Package ‘sistmr’

March 24, 2022

Type Package

Title A Collection of Utility Function from the Inserm/Inria SISTM Team

Version 0.1.1

Author Boris Hejblum [aut], Mélanie Huchon [aut, cre]

Maintainer Mélanie Huchon <melanie.huchon@u-bordeaux.fr>

Description Functions common to members of the SISTM team.

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Encoding UTF-8

RoxygenNote 7.1.2

Imports BlandAltmanLeh, dplyr, ggbeeswarm, ggplot2, ggrepel, rlang, scales, stats

NeedsCompilation no

Repository CRAN

Date/Publication 2022-03-24 08:30:02 UTC

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**BlandAltmanPlot**  
*Bland-Altman plot function*

### Description

Bland-Altman plot function

### Usage

```r
BlandAltmanPlot(
  var1,
  var2,
  with_gradient = FALSE,
  line_color = c("blue", "lightblue"),
  extremum_pctg = TRUE
)
```

### Arguments

- **var1**: a vector of numerics for the 1st group to be compared.
- **var2**: a vector of numerics for the 2nd group to be compared.
- **with_gradient**: a logical indicating if you have a lot of measures, use `with_gradient=TRUE` to have gradient scale and not points. Default value is `FALSE`.
- **line_color**: a vector of color for the three lines: average difference and upper and lower limits of the confidence interval for the average difference.
- **extremum_pctg**: a logical indicating if you want to add the percentage of points outside the confidence interval for the upper and lower limits. Default is `TRUE`.

### Value

a `ggplot2` object

### Examples

```r
library(ggplot2)

# Small sample
# Generate data
x <- rnorm(30)
y <- rnorm(30, mean = 5, sd = 3)
# Plotting
BlandAltmanPlot(var1 = x, var2 = y)
# Add color by group
gr <- c(rep("G1", 15), rep("G2", 15))
BlandAltmanPlot(var1 = x, var2 = y) + geom_point(aes(color = gr))
```
#High sample
#Generate data
x <- rnorm(10000)
y <- rnorm(10000, mean = 5, sd = 3)
#Plotting with gradient
BlandAltmanPlot(var1 = x, var2 = y, with_gradient = TRUE)

## multipleBoxplots

Multiple boxplots for many times

### Description

Multiple boxplots for many times

### Usage

`multipleBoxplots(data, x_var, y_var, add_points = TRUE)`

### Arguments

- **data**: a dataset from which the variable `x_var` and `y_var` should be taken.
- **x_var**: corresponding to the x coordinates for the plot, it must be a factor to obtain multiple boxplots.
- **y_var**: corresponding to the y coordinates for the plot.
- **add_points**: if you want to add points on boxplots. Default value is `TRUE`.

### Value

a `ggplot2` object

### Examples

```r
library(ggplot2)

#Generate data
dx_ex <- factor(c(rep("J0", 10), rep("J7", 10), rep("J14", 10)), levels = c("J0", "J7", "J14"))
dy_ex <- rnorm(30)
data_ex <- cbind.data.frame(x_ex, dy_ex)

#Plotting
multipleBoxplots(data = data_ex, x_var = x_ex, y_var = dy_ex)
multipleBoxplots(data = data_ex, x_var = x_ex, y_var = dy_ex) +
  labs(x = "Time", y = "Value") +
  theme(legend.position = "none")
```
normal_distribution Functions

Description
Functions

Usage
normal_distribution(vec)

Arguments
vec  a vector

Value
a vector

sistmr sistmr.

Description
This package contains functions common to members of the SISTM team.

volcanoPlot Volcano plot function

Description
Volcano plot function

Usage
volcanoPlot(
  log2fc,
  pValue,
  data,
  FDR_threshold = 0.05,
  LFC_threshold = log2(1.5),
  color = c("red", "black"),
  geneNames = NULL,
  nb_geneTags = 20,
  logTransformPVal = TRUE
)
volcanoPlot

Arguments

tlog2fc a magnitude of change (fold-change) in base log 2 corresponding to the x-axis.
pValue a statistical significance (p-value) corresponding to the y-axis.
data a data.frame of differentially expressed results from which the variable log2fc, pValue and geneNames (if it is used) should be taken.
FDR_threshold a threshold of false discovery rate.
LFC_threshold a threshold of log fold change.
color a vector of two colors for significant or not significant points.
geneNames a vector of gene names if you want to put gene tags on the volcano plot. Default is NULL.
nb_geneTags number of tags for the significant genes if geneNames is not NULL. Default is 20 to obtain the 20 first significant genes.
logTransformPVal If TRUE, the p-values will have a negative logarithm transformation (base 10). Default is TRUE.

Value

a ggplot2 object

Examples

genes <- paste0("G", 1:500)
pval <- runif(500, max = 0.5)
log2FC <- runif(500, min = -4, max = 4)
data <- cbind.data.frame(genes, pval, log2FC)
rm(genes, pval, log2FC)
volcanoPlot(log2FC, pval, data, geneNames = genes)
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