

# Package ‘mcaGUI’

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**Version** 1.4.0

**Title** Microbial Community Analysis GUI

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**Depends** lattice, MASS, proto, foreign, gWidgets(>= 0.0-36),gWidgetsRGtk2(>= 0.0-53), OTUbase, vegan, bpca

**Suggests**

**Enhances** iplots, reshape, ggplot2, cairoDevice, OTUbase

**Description** Microbial community analysis GUI for R using gWidgets.

**biocViews** GUI, Visualization, Bioinformatics, Clustering, Sequencing

**License** GPL (>= 2)

**URL** <http://www.ibest.uidaho.edu/ibest/index.php>

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ibestGUI-package      *ibestGUI*

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### Description

mcaGUI is a Simple GUI used in the analysis of microbial communities using RGtk2 and gWidgetsRGtk.

### Details

Further information is available in the following vignettes:

manual    pmg (source, pdf)

### Author(s)

Wade Copeland with original PMG source by John Verzani Authors: Wade K. Copeland, Vandhana Krishnan, Daniel Beck, Matt Settles, Zaid Abdo

Authors: Wade K. Copeland, Vandhana Krishnan, Daniel Beck, Matt Settles, James Foster, Kyu-Chul Cho Mitch Day, Roxana Hickey, Ursel M.E. Schutte, Xia Zhou, Chris Williams, Larry J. Forney, Zaid Abdo

Additional Input and Suggestions: John Verzani - Author of Original of the PMG Source Code used as a backend for mcaGUI.

Maintainer: Wade K. Copeland <wade@kingcopeland.com> URL: <http://www.ibest.uidaho.edu/ibest/index.php>

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mcaGUI                      *A function to start the ibest GUI*

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### Description

The mcaGUI is a simple GUI for R using RGtk2 as the graphical toolkit. The GUI is written using the gWidgets interface to a toolkit.

### Usage

```
mcaGUI(cliType="console", width=850, height=.75*width,guiToolkit="RGtk2")
```

```
pmg.add(widget,label)
```

```
pmg.gw(lst, label=NULL)
```

```
pmg.addMenubar(menuList)
```

```
pmg.eval(command, assignto=NULL)
```

**Arguments**

<code>cliType</code>	Where to send output of function called within <code>ibestGUI</code> function? This can be either "console" to put output into console that called <code>ibestGUI</code> , or "GUI" to put output into a widget.
<code>width</code>	Width in pixels of initial window
<code>height</code>	height in pixels of initial window
<code>guiToolkit</code>	Specify toolkit to use with <code>gWidgets</code>
<code>widget</code>	A <code>gWidgets</code> widget to add to the main notebook for holding dialogs
<code>label</code>	A string containing a label to put on the tab when adding a widget to the main notebook for holding dialogs
<code>lst</code>	A value passed to <code>ggenericwidget</code> . Can be a list, a function name or a function
<code>menulist</code>	A list passed to <code>gmenu</code> for adding to the menubar
<code>command</code>	A string containing a command to be parsed and evaluated in the global environment
<code>assignto</code>	If non-NULL, a variable name to assign the output generated from evaluating the command

**Details**

The user can add to the menubar at start up time by defining a list that is called by `gmenu`. `IBESTgui` look for a variable `pmg.user.menu`. This is a list with named components. Each name becomes the menubar entry top level, and each component is called by `gmenu` to populate the menubar entry.

The functions `pmg.add`, `pmg.gw`, `pmg.addMenubar`, and `pmg.eval` are used to extend the GUI.

**pmg.add** This is used to add a widget to the main notebook containing the dialogs

**pmg.gw** This is used to add a `ggenericwidget` instance to the main notebook containing the dialogs. These widgets can be generated from a function name using the values from `formals`

**pmg.addMenubar** Used to add top-level entries to the main menubar

**pmg.eval** Used to send a command, as a string, to the Commands area to be evaluated. Evaluation is done in the global environment.

**Author(s)**

Origan function John Verzani with modifications by Wade K. Copeland

**Examples**

```
## Not run:
## this restarts the GUI if the main window has been closed
mcaGUI()

## End(Not run)
```

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 pmg-dynamic

*"Dynamic" widgets for pmg*


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## Description

We call a widget "dynamic" if it updates itself immediately when an event occurs, such as a drag and drop, or a change in some value. The dynamic widgets documented here, are meant to provide quick, easy (but limited) access to R's modeling functions, R's significance tests, and R's lattice functions

## Usage

```
dLatticeExplorer(container = NULL, ...)
```

## Arguments

container	A container to attach the object to
...	Currently ignored

## Details

For each "dynamic" widget, the variables can be specified by drag and drop, or by editing the widget. The bold-face areas of each widget can be edited by clicking on them or by dropping values. If the drop value comes from a column of an `idf` instance, then when that column is edited, the dynamic widget is updated. Such variables can not be edited or changed. Other variables may, such as writing powers, or applying functions.

The "dynamic" widgets are meant for easy exploration, but not for saving of actions.

The `ilatticeexplorer` function creates a dynamic graphing widget based on lattice graphics. Up to three variables (only 2 for univariate graphs) may be dropped on the widget. The order is for univariate graphs:  $\sim x$  then  $\sim x \mid y$ . And for bivariate graphs  $x$ ,  $x \sim y$ ,  $x \sim y \mid z$ . The panel functions add to the plots of dots by, typically, incorporating some trend line.

## Value

Although there are methods for `dModelsDialog`, these widgets aren't meant to be interacted with from the command line.

## Note

Some of the usability was inspired by the Fathom software.

## Author(s)

John Verzani

## Examples

```
## Not run:
dLatticeExplorer()

## End(Not run)
```

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pmg-undocumented	<i>Undocumented, but exported, functions</i>
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**Description**

These functions are used in the global environment and so must be exported. However, they are not intended for general use.

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pmgRepeatTrials	<i>A function to simplify simulations</i>
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**Description**

A simple function to repeat an expression several times as an aid to simplifying simulations.

**Usage**

```
pmgRepeatTrials(expr, n = 10)
```

**Arguments**

expr	An R expression, such as <code>rnorm(1)</code> or <code>{x &lt;- rnorm(10); t.test(x)\$p.value}</code> that will be repeated <code>n</code> times.
n	Number of times to repeat the expressions. The default is 10.

**Details**

This function aids in doing simulations. Rather than explicitly write a for loop or use `sapply` this function will call `sapply` on the expression.

A GUI for this appears in pmg under the Simulation tab. The "quick action" will call the function on the results of the simulation.

**Value**

The output of a `sapply` call can be a vector, matrix, ... If it is a vector, it is transposed/

**Note**

This function and GUI was suggested by Daniel Kaplan at useR!2007

**Author(s)**

John Verzani

**Examples**

```
res <- pmgRepeatTrials(rnorm(1))
hist(res)

g = data.frame(
  father = c(78.5, 78.5, 77.5, 76.0, 75.5),
  mother = c(67.0, 68.0, 66.0, 65.5, 62.0),
  sex    = c("M", "M", "F", "F", "M"),
  nkids  = c(4, 4, 1, 2, 5)
)
res <- pmgRepeatTrials(coef(lm(father~ sex + sample(nkids),data=g)),100)
print(res)
```

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