Package: leem (via r-universe)

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Type Package

Title Laboratory of Teaching to Statistics and Mathematics

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Description An educational package for the teaching of statistics and mathematics in primary and higher education. The objective is to assist in teaching/learning for both student study planning and teacher teaching strategies. The leem package will try to bring, in a simple and at the same time in-depth, knowledge of statistics and mathematics to everyone who wants to study these areas of knowledge. The main function of the package is 'leem' function.

Imports tcltk, tkrplot, tkRplotR, manipulate, crayon, grDevices, graphics, utils, diagram

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URL `https://bendeivide.github.io/project/leem/`, `https://github.com/bendeivide/leem`

BugReports `https://github.com/bendeivide/leem/issues`

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RemoteUrl https://github.com/bendeivide/leem

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Contents

`amplitude` *Range*

Description

Compute the sample range

Usage

```
amplitude(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
set.seed(10)
rpois(30, 2.5) |>
  new_leem() |>
  amplitude(grouped = FALSE)
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  amplitude()
```

`apf` *Plot of probability function of any discrete variable*

Description

Help in building the plot of the probability function of any discrete variable

Usage

```
apf(x, p, main = NULL, xlab = NULL, ylab = NULL, ...)
```

Arguments

`x`	numeric vector of values of X. See **Details**.
`p`	numeric vector of $p_X(x)$. See **Details**.
`main`	main title for the plot.
`xlab`	a label for the x axis.
`ylab`	a label for the y axis.

Details

Consider the X distribution:

$$\begin{array}{rccccc} p_X(x): & 0.23 & 0.27 & 0.30 & 0.12 & 0.08 \\ x: & 1 & 2 & 3 & 4 & 5 \end{array}$$

where $p_X(x)$ and x are probability function and values of X. See *Example 1*.

Value

The output is plot of distribution function. See *Example 1*.

Examples

```
# Example 1
x <- 1:5
p <- c(0.23, 0.27,0.30, 0.12, 0.08)
apf(x, p)
```

`barplot.leem` *Barplot graph*

Description

Class method leem for generic barplot

Usage

```
barplot(x, ...)

## Leem S3 method:
barplot.leem(x, freq = "a", bg = TRUE, main = NULL, xlab = NULL, ylab = NULL,
  grids = grid(col = "white"), bgcol = "gray", bgborder = NA,
  barcol = "yellow", barborder = "gray", posx1 = 0, posx2 = 0,
  xang = 0, labels = NULL, ...)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`freq`	Character argument. Type of frequency with options: `"a"` (absolute and default), `"r"` relative and `"p"` percentage.
`bg`	Logical argument. Default is `TRUE`, it displays the background, and `bg = FALSE` otherwise.
`main`	Character argument. Insert the plot title. The default is `NULL`.
`xlab`	Character argument. Insert the title of the x-axis graphic label. The default is `NULL`.
`ylab`	Character argument. Insert the title of the y-axis graphic label. The default is `NULL`.

`grids`	Insert grids to plot. The default is `grid(col = "white")`.
`bgborder`	Character argument. Insert the background border color. This argument is only valid when bg = `TRUE`. The default is bgborder = NA.
`barcol`	Character argument. Insert the barplot color. The default is `barcol = "yellow"`. This argument is only valid when `bars = TRUE`.
`barborder`	Numeric argument. Insert the barplot border color. This argument is only valid when `bars = TRUE`. The default is barborder = "gray".
`posx1`	Numeric argument.Distance of the labels (horizontal) in relation to the x axis.
`posx2`	Numeric argument.Distance of the labels (vertical) in relation to the x axis.
`xang`	Numeric argument.Angle of the labels in relation to the x axis
`labels`	Character argument. Labels name vector.
`...`	further arguments passed to or from other methods.

Examples

```
library(graphics)
# Example 1 - Simple example
library(leem)
rep(1:5, 5:1) |>
  new_leem() |>
  barplot()
# Example 2 - Color bars
rep(1:5, 5:1) |>
  new_leem() |>
  barplot(barcol = heat.colors(5))
# Example 3 - Ordered data
library(leem)
school <- rep(c("high", "university", "basic"), 3:5)
sample(school, 30, TRUE) |>
 new_leem() |>
 tabfreq(ordered = c("basic", "high", "university")) |>
 barplot(xang = 15, posx2 = -0.2)
# Example 4 - Coerced to histogram
rnorm(100, 10, 2) |>
  new_leem(variable = 2) |>
  barplot(barcol = heat.colors(10))
```

`boxplot.leem` *Box plot*

Description

Produce box-and-whisker plot(s) of leem class object and computes the necessary values for the development of the plot.

Usage

```
## S3 method for class 'leem'
boxplot(
  x,
  type = "rawdata",
  details = FALSE,
  horizontal = FALSE,
  coef = 1.5,
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  col = rgb(0, 175, 239, maxColorValue = 255),
  ...
)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`type`	character argument. Default is `rawdata`. If `type = "classes"`, the function returns a boxplot plot for each set of data grouped of classes of `x` object.
`details`	Logical argument. Default is `FALSE`, otherwise, in addition to the plot, the measurements necessary for the development of the plot will be displayed on the console.
`horizontal`	Logical argument indicating if the boxplots should be horizontal; default `FALSE` means vertical boxes.
`coef`	this determines how far the plot whiskers extend out from the box. If `coef` is positive, the whiskers extend to the most extreme data point which is no more than `coef` times the interquartile range from the box. A value of zero causes the whiskers to extend to the data extremes.
`main`	Title name. Defaults is `NULL`.
`xlab`	a label for the `x` axis. Defaults is `NULL`.
`ylab`	a label for the `y` axis. Defaults is `NULL`.
`col`	Character vector. Default `col = rgb(0, 175, 239, maxColorValue = 255)`.
`...`	further arguments passed to or from other methods.

Examples

```
library(leem)
library(boxplot)
# Example 1
x <- rnorm(30, 100, 2) |>
  new_leem(variable = 2) |>
  tabfreq()
boxplot(x, details = TRUE)
# Example 2
boxplot(x, type = "classes")
```

`cdfd` *Plot of cumulative distribution function of any discrete variable*

Description

Help in building the plot of the cumulative distribution function of any discrete variable

Usage

```
cdfd(x, fda, main = NULL, xlab = NULL, ylab = NULL)
```

Arguments

`x`	numeric vector of values of X. See **Details**.
`fda`	numeric vector of $F_X(x)$. See **Details**.
`main`	main title for the plot.
`xlab`	a label for the x axis.
`ylab`	a label for the y axis.

Details

Consider the X distribution:

$$\begin{array}{rccccc} p_X(x): & 0.23 & 0.27 & 0.30 & 0.12 & 0.08 \\ x: & 1 & 2 & 3 & 4 & 5 \end{array}$$

where $p_X(x)$ and x are probability function and values of X. Consider also the X distribution function:

$$F_X(x) = \begin{cases} 0, & \text{if } x < 1; \\ 0.23, & \text{if } 1 \leq x < 2; \\ 0.50, & \text{if } 2 \leq x < 3; \\ 0.80, & \text{if } 3 \leq x < 4; \\ 0.92, & \text{if } 4 \leq x < 5; \\ 1.00 & \text{if } x \geq 5. \end{cases}$$

This way, the `cdfd` function needs to consider only the vectors `x <- 1:5` and `fda <- c(0.23, 0.50, 0.80, 0.92, 1)`, that is, only the equality conditions for x. See *Example 1*.

Value

The output is plot of distribution function. See *Example 1*.

Examples

```
# Example 1
x <- 1:5
fda <- c(0.23, 0.5, 0.8, 0.92, 1)
cdfd(x, fda)
```

`cv` *Coefficient of variation*

Description

Compute the sample coeffient of variation

Usage

```
cv(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
rpois(30, 2.5) |>
  new_leem() |>
  cv()
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  cv(grouped = FALSE)
```

`hist.leem` *Histogram graph*

Description

Class method leem for generic hist

Usage

```
hist(x, ...)

## Leem S3 method:
hist.leem(x, bg = TRUE, main = NULL, xlab = NULL, ylab = NULL,
          grids = grid(col = "white"), bgcol = "gray", bgborder = NA,
          barcol = "yellow", barborder = "gray", ...)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`freq`	Character argument. Type of frequency with options: `"a"` (absolute and default), `"r"` relative and `"p"` percentage.
`bg`	Logical argument. Default is `TRUE`, it displays the background, and `bg = FALSE` otherwise.
`main`	Insert the plot title. The default is `NULL`.
`xlab`	Insert the title of the x-axis graphic label. The default is `NULL`.
`ylab`	Insert the title of the y-axis graphic label. The default is `NULL`.
`grids`	Insert grids to plot. The default is `grid(col = "white")`.
`bgcol`	Insert the background color. This argument is only valid when `bg = TRUE`. The default is `bgcol="gray"`.
`bgborder`	Insert the background border color. This argument is only valid when `bg = TRUE`. The default is bgborder = NA.
`barcol`	Insert the barplot color. The default is `barcol = "yellow"`. This argument is only valid when `bars = TRUE`.
`...`	further arguments passed to or from other methods.

Examples

```
# Example 1
library(leem)
rnorm(36, 100, 50) |> new_leem(variable = "continuous") |> tabfreq() |> hist()

# Example 2
library(leem)
school <- rep(c("high", "university", "basic"), 3:5)
sample(school, 30, TRUE) |>
```

```
new_leem() |>
tabfreq(ordered = c("basic", "high", "university"))
```

`insert` *Insert measures of position in plot*

Description

Generic function that allows inserting measures of position in plots

Usage

```
insert(dados, ...)

## Leem S3 method:
insert(x, type = "black", lcol, tcol = lcol, acol = lcol, parrow = 0.5,
       larrow = 0.2, ptext = 0.6, side = "right", lwd = 2, lwdarrow = lwd)

## Default S3 method:
insert(x)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`type`	Type of measure of position. The default is `type = "mean"`. Other options: `"median"`, `"mode"` or `"all"`.
`lcol`	Vertical line color type. The default is `lpcol = "black"`. This argument must be the same length as the `type` argument.
`tcol`	Text color type. The default is `tcol = lcol`.
`acol`	Arrow color type. The default is `acol = lcol`.
`parrow`	Text and arrow height. The default is `parrow = 0.5`. This argument must be the same length as the `type` argument.
`larrow`	Text and arrow length. The default is `larrow = 0.6`.
`ptext`	Distance between lines of text. The default is `ptext = 0.06`.
`side`	Side to insert the text. The default is `side = "right"`. This argument must be the same length as the `type` argument.
`lwd`	numeric argument. The vertical line width. The default is `lwd = 2`.
`lwdarrow`	numeric argument. The arrow width. The default is `lwdarrow = lwd`.

Value

The result of `tabfreq()` is a list. This list has two elements: `table` and `statistics`. The first is the data frequency table, and the second represents some useful statistics for methods of leem class.

Examples

```
# Example 1
library(leem)
set.seed(10)
rnorm(36, 100, 50) |>
 new_leem(variable = "continuous") |>
 tabfreq() |>
 hist() |>
 insert(
  lcol = "black",
  tcol = "purple",
  acol = "brown",
  parrow = 0.6,
  larrow = 0.6,
  ptext = 0.4,
  side = "left",
  lwd = 2,
  lwdarrow = 4
 )
```

`leem` *Graphical User Interface for leem package*

Description

`leem` A Graphical User Interface (GUI) for the leem package

Usage

```
leem(gui = TRUE)
```

Arguments

`gui`	Logical argument, `TRUE` or `FALSE`. The default is `TRUE`

Value

`leem` presents GUI with various problems for the teaching of statistics and mathematics. The idea is to use this package to learn these subjects without necessarily programming in R

Examples

```
# Loading package
library(leem)
if (interactive()) {
  leem(gui = FALSE)
}
```

---

madev *Mean absolute deviation*

Description

Compute the sample mean absolute deviation

Usage

```
madev(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
set.seed(10)
rpois(30, 2.5) |>
  new_leem() |>
  madev(grouped = FALSE)
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  madev()
```

---

mean.leem *Arithmetic mean Class method leem for the generic mean function*

Description

Arithmetic mean Class method leem for the generic mean function

Usage

```
## S3 method for class 'leem'
mean(
  x,
  trim = 0,
  na.rm = FALSE,
  rounding = 2,
  grouped = TRUE,
  details = FALSE,
  ...
)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function. Complex vectors are allowed for `trim = 0`, only.
`trim`	The fraction (0 to 0.5) of observations to be trimmed from each end of x before the mean is computed. Values of trim outside that range are taken as the nearest endpoint.
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).
`details`	Logical object. Details of data (default `FALSE`).
`...`	further arguments passed to or from other methods.

Examples

```
# Example 1
set.seed(10)
x <- rnorm(36, 100, 50)
y <- rbinom(36, 10, 0.8)
y <- rep(letters[1:4], 1:4)
y |> new_leem(variable = "discrete") |> tabfreq() |> mean()
x |> new_leem(variable = "continuous") |> tabfreq() |> mean()
```

`medev` *Median absolute deviation*

Description

Compute the sample median absolute deviation

Usage

```
medev(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
set.seed(10)
rpois(30, 2.5) |>
  new_leem() |>
  medev(grouped = FALSE)
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  medev()
```

`median.leem` *Median value*

Description

Class method leem for the generic median function

Usage

```
## S3 method for class 'leem'
median(x, na.rm = FALSE, rounding = 2, grouped = TRUE, details = FALSE, ...)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).

`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).
`details`	Logical object. Details of data (default `FALSE`).
`...`	further arguments passed to or from other methods.

Examples

```
library(leem)
library(stats)
# Examples
rnorm(36, 100, 50) |> new_leem(variable = 2) |> tabfreq() |> median()
```

`mfreq` *Mode value*

Description

Compute the sample mode.

Usage

```
mfreq(x, na.rm = FALSE, rounding = 2, grouped = TRUE, details = FALSE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default 2).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).
`details`	Logical object. Details of data (default `FALSE`).
`...`	further arguments passed to or from other methods.

Examples

```
library(leem)
# set.seed(10)
x <- rnorm(36, 100, 50)
set.seed(10)
y <- rbinom(36, 10, 0.8)
w <- rep(letters[1:4], 1:4)
(tab1 <- y |> new_leem(variable = "discrete") |> tabfreq())
(tab2 <- x |> new_leem(variable = "continuous") |> tabfreq())
(tab3 <- w |> new_leem(variable = "discrete") |> tabfreq())
y |> new_leem(variable = "discrete") |> tabfreq() |> mfreq()
```

```
x |> new_leem(variable = "continuous") |> tabfreq() |> mfreq()
w |> new_leem(variable = "discrete") |> tabfreq() |> mfreq()
```

`mpos` *Measures of position*

Description

Compute all measures of position

Usage

```
mpos(
  x,
  trim = 0,
  na.rm = FALSE,
  rounding = 2,
  grouped = TRUE,
  details = FALSE,
  ...
)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function. Complex vectors are allowed for `trim = 0`, only.
`trim`	The fraction (0 to 0.5) of observations to be trimmed from each end of x before the mean is computed. Values of trim outside that range are taken as the nearest endpoint.
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).
`details`	Logical object. Details of data (default `FALSE`).
`...`	further arguments passed to or from other methods.

Details

The measures of position are: average, median and mode.

Examples

```
# Example 1: Poisson data
rpois(30, 2.5) |>
  new_leem() |>
  mpos()
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  mpos(grouped = FALSE)
```

`mstde` *Mean standard error*

Description

Compute the sample mean standard error

Usage

```
mstde(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
set.seed(10)
rpois(30, 2.5) |>
  new_leem() |>
  mstde(rounding = 4)
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  mstde(grouped = FALSE)
```

`new_leem` *Constructor of object of leem class*

Description

Constructor of object of leem class

Usage

```
new_leem(x = vector(), variable = "discrete")
```

Arguments

`x`	R object (vector as data structure).
`variable`	Type of data. If `discrete` (default), the data are categorical (numeric or not). If continuous, the data are numeric.

Value

The `variable` argument also allows using `variable = 1` for categorical variable and `variable = 2` for continuous variable.

Examples

```
# Example 1
library(leem)
x <- rbinom(36, 10, 0.6)
new_leem(x, variable = 1)

# Example 2 (Pipe operator)
rnorm(36, 100, 4) |> new_leem(variable = 2)
```

`ogive` *Ogives Graph*

Description

Generic function that plots the culmulative frequency curve.

Usage

```
ogive(x, ...)

## Leem S3 method:
ogive(x, decreasing = FALSE, both = FALSE, bars = FALSE,
      histogram = FALSE, bg = TRUE, main = NULL, xlab = NULL, ylab = NULL,
      grids = grid(col = "white"), bgcol = "gray", bgborder = NA,
      barcol = "yellow", histcol = barcol, barborder = "gray",
      histborder = barborder, type = "b", lpcol = "black", lwd = 2,
      pch = 19, lty = 2)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`...`	further arguments passed to or from other methods.
`freq`	Character argument. Type of frequency with options: `"a"` (absolute and default), `"r"` relative and `"p"` percentage.
`decreasing`	Logical argument. Default is `FALSE`. If `decreasing = FALSE`, it represents the "ogive larger than", if `decreasing = TRUE`, it represents the "ogive less than".
`both`	Logical argument. Default is `FALSE`. If `both = TRUE`, both o will be plotted. If `both = FALSE` otherside.
`bars`	Logical argument. Default is `FALSE`. If `bars = TRUE`, the bars of the accumulated frequency will be inserted to plot, according to the `decreasing` argument. If `bars = FALSE` otherside.
`histogram`	Logical argument. Default is `FALSE`. If `histogram = TRUE`, the histogram will be inserted to plot.
`bg`	Logical argument. Default is `TRUE`, it displays the background, and `bg = FALSE` otherwise.
`main`	Insert the plot title. The default is `NULL`.
`xlab`	Insert the title of the x-axis graphic label. The default is `NULL`.
`ylab`	Insert the title of the y-axis graphic label. The default is `NULL`.
`grids`	Insert grids to plot. The default is `grid(col = "white")`.
`bgcol`	Insert the background color. This argument is only valid when `bg = TRUE`. The default is `bgcol="gray"`.
`bgborder`	Insert the background border color. This argument is only valid when `bg = TRUE`. The default is bgborder = NA.
`barcol`	Insert the barplot color. The default is `barcol = "yellow"`. This argument is only valid when `bars = TRUE`.
`histcol`	Insert the histogram color. The default is `histcol = barcol`. This argument is only valid when `histogram = TRUE`.
`barborder`	Insert the barplot border color. This argument is only valid when `bars = TRUE`. The default is barborder = "gray".

`histborder`	Insert the histogram border color. This argument is only valid when `histogram = TRUE`. The default is histborder = barborder.
`type`	Type of plot. The default is `type = "b"`, i.e., line and points. See `graphical parameter` for details.
`lpcol`	Type of line color. The default is `lpcol = "black"`.
`lwd`	numeric argument. The line width. The default is `lwd = 2`.
`pch`	Type of point. The default is `pch = 19`.
`lty`	Type of line. The default is `lty = 2`.

Examples

```
library(leem)
# Example 1 - Both ogives
rnorm(36, 100, 50) |> new_leem(variable = 2) |> tabfreq() |> ogive(both = TRUE)

# Example 2 - Insert barplot
rnorm(36, 100, 50) |> new_leem(variable = 2) |> tabfreq() |> ogive(both = TRUE, bars = TRUE)
# Example 3 - Insert histogram
rnorm(36, 100, 50) |> new_leem(variable = 2) |> tabfreq() |> ogive(both = TRUE, hist = TRUE)
```

`piechart` *Pie Chart*

Description

Draw a pie chart.

Usage

```
piechart(
  x,
  labels = NULL,
  col = heat.colors(5, 1),
  border = FALSE,
  main = NULL,
  ...
)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`labels`	One or more expressions or character strings giving names for the slices
`col`	Character vector. Default `col = heat.colors(5)`.
`border`	Logical argument (default `FALSE`).
`main`	Title name.
`...`	further arguments passed to or from other methods.

Examples

```
library(leem)
# Example 1
school <- rep(c("high", "university", "basic"), 3:5)
x <- sample(school, 30, TRUE) |>
  new_leem() |>
  tabfreq(ordered = c("basic", "high", "university"))
# Example 2
x <- rbinom(36, 10, 0.6)
x <- new_leem(x, variable = "discrete")
x <- tabfreq(x)
piechart(x)
```

`polyfreq` *Frequency polygon Graph*

Description

Generic function that plots the frequency polygon curve.

Usage

```
polyfreq(x, ...)

## Leem S3 method:
polyfreq.leem(x, type = "b", bars = TRUE, bg = TRUE, main = NULL,
                      xlab = NULL, ylab = NULL, grids = grid(col = "white"),
                      bgcol = "gray", bgborder = NA, barcol = "yellow",
                      barborder = "gray", lpcol = "black", lwd = 2, pch = 19,
                      lty = 2)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`...`	further arguments passed to or from other methods.
`freq`	Character argument. Type of frequency with options: `"a"` (absolute and default), `"r"` relative and `"p"` percentage.
`type`	Type of plot. The default is `type = "b"`, i.e., line and points. See `graphical parameter` for details.
`bars`	Logical argument. Default is `FALSE`. If `bars = TRUE`, the histogram will be inserted to plot.
`bg`	Logical argument. Default is `TRUE`, it displays the background, and `bg = FALSE` otherwise.
`main`	Insert the plot title. The default is `NULL`.
`xlab`	Insert the title of the x-axis graphic label. The default is `NULL`.

`ylab`	Insert the title of the y-axis graphic label. The default is `NULL`.
`grids`	Insert grids to plot. The default is `grid(col = "white")`.
`bgcol`	Insert the background color. This argument is only valid when `bg = TRUE`. The default is `bgcol="gray"`.
`bgborder`	Insert the background border color. This argument is only valid when `bg = TRUE`. The default is bgborder = NA.
`barcol`	Insert the barplot color. The default is `barcol = "yellow"`. This argument is only valid when `bars = TRUE`.
`histcol`	Insert the histogram color. The default is `histcol = barcol`. This argument is only valid when `histogram = TRUE`.
`barborder`	Insert the barplot border color. This argument is only valid when `bars = TRUE`. The default is barborder = "gray".
`histborder`	Insert the histogram border color. This argument is only valid when `histogram = TRUE`. The default is histborder = barborder.
`lpcol`	Type of line color. The default is `lpcol = "black"`.
`lwd`	numeric argument. The line width. The default is `lwd = 2`.
`pch`	Type of point. The default is `pch = 19`.
`lty`	Type of line. The default is `lty = 2`.

Examples

```
# Example 1
library(leem)
rnorm(36, 100, 50) |> new_leem(variable = "continuous") |> tabfreq() |> polyfreq()
```

`probnormal` *Draw a pie chart.*

Description

Draw a pie chart.

Usage

```
probnormal(
  a = 1,
  b = 2,
  col = "lightblue",
  mean = 0,
  sd = 1,
  type = 1,
  rounding = 4,
  zang = 0,
  xang = 0
)
```

Arguments

`col`	Character vector. Default `col` = `heat.colors(5)`.
`x`	R object (list) of class leem. Use `new_leem()` function.
`labels`	One or more expressions or character strings giving names for the slices
`border`	Logical argument (default `FALSE`).
`main`	Title name.
`...`	further arguments passed to or from other methods.

Examples

```
library(leem)
# Example 1
school <- rep(c("high", "university", "basic"), 3:5)
x <- sample(school, 30, TRUE) |>
  new_leem() |>
  tabfreq(ordered = c("basic", "high", "university"))
# Example 2
x <- rbinom(36, 10, 0.6)
x <- new_leem(x, variable = "discrete")
x <- tabfreq(x)
piechart(x)
```

`Q` *Quantile distribution function.*

Description

`Q` Quantile function for multiple distributions.

Usage

```
Q(
  p,
  dist = "normal",
  lower.tail = TRUE,
  two.sided = FALSE,
  rounding = 2,
  gui = "plot",
  mfrow = c(1, 2),
  type = "both",
  ...
)
```

Arguments

`p`	probability. The `p` argument need have length 1 and value lower then 1.
`dist`	distribution to use. The default is `'normal'`. Options: `'normal'`, `'t-student'`, `'gumbel'`, `'binomial'`, `'poisson'`, and ....
`lower.tail`	logical; if `TRUE` (default), the quantile function is computed; otherwise, the complement of the quantile function (survival function) will be computed. The `lower.tail` argument will only be valid for `two-sided = FALSE`.
`two.sided`	logical. if `TRUE` (default), the calculation of the quantile function and survival will be presented; otherwise the `Q()` function will be based according to the `lower.tail` argument.
`rounding`	numerical; it represents the number of decimals for calculating the probability.
`gui`	default is `'plot'`; it graphically displays the result of the probability. Others options are: `"plot"` and `"rstudio"` and `"tcltk"`.
`mfrow`	numerical vector. Considering the arguments `two.sided = TRUE` and `type = "both"`, the default will be to present two graphs (based on CDF and PDF) horizontally for the quantile function, that is, `mfrow = c(1, 2)` (default).
`type`	character argument. The default is `"both"`; the output will display two plots (based on CDF and PDF) to present the result of Q(). The other options are: `"cdf"` and `"pdf"`.
`...`	additional parameters according to the chosen distribution.

Details

The expression of quantile function is given by:

$$Q(p) = \inf x \in \mathbb{R} : p \leq F(x),$$

where `p` is the first argument of `Q()` and `x` its return value;

Value

`Q` returns the quantile and its graphical representation for a given distribution. The output is a vector.

Examples

```
# Attaching package
library(leem)
## Not run:
Q(p = 0.8, dist = "normal", mean = 200, sd=30)

## End(Not run)
```

`sdev` *Standard Deviation*

Description

Compute the sample standard deviation

Usage

```
sdev(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
rpois(30, 2.5) |>
  new_leem() |>
  sdev()
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  sdev(grouped = FALSE)
```

`showboxplot` *Undertanding a box plot*

Description

Detailing of a box plot, showing the main information contained in this type of graph

Usage

```
showboxplot(horizontal = FALSE, col = rgb(0, 175, 239, maxColorValue = 255))
```

Arguments

`horizontal`	Logical argument indicating if the boxplots should be horizontal; default `FALSE` means vertical boxes.
`col`	Character vector. Default `col = rgb(0, 175, 239, maxColorValue = 255)`.

Examples

```
library(leem)
# Example 1
showboxplot()
```

`showcdf` *Distribution Function Properties*

Description

Graphic presentation of properties for distribution function

Usage

```
showcdf(variable = "discrete", prop = NULL)
```

Arguments

`variable`	Variabe type. Defaults `variable = "discrete"`. The options are: `discrete` or `"1"` and `continuous` or `"2"`.
`prop`	Properties for distribution function. See Details.

Details

- `prop = 1`: $\lim_{x \to \infty} F_X(x) = 1$ and $\lim_{x \to -\infty} F_X(x) = 0$;
- `prop = 2`: $F_X(x) \leq F_X(y),\ x \leq y\ \forall x, y \in \mathbb{R}$;
- `prop = 3`: $\lim_{x_n \downarrow x} F_X(x_n) \downarrow F_X(x)$.

Examples

```
library(leem)
# Example 1
showcdf()
```

`showci` *Understanding the Confiance Indice*

Description

Detailing the confiance indice plot, showing the main information contained in this type of graph.

Usage

```
showci(dist = "normal", ci = "two.sided", main = NULL)
```

Arguments

`dist`	Parameter to indicate the distribution of the graphic, fixed for now.
`ci`	Parameter to indicate the region of the confiance indice.
`main`	Parameter to indicate the title of the graphic.

Examples

```
library(leem)
# Example 1
showci()
```

`showkur` *Plot of interpretation about Kurtosis*

Description

`showkur` Interpretation of kutosis

Usage

```
showkur()
```

Value

`showkur` returns a plot with the kurtosis characteristics.

Examples

```
# Loading package
library(leem)
## Not run:
showkur()

## End(Not run)
```

`showpar` *Interpretation of location and scale parameters*

Description

`showpar` Function that exemplifies the interpretation of location and scale parameters

Usage

```
showpar(gui = "rstudio")
```

Arguments

`gui`	character argument. The options are: `"rstudio"` (default) and `"tcltk"`.

Details

The result of the `showpar()` call will interactively present a plot of the normal distribution showing the behavior of the location and scale parameters via RStudio. For `showpar(gui = "tcltk")` the result will be displayed in a tcltk interface.

Value

`showpar` returns an interactive plot.

Examples

```
# Loading package
library(leem)
## Not run:
showpar()

## End(Not run)
```

`showskew` *Plot of interpretation about skewsness*

Description

`showskew` Interpretation of asymmetry based on frequency distributions

Usage

```
showskew(mpos = FALSE)
```

Arguments

`measures`	shows the measures of position or not (default `FALSE`).

Value

`showskew` returns a plot with the skewsness characteristics.

Examples

```
# Loading package
library(leem)
## Not run:
showskew()

## End(Not run)
```

`showtabnormal` *Understanding the Ztable.*

Description

Detailing of the Ztable, showing the main information contained in this type of table.

Usage

```
showtabnormal(z)
```

Arguments

`z`	Parameter for lacate the z value on the table; default `NULL` means error if not insert a number.

Examples

```
library(leem)
# Example 1
showtabnormal(zvalue)
```

`skewness` *Skewness value*

Description

Compute the skewness

Usage

```
skewness(
  x,
  type = "pearson",
  rounding = 2,
  na.rm = FALSE,
  details = FALSE,
  grouped = TRUE
)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
rpois(30, 2.5) |>
  new_leem() |>
  skewness()
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  skewness(grouped = TRUE)
```

`stickchart` *Stick chart*

Description

Stick chart for discrete data

Usage

```
stickchartunction(x, ...)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`freq`	Character argument. Type of frequency with options: `"a"` (absolute and default), `"r"` relative and `"p"` percentage.
`bg`	Logical argument. Default is `TRUE`, it displays the background, and `bg = FALSE` otherwise.
`main`	Insert the plot title. The default is `NULL`.
`xlab`	Insert the title of the x-axis graphic label. The default is `NULL`.
`ylab`	Insert the title of the y-axis graphic label. The default is `NULL`.
`grids`	Insert grids to plot. The default is `grid(col = "white")`.
`bgcol`	Insert the background color. This argument is only valid when `bg = TRUE`. The default is `bgcol="gray"`.
`bgborder`	Insert the background border color. This argument is only valid when `bg = TRUE`. The default is bgborder = NA.
`posx1`	Numeric argument.Distance of the labels (horizontal) in relation to the x axis.
`posx2`	Numeric argument.Distance of the labels (vertical) in relation to the x axis.
`xang`	Numeric argument.Angle of the labels in relation to the x axis
`labels`	Character argument. Labels name vector.
`lcol`	Line color. The default is `lcol = "black"`.
`pcol`	Point color. The default is `pcol = lcol`.
`pty`	Point type. The default is `pty = 19`.
`pwd`	Point width. The default is `pwd = 3`.
`lty`	Line type. The default is `lty = 2`.
`lwd`	Line width. The default is `lwd = 2`.
`...`	further arguments passed to or from other methods.

Value

The result of `stickchart()` is `x` object.

Examples

```
library(leem)
# Example 1
rbinom(30, 10, 0.4) |>
  new_leem() |>
  tabfreq() |>
  stickchart()
# Example 2
school <- rep(c("high", "university", "basic"), 3:5)
sample(school, 30, TRUE) |>
  new_leem() |>
  tabfreq(ordered = c("basic", "high", "university")) |>
  stickchart(xang = 15, posx2 = -0.5)
```

`tabfreq` *Frequency distribution table*

Description

Generic function that allows you to tabulate continuous and categorical data (quantitative or qualitative) in frequency distribution. Depending on the nature of the data, they can be grouped into class ranges or not.

Usage

```
tabfreq(dados, ...)

## Leem S3 method:
tabfreq(data, k = NULL, na.rm = FALSE, ordered = NULL, namereduction = TRUE, ...)

## Default S3 method:
tabfreq(data)
```

Arguments

`data`	R object (data structure vector) of class leem. Use `new_leem()` function.
`k`	Number of classes. Default is `NULL`.
`na.rm`	a logical evaluating to TRUE or FALSE indicating whether NA values should be stripped before the computation proceeds.
`ordered`	Ordered vector of the same length and elements of data object. Default is `NULL`.
`namereduction`	Logical argument. If `TRUE` (default), the group names are reduzed the 10 characters. If `FALSE`, otherwise.

Value

The result of `tabfreq()` is a list. This list has two elements: `table` and `statistics`. The first is the data frequency table, and the second represents some useful statistics for methods of leem class.

Examples

```
# Example 1
library(leem)
x <- rbinom(36, 10, 0.6)
x <- new_leem(x, variable = "discrete")
tabfreq(x)

# Example 2 (Pipe operator)
rnorm(36, 100, 4) |> new_leem(variable = "continuous") |> tabfreq()

# Example 3
x <- rbinom(36, 10, 0.6)
# Constructor (object of leem class)
x <- new_leem(x, variable = "discrete")
tab <- tabfreq(x)
# Details
tab$table
tab$statistics

# Example 3 - ordered categories ("d","a", "b", "c")
w <- rep(letters[1:4], 1:4)
w |> new_leem(variable = "discrete") |> tabfreq(ordered = c("d","a", "b", "c"))
```

`th` *Test of hypothesis*

Description

Performs hypothesis testing for various parameters of one or more populations

Usage

```
th(
  x,
  y = NULL,
  test = "ztest",
  h0,
  prop = FALSE,
  delta = 0,
  p,
  pa,
  alternative = c("two.sided", "L", "less", "greater", "G"),
  alpha = 0.05,
  exact = TRUE,
  correct = FALSE,
  paired = FALSE,
  plot = FALSE,
  ...
)
```

Arguments

`x`	R object. See in details.
`y`	an optional (non-empty) numeric vector of data values.
`test`	character value. The options are: `"ttest"`, `"ztest"`, `"ptest"`, `"chitest"`, `"ftest"`, `"anova"`, `"friedman"`, `"kruskal"`, `"mann whitney"`.
`h0`	numeric value. The hypothesized parameter.
`prop`	a logical indicating whether you want to use the proportion test of not. Default is `prop=FALSE`.
`alternative`	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
`alpha`	significance level of the test
`exact`	a logical indicating whether you want to use the exact test or not. Default is `exact=TRUE`.
`correct`	a logical indicating whether Yates' continuity correction should be applied where possible. This argument must be used when `exact = FALSE`.
`paired`	a logical indicating whether you want a paired t-test. Valid only for `test="ttest"`.
`plot`	a logical indicating whether you want a graph indicating the regions of rejection or not of the null hypothesis, as well as the test decision.

`variance` *Variance value*

Description

Compute the sample variance

Usage

```
variance(x, rounding = 2, na.rm = FALSE, details = FALSE, grouped = TRUE)
```

Arguments

`x`	R object (list) of class leem. Use `new_leem()` function.
`rounding`	Numerical object. Rounds the values in its first argument to the specified number of decimal places (default `2`).
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.
`details`	Logical object. Details of data (default `FALSE`).
`grouped`	Logical object. Determines whether the measure of position result will be based on grouped data or not (default `TRUE`).

Examples

```
# Example 1: Poisson data
rpois(30, 2.5) |>
  new_leem() |>
  variance()
# Example 2: Normal data
rnorm(50, 100, 2.5) |>
  new_leem(variable = 2) |>
  variance(grouped = FALSE)
```

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