Package 'TOmicsVis'

August 28, 2023

Type Package

Title Transcriptome Visualization Process Scheme

Version 2.0.0

Description Transcriptome visualization from sample trait statistics to gene expression analysis. Six categories include ``Samples Statistics'', ``Traits Analysis'', ``Differential Expression Analysis'', ``Advanced Analysis'', ``GO and KEGG Enrichment'', ``Tables Operations'', with complete sample data.

URL https://benben-miao.github.io/TOmicsVis/

BugReports https://github.com/benben-miao/TOmicsVis/issues/

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RoxygenNote 7.2.3

Encoding UTF-8

LazyData true

Depends R (>= 3.5), Biobase (>= 2.5.5), e1071 (>= 1.7-0)

Imports stats, utils, grid, graphics, grDevices, ggplot2, ggsci, reshape2, ggpubr, ggcorrplot, ggforce, vegan, venn, UpSetR, circlize, randomcoloR, ComplexHeatmap, EnhancedVolcano, GGally, survival, survminer, Rtsne, umap, dplyr, tidyr, clusterProfiler, enrichplot, ggnewscale, igraph, WGCNA, stringr, pheatmap, RColorBrewer, ggpolypath, factoextra, ggrepel, cowplot, ggplotify, plotrix, Mfuzz, shiny

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

`box_plot` *Box plot support two levels and multiple groups with P value.*

Description

Box plot support two levels and multiple groups with P value.

Usage

```
box_plot(
  data,
  test_method = "t.test",
  test_label = "p.format",
  notch = TRUE,
  group_level = "Three_Column",
  add_element = "jitter",
  my_shape = "fill_circle",
  sci_fill_color = "Sci_AAAS",
  sci_fill_alpha = 0.5,
  sci_color_alpha = 1,
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)
```

Arguments

`data`	Dataframe: Length, Width, Weight, and Sex traits dataframe (1st-col: Value, 2nd-col: Traits, 3rd-col: Sex).
`test_method`	Character: test methods of P value. Default: "t.test", options: "wilcox.test", "t.test", "anova", "kruskal.test".
`test_label`	Character: test label of P value. Default: "p.format", options: "p.signif", "p.format". c(0, 0.0001, 0.001, 0.01, 0.05, 1).
`notch`	Logical: Box notch or none. Default: TRUE, options: TRUE, FALSE.
`group_level`	Character: group levels. Default: "Three_Column", options: "Two_Column", "Three_Column".

add_element	Character: add new plot. Default: "jitter", options: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range".
my_shape	Character: box scatter shape. Default: "fill_circle", options: "border_square", "border_circle", "border_triangle", "plus", "times", "border_diamond", "border_triangle_down", "square_times", "plus_times", "diamond_plus", "circle_plus", "di_triangle", "square_plus", "circle_times","square_triangle", "fill_square", "fill_circle", "fill_triangle", "fill_diamond", "large_circle", "small_circle", "fill_border_circle", "fill_border_square", "fill_border_diamond", "fill_border_triangle".
sci_fill_color	Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
sci_fill_alpha	Numeric: ggsci fill color alpha. Default: 0.50, min: 0.00, max: 1.00.
sci_color_alpha	Numeric: ggsci border color alpha. Default: 1.00, min: 0.00, max: 1.00.
legend_pos	Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".
legend_dir	Character: legend direction. Default: "vertical", options: "horizontal", "vertical".
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: box plot support two levels and multiple groups with P value.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(traits_sex)
head(traits_sex)

# 3. Default parameters
box_plot(traits_sex)

# 4. Set test_label = "p.signif",
box_plot(traits_sex, test_label = "p.signif")

# 5. Set notch = FALSE
```

```
box_plot(traits_sex, notch = FALSE)

# 6. Set group_level = "Two_Column"
box_plot(traits_sex, group_level = "Two_Column")

# 7. Set add_element = "point"
box_plot(traits_sex, add_element = "point")
```

---

chord_plot *Chord plot for visualizing the relationships of pathways and genes.*

Description

Chord plot is used to visualize complex relationships between samples and genes, as well as between pathways and genes.

Usage

```
chord_plot(
  data,
  multi_colors = "VividColors",
  color_seed = 10,
  color_alpha = 0.3,
  link_visible = TRUE,
  link_dir = -1,
  link_type = "diffHeight",
  sector_scale = "Origin",
  width_circle = 3,
  dist_name = 3,
  label_dir = "Vertical",
  dist_label = 0.3,
  label_scale = 0.8
)
```

Arguments

data	Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).
multi_colors	Character: color palette. Default: "VividColors", options: "VividColors", "RainbowColors".
color_seed	Numeric: rand seed for VividColors. Default: 10.
color_alpha	Numeric: color alpha. Default: 0.50, min: 0.00, max: 1.00.
link_visible	Logical: links visible. Default: TRUE, options: TRUE, FALSE.
link_dir	Numeric: links direction, use with link_type. Default: -1, options: -1, 0, 1, 2.

link_type	Character: links type, use with link_dir. Default: "diffHeight", options: "diffHeight", "arrows".
sector_scale	Character: sector scale method. Default: "Origin", options: "Origin", "Scale".
width_circle	Numeric: outside circle width. Default: 3.0, min: 0.0, max: 10.0.
dist_name	Numeric: the distance of name and circle. Default: 3.0, min: 0.0, max: 10.0.
label_dir	Character: label director. Default: "Vertical", options: "Horizontal", "Vertical".
dist_label	Numeric: the distance of label and circle. Default: 0.3, min: 0.0.
label_scale	Numeric: labels font size sclae. Default: 0.8, min: 0, max: NULL.

Value

Plot: chord plot is used to visualize complex relationships between samples and genes, as well as between pathways and genes.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression2)
head(gene_expression2)

# 3. Default parameters
chord_plot(gene_expression2[1:20,])
```

---

circos_heatmap *Circos heatmap plot for visualizing gene expressing in multiple samples.*

Description

Circos heatmap plot for visualizing gene expressing in multiple samples.

Usage

```
circos_heatmap(
  data,
  low_color = "#0000ff",
  mid_color = "#ffffff",
  high_color = "#ff0000",
  gap_size = 25,
```

```
  cluster_run = TRUE,
  cluster_method = "complete",
  distance_method = "euclidean",
  dend_show = "inside",
  dend_height = 0.2,
  track_height = 0.3,
  rowname_show = "outside",
  rowname_size = 0.8
)
```

Arguments

data	Dataframe: Shared degs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).
low_color	Character: min value color (color name or hex value). Default: "#0000ff".
mid_color	Character: middle value color (color name or hex value). Default: "#ffffff".
high_color	Character: high value color (color name or hex value). Default: "#ff0000".
gap_size	Numeric: heatmap gap size. Default: 25, min: 0.
cluster_run	Logical: running cluster algorithm. Default: TRUE, options: TRUE, FALSE.
cluster_method	Character: cluster methods. Default: "complete", options: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid".
distance_method	Character: distance methods. Default: "euclidean", options: "euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski".
dend_show	Character: control dendgram display and position. Default: "inside", options: "none", "outside", "inside".
dend_height	Numeric: dendgram height. Default: 0.20, min: 0.00, max: 0.50.
track_height	Numeric: heatmap track height. Default: 0.30, min: 0.00, max: 0.50.
rowname_show	Character: control rownames display and position. Hind first rowname by running rownames(data). Default: "outside", options: "none", "outside", "inside".
rowname_size	Numeric: rowname font size. Default: 0.80, min: 0.10, max: 10.00.

Value

Plot: circos heatmap plot for visualizing gene expressing in multiple samples.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
```

```
data(gene_expression2)
head(gene_expression2)

# 3. Default parameters
circos_heatmap(gene_expression2[1:50,])
```

---

corr_heatmap *Correlation Heatmap for samples/groups based on Pearson algorithm.*

Description

Correlation Heatmap for samples/groups based on Pearson algorithm.

Usage

```
corr_heatmap(
  data,
  corr_method = "pearson",
  cell_shape = "square",
  fill_type = "full",
  lable_size = 3,
  axis_angle = 45,
  axis_size = 12,
  lable_digits = 3,
  color_low = "blue",
  color_mid = "white",
  color_high = "red",
  outline_color = "white",
  ggTheme = "theme_light"
)
```

Arguments

data	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
corr_method	Character: correlation method. Default: "pearson", options: "pearson", "spearman", "kendall".
cell_shape	Character: heatmap cell shape. Default: "square", options: "circle", "square".
fill_type	Character: heatmap fill type. Default: "full", options: "upper", "low", "full".
lable_size	Numeric: heatmap label size. Default: 3, min: 0.
axis_angle	Numeric: axis rotate angle. Default: 45, min: 0, max: 360.
axis_size	Numberic: axis font size. Default: 12, min: 0.
lable_digits	Numeric: heatmap label digits. Default: 3, min: 0, max: 3.
color_low	Character: low value color name or hex value. Default: "blue".

color_mid	Character: middle value color name or hex value. Default: "white".
color_high	Character: high value color name or hex value. Default: "red".
outline_color	Character: outline color name or hex value. Default: "white".
ggTheme	Character: ggplot2 theme. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void".

Value

Plot: heatmap plot filled with Pearson correlation values and P values.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset gene_exp
data(gene_expression)
head(gene_expression)

# 3. Default parameters
corr_heatmap(gene_expression)

# 4. Set color_low = "#008800"
corr_heatmap(gene_expression, color_low = "#008800")

# 5. Set cell_shape = "circle"
corr_heatmap(gene_expression, cell_shape = "circle")
```

---

degs_lists *Paired comparisons differentially expressed genes (degs) among groups.*

Description

Paired comparisons differentially expressed genes (degs) among groups.

Usage

```
data(degs_lists)
```

Format

Dataframe: Paired comparisons differentially expressed genes (degs) among groups (1st-col~: degs of paired comparisons).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/VennPlot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(degs_lists)

# 3. View example data
degs_lists
```

---

degs_stats *All DEGs of paired comparison CT-vs-LT12 stats dataframe.*

Description

All DEGs of paired comparison CT-vs-LT12 stats dataframe.

Usage

```
data(degs_stats)
```

Format

Dataframe: All DEGs of paired comparison CT-vs-LT12 stats dataframe (1st-col: Genes, 2nd-col: log2FoldChange, 3rd-col: Pvalue, 4th-col: FDR).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/VolcanoPlot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(degs_stats)

# 3. View example data
degs_stats
```

`degs_stats2` *All DEGs of paired comparison CT-vs-LT12 stats2 dataframe.*

Description

All DEGs of paired comparison CT-vs-LT12 stats2 dataframe.

Usage

```
data(degs_stats2)
```

Format

Dataframe: All DEGs of paired comparison CT-vs-LT12 stats2 dataframe (1st-col: Gene, 2nd-col: baseMean, 3rd-col: Log2FoldChange, 4th-col: FDR).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/MversusA/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(degs_stats2)

# 3. View example data
degs_stats2
```

dendro_plot *Dendrograms for multiple samples/groups clustering.*

Description

Dendrograms for multiple samples/groups clustering.

Usage

```
dendro_plot(
  data,
  dist_method = "euclidean",
  hc_method = "ward.D2",
  tree_type = "rectangle",
  k_num = 5,
  palette = "npg",
  color_labels_by_k = TRUE,
  horiz = FALSE,
  label_size = 1,
  line_width = 1,
  rect = TRUE,
  rect_fill = TRUE,
  xlab = "Samples",
  ylab = "Height",
  ggTheme = "theme_light"
)
```

Arguments

data	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
dist_method	Character: distance measure method. Default: "euclidean", options: "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".
hc_method	Character: hierarchical clustering method. Default: "ward.D2", options: "ward.D", "ward.D2", "single", "complete","average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
tree_type	Character: plot tree type. Default: "rectangle", options: "rectangle", "circular", "phylogenic".
k_num	Numeric: the number of groups for cutting the tree. Default: 3.
palette	Character: color palette used for the group. Default: "npg", options: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
color_labels_by_k	Logical: labels colored by group. Default: TRUE, options: TRUE or FALSE.
horiz	Logical: horizontal dendrogram. Default: FALSE, options: TRUE or FALSE.
label_size	Numeric: tree label size. Default: 0.8, min: 0.

line_width	Numeric: branches and rectangle line width. Default: 0.7, min: 0.
rect	Logical: add a rectangle around groups. Default: TRUE, options: TRUE or FALSE.
rect_fill	Logical: fill the rectangle. Default: TRUE, options: TRUE or FALSE.
xlab	Character: title of the xlab. Default: "".
ylab	Character: title of the ylab. Default: "Height".
ggTheme	Character: ggplot2 theme. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void".

Value

Plot: dendrogram for multiple samples clustering.

Author(s)

wei dong

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset gene_expression
data(gene_expression)
head(gene_expression)

# 3. Default parameters
dendro_plot(gene_expression)

# 4. Set palette = "aaas"
dendro_plot(gene_expression, palette = "aaas")

# 5. Set tree_type = "circular"
dendro_plot(gene_expression, tree_type = "circular")
```

---

flower_plot *Flower plot for stat common and unique gene among multiple sets.*

Description

Flower plot for stat common and unique gene among multiple sets.

Usage

```
flower_plot(
  flower_dat,
  angle = 90,
  a = 1,
  b = 2,
  r = 1,
  ellipse_col_pal = "Spectral",
  circle_col = "white",
  label_text_cex = 1
)
```

Arguments

flower_dat	Dataframe: Paired comparisons differentially expressed genes (degs) among groups (1st-col~: degs of paired comparisons).
angle	Number: set the angle of rotation in degress. Default: 90.
a	Number: set the radii of the ellipses along the x-axes. Default: 0.5.
b	Number: set the radii of the ellipses along the y-axes. Default: 2.
r	Number: set the radius of the circle. Default: 1.
ellipse_col_pal	Character: set the color palette for filling the ellipse. Default: "Spectral", options: 'Spectral', 'Set1', 'Set2', 'Set3', 'Accent', 'Dark2', 'Paired', 'Pastel1', 'Pastel2'.
circle_col	Character: set the color for filling the circle. Default: "white".
label_text_cex	Number: set the label text cex. Default: 1.

Value

Plot: Flower plot for stat common and unique gene among multiple sets.

Author(s)

wei dong

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(degs_lists)
head(degs_lists)

# 3. Default parameters
flower_plot(degs_lists)

# 4. Set angle = 60
```

```
flower_plot(degs_lists, angle = 60)

# 5. Set ellipse_col_pal = "Accent"
flower_plot(degs_lists, ellipse_col_pal = "Accent")

# 6. Set a = 1, b = 2, r = 1
flower_plot(degs_lists, a = 1, b = 2, r = 1, ellipse_col_pal = "Set2")
```

`gene_cluster_trend` *Gene cluster trend plot for visualizing gene expression trend profile in multiple samples.*

Description

Gene cluster trend plot for visualizing gene expression trend profile in multiple samples.

Usage

```
gene_cluster_trend(
  data,
  thres = 0.25,
  min_std = 0.2,
  palette = "PiYG",
  cluster_num = 4
)
```

Arguments

`data`	Dataframe: Shared DEGs of all paired comparisons in all groups expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~n-1-col: Groups, n-col: Pathways).
`thres`	Number: set the threshold for excluding genes. Default: 0.25.
`min_std`	Number: set the threshold for minimum standard deviation. Default: 0.2.
`palette`	Character: set the color palette to be used for plotting. Default: "PiYG", options: 'Spectral', 'BrBG', 'PiYG', 'PRGn', 'PuOr', 'RdBu', 'RdGy', 'RdYlBu', 'RdYlGn'.
`cluster_num`	Number: set the number of clusters. Default: 4.

Value

Plot: Gene cluster trend plot for visualizing gene expression trend profile in multiple samples.

Author(s)

wei dong

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset gene_cluster_data
data(gene_expression3)
head(gene_expression3)

# 3. Default parameters
gene_cluster_trend(gene_expression3[,-7])

# 4. Set palette = "RdBu"
gene_cluster_trend(gene_expression3[,-7], palette = "RdBu")

# 5. Set cluster_num = 6
gene_cluster_trend(gene_expression3[,-7], cluster_num = 6, palette = "Spectral")
```

---

gene_expression *All genes in all samples expression dataframe of RNA-Seq.*

Description

All genes in all samples expression dataframe of RNA-Seq.

Usage

```
data(gene_expression)
```

Format

Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/CorPlot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example dataset gene_expression
data(gene_expression)
```

```
# 3. View gene_expression
gene_expression
```

---

gene_expression2 *Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq.*

Description

Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq.

Usage

```
data(gene_expression2)
```

Format

Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/CorPlot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example dataset
data(gene_expression2)

# 3. View gene_expression2
gene_expression2
```

gene_expression3 *Shared DEGs of all paired comparisons in all groups expression dataframe of RNA-Seq.*

Description

Shared DEGs of all paired comparisons in all groups expression dataframe of RNA-Seq.

Usage

```
data(gene_expression3)
```

Format

Dataframe: Shared DEGs of all paired comparisons in all groups expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~n-1-col: Groups, n-col: Pathways).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/CorPlot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example dataset
data(gene_expression3)

# 3. View gene_expression3
gene_expression3
```

gene_go_kegg *GO and KEGG annotation of background genes.*

Description

GO and KEGG annotation of background genes.

Usage

```
data(gene_go_kegg)
```

Format

Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/GOenrichStat/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(gene_go_kegg)

# 3. View example data
gene_go_kegg
```

---

gene_go_kegg2 *GO and KEGG annotation of background genes.*

Description

GO and KEGG annotation of background genes.

Usage

```
data(gene_go_kegg2)
```

Format

Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/GOenrichStat/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(gene_go_kegg2)

# 3. View example data
gene_go_kegg2
```

`gene_rank_plot` *Gene ranking dotplot for visualizing differentailly expressed genes.*

Description

Gene ranking dotplot for visualizing differentailly expressed genes.

Usage

```
gene_rank_plot(
  data,
  log2fc = 1,
  palette = "Spectral",
  top_n = 10,
  genes_to_label = NULL,
  label_size = 5,
  base_size = 12,
  title = "Gene ranking dotplot",
  xlab = "Ranking of differentially expressed genes",
  ylab = "Log2FoldChange"
)
```

Arguments

`data`	Dataframe: All DEGs of paired comparison CT-vs-LT12 stats dataframe (1st-col: Genes, 2nd-col: log2FoldChange, 3rd-col: Pvalue, 4th-col: FDR).
`log2fc`	Numeric: log2(FoldChange) cutoff log2(2) = 1. Default: 1.0, min: 0.0, max: null.
`palette`	Character: color palette used for the point. Default: "spectral", options: 'Spectral', 'BrBG', 'PiYG', 'PRGn', 'PuOr', 'RdBu', 'RdGy', 'RdYlBu', 'RdYlGn'.
`top_n`	Numeric: number of top differentailly expressed genes. Default: 10, min: 0.
`genes_to_label`	Character: a vector of selected genes. Default: "NULL".
`label_size`	Numeric: gene label size. Default: 5, min: 0.
`base_size`	Numeric: base font size. Default: 12, min: 0.

title	Character: main plot title. Default: "Gene ranking dotplot".
xlab	Character: title of the xlab. Default: "Ranking of differentially expressed genes".
ylab	Character: title of the ylab. Default: "Log2FoldChange".

Value

Plot: Gene ranking dotplot for visualizing differentailly expressed genes.

Author(s)

wei dong

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(degs_stats)
head(degs_stats)

# 3. Default parameters
gene_rank_plot(degs_stats)

# 4. Set top_n = 5
gene_rank_plot(degs_stats, top_n = 5, palette = "PiYG")

# 5. Set genes_to_label = c("SELL","CCR7","KLRG1","IL7R")
gene_rank_plot(degs_stats, genes_to_label = c("SELL","CCR7","KLRG1","IL7R"), palette = "PuOr")
```

---

go_enrich *GO enrichment analysis based on GO annotation results (None/Exist Reference Genome).*

Description

GO enrichment analysis based on GO annotation results (None/Exist Reference Genome).

Usage

```
go_enrich(
  go_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05
)
```

Arguments

go_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.

Value

Table: include columns ("ID", "ontology", "Description", "GeneRatio", "BgRatio", "pvalue", "p.adjust", "qvalue", "geneID", "Count").

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
res <- go_enrich(gene_go_kegg[,-5], gene_go_kegg[100:200,1])
head(res)

# 4. Set padjust_method = "BH"
res <- go_enrich(gene_go_kegg[,-5], gene_go_kegg[100:200,1], padjust_method = "BH")
head(res)

# 5. Set pvalue_cutoff = 0.10
res <- go_enrich(gene_go_kegg[,-5], gene_go_kegg[100:200,1], pvalue_cutoff = 0.10)
head(res)
```

---

go_enrich_bar *GO enrichment analysis and bar plot (None/Exist Reference Genome).*

Description

GO enrichment analysis and bar plot (None/Exist Reference Genome).

Usage

```
go_enrich_bar(
  go_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  sign_by = "p.adjust",
  category_num = 30,
  font_size = 12,
  low_color = "#ff0000aa",
  high_color = "#008800aa",
  ggTheme = "theme_light"
)
```

Arguments

go_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
sign_by	Character: significant by. Default: "p.adjust", options: "pvalue", "p.adjust", "qvalue".
category_num	Numeric: categories number to display. Default: 30, min: 1, max: NULL.
font_size	Numeric: category font size. Default: 12.
low_color	Character: low value (p-value or q-value) color (color name or hex value).
high_color	Character: high value (p-value or q-value) color (color name or hex value).
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: GO enrichment analysis and bar plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
go_enrich_bar(gene_go_kegg[,-5], gene_go_kegg[100:200,1])

# 4. Set padjust_method = "BH"
go_enrich_bar(gene_go_kegg[,-5], gene_go_kegg[100:200,1], padjust_method = "BH")

# 5. Set category_num = 10
go_enrich_bar(gene_go_kegg[,-5], gene_go_kegg[100:200,1], category_num = 10)

# 6. Set ggTheme = "theme_bw"
go_enrich_bar(gene_go_kegg[,-5], gene_go_kegg[100:200,1], ggTheme = "theme_bw")
```

---

go_enrich_dot *GO enrichment analysis and dot plot (None/Exist Reference Genome).*

Description

GO enrichment analysis and dot plot (None/Exist Reference Genome).

Usage

```
go_enrich_dot(
  go_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  sign_by = "p.adjust",
  category_num = 30,
  font_size = 12,
  low_color = "#ff0000aa",
  high_color = "#008800aa",
  ggTheme = "theme_light"
)
```

Arguments

go_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).

degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
sign_by	Character: significant by. Default: "p.adjust", options: "pvalue", "p.adjust", "qvalue".
category_num	Numeric: categories number to display. Default: 30, min: 1, max: NULL.
font_size	Numeric: category font size. Default: 12.
low_color	Character: low value (p-value or q-value) color (color name or hex value).
high_color	Character: high value (p-value or q-value) color (color name or hex value).
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: GO enrichment analysis and dot plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
go_enrich_dot(gene_go_kegg[,-5], gene_go_kegg[100:200,1])

# 4. Set padjust_method = "BH"
go_enrich_dot(gene_go_kegg[,-5], gene_go_kegg[100:200,1], padjust_method = "BH")

# 5. Set category_num = 10
go_enrich_dot(gene_go_kegg[,-5], gene_go_kegg[100:200,1], category_num = 10)

# 6. Set ggTheme = "theme_bw"
go_enrich_dot(gene_go_kegg[,-5], gene_go_kegg[100:200,1], ggTheme = "theme_bw")
```

go_enrich_net *GO enrichment analysis and net plot (None/Exist Reference Genome).*

Description

GO enrichment analysis and net plot (None/Exist Reference Genome).

Usage

```
go_enrich_net(
  go_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  category_num = 20,
  net_layout = "circle",
  net_circular = TRUE,
  low_color = "#ff0000aa",
  high_color = "#008800aa"
)
```

Arguments

go_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
category_num	Numeric: categories number to display. Default: 20, min: 1, max: NULL.
net_layout	Character: network layout. Default: "circle", options: 'star', 'circle', 'gem', 'dh', 'graphopt', 'grid', 'mds', 'randomly', 'fr', 'kk', 'drl' or 'lgl'.
net_circular	Logical: network circular. Default: TRUE, options: TRUE, FALSE.
low_color	Character: low value (p-value or q-value) color (color name or hex value).
high_color	Character: high value (p-value or q-value) color (color name or hex value).

Value

PLot: GO enrichment analysis and net plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
go_enrich_net(gene_go_kegg[,-5], gene_go_kegg[100:200,1])
```

---

go_enrich_stat *GO enrichment analysis and stat plot (None/Exist Reference Genome).*

Description

GO enrichment analysis and stat plot (None/Exist Reference Genome).

Usage

```
go_enrich_stat(
  go_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  max_go_item = 15,
  strip_fill = "#CDCDCD",
  xtext_angle = 45,
  sci_fill_color = "Sci_AAAS",
  sci_fill_alpha = 0.8,
  ggTheme = "theme_light"
)
```

Arguments

go_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".

pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
max_go_item	Numeric: max BP/CC/MF terms. Default: 15, min: 1, max: NULL.
strip_fill	Character: strip fill color (color name or hex value). Default: "#CDCDCD".
xtext_angle	Numeric: x axis texts angle. Default: 45, min: 0, max: 360.
sci_fill_color	Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
sci_fill_alpha	Numeric: ggsci fill color alpha. Default: 0.80, min: 0.00, max: 1.00.
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: GO enrichment analysis and stat plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
go_enrich_stat(gene_go_kegg[,-5], gene_go_kegg[100:200,1])

# 4. Set padjust_method = "BH"
go_enrich_stat(gene_go_kegg[,-5], gene_go_kegg[100:200,1], padjust_method = "BH")

# 5. Set max_go_item = 10
go_enrich_stat(gene_go_kegg[,-5], gene_go_kegg[100:200,1], max_go_item = 10)

# 6. Set strip_fill = "#008888"
go_enrich_stat(gene_go_kegg[,-5], gene_go_kegg[100:200,1], strip_fill = "#008888")

# 7. Set sci_fill_color = "Sci_JAMA"
go_enrich_stat(gene_go_kegg[,-5], gene_go_kegg[100:200,1], sci_fill_color = "Sci_JAMA")
```

heatmap_cluster *Heatmap cluster for visualizing clustered gene expression data.*

Description

Heatmap cluster for visualizing clustered gene expression data.

Usage

```
heatmap_cluster(
  data,
  dist_method = "euclidean",
  hc_method = "average",
  k_num = 5,
  show_rownames = FALSE,
  palette = "RdBu",
  cluster_pal = "Set1",
  border_color = "#ffffff",
  angle_col = 45,
  label_size = 10,
  base_size = 12,
  line_color = "#0000cd",
  line_alpha = 0.2,
  summary_color = "#0000cd",
  summary_alpha = 0.8
)
```

Arguments

data	Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).
dist_method	Character: distance measure method. Default: "euclidean", options: "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".
hc_method	Character: hierarchical clustering method. Default: "average", options: "ward.D", "ward.D2", "single", "complete","average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
k_num	Numeric: the number of groups for cutting the tree. Default: 5.
show_rownames	Logical: boolean specifying if column names are be shown. Default: FALSE, options: TRUE or FALSE.
palette	Character: color palette used in heatmap. Default: "RdBu", options: 'Spectral', 'BrBG', 'PiYG', 'PRGn', 'PuOr', 'RdBu', 'RdGy', 'RdYlBu', 'RdYlGn'.
cluster_pal	Character: color palette used for the cluster. Default: "Set1", options: 'Set1', 'Set2', 'Set3', 'Accent', 'Dark2', 'Paired', 'Pastel1', 'Pastel2'.
border_color	Character: cell border color (color name or hex value). Default: "#ffffff".
angle_col	Numeric: angle of the column labels. Default: 45.

label_size	Numeric: fontsize for the plot. Default: 10, min: 0.
base_size	Numeric: base font size. Default: 12, min: 0.
line_color	Character: trend lines color. Default: "#0000cd".
line_alpha	Numeric: trend lines alpha. Default: 0.20, min: 0.00, max: 1.00.
summary_color	Charater: summary line color. Default: "#0000cd".
summary_alpha	Numeric: summary line alpha. Default: 0.80, min: 0.00, max: 1.00.

Value

Plot: Heatmap cluster for visualizing clustered gene expression data.

Author(s)

wei dong

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression2)
head(gene_expression2)

# 3. Default parameters
heatmap_cluster(gene_expression2)

# 4. Set palette = "PuOr"
heatmap_cluster(gene_expression2, palette = "PuOr")

# 5. Set line_color = "#ff0000", summary_color = "#ff0000"
heatmap_cluster(gene_expression2, line_color = "#ff0000", summary_color = "#ff0000")
```

---

heatmap_group *Heatmap group for visualizing grouped gene expression data.*

Description

Heatmap group for visualizing grouped gene expression data.

Usage

```
heatmap_group(
  sample_gene,
  group_sample,
  scale_data = "row",
```

```
  clust_method = "complete",
  border_show = TRUE,
  border_color = "#ffffff",
  value_show = TRUE,
  value_decimal = 2,
  value_size = 5,
  axis_size = 8,
  cell_height = 10,
  low_color = "#00880055",
  mid_color = "#ffffff",
  high_color = "#ff000055",
  na_color = "#ff8800",
  x_angle = 45
)
```

Arguments

sample_gene	Dataframe: Shared degs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).
group_sample	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).
scale_data	Character: scale data. Default: "row", options: "row", "column", "none".
clust_method	Character: cluster method. Default: "complete", options: "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
border_show	Logical: show border. Default: TRUE, options: TRUE, FALSE.
border_color	Character: cell border color (color value or hex value with alpha). Default: "#ffffff".
value_show	Logical: show value in cell. Default: TRUE, options: TRUE, FALSE.
value_decimal	Numeric: cell value decimal. Default: 2, min: 0, max: 5.
value_size	Numeric: cell value font size. Default: 5, min: 0, max: NULL.
axis_size	Numeric: axis title font size. Default: 8, min: 0, max: NULL.
cell_height	Numeric: cell height for value size and axis size. Default: 10.
low_color	Character: min value color (color value or hex value with alpha). Default: "#00880055".
mid_color	Character: min value color (color value or hex value with alpha). Default: "#ffffff".
high_color	Character: min value color (color value or hex value with alpha). Default: "#ff000055".
na_color	Character: min value color (color value or hex value with alpha). Default: "#ff8800".
x_angle	Numeric: x axis text angle. Default: 45, min: 0, max: 360.

Value

Plot: Heatmap group for visualizing grouped gene expression data.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression2)
head(gene_expression2)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
heatmap_group(gene_expression2[1:50,], samples_groups)

# 4. Set scale_data = "column"
heatmap_group(gene_expression2[1:50,], samples_groups, scale_data = "column")

# 5. Set value_show = FALSE
heatmap_group(gene_expression2[1:50,], samples_groups, value_show = FALSE)

# 6. Set low_color = "#00008888"
heatmap_group(gene_expression2[1:50,], samples_groups, low_color = "#00008888")
```

`kegg_enrich` *KEGG enrichment analysis based on KEGG annotation results (None/Exist Reference Genome).*

Description

KEGG enrichment analysis based on KEGG annotation results (None/Exist Reference Genome).

Usage

```
kegg_enrich(
  kegg_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05
)
```

Arguments

kegg_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.

Value

Table: include columns ("ID", "Description", "GeneRatio", "BgRatio", "pvalue", "p.adjust", "qvalue", "geneID", "Count").

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
res <- kegg_enrich(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1])
head(res)

# 4. Set padjust_method = "BH"
res <- kegg_enrich(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], padjust_method = "BH")
head(res)

# 5. Set pvalue_cutoff = 0.80
res <- kegg_enrich(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], pvalue_cutoff = 0.80)
head(res)
```

---

kegg_enrich_bar *KEGG enrichment analysis and bar plot (None/Exist Reference Genome).*

Description

KEGG enrichment analysis and bar plot (None/Exist Reference Genome).

Usage

```
kegg_enrich_bar(
  kegg_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  sign_by = "p.adjust",
  category_num = 30,
  font_size = 12,
  low_color = "#ff0000aa",
  high_color = "#008800aa",
  ggTheme = "theme_light"
)
```

Arguments

kegg_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
sign_by	Character: significant by. Default: "p.adjust", options: "pvalue", "p.adjust", "qvalue".
category_num	Numeric: categories number to display. Default: 30, min: 1, max: NULL.
font_size	Numeric: category font size. Default: 12.
low_color	Character: low value (p-value or q-value) color (color name or hex value).
high_color	Character: high value (p-value or q-value) color (color name or hex value).
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void".

Value

Plot: KEGG enrichment analysis and bar plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
kegg_enrich_bar(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1])

# 4. Set padjust_method = "BH"
kegg_enrich_bar(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], padjust_method = "BH")

# 5. Set category_num = 10
kegg_enrich_bar(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], category_num = 10)

# 6. Set ggTheme = "theme_bw"
kegg_enrich_bar(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], ggTheme = "theme_bw")
```

---

kegg_enrich_dot *KEGG enrichment analysis and dot plot (None/Exist Reference Genome).*

Description

KEGG enrichment analysis and dot plot (None/Exist Reference Genome).

Usage

```
kegg_enrich_dot(
  kegg_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  sign_by = "p.adjust",
  category_num = 30,
  font_size = 12,
  low_color = "#ff0000aa",
  high_color = "#008800aa",
  ggTheme = "theme_light"
)
```

Arguments

kegg_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
sign_by	Character: significant by. Default: "p.adjust", options: "pvalue", "p.adjust", "qvalue".
category_num	Numeric: categories number to display. Default: 30, min: 1, max: NULL.
font_size	Numeric: category font size. Default: 12.
low_color	Character: low value (p-value or q-value) color (color name or hex value).
high_color	Character: high value (p-value or q-value) color (color name or hex value).
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: KEGG enrichment analysis and dot plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
kegg_enrich_dot(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1])

# 4. Set padjust_method = "BH"
kegg_enrich_dot(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], padjust_method = "BH")

# 5. Set category_num = 10
kegg_enrich_dot(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], category_num = 10)

# 6. Set ggTheme = "theme_bw"
kegg_enrich_dot(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], ggTheme = "theme_bw")
```

kegg_enrich_net *KEGG enrichment analysis and net plot (None/Exist Reference Genome).*

Description

KEGG enrichment analysis and net plot (None/Exist Reference Genome).

Usage

```
kegg_enrich_net(
  kegg_anno,
  degs_list,
  padjust_method = "fdr",
  pvalue_cutoff = 0.05,
  qvalue_cutoff = 0.05,
  category_num = 20,
  net_layout = "circle",
  net_circular = TRUE,
  low_color = "#ff0000aa",
  high_color = "#008800aa"
)
```

Arguments

kegg_anno	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
degs_list	Dataframe: degs list.
padjust_method	Character: P-value adjust to Q-value. Default: "fdr" (false discovery rate), options: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
pvalue_cutoff	Numeric: P-value cutoff. Recommend: small than 0.05.
qvalue_cutoff	Numeric: Q-value cutoff. Recommend: small than 0.05.
category_num	Numeric: categories number to display. Default: 20, min: 1, max: NULL.
net_layout	Character: network layout. Default: "circle", options: 'star', 'circle', 'gem', 'dh', 'graphopt', 'grid', 'mds', 'randomly', 'fr', 'kk', 'drl' or 'lgl'.
net_circular	Logical: network circular. Default: TRUE, options: TRUE, FALSE.
low_color	Character: low value (p-value or q-value) color (color name or hex value).
high_color	Character: high value (p-value or q-value) color (color name or hex value).

Value

Plot: KEGG enrichment analysis and net plot (None/Exist Reference Genome).

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
kegg_enrich_net(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1])

# 4. Set category_num = 10
kegg_enrich_net(gene_go_kegg[,c(1,5)], gene_go_kegg[100:200,1], category_num = 10)
```

---

ma_plot *MversusA plot for visualizing differentially expressed genes.*

Description

MversusA plot for visualizing differentially expressed genes.

Usage

```
ma_plot(
  data,
  foldchange = 1,
  fdr_value = 0.05,
  point_size = 3,
  color_up = "#FF0000",
  color_down = "#008800",
  color_alpha = 0.5,
  top_method = "fc",
  top_num = 20,
  label_size = 8,
  label_box = TRUE,
  title = "CT-vs-LT12",
  xlab = "Log2 mean expression",
  ylab = "Log2 fold change",
  ggTheme = "theme_light"
)
```

Arguments

data	Dataframe: differentially expressed genes (DEGs) stats 2 (1st-col: Gene, 2nd-col: baseMean, 3rd-col: Log2FoldChange, 4th-col: FDR).
foldchange	Numeric: fold change value. Default: 1.0, min: 0.0, max: null.
fdr_value	Numeric: false discovery rate. Default: 0.05, min: 0.00, max: 1.00.
point_size	Numeric: point size. Default: 1.0, min: 0.0, max: null.
color_up	Character: up-regulated genes color (color name or hex value). Default: "#FF0000".
color_down	Character: down-regulated genes color (color name or hex value). Default: "#008800".
color_alpha	Numeric: point color alpha. Default: 0.50, min: 0.00, max: 1.00.
top_method	Character: top genes select method. Default: "fc" (fold change), options: "padj" (p-adjust), "fc".
top_num	Numeric: top genes number. Default: 20, min: 0, max: null.
label_size	Numeric: label font size. Default: 8.00, min: 0.00, max: null.
label_box	Logical: add box to label. Default: TRUE, options: TRUE, FALSE.
title	Character: plot title. Default: "CT-vs-Trait1".
xlab	Character: x label. Default: "Log2 mean expression".
ylab	Character: y label. Default: "Log2 fold change".
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: MversusA plot for visualizing differentially expressed genes.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(degs_stats2)
head(degs_stats2)

# 3. Default parameters
ma_plot(degs_stats2)

# 4. Set color_up = "#FF8800"
ma_plot(degs_stats2, color_up = "#FF8800")
```

```
# 5. Set top_num = 10
ma_plot(degs_stats2, top_num = 10)
```

`network_data` *Network data from WGCNA tan module top-200 dataframe.*

Description

Network data from WGCNA tan module top-200 dataframe.

Usage

```
data(network_data)
```

Format

Dataframe: Network data from WGCNA tan module top-200 dataframe (1st-col: Source, 2nd-col: Target).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/NetworkPlot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(network_data)

# 3. View example data
network_data
```

network_plot *Network plot for analyzing and visualizing relationship of genes.*

Description

Network plot for analyzing and visualizing relationship of genes.

Usage

```
network_plot(
  data,
  calc_by = "degree",
  degree_value = 0.5,
  normal_color = "#008888cc",
  border_color = "#FFFFFF",
  from_color = "#FF0000cc",
  to_color = "#008800cc",
  normal_shape = "circle",
  spatial_shape = "circle",
  node_size = 25,
  lable_color = "#FFFFFF",
  label_size = 0.5,
  edge_color = "#888888",
  edge_width = 1.5,
  edge_curved = TRUE,
  net_layout = "layout_on_sphere"
)
```

Arguments

data	Dataframe: Network data from WGCNA tan module top-200 dataframe (1st-col: Source, 2nd-col: Target).
calc_by	Character: calculate relationship by "degree", "node". Default: "degree".
degree_value	Numeric: degree value when calc_by = "degree". Default: 0.05, min: 0.00, max: 1.00.
normal_color	Character: normal relationship nodes color (color name of hex value).
border_color	Character: node border color (color name or hex value).
from_color	Character: the start color of nodes that meet degree_value.
to_color	Character: the end color of nodes that meet degree_value.
normal_shape	Character: normal node shape. Default: "circle", options: "circle", "crectangle", "csquare", "none", "pie", "raster", "rectangle", "sphere", "square", "vrectangle".
spatial_shape	Character: meet degree_value node shape. Default: "csquare", options: "circle", "crectangle", "csquare", "none", "pie", "raster", "rectangle", "sphere", "square", "vrectangle".

node_size	Numeric: node size. Default: 10, min: 0, max: NULL.
lable_color	Character: gene labels color. Default: "#FFFFFF".
label_size	Numeric: node label size. Default: 0.5, min: 0, max: NULL.
edge_color	Character: edges color. Default: "#888888".
edge_width	Numeric: edges width. Default: 1.5.
edge_curved	Logical: curved edges. Default: TRUE, options: TRUE, FALSE.
net_layout	Character: network layout. Default: "layout_on_sphere", options: "layout_as_bipartite", "layout_as_star", "layout_as_tree", "layout_components", "layout_in_circle", "layout_nicely", "layout_on_grid", "layout_on_sphere","layout_randomly","layout_with_dh","layout_with_c

Value

Plot: network plot for analyzing and visualizing relationship of genes.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(network_data)
head(network_data)

# 3. Default parameters
network_plot(network_data)

# 4. Set calc_by = "node"
network_plot(network_data, calc_by = "node")

# 5. Set degree_value = 0.1
network_plot(network_data, degree_value = 0.1)

# 6. Set normal_color = "#ff8800cc"
network_plot(network_data, normal_color = "#ff8800cc")

# 7. Set net_layout = "layout_as_tree"
network_plot(network_data, net_layout = "layout_as_tree")
```

pca_analysis *PCA dimensional reduction analysis for RNA-Seq.*

Description

PCA dimensional reduction analysis for RNA-Seq.

Usage

```
pca_analysis(sample_gene, group_sample)
```

Arguments

sample_gene	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
group_sample	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Value

Table: PCA dimensional reduction analysis for RNA-Seq.

Author(s)

benben-miao

Examples

```
# 1. Library package TOmicsVis
library(TOmicsVis)

# 2. Load example datasets
data(gene_expression)
head(gene_expression)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
res <- pca_analysis(gene_expression, samples_groups)
head(res)
```

pca_plot *PCA dimensional reduction visualization for RNA-Seq.*

Description

PCA dimensional reduction visualization for RNA-Seq.

Usage

```
pca_plot(
  sample_gene,
  group_sample,
  xPC = 1,
  yPC = 2,
  multi_shape = TRUE,
  point_size = 5,
  point_alpha = 0.8,
  text_size = 5,
  fill_alpha = 0.05,
  border_alpha = 0,
  sci_fill_color = "Sci_AAAS",
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)
```

Arguments

sample_gene	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
group_sample	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).
xPC	Numeric: PC index at x axis. Default: 1, options: 1, 2, 3, ...
yPC	Numeric: PC index at y axis. Default: 2, options: 2, 3, 4, ...
multi_shape	Logical: groups as shapes. Default: TRUE, options: TRUE, FALSE.
point_size	Numeric: PCA plot point size. Default: 5, min: 0.
point_alpha	Numeric: point color alpha. Default: 0.80, min: 0.00, max: 1.00.
text_size	Numeric: PCA plot annotation size. Default: 5, min: 0.
fill_alpha	Numeric: ellipse fill color alpha. Default: 0.10, min: 0.00, max: 1.00.
border_alpha	Numeric: ellipse border color alpha. Default: 0.10, min: 0.00, max: 1.00.
sci_fill_color	Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".

legend_pos	Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".
legend_dir	Character: legend director. Default: "vertical", options: "horizontal", "vertical".
ggTheme	Character: ggplot2 theme. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void".

Value

Plot: PCA dimensional reduction visualization for RNA-Seq.

Author(s)

benben-miao

Examples

```
# 1. Library package TOmicsVis
library(TOmicsVis)

# 2. Load example datasets
data(gene_expression)
head(gene_expression)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
pca_plot(gene_expression, samples_groups)

# 4. Set multi_shape = FALSE
pca_plot(gene_expression, samples_groups, multi_shape = FALSE)

# 5. Set sci_fill_color = "Sci_NPG", fill_alpha = 0.10
pca_plot(gene_expression, samples_groups, sci_fill_color = "Sci_NPG", fill_alpha = 0.10)
```

---

quantile_plot *Quantile plot for visualizing data distribution.*

Description

Quantile plot for visualizing data distribution.

Usage

```
quantile_plot(
  data,
  my_shape = "fill_circle",
  point_size = 1.5,
  conf_int = TRUE,
  conf_level = 0.95,
  split_panel = "Split_Panel",
  legend_pos = "right",
  legend_dir = "vertical",
  sci_fill_color = "Sci_NPG",
  sci_color_alpha = 0.75,
  ggTheme = "theme_light"
)
```

Arguments

data	Dataframe: Weight and Sex traits dataframe (1st-col: Weight, 2nd-col: Sex).
my_shape	Character: scatter shape. Default: "fill_circle", options: "border_square", "border_circle", "border_triangle", "plus", "times", "border_diamond", "border_triangle_down", "square_times", "plus_times", "diamond_plus", "circle_plus", "di_triangle", "square_plus", "circle_times","square_triangle", "fill_square", "fill_circle", "fill_triangle", "fill_diamond", "large_circle", "small_circle", "fill_border_circle", "fill_border_square", "fill_border_diamond", "fill_border_triangle".
point_size	Numeric: point size. Default: 1.5, min: 0.0, max: not required.
conf_int	Logical: confidence interval (CI). Default: TRUE, options: TRUE or FALSE.
conf_level	Numeric: confidence interval value. Default: 0.95, min: 0.00, max: 1.00.
split_panel	Character: split panel by groups. Default: "Split_Panel", options: "One_Panel", "Split_Panel".
legend_pos	Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".
legend_dir	Character: legend direction. Default: "vertical", options: "horizontal", "vertical".
sci_fill_color	Character: ggsci fill or color palette. Default: "Sci_NPG", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
sci_color_alpha	Numeric: ggsci border color alpha. Default: 0.75, min: 0.00, max: 1.00.
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void".

Value

Plot: quantile plot for visualizing data distribution.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(weight_sex)
head(weight_sex)

# 3. Default parameters
quantile_plot(weight_sex)

# 4. Set split_panel = "Split_Panel"
quantile_plot(weight_sex, split_panel = "Split_Panel")

# 5. Set sci_fill_color = "Sci_Futurama"
quantile_plot(weight_sex, sci_fill_color = "Sci_Futurama")

# 6. Set conf_int = FALSE
quantile_plot(weight_sex, conf_int = FALSE)
```

---

samples_groups *Samples and groups for gene expression.*

Description

Samples and groups for gene expression.

Usage

```
data(samples_groups)
```

Format

Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/PCAplot/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example dataset samples_groups
data(samples_groups)

# 3. View samples_groups
samples_groups
```

`survival_data` *Survival data as example data for survival_plot function.*

Description

Survival data as example data for survival_plot function.

Usage

```
data(survival_data)
```

Format

Dataframe: survival record data (1st-col: Time, 2nd-col: Status, 3rd-col: Group).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/SurvivalAnalysis/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(survival_data)

# 3. View example data
survival_data
```

survival_plot *Survival plot for analyzing and visualizing survival data.*

Description

Survival plot for analyzing and visualizing survival data.

Usage

```
survival_plot(
  data,
  curve_function = "pct",
  conf_inter = TRUE,
  interval_style = "ribbon",
  risk_table = TRUE,
  num_censor = TRUE,
  sci_palette = "aaas",
  ggTheme = "theme_light",
  x_start = 0,
  y_start = 0,
  y_end = 100,
  x_break = 10,
  y_break = 10
)
```

Arguments

data	Dataframe: survival record data (1st-col: Time, 2nd-col: Status, 3rd-col: Group).
curve_function	Character: an arbitrary function defining a transformation of the survival curve. Often used transformations can be specified with a character argument: "event" plots cumulative events (f(y) = 1-y), "cumhaz" plots the cumulative hazard function (f(y) = -log(y)), and "pct" for survival probability in percentage.
conf_inter	Logical: confidence interval. Default: TRUE, options: TRUE, FALSE.
interval_style	Character: confidence interval style. Default: "ribbon", options: "ribbon", "step".
risk_table	Logical: show cumulative risk table. Default: TRUE, options: TRUE, FALSE.
num_censor	Logical: show cumulative number of censoring. Default: TRUE, options: TRUE, FALSE.
sci_palette	Character: ggsci color palette. Default: "aaas", options: "aaas", "npg", "lancet", "jco", "ucscgb", "uchicago", "simpsons", "rickandmorty".
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"
x_start	Numeric: x-axis start value. Default: 0, min: 0, max: null.

y_start	Numeric: y-axis start value. Default: 0, min: 0, max: 100.
y_end	Numeric: y-axis end value. Default: 100, min: 0, max: 100.
x_break	Numeric: x-axis break value. Default: 10, min: 0, max: null.
y_break	Numeric: y-axis break value. Default: 10, min: 0, max: 100.

Value

Plot: survival plot for analyzing and visualizing survival data.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(survival_data)
head(survival_data)

# 3. Default parameters
survival_plot(survival_data)

# 4. Set conf_inter = FALSE
survival_plot(survival_data, conf_inter = FALSE)

# 5. Set sci_palette = "jco"
survival_plot(survival_data, sci_palette = "jco")
```

---

table_cross *Table cross used to cross search and merge results in two tables.*

Description

Table cross used to cross search and merge results in two tables.

Usage

```
table_cross(
  data1,
  data2,
  inter_var = "Genes",
  left_index = TRUE,
  right_index = TRUE
)
```

Arguments

data1	Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).
data2	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
inter_var	Character: Intersecting variable (column name). Default: "geneID" in example data.
left_index	Logical: left table as index. Default: TRUE, options: TRUE, FALSE.
right_index	Logical: right table as index. Default: FALSE, options: TRUE, FALSE.

Value

Table: include multiple columns.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression2)
head(gene_expression2)

data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
res <- table_cross(gene_expression2, gene_go_kegg, inter_var = "Genes")
head(res)

# 4. Set left_index = TRUE, right_index = FALSE
res <- table_cross(gene_expression2, gene_go_kegg,
inter_var = "Genes", left_index = TRUE, right_index = FALSE)
head(res)

# 5. Set left_index = FALSE, right_index = TRUE
res <- table_cross(gene_expression2, gene_go_kegg,
inter_var = "Genes", left_index = FALSE, right_index = TRUE)
head(res)
```

table_filter *Table filter used to filter row by column condition.*

Description

Table filter used to filter row by column condition.

Usage

```
table_filter(data, ...)
```

Arguments

data	Dataframe: Length, Width, Weight, and Sex traits dataframe (1st-col: Value, 2nd-col: Traits, 3rd-col: Sex).
...	Expression: multiple expressions.

Value

Table: table filter used to filter row by column condition.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(traits_sex)
head(traits_sex)

# 3. Set height > 100 & eye_color == "black"
res <- table_filter(traits_sex, Sex == "Male" & Traits == "Weight" & Value > 40)
head(res)
```

table_merge *Table merge used to merge multiple variables to on variable.*

Description

Table merge used to merge multiple variables to on variable.

Usage

```
table_merge(
  data,
 merge_vars = c("biological_process", "cellular_component", "molecular_function"),
  new_var = "go_category",
  new_value = "go_term",
  na_remove = FALSE
)
```

Arguments

data	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
merge_vars	Vector: include merged variable (column) names. Default: c("Ozone", "Solar.R", "Wind", "Temp") in example data.
new_var	Character: new variable (column) name. Default: "Variable".
new_value	Character: new variable (column) value name. Default: "Value".
na_remove	Logical: remove NA value. Default: FALSE, options: TRUE, FALSE.

Value

Table: include multiple variables.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg)
head(gene_go_kegg)

# 3. Default parameters
res <- table_merge(gene_go_kegg)
```

```
head(res)

# 4. Set new_var = "GO", new_value = "Terms"
res <- table_merge(gene_go_kegg, new_var = "GO", new_value = "Terms")
head(res)
```

`table_split` *Table split used for splitting a grouped column to multiple columns.*

Description

Table split used for splitting a grouped column to multiple columns.

Usage

```
table_split(
  data,
  grouped_var = "go_category",
  value_var = "go_term",
  miss_drop = TRUE
)
```

Arguments

`data`	Dataframe: GO and KEGG annotation of background genes (1st-col: Genes, 2nd-col: biological_process, 3rd-col: cellular_component, 4th-col: molecular_function, 5th-col: kegg_pathway).
`grouped_var`	Character: grouped column name. Default: "go_category".
`value_var`	Character: value column name. Default: "go_term".
`miss_drop`	Logical: drop missing values or NA values. Default: TRUE, options: TRUE, FALSE.

Value

Table: table split used for splitting a grouped column to multiple columns.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_go_kegg2)
head(gene_go_kegg2)

# 3. Default parameters
res <- table_split(gene_go_kegg2)
head(res)
```

`tomicsvis` *TOmicsVis shiny app start function.*

Description

TOmicsVis shiny app start function.

Usage

```
tomicsvis()
```

Value

Shinyapp: TOmicsVis shiny app.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)
```

traits_sex *Length, Width, Weight, and Sex traits dataframe.*

Description

Length, Width, Weight, and Sex traits dataframe.

Usage

```
data(traits_sex)
```

Format

Dataframe: Length, Width, Weight, and Sex traits dataframe (1st-col: Value, 2nd-col: Traits, 3rd-col: Sex).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/BoxStat/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(traits_sex)

# 3. View example data
traits_sex
```

trend_plot *Trend plot for visualizing gene expression trend profile in multiple traits.*

Description

Trend plot for visualizing gene expression trend profile in multiple traits.

Usage

```
trend_plot(
  data,
  scale_method = "centerObs",
  miss_value = "exclude",
  line_alpha = 0.5,
  show_points = TRUE,
  show_boxplot = TRUE,
  num_column = 1,
  xlab = "Traits",
  ylab = "Genes Expression",
  sci_fill_color = "Sci_AAAS",
  sci_fill_alpha = 0.8,
  sci_color_alpha = 0.8,
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)
```

Arguments

data	Dataframe: Shared degs of all paired comparisons in all groups expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~n-1-col: Groups, n-col: Pathways).
scale_method	Character: data scale methods. Default: "globalminmax" (global min and max values), options: "std" (standard), "robust", "uniminmax" (unique min and max values), "globalminmax", "center", "centerObs" (center observes).
miss_value	Character: deal method for missing values. Default: "exclude", options: "exclude", "mean", "median", "min10", "random".
line_alpha	Numeric: lines color alpha. Default: 0.50, min: 0.00, max: 1.00.
show_points	Logical: show points at trait node. Default: TRUE, options: TRUE, FALSE.
show_boxplot	Logical: show boxplot at trait node. Default: TRUE, options: TRUE, FALSE.
num_column	Logical: column number. Default: 2, min: 1, max: null.
xlab	Character: x label. Default: "Traits".
ylab	Character: y label. Default: "Genes Expression".
sci_fill_color	Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
sci_fill_alpha	Numeric: ggsci fill color alpha. Default: 0.50, min: 0.00, max: 1.00.
sci_color_alpha	Numeric: ggsci border color alpha. Default: 1.00, min: 0.00, max: 1.00.
legend_pos	Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".
legend_dir	Character: legend direction. Default: "vertical", options: "horizontal", "vertical".

ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: box plot support two levels and multiple groups with P value.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression3)
head(gene_expression3)

# 3. Default parameters
trend_plot(gene_expression3[1:50,])

# 4. Set line_alpha = 0.30
trend_plot(gene_expression3[1:50,], line_alpha = 0.30)

# 5. Set sci_fill_color = "Sci_NPG"
trend_plot(gene_expression3[1:50,], sci_fill_color = "Sci_NPG")
```

---

tsne_analysis *TSNE analysis for analyzing and visualizing TSNE algorithm.*

Description

TSNE analysis for analyzing and visualizing TSNE algorithm.

Usage

```
tsne_analysis(sample_gene, group_sample, seed = 1, tsne_dims = 2)
```

Arguments

sample_gene	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
group_sample	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).
seed	Numeric: set seed for robust result. Default: 1.
tsne_dims	Numeric: TSNE dimensionality number. Default: 2.

Value

Table: TSNE analysis for analyzing and visualizing TSNE algorithm.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression)
head(gene_expression)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
res <- tsne_analysis(gene_expression, samples_groups)
head(res)

# 4. Set tsne_dims = 3
res <- tsne_analysis(gene_expression, samples_groups, tsne_dims = 3)
head(res)
```

---

tsne_plot *TSNE plot for analyzing and visualizing TSNE algorithm.*

Description

TSNE plot for analyzing and visualizing TSNE algorithm.

Usage

```
tsne_plot(
  sample_gene,
  group_sample,
  seed = 1,
  multi_shape = FALSE,
  point_size = 5,
  point_alpha = 0.8,
  text_size = 5,
  text_alpha = 0.8,
  fill_alpha = 0.1,
  border_alpha = 0,
```

```
  sci_fill_color = "Sci_AAAS",
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)
```

Arguments

sample_gene	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
group_sample	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).
seed	Numeric: set seed for robust result. Default: 1.
multi_shape	Logical: groups as shapes. Default: FALSE, options: TRUE, FALSE.
point_size	Numeric: point size. Default: 5, min: 0, max: null.
point_alpha	Numeric: point color alpha. Default: 0.80, min: 0.00, max: 1.00.
text_size	Numeric: text size. Default: 5, min: 0 (hind), max: null.
text_alpha	Numeric: text alpha. Default: 0.80, min: 0.00, max: 1.00.
fill_alpha	Numeric: ellipse alpha. Default: 0.30, min: 0.00, max: 1.00.
border_alpha	Numeric: ellipse border color alpha. Default: 0.10, min: 0.00, max: 1.00.
sci_fill_color	Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
legend_pos	Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".
legend_dir	Character: legend direction. Default: "vertical", options: "horizontal", "vertical".
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: TSNE plot for analyzing and visualizing TSNE algorithm.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression)
```

```
head(gene_expression)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
tsne_plot(gene_expression, samples_groups)

# 4. Set sci_fill_color = "Sci_NPG", seed = 6
tsne_plot(gene_expression, samples_groups, sci_fill_color = "Sci_NPG", seed = 6)

# 5. Set multi_shape = TRUE, fill_alpha = 0.00
tsne_plot(gene_expression, samples_groups, multi_shape = TRUE, fill_alpha = 0.00)
```

`umap_analysis` *UMAP analysis for analyzing RNA-Seq data.*

Description

UMAP analysis for analyzing RNA-Seq data.

Usage

```
umap_analysis(sample_gene, group_sample, seed = 1, method = "naive")
```

Arguments

`sample_gene`	Dataframe: gene expression dataframe (1st-col: Transcripts or Genes, 2nd-col~: Samples).
`group_sample`	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).
`seed`	Numeric: set seed for robust result. Default: 1.
`method`	Character: 'naive' (an implementation written in pure R) and 'umap-learn' (requires python package 'umap-learn').

Value

Table: UMAP analysis for analyzing RNA-Seq data.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression)
head(gene_expression)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
res <- umap_analysis(gene_expression, samples_groups)
head(res)
```

`umap_plot` *UMAP plot for analyzing and visualizing UMAP algorithm.*

Description

UMAP plot for analyzing and visualizing UMAP algorithm.

Usage

```
umap_plot(
  sample_gene,
  group_sample,
  seed = 1,
  multi_shape = TRUE,
  point_size = 5,
  point_alpha = 1,
  text_size = 5,
  text_alpha = 0.8,
  fill_alpha = 0,
  border_alpha = 0,
  sci_fill_color = "Sci_AAAS",
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)
```

Arguments

`sample_gene`	Dataframe: gene expression dataframe (1st-col: Transcripts or Genes, 2nd-col~: Samples).
`group_sample`	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

seed	Numeric: set seed for robust result. Default: 1.
multi_shape	Logical: groups as shapes. Default: FALSE, options: TRUE, FALSE.
point_size	Numeric: point size. Default: 5, min: 0, max: null.
point_alpha	Numeric: point color alpha. Default: 0.80, min: 0.00, max: 1.00.
text_size	Numeric: text size. Default: 5, min: 0 (hind), max: null.
text_alpha	Numeric: text alpha. Default: 0.80, min: 0.00, max: 1.00.
fill_alpha	Numeric: ellipse alpha. Default: 0.30, min: 0.00, max: 1.00.
border_alpha	Numeric: ellipse border color alpha. Default: 0.10, min: 0.00, max: 1.00.
sci_fill_color	Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
legend_pos	Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".
legend_dir	Character: legend direction. Default: "vertical", options: "horizontal", "vertical".
ggTheme	Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: UMAP plot for analyzing and visualizing UMAP algorithm.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression)
head(gene_expression)

data(samples_groups)
head(samples_groups)

# 3. Default parameters
umap_plot(gene_expression, samples_groups)

# 4. Set sci_fill_color = "Sci_Simpsons", seed = 6
umap_plot(gene_expression, samples_groups, sci_fill_color = "Sci_Simpsons", seed = 6)

# 5. Set fill_alpha = 0.10
umap_plot(gene_expression, samples_groups, fill_alpha = 0.10)
```

upsetr_plot *UpSet plot for stat common and unique gene among multiple sets.*

Description

UpSet plot for stat common and unique gene among multiple sets.

Usage

```
upsetr_plot(
  data,
  sets_num = 4,
  keep_order = FALSE,
  order_by = "freq",
  decrease = TRUE,
  mainbar_color = "#006600",
  number_angle = 45,
  matrix_color = "#cc0000",
  point_size = 4.5,
  point_alpha = 0.5,
  line_size = 0.8,
  shade_color = "#cdcdcd",
  shade_alpha = 0.5,
  setsbar_color = "#000066",
  setsnum_size = 6,
  text_scale = 1.2
)
```

Arguments

data	Dataframe: Paired comparisons differentially expressed genes (degs) among groups (1st-col~: degs of paired comparisons).
sets_num	Numeric: sets number. Default: 4, min: 2, max: NULL.
keep_order	Logical: keep sets in the order entered using the sets parameter. Default: FALSE, options: TRUE, FALSE.
order_by	Character: intersections in the matrix should be ordered by. Default: "freq" (frequency), options: "freq", "degree", "both".
decrease	Logical: order by decrease. Default: TRUE, options: TRUE, FALSE.
mainbar_color	Charactor: mainbar color (color name or hex value). Default: "#006600".
number_angle	Numeric: number display angle. Default: 45, min: 0, max: 360.
matrix_color	Charactor: matrix point color (color name or hex value). Default: "#cc0000".
point_size	Numeric: point size. Default: 4.5, min: 0.0, max: NULL.
point_alpha	Numeric: point color alpha. Default: 0.50, min: 0.00, max: 1.00.
line_size	Numeric: connection line size. Default: 0.8, min: 0.00, max: NULL.

shade_color	Character: matrix shade color. Default: "#cdcdcd".
shade_alpha	Numeric: shade color alpha. Default: 0.50, min: 0.00, max: 1.00.
setsbar_color	Character: sets bar color. Default: "#000066".
setsnum_size	Numeric: sets bar number size. Default: 6.
text_scale	Numeric: all text scale. Default: 1.2, min: 0.01, max: NULL.

Value

Plot: UpSet plot for stat common and unique gene among multiple sets.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(degs_lists)
head(degs_lists)

# 3. Default parameters
upsetr_plot(degs_lists)

# 4. Set keep_order = TRUE, order_by = "degree"
upsetr_plot(degs_lists, keep_order = TRUE, order_by = "degree")

# 5. Set mainbar_color = "#333333", number_angle = 0
upsetr_plot(degs_lists, mainbar_color = "#333333", number_angle = 0)

# 6. Set shade_color = "#ffcc00", setsbar_color = "#0000cc"
upsetr_plot(degs_lists, shade_color = "#ffcc00", setsbar_color = "#0000cc")
```

---

venn_plot *Venn plot for stat common and unique gene among multiple sets.*

Description

Venn plot for stat common and unique gene among multiple sets.

Usage

```
venn_plot(
  data,
  title_size = 1,
  label_show = TRUE,
  label_size = 0.8,
  border_show = TRUE,
  line_type = "longdash",
  ellipse_shape = "circle",
  sci_fill_color = "Sci_AAAS",
  sci_fill_alpha = 0.65
)
```

Arguments

data	Dataframe: Paired comparisons differentially expressed genes (degs) among groups (1st-col~: degs of paired comparisons).
title_size	Numeric: sets title size. Default: 1, min: 0, max: NULL.
label_show	Logical: show intersection labels. Default: TRUE, options: TRUE, FALSE.
label_size	Numeric: intersection labels size. Default: 0.8, min: 0, max: NULL.
border_show	Logical: show border line. Default: TRUE, options: TRUE, FALSE.
line_type	Character: ellipse border line type. Default: "blank", options: "blank", "solid", "dashed", "dotted", "dotdash", "longdash", "twodash".
ellipse_shape	Character: ellipse shape. Default: "circle", options: "circle", "ellipse".
sci_fill_color	Character: ggsci color palette. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".
sci_fill_alpha	Numeric: ggsci fill color alpha. Default: 0.65, min: 0.00, max: 1.00.

Value

Plot: venn plot for stat common and unique gene among multiple sets.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(degs_lists)
head(degs_lists)

# 3. Default parameters
```

```
venn_plot(degs_lists)

# 4. Set line_type = "blank"
venn_plot(degs_lists, line_type = "blank")

# 5. Set ellipse_shape = "ellipse"
venn_plot(degs_lists, ellipse_shape = "ellipse")

# 6. Set sci_fill_color = "Sci_IGV"
venn_plot(degs_lists, sci_fill_color = "Sci_IGV")
```

`violin_plot` *Violin plot support two levels and multiple groups with P value.*

Description

Violin plot support two levels and multiple groups with P value.

Usage

```
violin_plot(
  data,
  test_method = "t.test",
  test_label = "p.format",
  group_level = "Three_Column",
  violin_orientation = "vertical",
  add_element = "boxplot",
  element_alpha = 0.5,
  my_shape = "plus_times",
  sci_fill_color = "Sci_AAAS",
  sci_fill_alpha = 0.5,
  sci_color_alpha = 1,
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)
```

Arguments

`data`	Dataframe: Length, Width, Weight, and Sex traits dataframe (1st-col: Value, 2nd-col: Traits, 3rd-col: Sex).
`test_method`	Character: test methods of P value. Default: "t.test", options: "wilcox.test", "t.test", "anova", "kruskal.test".
`test_label`	Character: test label of P value. Default: "p.format", options: "p.signif", "p.format". c(0, 0.0001, 0.001, 0.01, 0.05, 1).

group_level Character: group levels. Default: "Three_Column", options: "Two_Column", "Three_Column".

violin_orientation
Character: violin orientation. Default: "vertical", options: "vertical", "horizontal", "reverse".

add_element Character: add new plot. Default: "boxplot", options: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range".

element_alpha Numeric: element color alpha. Default: 0.50, min: 0.00, max: 1.00.

my_shape Character: box scatter shape. Default: "plus_times", options: "border_square", "border_circle", "border_triangle", "plus", "times", "border_diamond", "border_triangle_down", "square_times", "plus_times", "diamond_plus", "circle_plus", "di_triangle", "square_plus", "circle_times","square_triangle", "fill_square", "fill_circle", "fill_triangle", "fill_diamond", "large_circle", "small_circle", "fill_border_circle", "fill_border_square", "fill_border_diamond", "fill_border_triangle".

sci_fill_color Character: ggsci color pallet. Default: "Sci_AAAS", options: "Sci_AAAS", "Sci_NPG", "Sci_Simpsons", "Sci_JAMA", "Sci_GSEA", "Sci_Lancet", "Sci_Futurama", "Sci_JCO", "Sci_NEJM", "Sci_IGV", "Sci_UCSC", "Sci_D3", "Sci_Material".

sci_fill_alpha Numeric: ggsci fill color alpha. Default: 0.50, min: 0.00, max: 1.00.

sci_color_alpha
Numeric: ggsci border color alpha. Default: 1.00, min: 0.00, max: 1.00.

legend_pos Character: legend position. Default: "right", options: "none", "left", "right", "bottom", "top".

legend_dir Character: legend direction. Default: "vertical", options: "horizontal", "vertical".

ggTheme Character: ggplot2 themes. Default: "theme_light", options: "theme_default", "theme_bw", "theme_gray", "theme_light", "theme_linedraw", "theme_dark", "theme_minimal", "theme_classic", "theme_void"

Value

Plot: violin plot support two levels and multiple groups with P value.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(traits_sex)
head(traits_sex)
```

```
# 3. Default parameters
violin_plot(traits_sex)

# 4. Set test_label = "p.signif",
violin_plot(traits_sex, test_label = "p.signif")

# 5. Set violin_orientation = "horizontal"
violin_plot(traits_sex, violin_orientation = "horizontal")

# 6. Set group_level = "Two_Column"
violin_plot(traits_sex, group_level = "Two_Column")

# 7. Set add_element = "jitter"
violin_plot(traits_sex, add_element = "jitter")
```

`volcano_plot` *Volcano plot for visualizing differentailly expressed genes.*

Description

Volcano plot for visualizing differentailly expressed genes.

Usage

```
volcano_plot(
  data,
  title = "CT-vs-LT12",
  log2fc_cutoff = 1,
  pq_value = "pvalue",
  pq_cutoff = 0.05,
  cutoff_line = "longdash",
  point_shape = "large_circle",
  point_size = 2,
  point_alpha = 0.5,
  color_normal = "#888888",
  color_log2fc = "#008000",
  color_pvalue = "#0088ee",
  color_Log2fc_p = "#ff0000",
  label_size = 3,
  boxed_labels = FALSE,
  draw_connectors = FALSE,
  legend_pos = "right"
)
```

Arguments

`data`	Dataframe: differentially expressed genes (DEGs) stats (1st-col: Genes, 2nd-col: log2FoldChange, 3rd-col: Pvalue, 4th-col: FDR).

title	Character: title of plot. Default: CT-vs-LT12.
log2fc_cutoff	Numeric: log2(FoldChange) cutoff log2(2) = 1. Default: 1.0, min: 0.0, max: null.
pq_value	Character: select pvalue or qvalue. Default: "pvalue", options: "pvalue", "padj".
pq_cutoff	Numeric: pvalue or qvalue cutoff. Default: 0.005, min: 0.000, max: 1.000.
cutoff_line	Character: cutoff line type. Default: "longdash", options: "blank", "solid", "dashed", "dotted", "dotdash", "longdash", "twodash".
point_shape	Character: point shape. Default: "large_circle", options: "border_square", "border_circle", "border_triangle", "plus", "times", "border_diamond", "border_triangle_down", "square_times", "plus_times", "diamond_plus", "circle_plus", "di_triangle", "square_plus", "circle_times","square_triangle", "fill_square", "fill_circle", "fill_triangle", "fill_diamond", "large_circle", "small_circle", "fill_border_circle", "fill_border_square", "fill_border_diamond", "fill_border_triangle".
point_size	Numeric: point size. Default: 1.0, min: 0.0, max: null.
point_alpha	Numeric: point color alpha. Default: 0.50, min: 0.00, max: 1.00.
color_normal	Character: normal genes color (color name or hex value). Default: "#888888".
color_log2fc	Character: genes color that log2fc >= log2fc_cutoff. Default: "#008000".
color_pvalue	Character: genes color that pvalue > pq_cutoff. Default: "#0088ee".
color_Log2fc_p	Character: genes color that log2fc >= log2fc_cutoff and pvalue > pq_cutoff. Default: "#ff0000".
label_size	Numeric: DEG labels size. Default: 3.0, min: 0.0, max: null.
boxed_labels	Logical: add box to every DEG label. Default: FALSE.
draw_connectors	Logical: add connector between DEGs and labels. Default: FALSE.
legend_pos	Character: legend position. Default: "right", options: "right", "left", "top", "bottom".

Value

Plot: volcano plot for visualizing differentailly expressed genes.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(degs_stats)
head(degs_stats)

# 3. Default parameters
```

```
volcano_plot(degs_stats)

# 4. Set color_Log2fc_p = "#ff8800"
volcano_plot(degs_stats, color_Log2fc_p = "#ff8800")

# 5. Set boxed_labels = TRUE
volcano_plot(degs_stats, boxed_labels = TRUE)
```

`weight_sex` *Weight and Sex traits dataframe.*

Description

Weight and Sex traits dataframe.

Usage

```
data(weight_sex)
```

Format

Dataframe: Weight and Sex traits dataframe (1st-col: Weight, 2nd-col: Sex).

Author(s)

benben-miao

References

https://github.com/BioSciTools/BioSciToolsDatasets/tree/main/QuantileQuantile/

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Load example data
data(weight_sex)

# 3. View example data
weight_sex
```

wgcna_pipeline *WGCNA analysis pipeline for RNA-Seq.*

Description

WGCNA analysis pipeline for RNA-Seq.

Usage

```
wgcna_pipeline(
  sample_gene,
  group_sample,
  R_cutofff = 0.85,
  max_block = 5000,
  min_module = 20,
  network_type = "unsigned",
  merge_cutoff = 0.15,
  cor_type = "pearson",
  na_color = "#cdcdcd",
  xlab_angle = 45,
  text_size = 0.7
)
```

Arguments

sample_gene	Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).
group_sample	Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).
R_cutofff	Numeric: Rsquare cutoff. Default: 0.85, min: 0.00, max: 1.00.
max_block	Numeric: max block size. Default: 5000.
min_module	Numeric: min module gene number. Default: 20.
network_type	Character: network type. Default: "unsigned", options: "unsigned", "signed", "signed hybrid".
merge_cutoff	Numeric: merge modules cutoff. Default: 0.15.
cor_type	Character: correlation type. Default: "pearson", options: "pearson", "bicor".
na_color	Character: NA value color (color name or hex value). Default: "#cdcdcd".
xlab_angle	Numeric: X axis lable angle. Default: 45, min: 0, max: 360.
text_size	Numeric: cell text size. Default: 0.7, min: 0, max: NULL.

Value

WGCNA results in tempdir() directory of current session.

Author(s)

benben-miao

Examples

```
# 1. Library TOmicsVis package
library(TOmicsVis)

# 2. Use example dataset
data(gene_expression)
head(gene_expression)

data(samples_groups)
head(samples_groups)
```

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