Package 'plotGrouper'

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Title Shiny app GUI wrapper for ggplot with built-in statistical analysis

Version 1.30.0

Description A shiny app-based GUI wrapper for ggplot with built-in statistical analysis. Import data from file and use dropdown menus and checkboxes to specify the plotting variables, graph type, and look of your plots. Once created, plots can be saved independently or stored in a report that can be saved as a pdf. If new data are added to the file, the report can be refreshed to include new data. Statistical tests can be selected and added to the graphs. Analysis of flow cytometry data is especially integrated with plotGrouper. Count data can be transformed to return the absolute number of cells in a sample (this feature requires inclusion of the number of beads per sample and information about any dilution performed).

Depends R (>= 3.5)

Imports ggplot2 (>= 3.0.0), dplyr (>= 0.7.6), tidyr (>= 0.2.0), tibble (>= 1.4.2), stringr (>= 1.3.1), readr (>= 1.1.1), readxl (>= 1.1.0), scales (>= 1.0.0), stats, grid, gridExtra (>= 2.3), egg (>= 0.4.0), gtable (>= 0.2.0), ggpubr (>= 0.1.8), shiny (>= 1.1.0), shinythemes (>= 1.1.1), colourpicker (>= 1.0), magrittr (>= 1.5), Hmisc (>= 4.1.1), rlang (>= 0.2.2)

Suggests knitr, htmltools, BiocStyle, rmarkdown, testthat

VignetteBuilder knitr

biocViews ImmunoOncology, FlowCytometry, GraphAndNetwork, StatisticalMethod, DataImport, GUI, MultipleComparison

URL https://jdgagnon.github.io/plotGrouper/

BugReports https://github.com/jdgagnon/plotGrouper/issues

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Contents

gplot 2
organizeData 4
plotGrouper 5
readData 6
readData_example 6
%>% 7

Index **8**

`gplot` *A function to create a grouped plot and return a table grob.*

Description

This function allows you to create a grouped plot and return a table grob. It takes a tidy dataset containing sample replicate values for at least one variable, a column organizing each replicate into the proper comparison group, and a column that groups the variables to be plotted. Additional arguments allow for the re-ordering of the variables and the comparisons being ploted, selection of the type of graph to display (e.g., bar graph, boxplot, violin plot, points, statistical summary, etc...), as well as other aesthetics of the plot.

Usage

```
gplot(dataset = NULL, comparison = NULL, group.by = NULL,
  levs = TRUE, val = "value", geom = c("bar", "errorbar", "point",
  "stat", "seg"), p = "p.signif", ref.group = NULL,
  p.adjust.method = "holm", comparisons = NULL, method = "t.test",
  paired = FALSE, errortype = "mean_sdl", y.lim = NULL,
  y.lab = NULL, trans.y = "identity", x.lim = c(NA, NA),
  expand.y = c(0, 0), x.lab = NULL, trans.x = "identity",
  sci = FALSE, angle.x = FALSE, levs.comps = TRUE,
  group.labs = NULL, stats = FALSE, split = TRUE, split_str = NULL,
  trim = "none", leg.pos = "top", stroke = 0.25, font_size = 9,
  size = 1, width = 0.8, dodge = 0.8, plotWidth = 30,
  plotHeight = 40, shape.groups = c(19, 21),
  color.groups = c("black", "black"), fill.groups = c("#444444", NA,
  "#A33838"))
```

Arguments

dataset	Define your data set which should be a gathered tibble
comparison	Specify the comparison you would like to make (e.g., Genotype)
group.by	Specify the variable to group by (e.g., Tissue).
levs	Specify the order of the grouping variables
val	Specify column name that contains values (optional)
geom	Define the list of geoms you want to plot
p	Specify representation of pvalue (p.signif = astrisk representation of the raw p value; p.format = 'p = 0.05'; p.adj = adjusted p-value; p.adj.signif = astrisk representation of the adjusted p value)
ref.group	Specify a reference group to compare all other comparisons to
p.adjust.method	Method used for adjusting the pvalue
comparisons	Specify which of the available comparisons within your data you would like to plot
method	Specify the statistical test to be used
paired	Specify whether or not the statistical comparisons should be paired
errortype	Specify the method of statistical error to plot
y.lim	Specify the min and max values to be used for the y-axis
y.lab	Specify a custom y-axis label to use
trans.y	Specify the transformation to perform on the dependent variable
x.lim	Specify the min and max values to be used for the x-axis
expand.y	Specify values to expand the y-axis
x.lab	Specify a custom x-axis label to use
trans.x	Specify the transformation to perform on the independent variable
sci	Specify whether or not to display the dependent variable using scientific notation
angle.x	Specify whether or not to angle the x-axis text 45deg
levs.comps	Specify the order in which to plot the comparisons
group.labs	Specify custom labels for the independent variables
stats	Specify whether or not to output the statistics table
split	Specify whether or not to split the x-axis label text
split_str	Specify the string to split the x-axis label text by; uses regex
trim	Specify the string to trim text from the right side of the x-axis label text; uses regex
leg.pos	Specify where to place the legend
stroke	Specify the line thickness to use
font_size	Specify the font size to use
size	Specify the size of the points to use

width	Specify the width of groups to be plotted
dodge	Specify the width to dodge the comparisons by
plotWidth	Specify the length of the x-axis in mm
plotHeight	Specify the length of the y-axis in mm
shape.groups	Specify the default shapes to use for the comparisons
color.groups	Specify the default colors to use for the comparisons
fill.groups	Specify the default fills to use for the comparisons

Value

Table grob of the plot

Examples

```
iris %>% dplyr::mutate(Species = as.character(Species)) %>%
dplyr::group_by(Species) %>%
dplyr::mutate(Sample = paste0(Species, "_", dplyr::row_number()),
Sheet = "iris") %>%
dplyr::select(Sample, Sheet, Species, dplyr::everything()) %>%
tidyr::gather(variable, value, -c(Sample, Sheet, Species)) %>%
dplyr::filter(variable == "Sepal.Length") %>%
plotGrouper::gplot(
comparison = "Species",
group.by = "variable",
shape.groups = c(19,21,17),
color.groups = c(rep("black",3)),
fill.groups = c("black","#E016BE", "#1243C9")) %>%
gridExtra::grid.arrange()
```

---

organizeData *A function to organize a tibble into tidy format and perform count transformations*

Description

This function will organize a tibble into tidy format and perform count transformations if appropriate columns are specified.

Usage

```
organizeData(data = NULL, exclude = NULL, comp = NULL,
  comps = NULL, variables = NULL, id = NULL, beadColumn = NULL,
  dilutionColumn = NULL)
```

Arguments

data	A tibble
exclude	A list of columns to exclude from gather
comp	the name of comparison column
comps	A vector of names of the comparisons
variables	A vector of the variables to be plotted
id	The name of unique identifier column
beadColumn	The column name that has total number of beads/sample
dilutionColumn	The column name that has dilution factor for each sample 1/x

Value

Tibble in tidy format based on columns chosen to be excluded. Count data will be transformed if appropriate columns are present.

Examples

```
iris %>% dplyr::mutate(Species = as.character(Species)) %>%
dplyr::group_by(Species) %>%
dplyr::mutate(Sample = paste0(Species, "_", dplyr::row_number()),
Sheet = "iris") %>%
dplyr::select(Sample, Sheet, Species, dplyr::everything()) %>%
plotGrouper::organizeData(data = .,
exclude = c("Sample", "Sheet", "Species"),
comp = "Species",
comps = c("setosa", "versicolor", "virginica"),
variables = "Sepal.Length",
id = "Sample",
beadColumn = "none",
dilutionColumn = "none")
```

---

plotGrouper *A function to run the plotGrouper shiny app*

Description

This function runs the plotGrouper app

Usage

```
plotGrouper(...)
```

Arguments

...	Any argument that you can pass to shiny::runApp

Value

Runs the plotGrouper shiny app.

Examples

```
# plotGrouper()
```

`readData` *A function to read an excel file and combine its sheets into a single dataframe.*

Description

This function will read an excel file and combine its sheets into a single dataframe.

Usage

```
readData(file = NULL, sheet = NULL)
```

Arguments

`file`	Takes an excel file to be read from
`sheet`	Takes a vector of sheets to be read

Value

Tibble assembled from the sheets selected from the file

Examples

```
datasets <- readData_example("iris.xlsx")
readData(datasets, "iris")
```

`readData_example` *Get path to readData example*

Description

readData comes bundled with a example files in its 'inst/applications/www' directory. This function makes them easy to access.

Usage

```
readData_example(path = NULL)
```

Arguments

path	Name of file. If 'NULL', the example files will be listed.

Value

Located example excel file in package

Examples

```
readData_example(path = "iris.xlsx")
```

%>% *Pipe graphics*

Description

Like dplyr, ggvis also uses the pipe function, %>% to turn function composition into a series of imperative statements.

Arguments

lhs, rhs	A visualisation and a function to apply to it

Examples

```
# Instead of
dplyr::mutate(dplyr::filter(iris, Species == "versicolor"),
"Sample" = paste0(Species, dplyr::row_number()))
# You can write
dplyr::filter(iris, Species == "versicolor") %>%
dplyr::mutate("Sample" = paste0(Species, "_", dplyr::row_number()))
```

Index

∗ **organizeData**
organizeData, 4
∗ **readData**
readData, 6
%>%, 7

gplot, 2

organizeData, 4

plotGrouper, 5

readData, 6
readData_example, 6