# Package 'ade4TkGUI'

July 2, 2014

**Version** 0.2-6

**Date** 2012/11/07

**Title** ade4 Tcl/Tk Graphical User Interface

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**Depends** ade4 (>= 1.4-3), tcltk

**Suggests** tkrplot, pixmap

**Description** a Tcl/Tk GUI for some basic functions in the ade4 package

**License** GPL (>= 2)

**URL** <http://pbil.univ-lyon1.fr/ade4TkGUI>, Mailing list:
<http://listes.univ-lyon1.fr/wws/info/adelist>

**Repository** CRAN

**Repository/R-Forge/Project** ade4tkgui

**Repository/R-Forge/Revision** 17

**Repository/R-Forge/DateTimeStamp** 2012-11-07 16:04:55

**Date/Publication** 2012-11-13 06:57:22

**NeedsCompilation** no

## R topics documented:

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ade4TkGUI                                      *Tcl/Tk GUI for the ade4 package*

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### Description

A Tcl/Tk GUI for some basic functions in the ade4 package.

### Usage

```
ade4TkGUI(show = FALSE, history = FALSE)
```

### Arguments

show
: a logical value. If TRUE, R commands executed in the GUI are echoed to the console.

history
: a logical value. If TRUE, R commands executed in the GUI are stored in the R session history.

### Details

Right-click on ade4 function buttons to get help on these functions. You can also click on the questionhead icon in the dialog windows. This displays the R help for the corresponding function.

In all dialog windows, entries can either be filled with a "set" button, or typed directly in the entry field. The "set" button displays a listbox with a list of available objects in the global environment. This list is restricted to objects with an adequate type (dataframe, dudi, factor, etc). Entries can also be filled directly by typing the desired value. In this case, R expressions can also be entered, for example c("red", "green", "blue"), doubs$mil[1:20,1:5], meau$plan$dat , or 1:20.

### Buttons

The first row of buttons (- Data sets -) is used to load data sets, either from a tab-delimited text file exported from Excel (Read data file button), or from the ade4 package built-in datasets (Load a data set button; right-click to get help on the selected dataset).

The second block of buttons (- One table analyses -) gives access to simple analyses (like pca), in which only one table is analysed.

The third block (- One table with groups -) is for analyses in which the rows of the table belong to several groups. This is the case for example for discriminant analysis (discrimin) and for the within and between analyses (see ade4 documentation).

The fourth block (- Two tables analyses -) gives access to three analyses in which the relationships between two data tables are analysed. cca is the well known (at least in ecology) canonical correspondence analysis, coinertia can be seen as a robust alternative to cca when the number of samples is low, and pcaiv is principal components analyses with respect to instrumental variables (see ade4 documentation).

The fifth block (- Graphic functions -) contains three buttons that launch the dialog windows for three basic graphic functions in ade4 : s.label (scatter diagram of a factor map), s.class (scatter diagram with groups), s.value (scatter diagram with squares proportional to one variable).

Other graphic functions are available in the Graphics menu : s.corcircle (correlation circle in normed pca), s.chull (scatter diagram with convex hulls), and s.match (scatter diagram of two paired clouds of points)

The sixth block (- Advanced graphics -) can be used for several things:

- Display dudi displays a dialog window grouping all the components of a dudi. Each of these components is represented by a button which action is to draw a graphical display of the corresponding component. The axes used to draw theses graphics can be set by the user. The last row of buttons gives access to particular graphic functions that can be used according to the dudi type.

- Graph explore is a dynamic graphic exploration of factor maps (it needs the tkrplot package). It allows dynamic operations like zooming, panning, and identifying points. This is particularly usefull when many points are superimposed.

- Monte-Carlo tests displays a dialog window for computing Monte-Carlo tests after (e.g.) a between or coinertia analysis.

### Menu bar

The menu bar at the top of the window can be used to launch the same functions, plus several others. All theses menus are tear-off.

The File menu can be used to read and load files and datasets, to edit a dataframe, and to quit R :

- Read text file allows to read a data file and store the result in a dataframe. It can be used to read standard Excel tab-delimited text files (with variable names on the first row and sample names in the first column, leaving the first cell empty). The name "clipboard" can be used to read a data table just copied from an Excel data sheet (so it is not necessary to save the data in a text file).

- Load data set allows to load a data set from the ade4 package.

- Edit data frame can be used to edit a dataframe.

- Quit R opens a dialog window to ask if the environment should be saved before quitting R.

The Windows menu allows to manage several graphical windows :

- New graphic window opens a new graphic window and makes it the active window. This is usefull to compare easily several graphics.

- Change graphic window changes the active window (i.e., the one into which the next graphic will be drawn).

- Save graphic window saves the graphic drawn in the active window into a disk file in several formats (postscript, pdf, etc).

The 1table, 1table+groups, 2tables, and Graphics menus give access to several other analysis methods and graphics.

### History and command line echoing

If the show argument is set to TRUE, then all the commands executed in the GUI are echoed to the console. This is handy for complex commands, as it allows to check the exact syntax of the command that was executed.

If the `history` argument is set to TRUE, then the commands executed in the GUI (the same as the commands which are echoed to the console) are stored in the R session history buffer. For each command, the history buffer is written to a temporary disk file with `savehistory()`, the command is appended to this file, and the file is reread in memory with `loadhistory()`.

The value (T/F) of both arguments is recalled in the title of the window (ade4TkGUI), so that different instances of the GUI launched simultaneously with different values for these arguments can be easily recognized.

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### Examples

```
## Not run:
## Start the GUI
ade4TkGUI()

## End(Not run)
```

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  ade4TkGUI-internal        *Internal functions for the ade4TkGUI package.*

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### Description

Internal functions for the ade4TkGUI package

### Details

These are not to be called by the user.

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  explore                   *Factor map dynamic exploration function*

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### Description

This function provides graphical tools for dynamically exploring the factor maps obtained in multivariate data analysis. Many operations like zooming, panning, and searching are possible. This is particularly usefull for large datasets, as it is very difficult to identify one particular item on a cluttered factor map.

### Usage

```
explore(call.graph, scale.graph=1.3)
```

## Arguments

call.graph    a call to a graphical function of the ade4 package (s.label, s.arrow, s.class, or s.value).

scale.graph   a scale factor used to resize the drawing. This is particularly usefull for small laptop screens.

## Details

The main window displays the factor map corresponding to the first argument function call. Under this graph, three buttons can be used to close the window, save the graph in a file, and redraw the original graph. A scale widget allows to zoom in or out on the graph (this operation can be slow when the number of points is high).

In the top-right part of the main window, a small graph shows the density distribution of points on the factor map, and a red rectangle shows which part of the graph has been zoomed in.

Under this small graph, four radiobuttons can be used to set the operation mode (see below Operation modes). The Show commands in R console checkbox button allows to echoe the commands to the console.

The Find a point panel gives a list of the labels. Clicking on one label redraws the main graph, centering it around the selected item and displaying it in red. This is handy to locate rapidly a particular item. The text field just above the listbox can be used to type a character string. The list of labels is then searched dynamically as characters are typed and the list is restricted to labels matching the typed string.

The Label options panel is used only when in Labels mode (see below Operation modes).

At the bottom-right of the window, the Information panel lists item labels and x & y coordinates in a listbox.

## Operation modes

Zoom mode is the default mode: clicking in the main graph window increases the zoom factor around the coordinates of the click. If a drag operation is performed (button press, mouse move, button release), then the zone defined by this operation is zoomed in.

Pan mode just moves the center of the main graph to the coordinates where the click occured.

Labels mode gives access to the four buttons of the label options panel. The two buttons Add all and Remove all remove all the labels (leaving only small black dots) or set them back in the graph. The Select... button display a listbox with all the labels, allowing to select some of them, which are then displayed on the factor map. The By values... button also allows to select labels, but based on the x and y numerical ranges.

Identify mode is usefull when labels are not displayed. It gives the label of the nearest item after a mouse click in the main graph window. Typical use is after zooming to separate cluttered points.

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**Examples**

```
## Not run:
## Start the GUI
data(meau)
acpmil <- dudi.pca(meau$mil, scannf=F)
explore(s.label(acpmil$li))

## End(Not run)
```

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ordiClust                          *Ordination and Cluster analysis*

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**Description**

This function does cluster analysis on ordination scores, providing a dynamic exploration of the clusters on the factor maps. As a first step, an ordination method computes the row scores of the input data table. In a second step, cluster analysis is used on these row scores to obtain groups. The dudi and the factor are available in the global environment under the names ordiClust.dudi and ordiClust.factor.

**Usage**

```
ordiClust(datatab=NULL, hscalef=1.2, vscalef=1.2, maxgr=20)
```

**Arguments**

| | |
|---|---|
| datatab | a dataframe containing the data table to analyse, or directly a dudi. |
| hscalef | horizontal scale factor used to resize the drawing in the tkrplot window. |
| vscalef | vertical scale factor used to resize the drawing in the tkrplot window. |
| maxgr | maximum number of groups displayed on the ordination factor map. |

**Details**

The GUI is divided in a graph panel on the right and several dialog panels on the left.

Under the graph panel, a scale widget can be used to set the number of groups, and three buttons allow to change the graphical parameters (ellipses or convex hulls, and color or black & white). The `Submit` button under the graph (or the return key) draws the groups on the factor map. `Up arrow` and `Down arrow` keys (or the scale widget) can be used to increase or decrease the number of groups. Choosing another clustering algorithm or another distance automatically updates the graph, allowing easy comparisons. The `Dismiss` button at the bottom of the window closes the ordiClust window, and the `Save` button can be used to save the current graphic in a disk file.

From top to bottom the left panels are :

`Input data frame` : this is the data table that will be analysed. The user can set it with the `Set` button.

`Input dudi` : this is directly the dudi that will be analysed. The user can set it with the `Set` button. No ordination method should be used when a dudi is selected here: cluster analysis will be done on the row scores of this dudi.

`Ordination method` : the user can choose between principal component analysis (centered or normed), correspondence analysis, and multiple correspondence analysis. After computations are finished, the eigenvalues bar chart is displayed in the right panel. The user can then set the number of principal components (axes) on which cluster analysis will be done with the `Set` button (defaults to 2). If no number is chosen, then all axes are kept.

`Ordination graph` : draw the factor maps for rows or columns. Axis numbers can be chosen (default is 1 for X axis and 2 for Y axis).

`Cluster analysis - Distance` : choose the way distances are computed among rows. See help("dist"). The dudi option is a special case: computations are done with the `dist.dudi` function of the ade4 package (i.e., for a normed PCA this is the Euclidean distance computed on normed variables).

`Cluster analysis - Cluster method` : choose the clustering algorithm. See help("hclust"). The `Submit` button starts the computations and the hierarchical tree is displayed in the right panel. Choosing another algorithm or another distance automatically updates the graph, allowing easy comparisons.

`Number of groups` : this is the number of groups used to cut the tree computed by cluster analysis. The `Cut tree` button cuts the tree and draws a red line on the right panel. `Up arrow` and `Down arrow` keyboard keys (or the scale widget) can be used to increase or decrease this value respectively.

`Level height` : height of the cut level in the tree computed by cluster analysis. The `Cut tree` button cuts the tree and draws a red line on the right panel.

`Inertia ratio` : this is the between group to total inertia ratio (percentage of explained vari-

ance). The `Draw curve` button draws the curve of this ratio as a function of the number of groups. Steps on this curve can be used to choose the number of groups. The red cross on this graph gives the number of groups and the corresponding percentage of between-groups inertia. `Up arrow` and `Down arrow` keys (or the scale widget) can be used to increase or decrease the number of groups. Choosing another clustering algorithm or another distance automatically updates the graph, allowing easy comparisons.

`BGA MCTest p-value` : p-value of the Between Groups Analysis Monte-Carlo test (BGA, ade4 `between` function).

The dudi and the factor used to draw the graphs are available in the global environment, withe the names `ordiClust.dudi` and `ordiClust.factor`.

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### Examples

```
## Not run:
## Start the GUI form the console
data(meau)
ordiClust(dudi.pca(meau$mil,scan=F))

## End(Not run)
```

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