

Package ‘RcmdrPlugin.BiclustGUI’

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Type Package

Title 'Rcmdr' Plug-in GUI for Biclustering

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Description A plug-in for R Commander ('Rcmdr'). The package is a Graphical User Interface (GUI) in which several biclustering methods can be executed, followed by diagnostics and plots of the results. Further, the GUI also has the possibility to connect the methods to more general diagnostic packages for biclustering. Biclustering methods from 'biclust', 'fabia', 's4vd', 'iBBiG', 'isa2', 'BiBitR', 'rqubic' and 'BicARE' are implemented. Additionally, 'superbiclust' and 'BcDiag' are also implemented to be able to further investigate results. The GUI also provides a couple of extra utilities to export, save, search through and plot the results. 'RcmdrPlugin.BiclustGUI' also provides a very specific framework for biclustering in which new methods, diagnostics and plots can be added. Scripts were prepared so that R-package developers can freely design their own dialogs in the GUI which can then be added by the maintainer of 'RcmdrPlugin.BiclustGUI'. These scripts do not required any knowledge of 'tcltk' and 'Rcmdr' and are easy to fill in. (Note: rqubic currently requires manual installation through BiocManager::install('rqubic').)

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Depends biclust, fabia, iBBiG,superbiclust(>= 1.1),BcDiag(>= 1.0.10),
BicARE, s4vd, BiBitR(>= 0.3.1)

Imports Rcmdr, tcltk, gplots, grDevices, graphics, methods, utils,
viridis

VignetteBuilder knitr

Suggests knitr, rqubic, BiocManager

NeedsCompilation no

RoxygenNote 7.1.1

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RcmdrPlugin.BiclustGUI-package
The BiclustGUI package

Description

RcmdrPlugin.BiclustGUI is a plug-in package for R Commander (Rcmdr). The package is a *Graphical User Interface* (GUI) in which several *biclustering* methods can be executed, followed by diagnostics and plots of the results. Further, the GUI also has the possibility to connect the methods to more general diagnostic packages for biclustering. Biclustering methods from **biclust**, **fabia**, **iBBiG**, **isa2**, **BiBitR** **rqubic** and **BicARE** are implemented. Additionally, **superbiclust** and **BcDiag** are also implemented to be able to further investigate results. The GUI also provides a couple of extra utilities to export, save, search through and plot the results.

RcmdrPlugin.BiclustGUI also provides a very specific framework for biclustering in which new methods, diagnostics and plots can be added. Scripts were prepared so that R-package developers can freely design their own dialogs in the GUI which can then be added by the maintainer of RcmdrPlugin.BiclustGUI. These scripts do not required any knowledge of **tcltk** and **Rcmdr** and are easy to fill in.

Details

More detailed information about all the implementations and scripting of RcmdrPlugin.BiclustGUI can be found in the vignette. (See the doc folder of package)

Author(s)

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References

Kasim, A., Shkedy, Z., Kaiser, S., Hochreiter, S. and Talloen W. (2016), “Applied Biclustering Methods for Big and High Dimensional Data Using R”, *CRC*

See Also

The Bicluster algorithms in the packages: [biclust](#), [fabia](#), [iBBiG](#), [rqubic](#) and [BicARE](#).
 Additional Plotting & Diagnostics packages: [superbiclust](#) and [BcDiag-package](#)

GUI Functions

GUI Functions

Description

List of GUI functions used for certain buttons.

Details

This list of GUI functions is a mix of 2 types of functions. Some of them simply consist out of combining several functions from a package, linking them all to a single button by placing them together in a function. The other type are special created functions to extract more bicluster information from certain object or bring more functionality to the GUI. Sometimes this last type is based on example code in package documentation, sometimes it is made from scratch. More information of these function can be found throughout the vignette of `RcmdrPlugin.BiclustGUI`.

In general these functions are not meant for public use.

Author(s)

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Internal Functions

List of Internal Functions

Description

List of internal functions used in various functions in the package.

Details

Not to be used by the users.

Author(s)

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Template Script Functions

Template Script Functions

Description

List of internal functions used in the template scripts.

Details

More information of the use of these functions can be found in the vignette. (Guide to New Implementations)

Author(s)

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Window Functions

Window Functions

Description

List of window functions, responsible for creating all the dialogs.

Usage

```

bicare_WINDOW()
bicarebiclust_WINDOW(methodname)
bcdiag_WINDOW(methodname)
bcdiagwrite_WINDOW(methodname, fabia.thresZ, fabia.thresL)
biclustbimax_WIN()
biclustCC_WIN()
biclustextraplots_WINDOW(methodname)
biclustplaid_WIN()
biclustquest_WIN()
biclustspectral_WIN()
biclustXMotif_WIN()
clearresults_WINDOW()
exportFURBY_WINDOW()
exportTXT_WINDOW()
extractbiclust_WINDOW()
fabibiclust_WINDOW(methodname, thresZ, thresL)
fabialaplace_WIN()
fabiapostprojection_WIN()
fabiasparsenessprojection_WIN()

```

```
fabiaSPARSE_WIN()
findbicclusters_WINDOW()
iBBiG_WIN()
image_WINDOW()
isadefault_WIN()
isaextraplots_WINDOW(methodname)
jaccard_WINDOW()
plotgridpref_WINDOW()
rqubic_WINDOW()
saveload_WINDOW()
s4vd_WIN()
search_WINDOW()
ssvd_WIN()
superbiclust_WINDOW(methodname,methodseed,methodsave)
MaxBC_WINDOW()
bibit_WIN()
bibit3_WIN()
bibitworkflow_WIN(methodname)
heatmapJI_WINDOW()
```

Arguments

methodname	These windows are called from a specific biclustering method window. The argument is a string containing the name of the method it is called from.
methodseed	Logical Value of methodseed option for the method chosen in methodname. Superbiclust window needs this information to generate the window correctly (e.g. the repeat analysis box)
methodsave	Logical Value of methodsave option for the method chosen in methodname. Superbiclust window needs this information to apply the repeat analysis correctly
thresZ	Fabia bicluster samples threshold
thresL	Fabia bicluster loadings threshold
fabia.thresZ	See thresZ
fabia.thresL	See thresL

Details

All these window functions for all the biclustering dialogs were created using the template scripts (`newmethod_script.R` & `newtool_script.R`). A detailed description with an example on how to use these scripts and how to create the dialogs, can be found in the appendix (Guideline to New Implementations).

Please note that these template scripts are also located in the doc subdirectory of the package.

Author(s)

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