

# The BioclustGUI R Package - 1.0.3

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## Contents

<b>1</b>	<b>Introduction</b>	<b>2</b>
1.1	R Commander . . . . .	3
1.2	Biclustering . . . . .	4
<b>2</b>	<b>Envelope Packages - Software Development using R</b>	<b>6</b>
<b>3</b>	<b>The BioclustGUI R Package</b>	<b>7</b>
3.1	GUI Structure . . . . .	7
3.2	Installing and Loading . . . . .	9
3.3	Data Input . . . . .	10
3.4	Extra Utilities . . . . .	11
3.4.1	Search Dialog . . . . .	11
3.4.2	Help Documentation & Scripts . . . . .	11
3.4.3	Plot Grid . . . . .	11
3.4.4	Draw Heatmaps . . . . .	12
3.4.5	Jaccard Index . . . . .	13
3.4.6	Clear Results . . . . .	13
3.4.7	Export Results . . . . .	13
3.4.8	Extract Biclusters . . . . .	14
3.4.9	Search for genes or samples in biclusters . . . . .	15
3.4.10	Save/Load . . . . .	16
3.5	biclust-package . . . . .	16
3.5.1	Plaid Biclustering . . . . .	16
3.5.2	CC( $\delta$ ) Biclustering . . . . .	18
3.5.3	XMotifs Biclustering . . . . .	18
3.5.4	Spectral Biclustering . . . . .	19
3.5.5	QuestMotif Biclustering . . . . .	20
3.5.6	Bimax Biclustering . . . . .	21
3.5.7	Biclust: Plots & Diagnostics . . . . .	22
3.6	fabia-package . . . . .	24
3.6.1	Laplace Prior . . . . .	25
3.6.2	Post-Projection . . . . .	26
3.6.3	Sparseness Projection . . . . .	26
3.6.4	SPARSE . . . . .	27
3.6.5	Fabia: Plots & Diagnostics . . . . .	28
3.7	isa2-package . . . . .	30
3.8	iBBiG-package . . . . .	32
3.9	rqubicc-package . . . . .	33
3.10	BicARE-package . . . . .	35
3.11	s4vd-package . . . . .	38
3.11.1	SSVD - Biclustering via Sparse Singular Value Decomposition . . . . .	38
3.11.2	S4VD - Robust biclustering by ssvd incorporating stability selection . . . . .	39
3.12	Diagnostic Packages . . . . .	41
3.12.1	BcDiag-package . . . . .	41
3.12.2	superbiclust-package . . . . .	43

<b>4 A Guideline to New Implementations</b>	<b>46</b>
4.1 Implementing a New Method . . . . .	46
4.1.1 New Method Script - ClusterTab & PlotDiagTab . . . . .	47
4.1.2 The Frame Scripts . . . . .	52
4.1.3 A quick example - Plaid . . . . .	58
4.2 Implementing a New Tool . . . . .	60
4.2.1 New Tool Script . . . . .	60
4.2.2 A quick example - BcDiag . . . . .	61
4.3 How to start? . . . . .	62
<b>5 Extensions - Shiny App &amp; REST</b>	<b>63</b>
<b>6 Appendix</b>	<b>66</b>
6.1 Introduction . . . . .	66
6.2 The BioclustGUI R Package . . . . .	66
6.2.1 Installing and Loading - Installing Script . . . . .	66
6.2.2 Extra Utilities . . . . .	67
6.2.3 biclust-package . . . . .	68
6.2.4 fabia-package . . . . .	71
6.2.5 isa2-package . . . . .	75
6.2.6 iBBiG-package . . . . .	75
6.2.7 BicARE-package . . . . .	76
6.2.8 BcDiag-package . . . . .	77
6.2.9 superbiclust-package . . . . .	79
6.3 Guideline - Template Scripts . . . . .	79
6.3.1 newmethod_script . . . . .	79
6.3.2 frames_script . . . . .	81
6.3.3 Quick Example - Plaid . . . . .	83
6.3.4 newtool_script . . . . .	93
6.3.5 Quick Example - BcDiag . . . . .	94
6.3.6 Extra Example - Superbiclust . . . . .	100

## 1 Introduction

Data obtained from microarrays has been subject to a variety of studies. The art of identifying differentially expressed genes, finding high predictive genes or groups of genes with respect to a response or conditions has been of major interest in order to explore the structure of these *gene expression datasets*.

Another way to investigate this kind of data is through the help of *clustering*. Through clustering gene expression matrices can be analyzed in both dimensions, the gene and condition dimension. This translates into the grouping of genes according to their expression under multiple conditions and the grouping of conditions based on the expression of a number of genes. These results can then for example be utilized for classification afterwards.

This procedure can be extended to clustering on the genes and conditions simultaneously which is called *biclustering*.

There exist a great deal of methods to do biclustering for which many R packages have been developed. For example **biclust** (Kaiser and Leisch, 2008), **fabia** (Hochreiter et al., 2010), **isa2** (Csárdi, 2014) and **iBBiG** (Gustenleitner et al., 2012) are some of these.

But while there are a lot of R packages available, not a lot of user-friendly graphical user interfaces (GUI) exist to execute these biclustering methods. This is particularly helpful for scientists with limited knowledge of R as they can apply the multitude of methods through simple point-and-click dialogs. Further, since the GUI is a plugin of **Rcmdr**, the user will also be exposed to the actual R commands of the implemented packages, making it a learning experience on the use of R.

The **RcmdrPlugin.BioclustGUI** is a continuation of the same-named package available on R-Forge, made by Setia Pramana. The already implemented biclustering algorithms were completely redone, adding extra parameter options in the process. New methods have been added as well as more options to graphically present the results of all methods. Further all biclustering procedures have been implemented in the GUI in a very specific framework which makes adding new packages in the future a quick and easy task with minimal interference of the maintainer. In short, the method/package developer will be able to create his own dialogs/windows for his procedure *without* having to rely on any knowledge of the **Rcmdr** or **tcltk** syntax which is normally necessary

to create these.

Thanks to this, the package has the potential to become a GUI from which a vast collection of biclustering methods can be accessed in the future.

Following on the introduction, there will be two major sections about the `RcmdrPlugin.BiclustGUI` package. In the first, the already implemented biclustering methods will be briefly explained followed by showcasing the functionality of the GUI. This will contain the executing of the procedure itself as well as the visualisation of the results through the appropriate plots.

In the second section, an extensive guideline will be presented with explanatory examples on how to create the appropriate scripts to add new biclustering procedures. The main idea is that these scripts can then be sent forward to the maintainer of `RcmdrPlugin.BiclustGUI` who can then easily add these new dialogs to the already implemented procedures.

It should be stressed that over the entirety of this vignette the focus will be on the software development of the GUI. While a multitude of biclustering methods will be visited, the goal is not to investigate into detail how they work, but how they are implemented in the GUI. What will be of interest though is the structure of the GUI, namely how the several methods are automatically linked to the plots and diagnostics without unnecessary interference of the user. Therefore the description of the implemented methods will be very brief and basic.

## 1.1 R Commander

R Commander, `Rcmdr`(Fox, 2005), is a GUI developed by John Fox from McMaster University, Canada. Originally it was conceived as a basic-statistics graphical user interface for R, but its capabilities have been extended substantially since. The `Rcmdr` package is based on the `tcltk` package (Dalgaard, 2001b) which provides an R interface to the *Tcl/Tk* GUI builder. Since `tcltk` is available on all the operating systems on which R is commonly run, the R Commander GUI will also run on all of these platforms.

The GUI is also very easy to start to use for beginners who do not have any or little experience with R. It will protect beginners from errors as the dialog boxes only have limited options related to the current context which minimizes the errors made by users. Further, since the users are exposed to the actual R commands through a script and output window, besides analyzing and managing the data in R easily, they can also learn how to do it in R without a GUI. Another advantage is that the script will be generated on the fly as the user applies the desired statistics through the point-and-click GUI. This means it can be easily saved at the end of a session which enables the user afterwards to recreate the results by running the R script without going through all the dialogs again. Advanced users can even adapt the created script to do some more detailed analysis. These are the main advantages `Rcmdr` has over other available RGUI packages.

Starting with version 1.3-0, `Rcmdr` also provides the possibility of *plug-in* packages which can augment the R Commander menus. These packages are developed, maintained, distributed and installed independently of `Rcmdr` and can provide a wide variety of new dialog boxes and statistical functionality. More information on developing such a plug-in can be found in Fox (2007).

It is through this functionality that the `RcmdrPlugin.BiclustGUI` has been created which brings a new menu to the R Commander GUI containing a collection of biclustering procedures.

As can be seen in Figure 1, the window is separated in three parts: a *script window*, an *output window* and a *messages window*. In the first the generated R commands from R Commander (and plug-ins) will appear. Users are also able to edit, enter and re-execute commands from this window. The second window is simply what would normally appear in the R-console window and the third displays error messages and warnings.

More information on the use of R commander can be found in ‘*Getting Started With the R Commander*’ by Fox (2007).

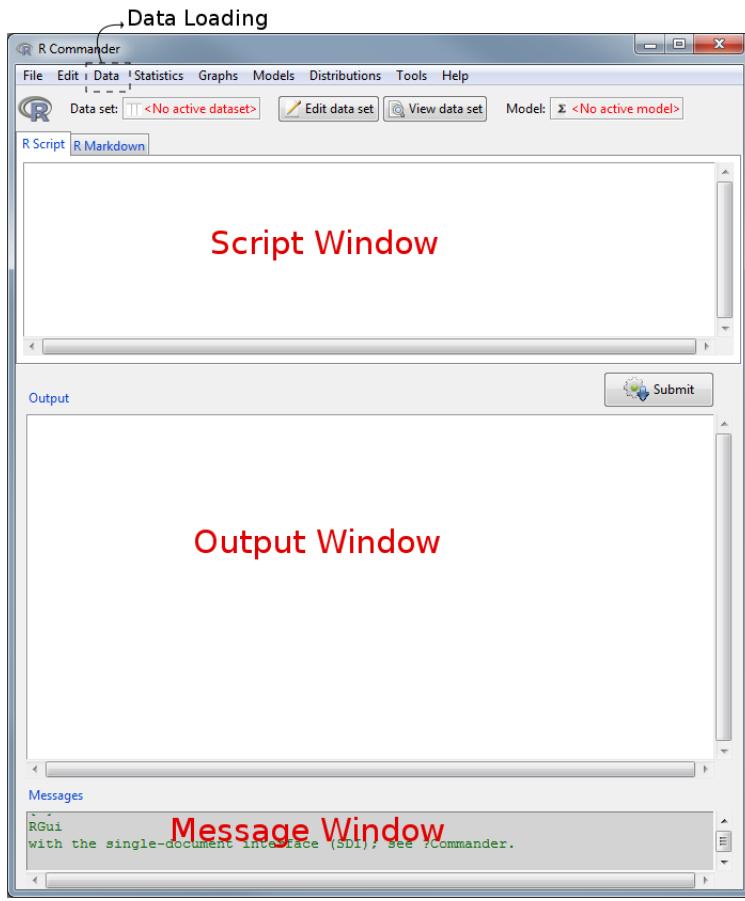


Figure 1: Default R Commander

## 1.2 Biclustering

Let  $\mathbf{Y}$  be a  $m \times n$  matrix. The goal of *biclustering* now is to find subgroups of rows and columns which are as similar as possible to each other and as different as possible to the rest (Kaiser and Leisch, 2008). This basically comes down to clustering on both the row and column dimension simultaneously and while clustering methods on 1 dimension derive a *global model*, biclustering algorithms will produce a *local model*. For example in clustering algorithms each row in a rowcluster is defined over all the columns, however a row in a bicluster is selected using only a subset of columns.

Going back to the matrix  $\mathbf{Y}$ , this corresponds to looking for submatrices with a high similarity of elements. This submatrix is what is called a *bicluster*.

$$Y = \begin{pmatrix} a_{11} & a_{12} & \cdots & a_{1n} \\ a_{21} & a_{22} & \cdots & a_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{m1} & a_{m2} & \cdots & a_{mn} \end{pmatrix}$$

While biclustering has its applications in many areas such as marketing and behavior science, a popular use of it is for the analysis of genetic data. The  $\mathbf{Y}$  matrix would then be a gene expression matrix in which the rows correspond with the genes and the columns with the conditions/samples. In this setting  $a_{mn}$  is the expression level of the  $m$ th gene under the  $n$ th condition and biclustering algorithms will identify groups of genes that show similar activity patterns under a specific subset of the conditions. Therefore, biclustering is the key technique in situations where a cellular process, in which only a small set of the genes participate, is of interest or in the situation that an interesting cellular process is active only in a subset of the conditions.

There exist a great deal of different biclustering algorithms today and several authors have provided extensive reviews, discussion and comparisons of these (Madeira and Oliveira, 2004, Tanay et al., 2004 and Prelić et al., 2006)

All these different algorithms are able to identify several types of biclusters which can be identified into four major classes:

1. Biclusters with constant values

2. Biclusters with constant values on rows or columns
3. Biclusters with coherent values
4. Biclusters with coherent evolutions

To briefly elaborate on this, coherent values would mean that each row and column can be obtained by adding a constant to each of the others or by multiplying each of the others by a constant value. Further in the evolution approaches, the elements of the matrix are viewed as symbolic values and biclusters with coherent behaviour will be discovered regardless of the exact numeric values in the matrix. These types of biclusters can be found in Figure 60 in the Appendix.

It is also interesting to know that while many biclustering algorithms perform simultaneous clustering on both dimensions of the data matrix, there also exist two-way clustering approaches. These use one-way clustering to produce clusters on both dimensions of the data matrix separately.

Finally, if a biclustering algorithm assumes the existence of several biclusters, several underlying structures of the data matrix can be considered. Madeira and Oliveira (2004) listed the following eight major types of underlying bicluster structures:

1. Exclusive row and column biclusters (rectangular diagonal blocks after row and column reorder).
2. Non-Overlapping biclusters with checkerboard structure.
3. Exclusive-rows biclusters.
4. Exclusive-columns biclusters.
5. Non-Overlapping biclusters with tree structure.
6. Non-Overlapping non-exclusive biclusters.
7. Overlapping biclusters with hierarchical structure.
8. Arbitrarily positioned overlapping biclusters.

These different structures are visualized in figure 61 in the Appendix.

## 2 Envelope Packages - Software Development using R

There exist a great number of packages for R. On CRAN for example there are almost 6000 packages available which handle many topics. Due to the fact that for each topic or area many packages can be installed, it can sometimes be challenging for new users to quickly execute a certain analysis of interest (e.g. dose-response modelling, biclustering methods, etc.).

The creation of '*envelope packages*', related to a common data analysis problem, can be a solution to this often-occurring problem. An attractive way to implement this, is with the help of a Graphical User Interface (= GUI).

The idea is to design a joint development programming environment in which methodological developers can include their packages in this 'envelope package' without too much programming effort.

Not only can multiple people contribute to this 'envelope package', the users will be able to make use of all of these packages in one clear environment. To clarify, all the implemented packages in the '*envelope package*' are still independent entities on CRAN or Bioconductor. This means the '*envelope*' package is simply depending on these other packages, not incorporating the actual code behind them. As a result, any updates by the authors on an outsourced package will also automatically update the '*envelope package*'. The main goal of the '*envelope package*' is to provide a solid and intuitive 'module-like' structure in which the external packages can fit in, while also providing the possibility of interconnecting these packages.

So while the packages are still independently developed, the end user will only need this 'envelope package' to carry out a specific analysis for which multiple methods exist. The 'envelope package' can make sure the output of implemented packages is processed in a similar way, providing a user-friendly environment to execute each step of an analysis. An example of this could be that after applying a certain analysis method, the results can immediately be visualized through an appropriate button in the GUI.

Further, such an 'envelope package' also introduces a lot of flexibility in the way several packages can be connected, providing an easier workflow. For example a package focused at the visualisation of results could easily be connected with other packages in a GUI, alleviating the work of the user in figuring the right data input for each function.

Also, by creating the GUI as a plug-in for R-Commander, it will not deny the user access to the actual R code which is used for applying a certain analysis. The R-Commander window will generate the actual R code on the fly which can be saved, re-executed and even edited. Before, in other GUI systems for R, this was not yet possible. They did not provide any insight for the user about the R code behind the functionalities.

It is this concept which was the basis for the development of the `RcmdrPlugin.BiclustGUI` package. The goal of this package is to serve as a platform from which several biclustering algorithms as well as the appropriate diagnostics and graphs can be accessed.

### 3 The BioclustGUI R Package

#### 3.1 GUI Structure

The **general structure** of a biclustering window is always the same for each method. This is shown in Figure 2. The method dialog consists out of two tabs: the *biclustering* tab and the *plots & diagnostics* tab.

In the first tab, the user will be able choose the appropriate parameters for a biclustering algorithm and then click the *Show Results* button to execute it. If relevant, there will also be a small seed box present to set your seed for this run in order to obtain reproducible results (this will appear as `set.seed(...)` in the script). In the second tab, one can find the *specific* plots and diagnostic tools for the chosen method or package. However, from this second tab you are also able to access more general diagnostics and plots obtained from an external package. Two which are already implemented are `BcDiag` and `superbiclust`. They can be easily accessed through a button, provided they are compatible with the chosen method. Clicking one of these buttons will open up a new window entirely with additional plotting and diagnostic tools.

When these diagnostics are opened up from a specific biclustering window, the plots and diagnostics will automatically choose the right object to apply their functions to. This way no extra interference of the user is necessary when applying their functionality and the user will not have to worry about the communication between these windows. (See Figure 4)



Figure 2: Default Window Structure

Note that when the graphs are produced they will appear in a separate graphics device window. Due to the variety of graphical parameters some diagnostic plots use, it might sometimes be necessary to close this graphics device down before utilizing a certain graph.(e.g. when you observe the size of a plot is considerably smaller and multiple are appearing in the same device). Further, if you would like the save a graph appearing in the device, simply select the device window and go to the working bar of R itself (not R Commander). Here, select *File, Save As* and then choose the desired extension (png, pdf,...).

Finally, each biclustering method can be accessed from the *Biclustering* menu (see Figure 3) in R commander which will appear after loading the plug-in.

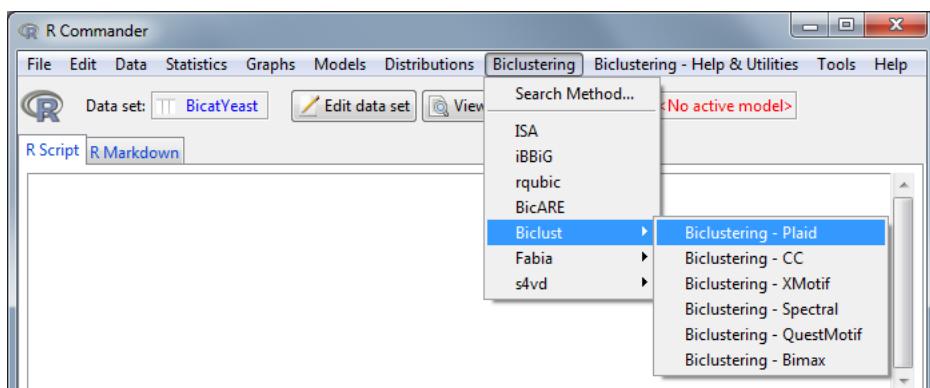


Figure 3: Biclustering Menu (Biclust submenu)

The implemented algorithms and diagnostic tools can be found in Table 1.

Type	Package	Method/Description
<i>Biclustering Algorithms</i>	<b>biiclust</b>	Plaid
		CC
		XMotif
		Spectral
		QuestMotif
		Bimax
<i>General Plots/Diagnostics</i>	<b>fabia</b>	Laplace Prior
		Post-Projection
		Sparseness Projection
		SPARSE
<i>Biclustering Algorithms</i>	<b>isa2</b>	The Iterative Signature Algorithm
	<b>iBBiG</b>	Iterative Binary Biclustering of Genesets
	<b>rqubic</b>	Qualitative Biclustering
	<b>BicARE</b>	Biclustering Analysis and Results Exploration
	<b>s4vd</b>	SSVD (Sparse Singular Value Decomposition) S4VD (SSVD incorporating stability correction)
<i>General Plots/Diagnostics</i>	<b>BcDiag</b>	Bicluster Diagnostics Plots
	<b>superbiiclust</b>	Generating Robust Biclusters from a Bicluster Set

Table 1: *Table of implemented packages*

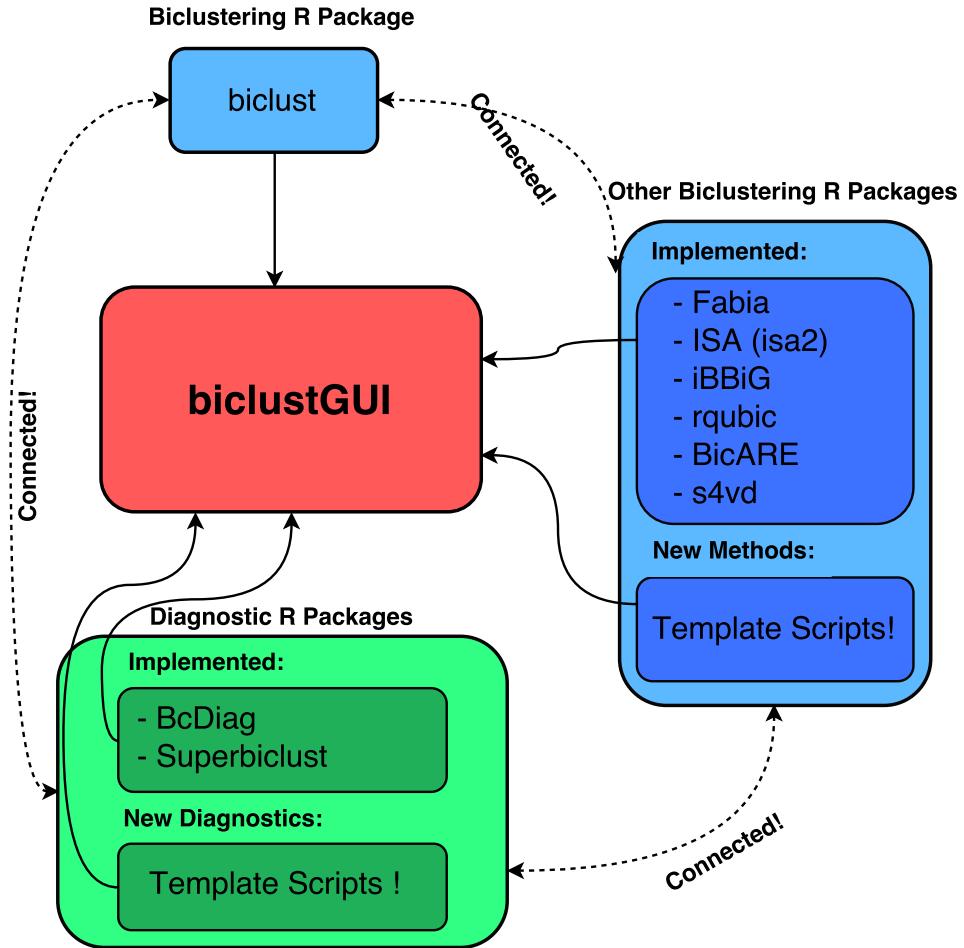


Figure 4: The BiclustGUI Structure

### 3.2 Installing and Loading

Like a lot of R packages, RcmdrPlugin.BiclustGUI can simply be downloaded from CRAN at <http://cran.r-project.org/web/packages/Rcmdr/index.html> or simply by using `install.packages` in the R console.

Since the BiclustGUI package relies on other biclustering packages, these should be installed as well as shown in the panels below. Note that some of the packages are located on CRAN,

```
## PACKAGES AVAILABLE ON CRAN ##
install.packages("biclust")
install.packages("BcDiag")
install.packages("superbiclust")
install.packages("Rcmdr")
install.packages("isa2")
install.packages("s4vd")
install.packages("gplots")
```

while others are available in Bioconductor

```
## PACKAGES AVAILABLE ON BIOCONDUCTOR ##
source("http://bioconductor.org/biocLite.R")
biocLite("iBBiG")
biocLite("fabia")
biocLite("rqubic")
biocLite("BicARE")
```

Once all R packages are installed we can install the GUI using the following code. You can either install the development version from the R-Forge repository or the release version from the CRAN repository.

```
## Bioclust GUI - In Development Version ##
install.packages("RcmdrPlugin.BioclustGUI",
repos="http://R-Forge.R-project.org")
## Bioclust GUI - Release Version ##
install.packages("RcmdrPlugin.BioclustGUI")
```

It could very well be that at first launch the GUI will still prompt to install some suggested packages. These can be installed by accepting the request.

After successfully installing the plug-in, the easiest way to load the BioclustGUI is by using the command

```
library(RcmdrPlugin.BioclustGUI}
```

in the R console. This will open up the main window of R Commander which can, if closed, be reopened with the `Commander()` command.

All the commands to install the necessary packages can also be found in the appendix.

### 3.3 Data Input

There are a couple of ways on how to load data into the Rcmdr package (Figure 5):

- Enter *new data* directly with: *Data* –> *New data set ...*
- Load an existing data set from the *R workspace*: *Data* –> *Load data set ...*
- Import existing data from a plain-text file, other statistical packages (SPSS, SAS, Minitab, STATA) or even an Excel file: *Data* –> *Import data* –> *(choose required option)*
- Use a data set which is included in an R package: *Data* –> *Data in packages* –> *Read data set from an attached package ...*

Once the data is loaded in, it will be the active data set in the form of a data frame (see Figure 6). Further note that in most cases the biclustering procedures require a data matrix with the rows as genes and the columns as conditions/samples.

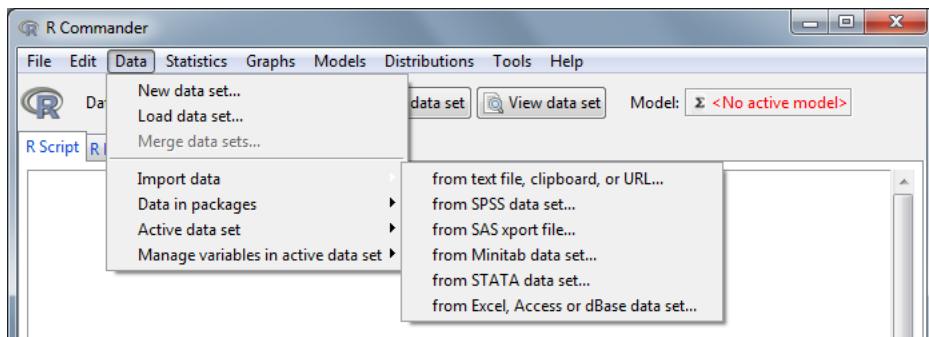


Figure 5: *R Commander - Data Menu*

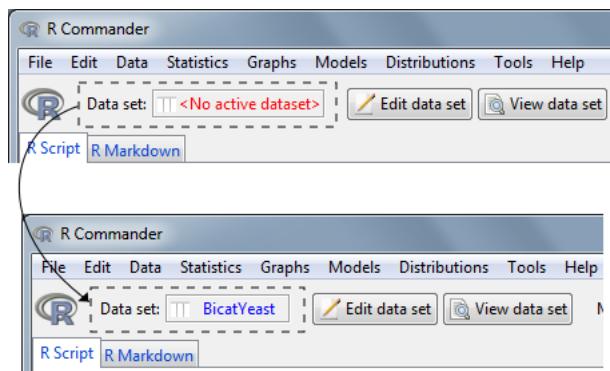


Figure 6: *R Commander - Active Dataset*

## 3.4 Extra Utilities

### Note on Active Dataset

Some of utilities also make use of the dataset which was used to obtain a certain biclustering result (e.g. Exporting Results). If the result was obtained in this session, the correct dataset will automatically be made the active one. Otherwise please make sure the correct corresponding dataset is chosen as the active one in R-Commander.

### 3.4.1 Search Dialog

In the *Biclustering* menu, there is also an option called ‘*Search Method...*’. This option will open up a small window (Figure 7) in which the user can query the available biclustering methods for several criteria. After the search, one of the methods (which appear in the list box) can be selected and then opened up with the *Go To* button.

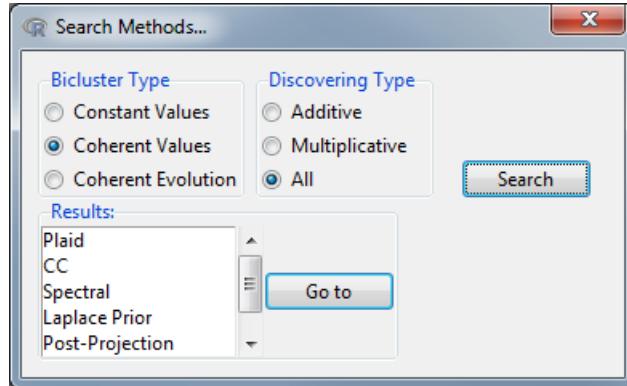


Figure 7: *Search Biclustering Method Dialog*

### 3.4.2 Help Documentation & Scripts

Next to the *Biclustering* menu is the *Biclustering - Help & Utilities* menu (See Figure 8). The first submenu *Help Documentation* contains three items. The first, *Helppage BiclustGUI*, will lead to the help files of the R package. The next, *Vignette BiclustGUI*, will open up the vignette for the BiclustGUI. This document contains information about the GUI itself as well as a guideline on how to implement new biclustering methods. The last item, *Template Scripts*, will open up the folder in which these scripts are localised. The developers can use these to create windows for their own package after which they can send them to the maintainer of the GUI who can include them in the next update.

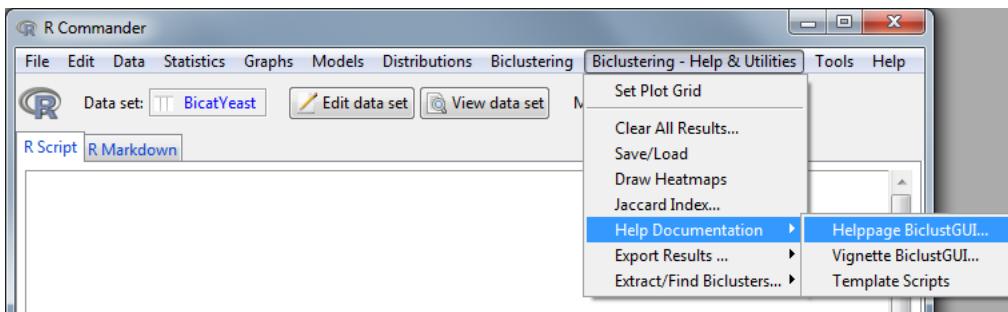


Figure 8: *Biclustering Helpmenu*

### 3.4.3 Plot Grid

Clicking on this item will bring up a small window (Figure 9) from which it is possible to set the grid of the graphics device in which the plots will be created. This can be helpful in order to show multiple plots on 1 graphics device. By default this setting is put to 1 by 1 (unless some specific plots require a different grid).

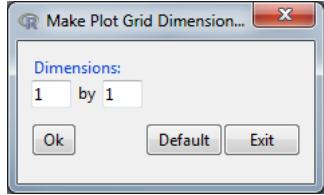


Figure 9: Set Plot Grid Window

**Note:** This option will mostly only work for the graphs which only contain 1 plot. If some graphs already require an own grid to be set with multiple plots (e.g. the visualisation of the bootstrap (1 by 2) ), it will not be compatible with this setting. (A new plot will however follow your own setting again.)

The only exception to this are the graphs from BcDiag which contain multiple plots. If your grid setting is large enough, they will simply be added into it.

Further, some more advanced grid settings, like for the General Plot for iBBiG, might require the user to re-apply your own settings.

### 3.4.4 Draw Heatmaps

The next utility is the ability to draw heatmaps of data or biclustering results. Clicking this button will open up a window which consists out of 2 tabs as shown in Figure 10.

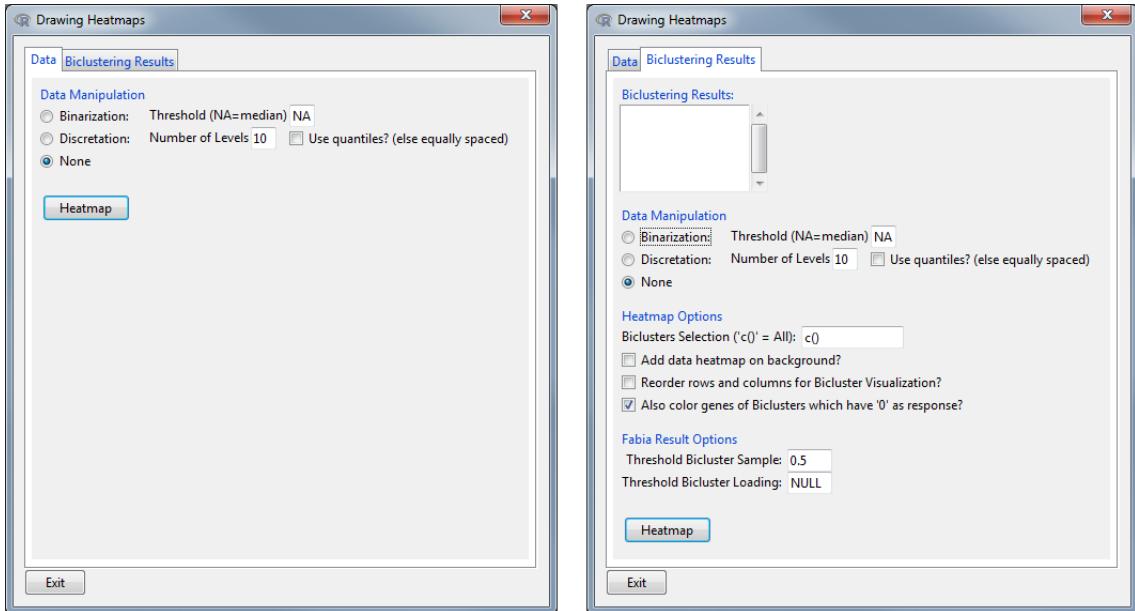


Figure 10: Draw Heatmaps Window

In the first tab of the window, a heatmap of the Active Dataset can be plotted. It is also possible, if necessary, to binarize or discretize the data beforehand. An example of these plots are given in Figure 62 and 63 in the Appendix.

The *biclustering results* tab provides all the tools to plot the heatmap of any of the results in the current session. Simply select a result in the result box and press the *Heatmap* button.

Further there are also some extra options under the *Heatmap Options* title. If required, only some specific biclusters can be plotted by putting a vector (e.g. `c(1,2,3)`) in the entry field. Next it is also possible to add the original data heatmap on the background in a transparent fashion (Again this background heatmap can be binarized or discretized with the options above). Also note that if binary data is being used (by default or through the transformation option), regardless of the fact if the background option is checked, the heatmap will look slightly different. The difference is that not all fields are white if they don't belong to a bicluster, they can also be gray. This simply means that this row and column combination had a '1' response, but was not included in a bicluster.

Next, the following option will reorder the rows and columns of the matrix so the resulted biclusters are generally put more together. The algorithm to accomplish this was borrowed from the heatmap plot in the **iBBiG** package. Finally, the last option will determine if row/column combinations in biclusters should also be colored

even if the response was '0'. This is mostly helpfull when investigating binary data if for example you know the resulting biclusters might still contain zeros (depending on the algorithm). In this case checking this option would show the full biclusters, but when unchecked, some fields of the biclusters might turn white.

Lastly, do take care that it is not possible to visualize overlapping biclusters that well in these 2D heatmaps. The biclusters are drawn in the order they appear in the legend so a higher numbered bicluster might be drawn on top of another (if the biclustering algorithm is able to find such biclusters). Drawing only a selection of biclusters might be helpfull in this scenario. Another solution could be to turn to software like FURBY for which the results can be exported.

### 3.4.5 Jaccard Index

In the Jaccard Index Window (Figure 11) it is possible to compute the Jaccard Index between 2 biclustering results which can be selected in the results box.

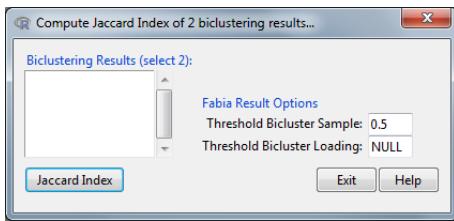


Figure 11: *Compute Jaccard Index Window*

### 3.4.6 Clear Results

The *Clear Results* button in the *Help & Utilities* menu will automatically clear this session of all biclustering results. This might be helpfull if one would like to investigate a new dataset.

### 3.4.7 Export Results

Further it is also possible to export the results either as a text file or in the necessary format for FURBY, Fuzzy Force-Directed Bicluster Visualization (<http://caleydo.github.io/projects/furby/>).

Note that all the results will appear in the result box. This means that those result object which are for example manually named by the user will also appear in the box. Also take care that the correct data set is the active one in R Commander so that it corresponds with the chosen result (if the result was obtained in a previous session). the dialogs are shown in Figure 12.

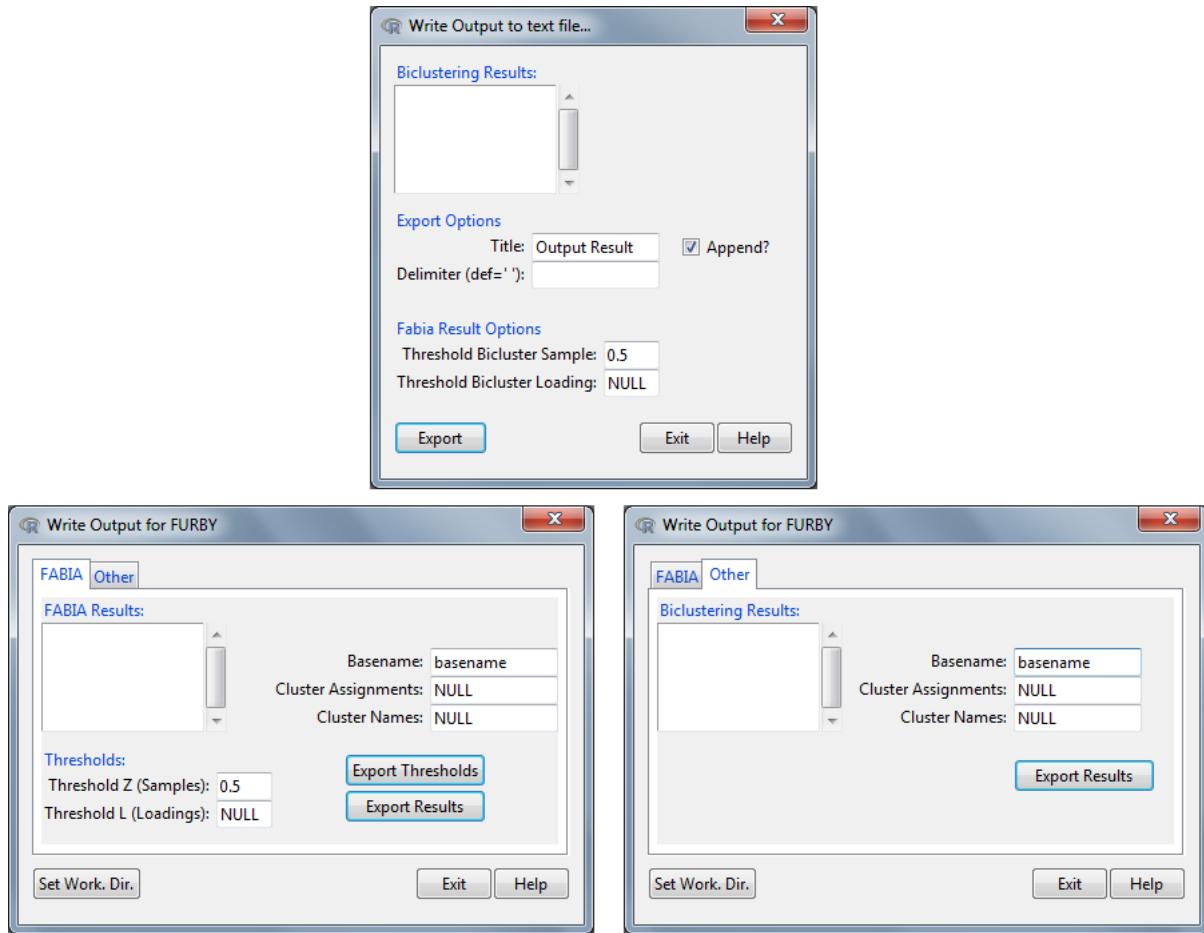


Figure 12: *Export Windows*

### 3.4.8 Extract Biclusters

Another option the user has is to extract the biclustering results in a list object through the *Extract Window* (Figure 13). The extracted object is a list object in which each element is a bicluster (in the form of again a list object). Each bicluster list element can contain the following items: the indices of the rows and/or columns in the bicluster and the corresponding names of these rows and/or columns.

First of all it is also possible to get a quick summary of the selected result with the *Summary* button. Below this button, the options for the actual extracting are situated. These options include the thresholds for fabia results, choosing which bicluster to extract and which dimensions to include in the resulting list object. The user can either choose to extract all biclusters, a certain range (e.g. from 2 to 6) or a specific selection (in the form of a vector: e.g. `c(3,6,11)`).

Finally, the user can also save the extracted list object in an .rData-object in the current working directory (which can be changed with the *Set Work Dir.* button). The name for this saved object will be determined by the entry in *Extract Name* (Note that this name also determines the name of the extracted object in the workspace, even when not saving it).

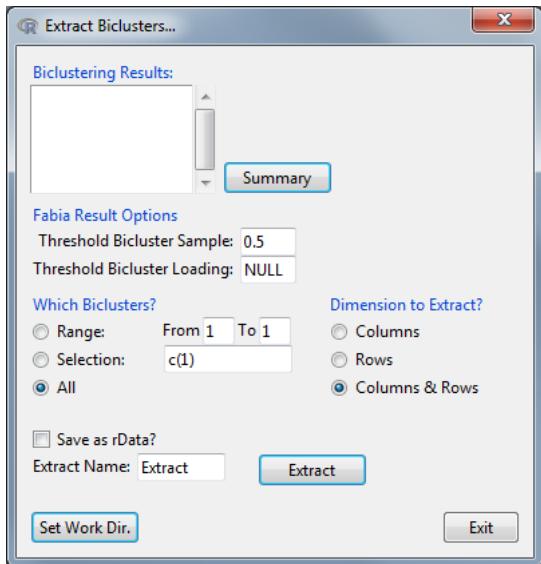


Figure 13: *Extract Window*

### 3.4.9 Search for genes or samples in biclusters

In this window (Figure 14) it is possible to go through several biclustering results and investigate if certain rows (= genes) or columns (= samples) are appearing together in a bicluster.

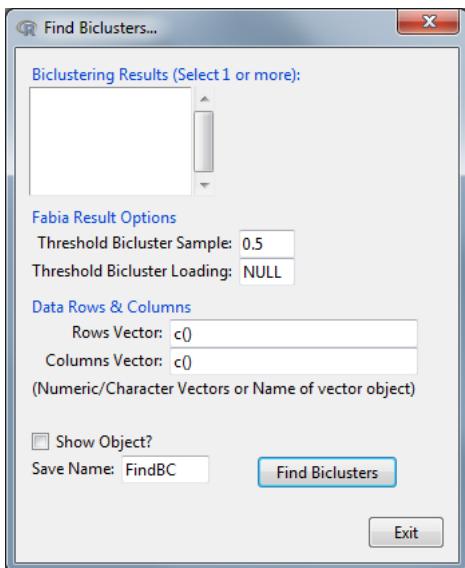


Figure 14: *Find Biclusters Window*

The way this is done is by simply selecting one or more of the available results in the list box, setting an optional threshold for the possible Fabia results (which will then all have the same threshold) and then simply making vectors containing the rows and/or columns of interest. These can either be the indices (e.g. `c(1,6,77)`) or the names (e.g. `c("249364_at","258239_at")`). It is also possible to simple enter the name of an R object containing such a vector.

After this, the user can enter the name in which the result is saved and then press the *Find Biclusters* button. This will execute the function, save the result and also give a small summary in the console. This small summary contains the total number of found biclusters and will also show how many biclusters were found in each result together with which ones they actually are (Figure 15).

The saved result is a list object containing the same information as well as information of the found biclusters itself (in the same format as in the extract window). The list object also has an element which contains which rows and columns were chosen to search through the biclusters. (The *Show Object* checkbox simple determines if the result should be printed afterwards or not.)

```

> FindBC <-
+   FindBiclusters(results=list(FabiaLaplacePrior=.fabia2biclust(FabiaLaplacePrior,
+   thresZ=0.5,thresL=NULL),ISA=isa.biclust(ISA),Plaid=Plaid,XMotifs=XMotifs),
+   rows=c(15,16,17),cols=c(),data=as.matrix(BicatYeast))
Total Number of found BC's: 31

FabiaLaplacePrior
0 BC's
ISA
30 BC's: 71 87 90 93 98 101 108 115 120 123 126 127 128 129 133 138 140 143 146 147 162 163 166 167 169 170 171 172 173 174
Plaid
1 BC's: 4
XMotifs
0 BC's

```

Figure 15: *Find Biclusters Summary*

### 3.4.10 Save/Load

Another available option for the user is to *Save* a result from a certain method (as a **RData** or **rda** file) and to also *Load* it back in in a later session. This is done through the dialogs shown in Figure 16.

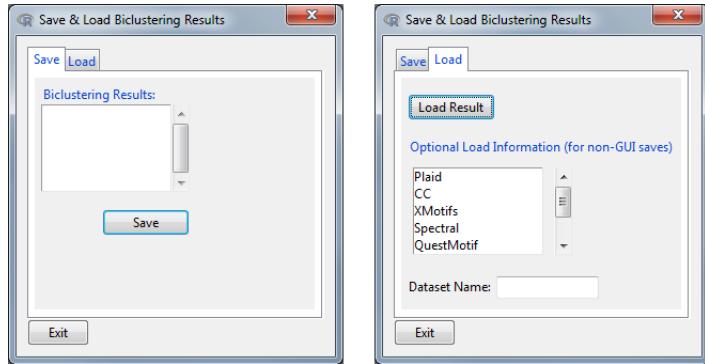


Figure 16: *Save & Load Windows*

In the first tab, the user can simply select the desired result and save it through the *Save* button. Note that in this **RData** object also some info will be stored on what method and which data were used.

In the second tab, if the result was saved with the button in the first tab, the **RData** object can be loaded into the GUI will the *Load Result* button. However if the **RData** object was not created through the save functionality of the GUI, the additional saved information will not be automatically available. In this case the user needs to select which method was used in the list box and fill in the name of the data as well. Please take care that the name of the object inside the **RData** file has the same name as the file itself.

*Note: Please note that if you are hiding the extensions of known files on your computer, during the save process the **RData** or **rda** extension might not be appended automatically. You will have to add it manually.*

## 3.5 biclust-package

### 3.5.1 Plaid Biclustering

The plaid biclustering in the GUI implements the plaid algorithm by Turner et al. (2005) which was proposed as an improvement of the plaid model discussed by Lazzeroni and Owen (2000). The plaid model is a biclustering method which takes the interactions between biclusters into consideration by defining the data structure (e.g. expression level) as a sum of layers. This model includes a background layer to capture the global effects and afterwards the method will construct a series of layers that represent the biclusters.

#### Plaid Model:

$$Y_{mn} = \theta_{mno} + \sum_{p=1}^P \theta_{mnp} \gamma_{mp} \eta_{np} + \epsilon_{mn} \quad (1)$$

$$\gamma_{mp} = \begin{cases} 1 & m \in p \\ 0 & otherwise \end{cases}, \text{ and } \eta_{np} = \begin{cases} 1 & n \in p \\ 0 & otherwise \end{cases} \quad (2)$$

$$\theta_{mnp} = \begin{cases} \mu_p & (3.1) \\ \mu_p + \alpha_{mp} & (3.2) \\ \mu_p + \beta_{np} & (3.3) \\ \mu_p + \alpha_{mp} + \beta_{np} & (3.4) \end{cases} \quad (3)$$

In (1),  $Y_{mn}$  is the expression level of gene  $m$  in condition  $n$  with  $m = 1, \dots, M$  and  $n = 1, \dots, N$ . Further,  $p$  is the layer index,  $P$  is the number of biclusters,  $\theta_{mno}$  is a sum of overall mean and  $\epsilon_{mn}$  is a random error with mean zero. The model also contains two indicator variables,  $\gamma_{mp}$  and  $\eta_{np}$  which represent the membership of the gene/condition in a bicluster  $p$  as formulated in (2). Finally  $\theta_{mnp}$  is the mean gene expression which can take four possible forms as shown in (3). In this formula, (3.1) implies a constant bicluster whereas (3.2) and (3.3) respectively imply biclusters with constant rows or columns. The last one, (3.4) implies a bicluster with coherent values across the genes and conditions in a bicluster.

The estimation of the plaid method is done with an iterative algorithm. First the background layer is fitted, then the bicluster-specific layers are added one at a time. In each iteration the algorithm will estimate the parameters with binary least squares after which a permutation test is performed which is a built-in protection against the discovery of random biclusters. This procedure is repeated until no layer is found anymore or until the maximum amount of layers as been reached. More detailed information about these steps can be found in Lazzeroni and Owen (2000) and Turner et al. (2005).

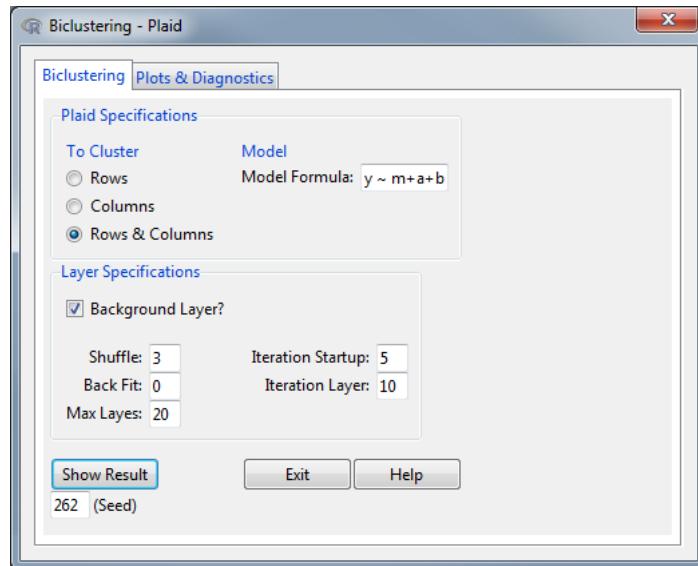


Figure 17: *Plaid Window*

In Figure 17, the standard *Plaid window* can be found which contains all the necessary parameters to apply plaid biclustering. First the user is able to decide they only want to cluster the rows and columns, or on both (recommended). Next the model which is fitted to each layer can be specified in the *Model Box*. This coincides with formula (3) and is defaulted to  $y \sim m + a + b$  ( $m$ =constant for all elements in bicluster;  $a$ =constant for all rows in bicluster;  $b$ =constant for all columns in bicluster).

The remaining parameters are there to further specify the layer options in the algorithm. The *background* check specifies if there is a background layer present in the data. *Iteration startup* and *layer* define the number of iterations to find respectively the starting values and each layer. And as already explained earlier, *max layers* will determine the maximum number of layers to include in the model and therefore the maximum number of biclusters.

Finally, *Back Fit* specifies the additional iterations to refine the fitting of the layer and *Shuffle* is a parameter connected with the permutation test. Before a layer is added, its statistical significance is compared against a number of random obtained layers, defined by this parameter.

### 3.5.2 CC( $\delta$ ) Biclustering

The  $\delta$  biclustering, also known as CC algorithm is based on the framework by Cheng and Church (2000). The algorithm discovers biclusters one at time and considers a bicluster as a subset of rows and columns that show coherent values. The method is a combination of data analysis based on an *ANOVA model* and a *node deletion algorithm*.

Let  $\mathbf{A}_{IJ}$  be a submatrix, i.e. a  $\delta$ -bicluster, in the data matrix  $\mathbf{A}$  ( $I = (i_1, \dots, i_k); J = (j_1, \dots, j_k)$ ). Note that  $a_{ij}$  is the expression level of gene  $i$  in condition  $j$ .

Now Cheng and Church defined a *mean residual score* (MSR) as follows

$$H_{IJ} = \frac{1}{|I||J|} \sum_{i \in I, j \in J} r_{ij}^2$$

where  $r_{ij} = a_{ij} - a_{iJ} - a_{IJ} + a_{JJ}, i \in I, j \in J$ .

A submatrix is now called a bicluster if the MSR is less than a pre-defined threshold  $\delta$ .

In order to find these  $\delta$ -biclusters, the algorithm will start with the full matrix and calculates the MSR. Now the MSR will be minimized by deleting/including rows and columns in the matrix. Since the *brute-force approach* is computationally not time-efficient, *node deletion* algorithms were developed (single & multiple) which is a *greedy* algorithm. These algorithms iterate the process of choosing a row and column with the largest MSR and removing them from the data matrix until the desired submatrix is found. Note that after the node deletion, the bicluster may not be maximal (some rows/columns may be added without increasing the MSR) so therefore node addition is performed by again adding rows and columns one by one (if it does not increase the MSR). More about both algorithms and the CC biclustering can be found in Cheng and Church (2000).

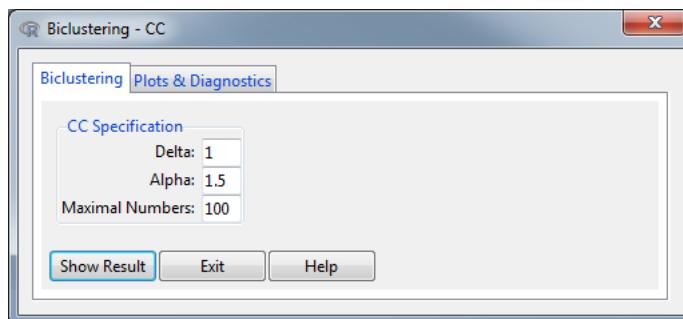


Figure 18: CC Window

As can be seen in Figure 18, there are not a lot of input parameters in the *CC window* for the  $\delta$ -biclustering. The most important parameter is of course *Delta*, the maximal accepted score which will be compared with the MSR. The choice of this variable should depend on the total variability of the data, taking into account both the assumed variability of the noise and bicluster values. Next, *Alpha* is a scaling factor. It is a parameter for the multiple node deletion and takes part in the three major steps of the algorithm:

1. Deleting rows and columns with a score larger than *Alpha* times the matrix score.
2. Deleting the rows and columns with the largest scores.
3. Adding rows or columns until *Alpha* level is reached.

Finally, the user is also able to set a maximum number of clusters to be found with the *Maximal Numbers* input parameter. The algorithm will stop until no bicluster is found or until this threshold is reached.

### 3.5.3 XMotifs Biclustering

The XMotifs biclustering algorithm was proposed by Murali and Kasif (2003) and looks for conserved gene expression motifs in a discretized version of the data matrix. This is achieved by searching for rows with constant values over a set of columns. The authors assume in their model that the gene can be expressed in a finite number of states (e.g. 2 states: up- and downregulated). The states of the gene expression matrix can also be defined by a fold change, represented by quantile discretization of the original matrix with log-transformed values. A conserved gene expression motif is now defined as a submatrix of *maximum size* for which the values within each row are equal to the same level.

Following the discretization, the biclusters are discovered with an iterative procedure which will be briefly touched upon down below while explaining the input parameters of the window. More detailed information can be found in Murali and Kasif (2003).

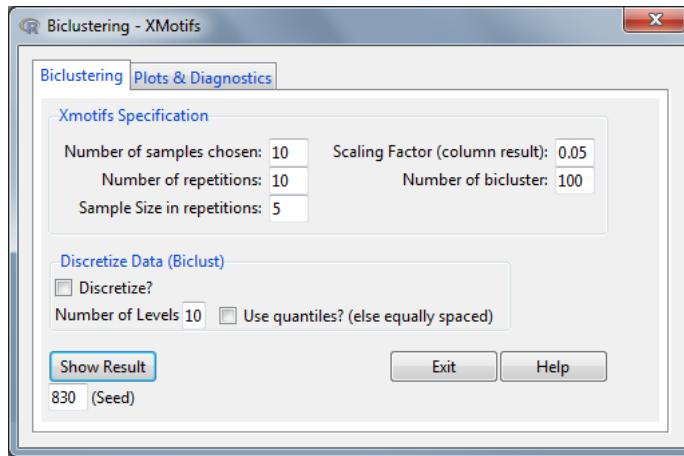


Figure 19: *XMotifs Window*

In Figure 19, the *Xmotifs window* is displayed which contains all the necessary input parameters for the algorithm. Note that in the bottom box, the user is able to discretize the active data set in the R commander session if necessary. This is done with the `discretize` function in the `biclust` package. For plotting however, the original matrix will be used.

After the discretization, the algorithm first needs a number of samples/columns (= ‘Number of samples chosen’) to be randomly selected as a seed. Then a number of sets of samples (= ‘Number of repetitions’) of a defined size (= ‘Sample size in repetitions’) needs to be inputted which will be randomly selected from the samples that were not in the *number of samples chosen*.

After this is done, the following steps are performed as described in Kaiser and Leisch (2008):

1. Choose a subset from these columns and collect all rows with equal state in this subset.
2. Collect all columns where these rows have the same state.
3. Return the bicluster if it has the most rows from all found and is also larger than a  $\alpha$  (= ‘Scaling factor’) fraction of the data.

To collect more than one bicluster, the calculation is rerun without the rows and columns already found (or return the smaller combinations found). This is done until the maximum number of biclusters (= ‘Number of biclusters’) is achieved or until no clusters can be found anymore.

### 3.5.4 Spectral Bioclustering

Spectral bioclustering is a method developed by Kluger et al. (2003), used for discovering multiplicative biclusters of coherent values. First of all it assumes that the gene expression matrix assumes a checkerboard structure after normalization therefore resulting in non-overlapping biclusters. These biclusters are called multiplicative because each bicluster element ( $a_{ij}$ , expression level gene  $i$ , condition  $j$ ) can be defined as a product of three terms: overall mean ( $\mu$ ), row-specific ( $\alpha_i$ ) and column-specific ( $\beta_j$ ) means ( $a_{ij} = \mu \times \alpha_i \times \beta_j$ ).

The spectral bioclustering is mostly based on a singular value decomposition (SVD) of the normalized data matrix and consists out of the following steps Kaiser and Leisch (2008):

1. Re-order the data matrix and apply one of the three normalization methods (independent rescaling, bistochasticization or log-interactions).
2. Obtaining eigenvalues and eigenvectors using SVD.
3. Depending on the normalization method, the biclusters are constructed beginning from the largest or second largest eigenvalue. The eigenvectors (left & right) corresponding to the largest eigenvalues are expected to provide optimal clustering of rows and columns.
4. The data is projected on the best two or three eigenvectors and  $k$ -means clustering is run to get the grouping.

More detailed descriptions of the above steps can be read in Kluger et al. (2003).

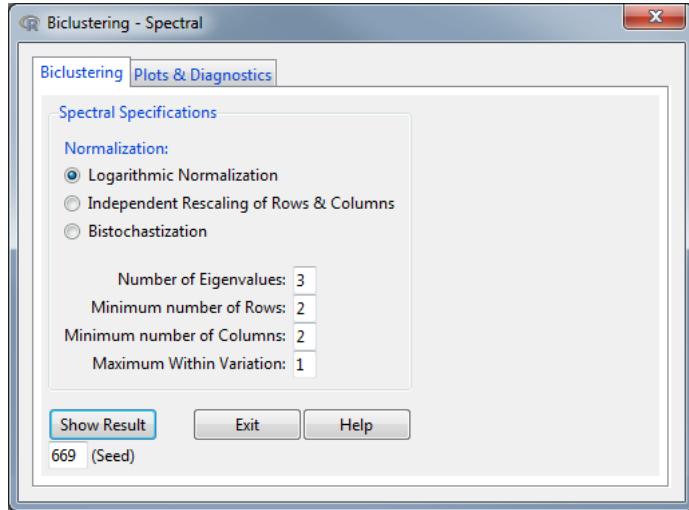


Figure 20: *Spectral Window*

In Figure 20 above, the *Spectral window* is shown which contains the major steps of the spectral biclustering, namely the normalization and the SVD.

As already explained earlier, the data matrix need to be normalized first as this is necessary for a checkboard structure to be discovered by the use of Singular Value Decomposition. The user is able to choose out of three different options for this step. The *Independent Rescaling of Rows & Columns* assumes the non-normalized matrix is obtained by multiplying each row and column with a scalar. *Bistochasticization* works by repeating the independent scaling of rows and columns until stability is reached. For this normalization, the final matrix has all rows sum to a constant and all columns sum to a different constant. The final method, *Logarithmic Normalization* (= log-interactions) assumes that after taking the logarithm, the original rows/columns differ by additive constants. Further each row and column is expected to have mean zero which is achieved with a transformation.

Finally, the user will have to specify the input parameters connected with the SVD. These include: *Number of Eigenvalues*, *Minimum number of Rows*, *Minimum number of columns*, *Maximum Within Variation*. Note the number of eigenvalues coincides with the number of biclusters that should be discovered.

### 3.5.5 QuestMotif Biclustering

The Questmotif Biclustering is based on the framework by Murali and Kasif (2003) and developed by Kaiser (2011). The algorithm will search for biclusters of questioners which have similar answer to the questions.

Following now is a short description of the algorithm with respect to the *Questmotif window* in Figure 21.

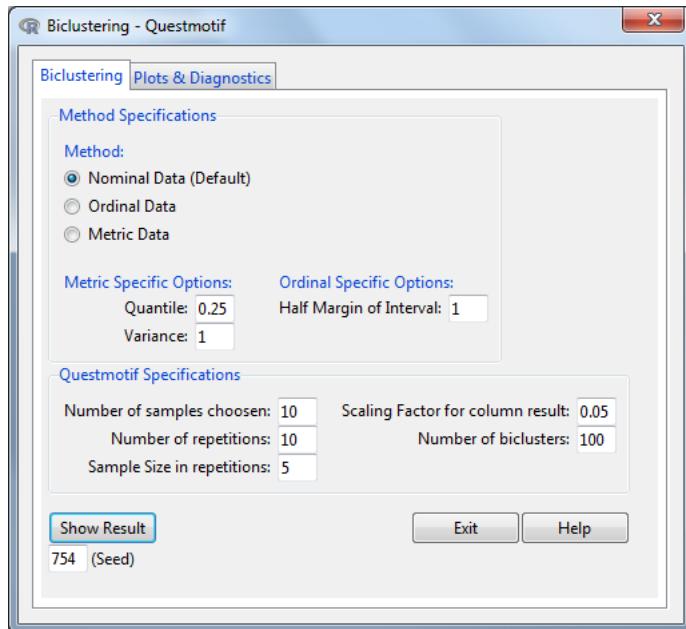


Figure 21: *QuestMotif Window*

The Quest algorithm contains three methods to deal with different scale levels data, especially for biclustering questionnaire data. All of the three methods can be selected by the user and depending on the choice, some additional parameters might have to be defined.

If the answers are given on a *nominal scale*, the algorithm simply works like the Xmotifs algorithm. For the *ordinal scale*, the algorithm will search for similar answers in an interval of a size set by the parameter '*Half Margin of Interval*' ( $= d$ ). This implies that the interval will be of the form  $[mean - d, mean + d]$ . In the continuous case, namely *metric data*, this interval is set by the quantile of a chosen distribution. It uses all previously found values to calculate the mean value and uses a given parameter for the variance of this distribution. Both the *Quantile* and *Variance* will have to be provided by the user in this case. (Since the normal scores are used in such data, the normal distribution is commonly used in this case.)

Finally, a couple of general input parameters, used by the algorithm, will have to be set by user in the *Questmotif Specifications* box. These include: *number of samples chosen*, *number of repetitions*, *sample size in repetitions*, *scaling factor for column result* and *number of biclusters*. Note that these are the same input parameters used by the Xmotif algorithm.

More insight and details about the algorithm itself can be found in Kaiser (2011).

### 3.5.6 Bimax Biclustering

The last implemented biclustering method from the *biclust* package is the *Bimax* (= binary inclusion-maximal) biclustering algorithm which was developed by Prelić et al. (2006). They advocated its use as a preprocessing step to identify potentially relevant biclusters that can be used as input for other methods. According to the authors, the main benefit of the method is the relatively small computation time while still providing relevant biclusters using a simple data model.

The Bimax algorithm works on a binarized data matrix in which the expression value is set to 1 if there is a change with respect to the control setting and to 0 otherwise. If a control setting is unavailable, one can simply take a threshold based on the distribution of the data values. The goal of the Bimax method is to find maximal inclusion biclusters. This means a Bimax bicluster spans a submatrix of 1's which cannot be part of a larger submatrix of 1's. The algorithm achieves this by applying a divide-and-conquer strategy in which the rows and columns are rearranged (to concentrate ones in the upper right corner of the matrix) before dividing the matrix into two submatrices.

More detailed information about the algorithm can be found in Prelić et al. (2006).

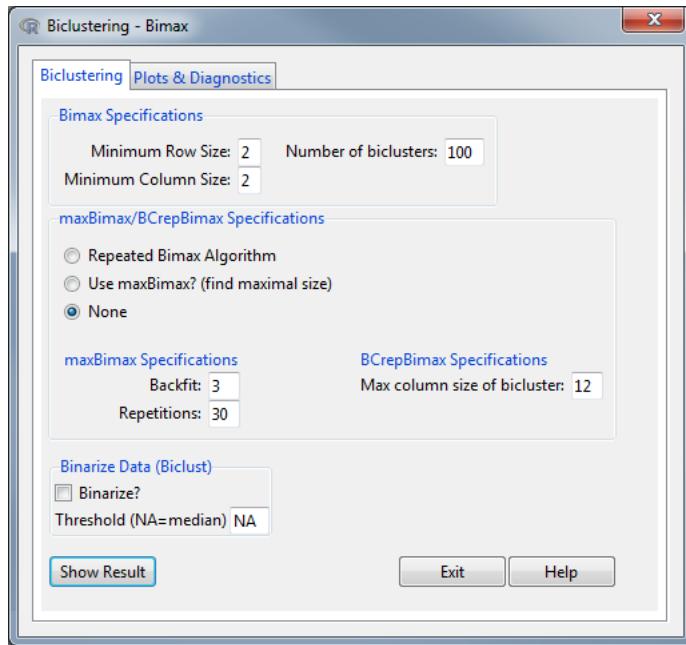


Figure 22: *Bimax Window*

The first box in the *Bimax window*, shown in figure 22, are general input parameters required by the algorithm. These include the *minimum row & column size* of a bicluster (for it to be included) and the *number of biclusters*. The algorithm will terminate when this boundary level of number of biclusters is achieved or when no more maximal inclusion biclusters can be found.

Further, Kaiser and Leisch (2008) suggested that in order to get satisfying results. the method should be iterated several times with different starting points. This can be accomplished with the '*Use maxBimax*' option in the second box for which the *number of repetitions* and *backfit* should be defined. With this option biclusters of maximal size will be discovered.

Finally, also the *Repeated Bimax Algorithm* is implemented in this window for which the *max column size of biclusters* should be inputted. More information about this last variation of Bimax can be found in Dolnicar et al. (2011).

Finally in the last box, the active data set in your R Commander session can be binarized if this is not a binary matrix by default. This is done through a available function `binarize` in the `biclust` package. A threshold can be set for this transformation or it can be left on the default option, namely the median. Do note that when plotting graphs (e.g. the biclust plots), the original data matrix will be used which is the active data set in your session.

### 3.5.7 Biclust: Plots & Diagnostics

After executing any of the bioclustering methods available in the `biclust` package, the user is now able to proceed to the second tab '*Plots & Diagnostics*' which is identical for all of these methods. No additional work is needed by the user for the plotting and diagnostic functions to use the correct results from the method which was applied in the first tab. An example (for the Plaid Bioclustering) of the *Plots & Diagnostics window* is given in Figure 23. Note that the second window in this figure is accessible through the *Extra Biclust Plots* button.

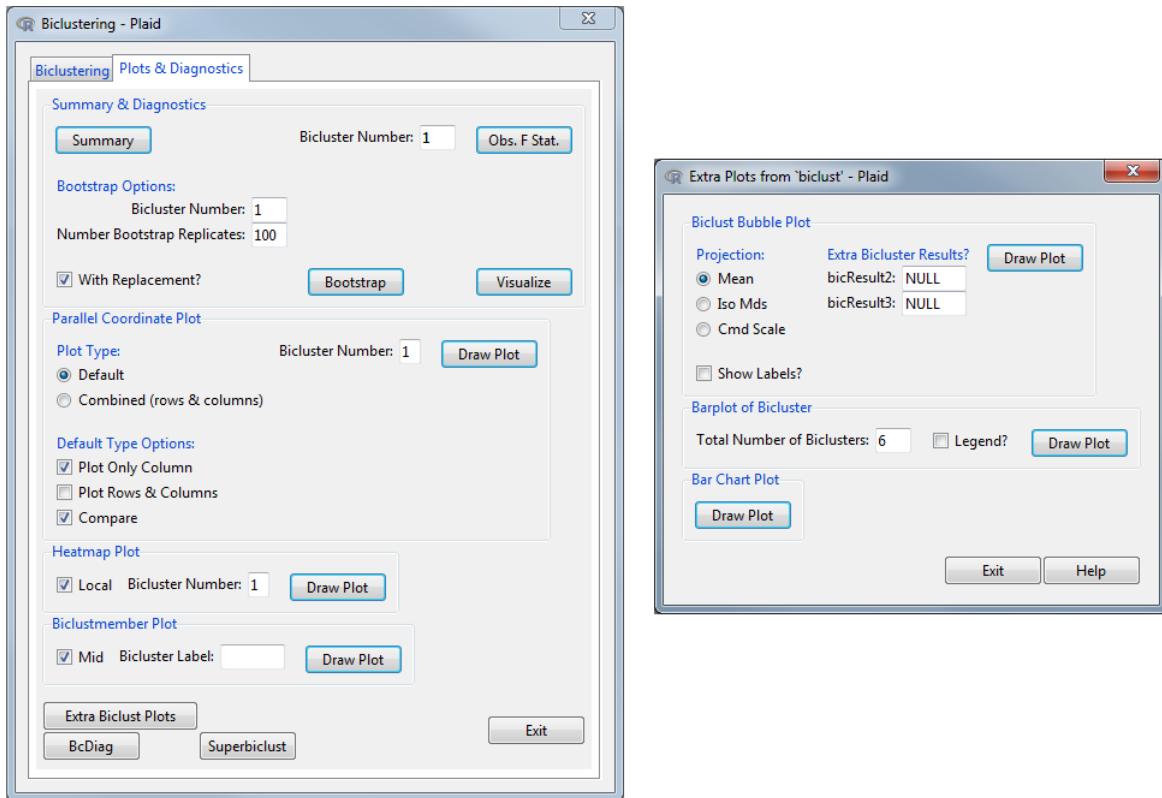


Figure 23: *Biclust - Plots & Diagnostics Tab*

### Summary & Diagnostics

In the first box, the summary of the biclustering result as well as some basic diagnostics can be called by the user. The *Summary* button will provide the user with the number of clusters found as well with the number of rows and columns each bicluster contains. Next, the *Obs. F Stat.* button will enable the user to compute some F-statistics about a specific bicluster, defined by the number in the *Bicluster Number* entry box. These F-statistics include the main effects, namely the row and column, and also the interaction effect. The first two F-statistics (main effects) are calculated from a two-way ANOVA with such row and column effect. Because the full model with interaction is unidentifiable, Tukey's test for non-additivity is used to detect an interaction within a bicluster. Lastly, the p-values are obtained from asymptotic F distributions.

The last option in this first box, is the ability to calculate p-values of earlier F-statistics but now with the help of bootstrapping. This means the p-values are now calculated by taking the number of bootstrap replicates which are larger than the observed F-statistics and divide it by the total number of replicates plus one. This number can be set by the *Number Bootstrap Replicates* entry box and the user can also decide to bootstrap with or without replacement with the corresponding checkbox. The bootstrapping on the defined *Bicluster Number* is executed through the *Bootstrap* button after which the user can use the *Visualize* button to obtain histograms of the bootstrap results of the row and column tests. An example of this graph (and bootstrapping output) can be found in the Appendix in figure 64. Note that the vertical green line represents the observed F-statistic.

### Parallel Coordinate Plot

In the next box the user is able to produce a variety of parallel coordinate plot. The graphs make use of the expression levels in the original data matrix (unaffected by discretization or binarization). The plot represents these levels through gene and/or condition profiles in a bicluster as lines. The bicluster which will be drawn is once again defined by a *Bicluster Number* entry box.

The first *Plot Type* is the default one for which extra options are available in the form of checkboxes. By checking only the *Plot Only Column*, the expression levels for the columns in the selected bicluster will be drawn. This means each line is a column profile with the genes on the x-axis. By checking *Plot Rows & Columns* a second plot will be added to the graphics device, but now with the row/gene profiles with the columns/conditions on the x-axis. The last checkbox, *Compare*, will make sure the other profiles, not in the chosen bicluster, are also plotted in a light-gray colour.

Finally the second type, *Combined (rows & columns)*, in a way combines the information about the bicluster grouping of rows and columns. Again, each line is a gene/row profile, but the columns/conditions on the x-axis are reordered in such a way that the columns belonging to the bicluster come first. This is visualized by showing a red line when belonging to the selected bicluster and black one when not.

An example of these parallel coordinate plots (or profile plots), can be found in the Appendix in Figure 65.

### Heatmap Plot

In this box, the user can visualize the gene expression data matrix as a heatmap. The rows and columns will be reordered so that the inputted bicluster in the *Bicluster Number* entry box will appear in the top-left of the matrix. However, by checking the *Local* option, only the heatmap of the bicluster will be drawn, omitting the rest of the matrix.

An example is given in the Appendix in Figure 66.

### Biclustmember Plot

The last box on this window contains the options to draw a Biclustmember Plot. This plot can primarily be used to compare the discovered biclusters against each other. On this graph, as given in the Appendix in figure 67, one can find multiple columns of stacked rectangles. Each such column is a representation of a bicluster and each rectangle inside represents a column/condition/sample of the data matrix. Basically if in a column of these stacked rectangles, a rectangle is coloured, it means that this condition is part of that particular bicluster. Now, if the *Mid* box is not checked, a coloured rectangle consists out of two parts, left and right. The left colour represents the mean of this condition for all the genes within the biclusters. However, the right colour contains the global mean value for this condition. If the *Mid* option is checked though, the rectangle exist out of three colours with the global mean in the middle and the bicluster mean on the left and right.

Finally, the user is also able to set a label which will come in front of the cluster number with the *Bicluster Label* entry box.

### Biclust Bubble Plot

The first plot the user can create from the extra window, is the Biclust Bubble Plot. The bubbleplot is a 2D-projection of the biclusters, done through multidimensional scaling based on the gene and condition profiles. It is used as a tool to help understand the overall behaviour of biclustering methods, detect trends, outliers, etc. Each bicluster is represented as a circle of which the brightness represents the homogeneity (darker, less homogeneous). The size on the other hand represents the size of the biclusters, as rows  $\times$  columns. The user is able to add up to three bicluster results in the *Extra Bicluster Results* entry boxes, obtained from earlier runs of methods from `biclust`. Note that each bicluster set will get a different colour in the plot.

Further, the user is also able to choose between three different kind of projections, namely *mean*, *Iso Mds* and *CmdScale* of which more information can be found in the help files (note that this *Help* button is linked to the bubbleplot help page).

Lastly the *Show Labels* checkbox will give each bicluster the corresponding bicluster number if checked. An example of this type of graph can be found in the Appendix in Figure 68.

### Barplot of Bicluster

The graph available in this box is a barplot of biclusters which is used to compare the values inside a bicluster with the values outside of the bicluster. For each bicluster, three bars are drawn per column/condition part of the bicluster. The darkest represents the values inside of the bicluster and the other two the mean and median of the values outside of the cluster. The user is able to draw a legend yes or no with the *Legend* checkbox and can also determine the number of biclusters which should be drawn with the *Total Number of Biclusters* entry box. However this works in a slightly different way, namely on each graphics output device, only 6 bicluster barplots can fit. Further the spot such barplot will get on this ‘grid’ will always be the same. For example, if you would take as input the number 14, only bicluster 13 and 14 would appear on the device. If you would put in the number 12, bicluster 7 to 12 would appear.

An example is given in the Appendix in Figure 69.

### Bar Chart Plot

The final graph in this window will create a barchart for all the biclusters, representing the columns. Each block represents one bicluster and the bars inside of it represent the means of bicluster values for the corresponding column.

An example of this is also given in the Appendix in figure 70.

## 3.6 fabia-package

The biclustering algorithm FABIA or Factor Analysis for Bicluster Acquisition was proposed by Hochreiter et al. (2010). A couple of variations are available in the `fabia` packages of which the *Laplace Prior*, *Post-Projection*, *Sparseness Projection* and *SPARSE* are implemented in the GUI.

The main description of fabia will be given for the Laplace prior implementation. For the others, the differences between the windows will be briefly touched upon.

### 3.6.1 Laplace Prior

Factor Analysis for Bicluster Acquisition with Laplace Prior is an algorithm based on factor analysis where the homogeneity is based on the latent relationship between the variables in the data. The method will discover multiplicative biclusters which are found by sparse factor analysis where both the factors and loadings are sparse. This assumption of sparseness comes from the gene expression data, where normally only a small fraction of the genes is active under a small subset of conditions (Khamiakova, 2013). Further, the model assumes non-Gaussian signal distributions with heavy tails.

Now, a factor model for data matrix  $Y$  with  $P$  factors can be described as follows

$$\mathbf{Y} = \sum_{p=1}^P \lambda_p Z_p + \epsilon$$

where  $Z_p$  is the  $p$ th factor,  $\lambda_p$  is the vector of factor loadings for  $Z_p$  and where additive random noise is assumed to be normally distributed,  $\epsilon \sim N(0, \Psi)$ . Furthermore, the model assumes that  $\Psi$  is a diagonal matrix, i.e. the error terms  $\epsilon$  are independently and normally distributed given the  $p$  factors in the model. Another assumption is that  $\mathbf{Z}$  and  $\Psi$  are independent which implies that the noise is independent of the signal strength. Lastly, as said before, the factor model assumes sparseness of factors and their loadings and this is reflected by the choice of the corresponding prior on loadings and factors (i.e. a Laplace Distribution).

Using this factor model, biclusters can be obtained as following. On a side note, it is important to mention that the method requires normalized and centered data. Now, the algorithm will estimate the parameters and factors through maximizing the posterior of  $\Lambda$ ,  $\Psi$  and  $\mathbf{Z}$  with the help of a variational EM algorithm. Using the estimates for  $\Lambda$  and  $\mathbf{Z}$ , the denoized data is obtained and the biclusters are derived from  $\lambda_p Z_p$ . This means that this component can be seen as a bicluster of which the non-zero genes and samples are members of the bicluster.

More intricate details and information about the method and its variations, can be found in Hochreiter et al. (2010) and Hochreiter (2014a).

The *Fabia with Laplace Prior* window is shown in figure 24 in which the fabia specifications as well as some data manipulation can be decided upon.

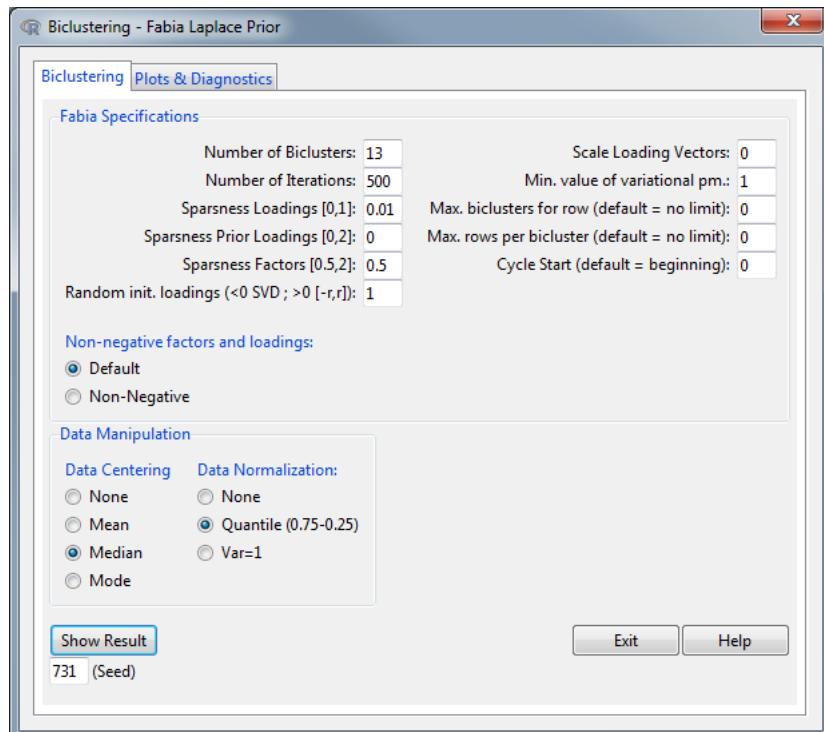


Figure 24: *FABIA (Laplace Prior) Window - Clustering Tab*

As one can see there are a lot of input parameters which can be specified. The most important ones are the *Number of Biclusters* which is equal to the number of factors and can be set to the upper boundary. The other parameters of importance are responsible for the specification of the sparseness such as the *Loadings*, *Prior Loadings*, *Factors*, etc. These depend on the noise level in the data and also the size of the data set.

The user can also select if the factors and loadings are non-negative or not.

Finally, the user can also apply some data manipulation before the method is executed, namely *Centering* and *Normalizing* the data matrix.

### 3.6.2 Post-Projection

For *Fabia Post-Projection*, some post-processing is present. Namely the final results of the loadings and the factors are projected to a sparse vector according to Hoyer (2004). This means: given an  $l_1$ -norm and an  $l_2$ -norm, minimize the Euclidean distance to the original vector (currently the  $l_2$ -norm is fixed to 1). The *Fabia Post-Projection* window is given in figure 25.

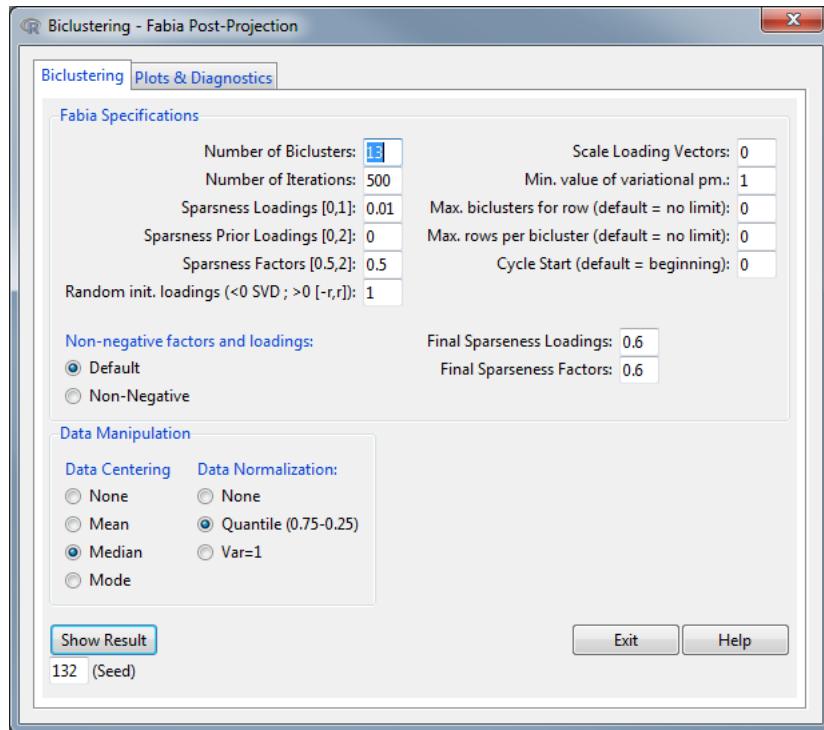


Figure 25: *FABIA (Post-Projection)* Window - Clustering Tab

As one can see, the window is primarily the same as the *Laplace Prior* one, but the user can now also define the *Final Sparseness Loadings* and *Final Sparseness Factors*.

### 3.6.3 Sparseness Projection

The next implemented fabia algorithm is fabia with *Sparseness Projection*. In this version, the prior has finite support, therefore after each update of the loadings they are projected to this finite support. This projection is again done according to Hoyer (2004) (See *Post-Projection*). Figure 26 shows the *Fabia Sparseness Projection* window.

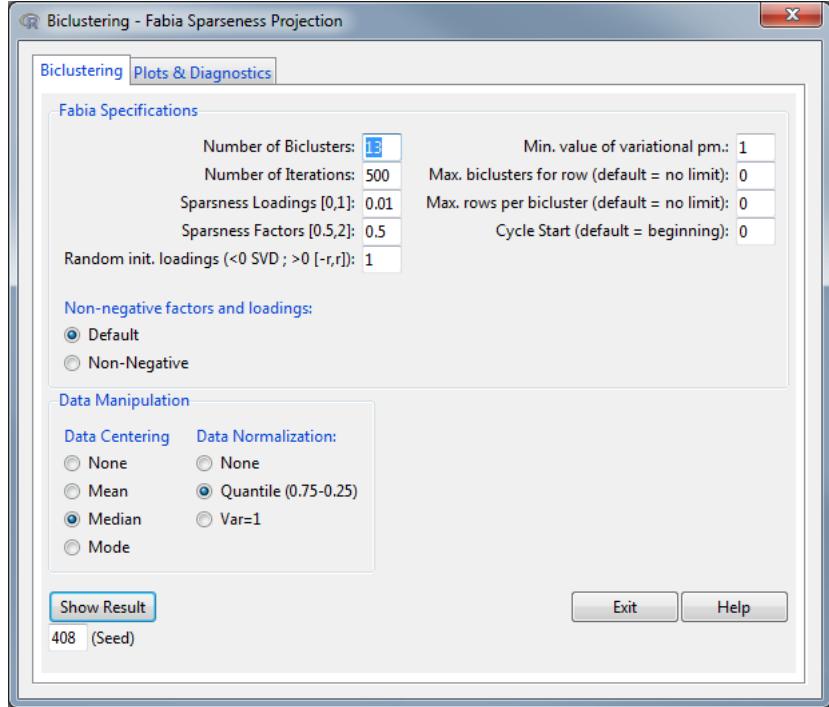


Figure 26: *FABIA (Sparseness Projection) Window - Clustering Tab*

The only difference with *Laplace Prior* is that some options in the specifications have disappeared. These include the *Sparseness Prior Loadings* and the *Scale Loading Vectors*.

### 3.6.4 SPARSE

This is a version of fabia for a sparse data matrix. The matrix is directly scanned by C-code and therefore must be in sparse matrix format as described in Hochreiter et al. (2010) and Hochreiter (2014a).

Again biclusters are discovered through sparse factor analysis and the model selection is performed by a variational approach according to Girolami (2001) and Palmer et al. (2006). Further a prior on the parameters is included and a lower bound on the posterior of the parameters is minimized, given the data. The update of the loadings includes an additive term which pushes the loadings towards zero (Gaussian prior leads to a multiplicative factor).

More detailed information about this algorithm and its methodology can be found in Hochreiter et al. (2010) and Hochreiter (2014a). The *Fabia SPARSE window* is shown in Figure 27.

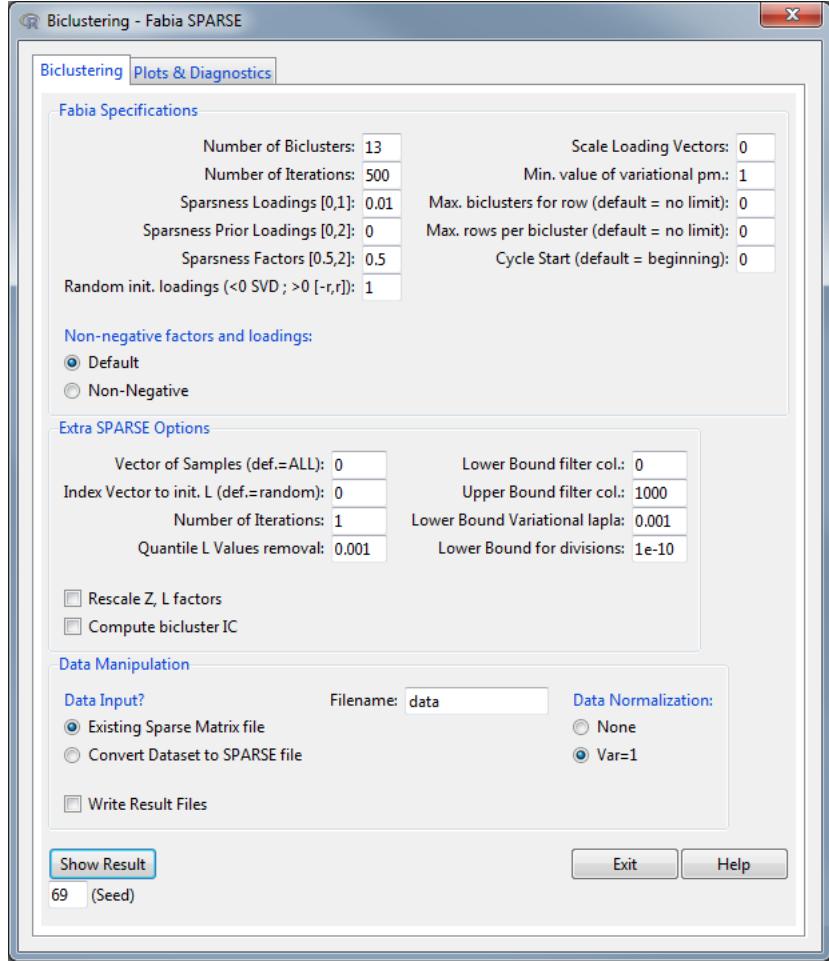


Figure 27: *FABIA (SPARSE) Window - Clustering Tab*

Once again, the same specifications as for the *Laplace Prior* are available in this window. However the options for *Data Centering* and *Quantile Normalization* are not available anymore.

In the second box, *Extra SPARSE Options*, more specifications are given, specific for the SPARSE algorithm. More information about these can be found in the reference manual and vignette of **fabia** (Hochreiter, 2014b).

As explained earlier, the algorithm requires the data matrix in a special sparse format so therefore, the data input for this method works slightly different. Namely the function requires the data to be located in a plain text file in said format. There are two options of inputting the data into this algorithm which will now be explained.

The first option assumes that the user already has this text file which contains the data matrix in sparse format. In this case the *Existing Sparse Matrix file* option should be used and the *Filename* entry box should contain the name of this file (without the extension). Upon pressing the *Show Result* button, the GUI will prompt the user with a directory window in which they have to select the folder where this file is located.

The second option, *Convert Dataset to SPARSE file*, will -as the option states- transform the active dataset in the R commander session to a data matrix in sparse format. With this option a plain text file will be generated, containing the data matrix in sparse format with the name inputted in the *Filename* entry box. Now upon pressing the *Show Result* button, the user chooses the folder where this file will be saved. Note that the code behind this transformation was based on example R-code, available in the **fabia** vignette (Hochreiter, 2014a). Finally, the user can also check the *Write Result Files* which will enable the results being saved in the chosen folder location in the form of plain text files.

### 3.6.5 Fabia: Plots & Diagnostics

Similar to the ‘*Plots & Diagnostics*’ of **biclust**, also for **fabia** the second tab is the same for all of the methods implemented from this package. The idea is to proceed to this tab after executing the biclustering method in the first one so that the biclustering result object is available for the plotting functions. The structure of this *Plots & Diagnostics* window is given in Figure 28 which, in this example, is part of the Laplace Prior dialog.

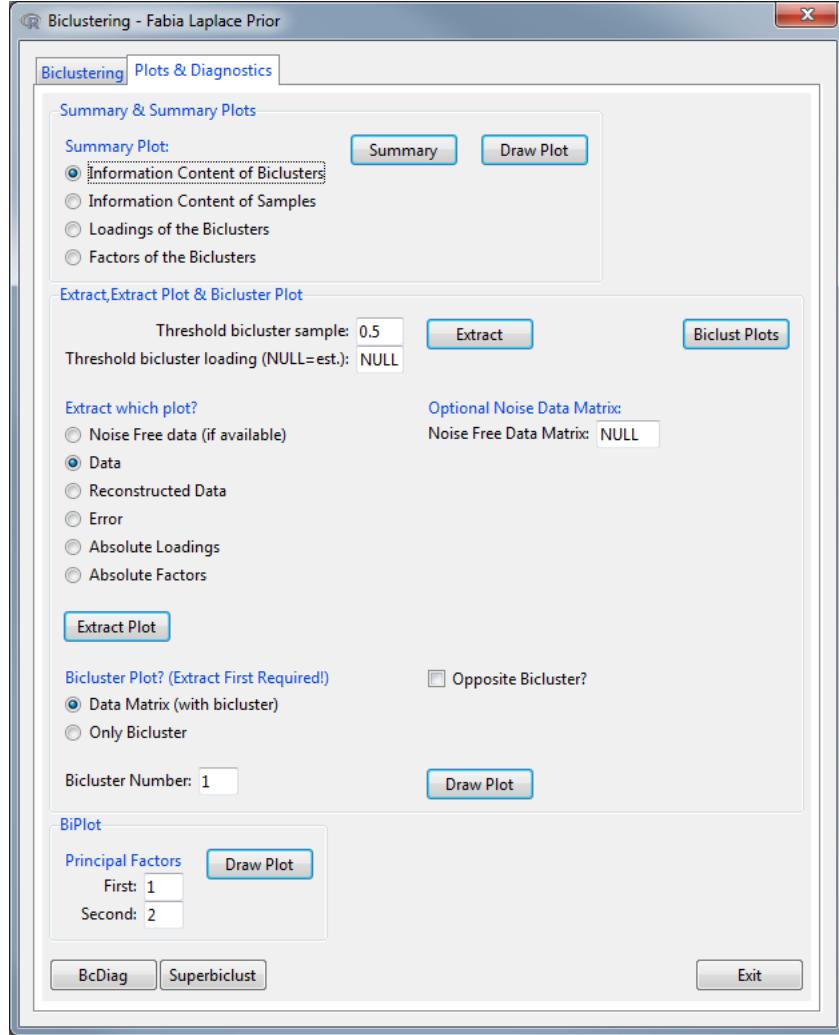


Figure 28: *Fabia Window - Plots & Diagnostics*

### Summary & Summary Plots

By clicking the *Summary* button, the user will receive some general information about the fabia result. Information such as the number of rows and columns in the data matrix, the number of biclusters, the information content of the biclusters & samples and finally some summary statistics of the column clusters/factors and row clusters/loadings, will be printed in the output window.

Further in this first box, the user can also plot several graphs containing the information which was outputted by the *Summary* button. The first two are histograms containing the *Information Content of Biclusters* and *Information Content of Samples*. The other two options are boxplots of the *Loadings of the Biclusters* and the *Factors of the Biclusters*. Examples of these four types of graphs can be found in the Appendix in figures 71 and 72.

More information about the calculation of the information content can be found in the `fabia` vignette (Hochreiter, 2014). Basically it is a way to rank the discovered biclusters analogously to principal components which are ranked according to the data variance they explain. In this case the biclusters are ranked according to the information they contain about the data.

### Extract, Extract Plot & Biocluster Plot

First of all, in the top of this box, the user is able to extract the bicluster results from the fabia results object so it can be used for other applications. This is achieved by using the *Extract* button. Before doing this, 2 thresholds should be set, namely the '*Threshold bicluster sample*' which is a threshold determining when a sample belongs to a bicluster and the '*Threshold bicluster loading*' which is, unsurprisingly, the threshold determining when a loading (=row) belongs to a bicluster. Note that by default this last one is estimated. The result of this extraction is a list object which contains the following items: the extracted biclusters and their indices, the extracted opposite biclusters and their indices, the scaled and centered data matrix and lastly the number of biclusters. (Opposite means that the negative pattern is present.)

To the right of this button is the *Biclust Plots* button which will extract the biclusters based on the earlier

mentioned thresholds and then open up a new window. This new window contains all the plots and diagnostics from the `biclust` package.

The next option in this box is the ability to extract more useful plots from the fabia result. Note that again that the threshold for samples and loadings apply to these graphs as well. The user is able to pick out of a multiple of plots, namely the *Data*, *Reconstructed Data*, *Error*, *Absolute Factors*, *Absolute Factors* and (if available) the *Noise Free data*. For the latter the object name of the noise free matrix should be entered in the *Noise Free Data Matrix* entry box. Interesting to know is that to achieve sorting, k-means is performed so that the vectors belonging to the same cluster can be put together. However, in general this sorting is not able to visualize all biclusters as blocks, namely if they overlap. Several examples of these plots are given in Figure 73 in the Appendix.

The final plot in this particular box is the *Bicluster Plot* which is basically the same as the heatmap available in `biclust`. The user is able to choose a specific bicluster in the *Bicluster Number* entry box and then draw only the bicluster (*Only Bicluster*) or the entire data matrix with the bicluster in the top-left (*Data Matrix (with bicluster)*). Further the user can also decide to plot the opposite bicluster with the *Opposite Bicluster* checkbox. Note that the bicluster plot will *only* work if the extraction in the first part of this box is executed as it requires this output to draw the biclusters. An example of both graphs can be found in figure 74 in the Appendix.

### BiPlot

The final implemented plot in the last box is the *BiPlot* for the matrix factorization result. The user will have to specify the *Principal Factors* that are plotted along the horizontal (*First*) and vertical (*Second*) axis. On this biplot, the row-items/genes are represented as circles with their areas proportional to the row weighting. The most informative genes are those that are the most distant from the center of the plot. Note that the column-items are represented by squares. Also for this last plot type, an example is available in the Appendix in Figure 75.

## 3.7 isa2-package

The ISA biclustering or *Iterative Signature Algorithm* (Bergman et al., 2003) is a semi-supervised method, designed to decompose a large set of data into *modules*. These modules or biclusters consist of subsets of genes (rows) that exhibit a coherent expression profile only over a subset of samples/conditions/experiments (columns). ISA does allow for overlapping modules (rows and columns belonging to multiple modules) and it is developed to find biclusters that have correlated rows and columns which are identified through an iterative procedure. A standard ISA procedure starts with normalizing the data first and then generates random input seeds which correspond to some set of genes or samples. This is refined at each iteration by adding and/or removing genes and/or samples until the process converges to a stable set, the *transcription module*. Following now will be the explanation of the *ISA window* in Figure 29 with some more basic information about the important parameters of the algorithm. More detailed information can however be found in Bergman et al. (2003) and the `isa2` documentation.

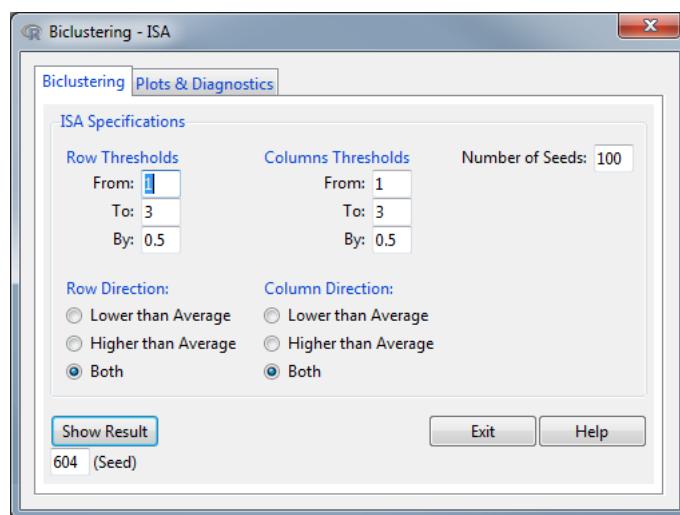


Figure 29: *ISA Window - Clustering Tab*

The two main parameters of ISA are the two thresholds (for rows & columns). If the row threshold is high, then the modules will have very similar rows, if the threshold is mild, the modules will be bigger but with

less similar rows (analogous for columns). The user is able to set a sequence of thresholds for both the rows and the columns (default: `c(1,1.5,2,2.5,3)`) and ISA will run over all combinations of these sequences. For each threshold combination the similar modules will be merged and as a last step again similar modules will be merged but now across all threshold combinations. In this last step, if two modules are similar, then the larger one (with milder thresholds) is kept.

Another interesting parameter the user can set is the direction of rows and columns. This will determine if you are interested in rows/columns that are higher or lower than the average or even both.

The final input value is the number of seeds which are generated to start the ISA algorithm with. For now the GUI only allows for random seeding, but advanced user can use the `isa2` package to set non-random seeds which are based on knowledge of the data (e.g. gene sets).

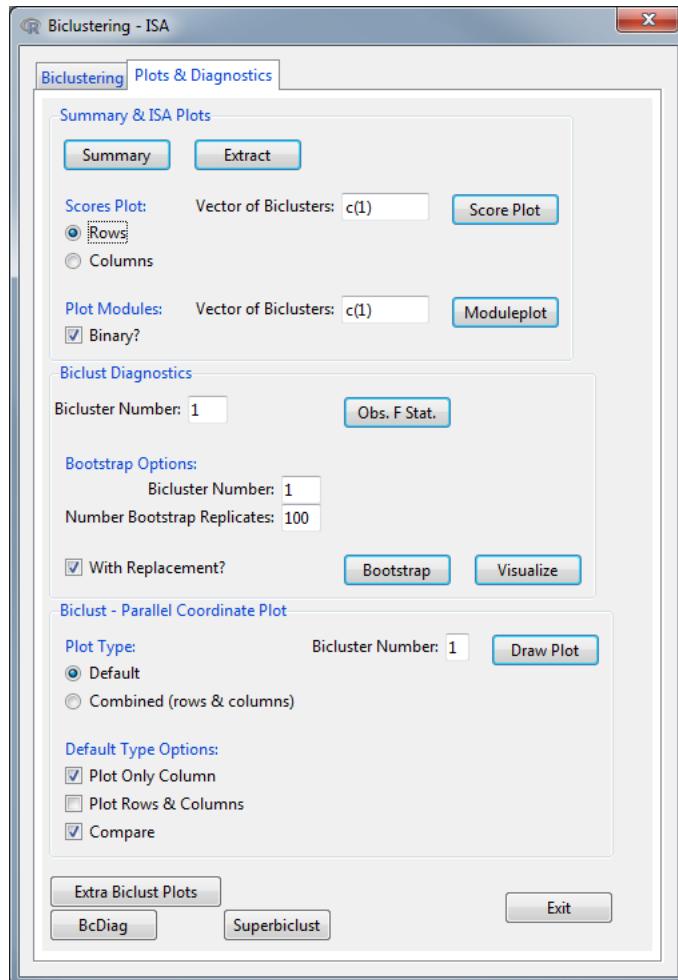


Figure 30: *ISA Window - Plots & Diagnostics Tab*

In Figure 30 above, the the second tab for the ISA method can be found. Apart from the first box ‘*Summary & ISA Plots*’ the plotting and diagnostic options are the same as for the `biclust` methods therefore they will not be elaborated on.

The *Summary* button will give some information about the bicluster result of `isa2`. It will give the number of found biclusters and report the top 10 biclusters based on the robustness score which is a measure of how well the rows and columns are correlated. The next button *Extract* will transform the result of `isa` to a list of biclusters and save it in an list-object called `Extract`. Each entry of this list will have two sublists, `rows` and `columns` which contain the indices of the subset of rows and columns.

The last two buttons in this box will create graphs based on a user-defined vector of biclusters (e.g. `c(1,2,3) = bicluster 1, 2 and 3`). The first, *Scores Plot*, will plot either the row or columns scores (depending on the radio button selection) which is a number between -1 and 1. The further this number is from zero, the stronger the association of the given *row* or *column* to the bicluster. The last, *Moduleplot*, will create image plots for the chosen set of modules as well as the matrix of the original data. The binary check box will determine whether to binarize the biclusters before plotting or use the actual ISA scores. An example of these last two graphs can be find in Figure 76 in the Appendix.

On a final note it should be mentioned that while the *extract* and *score plot* functions were not available in the *isa2* package, they were based on the author's code in the examples of Csárdi (2013).

### 3.8 iBBiG-package

**iBBiG** or *Iterative Binary Bi-clustering of Gene Sets* is a biclustering algorithm proposed by Gustenleitner et al. (2012) which, similar to *Bimax*, will look for submatrices (= modules) of 1's in a sparse binary matrix. But because it works under the assumption of noisy data (non-perfect binarization), a number of 0's are tolerated within a bicluster. Further, it also allows for discovery of overlapping biclusters and the method is optimized for finding modules in matrices of discretized p-values from gene set enrichment analysis (GSA). However this does not prevent one to apply it to any kind of binary matrix. Another attractive feature of iBBiG is that it does not require prior knowledge or limit the number or size of clusters.

In short, the iBBiG algorithm consists out of three main components: 1) a module *fitness score* 2) a heuristic search algorithm to identify and grow modules in a high dimensional search space (*Genetic Algorithm*) and 3) an iterative extraction method to mask the signal of modules that have already been discovered (*Iterative Module Extraction*). Further information can be found in Gustenleitner et al. (2012).

The *iBBiG* window is shown in Figure 31 which contains the parameters which iBBiG needs to execute its algorithm.

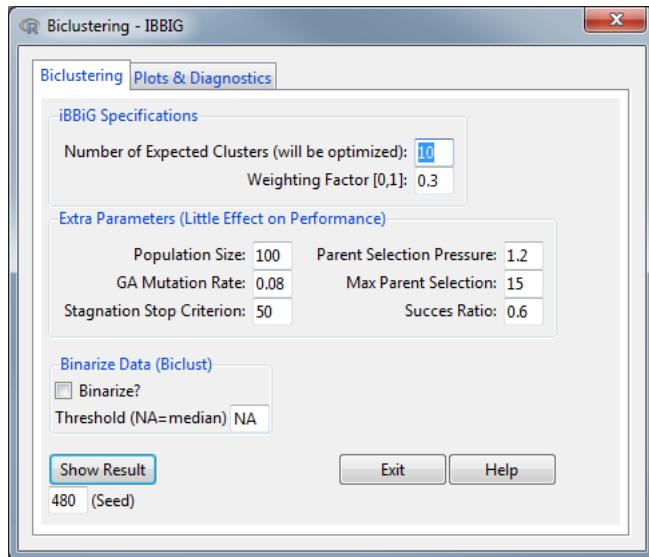


Figure 31: *iBBiG - Clustering Tab*

The most important parameter is  $\alpha$ , the weighting factor, which is responsible for the balance between module *homogeneity* and module *size* when computing the fitness score (number of phenotypes versus number of gene-sets, consequently tradeoff between specificity and sensitivity). A small  $\alpha$  will give more weight to the module size while a large one gives more weight to the homogeneity. However the authors showed in simulated studies that a range of 0.3-0.5 is appropriate with an optimal default value of 0.3 (Gustenleitner et al., 2012). However own investigation for a good value for your particular data or research question is still advised.

The other important parameter is the number of expected biclusters, but because the algorithm is optimized to find a minimal number, this parameter can be larger than the expected value. This means it is recommended to choose an upper boundary for this parameter.

All the other parameters are linked to the genetic algorithm which is a class of heuristic search algorithms based on evolutionary concepts. It is however recommended to keep these on default as these input parameters were reported to have little effect on the results.

Finally, the active data set in your R Commander session can be binarized if this is not a binary matrix by default. (This uses the same function available in *biclust*.) Do note that when plotting graphs (e.g. the biclust plots), the original data matrix will be used which is the active data set in your session.

*Attention! Results from iBBiG are not reproducible, even when setting a seed beforehand. The result should be saved if it is to be investigated later.*

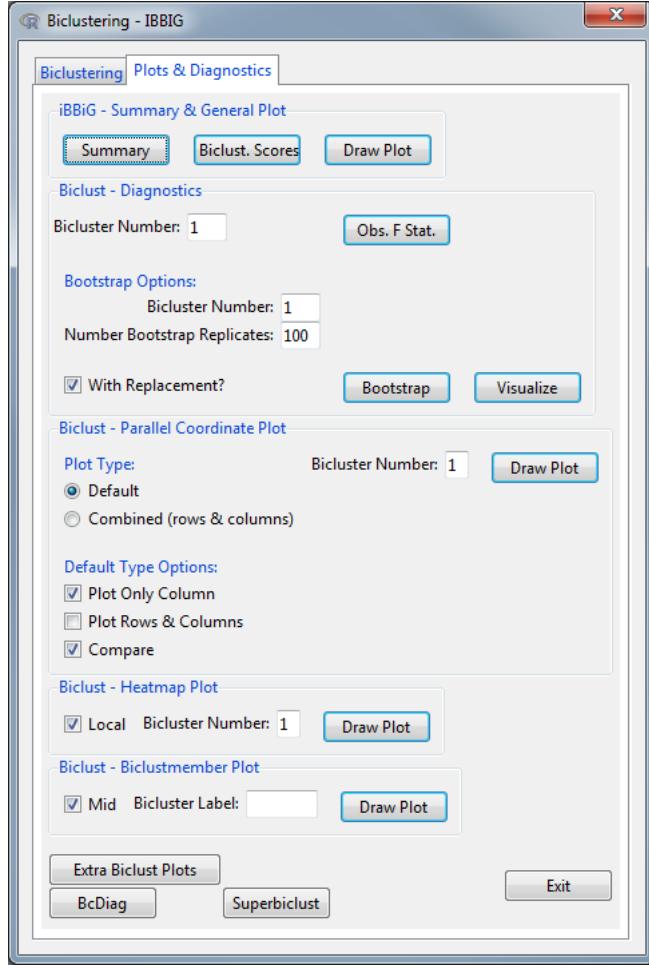


Figure 32: *iBBiG - Plots & Diagnostics Tab*

As can be seen in Figure 32, a lot of the functionality is the same as for the `biclust` algorithms (Section 3.5.7) so it therefore will not be explained again here.

On the top, three `iBBiG` specific buttons can be found. The *summary* button will give some basic information about the number of clusters found and first five biclusters of which the number of rows and columns will be reported. The next button, *Cluster Scores*, will give the module score of the clusters and the third one, *Draw Plot*, will create a general graph of the biclustering result. This graph contains a plot of all the modules colour-labeled in the matrix, as well as some histograms with the module sizes, module scores and weighted scores. An example of this can be found in the Appendix in Figure 77.

### 3.9 `rqubic`-package

The `rqubic` package is the R implementation of QUBIC (Li et al., 2009), a qualitative biclustering algorithm. The algorithm will first apply quantile discretization (e.g. 3 levels: unchanged or up- and downregulated) after which a heuristic algorithm is used to identify the biclusters. In this last step, seeds will be set which are pairs of gene sharing expression patterns in a number of samples. By searching for other genes sharing these expression patterns or genes with an even similar match, the biclusters are identified from this set of seeds. This is repeated for all the generated seeds and a number of maximal biclusters (defined as the number of genes times the number of conditions in that bicluster) are reported.

More detailed information about QUBIC can be found in Li et al. (2009).

In Figure 33, the *rqubic* window can be found in which all the steps of the algorithm can be set up.

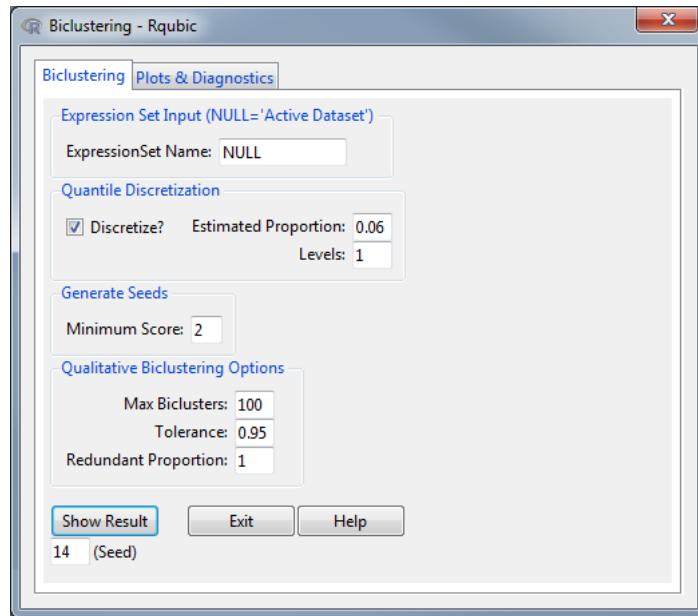


Figure 33: *Rqubic Window - Clustering Tab*

Before deciding the parameters, the users has the possibility to use an ExpressionSet object (**Biobase** package). This was implemented since the functions of this package primarily accept this kind of object. If no Expression Set (= eSet) is given here, the active data set will simple be converted to such an eSet though it will be lack all the additional information an eSet normally contains (it will only contain the expression matrix). However if the name of an eSet is given, the expression matrix part of this object will be made the active data set with the same name as the eSet, appended with ‘\_expr’. This is done so it can be used for plotting and diagnostics purposes.

In the next part of the dialog, the user gets the option to apply quantile discretization for which both the number of levels (e.g. level 1 means -1, 0, 1 label) and the estimated proportion of conditions where a gene is up- or downregulated can be set.

The next option is to set the minimum score for the generation of seeds. A seed is chosen by picking edges with higher scores than this value after composing a complete graph of all genes with coincidence score as weights. This score is the number of samples in which the connected gene pair has the same expression level.

Finally, the parameters for the bicluster identifying process can be decided upon. Parameters such as the maximum number of biclusters (*Max Biclusters*), the percentage of tolerated incoherent samples (*Tolerance*) and the proportion of a cluster over which the cluster is considered as redundant (*Redundant Proportion*).

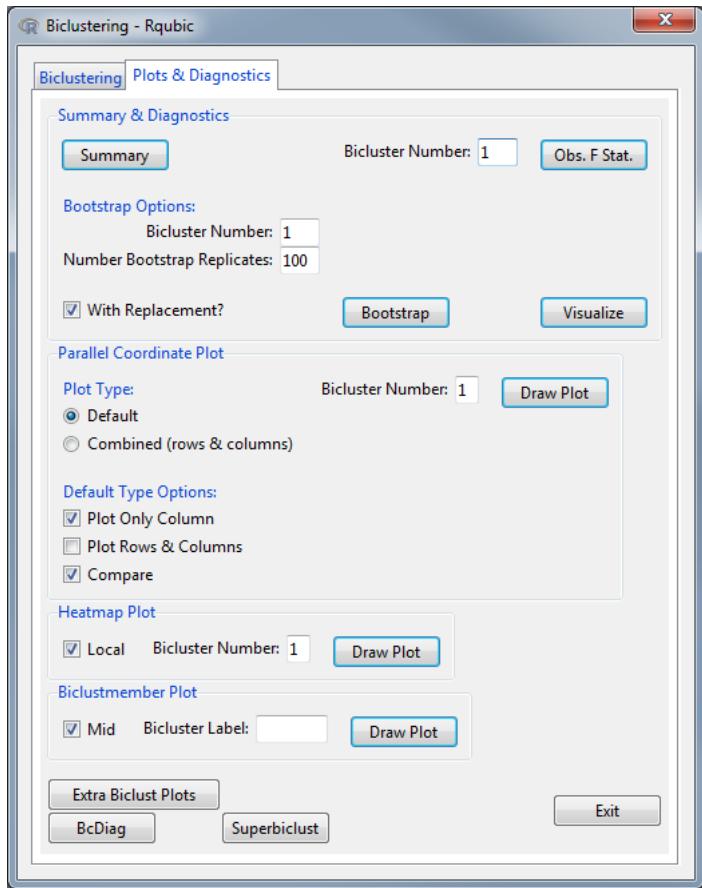


Figure 34: *Rqubic - Plots & Diagnostics Tab*

The second tab (Figure 34) contains the plotting and diagnostics options which is completely the same as options for the methods in the **biclust** package.

### 3.10 BicARE-package

The **BicARE** package (Gestraud and Barillot, 2014), ‘Biclustering Analysis and Results Exploration, is centered around the FLOC algorithm (Yang et al., 2005) of which a modified version is implemented.

FLOC is a probabilistic *move-based* algorithm that can discover a set of possibly overlapping biclusters simultaneously and is also centered around the idea of reducing the mean squared residue (Cheng and Church, 2000). The authors compared the results of FLOC on the same yeast data with the algorithms by Cheng and Church (2000) and they reported that the biclusters returned by FLOC, on average, have a comparable mean squared residue but a larger size. Further they also reported that FLOC was able to locate these biclusters much faster than the algorithms proposed in Cheng and Church (2000).

The FLOC algorithm has two phases. In the first phase, a number of initial biclusters are constructed by a random process which determines whether a row or column should be included. Next, the second phase is an iterative process to improve the quality of the biclusters continuously. In each iteration of the second phase, each row and column are examined in order to determine the best action (including/deleting rows/columns,...) towards reducing the overall mean squared residue. Note that sometimes an action even may be blocked temporarily during an iteration due to a violation of some constraint. The result of each iteration will be used as the initial biclustering for the next iteration.

A much more detailed description about the algorithm itself and the incorporation of the parameters which you can set in this algorithm can be found in Yang et al. (2005). It also provides more ideas about improvements on the basic FLOC algorithm, the inclusion of inverted rows (for discovering genes with opposite regulation) and more.

The *BicAre* window is now shown in Figure 35.

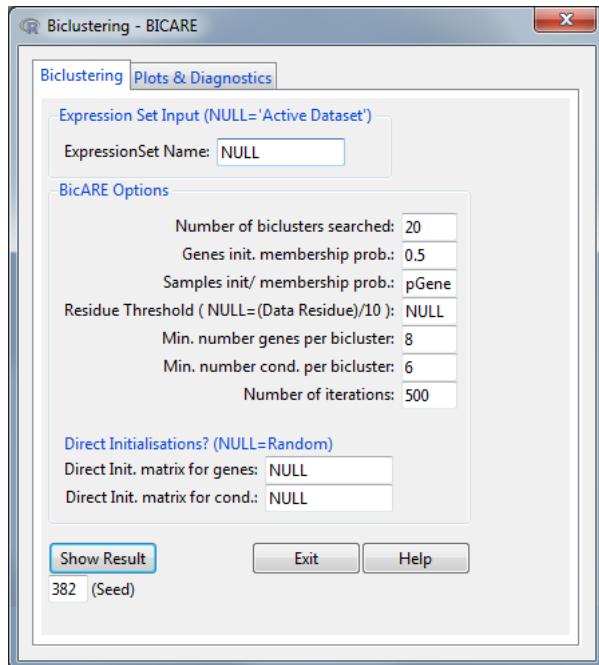


Figure 35: *BicARE Window - Clustering Tab*

Just as for the implementation of the `rqubic` package in the GUI, the user again gets the possibility to use an ‘external’ Expression Set instead of only a matrix provided by the Active Dataset (see section 3.9 for more explanation). For the implementation of this package it is even more interesting to use an Expression Set object as it will enable the user to apply gene and sample enrichment in the second tab.

In the second box of the biclustering dialog, the user can fill in all the necessary parameters for the FLOC algorithm which are fairly self-explanatory. Namely the maximum number of biclusters, the initial membership probability for genes and samples (in first phase), the residue threshold, the minimum number of genes and conditions in a bicluster and finally the number of iterations in phase two.

Lastly, instead of random initialisations, the user can also give the names of matrices which contain information about direct initialisation of the genes and conditions. These are boolean matrices indicating the membership of the elements to the biclusters

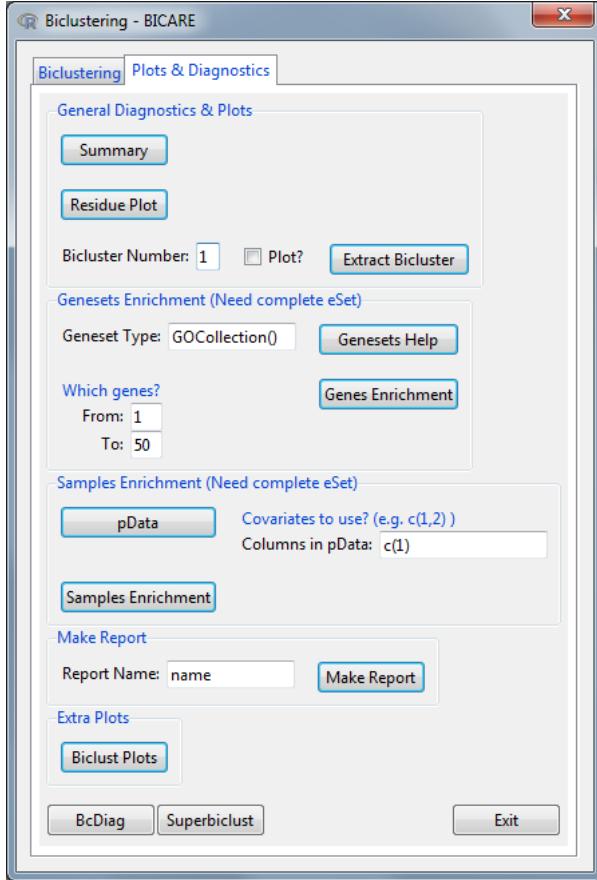


Figure 36: *BicARE - Plots & Diagnostics Tab*

After applying the algorithm, some BicARE specific plots and diagnostics are available in the second tab (Figure 36).

### General Diagnostics & Plots

The first button in this box, *Summary*, will simply print the object as it is printed when the calculation of the algorithm is done. The next button, *Residue Plot*, will create a plot showing the residues of each of the discovered biclusters. An example of this graph can be found in the Appendix in Figure 78. The final button in this box, namely *Extract Bicluster*, will extract the submatrix of the expression matrix corresponding with the chosen bicluster with the *Bicluster Number*. The user can also plot this bicluster by checking the *Plot* option (Figure 79 in the Appendix).

### Genesets Enrichment

In this box, a functional view of the biclusters can be obtained by testing the over-representation of a priori defined genesets. This over-representation is evaluated by an hypergeometric test of which the p-values and the adjusted p-values will be reported. The available genesets are in the GeneSetCollection format and the *Genesets Help* button can be used to query which genesets are available. These can then be filled in in the *Geneset Type* field. Lastly the user can also decide upon which genes should be used in the generating of the geneset collection.

After the analysis is completed with the *Genes Enrichment* button, the results will be added to the biclustering result object and the p-values will be printed. It may however be easier to explore these results with the *Make Report* button (see further).

Note that this analysis is *only* possible when a complete eSet has been used in the first biclustering tab.

### Samples Enrichment

This part of the dialog provides the tools to the user to apply a sample covariates enrichment. First, a button *pData* is provided to print the covariates information of the samples. The user can then choose those columns from this previous print and put them in vector format. These will be the covariates which will be used in the actual testing step. Namely for each bicluster, the enrichment of each level of the covariates will be evaluated with a  $\chi^2$  test of adequation.

Once again these results will be added to the biclustering results object and a small part of them will be printed.

It is however more convenient to explore these results afterwards after making the automatic report (see further).

Note that again this is only possible if the pData information is available in the eSet object you have chosen in the first tab.

### Make Report

Another feature of the **BicARE** package is to build an automatically generated html report of the biclustering results (and genes/samples enrichment if this was applied). The user simply needs to provide a name to the report and then click the *Make Report* button. First small window will pop up to choose the directory in which to put this report after which it will automatically open in the default web browser (Figure 80 in the Appendix).

### Extra Plots

Finaly, the user can find a button here which will open up a new window which contains all the **biclust** plots and diagnostics. The correct information from the **BicARE** will be used and does not require any intervention from the user itself.

## 3.11 s4vd-package

### 3.11.1 SSVD - Biclustering via Sparse Singular Value Decomposition

Sparse singular value decomposition (SSVD) was first proposed as a biclustering algorithm by Lee et al. (2010). It seeks a low-rank checkerboard structured matrix approximation to data matrices through SVD.

For example the following formula shows a rank- $K$  approximation to  $\mathbf{X}$  with SVD

$$\mathbf{X} \approx \mathbf{X}^{(K)} = \sum_{k=1}^K s_k \mathbf{u}_k \mathbf{v}_k^T$$

in which  $\mathbf{u}_k$  and  $\mathbf{v}_k$  are the left and right singular vector.

In the SSVD algorithm, biclusters are discovered by forcing the singular vectors of SVD to be sparse. This is achieved by interpreting the singular vectors as regression coefficients of a linear model. The algorithm alternately fits penalized least squares regression models (Adaptive Lasso or Hard Threshold) to the singular vector pair (left and right) to obtain a sparse matrix decomposition which will then represent the desired checkerboard structure.

This procedure minimizes the following formula with respect to the triplet  $(s, \mathbf{u}, \mathbf{v})$  in which  $P_1(s\mathbf{u})$  and  $P_2(s\mathbf{v})$  are the sparsity-inducing penalty terms, and  $\lambda_u$  and  $\lambda_v$  the nonnegative penalty parameters

$$\|\mathbf{X} - s\mathbf{u}\mathbf{v}^T\|_F^2 + \lambda_u P_1(s\mathbf{u}) + \lambda_v P_2(s\mathbf{v})$$

The penalty parameters for the optimal degree of sparsity (number of non-zero coefficients in the singular vector) are determined by minimizing the Bayesian information criterion (BIC).

The SSVD algorithm, to estimate the sparse singular vector pair, is run on the original data matrix to find the first layer or bicluster. To find the subsequent biclusters, the algorithm is run on the residual matrix after subtracting the original matrix with the previous Sparse SVD layer..

While R code for the algorithm was written, it was only later included in the **s4vd** R package by Sill and Kaiser (2011) which this GUI uses.

Figure 37 shows the *SSVD window*.

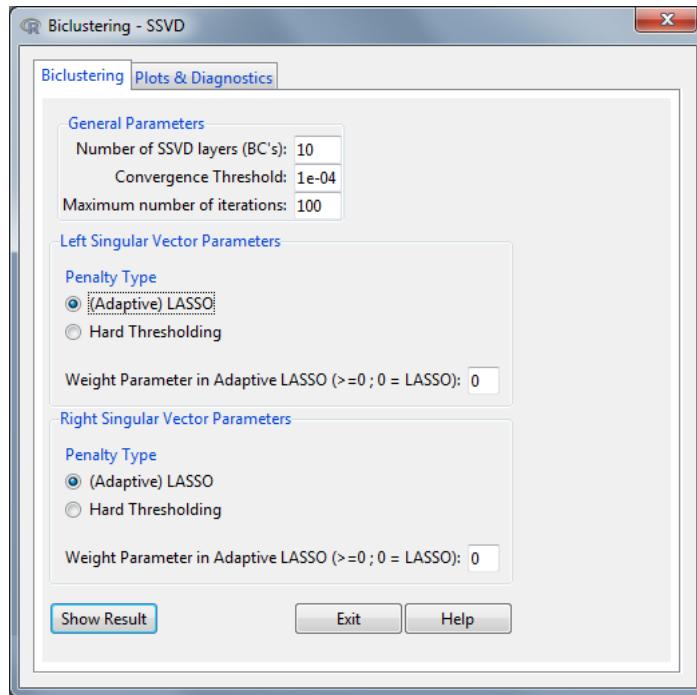


Figure 37: SSVD Window - Clustering Tab

The biclustering tab with the parameters of the algorithm consists out of 3 parts. The first part contains some general parameters such as the *number of biclusters* (= SSVD Layers), the *number of iterations* and *convergence threshold*.

The second and third part contain the penalty type for respectively the left and right singular vector. Note that for the Adaptive LASSO, the user can specify the weight. A zero weight would coincide with the normal LASSO.

The second tab is completely similar to the plots & diagnostics tab of the `biclust` packages in Section 3.5.7 so it will not be discussed here again.

### 3.11.2 S4VD - Robust biclustering by ssvd incorporating stability selection

The S4VD algorithm by Sill et al. (2011) is an extension of the SSVD algorithm. They proposed to incorporate stability selection in the original algorithm, which is a subsampling-based variable selection that allows to control Type I error rates. The goal was to improve both the selection of penalization parameters and the control of the degree of sparsity. Furthermore, the error control also serves as a stopping criterion for the S4VD algorithm and determines the number of reasonable layers or biclusters.

In brief, in each iteration of the alternate estimation and updating of the singular vector pair, for each possible penalty parameter (separately of the left and right singular vector) subsamples are drawn and the relative selection probability of respectively the rows and columns is estimated. By doing this a stable set of non-zero rows and columns is created which is then used in the last step to determine the final left and right sparse singular vectors.

Just like for SSVD, this algorithm is applied to find the first layer or bicluster. To find the next one, the same steps are applied to the residual matrix after subtracting the rank-one approximation derived by applying a regular SVD to the submatrix defined by the stable set of left and right singular vectors.

Presented in Figure 38 is the *window for S4VD*.

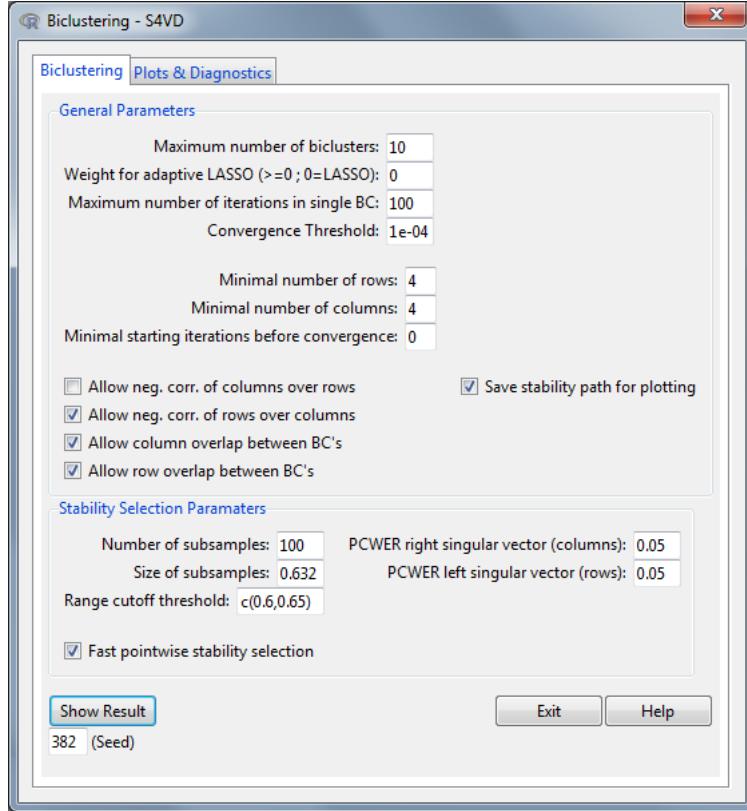


Figure 38: *S4VD Window - Clustering Tab*

This time the window is built out of 2 parts. In the first part, which contains the general parameters, there are some similar parameters as for the the SSVD algorithm (e.g. *Number of biclusters*, *Max Iterations*, *Weight Parameter*, *Convergence threshold*,...). There are also additional parameters such as the option to save the stability path in order to plot it later on. However for extreme high dimensional data set, this option might need to be disabled as the resulting object may exceed the available memory.

The second and last part is dedicated to the Stability Selection segment of the algorithm which contains parameters such as the error rates (= *PCWER*). Since the subsampling steps of the stability selection makes the S4VD algorithm computationally very demanding, the option is given to use the pointwise error control to reduce the computation time.

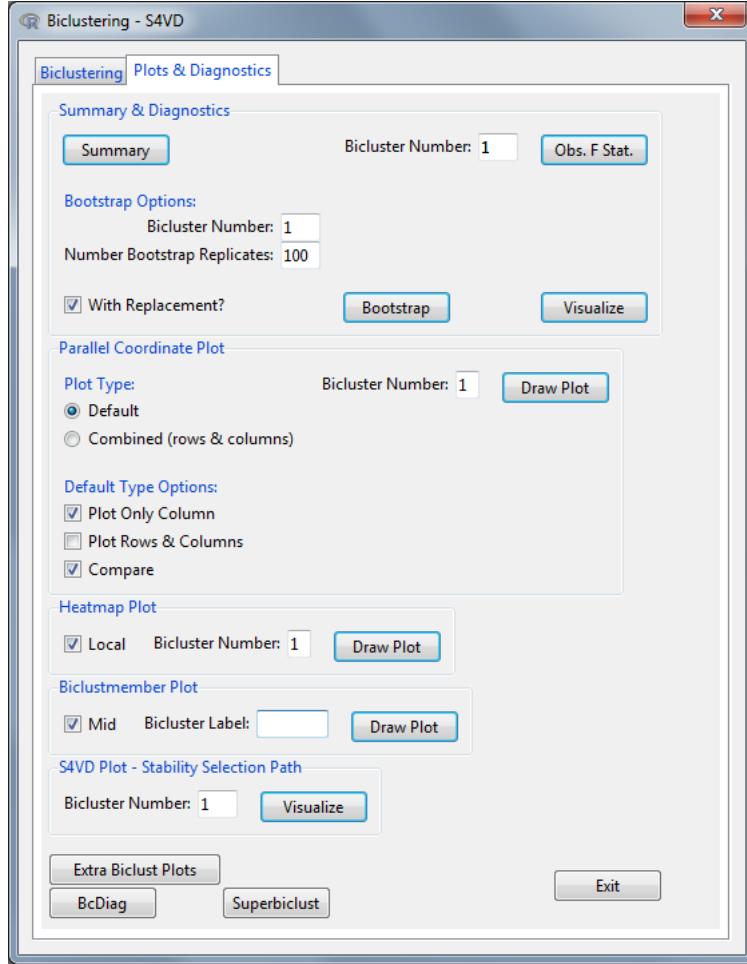


Figure 39: *S4VD Window - Plots & Diagnostics Tab*

Finally, Figure 39 shows the *Plots & Diagnostics* window for *S4VD*. It is nearly completely the same as the window in Section 3.5.7 for the *biclust* package apart from one addition at the bottom. Here it is possible to plot the stability path for the rows and columns in a specified bicluster regarding the last iteration. The path in the plot is basically the selection probabilities for the rows and columns for the possible penalty parameters. However note that if the pointwise error control was used, only the final selection probabilities (for the final penalty parameter) for the rows and columns will be plotted.

## 3.12 Diagnostic Packages

### 3.12.1 BcDiag-package

The first implemented diagnostics package is *BcDiag* which is compatible with *biclust*, *fabia* and *isa2*. Since the output of *iBBiG* is an extension of *biclust*, the diagnostics will also work on this package.

*BcDiag*'s task is the visualisation of bicluster data which can be categorized in three sections:

1. Profiling and Summarising the biclustered versus the clustered data simultaneously.
2. Profiling and Summarising the biclustered data only.
3. Exploring the biclustered data using *anova* and *median polish* techniques.

A general overview will follow, but more detailed descriptions can be found in Aregay et al. (2014).

In Figure 40, the *BcDiag Window* with the accompanying *output summary* window are shown. Note that in this example the diagnostics window was called from a *Plaid Window* as can be read in the window title.

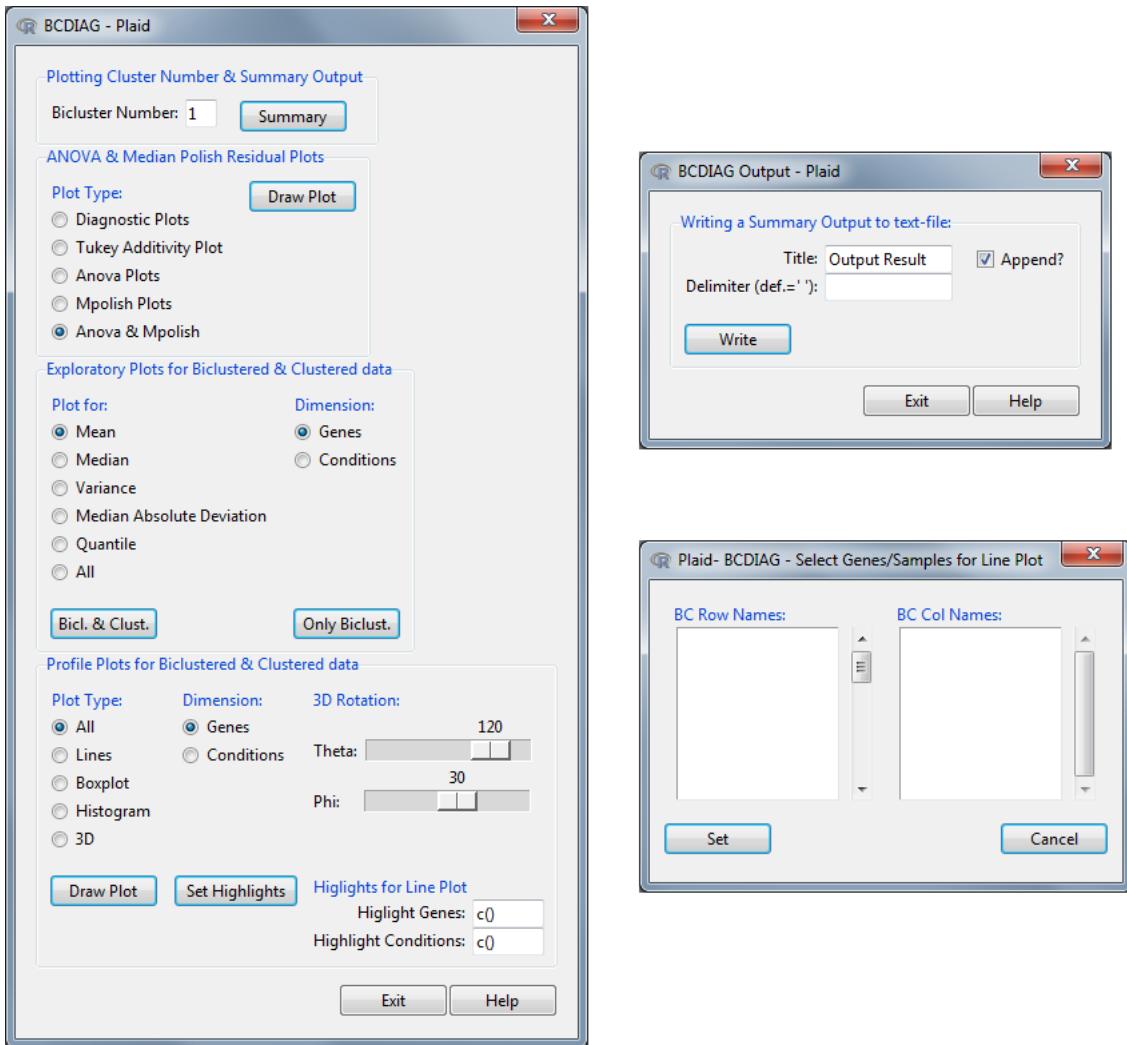


Figure 40: *BcDiag Window with Summary Output Window*

## Summary Output

Using the *Summary* button will open up a small new window which can be seen at the right in Figure 40. With the use of this window a summary output in text format can be created. The user needs to provide a *title* and can also decide on which *delimiter* to use (default=space). Pressing the *write* button will then open up a save window in which the user can decide on the location and name of the text file which will be created afterwards. The original function was developed in the *biclust* package and will create a text file with the total number of biclustered, the dimension and the name of biclustered rows and columns.

## Bicluster Number

At the top of the *BcDiag Window* the user can set the number of the bicluster for which the graphs should be created. This value is used for all the plots down in the window apart from of course the summary button which extracts all biclusters.

## ANOVA & Median Polish Residual Plots

Here residual plots or residual box plots for a bicluster can be created. These can be diagnostic plots (fitted vs residual, QQ,...), *Tukey additivity plots*, *anova* and *mpolish* plots. An example of some of these graphs can be found in the Appendix in Figure 81.

## Profile Plots

With this graph, profile plots for biclustered data can be created. These profile plots can either be in *lines*, *boxplot*, *histogram* or even *3D* format. For this last type the rotation can be controlled by the *theta* and *phi* parameter, respectively the *z* and *y* axis. Further, the user can decide to either to make these profile plots on the *genes* (=rows) or *conditions* (=columns) dimension. If for example you would choose the *conditions* dimension and *lines* as type, you would get the same result as the *parallel coordinates plot* (combined type) from the *biclust* plots. In this scenario each line is a gene in the bicluster and it gets a red colour labeling if

the column also is a part of the bicluster. The other way around, namely choosing the genes dimension, would mean that each line is one condition which is red when the gene on the x-axis is part of the bicluster. Some examples of these are shown in Figure 82 in the Appendix.

Further, there is also an option to highlight gene or condition profiles for the line plot type. Either give a vector with indicies or character names in the *Highlight Genes/Conditions* boxes, or use the *Set Highlights* button to open up a new window as shown in Figure 40. This dialog will show a list of the gene and conditions names of the chosen bicluster. From this list the to-be-highlighted members can be selected and after pressing *Set*, the highlight vectors will be filled out corresponding to this selection.

### Exploratory Plots

These plots are summary plots for the *mean*, *median*, *variance*, *MAD* and *quantiles* of the data. Just like for the profile plots, the dimension can be chosen here as well. Lastly the user can decide to show both the in-bicluster and out-bicluster information with the left button *Bicl.* & *Clust.* (as is always the case for the profile plots) or only the in-bicluster information with the *Only Biclust.* button. This is basically just the first part of the graph with both the in- and out-bicluster information as can been seen in figure 83 in the Appendix.

### Note on FABIA Results

For results from FABIA it is possible to set sample and loading thresholds to determine the biclusters (Figure 41).



Figure 41: *BcDiag - Fabia Thresholds*

### 3.12.2 superbiclust-package

A central issue of biclustering is its stability which can highly influence the ability to interpret the results of a biclustering analysis. The stability can be affected by initialisation, parameter settings and perturbations such as random noise. Shi et al. (2010) introduced a novel procedure for obtaining robust biclusters from a set of initial values which is exactly what **superbiclust** will accomplish. It will construct a hierarchy of biclusters based on for example the Jaccard index from which the robust biclusters based on this ‘superbiclust’ concept can be extracted.

Starting now, the functionality of the *superbiclust* window will be explained, following the default structure of a superbiclust analysis. However, for more information about the architecture of **superbiclust**, see Khamiakova (2013) and see Shi et al. (2010) for more details about the ‘superbiclust’ concept itself.

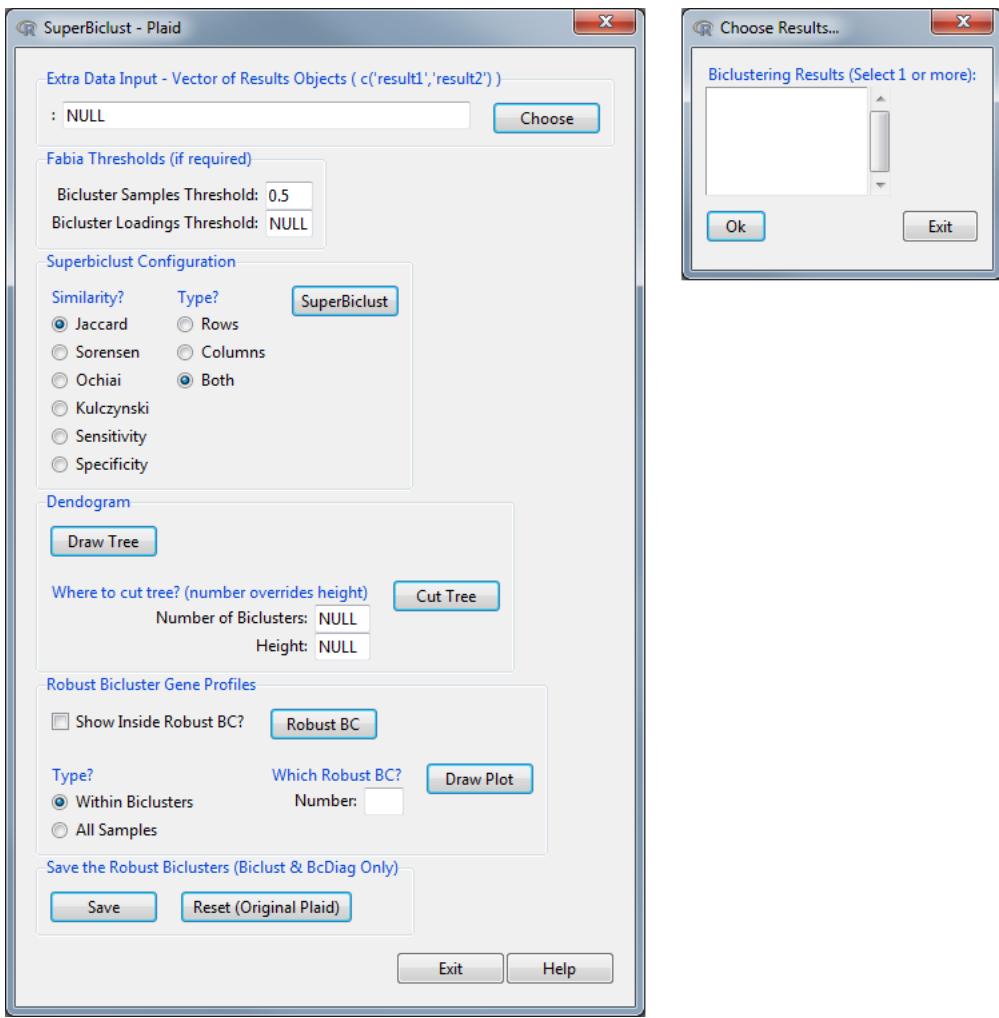


Figure 42: *Superbiclust Window*

### Extra Data Input

First of all, at the top of the window in Figure 42, there is room to add other biclustering results objects which are loaded in the R workspace. The format should be as in the given example: `c('result1','result2')`. The easiest way to do this is to use the *Choose* button. This will open up a small new window in which the user can select those results of interest. After pressing *Ok*, they will be immediately filled in in the entry field.

### Fabia Thresholds

In this small box, the user can set the thresholds for biclustering results from **Fabia**. These thresholds will apply for all the selected fabia results for the extra data input as well as for fabia result on which the superbiclust might be originally used. This means that the box will always be available.

### Superbiclust Configuration

In this box, the first part of a superbiclust analysis is executed, namely the computation of the similarity matrix of the biclusters. In this figure, we are working with the results of the plaid method as can be seen in the title window. This matrix can be based on several types of similarity and the user can also decide to base it on the rows, columns or on both (as is suggested for bicluster results). (Note that for fabia results, the default threshold is used to determine the biclusters.)

### Dendrogram

In the next step, the similarity matrix will be used to construct a hierarchical tree. This is visualised in a dendrogram which can be drawn with the *Draw Tree* button of which an example is given in Figure 84 (Appendix). By cutting this tree now, the *robust* or *super biclusters* can be obtained. This user can do this either by setting a *number* of desired *biclusters* or by choosing an appropriate *height* to cut the tree at before using the *Cut Tree* button.

### Robust Bicluster Gene Profiles

After cutting the tree, some information can be called with the *Robust BC* button with or without the *Show Inside* checkbox. The result of this can be found in Figure 85 in the Appendix. In first part a matrix is presented with in the first row the index of the robust bicluster and in the second row the number of original biclusters it contains. Note that only those robust biclusters created from more than one bicluster will be displayed. The second part, which will appear if you check the *Show Inside* option, will tell you the indices of the original biclusters in a robust bicluster.

In the last part of this box, the user is able to quickly draw a profile plot of a robust bicluster of choice. Just like in the *Bcdiag Window*, either all the data (in-bicluster + out-bicluster) or only the in-bicluster data can be drawn.

### Save the Robust Biclusters

The last box gives the user the option to *save* the robust biclusters. By doing this, the user can go back to the previous window (plots & diagnostics tab) or even to the *bcdiag* window (or extra *biclust plots*). If the user creates the graphs now, they will be based on the robust biclusters instead of the original ones. However, take note that this only applies to the *biclust-plots/diagnostics* and the plots created by *bcdiag*. For example in the case of *isa2*, the user will not be able to create the correct scores or modules plots as this information is lost after combining biclusters into a robust one. Another example would be the buttons in the ‘*summary & general plot*’ box of *iBBIG*. Same goes for *fabia*, only the plots from *biclust* and *BcDiag* will now work. If you would like to go back to the original bicluster result, simply click the *Reset Button*.

## 4 A Guideline to New Implementations

Thanks to the easy plug-in extensibility of R Commander, adding new dialogs is very simple. One only needs to make the desired window function and then add this to the `menus.txt` file situated in the plugin package folder (`package -> inst -> etc`) as explained in Fox (2007).

If you are familiar with the `Rcmdr` and `tcltk` syntax, you can make your own customized dialog functions and then send these to the maintainer of `RcmdrPlugin.BioclustGUI`.

However, if you are new to these two packages or simply want an easier and quicker way to construct your biclustering dialogs, *template functions* have been created to help with this process. In the following sections, an explanation will be given on *two kinds of scripts* in which these functions are called to create your desired window.

- **New Method Script:** The *first* type of *script* will address the creation of a dialog to execute biclustering methods.
- **New Tool Script:** The *second* type of *script* addresses the creation of an extra tool window. This last one can serve as either an extension of the first (through buttons) or can be a general diagnostic window compatible with multiple methods. This will be further discussed in a later section.

It should also be noted that these templates are specifically tailored to biclustering methods and that all of the already implemented methods are done through these scripts.

In the end, what should be given to the maintainer to implement a new method are the following items:

1. The necessary window scripts (manually or through the templates)
2. A simple description of how the menu should look like in R Commander (e.g. Bioclust menu opens up into several subitems like plaid, Xmotifs,...).
3. A function to transform the results object of the new method to a `bioclust` object. This is a S4 class object of which the most important slots are `RowxNumber`, `NumberxCol` and `Number` (see `Bioclust-class` in the `bioclust` reference manual (Kaiser et al., 2014)). This ensures that the new package will be immediately compatible with the `BcDiag` and `superbioclust` packages as well as all the *Extra Utilities* the GUI offers.
4. *Optional:* The correct criteria which should be used in the *Search Window*

### 4.1 Implementing a New Method

For starters, each biclustering window is made out of two tabs. One to execute the method and one to show diagnostics and plots. Both tabs have some standard buttons which will appear at the bottom as well as some optional ones as depicted in Figure 43.



Figure 43: *Standard Tab Buttons*

As will become clear later, the clustering tab will contain the parameters of the biclustering method while the second tab will contain diagnostics and plots *specific* to this method. The concept is that the optional buttons will lead to new windows of general diagnostic packages, compatible with multiple biclustering methods.

Secondly, the idea is to have one biclustering function/method for each biclustering dialog and tailor it towards this.

Lastly, also note that the generation of the R code in the script window, one of R Commander's advantages, is also done automatically through the use of the template scripts.

#### 4.1.1 New Method Script - ClusterTab & PlotDiagTab

We will now start going through `newmethod_script.R` which can be found in the Appendix.

The script `newmethod_script.R`, the first type of the mentioned scripts, can be used in order to create a new window for a new application.

##### General Method Information

The script begins by opening a function which will be closed again after the final step of the script. Here, this function is called `newmethod_WINDOW`, but this can be changed to one's own window name. This function will be called by R Commander to make the accompanying window appear when accessing the menus.

Next, some objects are initialized (`new.frames`, `grid.config` and `grid.rows`). These will be used to store information in about your window you are about to create.

```
newmethod_WINDOW <- function(){

    new.frames <- .initialize.new.frames()
    grid.config <- .initialize.grid.config()
    grid.rows <- .initialize.grid.rows()

    ##### GENERAL INFORMATION ABOUT THE NEW METHOD/WINDOW #####
    #### GENERAL INFORMATION ABOUT THE NEW METHOD/WINDOW ##

    methodname <- "A new method"

    methodfunction <- "methodfunction"
    data.arg <- "d"
    methodshow <- TRUE
    methodsave <- TRUE
    other.arg <- ""
    methodhelp <- ""

    # Transform the data from data.arg
    data.transf <- "matrix" # Values: "matrix" (default), "ExprSet"

    # Extra Data Conversion Boxes
    data.dscr <- FALSE
    data.bin <- FALSE

    # Possibility to give a seed ?
    methodseed <- TRUE

    ## COMPATIBILITY? ##

    # BcDiag
    bcdiag.comp <- FALSE

    # SuperBiiclust
    superbiclust.comp <- FALSE

} # Note: The curly bracket is placed here for syntax reasons.
#       It should be placed after the call of cluster_template.
```

The script starts by filling in some information about your biclustering method. A clarifying example follows later, filling in this information for the Plaid method.

- **methodname:** The title of the window which will be shown on top. It may contain no special characters besides ‘-’. It is important to know that the result of your biclustering function will be saved in a global variable, named `methodname` without the spaces and ‘-’ symbols. Therefore, do not make this string too elaborate.
- **methodfunction:** A string which contains the name of your biclustering method’s function. By this the actual R function, corresponding with the method, is meant. Note that the R command (which is printed in the

script window of R Commander) to execute the biclustering algorithm actually starts with this string. New arguments are appended to this string until the R command is fully constructed.

- **data.arg:** The name of the argument which needs the data.
- **methodshow:** Logical value which decides if the object in which the clustering result is saved, should be printed. See figure 44.
- **methodsave: -Warning: Experienced Users-** A logical value which decides if the the result of the *method*-function should be saved or not. Putting this argument to FALSE is only advised when knowing the use of `doItAndPrint()` and `justDoIt()`. This option can be useful in the scenario where the biclustering method actually consists out of multiple steps of functions. You can then create a general ‘GUI’ function which does not return an object (therefore the saving is not required), but will use `doItAndPrint()` to execute the different functions. However do make sure that eventually the result is saved in an object as described in the explanation of `methodname`. This is to ensure the plotting functions can use the correct result. (The `rqubic` implementation is an example of this) (Note that putting `methodsave` to FALSE will also put `methodshow` to FALSE)
- **other.arg:** A string containing extra arguments that cannot be changed by the user. For example, in the plaid window, it is used as follows. Since the biclust package uses only one function to execute all the different methods, namely `biclust()`, for the plaid method the string ",`method='BCPlaid'`" is added. Note the use of the comma in the beginning of the string! This is because this string is not restricted to only one argument, it could contain several of them. They simply need to be added in this string as they would be added inside the function itself.
- **methodhelp:** The name of the helppage the help button should be directed to. (`help(methodhelp)`)
- **data.transf:** Value which will determine if the data for `data.arg` should be transformed or not. Possible values are "" for no conversion, "`matrix`"(default) for `as.matrix` and "`ExprSet`" to convert it to an ExpressionSet obect (`Biobase`-package).
- **data.discr:** Logical value determining if a frame should be added above the *Show Results* button with the option to discretize the data. The `discretize` function from the `biclust` package is used to achieve this. See Figure 45.
- **data.bin:** Logical value determining if a frame should be added above the *Show Results* button with the option to binarize the data. The `binarize` function from the `biclust` package is used to achieve this. See Figure 45.
- **methodseed:** Logical value determining if there should be a seed box below the *Show Results* button. This will make sure a `set.seed()` is executed before the biclustering function.
- **bcdiag.comp & superbiclust.comp :** Logical value determining compatibility with the `BcDiag` and `superbiclust` package respectively. Please note that this only enables the appearance of the buttons in the second tab. For a button to function properly, some minor coding needs to be carried out by the maintainer. (Note that if a transformation function to a `biclust` object is given, namely the format in which the results of methods in the `biclust` package are, this almost requires no work on the maintainer’s side)

```

R Script | R Markdown
data(BicatYeast, package="biclust")
BicatYeast <- as.data.frame(BicatYeast)
names(BicatYeast) <- make.names(names(BicatYeast))
set.seed(189)
Plaid<-biclust(x=as.matrix(BicatYeast),method=BCPlaid(),cluster='b',
fit.model=y ~ m+a+b,background=TRUE,shuffle=3,back.fit=0,max.layers=20,
iter.startup=5,iter.layer=10)
Plaid!
-----'

Output
> Plaid
An object of class Biclust
call:
-----'

```

Figure 44: Example of Plaid Biclustering - With `method.show=TRUE`

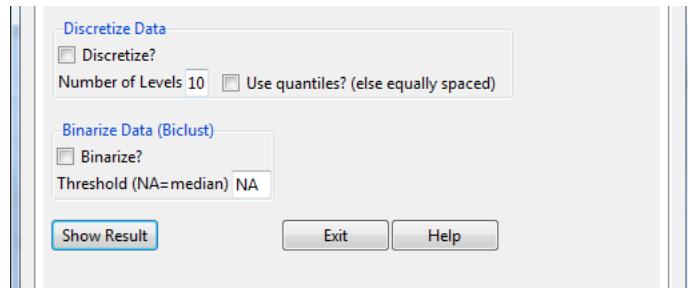


Figure 45: Example of discretize and binarize frames.

### Cluster Tab

After providing the information about the new biclustering method, the window for it can be created. Note that what follows is simply appended to the previous part of the script, but still inside the `newmethod_WINDOW` function which was opened in the very beginning.

Both the clustering tab and the plotting & diagnostics tab are created in three easy steps as shown in Figure 46:

1. Making the frames
2. Configuring the frames into a grid
3. Combining rows into a box

#### 1. Making the Frames

#### 2. Configuring the Grid

#### 3. Combining Rows

- Combine row 1  
("Plaid Specifications" Title)
- Combine row 2 & 3  
("Layer Specifications" Title)

Figure 46: Making windows in 3 steps

```
#####
### CLUSTERING TAB #####
#####

input <- "clusterTab"
```

```

### 1. ADDING THE FRAMES ###

# Add frames here

### 2. CONFIGURING THE GRID ###

grid.config <- .grid.matrix(input=input, c("frame1", "frame2", "frame3", NA, "frame4", NA),
                           nrow=3, ncol=2, byrow=TRUE, grid.config=grid.config)

### 3. COMBING THE ROWS ###

grid.rows <- .combine.rows(input=input, rows=c(1), title="A nice box: ",
                           border=TRUE, grid.rows=grid.rows, grid.config=grid.config)
grid.rows <- .combine.rows(input=input, rows=c(2,3), title="A nice box: ",
                           border=TRUE, grid.rows=grid.rows, grid.config=grid.config)

```

Looking at the script, you can see it starts with putting the `input` to `clusterTab`. This will make sure everything you are creating and saving now will be done for the first tab, namely the clustering tab.

#### *Step 1:*

As already explained earlier, the first step will be to create the frames in which you want to put your function arguments. A variety of frames can be created, but these will be explained in more detail in the following section. To give a quick summary, here is the list of the types of frames which can be generated in the clustering tab.

- Check Boxes
- Radio Buttons
- Entry Fields
- Sliders
- Spinboxes
- Manual Buttons (only for plot & diagnostics tab)

In future updates, there is still the possibility to add even more types if required.

#### *Step 2:*

During the creation of the frames in the previous step, you will have given each of them a unique name. Using these framenames, the next step will be to simply order them into a matrix grid, filling in the empty spots with NA's. This is achieved with the `.grid.matrix` function. The function accepts the exact same arguments as the `matrix` function apart from two new ones, namely `input` and `grid.config`. The first is to make sure the template function knows we are adding frames in the first tab, while second one is there to ensure that the new information is added to the old `grid.config` object and that old information is not lost.

Further, it is important to know that the inserted frames will *always* be pulled towards the north-west as much as possible. Therefore in a 1-row matrix, something like `c(NA, "frame1")` or `c("frame1", NA)` would give exactly the same result.

#### *Step 3:*

The final step will enable you to put one or multiple rows in a separate box which can serve two different purposes. The first is to add some visual distinction between rows with the help of a title with or without a border around the row(s).

The second purpose is connected to the way frames are added in this `grid`. Sometimes if frames have a large difference in size, other frames might seem to be jumping to the right, trying to fit in one general grid. In general if you see this happening, putting this row(s) in a box will solve this problem and the frames will again be pulled towards the left (see Figure 47 for an example). This works because now the grid exists 'locally' in this row box.

Creating these boxes by combining rows is very easy, simply use the `.combine.rows` function which will save the necessary information in the `grid.rows` object. The function only has three arguments that should be changed: (1) `rows` - a vector containing the rows you wish to combine, (2) `title` - give the box a title ("")

means no title) and (3) **border** - determines if there should be a border.

Note that in contrast to the grid configuration, you can call this function multiple times until the desired result is obtained.

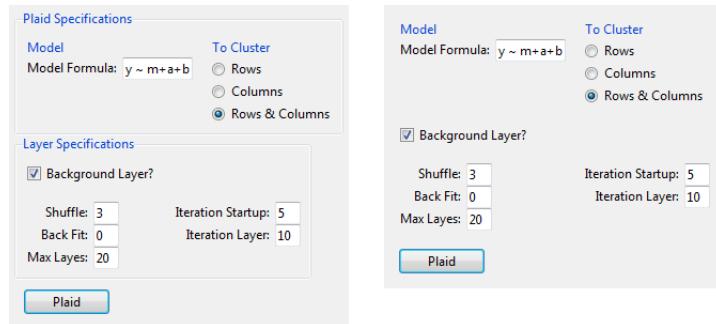


Figure 47: *Left:* Rows 1 and 2+3 were combined with boxes and titles ; *Right:* No rows combined. Frames are stuck in a general grid and jump more to the right instead of in a ‘local’ grid in a row box

## **PlotDiag Tab**

The clustering tab configuration is immediately followed by making the second tab.

```
#####
##### PLOTTING & DIAGNOSTICS TAB #####
#####
{ # ignore this bracket

  input <- "plotdiagTab"

  ### 1. ADDING THE FRAMES ###

  # Add frames here

  ### 2. CONFIGURING THE GRID ###

  grid.config <- .grid.matrix(input=input,c("frame5","frame6"),nrow=1,ncol=2,
    byrow=TRUE,grid.config=grid.config)

  ### 3. COMBING THE ROWS ###

  grid.rows <- .combine.rows(input=input,rows=c(1),title="Plot 1",border=TRUE,
    grid.rows=grid.rows,grid.config=grid.config)

#####
## USE ALL THE ARGUMENTS IN THE GENERAL CLUSTERTEMPLATE FUNCTION ##
#####

cluster_template(methodname=methodname,methodfunction=methodfunction,
  methodhelp=methodhelp,data.arg=data.arg,other.arg=other.arg,
  methodseed=methodseed,grid.config=grid.config,grid.rows=grid.rows,
  new.frames=new.frames,superbiclust.comp=superbiclust.comp,
  bcdiag.comp=bcdiag.comp,data.transf=data.transf,
  data.dscr=data.dscr,data.bin=data.bin,methodshow=methodshow,
  methodsave=methodsav)
}
```

Analogous to the first tab, this part of the script starts by putting the `input` variable to `plotdiagTab`. Next the same three steps are repeated as for the clustering tab. There is only one difference and that is the addition of one new type of frame which can be created in the plots & diagnostics tab. This is the *manual button frame* which will also be explained in more detail down below. Basically a manual button can serve two purposes, it can be tied to a plot or diagnostics function which uses some arguments (and then create a graph) or it can lead to a new window entirely which can be created with the *new tool script*.

Finally at the end of the script, all the variables and created objects are used in the `cluster_template` function which will create the actual window.

This `cluster_template` call is the final line of the function `newmethod_WINDOW` we started creating in Section 4.1.1. It is now ready to be used by R Commander to be called upon as a window.

### **4.1.2 The Frame Scripts**

In this section, the several types of frames which can be used in the `newmethod_script` will be showcased. The idea is that these parts of the R-code (which are also in the Appendix) are copy-pasted into the `newmethod_script` and are adjusted as deemed necessary.

All the frame types have the `title` and `border` option in common. The results of these options can be seen in figure 48. Also note that for each frametype the information is saved in one object, namely `new.frames`. Just as the grid and row configuration earlier, new information will keep on getting added to this object, now with the help of the `.add.frame` function. Lastly, at the start of each frame script, a `type` variable will be set to determine the type of frame for this previous mentioned `.add.frame` function.

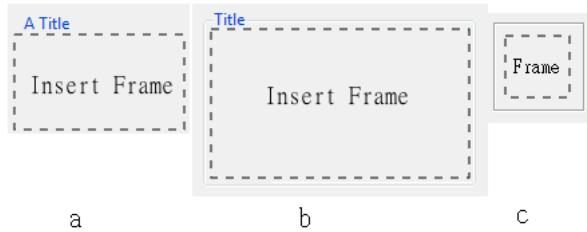


Figure 48: **a.** Title & No Border **b.** Title & Border **c.** No Title & Border

### Entry Fields

The first type of frame is the entry fields frame. It can be used for both numerical arguments and character arguments of your biclustering function. Multiple entries can be added in one frame which will be placed below each other.

```
#### ENTRY FIELDS FRAME ####

type <- "entryfields"

# Change variables accordingly:
frame.name <- "entryframe1"
argument.names <- c("Argument 1","Argument 2","Argument 3")
argument.types <- c("num","num","char")
arguments <- c("arg1","arg2","arg3")
initial.values <- c(1,2,"a")
title <- "A Title"
border <- FALSE
entry.width <- c("2","2","6")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type
                           ,frame.name=frame.name,argument.names=argument.names
                           ,arguments=arguments,initial.values=initial.values
                           ,title=title,border=border,entry.width=entry.width
                           ,argument.types=argument.types ,new.frames=new.frames)
```

Figure 49: Entry Fields: Code + Example

#### Entry Fields Variables:

- **frame.name:** The unique name of this frame. (Which is used in the grid matrix)
- **argument.names:** The argument names how they will appear in the window.
- **argument.types:** A vector defining if the argument is "num" or "char". This basically just means if there should be a '' around the value when filling it in in the biclustering function. (e.g. In Figure 49 the arguments would be filled in as ,arg1=1,arg2=2,arg3='a')
- **arguments:** The actual argument names, used for the biclustering function.
- **initial.values:** A vector containing the initial values in the entry fields.
- **title:** Optional title for the frame (" " means no title)
- **border:** Logical value determining the presence.
- **entry.width:** A vector containing the width of the entry fields (1 width = 1 number/character).

### Check Boxes

The second type of frame is the check boxes frame which is used for TRUE/FALSE arguments. Just like for entry fields, multiple check boxes can be added below each other.

```

##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "checkboxframe1"
argument.names <- c("Check 1","Check 2","Check 3")
arguments <- c("checkboxarg1","checkboxarg2","checkboxarg3")
initial.values <- c(0,1,1)
title <- "title"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type
    ,frame.name=frame.name,argument.names=argument.names
    ,arguments=arguments,initial.values=initial.values
    ,title=title,border=border,new.frames=new.frames)

```



Figure 50: *Check Boxes: Code + Example*

#### *Check Boxes Variables:*

- **frame.name:** The unique name of this frame. (Which is used in the grid matrix)
- **argument.names:** The argument names how they will appear in the window.
- **arguments:** The actual argument names, used for the biclustering function.
- **initial.values:** A vector containing the initial values in the entry fields. (0 for FALSE, 1 for TRUE)
- **title:** Optional title for the frame (" " means no title)
- **border:** Logical value determining the presence.

#### **Radio Buttons**

The next type is radio buttons, which is used for only one argument with a finite number of values.

```

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radioframe1"
argument.names <- c("Button 1","Button 2","Button 3")
arguments <- c("buttonarg")
argument.types <- "char"
argument.values <- c("b1","b2","b3")
initial.values <- "b3"
title <- "Button Options"
border <- TRUE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type
    ,frame.name=frame.name,argument.names=argument.names
    ,arguments=arguments,argument.values=argument.values
    ,initial.values=initial.values,title=title,border=border
    ,new.frames=new.frames,argument.types=argument.types)

```

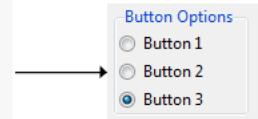


Figure 51: *Radio Buttons: Code + Example*

#### *Radio Buttons Variables:*

- **frame.name:** The unique name of this frame. (Which is used in the grid matrix)
- **argument.names:** The names of the buttons how they will appear in the window.
- **arguments:** The actual argument name, used for the biclustering function.
- **argument.types:** Just as for the entry fields, this will determine of the values are filled in with or without ". The two options are again "num" and "char", but in contrast with the entry fields it is now only one value and not a vector..

- **argument.values:** The actual values of the radio buttons that correspond to the values passed to biclustering function.
- **initial.values:** The initial value of the radio buttons. It will determine which button is selected on opening the window.
- **title:** Optional title for the frame (" " means no title)
- **border:** Logical value determining the presence.

### Value Sliders

The following type will create value sliders which can only be used for numerical values. Again multiple sliders can be placed under each other. The current value of the slider will always appear on top of it.

```
#### VALUE SLIDER FRAME ####

type <- "valuesliders"

# Change variables accordingly:
frame.name <- "sliderframe1"
argument.names <- c("Slider 1 ","Slider 2 ","Slider 3 ")
arguments <- c("sliderarg1","sliderarg2","sliderarg3")
initial.values <- c(1,5,10)
from <- c(1,1,1)
to <- c(5,50,500)
by <- c(1,10,50)
length <- c(50,100,150)
title <- "Title"
border <- TRUE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,
  title=title,border=border,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,
  initial.values=initial.values,from=from,to=to,by=by,
  length=length,new.frames=new.frames)
```

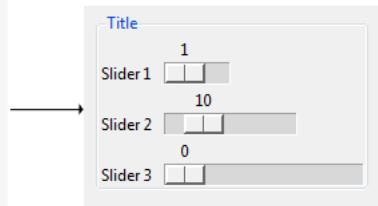


Figure 52: *Value Slider: Code + Example*

#### *Value Sliders Variables:*

- **frame.name:** The unique name of this frame. (Which is used in the grid matrix)
- **argument.names:** The argument names how they will appear in the window.
- **arguments:** The actual argument names, used for the biclustering function.
- **initial.values:** Vector of initial values of the sliders.
- **from:** Vector of starting points of the sliders.
- **to:** Vector of ending points of the sliders.
- **by:** Vector with the values determining how one movement of the sliders will change the current value.
- **length:** Vector containing the lengths of the sliders.
- **title:** Optional title for the frame (" " means no title)
- **border:** Logical value determining the presence.

### Spin Boxes

This type will create spin boxes which are again solely used for numerical values. Just as for sliders, multiple spin boxes can be placed below each other.

```

##### SPIN BOX FRAME #####
type <- "spinboxes"

# Change variables accordingly:
frame.name <- "spinboxframe1"
argument.names <- c("Spin Box 1: ","Spin Box 2: ","Spin Box 3: ")
arguments <- c("spinarg1","spingarg2","spingarg3")
initial.values <- c(5,10,20)
from <- c(1,5,10)
to <- c(10,20,30)
by <- c(1,1,1)
entry.width <- "2"
title <- "Spin Box !"
border <- TRUE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,
                           frame.name=frame.name,argument.names=argument.names,
                           arguments=arguments,initial.values=initial.values,
                           from=from,to=to,by=by,entry.width=entry.width,
                           title=title,border=border,new.frames=new.frames)

```

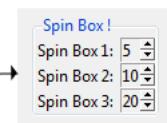


Figure 53: *Spin Boxes: Code + Example*

#### *Spin Boxes Variables:*

- **frame.name:** The unique name of this frame. (Which is used in the grid matrix)
- **argument.names:** The argument names how they will appear in the window.
- **arguments:** The actual argument names, used for the biclustering function.
- **initial.values:** Vector of initial values of the spin boxes.
- **from:** Vector of starting points of the spin boxes.
- **to:** Vector of ending points of the spin boxes.
- **by:** Vector with the values determining how much one click will change the current value.
- **entry.width:** Width of all the spinboxes (one value which applies to all of them)
- **title:** Optional title for the frame (" " means no title)
- **border:** Logical value determining the presence.

#### **Manual Buttons**

The last type of frame which can be utilized, is making manual buttons which will *only* work in the plot & diagnostics tab. As already explained earlier, there are two primary uses for these buttons. The first use is to simple execute a plot or diagnostic function, based on the arguments of other frames in the window. The second application is to tie the button to another window function (created with `newtool_script`) to open up more options.

```

##### MANUAL BUTTONS FRAME #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "buttonframe1"
button.name <- "Button 1"
button.function <- "buttonfunction"
button.data <- "d"
button.biclus <- "biclus"
button.width <- "12"
button.data.transf <- "matrix"

arg.frames <- c("frame1", "frame2")

save <- TRUE
show <- TRUE
button.otherarg <- ""

# Do not change this line:
new.frames <- .add.frame(input=input, frame.name=frame.name,
                           type=type, button.name=button.name,
                           button.function=button.function, button.data=button.data,
                           button.biclus=button.biclus, button.otherarg=button.otherarg,
                           button.width=button.width, button.data.transf=button.data.transf,
                           arg.frames=arg.frames, save=save, show=show, new.frames=new.frames)

```

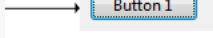


Figure 54: Manual Button: Code + Example

#### Manual Button Variables:

- **frame.name:** The unique name of this frame. (Which is used in the grid matrix)
- **button.name:** The text which will appear on the button. No special characters are allowed and if the result of the button is saved, it will be in an object with this name without the spaces.
- **button.function:** A string of the function which should be tied to this button. This could either be a plot, diagnostic or simple summary. Another useful practice is to actually make an entire new function for this manual button. This new function could then for example contain a series of diagnostic functions which would then be carried out all at the same time when clicking on this button.
- **button.data:** The name of the data argument the button function. The data which is loaded in R Commander will then be pasted after this argument. (Simply put "" when this is not necessary)
- **button.biclus:** The name of the biclustering result argument in the button function. Here the saved result after using the *Show Results* button will be pasted.
- **button.width:** Character containing the width of the button. (Default = "12")
- **button.data.transf:** Character determining if the data for **button.data** should be transformed. (Values: "matrix" (default), "ExprSet")
- **button.otherarg:** Just like for the biclustering function (**other.arg**), this is the variable in which one can add arguments to the function which should not be controlled by the user (e.g. ",type='biclus'"). Again, do not forget to add a comma in the beginning.
- **arg.frames:** A vector containing the names of those frames from which this button function should pull its arguments.
- **save:** Logical value determining if the result of the button function should be saved. For example for a plotting function this is mostly likely not necessary, however for a diagnostic result it is. The difference between a **TRUE** and **FALSE** option is shown in figure 55.
- **show:** Logical value determining if the button function should be shown in R Commander. It is good practice to do this for the plotting and diagnostics functions however if is a function to create a new window, it is probably not necessary to show it.

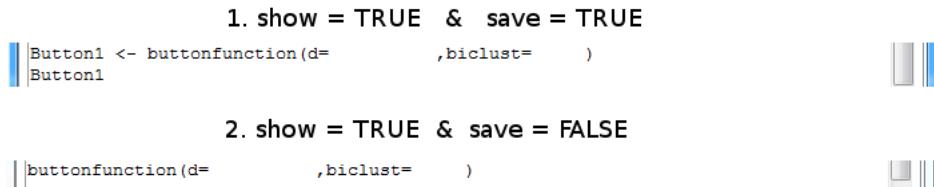


Figure 55: *Manual Buttons - save option*

#### 4.1.3 A quick example - Plaid

The entire script to construct the *Plaid Window* can be found in the Appendix. In this small section, some parts will be highlighted and explained in their context.

```
#####
## GENERAL INFORMATION ABOUT THE NEW METHOD/WINDOW ##
#####

methodname <- "Plaid"
methodfunction <- "biclust"
data.arg <- "x"
other.arg <- ",method=BCPlaid()"
methodhelp <- "BCPlaid"
methodseed <- TRUE
data.discr <- FALSE
data.bin <- FALSE
bcdiag.comp <- TRUE
superbiclust.comp <- TRUE

# Biclust only (Not for public use)
extrabiclustplot <- TRUE
```

First of all, the general information is filled in for the plaid method as shown in the script above. Please note that the `extrabiclustplot` is a biclust-only variable and will not be elaborated on.

Next, in Figure 56 we can see the code which makes the two frames in the top row.

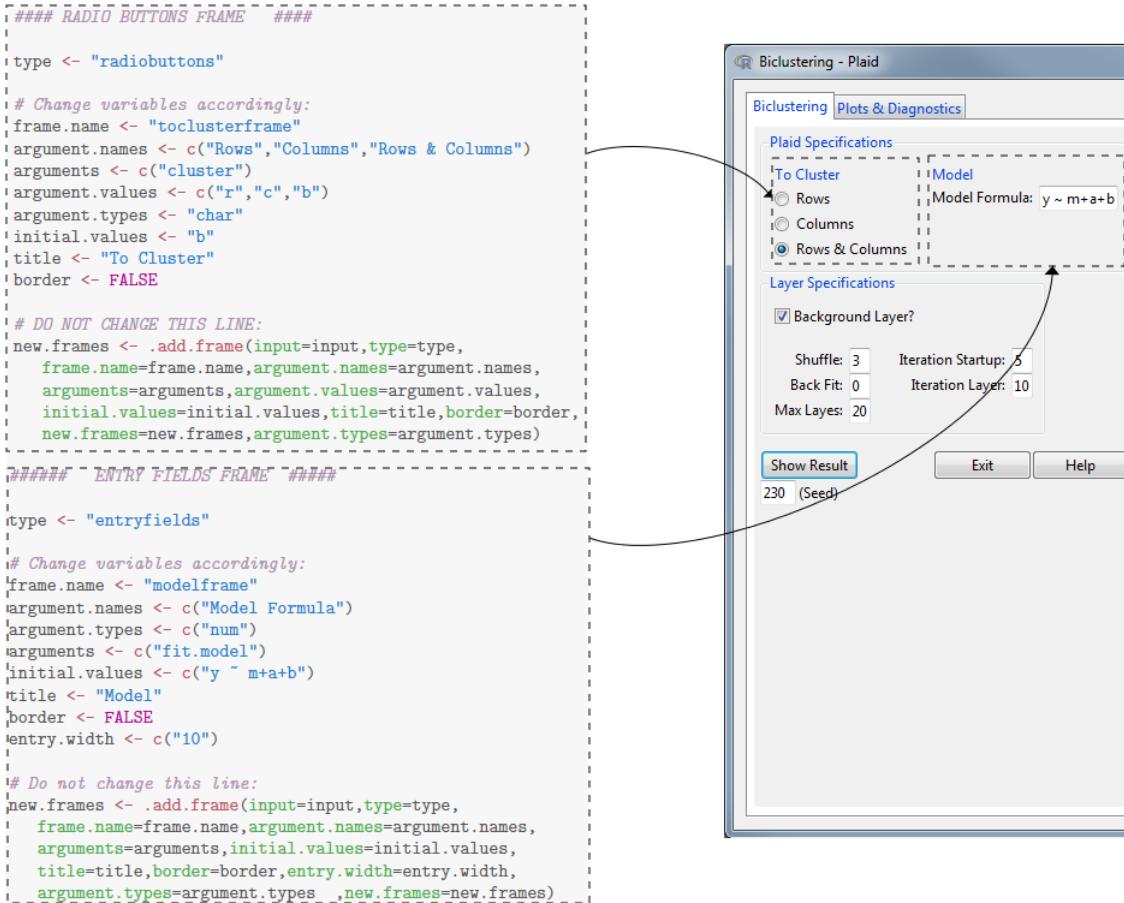


Figure 56: Building the Plaid Window - ClusterTab

After adding the frame scripts, the next step is the grid configuring and the row combining of the cluster tab. In this extract of the script, one can see the two frames from Figure 56 being placed in the top row of the matrix after which the first row is made into a box with border and *Plaid Specifications* title.

```

### 2. CONFIGURING THE GRID ####
grid.config <- .grid.matrix(input=input, c("toclusterframe", "modelframe",
  "backgroundcheckframe", NA, "backgroundentryframe1", "backgroundentryframe2"),
  byrow=TRUE, nrow=3, ncol=2, grid.config=grid.config)

### 3. COMBINING THE ROWS ####
grid.rows <- .combine.rows(input=input, rows=c(1), title="Plaid Specifications",
  border=TRUE, grid.rows=grid.rows, grid.config=grid.config)
grid.rows <- .combine.rows(input=input, rows=c(2,3), title="Layer Specifications",
  border=TRUE, grid.rows=grid.rows, grid.config=grid.config)

```

Finally, an example of the creation of manual buttons is shown in Figure 57. Note that the line of code containing the `.add.frame` has been omitted here for better clarity of the code. The button here is tied to the function `"drawHeatmap"` and draws its arguments from `"heatplotcheckframe"` and `"heatplotentryframe"` which are both defined in `arg.frames`.

Naturally the creations of all the other frames, together with the configuring of the grid and combining of the rows follows after.

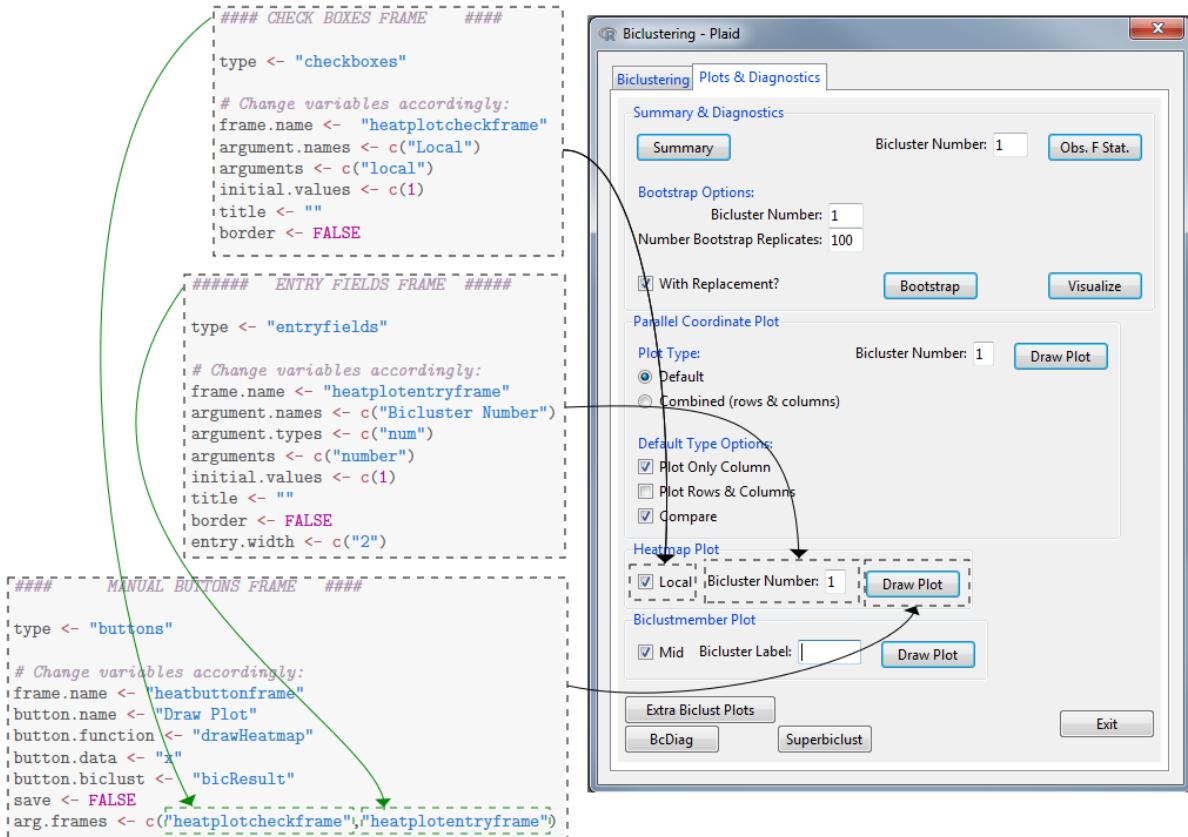


Figure 57: Building the Plaid Window - PlotDiagTab

## 4.2 Implementing a New Tool

The second template script (which is also available in the Appendix) is `newtool_script.R`. With the help of this script one can make a new window which can for example be tied to a manual button in the second tab of a clustering window. Another possibility is to make another general diagnostics window compatible with several other biclustering packages. This is for example already done with the `BcDiag` and `superbiclust` package for which the button appears in the second tab of the compatible methods. Also just as for these two packages, a compatibility variable could then be added in the begin of the `newmethod_script` to decide if the button for your new general diagnostics package should appear for a specific method.

### 4.2.1 New Tool Script

```
newtool_WINDOW <- function(methodname){

  new.frames <- .initialize.new.frames()
  grid.config <- .initialize.grid.config()
  grid.rows <- .initialize.grid.rows()

  #####
  ## GENERAL INFORMATION ABOUT THE NEW TOOL    ##
  #####

  toolname <- "A new tool"
  toolhelp <- "helppage"

  # Do not change this line:
  input <- "plotdiagTab"

  #### ADDING FRAMES ####
}
```

```

# Analogous to plotdiag tab.

### CONFIGURING GRID ####
grid.config <- .grid.matrix(input=input,c(),nrow=1,ncol=2,
                           byrow=TRUE,grid.config=grid.config)

### COMBINING ROWS #####
grid.rows <- .combine.rows(input=input,rows=c(),title="Plot 1",
                           border=TRUE,grid.rows=grid.rows,grid.config=grid.config)

#####
## USE ALL THE ARGUMENTS IN THE GENERAL NEW TOOL FUNCTION ##
#####

newtool_template(toolname=toolname,methodname=methodname,
                 toolhelp=toolhelp,grid.config=grid.config,
                 grid.rows=grid.rows,new.frames=new.frames)
}

```

Just as for `newmethod_script` the adjusting of the template starts with changing `newtool_WINDOW` to your own desired windowfunction name. Next at the start of the script again the necessary objects are initialized followed by some variables containing general information about the tool:

- **toolname:** The name of the tool appearing at the top of the window.
- **toolhelp:** The helppage the help button should be linked with. (`help(toolhelp)`)

After filling in these couple of variables, making this window is *exactly* the same as creating the second tab in `newmethod_script`. This means it is also possible to create manual buttons in this window. Note that even the `input` variable is again set to `plotdiagTab`. The only difference can be found in the last line where now the template function has changed to `newtool_template`.

Finally the attention should also be pointed to the fact that by default the `newtool_WINDOW` function has `methodname` as an argument. This means if this function is used inside a `newmethod_script`, the new tool window can behave differently depending on the method it is being called by. This will become clear in the example shortly.

#### 4.2.2 A quick example - BcDiag

We will now go through a couple of parts of the script responsible for the BcDiag window. The full script can once again be found in the Appendix.

```

bcdiag_WINDOW <- function(methodname){

  new.frames <- .initialize.new.frames()
  grid.config <- .initialize.grid.config()
  grid.rows <- .initialize.grid.rows()

  # Some extra code to determine the input type: "biclust", "fabia", "isa2"
  biclust.names <- c("Bimax","CC","Plaid","Questmotif","Spectral",
                    "XMotifs","IBBIG")
  fabia.names <- c("Fabia Laplace Prior","Fabia Post-Projection",
                  "Fabia Sparseness Projection","Fabia SPARSE")
  isa.names <- c("ISA")

  if(methodname %in% biclust.names){
    extra.arg <- ",mname='biclust'"
  }
  if(methodname %in% fabia.names){
    extra.arg <- ",mname='fabia'"
  }
  if(methodname %in% isa.names){

```

```

        extra.arg <- "mname='isa2'"
    }

#####
## GENERAL INFORMATION ABOUT THE NEW TOOL      ##
#####

toolname <- "BCDIAG"
toolhelp <- "BcDiag-package"

}#ignore

```

In the code above the variables containing the general information are filled in as expected, however just above some extra code has been added. These extra lines of code are simply determining what string should be saved in `extra.arg` based on the `methodname` given to `bcdiag_WINDOW`. This `extra.arg` variable will then be used later in the creation of a manual button as we will see now in Figure 58. Note that just as for the plaid example the `.add.frame` line has been omitted to maintain clarity.

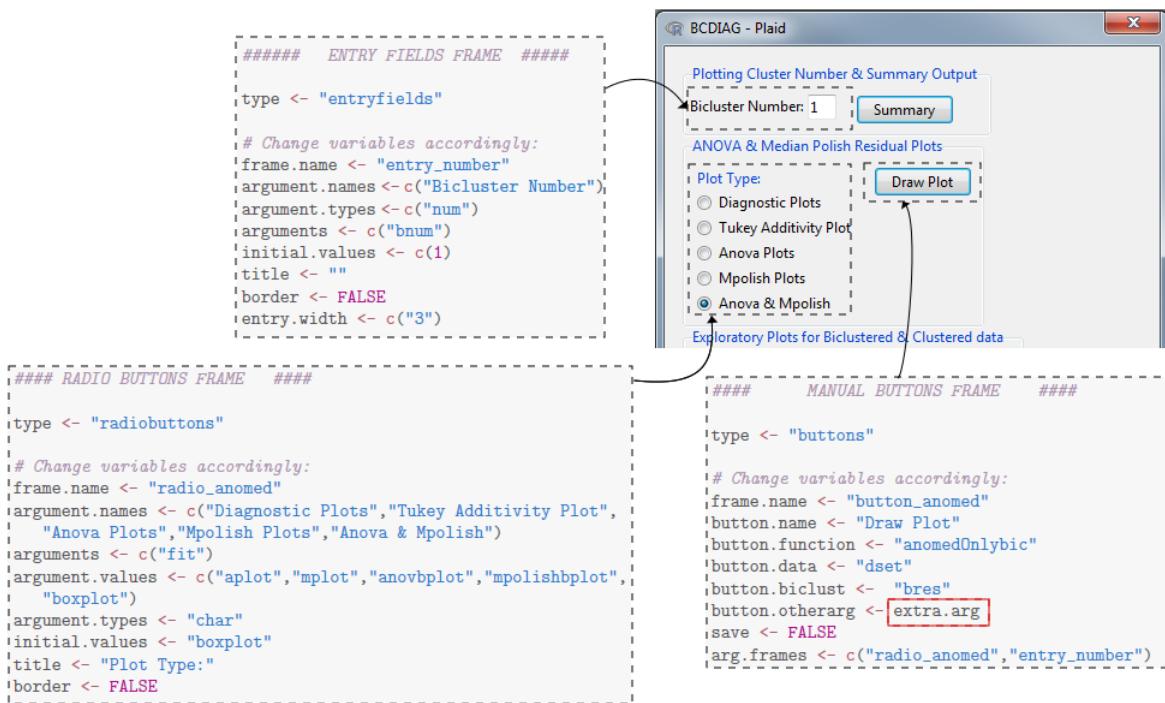


Figure 58: Building the *BcDiag* Window

Apart from the usual framebuilding, one can see that this earlier mentioned `extra.arg` is now used for the `button.otherarg` argument in the manual button setup.

This is only one of many ways in which you can tailor the tool window to a specific biclustering method. A more complicated example would be the implementation of the `superbiclust` window in which `methodname` is also transformed to `method_result` (`methodname` without spaces and ‘-’s) in order to make some distinctions. Further in this script a different `grid.config` and `grid.rows` will be created depending on `methodname`. Since apart from these additions the script is still very much the same as the others, it will not be elaborated on. It can however still be found in the Appendix.

### 4.3 How to start?

The easiest way to start making your own dialog, is to copy the `newmethod_script.R` (or `newtool_script.R`) to your own file. Next, simply change the variables so they fit your new application and add new frames by copying and adapting the default ones from `frames_scripts.R` inside your new file. Note that all of the above mentioned R files are available in the documentation folder of `RcmdrPlugin.BioclustGUI`. Finally, to test your new window, simply load in the `BioclustGUI` in R and run the `newmethod_WINDOW` function you’ve created.

## 5 Extensions - Shiny App & REST

The main functionality of the **BiclustGUI** was also recreated in the form of a Shiny Application. The **shiny** R package (Chang et al., 2015), developed by RStudio, allows the creation of web-based applications from R-code. Shiny Apps are very accessible since they do not require any installation on the user side. They can be hosted on a private website, Shiny Cloud and also Amazon Cloud. It is also possible to distribute them in a stand-alone version. The Shiny Apps are often highly interactive due to the use of reactive functions, allowing the App to immediately adapt to any input of the user. The **shiny** R package, provides a large amount of basic widgets, i.e. web elements users can interact with, of which some are built using the Bootstrap Project. Note that compared to the **BiclustGUI** in R Commander, the user will not see the generated R on the fly.

The **biclustGUI** Shiny App can be found at [ewouddetroyer.shinyapps.io/shiny-biclust](http://ewouddetroyer.shinyapps.io/shiny-biclust). It is also available as a stand-alone version to run locally on your pc at <http://www.xxxxxxx>. Simply extract the zip-file and double click the **LAUNCH.vbs** file (no installation, e.g. R, required!).



Figure 59: Shiny Example (iBBiG) - Biclusters Heatmap

The template scripts for biclustering windows were also the foundations for the **REST** package (De Troyer, 2015). With this package, it is possible to create plug-ins for R Commander without expert knowledge, providing a tool to create envelope GUI packages similar to **BiclustGUI**.

The **REST** package (**RmdrPlugin Easy Script Templates**) contains a generalization of the biclustering window scripts. These scripts, previously tailored towards a window structure for the biclustering dialogs, are now more general and flexible (i.e. allowing more tabs, more buttons, etc.).

The **REST** package allows a fast and easy creation of a R Commander plug-in without the **tcltk** syntax, can be used to create the windows for a new applications, and is freely available on CRAN with `install.packages("REST")` (Dependencies: **Rcmdr**).

The **REST** package also contains a vignette similar to Section 4 of this vignette. The guide is more general in its construction of a GUI window, but also contains some extra explanation and specializations.

## References

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## 6 Appendix

### 6.1 Introduction

<table border="1"> <tr><td>1.0</td><td>1.0</td><td>1.0</td><td>1.0</td></tr> <tr><td>1.0</td><td>1.0</td><td>1.0</td><td>1.0</td></tr> <tr><td>1.0</td><td>1.0</td><td>1.0</td><td>1.0</td></tr> <tr><td>1.0</td><td>1.0</td><td>1.0</td><td>1.0</td></tr> </table>	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	<table border="1"> <tr><td>1.0</td><td>1.0</td><td>1.0</td><td>0.0</td></tr> <tr><td>2.0</td><td>2.0</td><td>2.0</td><td>2.0</td></tr> <tr><td>3.0</td><td>3.0</td><td>3.0</td><td>3.0</td></tr> <tr><td>4.0</td><td>4.0</td><td>4.0</td><td>4.0</td></tr> </table>	1.0	1.0	1.0	0.0	2.0	2.0	2.0	2.0	3.0	3.0	3.0	3.0	4.0	4.0	4.0	4.0	<table border="1"> <tr><td>1.0</td><td>2.0</td><td>3.0</td><td>4.0</td></tr> <tr><td>1.0</td><td>2.0</td><td>3.0</td><td>4.0</td></tr> <tr><td>1.0</td><td>2.0</td><td>3.0</td><td>4.0</td></tr> <tr><td>1.0</td><td>2.0</td><td>3.0</td><td>4.0</td></tr> </table>	1.0	2.0	3.0	4.0	1.0	2.0	3.0	4.0	1.0	2.0	3.0	4.0	1.0	2.0	3.0	4.0	<table border="1"> <tr><td>1.0</td><td>2.0</td><td>5.0</td><td>0.0</td></tr> <tr><td>2.0</td><td>3.0</td><td>6.0</td><td>1.0</td></tr> <tr><td>4.0</td><td>5.0</td><td>8.0</td><td>3.0</td></tr> <tr><td>5.0</td><td>6.0</td><td>9.0</td><td>4.0</td></tr> </table>	1.0	2.0	5.0	0.0	2.0	3.0	6.0	1.0	4.0	5.0	8.0	3.0	5.0	6.0	9.0	4.0	<table border="1"> <tr><td>1.0</td><td>2.0</td><td>0.5</td><td>1.5</td></tr> <tr><td>2.0</td><td>4.0</td><td>1.0</td><td>3.0</td></tr> <tr><td>4.0</td><td>8.0</td><td>2.0</td><td>6.0</td></tr> <tr><td>3.0</td><td>6.0</td><td>1.5</td><td>4.5</td></tr> </table>	1.0	2.0	0.5	1.5	2.0	4.0	1.0	3.0	4.0	8.0	2.0	6.0	3.0	6.0	1.5	4.5
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Figure 60: Several Types of Biclusters

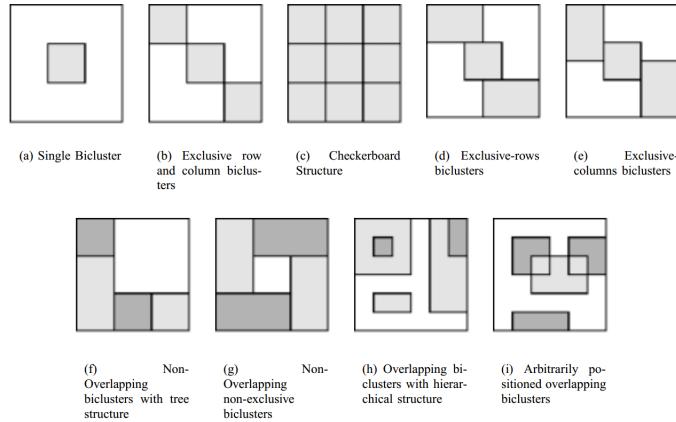


Figure 61: Underlying Bicluster Structures

## 6.2 The BioclustGUI R Package

### 6.2.1 Installing and Loading - Installing Script

```
## PACKAGES AVAILABLE ON CRAN ##
install.packages("bioclust")
install.packages("BcDiag")
install.packages("superbioclust")
install.packages("Rcmdr")
install.packages("isa2")

install.packages("gplots") # Extra package

## PACKAGES AVAILABLE ON BIOCONDUCTOR ##
source("http://bioconductor.org/biocLite.R")
biocLite("iBBiG")
biocLite("fabia")
biocLite("rqubic")
biocLite("BicARE")
```

```

## Bioclust GUI - Development Version ##
install.packages("RcmdrPlugin.BioclustGUI",
repos="http://R-Forge.R-project.org")

## Bioclust GUI - Release Version ##
install.packages("RcmdrPlugin.BioclustGUI")

```

### 6.2.2 Extra Utilities

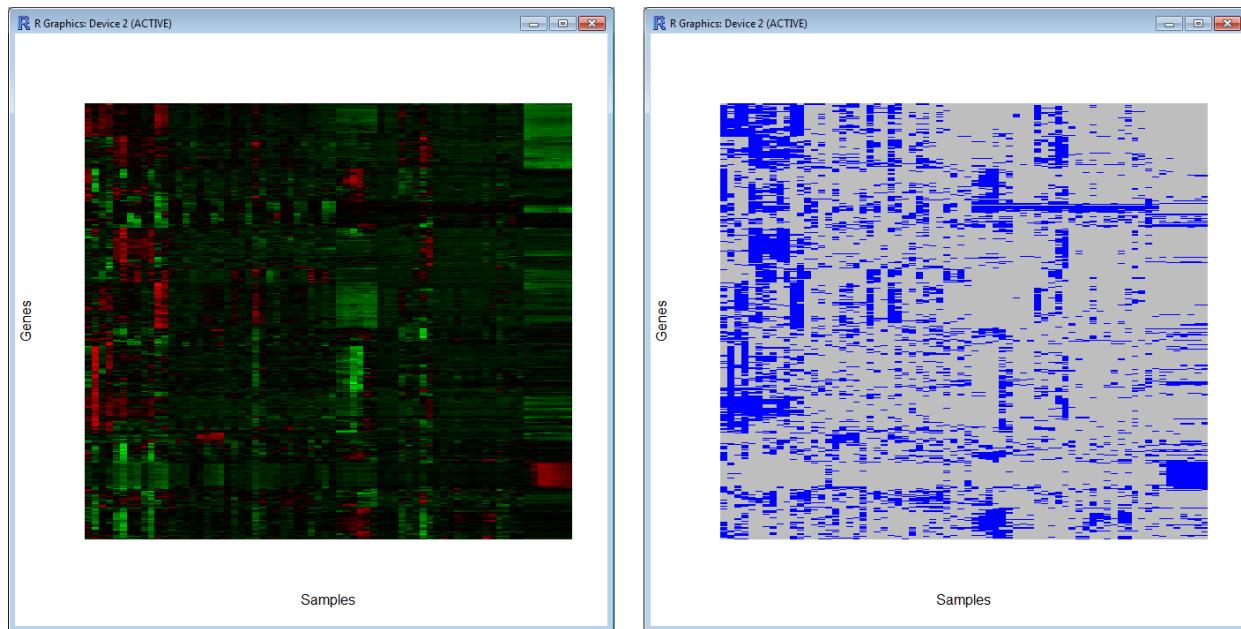


Figure 62: Data Heatmap - Normal & Binary

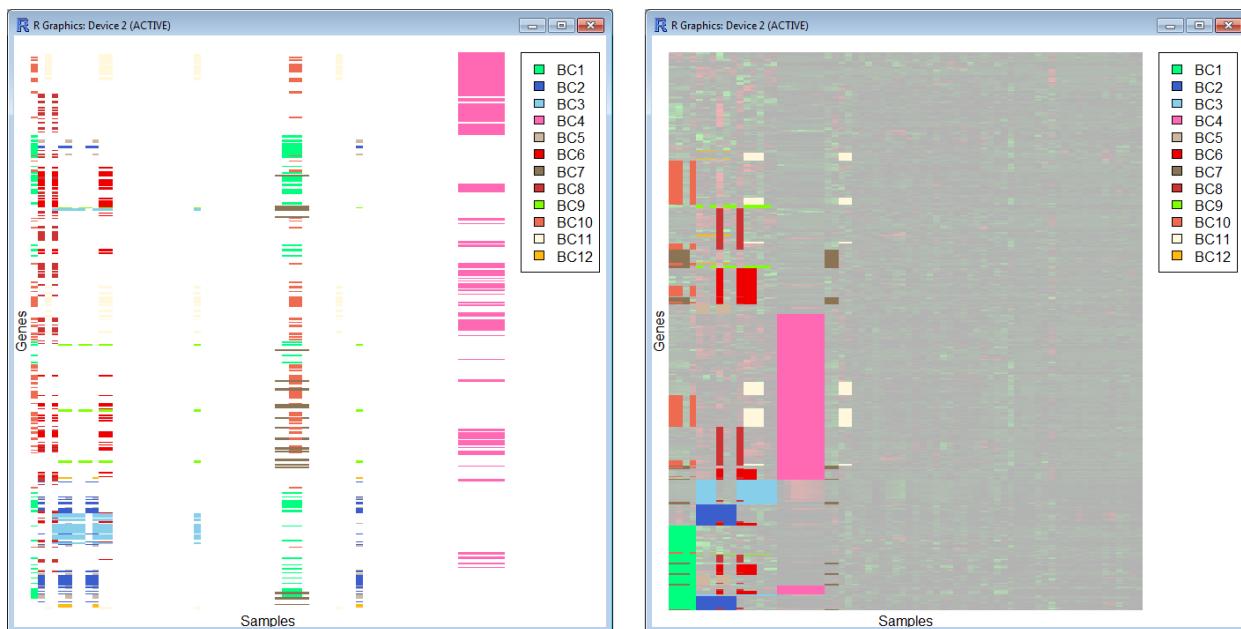


Figure 63: Result Heatmap - Default & Reordered with Background

### 6.2.3 biclust-package

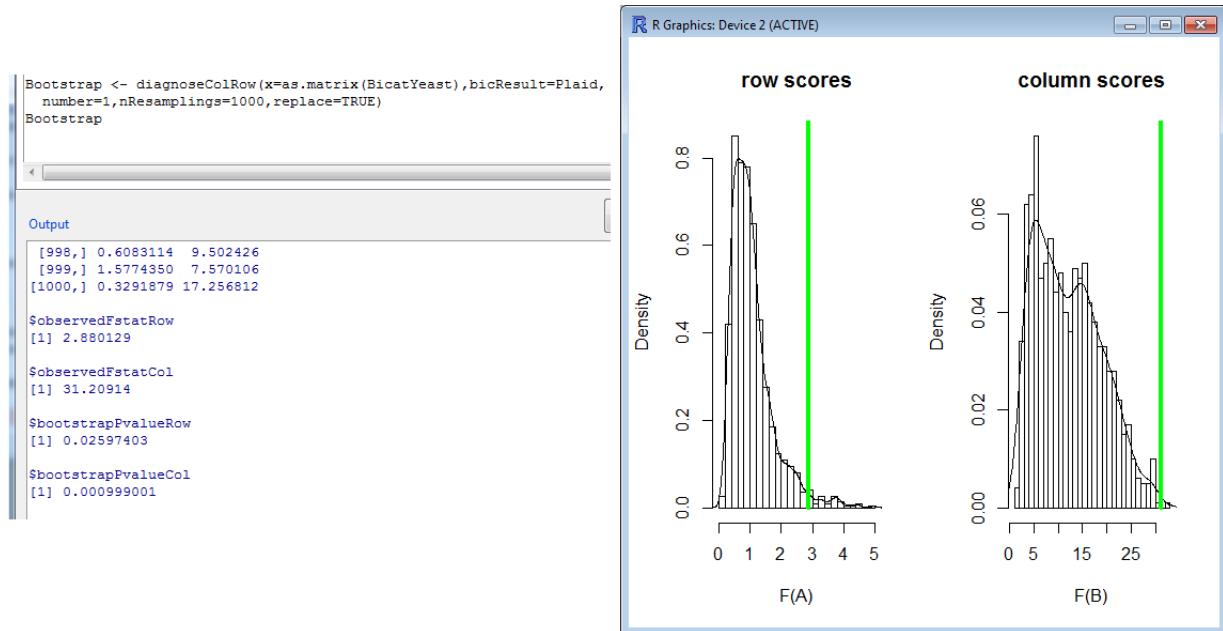


Figure 64: An example of bootstrap output & Histograms

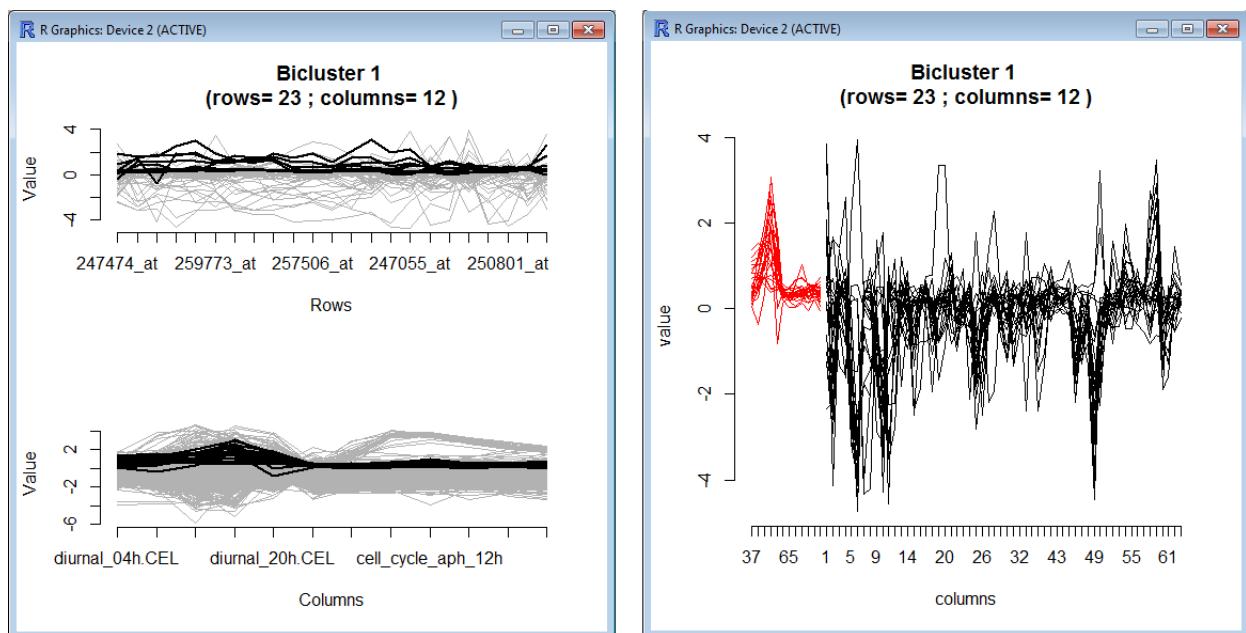


Figure 65: An example of Parallel Coordinates Plot - Default Type (row & column + Compare) & Combined Type

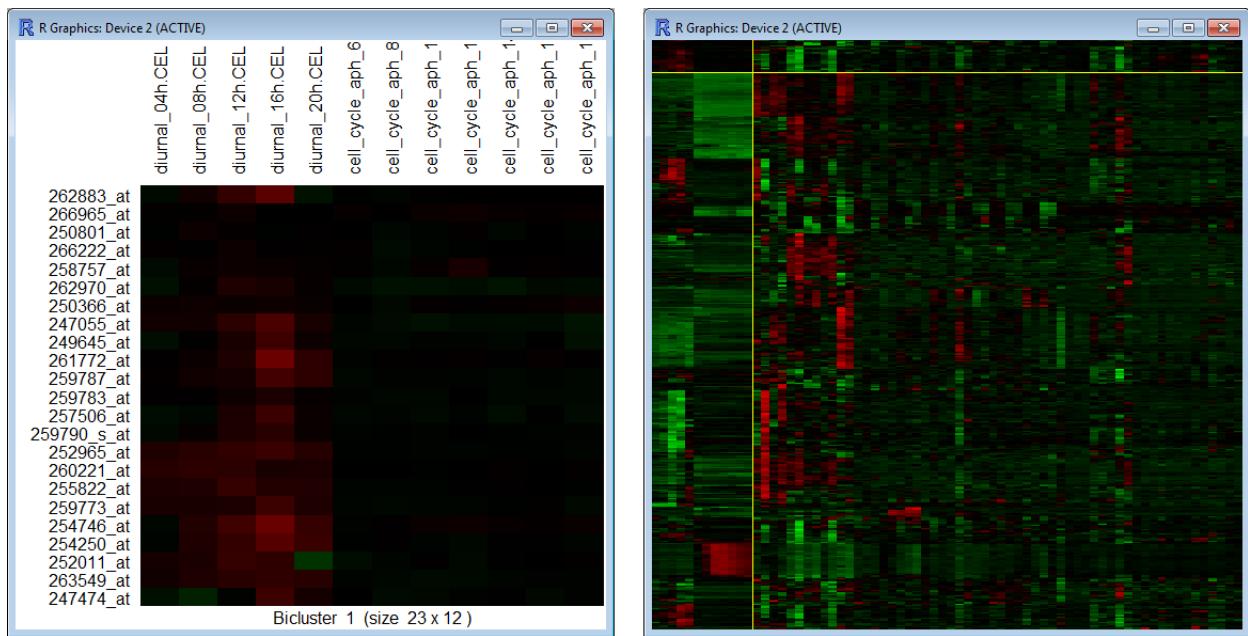


Figure 66: An example of the Heatmap - Local & Full Matrix

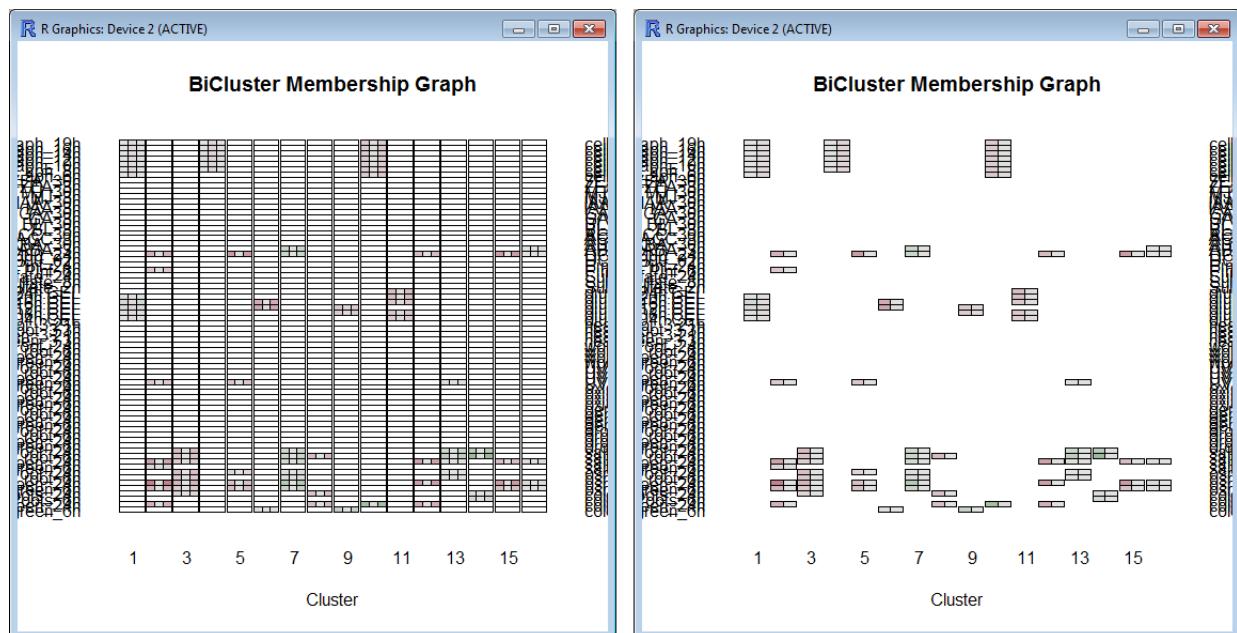


Figure 67: An example of BiclustMember Plot - Mid Checked & Mid Unchecked

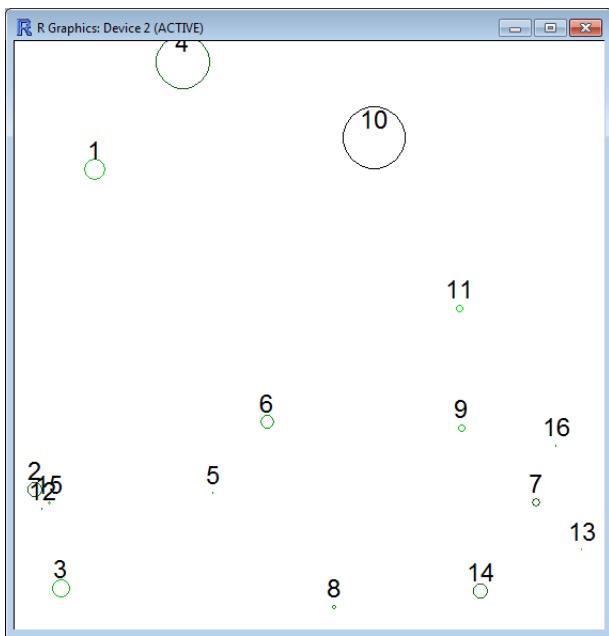


Figure 68: An example of Biclust Bubble Plot with Mean Projection

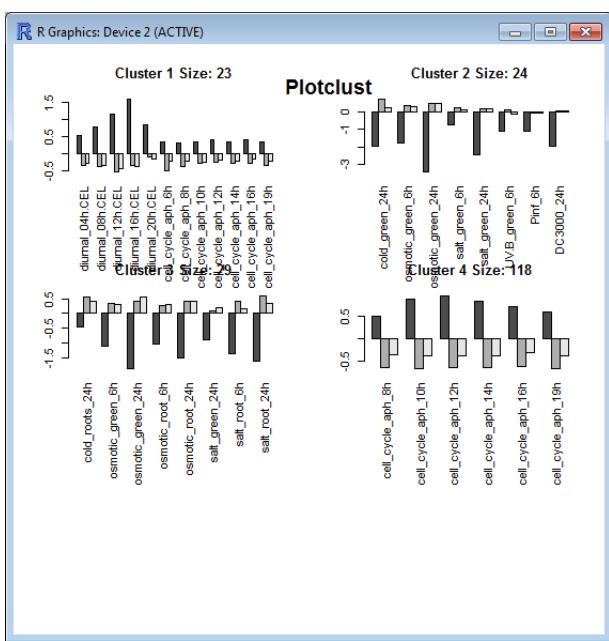


Figure 69: An example of the Barplots

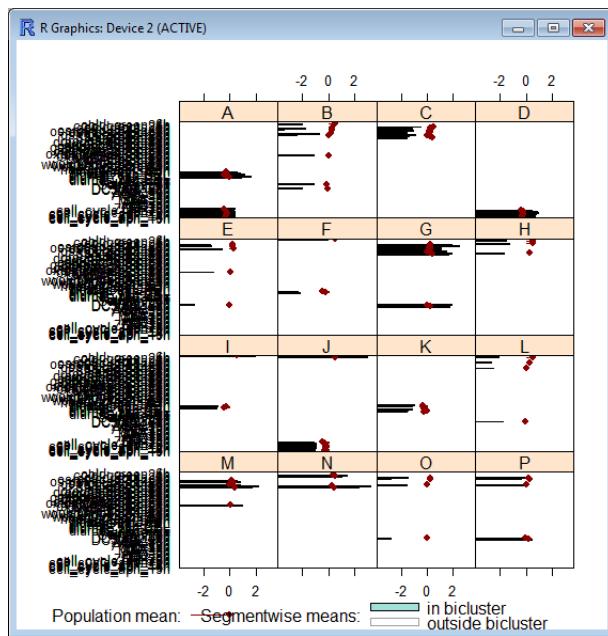


Figure 70: An example of Bicluster Barchart

#### 6.2.4 fabia-package

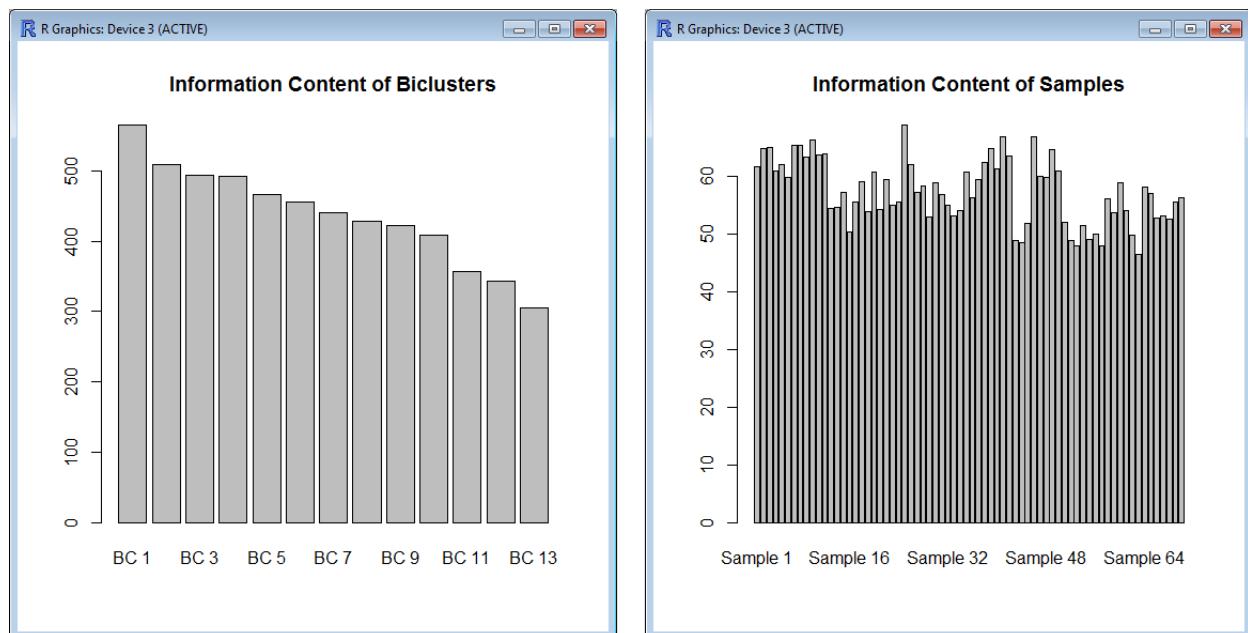


Figure 71: Examples of Information Content Histogram of biclusters and samples

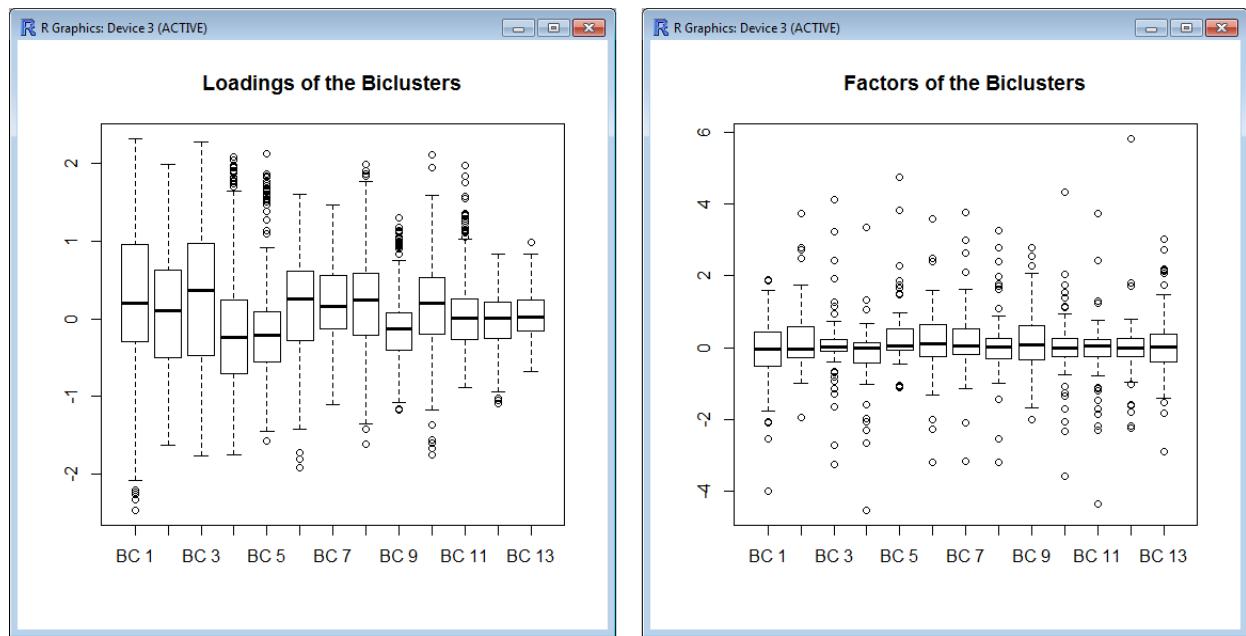


Figure 72: Examples of boxplots of Loadings & Factors

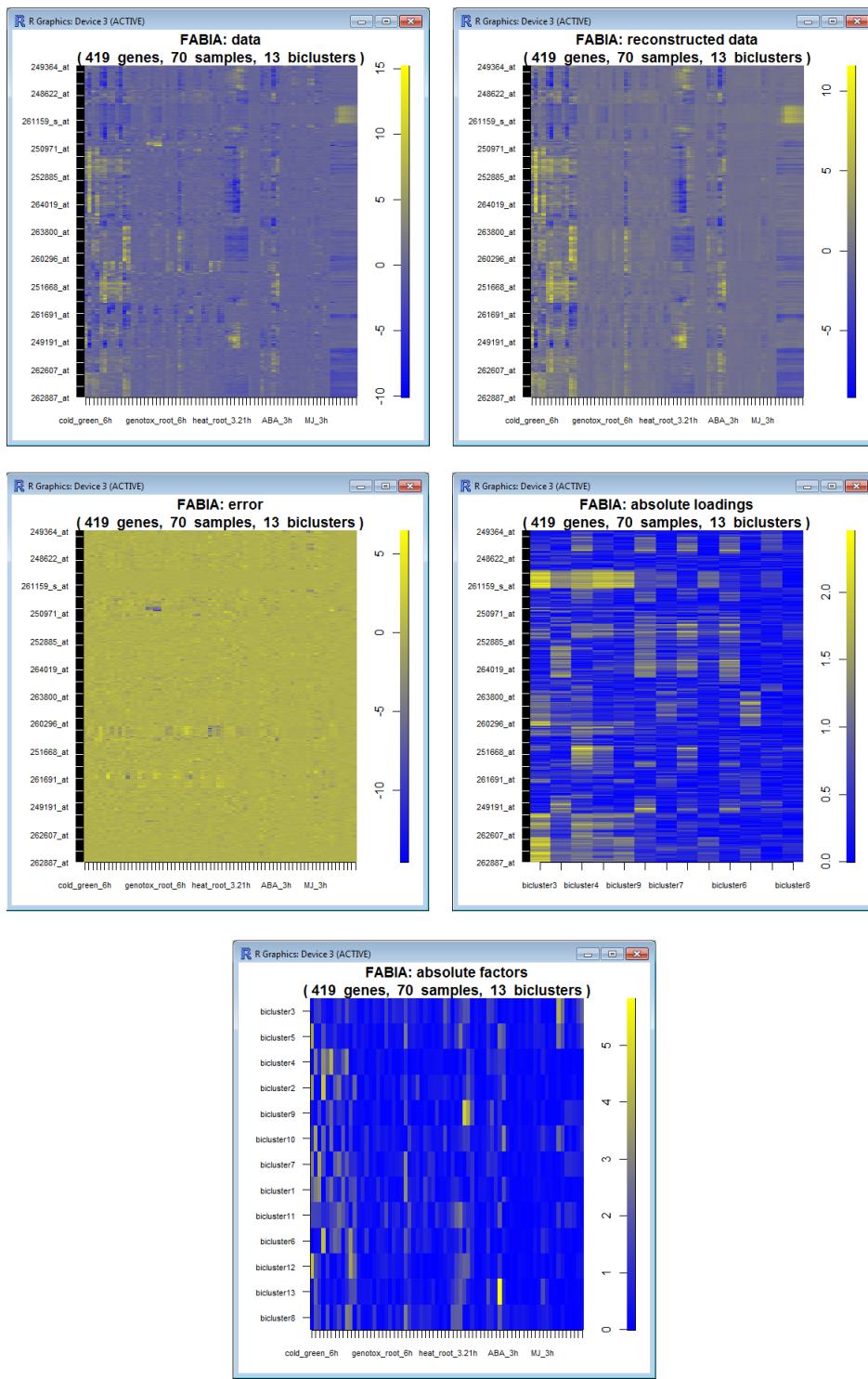


Figure 73: Examples Extract Plots

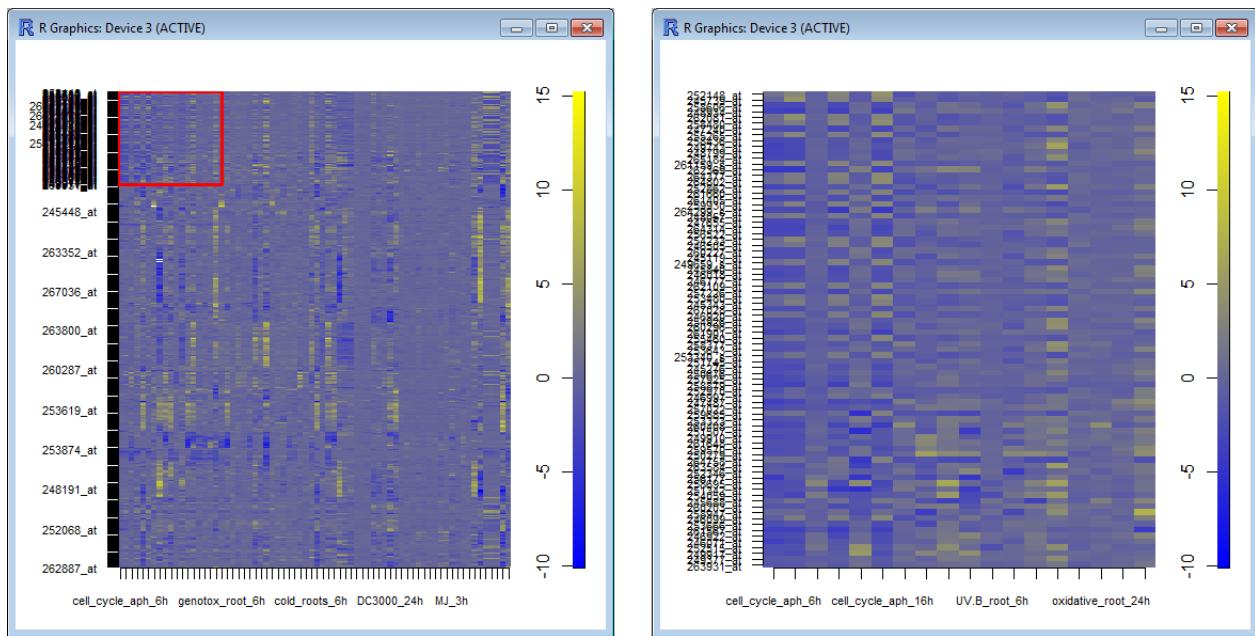


Figure 74: Example of Bicluster Plot - Full & Only Bicluster

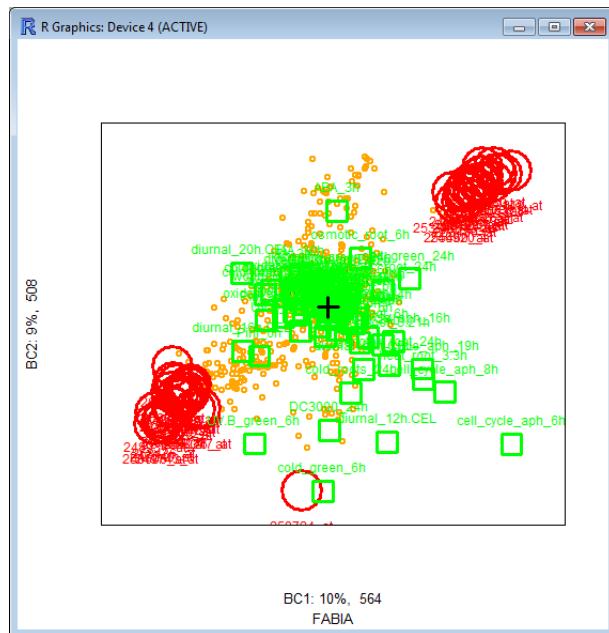


Figure 75: Example of BiPlot

### 6.2.5 isa2-package

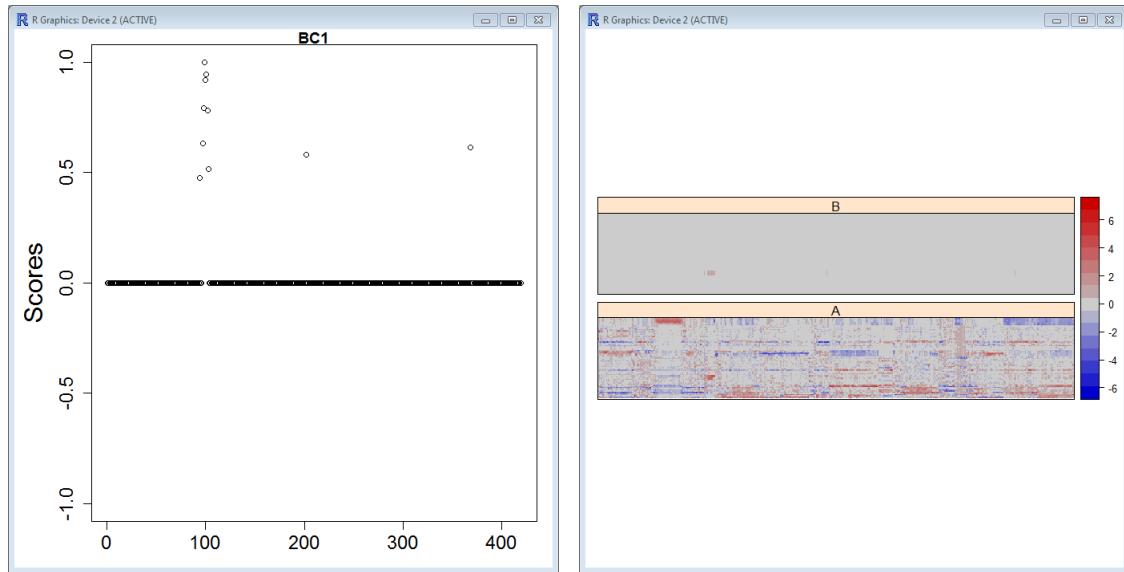


Figure 76: An example of score & module plot

### 6.2.6 iBBiG-package

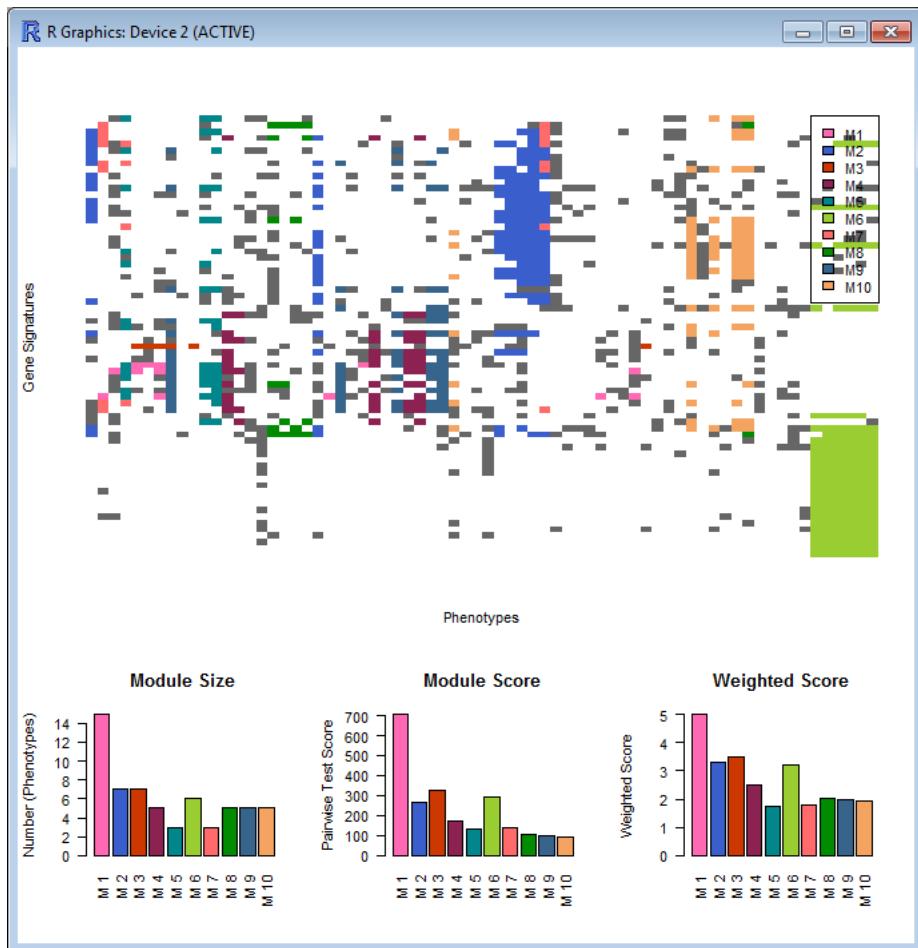


Figure 77: An example of the general iBBiG plot

### 6.2.7 BicARE-package

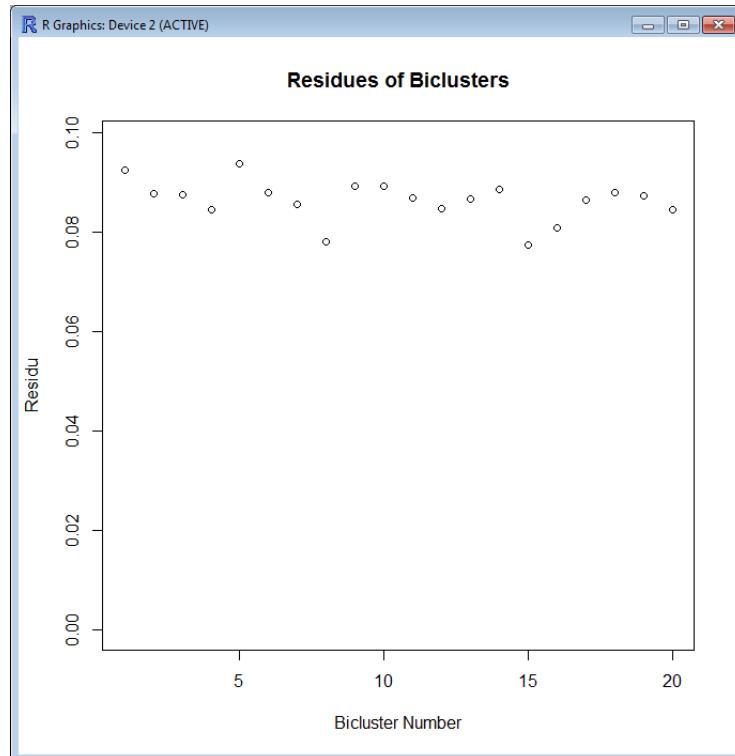


Figure 78: Example of Residue Plot

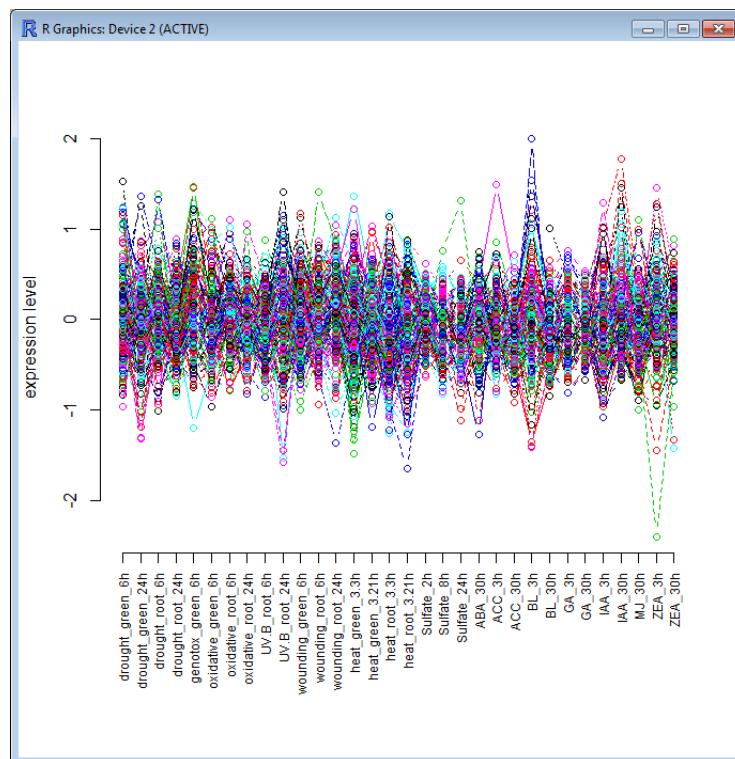


Figure 79: Example of Extract Bicluster Plot

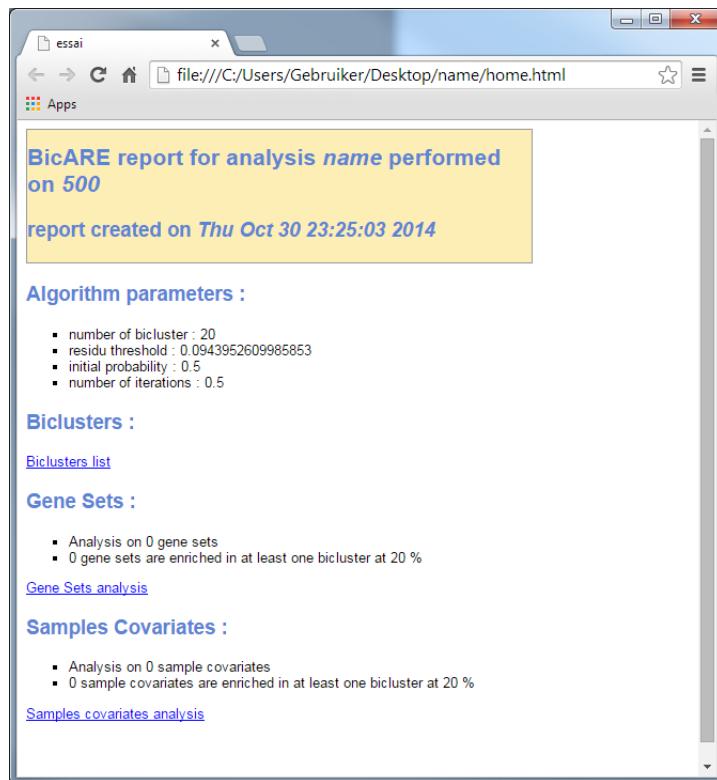


Figure 80: Example of the homepage of 'Make Report'

### 6.2.8 BcDiag-package

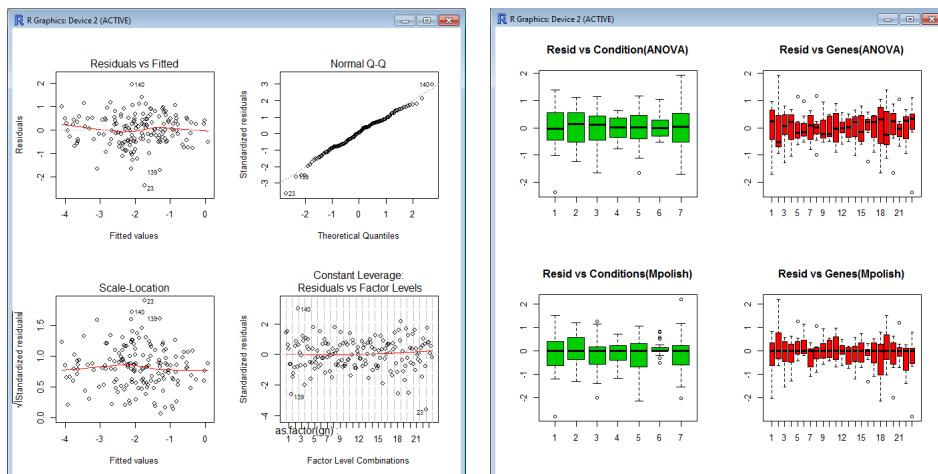


Figure 81: ANOVA & Residual Plots: Diagnostic Plots and ANOVA & Mpolish

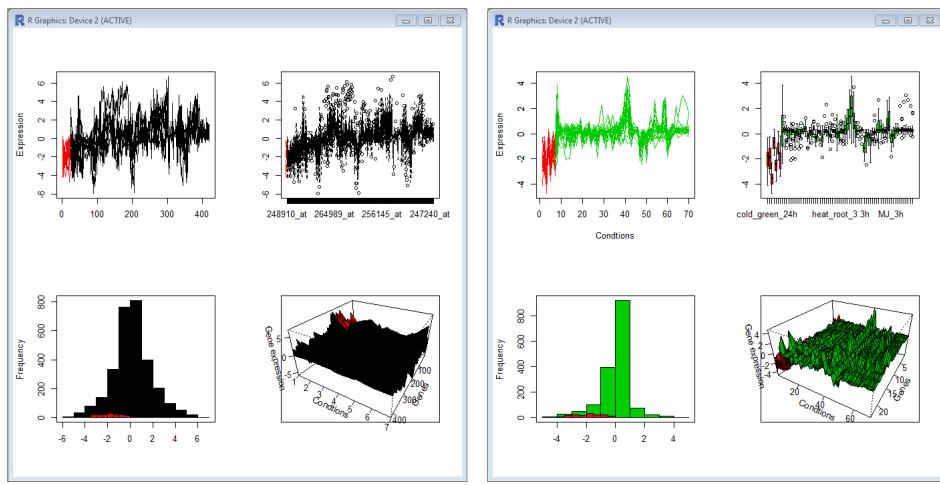


Figure 82: *Profile Plots: Example of all types for gene & condition dimension*

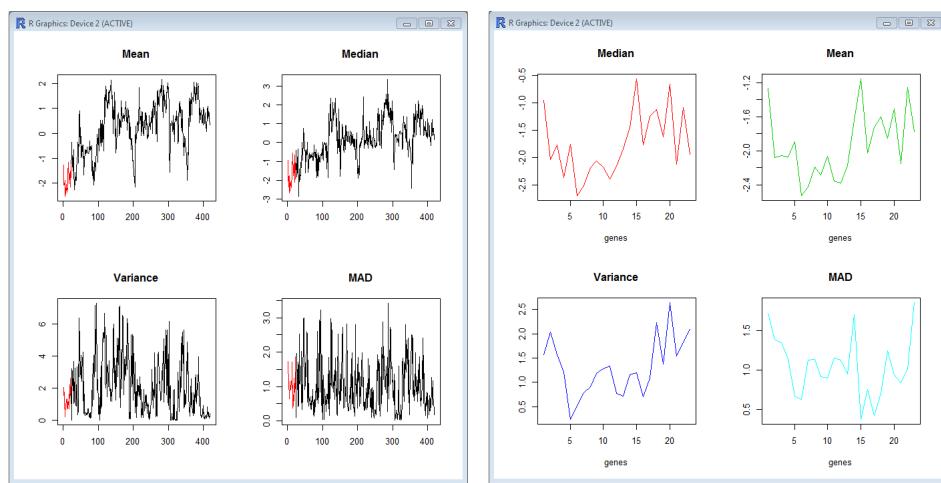


Figure 83: *Exploratory Plots: Left and right button for gene dimension*

### 6.2.9 superbiclust-package

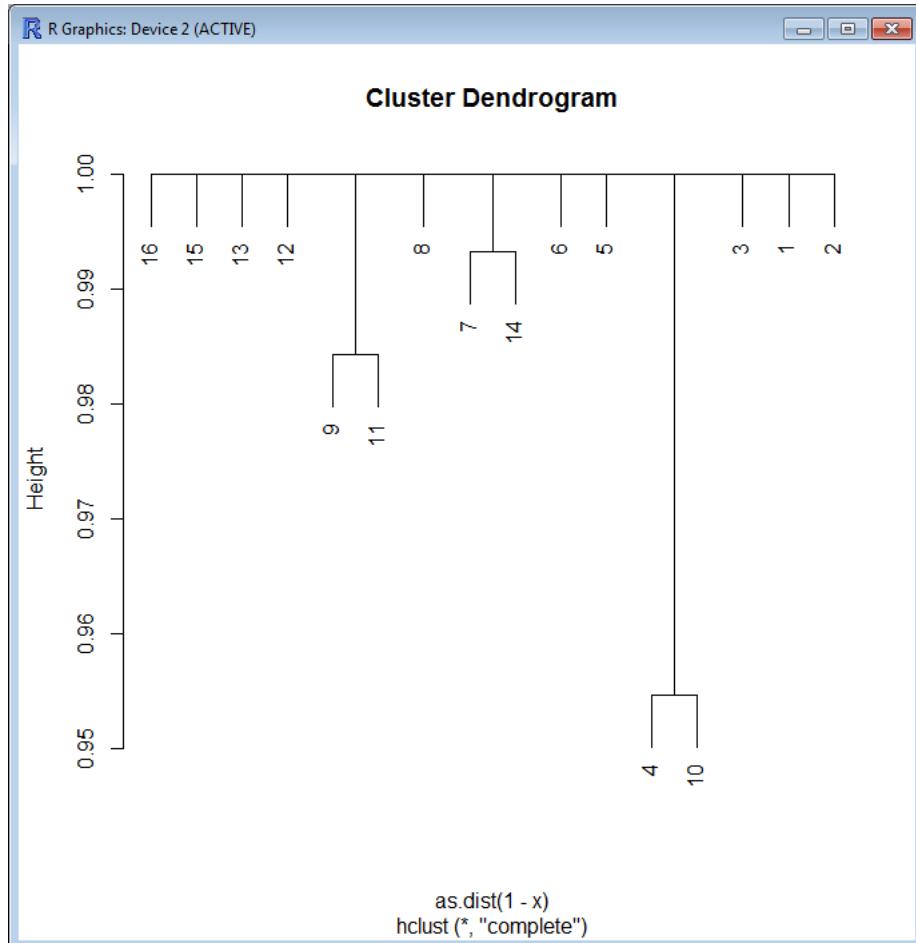


Figure 84: Example of a superbiclust tree (Note that this tree is only here for example purposes. All the biclusters here seem to be unique.)

```
> superbiclust.robust.GUI(CutTree=CutTree, show.which=TRUE)

Robust Biclusters created from more than 1 bicluster:
<NA> <NA>
Robust Bicluster:    4      9
#BC's inside:        2      2

Which Biclusters Inside?
Robust BC 4 :  4 10
Robust BC 9 :  9 11
```

Figure 85: Example of Robust BC button with Show Inside checked

## 6.3 Guideline - Template Scripts

### 6.3.1 newmethod\_script

This script can also be found in the doc subdirectory of the package.

```
newmethod_WINDOW <- function(){      # Change newmethod to your own method name

new.frames <- .initialize.new.frames()
grid.config <- .initialize.grid.config()
grid.rows <- .initialize.grid.rows()
```

```

#####
## GENERAL INFORMATION ABOUT THE NEW METHOD/WINDOW ##
#####

methodname <- "A new method"

methodfunction <- "methodfunction"
data.arg <- "d"
methodshow <- TRUE
other.arg <- ""
methodhelp <- ""

# Transform the data from data.arg
data.transf <- "matrix" # Values: "matrix" (default), "ExprSet"

# Extra Data Conversion Boxes
data.dscr <- FALSE
data.bin <- FALSE

# Possibility to give a seed ?
methodseed <- TRUE

## COMPATIBILITY? ##

# BcDiag
bcdiag.comp <- FALSE

# SuperBiclust
superbiclust.comp <- FALSE

#####
#### CLUSTERING TAB #####
#####

input <- "clusterTab"

### 1. ADDING THE FRAMES ###

# Add frames here

### 2. CONFIGURING THE GRID ###

grid.config <- .grid.matrix(input=input,c("frame1","frame2","frame3",NA
,"frame4",NA),nrow=3,ncol=2,byrow=TRUE,grid.config=grid.config)

### 3. COMBINING THE ROWS ###

grid.rows <- .combine.rows(input=input,rows=c(1),title="A nice box: "
,border=TRUE,grid.rows=grid.rows,grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(2,3),title="A nice box: "
,border=TRUE,grid.rows=grid.rows,grid.config=grid.config)

#####
#### PLOTTING & DIAGNOSTICS TAB #####
#####

input <- "plotdiagTab"

```

```

#### 1. ADDING THE FRAMES ####

# Add frames here

#### 2. CONFIGURING THE GRID ####

grid.config <- .grid.matrix(input=input,c("frame5","frame6"),nrow=1,
    ncol=2,byrow=TRUE,grid.config=grid.config)

#### 3. COMBING THE ROWS ####

grid.rows <- .combine.rows(input=input,rows=c(1),title="Plot 1",
    border=TRUE,grid.rows=grid.rows,grid.config=grid.config)

#####
## USE ALL THE ARGUMENTS IN THE GENERAL CLUSTERTEMPLATE FUNCTION ##
#####

cluster_template(methodname=methodname,methodfunction=methodfunction,
    methodhelp=methodhelp,data.arg=data.arg,other.arg=other.arg
    ,methodseed=methodseed,grid.config=grid.config,grid.rows=grid.rows,
    new.frames=new.frames,superbiclust.comp=superbiclust.comp,
    bcdiag.comp=bcdiag.comp,data.transf=data.transf,
    data.dscr=data.dscr, data.bin=data.bin,methodshow=methodshow,
    methodsave=methodsolve)

}


```

### 6.3.2 frames\_script

```

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "entryframe1"
argument.names <- c("Argument 1","Argument 2","Argument 3")
argument.types <- c("num","num","char")
arguments <- c("arg1","arg2","arg3")
initial.values <- c(1,2,"a")
title <- "A Title"
border <- FALSE
entry.width <- c("2","2","6")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type
    ,frame.name=frame.name,argument.names=argument.names
    ,arguments=arguments,initial.values=initial.values
    ,title=title,border=border,entry.width=entry.width
    ,argument.types=argument.types ,new.frames=new.frames)


```

### ##### RADIO BUTTONS FRAME #####

```

type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radioframe1"


```

```

argument.names <- c("Button 1","Button 2","Button 3")
arguments <- c("buttonarg")
argument.types <- "char"
argument.values <- c("b1","b2","b3")
initial.values <- "b3"
title <- "Button Options"
border <- TRUE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type
    ,frame.name=frame.name,argument.names=argument.names
    ,arguments=arguments,argument.values=argument.values
    ,initial.values=initial.values,title=title,border=border
    ,new.frames=new.frames,argument.types=argument.types)

##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "checkboxframe1"
argument.names <- c("Check 1","Check 2","Check 3")
arguments <- c("checkarg1","checkarg2","checkarg3")
initial.values <- c(0,1,1)
title <- "title"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type
    ,frame.name=frame.name,argument.names=argument.names
    ,arguments=arguments,initial.values=initial.values
    ,title=title,border=border,new.frames=new.frames)

##### VALUE SLIDER FRAME #####
type <- "valuesliders"

# Change variables accordingly:
frame.name <- "sliderframe1"
argument.names <- c("Slider 1 ","Slider 2 ","Slider 3 ")
arguments <- c("sliderarg1","sliderarg2","sliderarg3")
initial.values <- c(1,5,10)
from <- c(1,1,1)
to <- c(5,50,500)
by <- c(1,10,50)
length <- c(50,100,150)
title <- "Title"
border <- TRUE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,
    title=title,border=border,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,
    initial.values=initial.values,from=from,to=to,by=by,
    length=length,new.frames=new.frames)

##### SPIN BOX FRAME #####

```

```

type <- "spinboxes"

# Change variables accordingly:
frame.name <- "spinboxframe1"
argument.names <- c("Spin Box 1: ","Spin Box 2: ","Spin Box 3: ")
arguments <- c("spinarg1","spingarg2","spingarg3")
initial.values <- c(5,10,20)
from <- c(1,5,10)
to <- c(10,20,30)
by <- c(1,1,1)
entry.width <- "2"
title <- "Spin Box !"
border <- TRUE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,
                           frame.name=frame.name,argument.names=argument.names,
                           arguments=arguments,initial.values=initial.values,
                           from=from,to=to,by=by,entry.width=entry.width,
                           title=title,border=border,new.frames=new.frames)

##### MANUAL BUTTONS FRAME #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "buttonframe1"
button.name <- "Button 1"
button.function <- "buttonfunction"
button.data <- "d"
button.biclus <- "biclust"
button.width <- "12"
button.data.transf <- "matrix"

arg.frames <- c("frame1","frame2")

save <- TRUE
show <- TRUE
button.otherarg <- ""

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,
                           type=type,button.name=button.name,
                           button.function=button.function,button.data=button.data,
                           button.biclus=button.biclus,button.otherarg=button.otherarg,
                           button.width=button.width,button.data.transf=button.data.transf,
                           arg.frames=arg.frames,save=save,show=show,new.frames=new.frames)

```

### 6.3.3 Quick Example - Plaid

```

biclustplaid_WIN <- function(){

  new.frames <- .initialize.new.frames()
  grid.config <- .initialize.grid.config()
  grid.rows <- .initialize.grid.rows()

#####
## GENERAL INFORMATION ABOUT THE NEW METHOD/WINDOW ##

```

```

#####
methodname <- "Plaid"
methodfunction <- "biclust"
data.arg <- "x"
data.matrix <- TRUE
other.arg <- ",method=BCPlaid()"
methodhelp <- "BCPlaid"

# Possibility to give a seed ?
methodseed <- TRUE
# Add a discretize box?
data.dscr <- FALSE
# Add a binarize box?
data.bin <- FALSE

## COMPATIBILITY? ##

# BcDiag
bcdiag.comp <- TRUE

# SuperBiclust
superbiclust.comp <- TRUE

# Biclust only (Not for public use)
extrabiclustplot <- TRUE

#####
##### CLUSTERING TAB #####
#####

### 1. ADDING THE FRAMES ###

input <- "clusterTab"

#### RADIO BUTTONS FRAME ####

type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "toclusterframe"
argument.names <- c("Rows","Columns","Rows & Columns")
arguments <- c("cluster")
argument.values <- c("r","c","b")
argument.types <- "char"
initial.values <- "b"
title <- "To Cluster"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,
  frame.name=frame.name,argument.names=argument.names,
  arguments=arguments,argument.values=argument.values,
  initial.values=initial.values,title=title,border=border,
  new.frames=new.frames,argument.types=argument.types)

##### ENTRY FIELDS FRAME #####

```

```

type <- "entryfields"

# Change variables accordingly:
frame.name <- "modelframe"
argument.names <- c("Model Formula")
argument.types <- c("num")
arguments <- c("fit.model")
initial.values <- c("y ~ m+a+b")
title <- "Model"
border <- FALSE
entry.width <- c("10")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,initial.values=
  initial.values,title=title,border=border,entry.width=entry.width,
  argument.types=argument.types ,new.frames=new.frames)

##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "backgroundcheckframe"
argument.names <- c("Background Layer?")
arguments <- c("background")
initial.values <- c(1)
title <- ""
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=
  frame.name,argument.names=argument.names,arguments=arguments,
  initial.values=initial.values,title=title,border=border,new.frames=
  new.frames)

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "backgroundentryframe1"
argument.names <- c("Shuffle","Back Fit","Max Layes")
argument.types <- c("num","num","num")
arguments <- c("shuffle","back.fit","max.layers")
initial.values <- c(3,0,20)
title <- ""
border <- FALSE
entry.width <- c("2","2","2")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,initial.values=
  initial.values,title=title,border=border,entry.width=entry.width,
  argument.types=argument.types ,new.frames=new.frames)

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

```

```

# Change variables accordingly:
frame.name <- "backgroundentryframe2"
argument.names <- c("Iteration Startup","Iteration Layer")
argument.types <- c("num","num")
arguments <- c("iter.startup","iter.layer")
initial.values <- c(5,10)
title <- ""
border <- FALSE
entry.width <- c("2","2")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,initial.values=
  initial.values,title=title,border=border,entry.width=entry.width,
  argument.types=argument.types ,new.frames=new.frames)

### 2. CONFIGURING THE GRID ###

grid.config <- .grid.matrix(input=input,c("toclusterframe","modelframe",
  "backgroundcheckframe",NA,"backgroundentryframe1","backgroundentryframe2"),
  byrow=TRUE,nrow=3,ncol=2,grid.config=grid.config)

### 3. COMBING THE ROWS ###
grid.rows <- .combine.rows(input=input,rows=c(1),title="Plaid
  Specifications",border=TRUE,grid.rows=grid.rows,grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(2,3),title=
  "Layer Specifications",border=TRUE,grid.rows=grid.rows,
  grid.config=grid.config)

#####
##### PLOTTING & DIAGNOSTICS TAB #####
#####

input <- "plotdiagTab"

### 1. ADDING THE FRAMES ###

###          ###
## Parallel Coordinates Plot ##
###          ###

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "pplottypeframe"
argument.names <- c("Default","Combined (rows & columns)")
arguments <- c("type2")
argument.values <- c("default","combined")
argument.types <- "char"

```

```

initial.values <- "default"
title <- "Plot Type:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,argument.values=
  argument.values,initial.values=initial.values,title=title,border=border,
  new.frames=new.frames,argument.types=argument.types)

##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "pplotcheckboxframe"
argument.names <- c("Plot Only Column","Plot Rows & Columns","Compare")
arguments <- c("plotcol","plotBoth","compare")
initial.values <- c(1,0,1)
title <- "Default Type Options:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,initial.values=
  initial.values,title=title,border=border,new.frames=new.frames)

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "pplotentryframe"
argument.names <- c("Bicluster Number")
argument.types <- c("num")
arguments <- c("number")
initial.values <- c(1)
title <- ""
border <- FALSE
entry.width <- c("2")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,initial.values=
  initial.values,title=title,border=border,entry.width=entry.width,
  argument.types=argument.types ,new.frames=new.frames)

##### MANUAL BUTTONS FRAME #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "parallelbuttonframe"
button.name <- "Draw Plot"
button.function <- "parallelCoordinates3"

```

```

button.data <- "x"
button.bioclust <- "bicResult"
button.otherarg <- ""
save <- FALSE
arg.frames <- c("pplotcheckframe", "pplotentryframe", "pplottypeframe")

# Do not change this line:
new.frames <- .add.frame(input=input, frame.name=frame.name, save=save,
    type=type, button.name=button.name, button.otherarg=button.otherarg,
    button.function=button.function, button.data=button.data, button.bioclust=
    button.bioclust, arg.frames=arg.frames, new.frames=new.frames)

#####
#####

#####      Heatmap Plot #####
#####

##### CHECK BOXES FRAME #####
#####

type <- "checkboxes"

# Change variables accordingly:
frame.name <- "heatplotcheckframe"
argument.names <- c("Local")
arguments <- c("local")
initial.values <- c(1)
title <- ""
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input, type=type, frame.name=frame.name,
    argument.names=argument.names, arguments=arguments, initial.values=
    initial.values, title=title, border=border, new.frames=new.frames)

#####      ENTRY FIELDS FRAME #####
#####

type <- "entryfields"

# Change variables accordingly:
frame.name <- "heatplotentryframe"
argument.names <- c("Bicluster Number")
argument.types <- c("num")
arguments <- c("number")
initial.values <- c(1)
title <- ""
border <- FALSE
entry.width <- c("2")

# Do not change this line:
new.frames <- .add.frame(input=input, type=type, frame.name=frame.name,
    argument.names=argument.names, arguments=arguments, initial.values=
    initial.values, title=title, border=border, entry.width=entry.width,
    argument.types=argument.types , new.frames=new.frames)

#####      MANUAL BUTTONS FRAME #####
#####

type <- "buttons"

```

```

# Change variables accordingly:
frame.name <- "heatbuttonframe"
button.name <- "Draw Plot"
button.function <- "drawHeatmap"
button.data <- "x"
button.bioclust <- "bicResult"
save <- FALSE
arg.frames <- c("heatplotcheckframe","heatplotentryframe")

# Do not change this line: (without button.otherarg)
new.frames <- .add.frame(input=input,frame.name=frame.name,type=
    type,save=save,button.name=button.name,button.function=button.function,
    button.data=button.data,button.bioclust=button.bioclust,arg.frames=
    arg.frames,new.frames=new.frames)

#####
#####

#####
##      Bioclust Member Plot   ##
#####

##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "mplotcheckframe"
argument.names <- c("Mid")
arguments <- c("mid")
initial.values <- c(1)
title <- ""
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,initial.values=
    initial.values,title=title,border=border,new.frames=new.frames)

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "mplotentryframe"
argument.names <- c("Biocluster Label")
argument.types <- c("char")
arguments <- c("cl_label")
initial.values <- c("")
title <- ""
border <- FALSE
entry.width <- c("8")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,initial.values=
    initial.values,title=title,border=border,entry.width=entry.width,
    argument.types=argument.types ,new.frames=new.frames)

#####      MANUAL BUTTONS FRAME - EXAMPLE      #####

```

```

type <- "buttons"

# Change variables accordingly:
frame.name <- "memberbuttonframe"
button.name <- "Draw Plot"
button.function <- "biclustmember"
button.data <- "x"
button.biclust <- "bicResult"
save <- FALSE
arg.frames <- c("mplotcheckframe","mplotentryframe")

# Do not change this line: (without button.otherarg)
new.frames <- .add.frame(input=input,frame.name=frame.name,save=save,
    type=type,button.name=button.name,button.function=button.function,
    button.data=button.data,button.biclust=button.biclust,arg.frames=
    arg.frames,new.frames=new.frames)

#####
#####

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "summarybuttonframe"
button.name <- "Summary"
button.function <- "summary"
button.data <- ""
button.biclust <- "object"
arg.frames <- c()
save <- FALSE

# Do not change this line: (without button.otherarg)
new.frames <- .add.frame(input=input,frame.name=frame.name,save=save,
    type=type,button.name=button.name,button.function=button.function,
    button.data=button.data,button.biclust=button.biclust,arg.frames=
    arg.frames,new.frames=new.frames)

#####
#####

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "fstatbuttonframe"
button.name <- "Obs. F Stat."
button.function <- "computeObservedFstat"
button.data <- "x"
button.biclust <- "bicResult"
arg.frames <- c("fstatentryframe")

# Do not change this line: (without button.otherarg)

```

```

new.frames <- .add.frame(input=input,frame.name=frame.name,type=type,
    button.name=button.name,button.function=button.function,button.data=
    button.data,button.biclust=button.biclust,arg.frames=arg.frames,
    new.frames=new.frames)

#####
##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "fstatentryframe"
argument.names <- c("Bicluster Number")
argument.types <- c("num")
arguments <- c("number")
initial.values <- c("1")
title <- ""
border <- FALSE
entry.width <- c("4")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,initial.values=
    initial.values,title=title,border=border,entry.width=entry.width,
    argument.types=argument.types ,new.frames=new.frames)

#####
##### ENTRY FIELDS FRAME #####
#     #

type <- "entryfields"

# Change variables accordingly:
frame.name <- "bootstrapentryframe"
argument.names <- c("Bicluster Number","Number Bootstrap Replicates")
argument.types <- c("num","num")
arguments <- c("number","nResamplings")
initial.values <- c(1,100)
title <- "Bootstrap Options:"
border <- FALSE
entry.width <- c("4","4")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,initial.values=
    initial.values,title=title,border=border,entry.width=entry.width
    ,argument.types=argument.types ,new.frames=new.frames)

#####
##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "bootstrapreplacementframe"
argument.names <- c("With Replacement?")
arguments <- c("replace")
initial.values <- c(1)
title <- ""
border <- FALSE

```

```

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,initial.values=
    initial.values,title=title,border=border,new.frames=new.frames)

####      MANUAL BUTTONS FRAME      ####

type <- "buttons"

# Change variables accordingly:
frame.name <- "bootstrapbuttonframe"
button.name <- "Bootstrap"
button.function <- "diagnoseColRow"
button.data <- "x"
button.biclus <- "bicResult"
arg.frames <- c("bootstrapentryframe","bootstrapreplacementframe")

# Do not change this line: (without button.otherarg)
new.frames <- .add.frame(input=input,frame.name=frame.name,type=type,
    button.name=button.name,button.function=button.function,button.data=
    button.data,button.biclus=button.biclus,arg.frames=arg.frames,
    new.frames=new.frames)

####      MANUAL BUTTONS FRAME      ####

type <- "buttons"

# Change variables accordingly:
frame.name <- "bootstrapvisualbuttonframe"
button.name <- "Visualize"
button.function <- "diagnosticPlot"
button.data <- ""
button.biclus <- ""
button.otherarg <- "bootstrapOutput=Bootstrap"
save <- FALSE
arg.frames <- c()

# Do not change this line: (without button.otherarg)
new.frames <- .add.frame(input=input,frame.name=frame.name,save=save,
    type=type,button.name=button.name,button.function=button.function,
    button.data=button.data,button.biclus=button.biclus,arg.frames=
    arg.frames,new.frames=new.frames,button.otherarg=button.otherarg)

### 2. CONFIGURING THE GRID ###

grid.config <- .grid.matrix(input=input,c("summarybuttonframe",
    "fstatentryframe","fstatbuttonframe","bootstrapentryframe",NA,NA,
    "bootstrapreplacementframe","bootstrapbuttonframe",
    "bootstrapvisualbuttonframe" , "pplottypeframe","pplotentryframe",
    "parallelbuttonframe","pplotcheckframe",NA,NA,"heatplotcheckframe",
    "heatplotentryframe","heatbuttonframe","mplotcheckframe",
    "mplotentryframe","memberbuttonframe"),byrow=TRUE,nrow=7,ncol=3,
    grid.config=grid.config)

```

```

#### 3. COMBING THE ROWS ####

grid.rows <- .combine.rows(input=input,rows=c(1,2,3),title=
  "Summary & Diagnostics",border=TRUE,grid.rows=grid.rows,grid.config=
  grid.config)
grid.rows <- .combine.rows(input=input,rows=c(4,5),title=
  "Parallel Coordinate Plot",border=TRUE,grid.rows=grid.rows,grid.config=
  grid.config)
grid.rows <- .combine.rows(input=input,rows=c(6),title="Heatmap Plot"
  ,border=TRUE,grid.rows=grid.rows,grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(7),title="Biclusmember
  Plot",border=TRUE,grid.rows=grid.rows,grid.config=grid.config)

#####
## USE ALL THE ARGUMENTS ABOUT IN THE GENERAL CLUSTERTEMPLATE FUNCTION ##
#####

cluster_template(methodname=methodname,methodfunction=methodfunction,
  methodhelp=methodhelp,data.arg=data.arg,other.arg=other.arg,
  methodseed=methodseed,grid.config=grid.config,grid.rows=grid.rows,
  new.frames=new.frames,superbiclust.comp=superbiclust.comp,bcdiag.comp=
  bcdiag.comp,data.matrix=data.matrix,data.dscr=data.dscr,data.bin=
  data.bin,extrab biclustplot=extrab biclustplot)

}

```

#### 6.3.4 newtool\_script

This script can also be found in the doc subdirectory of the package.

```

newtool_WINDOW <- function(methodname){

  new.frames <- .initialize.new.frames()
  grid.config <- .initialize.grid.config()
  grid.rows <- .initialize.grid.rows()

#####

## GENERAL INFORMATION ABOUT THE NEW TOOL    ##
#####

toolname <- "A new tool"

toolhelp <- "helppage"

# Do not change this line:
input <- "plotdiagTab"

#####

## MAKING THE WINDOW ##

#####

### ADDING FRAMES ###

# Analogous to plotdiag tab.

#### CONFIGURING GRID ####

```

```

grid.config <- .grid.matrix(input=input,c(),nrow=1,ncol=2,byrow=TRUE
                           ,grid.config=grid.config)

#### COMBINING ROWS #####
grid.rows <- .combine.rows(input=input,rows=c(),title="Plot 1",
                           border=TRUE,grid.rows=grid.rows,grid.config=grid.config)

#####
## USE ALL THE ARGUMENTS IN THE GENERAL NEW TOOL FUNCTION ##
#####

newtool_template(toolname=toolname,methodname=methodname,toolhelp=toolhelp,
                 data.matrix=data.matrix,grid.config=grid.config,grid.rows=grid.rows,
                 new.frames=new.frames)

}

```

### 6.3.5 Quick Example - BcDiag

```

bcdiag_WINDOW <- function(methodname){

  new.frames <- .initialize.new.frames()
  grid.config <- .initialize.grid.config()
  grid.rows <- .initialize.grid.rows()

  # Some extra code to determine the input type: "biclust", "fabia", "isa2"
  biclust.names <- c("Bimax","CC","Plaid","Questmotif","Spectral",
                    "XMotifs","IBBIG")
  fabia.names <- c("Fabia Laplace Prior","Fabia Post-Projection",
                  "Fabia Sparseness Projection","Fabia SPARSE")
  isa.names <- c("ISA")

  if(methodname %in% biclust.names){
    extra.arg <- ",mname='biclust'"
  }
  if(methodname %in% fabia.names){
    extra.arg <- ",mname='fabia'"

    # Exception when superbiclust has been used on fabia:
    method_result <- gsub(" ","",methodname,fixed=TRUE)
    method_result <- gsub("-","",method_result,fixed=TRUE)
    eval(parse(text=paste("method_class <- class(",method_result,")",sep="")))
    if(method_class=="Biclust"){
      extra.arg <- ",mname='biclust'"
    }
  }
  if(methodname %in% isa.names){
    extra.arg <- ",mname='isa2'"
  }

#####
## GENERAL INFORMATION ABOUT THE NEW TOOL          ##
#####

toolname <- "BCDIAG"
toolhelp <- "BcDiag-package"

```

```

# Do not change this line:
input <- "plotdiagTab"

#### ADDING FRAMES ####

#####
## The anomedOnlybic Function ##
#####

#####

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radio_anomed"
argument.names <- c("Diagnostic Plots", "Tukey Additivity Plot",
  "Anova Plots", "Mpolish Plots", "Anova & Mpolish")
arguments <- c("fit")
argument.values <- c("aplot", "mplot", "anovbplot", "mpolishbplot",
  "boxplot")
argument.types <- "char"
initial.values <- "boxplot"
title <- "Plot Type:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input, type=type, frame.name=frame.name,
  argument.names=argument.names, arguments=arguments, argument.values=
  argument.values, initial.values=initial.values, title=title, border=border
, new.frames=new.frames, argument.types=argument.types)

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "entry_number"
argument.names <- c("Bicluster Number")
argument.types <- c("num")
arguments <- c("bnum")
initial.values <- c(1)
title <- ""
border <- FALSE
entry.width <- c("3")

# Do not change this line:
new.frames <- .add.frame(input=input, type=type, frame.name=
  frame.name, argument.names=argument.names, arguments=arguments,
  initial.values=initial.values, title=title, border=border,
  entry.width=entry.width, argument.types=argument.types ,
  new.frames=new.frames)

#### MANUAL BUTTONS FRAME ####

type <- "buttons"

# Change variables accordingly:

```

```

frame.name <- "button_anomed"
button.name <- "Draw Plot"
button.function <- "anomedOnlybic"
button.data <- "dset"
button.biclus <- "bres"
button.otherarg <- extra.arg
save <- FALSE
arg.frames <- c("radio_anomed","entry_number")

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,
  save=save,type=type,button.name=button.name,button.otherarg=
  button.otherarg,button.function=button.function,button.data=
  button.data,button.biclus=button.biclus,arg.frames=arg.frames,
  new.frames=new.frames)

#####
##      EXPLORATORY PLOTS (biclustered & Clustered Data) #####
#####

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radio1_explore"
argument.names <- c("Mean","Median","Variance","Median Absolute
  Deviation","Quantile","All")
arguments <- c("pfor")
argument.values <- c("mean","median","variance","mad","quant","all")
argument.types <- "char"
initial.values <- "mean"
title <- "Plot for:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,argument.values=
  argument.values,initial.values=initial.values,title=title,border=border
  ,new.frames=new.frames,argument.types=argument.types)

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radio2_explore"
argument.names <- c("Genes","Conditions")
arguments <- c("gby")
argument.values <- c("genes","conditions")
argument.types <- "char"
initial.values <- "genes"
title <- "Dimension:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,argument.values=
  argument.values,initial.values=initial.values,title=title,border=

```

```

border,new.frames=new.frames,argument.types=argument.types)

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "button_explore"
button.name <- "Bicl. & Clust."
button.function <- "exploreBic"
button.data <- "dset"
button.bioclust <- "bres"
button.otherarg <- extra.arg
save <- FALSE
arg.frames <- c("radio1_explore","radio2_explore","entry_number")

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,save=
  save,type=type,button.name=button.name,button.otherarg=button.otherarg,
  button.function=button.function,button.data=button.data,button.bioclust=
  button.bioclust,arg.frames=arg.frames,new.frames=new.frames)

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "button2_explore"
button.name <- "Only Bioclust."
button.function <- "exploreOnlybic"
button.data <- "dset"
button.bioclust <- "bres"
button.otherarg <- extra.arg
save <- FALSE
arg.frames <- c("radio1_explore","radio2_explore","entry_number")

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,
  save=save,type=type,button.name=button.name,button.otherarg=
  button.otherarg,button.function=button.function,button.data=
  button.data,button.bioclust=button.bioclust,arg.frames=arg.frames,
  new.frames=new.frames)

#####
#####      PROFILE PLOTS      #####
#####

#####      RADIO BUTTONS FRAME      #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radio1_profile"
argument.names <- c("All","Lines","Boxplot","Histogram","3D")
arguments <- c("bplot")
argument.values <- c("all","lines","boxplot","histogram","threeD")
argument.types <- "char"
initial.values <- "all"
title <- "Plot Type:"

```

```

border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,argument.values=
    argument.values,initial.values=initial.values,title=title,border=border
    ,new.frames=new.frames,argument.types=argument.types)

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "radio2_profile"
argument.names <- c("Genes","Conditions")
arguments <- c("gby")
argument.values <- c("genes","conditions")
argument.types <- "char"
initial.values <- "genes"
title <- "Dimension:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name
    ,argument.names=argument.names,arguments=arguments,argument.values=
    argument.values,initial.values=initial.values,title=title,border=
    border,new.frames=new.frames,argument.types=argument.types)

##### VALUE SLIDER FRAME - EXAMPLE #####
# Only for numerical values
type <- "valuesliders"

# Change variables accordingly:
frame.name <- "slider_profile"
argument.names <- c("Theta: ","Phi:      ")
arguments <- c("teta","ph")
initial.values <- c(120,30)
from <- c(-180,-180)
to <- c(180,180)
by <- c(10,10)
length <- c(125,125)
title <- "3D Rotation:"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,title=title,
    border=border,frame.name=frame.name,argument.names=argument.names,
    arguments=arguments,initial.values=initial.values,from=from,to=to,
    by=by,length=length,new.frames=new.frames)

#### MANUAL BUTTONS FRAME #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "button_profile"

```

```

button.name <- "Draw Plot"
button.function <- "profileBic"
button.data <- "dset"
button.biclus <- "bres"
button.otherarg <- extra.arg
save <- FALSE
arg.frames <- c("radio1_profile","radio2_profile","entry_number",
               "slider_profile")

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,
                           save=save,type=type,button.name=button.name,button.otherarg=
                           button.otherarg,button.function=button.function,button.data=
                           button.data,button.biclus=button.biclus,arg.frames=arg.frames,
                           new.frames=new.frames)

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "button_summaryoutput"
button.name <- "Summary"
button.function <- "bcdiagwrite_WINDOW"
button.data <- ""
button.biclus <- ""

temp <- paste("methodname='",methodname,"'",sep="")
button.otherarg <- temp
save <- FALSE
show <- FALSE
arg.frames <- c()

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,
                           show=show,save=save,type=type,button.name=button.name,
                           button.otherarg=button.otherarg,button.function=button.function,
                           button.data=button.data,button.biclus=button.biclus,arg.frames=
                           arg.frames,new.frames=new.frames)

### CONFIGURING GRID ###

grid.config <- .grid.matrix(input=input,c("entry_number",
                                           "button_summaryoutput",NA,"radio_anomed","button_anomed",NA,
                                           "radio1_explore","radio2_explore",NA,"button_explore","button2_explore"
                                           ,NA,"radio1_profile","radio2_profile","slider_profile","button_profile"
                                           ,NA,NA),byrow=TRUE,nrow=6,ncol=3,grid.config=grid.config)

### COMBINING ROWS ###
grid.rows <- .combine.rows(input=input,rows=c(1),title=
                           "Plotting Cluster Number & Summary Output",border=TRUE,grid.rows=
                           grid.rows,grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(2),title=
                           "ANOVA & Median Polish Residual Plots",border=TRUE,grid.rows=grid.rows,
                           grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(3,4),title=
                           "Exploratory Plots for Biclustered & Clustered data",border=TRUE,
                           grid.rows=grid.rows,grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(5,6),title=

```

```

"Profile Plots for Biclustered & Clustered data",border=TRUE,
grid.rows=grid.rows,grid.config=grid.config)

#####
## USE ALL THE ARGUMENTS ABOUT IN THE GENERAL NEW TOOL FUNCTION ##
#####

newtool_template(toolname=toolname,methodname=methodname,toolhelp=
  toolhelp,grid.config=grid.config,grid.rows=
  grid.rows,new.frames=new.frames)
}

```

### 6.3.6 Extra Example - Superbiclust

```

superbiclust_WINDOW <- function(methodname){

new.frames <- .initialize.new.frames()
grid.config <- .initialize.grid.config()
grid.rows <- .initialize.grid.rows()

method_result <- gsub(" ","",methodname,fixed=TRUE)
method_result <- gsub("-","",method_result,fixed=TRUE)

biclust.names <- c("Bimax","CC","Plaid","Questmotif",
  "Spectral","XMotifs","IBBIG","Rqubic")
fabia.names <- c("Fabia Laplace Prior","Fabia Post-Projection",
  "Fabia Sparseness Projection","Fabia SPARSE")
isa.names <- c("ISA")

if(methodname %in% biclust.names){
#extra.arg <- paste("x=",method_result,sep="")
extra.arg <- paste(",method_result='",method_result,"',
  type.method='biclust'",sep="")
#isa2 <- FALSE
biclust.combine <- TRUE
make.save.button <- TRUE
save.type <- "biclust"
}
if(methodname %in% fabia.names){
#extra.arg <- paste("x=",method_result,sep="")
extra.arg <- paste(",method_result='",method_result,"',
  type.method='fabia'",sep="")
#isa2 <- FALSE
biclust.combine <- FALSE
make.save.button <- TRUE
save.type <- "fabia"
}
if(methodname %in% isa.names){
#extra.arg <- paste("x=isa.biclust",method_result,")",sep="")
extra.arg <- paste(",method_result='",method_result,"',
  type.method='isa'",sep="")
#isa2 <- TRUE
biclust.combine <- FALSE
make.save.button <- TRUE
save.type <- "isa"
}

#####

```

```

## GENERAL INFORMATION ABOUT THE NEW TOOL      ##
#####
##### toolname <- "SuperBiclust"
##### toolhelp <- "superbiclust"

# Do not change this line:
input <- "plotdiagTab"

#####
## MAKING THE WINDOW ##
#####

#### ADDING FRAMES ####

#####
## EXTRA DATA INPUT ##
#####

#####
ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "biclustcombine"
argument.names <- c("")
argument.types <- c("num")
arguments <- c("extra.biclust")
initial.values <- c("NULL")
title <- "Vector of Biclust Objects (Example: c('biclust2','biclust3') )"
border <- FALSE
entry.width <- c("50")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=
  frame.name,argument.names=argument.names,arguments=arguments,
  initial.values=initial.values,title=title,border=border,entry.width=
  entry.width,argument.types=argument.types ,new.frames=new.frames)

#####
## SUPERBICLUST CONFIGURATION ##
#####

#####
RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "indexradio"
argument.names <- c("Jaccard","Sorensen","Ochiai","Kulczynski",
  "Sensitivity","Specificity")
arguments <- c("index")
argument.values <- c("jaccard","sorensen","ochiai","kulczynski",
  "sensitivity","specificity")

```

```

argument.types <- "char"
initial.values <- "jaccard"
title <- "Similarity?"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,argument.values=
  argument.values,initial.values=initial.values,title=title,border=border
, new.frames=new.frames,argument.types=argument.types)

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "typeradio"
argument.names <- c("Rows","Columns","Both")
arguments <- c("type")
argument.values <- c("rows","cols","both")
argument.types <- "char"
initial.values <- "both"
title <- "Type?"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,argument.values=
  argument.values,initial.values=initial.values,title=title,border=
  border,new.frames=new.frames,argument.types=argument.types)

##### MANUAL BUTTONS FRAME #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "superbiclust"
button.name <- "SuperBiclust"
button.function <- "superbiclust.GUI"
button.data <- ""
button.biclust <- "x"
button.otherarg <- extra.arg
save <- FALSE
show <- FALSE

if(biclust.combine==TRUE){
  arg.frames <- c("indexradio","typeradio","biclustcombine")
}
else{
  arg.frames <- c("indexradio","typeradio")
}

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,show=
  show,save=save,type=type,button.name=button.name,button.otherarg=
  button.otherarg,button.function=button.function,button.data=
  button.data,button.biclust=button.biclust,arg.frames=arg.frames,
  new.frames=new.frames)

#####

```

```

## DENDOGRAM ##
####      ####

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "drawtree"
button.name <- "Draw Tree"
button.function <- "plot"
button.data <- ""
button.biclus <- ""
button.otherarg <- "x=superbiclus.tree"
save <- FALSE
show <- TRUE
arg.frames <- c()

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,show=show,
    save=save,type=type,button.name=button.name,button.otherarg=
    button.otherarg,button.function=button.function,button.data=button.data,
    button.biclus=button.biclus,arg.frames=arg.frames,new.frames=new.frames)

#####
ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "cutentry"
argument.names <- c("Number of Biclusters","Height")
argument.types <- c("num","num")
arguments <- c("k","h")
initial.values <- c("NULL","NULL")
title <- "Where to cut tree? (number overrides height)"
border <- FALSE
entry.width <- c("6","6")

# Do not change this line:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
    argument.names=argument.names,arguments=arguments,initial.values=
    initial.values,title=title,border=border,entry.width=entry.width,
    argument.types=argument.types ,new.frames=new.frames)

#####      MANUAL BUTTONS FRAME      #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "cutree"
button.name <- "Cut Tree"
button.function <- "cutree"
button.data <- ""
button.biclus <- ""
button.otherarg <- "tree=superbiclus.tree"
save <- TRUE
show <- TRUE
arg.frames <- c("cutentry")

```

```

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,show=show,
  save=save,type=type,button.name=button.name,button.otherarg=
  button.otherarg,button.function=button.function,button.data=button.data,
  button.biclust=button.biclust,arg.frames=arg.frames,new.frames=new.frames)

##### #####
## Plotting Robust Biclusters ##
##### #####
##### CHECK BOXES FRAME #####
type <- "checkboxes"

# Change variables accordingly:
frame.name <- "showrobust"
argument.names <- c("Show Inside Robust BC?")
arguments <- c("show.which")
initial.values <- c(0)
title <- ""
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input,type=type,frame.name=frame.name,
  argument.names=argument.names,arguments=arguments,initial.values=
  initial.values,title=title,border=border,new.frames=new.frames)

##### MANUAL BUTTONS FRAME #####
type <- "buttons"

# Change variables accordingly:
frame.name <- "robustbutton"
button.name <- "Robust BC"
button.function <- "superbiclust.robust.GUI"
button.data <- ""
button.biclust <- ""
button.otherarg <- "CutTree=CutTree"
save <- FALSE
show <- TRUE
arg.frames <- c("showrobust")

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,
  show=show,save=save,type=type,button.name=button.name,button.otherarg=
  button.otherarg,button.function=button.function,button.data=button.data,
  button.biclust=button.biclust,arg.frames=arg.frames,new.frames=new.frames)

##### RADIO BUTTONS FRAME #####
type <- "radiobuttons"

# Change variables accordingly:
frame.name <- "plottyperadio"
argument.names <- c("Within Biclusters","All Samples")
arguments <- c("type")

```

```

argument.values <- c("within", "all")
argument.types <- "char"
initial.values <- "within"
title <- "Type?"
border <- FALSE

# DO NOT CHANGE THIS LINE:
new.frames <- .add.frame(input=input, type=type, frame.name=frame.name,
    argument.names=argument.names, arguments=arguments, argument.values=
    argument.values, initial.values=initial.values, title=title, border=border,
    new.frames=new.frames, argument.types=argument.types)

##### ENTRY FIELDS FRAME #####
type <- "entryfields"

# Change variables accordingly:
frame.name <- "whichrobust"
argument.names <- c("Number")
argument.types <- c("num")
arguments <- c("which.robust")
initial.values <- c("")
title <- "Which Robust BC?"
border <- FALSE
entry.width <- c("4")

# Do not change this line:
new.frames <- .add.frame(input=input, type=type, frame.name=frame.name,
    argument.names=argument.names, arguments=arguments, initial.values=
    initial.values, title=title, border=border, entry.width=entry.width,
    argument.types=argument.types , new.frames=new.frames)

#### MANUAL BUTTONS FRAME ####
type <- "buttons"

# Change variables accordingly:
frame.name <- "superplot"
button.name <- "Draw Plot"
button.function <- "plotSuper.GUI"
button.data <- ""
button.biclus <- ""
button.otherarg <- "CutTree=CutTree"
save <- FALSE
show <- FALSE
arg.frames <- c("plottyperadio", "whichrobust")

# Do not change this line:
new.frames <- .add.frame(input=input, frame.name=frame.name, show=show,
    save=save, type=type, button.name=button.name, button.otherarg=
    button.otherarg, button.function=button.function, button.data=button.data,
    button.biclus=button.biclus, arg.frames=arg.frames, new.frames=new.frames)

### #####
## SAVE BUTTON ##
#### #####
# ONLY FOR BICLUS

```

```

#####      MANUAL BUTTONS FRAME      #####
#
# type <- "buttons"

# Change variables accordingly:
frame.name <- "savebutton"
button.name <- "Save"
button.function <- "biclust.robust.fuse"
button.data <- ""
button.biclust <- ""
button.otherarg <- paste("CutTree=CutTree", ",method_result='",
method_result,'',",type='',save.type,'',sep='')
save <- FALSE
show <- TRUE
arg.frames <- c()

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,show=show,
  save=save,type=type,button.name=button.name,button.otherarg=
  button.otherarg,button.function=button.function,button.data=
  button.data,button.biclust=button.biclust,arg.frames=arg.frames,
  new.frames=new.frames)

#####      MANUAL BUTTONS FRAME      #####
#
# type <- "buttons"

# Change variables accordingly:
frame.name <- "resetbutton"
button.name <- paste0("Reset (Original ",methodname,")")
button.function <- "robust.reset"
button.data <- ""
button.biclust <- ""
button.otherarg <- paste("method_result='",method_result,'',sep='')
button.width <- paste0(nchar(button.name)-2)
save <- FALSE
show <- FALSE
arg.frames <- c()

# Do not change this line:
new.frames <- .add.frame(input=input,frame.name=frame.name,button.width=
  button.width,show=show,save=save,type=type,button.name=button.name,
  button.otherarg=button.otherarg,button.function=button.function,
  button.data=button.data,button.biclust=button.biclust,arg.frames=
  arg.frames,new.frames=new.frames)

### CONFIGURING GRID ###

if(biclust.combine==TRUE){
if(make.save.button==TRUE){
grid.config <- .grid.matrix(input=input,c("biclustcombine",
NA,NA,"indexradio","typeradio","superbiclust","drawtree",NA,NA,
"cutentry","cutree",NA,"showrobust","robustbutton",NA,"plottyperadio",
"whichrobust","superplot","savebutton","resetbutton",NA),byrow=TRUE
}
}

```

```

    ,nrow=7,ncol=3,grid.config=grid.config)
}
else{
grid.config <- .grid.matrix(input=input,c("biclustcombine",NA
,"NA","indexradio","typeradio","superbiclust","drawtree",NA,NA,"cutentry"
,"cutree",NA,"showrobust","robustbutton",NA,"plottyperadio",
"whichrobust","superplot"),byrow=TRUE,nrow=6,ncol=3,grid.config=grid.config)

}
}
else{
if(make.save.button==TRUE){
grid.config <- .grid.matrix(input=input,c("indexradio",
"typeradio","superbiclust","drawtree",NA,NA,"cutentry","cutree",NA,
"showrobust","robustbutton",NA,"plottyperadio","whichrobust","superplot",
"savebutton","resetbutton",NA),byrow=TRUE,nrow=6,ncol=3,
grid.config=grid.config)

}
else{
grid.config <- .grid.matrix(input=input,c("indexradio",
"typeradio","superbiclust","drawtree",NA,NA,"cutentry","cutree",NA,
"showrobust","robustbutton",NA,"plottyperadio","whichrobust","superplot")
,byrow=TRUE,nrow=5,ncol=3,grid.config=grid.config)
}
}
}


```

```

### COMBINING ROWS ###

if(biclust.combine==TRUE){

grid.rows <- .combine.rows(input=input,rows=c(1),title=
"Extra Biclust Data Input",border=TRUE,grid.rows=grid.rows,
grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(2),
title="Superbiclust Configuration",border=TRUE,grid.rows=grid.rows,
grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(3,4),
title="Dendrogram",border=TRUE,grid.rows=grid.rows,grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(5,6),title=
"Robust Bicluster Gene Profiles",border=TRUE,grid.rows=grid.rows,
grid.config=grid.config)
if(make.save.button==TRUE){

grid.rows <- .combine.rows(input=input,rows=c(7),
title="Save the Robust Biclusters (Biclust Only)",border=TRUE,
grid.rows=grid.rows,grid.config=grid.config)
}

}
else{
grid.rows <- .combine.rows(input=input,rows=c(1),
title="Superbiclust Configuration",border=TRUE,grid.rows=grid.rows,
grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(2,3),
title="Superbiclust Configuration",border=TRUE,grid.rows=grid.rows,
grid.config=grid.config)
grid.rows <- .combine.rows(input=input,rows=c(4,5),
title="Robust Bicluster Gene Profiles",border=TRUE,grid.rows=grid.rows,

```

```

grid.config=grid.config)
if(make.save.button==TRUE){
grid.rows <- .combine.rows(input=input,rows=c(6),
  title="Save the Robust Biclusters (Biclus Only)",border=TRUE,
  grid.rows=grid.rows,grid.config=grid.config)

}
}

#####
## USE ALL THE ARGUMENTS ABOUT IN THE GENERAL NEW TOOL FUNCTION ##
#####

newtool_template(toolname=toolname,methodname=methodname,
  toolhelp=toolhelp,data.matrix=data.matrix,grid.config=grid.config,
  grid.rows=grid.rows,new.frames=new.frames)

}

```