

TOmicsVis

1. Introduction

1.1 Meta Information

TOmicsVis: TranscriptOmics Visualization.

Website: <https://benben-miao.github.io/TOmicsVis/> (<https://benben-miao.github.io/TOmicsVis/>)

1.2 Github and CRAN Install

downloads 542 (<https://cran.rstudio.com/web/packages/TOmicsVis/index.html>)

1.2.1 Install required packages from Bioconductor:

```
# Install required packages from Bioconductor
install.packages("BiocManager")
BiocManager::install(c("ComplexHeatmap", "EnhancedVolcano", "clusterProfiler", "enrichplot", "impute", "preprocessCore",
"Mfuzz"))
```

1.2.2 Github: <https://github.com/benben-miao/TOmicsVis/> (<https://github.com/benben-miao/TOmicsVis/>)

Install from Github:

```
install.packages("devtools")
devtools::install_github("benben-miao/TOmicsVis")

# Resolve network by GitClone
devtools::install_git("https://gitclone.com/github.com/benben-miao/TOmicsVis.git")
```

1.2.3 CRAN: <https://cran.r-project.org/package=TOmicsVis> (<https://cran.r-project.org/package=TOmicsVis>)

Install from CRAN:

```
# Install from CRAN
install.packages("TOmicsVis")
```

1.3 Articles and Courses

Videos Courses: <https://space.bilibili.com/34105515/channel/series>
(<https://space.bilibili.com/34105515/channel/series>)

Article Introduction: 全解TOmicsVis完美应用于转录组可视化R包
(https://mp.weixin.qq.com/s/g8sRcK_ExIsOFniMWEJnVQ)

Article Courses: TOmicsVis 转录组学R代码分析及可视化视频
(<https://mp.weixin.qq.com/s/mVXJmHPAnC9J1-zMj7eG7g>)

1.4 About and Authors

OmicsSuite: Omics Suite Github: <https://github.com/omicssuite/> (<https://github.com/omicssuite/>)

Authors:

- benben-miao Github: <https://github.com/benben-miao/> (<https://github.com/benben-miao/>)
- dongwei1220 Github: <https://github.com/dongwei1220/> (<https://github.com/dongwei1220/>)

2. Library packages

```
# 1. Library TOMicsVis package
library(TOMicsVis)
#> 载入需要的程辑包: Biobase
#> 载入需要的程辑包: BiocGenerics
#>
#> 载入程辑包: 'BiocGenerics'
#> The following objects are masked from 'package:stats':
#>
#>   IQR, mad, sd, var, xtabs
#> The following objects are masked from 'package:base':
#>
#>   anyDuplicated, aperm, append, as.data.frame, basename, cbind,
#>   colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
#>   get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
#>   match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
#>   Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort,
#>   table, tapply, union, unique, unsplit, which.max, which.min
#> Welcome to Bioconductor
#>
#>   Vignettes contain introductory material; view with
#>   'browseVignettes()'. To cite Bioconductor, see
#>   'citation("Biobase")', and for packages 'citation("pkgname")'.
#> 载入需要的程辑包: e1071
#>
#> Registered S3 method overwritten by 'GGally':
#>   method from
#>   +.gg   ggplot2
#>
#> 载入程辑包: 'DynDoc'
#> The following object is masked from 'package:BiocGenerics':
#>
#>   path

# 2. Extra package
# install.packages("ggplot2")
library(ggplot2)
```

3. Usage cases

3.1 Samples Statistics

3.1.1 quantile_plot

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

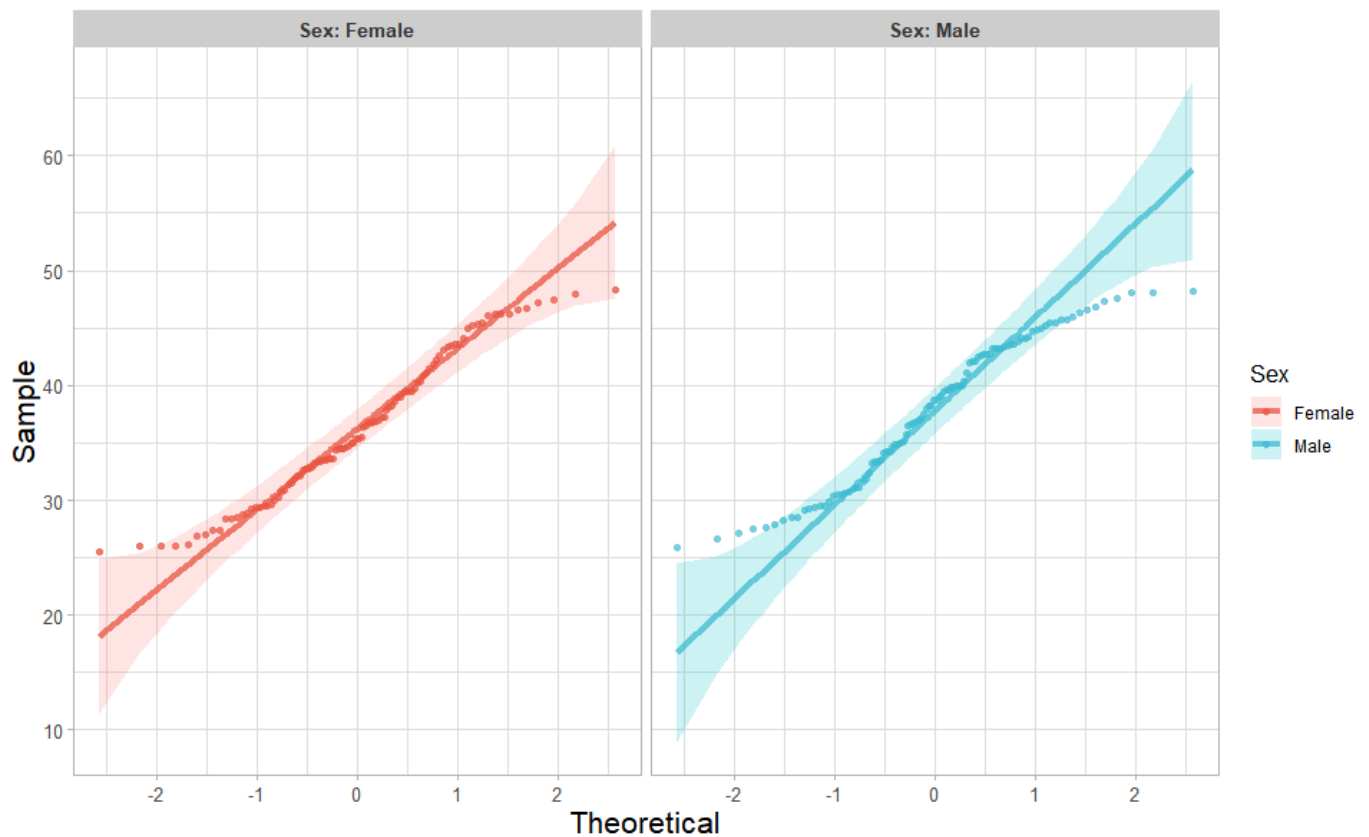
Output Plot: Quantile plot for visualizing data distribution.

```

# 1. Load example datasets
data(weight_sex)
head(weight_sex)
#> Weight Sex
#> 1 36.74 Female
#> 2 38.54 Female
#> 3 44.91 Female
#> 4 43.53 Female
#> 5 39.03 Female
#> 6 26.01 Female

# 2. Run quantile_plot plot function
quantile_plot(
  data = weight_sex,
  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"
)

```



Get help using command `?TomicsVis::quantile_plot` or reference page https://benben-miao.github.io/TomicsVis/reference/quantile_plot.html (https://benben-miao.github.io/TomicsVis/reference/quantile_plot.html).

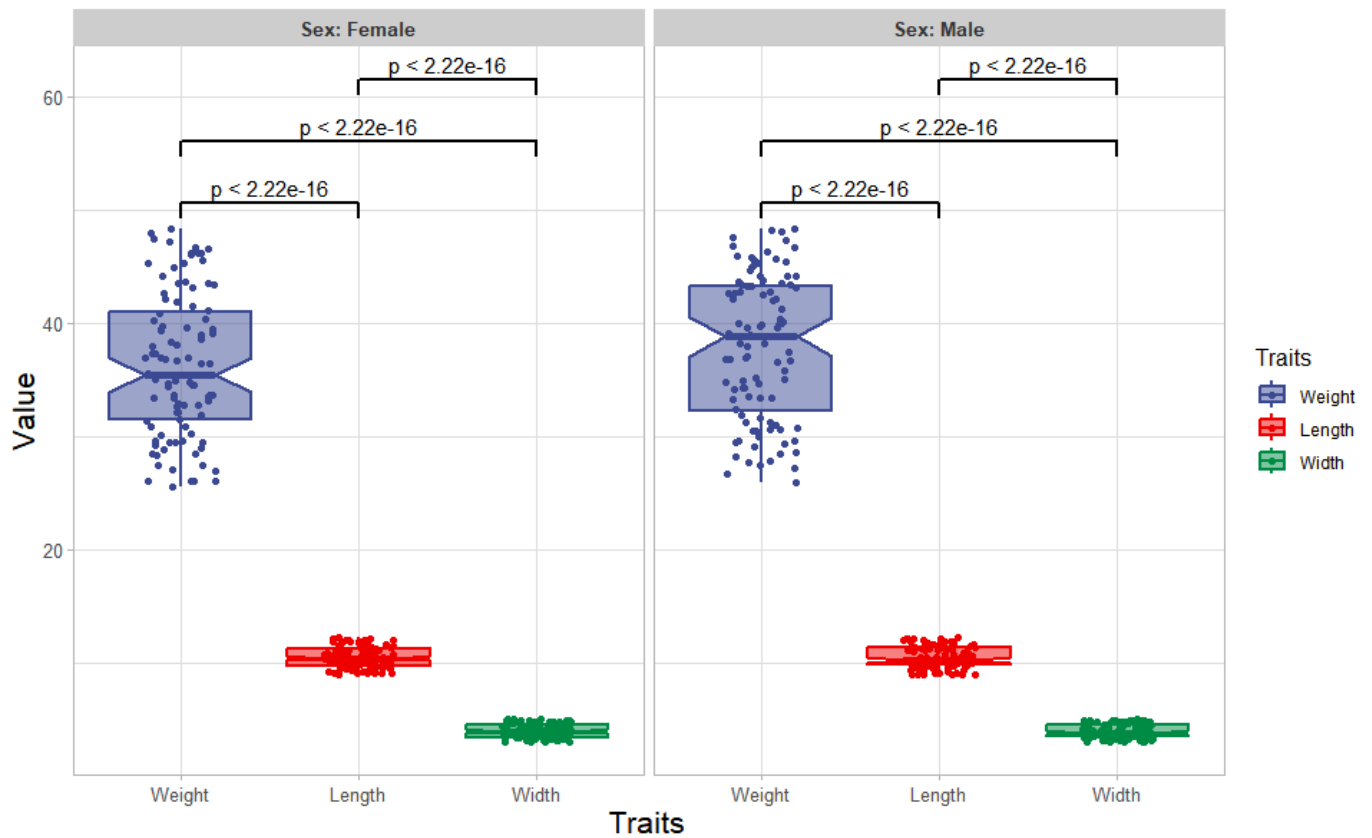
```
# Get help with command in R console.  
# ?TOMicsVis::quantile_plot
```

3.1.2 box_plot

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

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

```
# 1. Load example datasets  
data(traits_sex)  
head(traits_sex)  
#>  Value Traits  Sex  
#> 1 36.74 Weight Female  
#> 2 38.54 Weight Female  
#> 3 44.91 Weight Female  
#> 4 43.53 Weight Female  
#> 5 39.03 Weight Female  
#> 6 26.01 Weight Female  
  
# 2. Run box_plot plot function  
box_plot(  
  data = traits_sex,  
  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"  
)
```



Get help using command `?TOMicsVis::box_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/box_plot.html (https://benben-miao.github.io/TOMicsVis/reference/box_plot.html).

```
# Get help with command in R console.
# ?TOMicsVis::box_plot
```

3.1.3 violin_plot

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

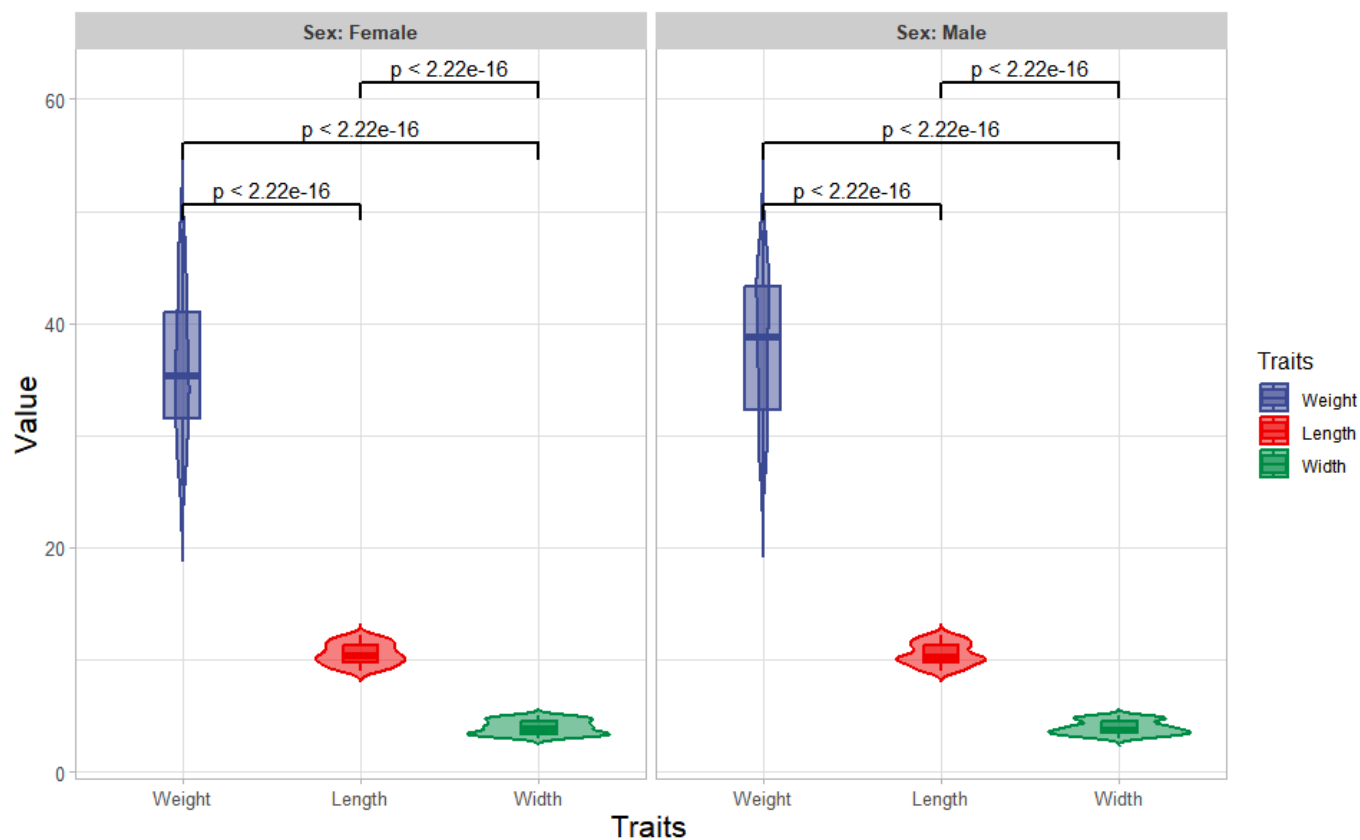
Output Plot: Plot: Violin plot support two levels and multiple groups with P value.

```
# 1. Load example datasets
```

```
data(traits_sex)
```

```
# 2. Run violin_plot plot function
```

```
violin_plot(  
  data = traits_sex,  
  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"  
)
```



Get help using command `?TOMicsVis::violin_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/violin_plot.html (https://benben-miao.github.io/TOMicsVis/reference/violin_plot.html).

```
# Get help with command in R console.
```

```
# ?TOMicsVis::violin_plot
```

3.1.4 survival_plot

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

Output Plot: Survival plot for analyzing and visualizing survival data.

1. Load example datasets

```
data(survival_data)
```

```
head(survival_data)
```

```
#> Time Status Group
```

```
#> 1 48 0 CT
```

```
#> 2 48 0 CT
```

```
#> 3 48 0 CT
```

```
#> 4 48 0 CT
```

```
#> 5 48 0 CT
```

```
#> 6 48 0 CT
```

2. Run survival_plot plot function

```
survival_plot(
```

```
  data = survival_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,
```

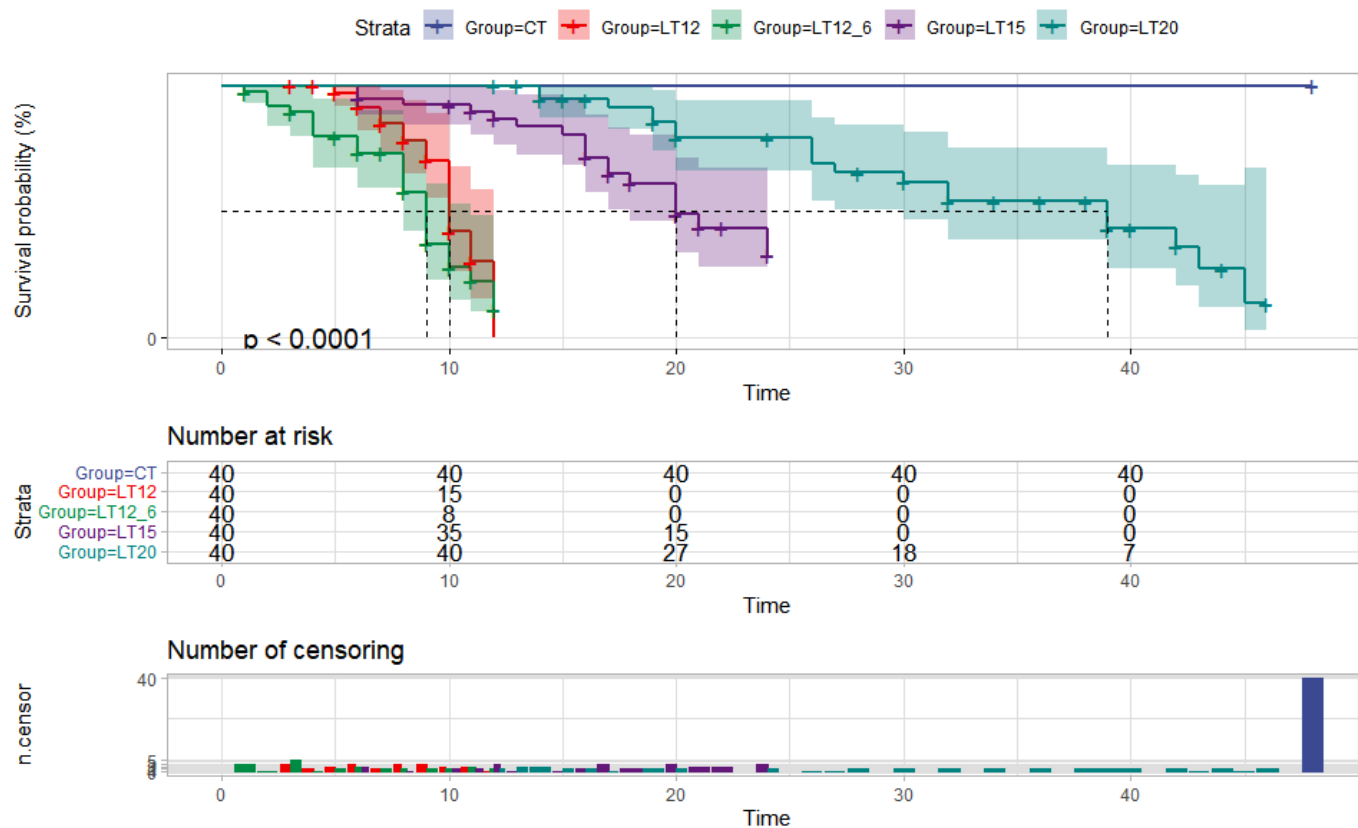
```
  y_start = 0,
```

```
  y_end = 100,
```

```
  x_break = 10,
```

```
  y_break = 10
```

```
)
```



Get help using command `?TOMicsVis::survival_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/survival_plot.html (https://benben-miao.github.io/TOMicsVis/reference/survival_plot.html).

```
# Get help with command in R console.  
# ?TOMicsVis::survival_plot
```

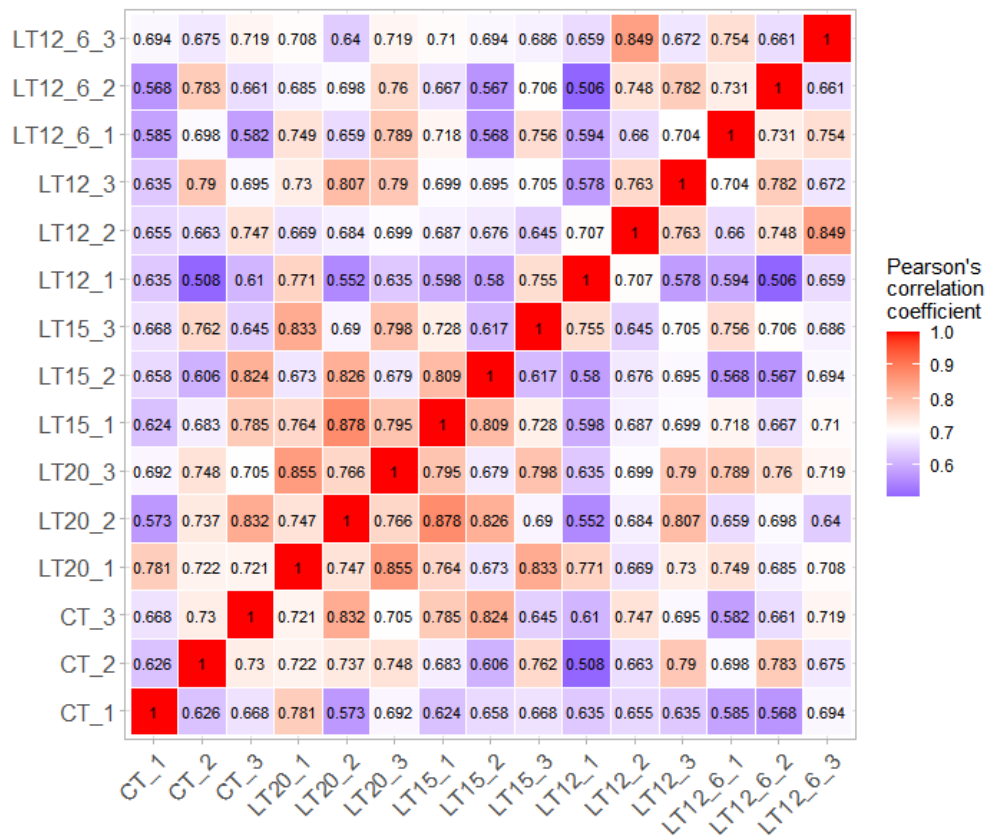
3.2 Traits Analysis

3.2.1 corr_heatmap

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

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

```
# 1. Load example dataset  
data(gene_expression)  
head(gene_expression)  
#>      Genes  CT_1  CT_2  CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2  
#> 1 transcript_0 655.78 631.08 669.89 654.21 402.56 447.09 510.08 442.22  
#> 2 transcript_1  92.72 112.26 150.30  88.35  76.35  94.55 120.24  80.89  
#> 3 transcript_10  21.74  31.11  22.58  15.09  13.67  13.24  12.48   7.53  
#> 4 transcript_100  0.00  0.00  0.00  0.00  0.00  0.00  0.00  0.00  
#> 5 transcript_1000  0.00 14.15 36.01  0.00  0.00 193.59 208.45  0.00  
#> 6 transcript_10000 89.18 158.04 86.28 82.97 117.78 102.24 129.61 112.73  
#>  LT15_3 LT12_1 LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3  
#> 1 399.82 483.30 437.89 444.06 405.43 416.63 464.75  
#> 2  73.94  96.25  82.62  85.48  65.12  61.94  73.44  
#> 3  13.35  11.16  11.36  6.96   7.82   4.01  10.02  
#> 4   0.00   0.00   0.00   0.00   0.00   0.00   0.00  
#> 5 232.40 148.58  0.00 181.61  0.02  12.18   0.00  
#> 6  85.70  80.89 124.11 115.25 113.87 107.69 119.83  
  
# 2. Run corr_heatmap plot function  
corr_heatmap(  
  data = gene_expression,  
  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"  
)  
#> Scale for fill is already present.  
#> Adding another scale for fill, which will replace the existing scale.
```

Get help using command `?TOMicsVis::corr_heatmap` or reference page https://benben-miao.github.io/TOMicsVis/reference/corr_heatmap.html (https://benben-miao.github.io/TOMicsVis/reference/corr_heatmap.html).

```
# Get help with command in R console.
# ?TOMicsVis::corr_heatmap
```

3.2.2 pca_analysis

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Output Table: PCA dimensional reduction analysis for RNA-Seq.

```
# 1. Load example datasets
data(gene_expression)

data(samples_groups)
head(samples_groups)
#> Samples Groups
#> 1 CT_1 CT
#> 2 CT_2 CT
#> 3 CT_3 CT
#> 4 LT20_1 LT20
#> 5 LT20_2 LT20
#> 6 LT20_3 LT20

# 2. Run pca_analysis plot function
res <- pca_analysis(gene_expression, samples_groups)
head(res)
#> PC1 PC2 PC3 PC4 PC5 PC6
#> CT_1 -27010.536 -18328.2803 5955.2569 46547.7319 11394.1043 -7197.285
#> CT_2 16248.651 29132.9251 -824.1857 20747.9618 -18798.8755 21096.088
#> CT_3 22421.017 -26832.3964 6789.4490 5864.1171 -15375.3418 17424.861
#> LT20_1 -18587.073 -472.9036 -21638.7836 7765.9575 114.1225 -3943.968
#> LT20_2 33275.933 -9874.9959 -14991.3942 -7443.9250 -4600.8302 -8072.298
#> LT20_3 -1596.255 11683.5426 -10892.8493 381.0795 11080.3560 -8994.187
#> PC7 PC8 PC9 PC10 PC11 PC12
#> CT_1 2150.6739 4850.320 4051.745 7666.9445 -3141.9327 -2487.939
#> CT_2 -12329.1138 -3353.734 4805.659 1503.8533 11184.0296 -4865.436
#> CT_3 12744.2255 -10037.516 -11468.842 202.4016 -11001.6260 -3847.291
#> LT20_1 8864.7482 -14171.127 -1968.082 -3562.1899 7446.2105 14831.486
#> LT20_2 -941.3943 -5072.401 5345.106 6494.1383 -3954.2153 9351.346
#> LT20_3 7263.9321 -7774.725 -1853.546 -21427.2641 -46.1503 -12507.011
#> PC13 PC14 PC15
#> CT_1 -2704.613 2396.7383 2.528517e-11
#> CT_2 -2633.057 -1375.3352 6.825657e-11
#> CT_3 5193.978 188.5601 2.255671e-11
#> LT20_1 3937.457 -7871.8062 4.864246e-11
#> LT20_2 -12904.673 6071.6618 -2.020696e-10
#> LT20_3 -5369.380 2606.1762 1.903509e-11
```

Get help using command `?TOMicsVis::pca_analysis` or reference page https://benben-miao.github.io/TOMicsVis/reference/pca_analysis.html (https://benben-miao.github.io/TOMicsVis/reference/pca_analysis.html).

```
# Get help with command in R console.
# ?TOMicsVis::pca_analysis
```

3.2.3 pca_plot

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Output Plot: Plot: PCA dimensional reduction visualization for RNA-Seq.

```
# 1. Load example datasets
```

```
data(gene_expression)
```

```
data(samples_groups)
```

```
head(samples_groups)
```

```
#> Samples Groups
```

```
#> 1 CT_1 CT
```

```
#> 2 CT_2 CT
```

```
#> 3 CT_3 CT
```

```
#> 4 LT20_1 LT20
```

```
#> 5 LT20_2 LT20
```

```
#> 6 LT20_3 LT20
```

```
# 2. Run pca_plot plot function
```

```
pca_plot(
```

```
  sample_gene = gene_expression,
```

```
  group_sample = samples_groups,
```

```
  xPC = 1,
```

```
  yPC = 2,
```

```
  point_size = 5,
```

```
  text_size = 5,
```

```
  fill_alpha = 0.10,
```

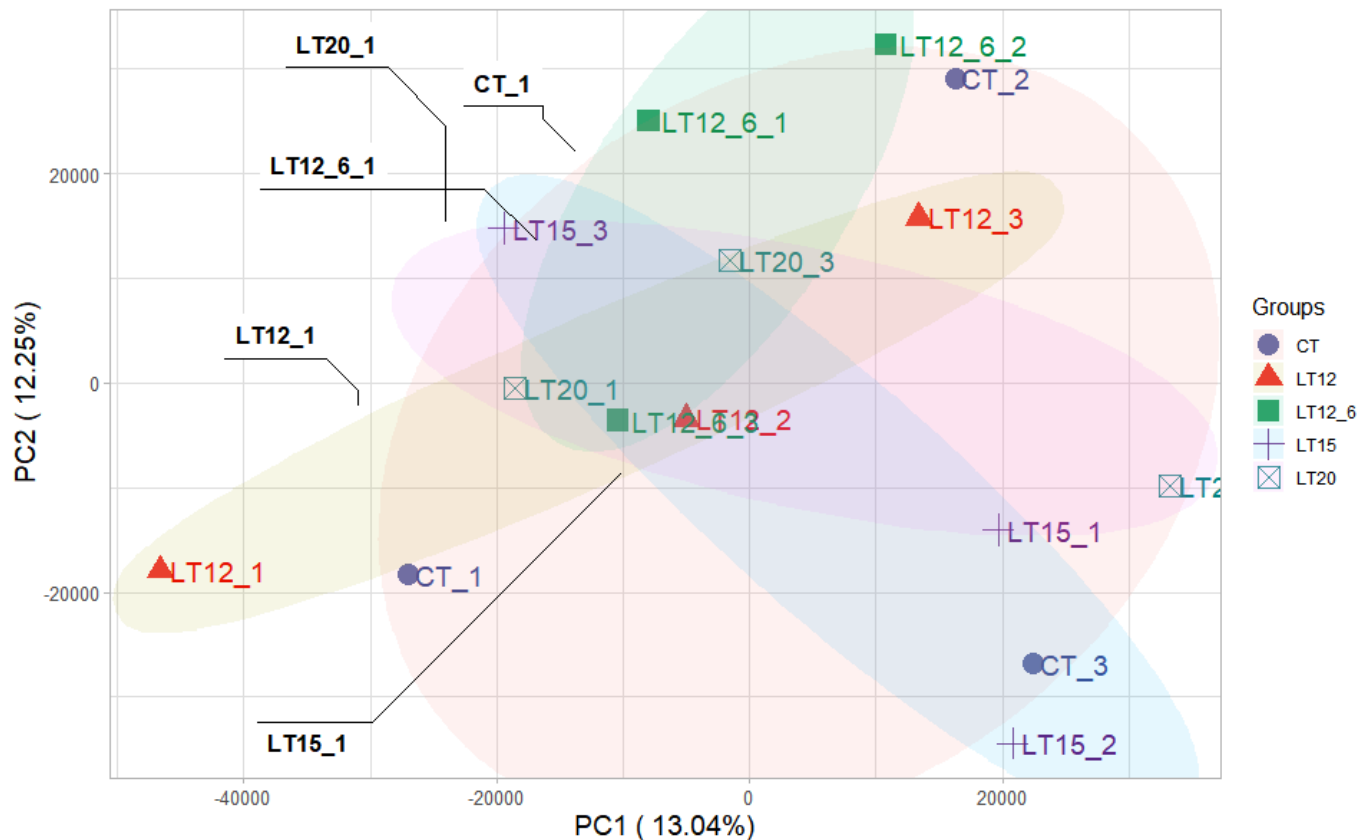
```
  border_alpha = 0.00,
```

```
  legend_pos = "right",
```

```
  legend_dir = "vertical",
```

```
  ggTheme = "theme_light"
```

```
)
```



Get help using command `?TOMicsVis::pca_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/pca_plot.html (https://benben-miao.github.io/TOMicsVis/reference/pca_plot.html).

```
# Get help with command in R console.  
# ?TOMicsVis::pca_plot
```

3.2.4 tsne_analysis

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Output Table: TSNE analysis for analyzing and visualizing TSNE algorithm.

```
# 1. Load example datasets  
data(gene_expression)  
data(samples_groups)  
  
# 2. Run tsne_analysis plot function  
res <- tsne_analysis(gene_expression, samples_groups)  
head(res)  
#>   TSNE1   TSNE2  
#> 1 -67.41252 -16.61397  
#> 2  43.08349 -34.02654  
#> 3 123.32273  54.14358  
#> 4 -42.52065 -31.30027  
#> 5  94.98790  48.97986  
#> 6 -23.90637 -22.26434
```

Get help using command `?TOMicsVis::tsne_analysis` or reference page https://benben-miao.github.io/TOMicsVis/reference/tsne_analysis.html (https://benben-miao.github.io/TOMicsVis/reference/tsne_analysis.html).

```
# Get help with command in R console.  
# ?TOMicsVis::tsne_analysis
```

3.2.5 tsne_plot

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

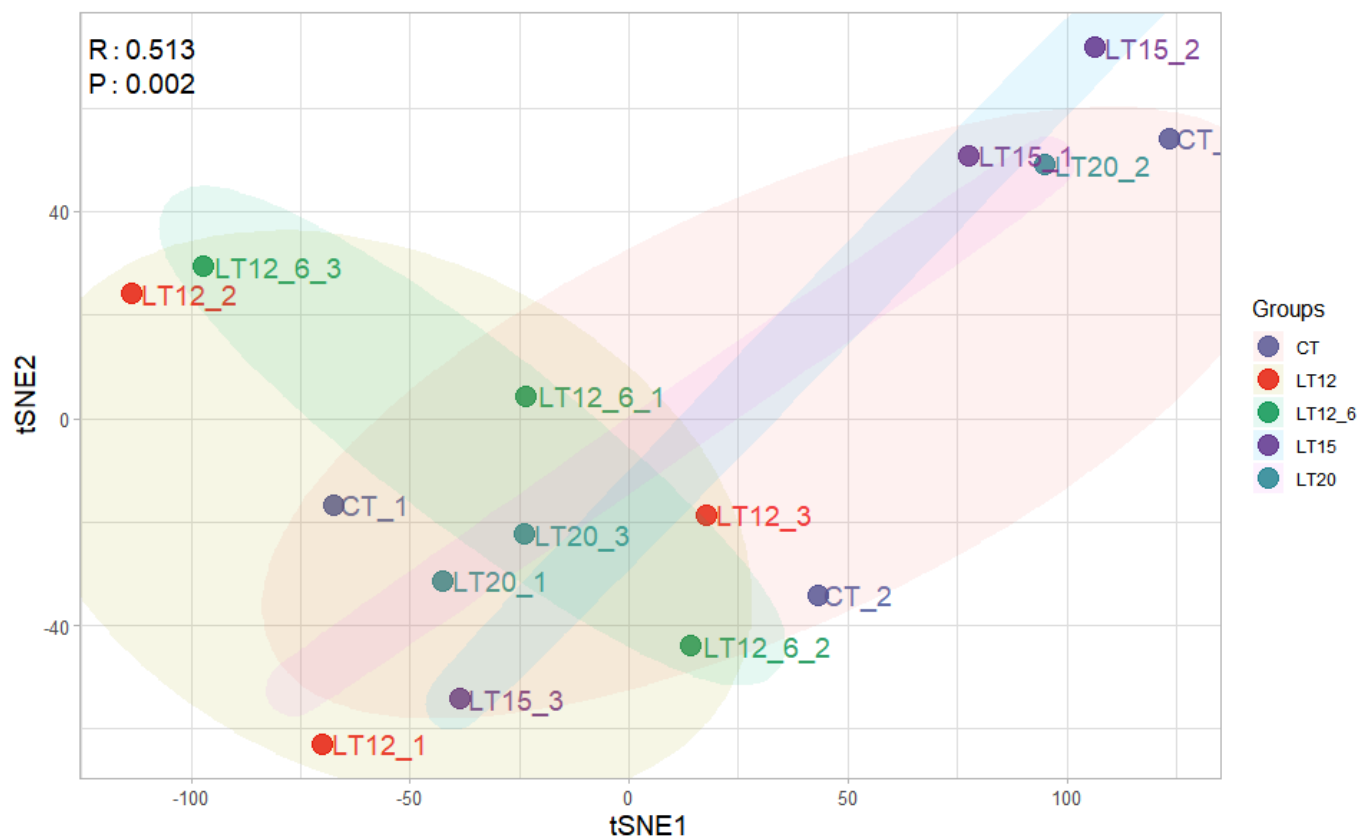
Output Plot: TSNE plot for analyzing and visualizing TSNE algorithm.

```

# 1. Load example datasets
data(gene_expression)
data(samples_groups)

# 2. Run tsne_plot plot function
tsne_plot(
  sample_gene = gene_expression,
  group_sample = samples_groups,
  seed = 1,
  multi_shape = FALSE,
  point_size = 5,
  point_alpha = 0.8,
  text_size = 5,
  text_alpha = 0.80,
  fill_alpha = 0.10,
  border_alpha = 0.00,
  sci_fill_color = "Sci_AAAS",
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)

```



Get help using command `?TOMicsVis::tsne_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/tsne_plot.html (https://benben-miao.github.io/TOMicsVis/reference/tsne_plot.html).

```

# Get help with command in R console.
# ?TOMicsVis::tsne_plot

```

3.2.6 umap_analysis

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Output Table: UMAP analysis for analyzing RNA-Seq data.

```
# 1. Load example datasets
data(gene_expression)
data(samples_groups)

# 2. Run tsne_plot function
res <- umap_analysis(gene_expression, samples_groups)
head(res)
#>      UMAP1    UMAP2
#> CT_1 -0.6752746 0.49425898
#> CT_2  1.0232441 0.03062202
#> CT_3 -0.4722297 -1.32183550
#> LT20_1 -0.2414214 0.13870703
#> LT20_2  0.1991701 -1.23434000
#> LT20_3  0.6431577 1.11879669
```

Get help using command `?TOMicsVis::umap_analysis` or reference page https://benben-miao.github.io/TOMicsVis/reference/umap_analysis.html (https://benben-miao.github.io/TOMicsVis/reference/umap_analysis.html).

```
# Get help with command in R console.
# ?TOMicsVis::umap_analysis
```

3.2.7 umap_plot

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

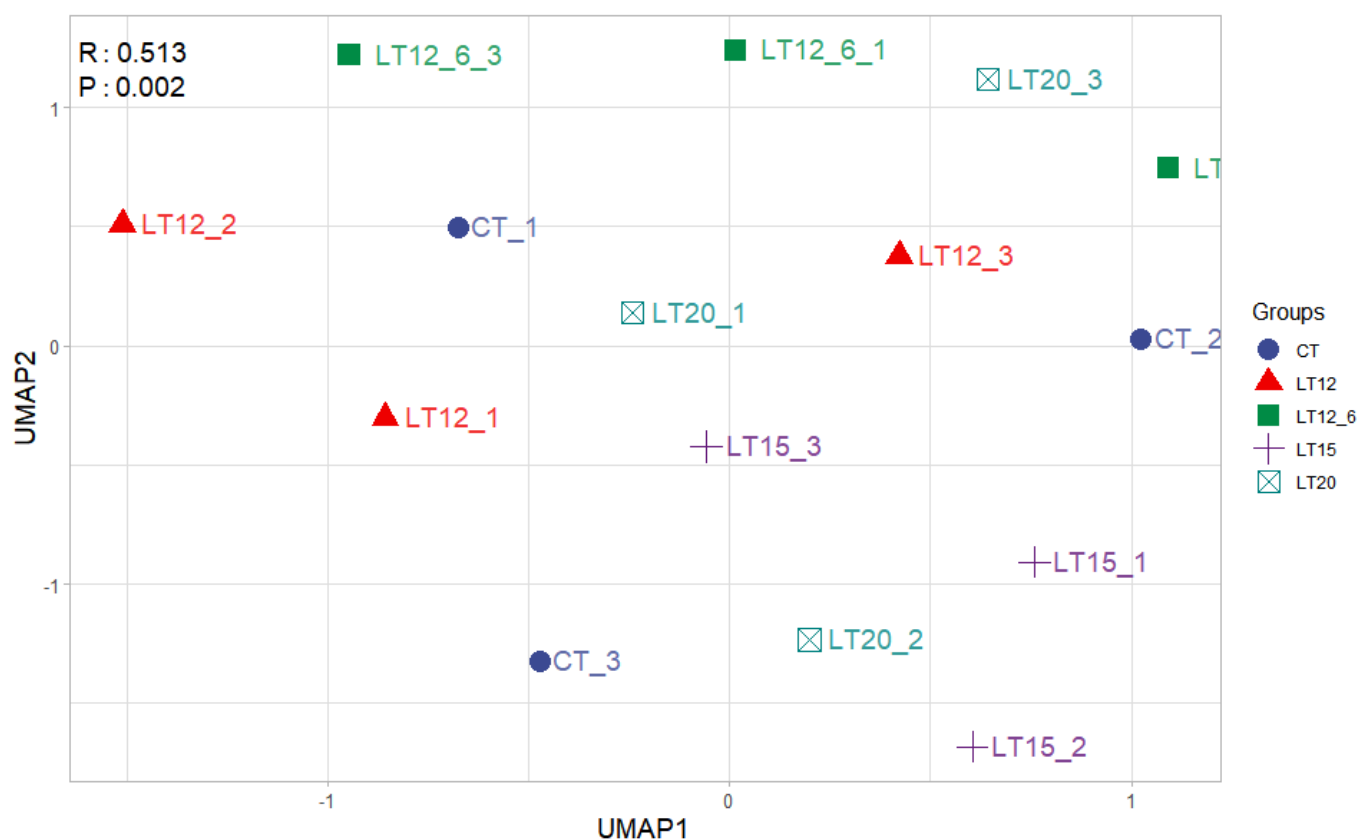
Output Plot: UMAP plot for analyzing and visualizing UMAP algorithm.

```

# 1. Load example datasets
data(gene_expression)
data(samples_groups)

# 2. Run tsne_plot plot function
umap_plot(
  sample_gene = gene_expression,
  group_sample = samples_groups,
  seed = 1,
  multi_shape = TRUE,
  point_size = 5,
  point_alpha = 1,
  text_size = 5,
  text_alpha = 0.80,
  fill_alpha = 0.00,
  border_alpha = 0.00,
  sci_fill_color = "Sci_AAAS",
  legend_pos = "right",
  legend_dir = "vertical",
  ggTheme = "theme_light"
)

```



Get help using command `?TOMicsVis::umap_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/umap_plot.html (https://benben-miao.github.io/TOMicsVis/reference/umap_plot.html).

```

# Get help with command in R console.
# ?TOMicsVis::umap_plot

```

3.2.8 dendro_plot

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

Output Plot: Plot: dendrogram for multiple samples clustering.

```
# 1. Load example datasets
```

```
data(gene_expression)
```

```
# 2. Run plot function
```

```
dendro_plot(
```

```
  data = gene_expression,
```

```
  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",
```

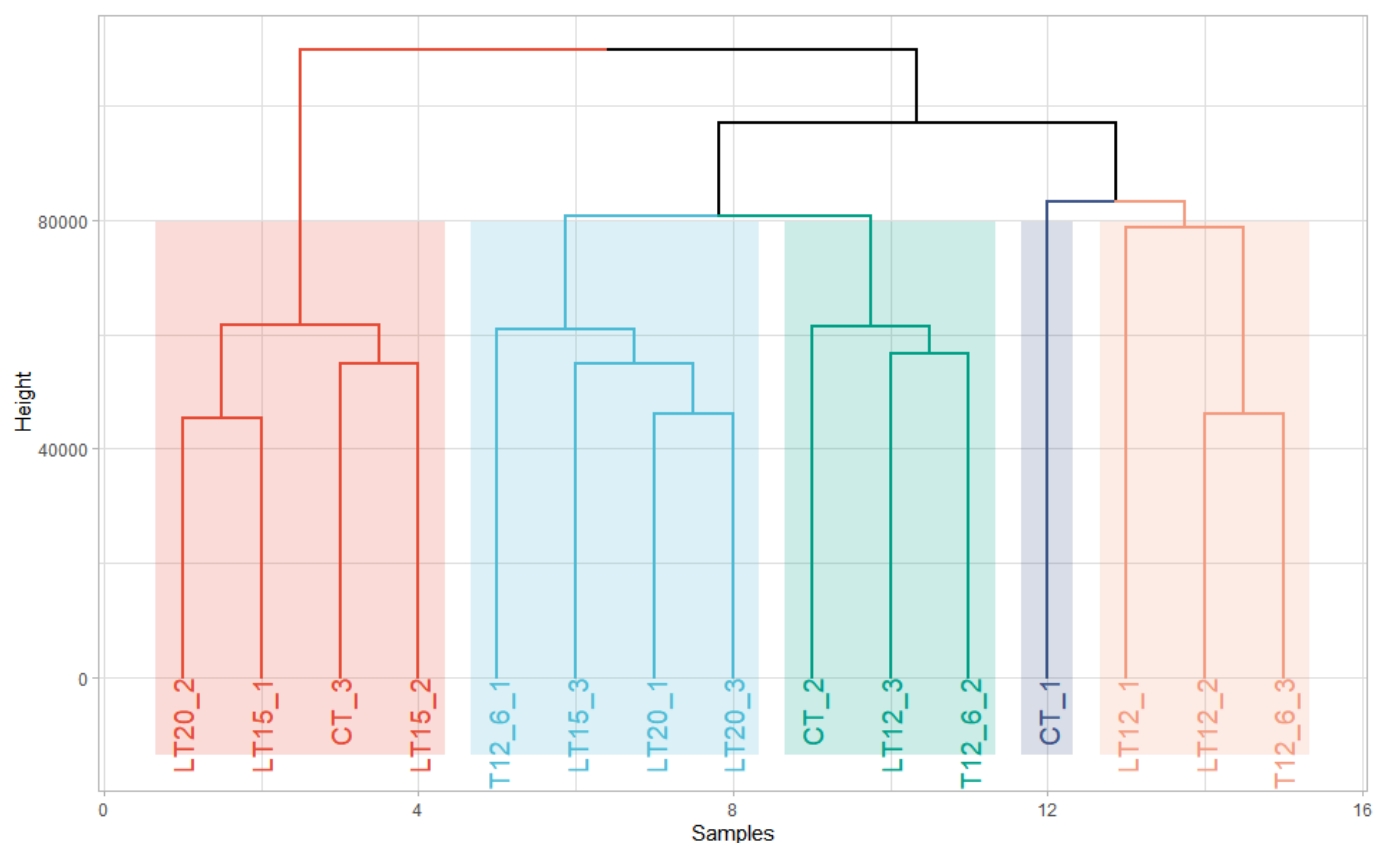
```
  ggTheme = "theme_light"
```

```
)
```

```
#> Registered S3 method overwritten by 'dendextend':
```

```
#> method from
```

```
#> rev.hclust vegan
```



Get help using command `?TomicsVis::dendro_plot` or reference page https://benben-miao.github.io/TomicsVis/reference/dendro_plot.html (https://benben-miao.github.io/TomicsVis/reference/dendro_plot.html).

```
# Get help with command in R console.  
# ?TomicsVis::dendro_plot
```

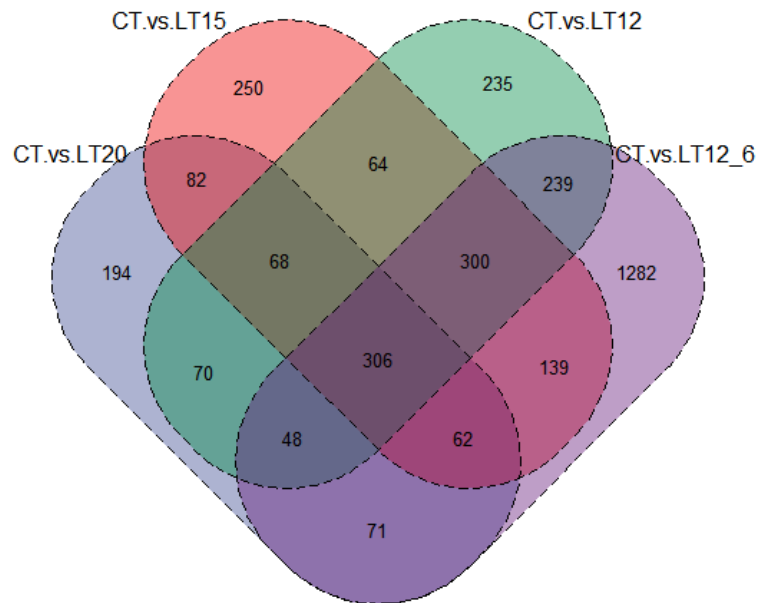
3.3 Differential Expression Analysis

3.3.1 venn_plot

Input Data2: Dataframe: Paired comparisons differentially expressed genes (deg) among groups (1st-col~: degs of paired comparisons).

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

```
# 1. Load example datasets  
data(degs_lists)  
head(degs_lists)  
#>      CT.vs.LT20  CT.vs.LT15  CT.vs.LT12  CT.vs.LT12_6  
#> 1 transcript_9024 transcript_4738 transcript_9956 transcript_10354  
#> 2 transcript_604 transcript_6050 transcript_7601 transcript_2959  
#> 3 transcript_3912 transcript_1039 transcript_5960 transcript_5919  
#> 4 transcript_8676 transcript_1344 transcript_3240 transcript_2395  
#> 5 transcript_8832 transcript_3069 transcript_10224 transcript_9881  
#> 6 transcript_74 transcript_9809 transcript_3151 transcript_8836  
  
# 2. Run venn_plot plot function  
venn_plot(  
  data = degs_lists,  
  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  
)
```



Get help using command `?TOMicsVis::venn_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/venn_plot.html (https://benben-miao.github.io/TOMicsVis/reference/venn_plot.html).

```
# Get help with command in R console.
# ?TOMicsVis::venn_plot
```

3.3.2 upsetr_plot

Input Data2: Dataframe: Paired comparisons differentially expressed genes (deg) among groups (1st-col~: degs of paired comparisons).

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

1. Load example datasets

```
data(degs_lists)
```

```
head(degs_lists)
```

```
#> CT.vs.LT20 CT.vs.LT15 CT.vs.LT12 CT.vs.LT12_6
```

```
#> 1 transcript_9024 transcript_4738 transcript_9956 transcript_10354
```

```
#> 2 transcript_604 transcript_6050 transcript_7601 transcript_2959
```

```
#> 3 transcript_3912 transcript_1039 transcript_5960 transcript_5919
```

```
#> 4 transcript_8676 transcript_1344 transcript_3240 transcript_2395
```

```
#> 5 transcript_8832 transcript_3069 transcript_10224 transcript_9881
```

```
#> 6 transcript_74 transcript_9809 transcript_3151 transcript_8836
```

2. Run upseotr_plot plot function

```
upseotr_plot(
```

```
  data = degs_lists,
```

```
  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",
```

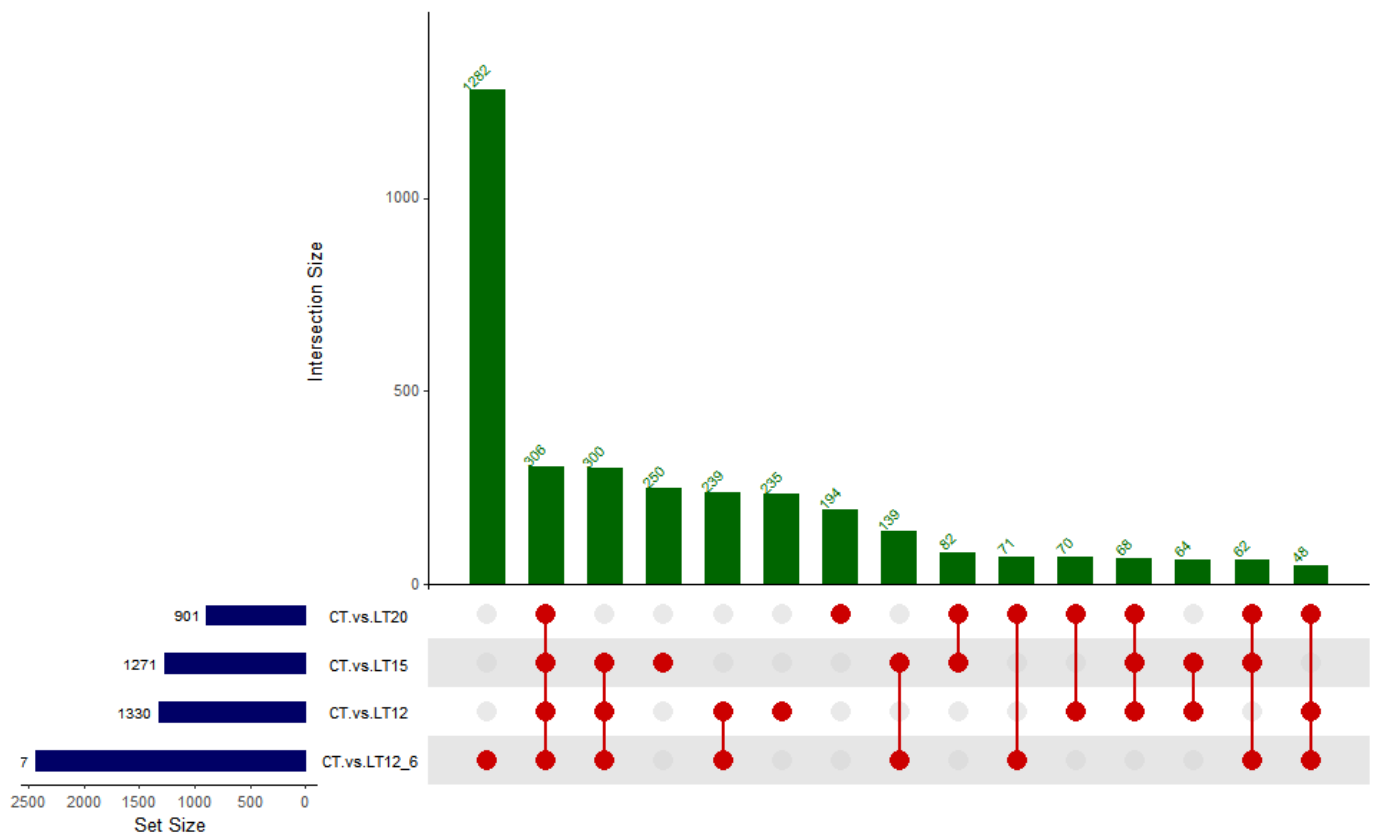
```
  shade_alpha = 0.5,
```

```
  setsbar_color = "#000066",
```

```
  setsnum_size = 6,
```

```
  text_scale = 1.2
```

```
)
```



Get help using command `?TOMicsVis::upsetr_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/upsetr_plot.html (https://benben-miao.github.io/TOMicsVis/reference/upsetr_plot.html).

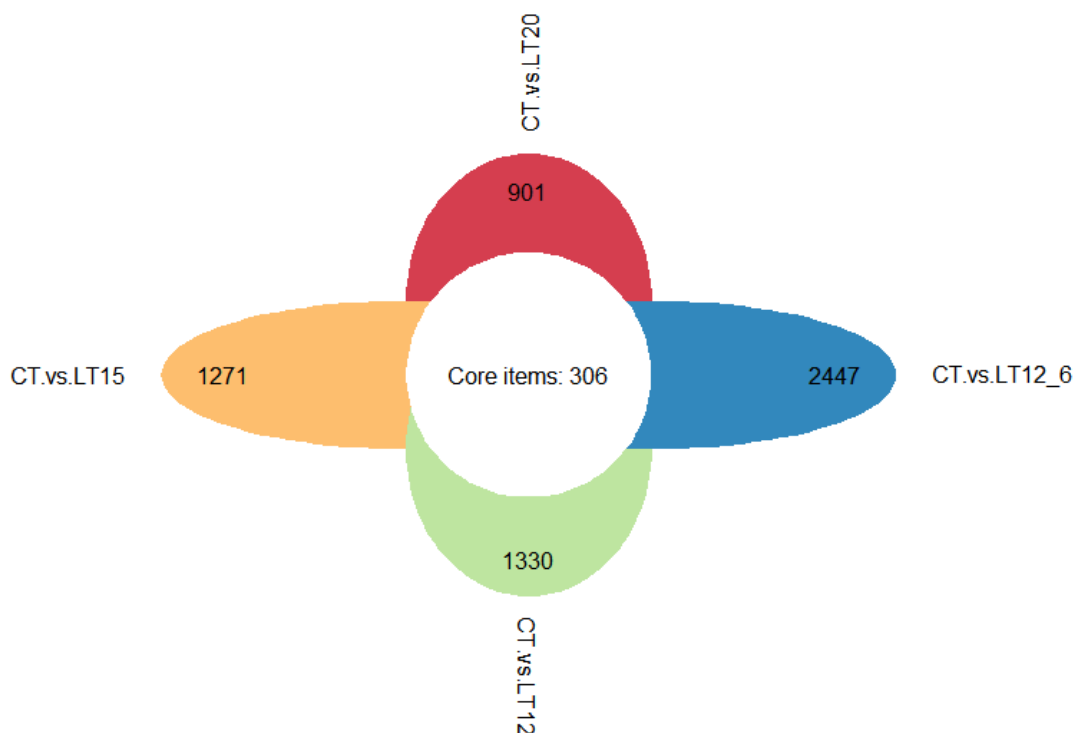
```
# Get help with command in R console.  
# ?TOMicsVis::upsetr_plot
```

3.3.3 flower_plot

Input Data2: Dataframe: Paired comparisons differentially expressed genes (degs) among groups (1st-col~: degs of paired comparisons).

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

```
# 1. Load example datasets  
data(degs_lists)  
  
# 2. Run plot function  
flower_plot(  
  flower_dat = degs_lists,  
  angle = 90,  
  a = 1,  
  b = 2,  
  r = 1,  
  ellipse_col_pal = "Spectral",  
  circle_col = "white",  
  label_text_cex = 1  
)
```



Get help using command `?TOMicsVis::flower_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/flower_plot.html (https://benben-miao.github.io/TOMicsVis/reference/flower_plot.html).

```
# Get help with command in R console.  
# ?TOMicsVis::flower_plot
```

3.3.4 volcano_plot

Input Data2: Dataframe: All DEGs of paired comparison CT-vs-LT12 stats dataframe (1st-col: Genes, 2nd-col: log2FoldChange, 3rd-col: Pvalue, 4th-col: FDR).

Output Plot: Volcano plot for visualizing differentially expressed genes.

```
# 1. Load example datasets  
data(degs_stats)  
head(degs_stats)  
#>   Gene log2FoldChange   Pvalue   FDR  
#> 1  AII3  -1.13855748 0.000111040 0.000862478  
#> 2  A1M   0.59076131 0.070988041 0.192551708  
#> 3  A2M   0.09297827 0.819706797 0.913893947  
#> 4 A2ML1  -0.26940689 0.745374782 0.874295125  
#> 5  ABAT   1.24811621 0.000001440 0.000016800  
#> 6 ABCC3  -0.72947545 0.005171574 0.024228298  
  
# 2. Run volcano_plot plot function  
volcano_plot(  
  data = degs_stats,  
  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"  
)
```



```
# 1. Load example datasets
```

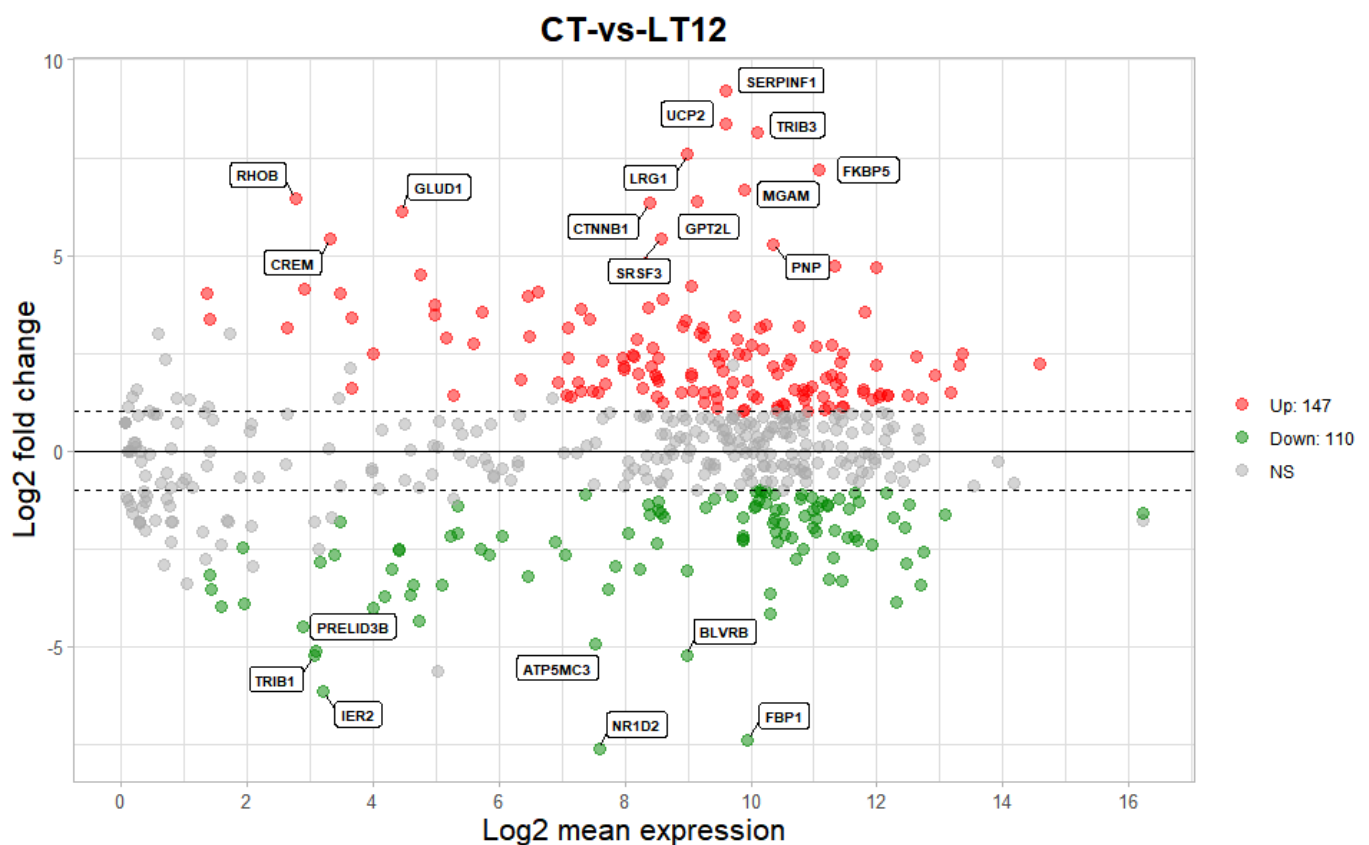
```
data(degs_stats2)
```

```
head(degs_stats2)
```

```
#>   name   baseMean log2FoldChange   padj
#> 1  A1I3  0.1184475   0.0000000    NA
#> 2  A1M 1654.4618140   0.6789538 5.280802e-02
#> 3  A2M  681.0463277   1.5263838 3.920000e-07
#> 4 A2ML1 389.7226640   3.8933573 1.180000e-14
#> 5  ABAT 364.7810090  -2.3554014 1.559230e-04
#> 6 ABCC3  1.1346239   1.2932740 4.491812e-01
```

```
# 2. Run volcano_plot plot function
```

```
ma_plot(
  data = degs_stats2,
  foldchange = 2,
  fdr_value = 0.05,
  point_size = 3.0,
  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"
)
```



Get help using command `?TomicsVis::ma_plot` or reference page https://benben-miao.github.io/TomicsVis/reference/ma_plot.html (https://benben-miao.github.io/TomicsVis/reference/ma_plot.html).

```
# Get help with command in R console.  
# ?TomicsVis::ma_plot
```

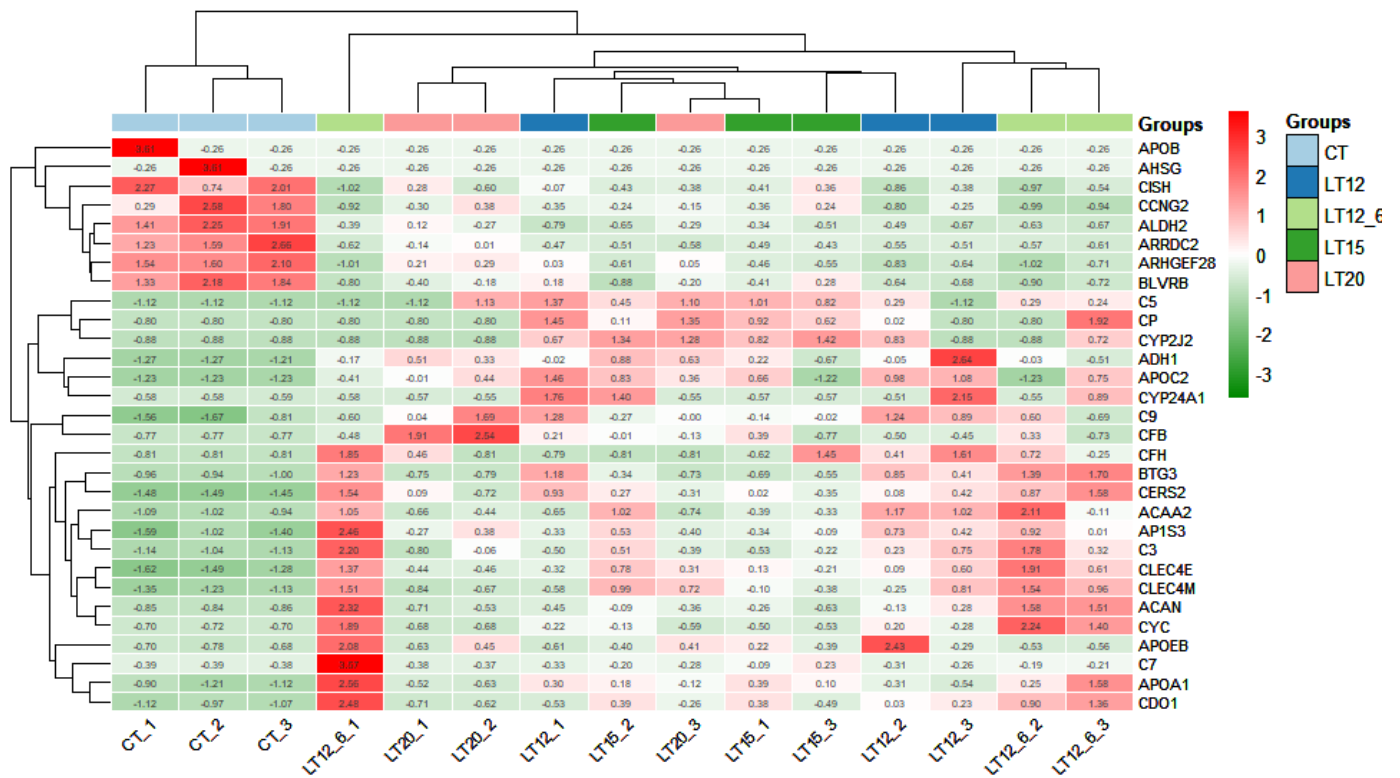
3.3.6 heatmap_group

Input Data1: Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Output Plot: Heatmap group for visualizing grouped gene expression data.

```
# 1. Load example datasets  
data(gene_expression2)  
data(samples_groups)  
  
# 2. Run heatmap_group plot function  
heatmap_group(  
  sample_gene = gene_expression2[1:30,],  
  group_sample = samples_groups,  
  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  
)
```

Get help using command `?TOmicsVis::heatmap_group` or reference page https://benben-miao.github.io/TOmicsVis/reference/heatmap_group.html (https://benben-miao.github.io/TOmicsVis/reference/heatmap_group.html).

```
# Get help with command in R console.
# ?TOmicsVis::heatmap_group
```

3.3.7 circos_heatmap

Input Data2: Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).

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

```
# 1. Load example datasets
```

```
data(gene_expression2)
```

```
head(gene_expression2)
```

```
#> Genes CT_1 CT_2 CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2 LT15_3 LT12_1
```

```
#> 1 ACAA2 24.50 39.83 55.38 114.11 159.32 96.88 169.56 464.84 182.66 116.08
```

```
#> 2 ACAN 14.97 18.71 10.30 71.23 142.67 213.54 253.15 320.80 104.15 174.02
```

```
#> 3 ADH1 1.54 1.56 2.04 14.95 13.60 15.87 12.80 17.74 6.06 10.97
```

```
#> 4 AHSB 0.00 1911.99 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
```

```
#> 5 ALDH2 2.07 2.86 2.54 0.85 0.49 0.47 0.42 0.13 0.26 0.00
```

```
#> 6 APIS3 6.62 14.59 9.30 24.90 33.94 23.19 24.00 36.08 27.40 24.06
```

```
#> LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3
```

```
#> 1 497.29 464.48 471.43 693.62 229.77
```

```
#> 2 305.81 469.48 1291.90 991.90 966.77
```

```
#> 3 10.71 30.95 9.84 10.91 7.28
```

```
#> 4 0.00 0.00 0.00 0.00 0.00
```

```
#> 5 0.28 0.11 0.37 0.15 0.11
```

```
#> 6 38.74 34.54 62.72 41.36 28.75
```

```
# 2. Run circos_heatmap plot function
```

```
circos_heatmap(
```

```
  data = gene_expression2[1:50,],
```

```
  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
```

```
)
```

```
#> Note: 15 points are out of plotting region in sector 'group', track
```

```
#> '3'.
```

```
#> Note: 15 points are out of plotting region in sector 'group', track
```

```
#> '3'.
```



```
# 1. Load chord_data example datasets
```

```
data(gene_expression2)
```

```
head(gene_expression2)
```

```
#> Genes CT_1 CT_2 CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2 LT15_3 LT12_1
```

```
#> 1 ACAA2 24.50 39.83 55.38 114.11 159.32 96.88 169.56 464.84 182.66 116.08
```

```
#> 2 ACAN 14.97 18.71 10.30 71.23 142.67 213.54 253.15 320.80 104.15 174.02
```

```
#> 3 ADH1 1.54 1.56 2.04 14.95 13.60 15.87 12.80 17.74 6.06 10.97
```

```
#> 4 AHSB 0.00 1911.99 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
```

```
#> 5 ALDH2 2.07 2.86 2.54 0.85 0.49 0.47 0.42 0.13 0.26 0.00
```

```
#> 6 APIS3 6.62 14.59 9.30 24.90 33.94 23.19 24.00 36.08 27.40 24.06
```

```
#> LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3
```

```
#> 1 497.29 464.48 471.43 693.62 229.77
```

```
#> 2 305.81 469.48 1291.90 991.90 966.77
```

```
#> 3 10.71 30.95 9.84 10.91 7.28
```

```
#> 4 0.00 0.00 0.00 0.00 0.00
```

```
#> 5 0.28 0.11 0.37 0.15 0.11
```

```
#> 6 38.74 34.54 62.72 41.36 28.75
```

```
# 2. Run chord_plot plot function
```

```
chord_plot(
```

```
  data = gene_expression2[1:30,],
```

```
  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
```

```
)
```

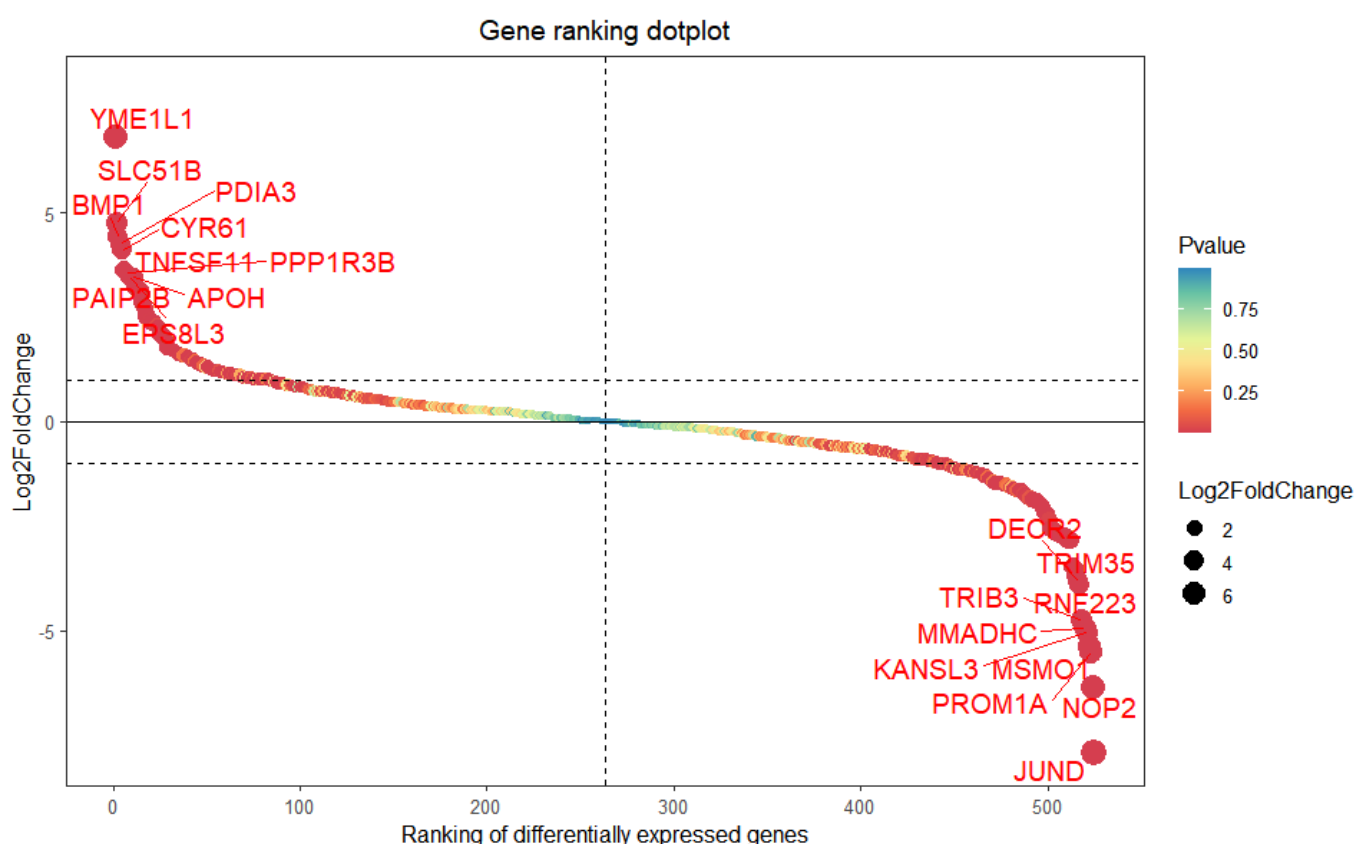


```
# 1. Load example datasets
```

```
data(degs_stats)
```

```
# 2. Run plot function
```

```
gene_rank_plot(
  data = degs_stats,
  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"
)
```



Get help using command `?TOMicsVis::gene_rank_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/gene_rank_plot.html (https://benben-miao.github.io/TOMicsVis/reference/gene_rank_plot.html).

```
# Get help with command in R console.
```

```
# ?TOMicsVis::gene_rank_plot
```

3.4.2 gene_cluster_trend

Input Data2: 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).

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

```
# 1. Load example datasets
```

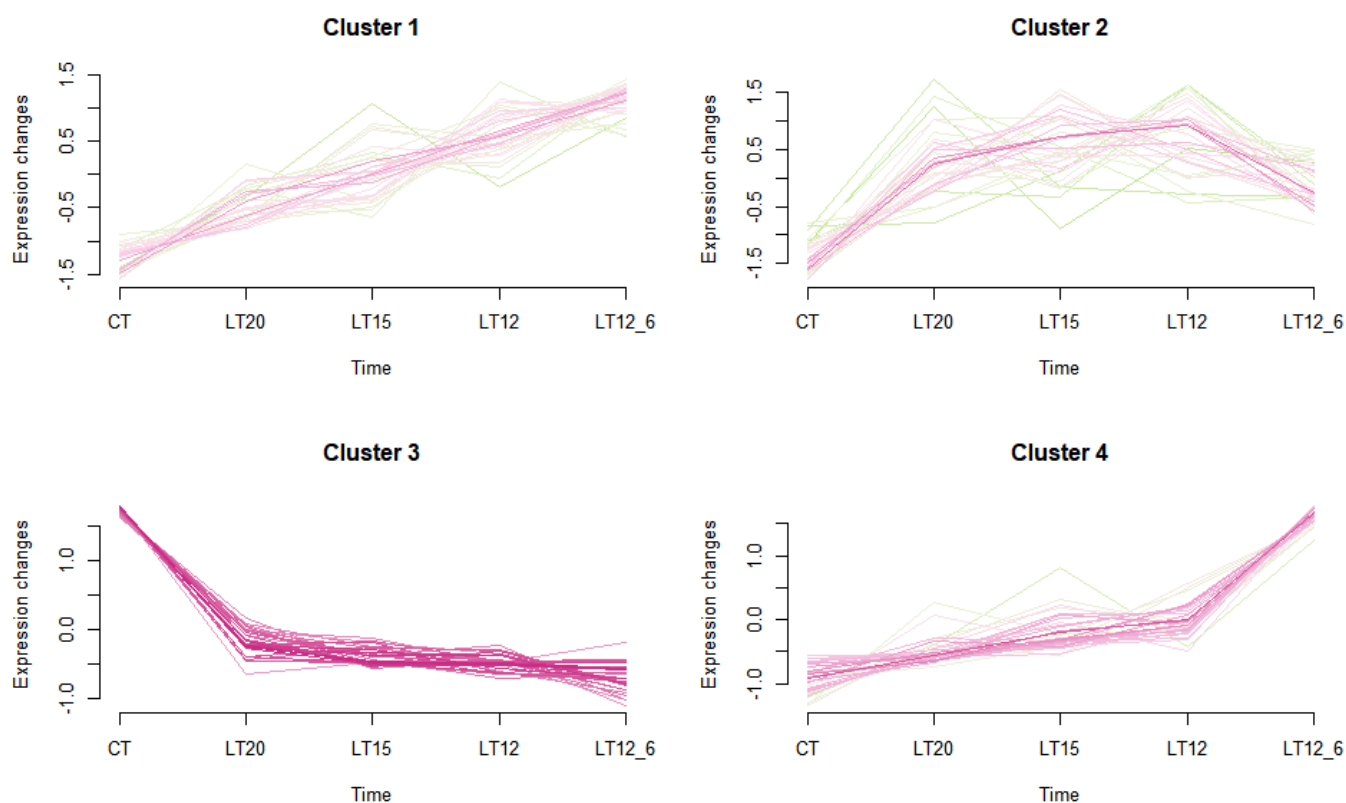
```
data(gene_expression3)
```

```
# 2. Run plot function
```

```
gene_cluster_trend(  
  data = gene_expression3[, -7],  
  thres = 0.25,  
  min_std = 0.2,  
  palette = "PiYG",  
  cluster_num = 4  
)
```

```
#> 0 genes excluded.
```

```
#> 0 genes excluded.
```



```
#> NULL
```

Get help using command `?TOMicsVis::gene_cluster_trend` or reference page https://benben-miao.github.io/TOMicsVis/reference/gene_cluster_trend.html (https://benben-miao.github.io/TOMicsVis/reference/gene_cluster_trend.html).

```
# Get help with command in R console.
```

```
# ?TOMicsVis::gene_cluster_trend
```

3.4.3 trend_plot

Input Data2: 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).

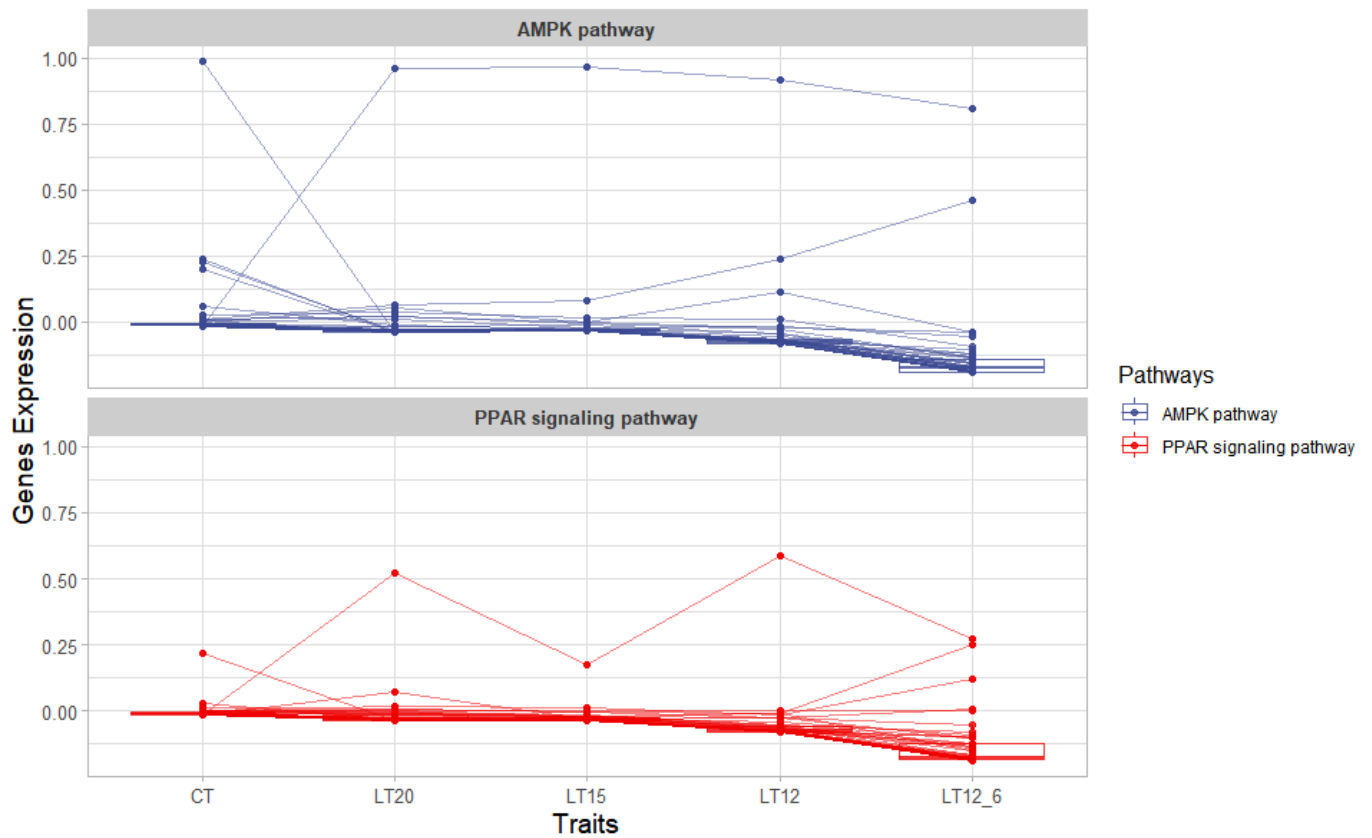
Output Plot: Trend plot for visualizing gene expression trend profile in multiple traits.

```

# 1. Load example datasets
data(gene_expression3)
head(gene_expression3)
#>   Genes      CT    LT20   LT15   LT12   LT12_6
#> 1 ACAA2 39.903333 123.4366667 272.3533 359.28333 464.940000
#> 2 ACAN 14.660000 142.4800000 226.0333 316.43667 1083.523333
#> 3 ADH1  1.713333 14.8066667 12.2000 17.54333  9.343333
#> 4 AHSB 637.330000 0.0000000 0.0000 0.00000 0.000000
#> 5 ALDH2 2.490000 0.6033333 0.2700 0.13000 0.210000
#> 6 AP1S3 10.170000 27.3433333 29.1600 32.44667 44.276667
#>      Pathways
#> 1 PPAR signaling pathway
#> 2 PPAR signaling pathway
#> 3 PPAR signaling pathway
#> 4 PPAR signaling pathway
#> 5 PPAR signaling pathway
#> 6 PPAR signaling pathway

# 2. Run trend_plot plot function
trend_plot(
  data = gene_expression3[1:100,],
  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"
)

```

Get help using command `?TOMicsVis::trend_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/trend_plot.html (https://benben-miao.github.io/TOMicsVis/reference/trend_plot.html).

```
# Get help with command in R console.
# ?TOMicsVis::trend_plot
```

3.4.4 wgcna_pipeline

Input Data1: Dataframe: All genes in all samples expression dataframe of RNA-Seq (1st-col: Genes, 2nd-col~: Samples).

Input Data2: Dataframe: Samples and groups for gene expression (1st-col: Samples, 2nd-col: Groups).

Output Plot: WGCNA analysis pipeline for RNA-Seq.

```

# 1. Load wgcna_pipeline example datasets
data(gene_expression)
head(gene_expression)
#>      Genes  CT_1  CT_2  CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2
#> 1 transcript_0 655.78 631.08 669.89 654.21 402.56 447.09 510.08 442.22
#> 2 transcript_1  92.72 112.26 150.30  88.35  76.35  94.55 120.24  80.89
#> 3 transcript_10 21.74  31.11  22.58 15.09 13.67 13.24 12.48  7.53
#> 4 transcript_100  0.00  0.00  0.00  0.00  0.00  0.00  0.00  0.00
#> 5 transcript_1000  0.00 14.15 36.01  0.00  0.00 193.59 208.45  0.00
#> 6 transcript_10000 89.18 158.04 86.28 82.97 117.78 102.24 129.61 112.73
#>      LT15_3 LT12_1 LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3
#> 1 399.82 483.30 437.89 444.06 405.43 416.63 464.75
#> 2  73.94  96.25  82.62  85.48  65.12  61.94  73.44
#> 3  13.35  11.16  11.36  6.96  7.82  4.01 10.02
#> 4   0.00   0.00   0.00   0.00   0.00   0.00   0.00
#> 5 232.40 148.58  0.00 181.61  0.02 12.18  0.00
#> 6  85.70  80.89 124.11 115.25 113.87 107.69 119.83

data(samples_groups)
head(samples_groups)
#> Samples Groups
#> 1  CT_1  CT
#> 2  CT_2  CT
#> 3  CT_3  CT
#> 4 LT20_1 LT20
#> 5 LT20_2 LT20
#> 6 LT20_3 LT20

# 2. Run wgcna_pipeline plot function
wgcna_pipeline(gene_expression[1:3000,], samples_groups)

```

Get help using command `?TOmicsVis::wgcna_pipeline` or reference page https://benben-miao.github.io/TOmicsVis/reference/wgcna_pipeline.html (https://benben-miao.github.io/TOmicsVis/reference/wgcna_pipeline.html).

```

# Get help with command in R console.
# ?TOmicsVis::wgcna_pipeline

```

3.4.5 network_plot

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

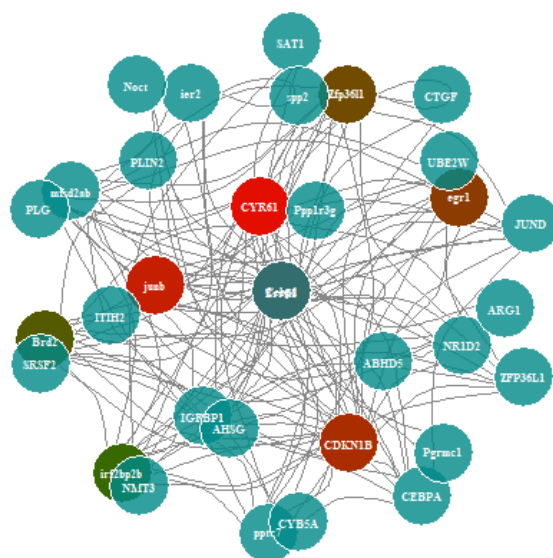
Output Plot: Network plot for analyzing and visualizing relationship of genes.

```

# 1. Load example datasets
data(network_data)
head(network_data)
#> Source Target
#> 1 Cebpd Cebpd
#> 2 CYR61 Cebpd
#> 3 Cebpd CDKN1B
#> 4 CYR61 CDKN1B
#> 5 junb Cebpd
#> 6 IGFBP1 Cebpd

# 2. Run network_plot plot function
network_plot(
  data = network_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,
  label_color = "#FFFFFF",
  label_size = 0.5,
  edge_color = "#888888",
  edge_width = 1.5,
  edge_curved = TRUE,
  net_layout = "layout_on_sphere"
)

```



Get help using command `?TOMicsVis::network_plot` or reference page https://benben-miao.github.io/TOMicsVis/reference/network_plot.html (https://benben-miao.github.io/TOMicsVis/reference/network_plot.html).

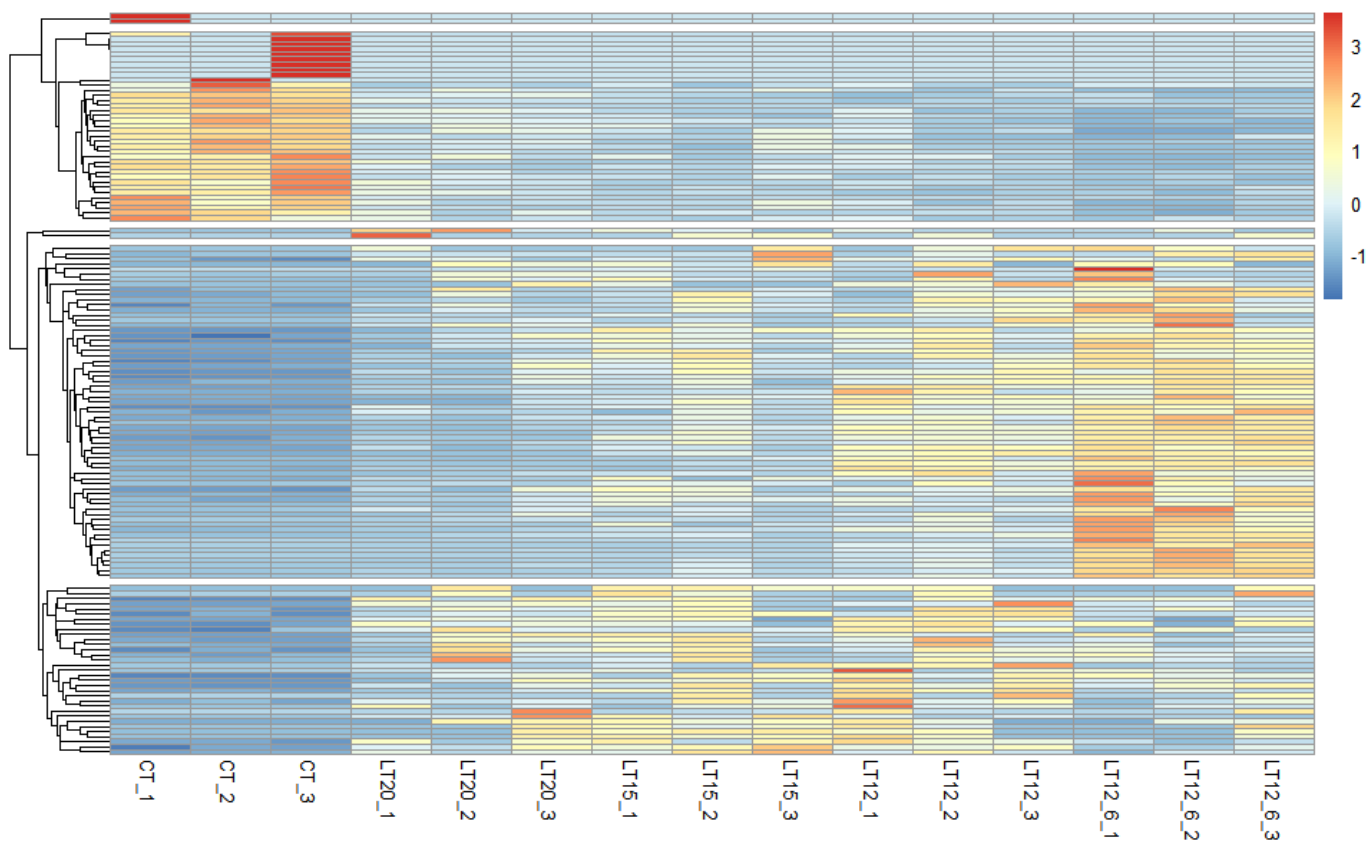
```
# Get help with command in R console.  
# ?TOMicsVis::network_plot
```

3.4.6 heatmap_cluster

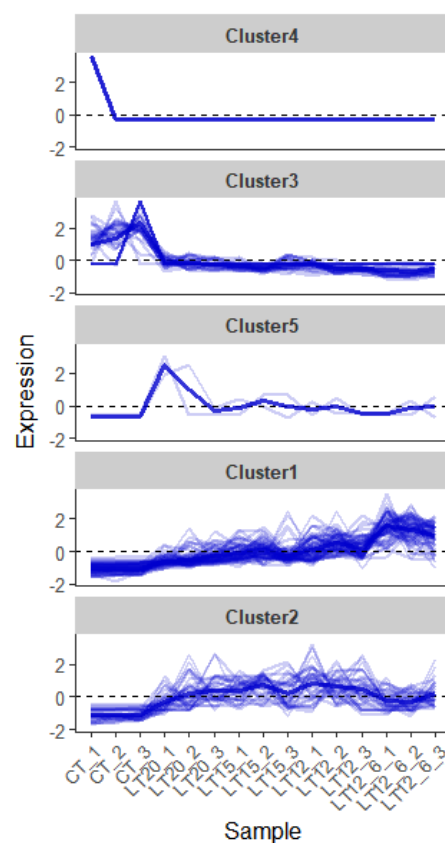
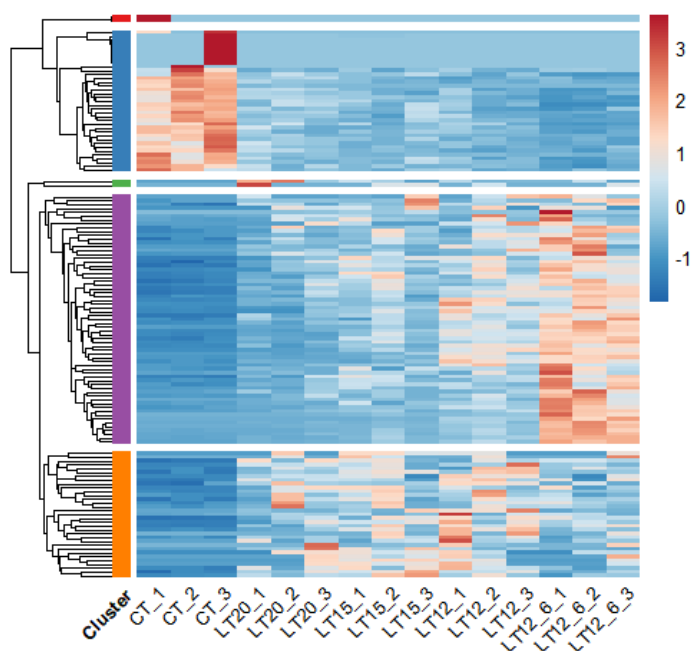
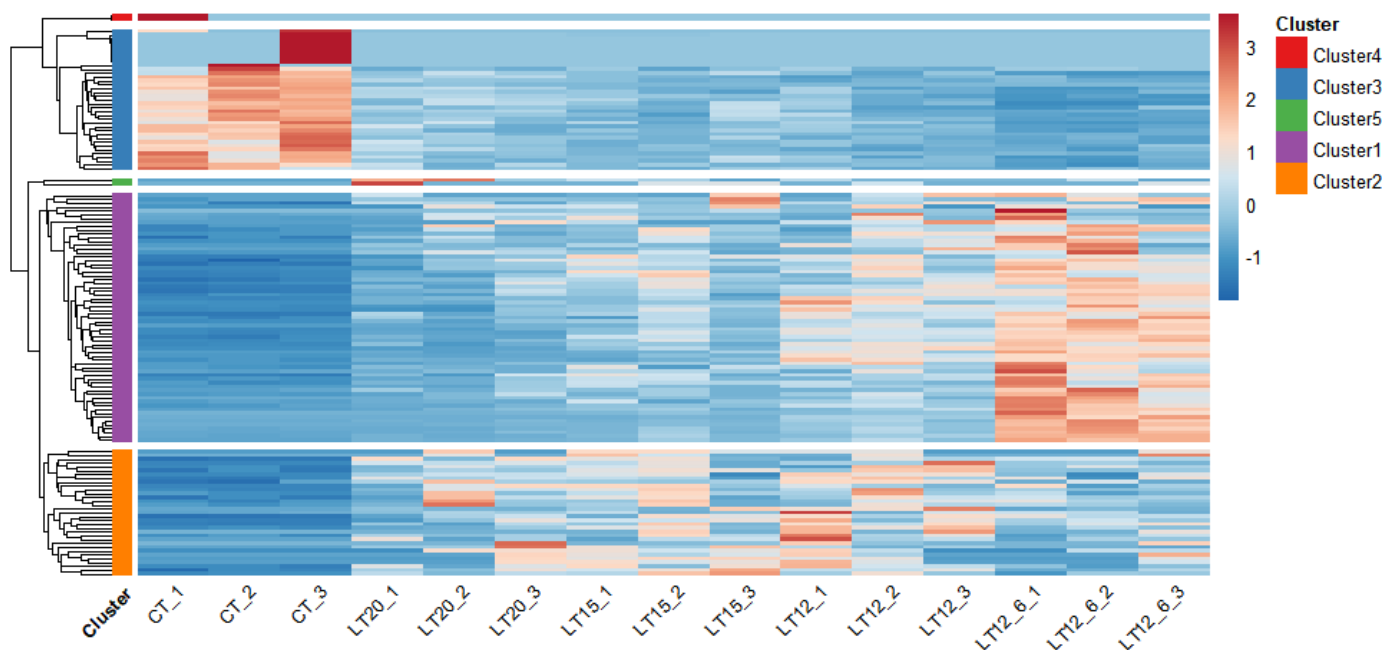
Input Data: Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).

Output Plot: Heatmap cluster plot for visualizing clustered gene expression data.

```
# 1. Load example datasets  
data(gene_expression2)  
head(gene_expression2)  
#> Genes CT_1 CT_2 CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2 LT15_3 LT12_1  
#> 1 ACAA2 24.50 39.83 55.38 114.11 159.32 96.88 169.56 464.84 182.66 116.08  
#> 2 ACAN 14.97 18.71 10.30 71.23 142.67 213.54 253.15 320.80 104.15 174.02  
#> 3 ADH1 1.54 1.56 2.04 14.95 13.60 15.87 12.80 17.74 6.06 10.97  
#> 4 AHSB 0.00 1911.99 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00  
#> 5 ALDH2 2.07 2.86 2.54 0.85 0.49 0.47 0.42 0.13 0.26 0.00  
#> 6 APIS3 6.62 14.59 9.30 24.90 33.94 23.19 24.00 36.08 27.40 24.06  
#> LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3  
#> 1 497.29 464.48 471.43 693.62 229.77  
#> 2 305.81 469.48 1291.90 991.90 966.77  
#> 3 10.71 30.95 9.84 10.91 7.28  
#> 4 0.00 0.00 0.00 0.00 0.00  
#> 5 0.28 0.11 0.37 0.15 0.11  
#> 6 38.74 34.54 62.72 41.36 28.75  
  
# 2. Run network_plot plot function  
heatmap_cluster(  
  data = gene_expression2,  
  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  
)
```



```
#> Using Cluster, gene as id variables
```



Get help using command `?TOMicsVis::heatmap_cluster` or reference page https://benben-miao.github.io/TOMicsVis/reference/heatmap_cluster.html (https://benben-miao.github.io/TOMicsVis/reference/heatmap_cluster.html).

```
# Get help with command in R console.
# ?TOMicsVis::heatmap_cluster
```

3.5 GO and KEGG Enrichment

3.5.1 go_enrich

Input 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).

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

```
# 1. Load example datasets
```

```
data(gene_go_kegg)
```

```
head(gene_go_kegg)
```

```
#>      Genes
```

```
#> 1      FN1
```

```
#> 2 14-3-3ZETA
```

```
#> 3      A1I3
```

```
#> 4      A2M
```

```
#> 5      AARS
```

```
#> 6      ABAT
```

```
#>
```

```
      biological_process
```

```
#> 1 GO:0003181(atrioventricular valve morphogenesis);GO:0003128(heart field specification);GO:0001756(somitogenesis)
```

```
#> 2                                     <NA>
```

```
#> 3                                     <NA>
```

```
#> 4                                     <NA>
```

```
#> 5                                     GO:0006419(alanyl-tRNA aminoacylation)
```

```
#> 6                                     GO:0009448(gamma-aminobutyric acid metabolic process)
```

```
#>
```

```
      cellular_component
```

```
#> 1 GO:0005576(extracellular region)
```

```
#> 2                                     <NA>
```

```
#> 3 GO:0005615(extracellular space)
```

```
#> 4 GO:0005615(extracellular space)
```

```
#> 5      GO:0005737(cytoplasm)
```

```
#> 6                                     <NA>
```

```
#>
```

```
      molecular_function
```

```
#> 1                                     <NA>
```

```
#> 2                                     GO:0019904(protein domain specific binding)
```

```
#> 3                                     GO:0004866(endopeptidase inhibitor activity)
```

```
#> 4                                     GO:0004866(endopeptidase inhibitor activity)
```

```
#> 5 GO:0004813(alanine-tRNA ligase activity);GO:0005524(ATP binding);GO:0000049(tRNA binding);GO:0008270(zinc ion binding)
```

```
#> 6      GO:0003867(4-aminobutyrate transaminase activity);GO:0030170(pyridoxal phosphate binding)
```

```
#>
```

```
kegg_pathway
```

```
#> 1      ko04810(Regulation of actin cytoskeleton);ko04510(Focal adhesion);ko04151(PI3K-Akt signaling pathway);ko04512(ECM-receptor interaction)
```

```
#> 2 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway - fly);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - worm)
```

```
#> 3      ko04610(Complement and coagulation cascades) ko0
```

```
4610(Complement and coagulation cascades)
```

```
#> 4      ko04610(Complement and coagulation cascades) ko0
```

```
4610(Complement and coagulation cascades)
```

```
#> 5
```

```
ko00970(Aminoacyl-tRNA biosynthesis)
```

```
#> 6      ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko00650(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synapse)
```

```
# 2. Run go_enrich analysis function
```

```
res <- go_enrich(
```

```
  go_anno = gene_go_kegg[,5],
```

```
  degs_list = gene_go_kegg[100:200,1],
```

```
  padjust_method = "fdr",
```

```
  pvalue_cutoff = 0.05,
```



```

qvalue_cutoff = 0.05
)
head(res)
#>      ID      ontology
#> 1 GO:0000221 cellular component
#> 2 GO:0000275 cellular component
#> 3 GO:0000276 cellular component
#> 4 GO:0000398 biological process
#> 5 GO:0000774 molecular function
#> 6 GO:0001671 molecular function
#>
#>      Description
#> 1      vacuolar proton-transporting V-type ATPase, VI domain
#> 2 mitochondrial proton-transporting ATP synthase complex, catalytic core F
#> 3 mitochondrial proton-transporting ATP synthase complex, coupling factor F
#> 4      mRNA splicing, via spliceosome
#> 5      adenyl-nucleotide exchange factor activity
#> 6      ATPase activator activity
#> GeneRatio BgRatio  pvalue  p.adjust  qvalue
#> 1  1/101  1/1279 7.896794e-02 1.110997e-01 9.458955e-02
#> 2  1/101  1/1279 7.896794e-02 1.110997e-01 9.458955e-02
#> 3  6/101  6/1279 2.109128e-07 1.075656e-05 9.158058e-06
#> 4  1/101 14/1279 6.858207e-01 7.363549e-01 6.269275e-01
#> 5  1/101  1/1279 7.896794e-02 1.110997e-01 9.458955e-02
#> 6  1/101  1/1279 7.896794e-02 1.110997e-01 9.458955e-02
#>
#>      geneID Count
#> 1      ATP6V1H  1
#> 2      ATP5F1E  1
#> 3 ATP5MC1/ATP5ME/ATP5MG/ATP5PB/ATP5PD/ATP5PF  6
#> 4      CDC40  1
#> 5      BAG2  1
#> 6      ATP1B1  1

```

Get help using command `?TOMicsVis::go_enrich` or reference page https://benben-miao.github.io/TOMicsVis/reference/go_enrich.html (https://benben-miao.github.io/TOMicsVis/reference/go_enrich.html).

```

# Get help with command in R console.
# ?TOMicsVis::go_enrich

```

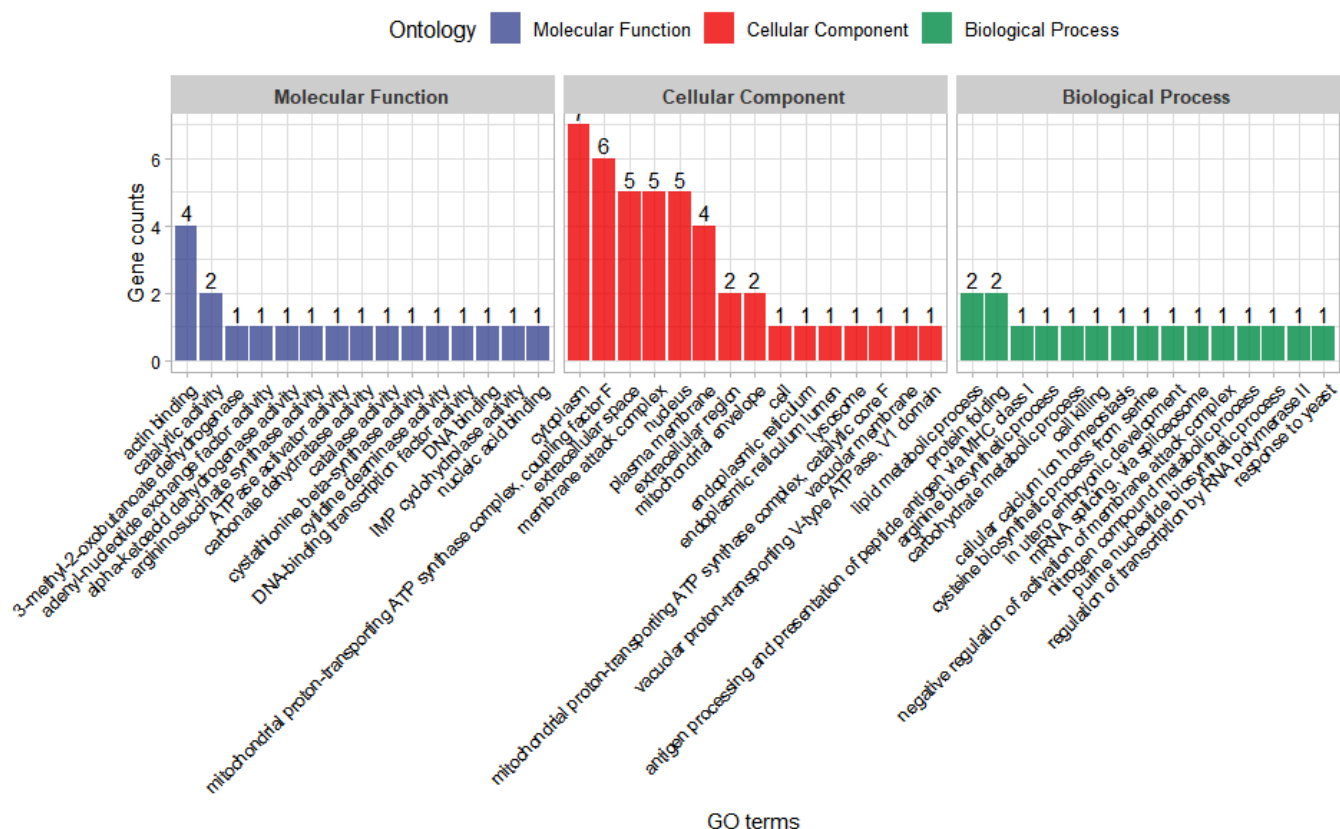
3.5.2 go_enrich_stat

Input 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).

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

```
# 1. Load example datasets
data(gene_go_kegg)

# 2. Run go_enrich_stat analysis function
go_enrich_stat(
  go_anno = gene_go_kegg[,-5],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
```



Get help using command `?TOMicsVis::go_enrich_stat` or reference page https://benbenmiao.github.io/TOMicsVis/reference/go_enrich_stat.html (https://benbenmiao.github.io/TOMicsVis/reference/go_enrich_stat.html).

```
# Get help with command in R console.
# ?TOMicsVis::go_enrich_stat
```

3.5.3 go_enrich_bar

Input 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).

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

```
# 1. Load example datasets
```

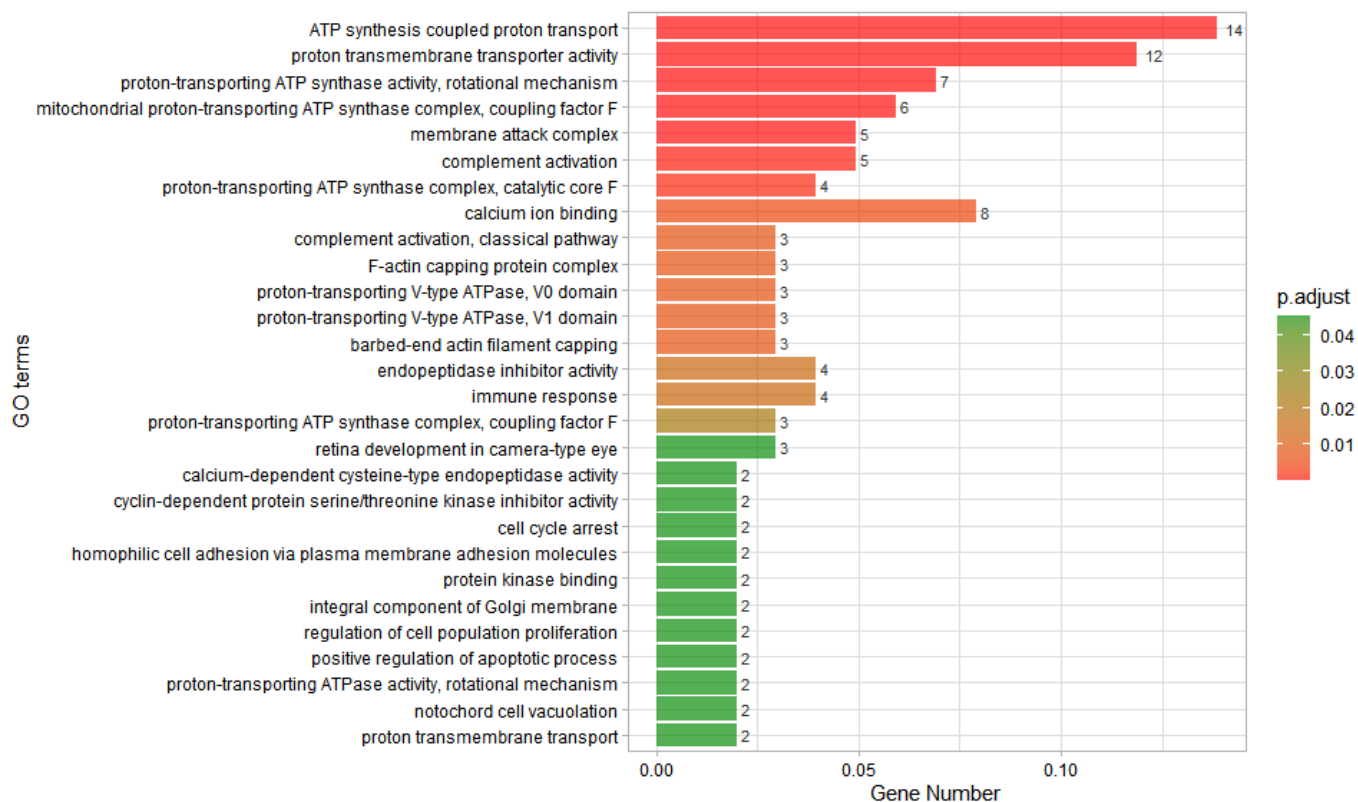
```
data(gene_go_kegg)
```

```
# 2. Run go_enrich_bar analysis function
```

```
go_enrich_bar(
  go_anno = gene_go_kegg[,5],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
```

```
#> Scale for fill is already present.
```

```
#> Adding another scale for fill, which will replace the existing scale.
```



Get help using command `?TOMicsVis::go_enrich_bar` or reference page https://benben-miao.github.io/TOMicsVis/reference/go_enrich_bar.html (https://benben-miao.github.io/TOMicsVis/reference/go_enrich_bar.html).

```
# Get help with command in R console.
```

```
# ?TOMicsVis::go_enrich_bar
```

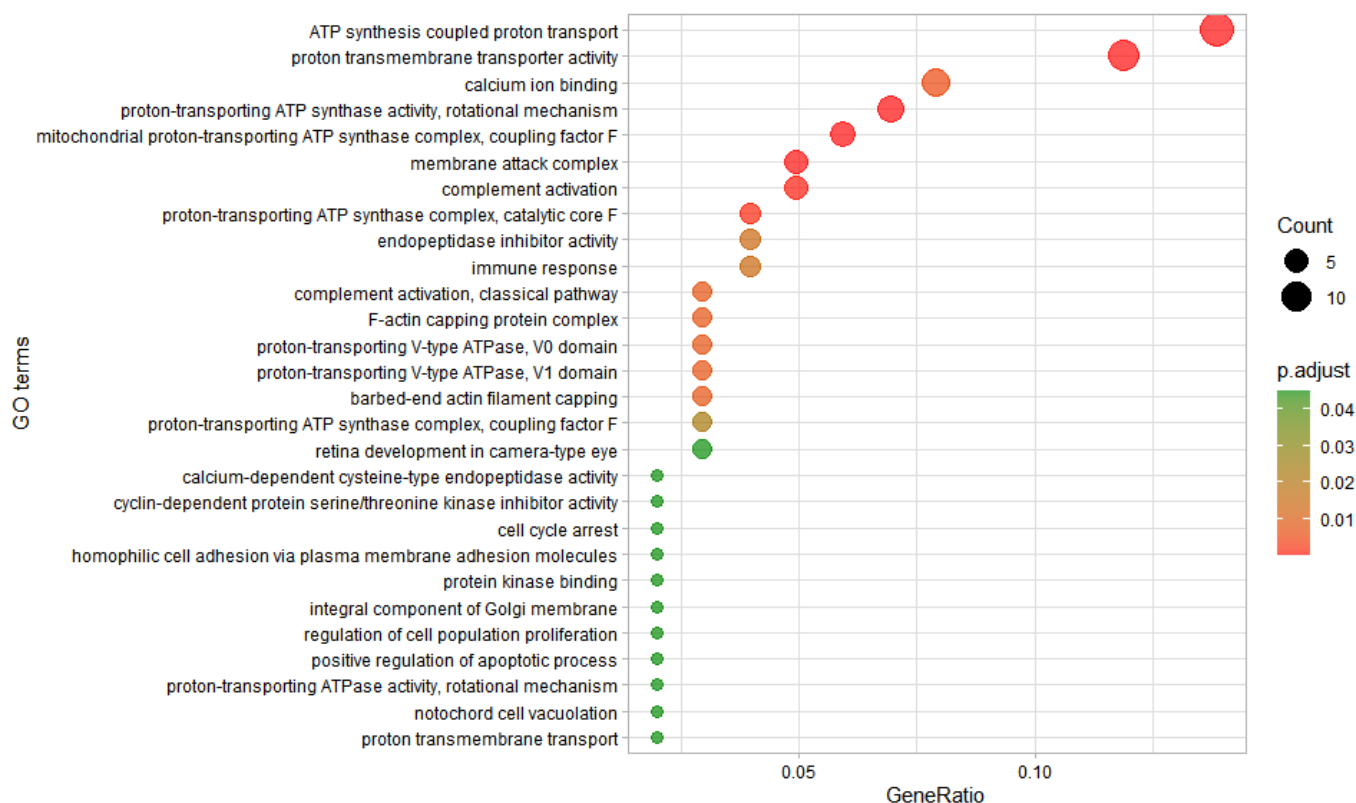
3.5.4 go_enrich_dot

Input 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).

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

```
# 1. Load example datasets
data(gene_go_kegg)

# 2. Run go_enrich_dot analysis function
go_enrich_dot(
  go_anno = gene_go_kegg[,5],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
#> Scale for colour is already present.
#> Adding another scale for colour, which will replace the existing scale.
```



Get help using command `?TOMicsVis::go_enrich_dot` or reference page https://benben-miao.github.io/TOMicsVis/reference/go_enrich_dot.html (https://benben-miao.github.io/TOMicsVis/reference/go_enrich_dot.html).

```
# Get help with command in R console.
# ?TOMicsVis::go_enrich_dot
```

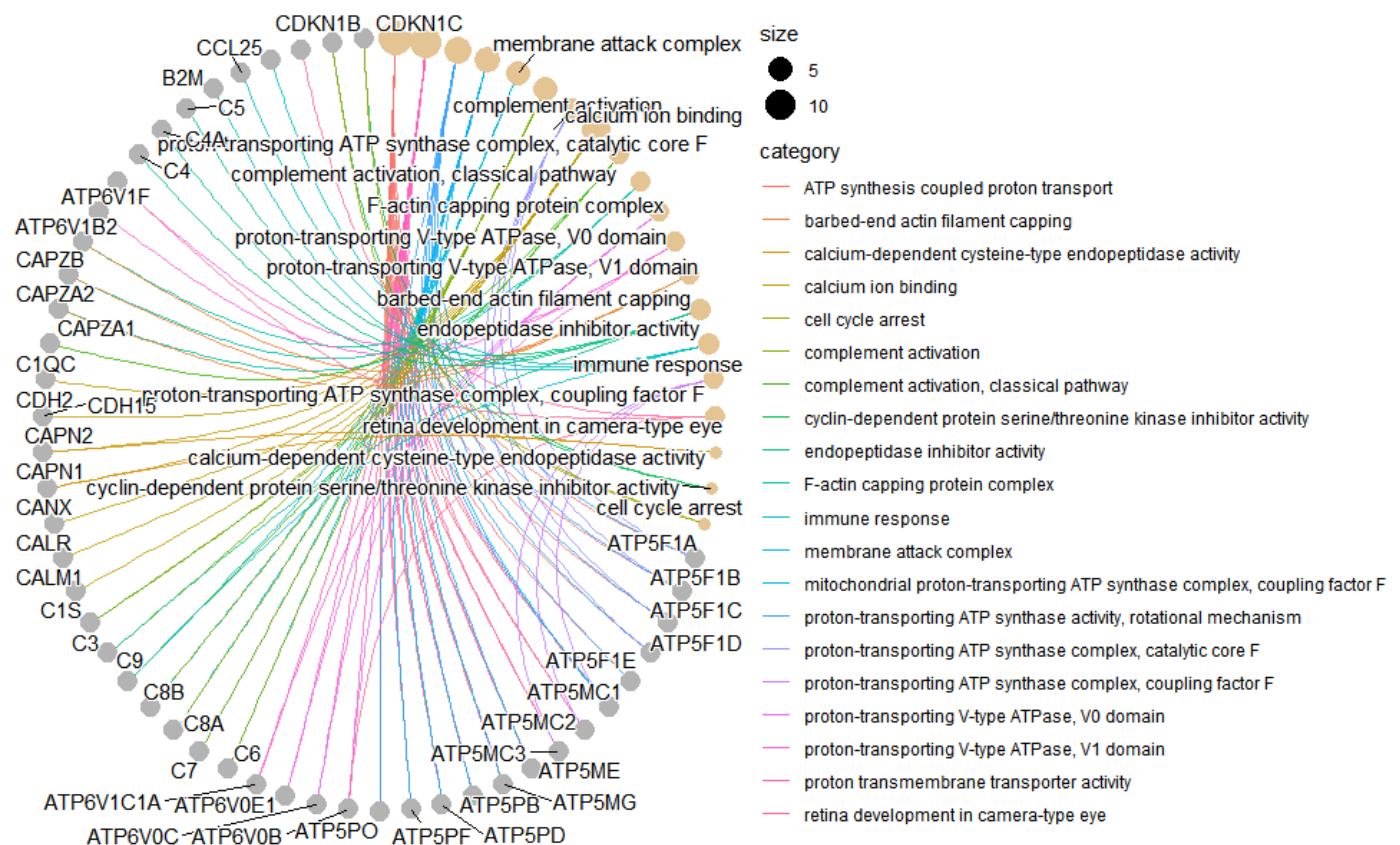
3.5.5 go_enrich_net

Input 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).

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

```
# 1. Load example datasets
data(gene_go_kegg)

# 2. Run go_enrich_net analysis function
go_enrich_net(
  go_anno = gene_go_kegg[,5],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
```



Get help using command `?TOMicsVis::go_enrich_net` or reference page https://benben-miao.github.io/TOMicsVis/reference/go_enrich_net.html (https://benben-miao.github.io/TOMicsVis/reference/go_enrich_net.html).

```
# Get help with command in R console.
# ?TOMicsVis::go_enrich_net
```

3.5.6 kegg_enrich

Input 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).

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

```
# 1. Load example datasets
```

```
data(gene_go_kegg)
```

```
head(gene_go_kegg)
```

```
#>      Genes
```

```
#> 1      FN1
```

```
#> 2 14-3-3ZETA
```

```
#> 3      A1I3
```

```
#> 4      A2M
```

```
#> 5      AARS
```

```
#> 6      ABAT
```

```
#>
```

```
      biological_process
```

```
#> 1 GO:0003181(atrioventricular valve morphogenesis);GO:0003128(heart field specification);GO:0001756(somitogenesis)
```

```
#> 2                                     <NA>
```

```
#> 3                                     <NA>
```

```
#> 4                                     <NA>
```

```
#> 5                                     GO:0006419(alanyl-tRNA aminoacylation)
```

```
#> 6                                     GO:0009448(gamma-aminobutyric acid metabolic process)
```

```
#>
```

```
      cellular_component
```

```
#> 1 GO:0005576(extracellular region)
```

```
#> 2                                     <NA>
```

```
#> 3 GO:0005615(extracellular space)
```

```
#> 4 GO:0005615(extracellular space)
```

```
#> 5      GO:0005737(cytoplasm)
```

```
#> 6                                     <NA>
```

```
#>
```

```
      molecular_function
```

```
#> 1                                     <NA>
```

```
#> 2      GO:0019904(protein domain specific binding)
```

```
#> 3      GO:0004866(endopeptidase inhibitor activity)
```

```
#> 4      GO:0004866(endopeptidase inhibitor activity)
```

```
#> 5 GO:0004813(alanine-tRNA ligase activity);GO:0005524(ATP binding);GO:0000049(tRNA binding);GO:0008270(zinc ion binding)
```

```
#> 6      GO:0003867(4-aminobutyrate transaminase activity);GO:0030170(pyridoxal phosphate binding)
```

```
#>
```

```
kegg_pathway
```

```
#> 1      ko04810(Regulation of actin cytoskeleton);ko04510(Focal adhesion);ko04151(PI3K-Akt signaling pathway);ko04512(ECM-receptor interaction)
```

```
#> 2 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway - fly);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - worm)
```

```
#> 3      ko04610(Complement and coagulation cascades) ko0
```

```
4610(Complement and coagulation cascades)
```

```
#> 4      ko04610(Complement and coagulation cascades) ko0
```

```
4610(Complement and coagulation cascades)
```

```
#> 5
```

```
ko00970(Aminoacyl-tRNA biosynthesis)
```

```
#> 6      ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko00650(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synapse)
```

```
# 2. Run go_enrich analysis function
```

```
res <- kegg_enrich(
```

```
  kegg_anno = gene_go_kegg[,c(1,5)],
```

```
  degs_list = gene_go_kegg[100:200,1],
```

```
  padjust_method = "fdr",
```

```
  pvalue_cutoff = 0.05,
```

```

qvalue_cutoff = 0.05
)
head(res)
#>      ID      Description GeneRatio BgRatio
#> ko04966 ko04966 Collecting duct acid secretion 7/101 7/1279
#> ko00190 ko00190 Oxidative phosphorylation 23/101 88/1279
#> ko04721 ko04721 Synaptic vesicle cycle 8/101 13/1279
#> ko04610 ko04610 Complement and coagulation cascades 13/101 43/1279
#> ko04145 ko04145 Phagosome 11/101 33/1279
#> ko04971 ko04971 Gastric acid secretion 4/101 4/1279
#>      pvalue p.adjust qvalue
#> ko04966 1.573976e-08 2.030430e-06 1.723090e-06
#> ko00190 5.232645e-08 3.375056e-06 2.864185e-06
#> ko04721 1.069634e-06 4.599427e-05 3.903227e-05
#> ko04610 1.078094e-05 3.476853e-04 2.950573e-04
#> ko04145 1.941460e-05 5.008968e-04 4.250776e-04
#> ko04971 3.679084e-05 7.910030e-04 6.712714e-04
#>
#>      geneID
#> ko04966 ATP6V0C/ATP6V0E1/ATP6V1B2/A
TP6V1C1A/ATP6V1F/ATP6V1G1/CA1
#> ko00190 ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5MC1/ATP5MC2/ATP5MC3/ATP5ME/ATP5MF/ATP5M
G/ATP5PB/ATP5PD/ATP5PF/ATP5PO/ATP6V0B/ATP6V0C/ATP6V0E1/ATP6V1B2/ATP6V1C1A/ATP6V1F/ATP6V1G1/ATP6
VIH
#> ko04721 ATP6V0B/ATP6V0C/ATP6V0E1/ATP6V1B
2/ATP6V1C1A/ATP6V1F/ATP6V1G1/ATP6V1H
#> ko04610 C1QC/C1S/C3/C4/C4A/C5/C
6/C7/C8A/C8B/C8G/C9/CD59
#> ko04145 ATP6V0B/ATP6V0C/ATP6V0E1/ATP6V1B2/ATP6V
1C1A/ATP6V1F/ATP6V1G1/ATP6V1H/C3/CALR/CANX
#> ko04971 ATP1B1/CA1/C
ALM1/CAMK2D
#>      Count
#> ko04966 7
#> ko00190 23
#> ko04721 8
#> ko04610 13
#> ko04145 11
#> ko04971 4

```

Get help using command `?TOMicsVis::kegg_enrich` or reference page https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich.html (https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich.html).

```

# Get help with command in R console.
# ?TOMicsVis::kegg_enrich

```

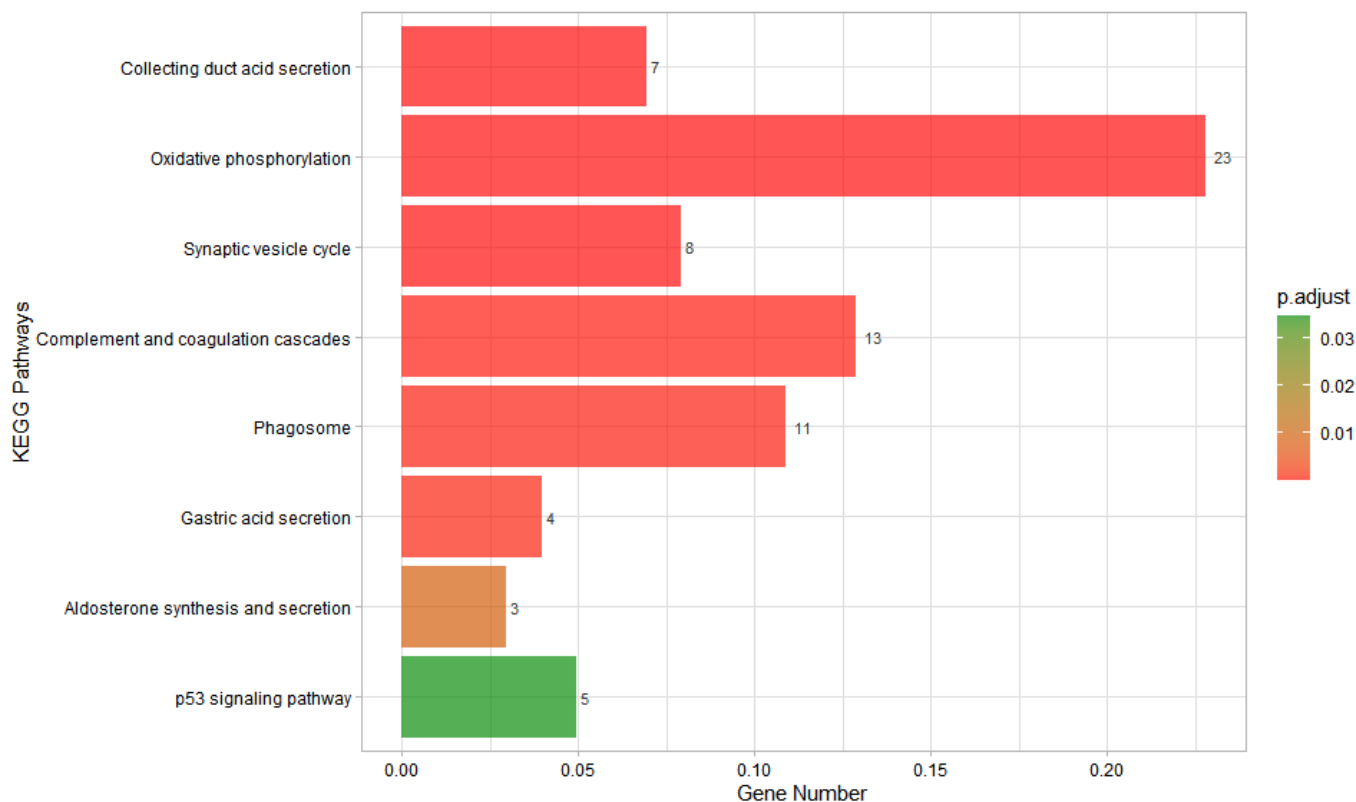
3.5.7 kegg_enrich_bar

Input 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).

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


```
# 1. Load example datasets
data(gene_go_kegg)

# 2. Run kegg_enrich_bar analysis function
kegg_enrich_bar(
  kegg_anno = gene_go_kegg[,c(1,5)],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
#> Scale for fill is already present.
#> Adding another scale for fill, which will replace the existing scale.
```



Get help using command `?TOMicsVis::kegg_enrich_bar` or reference page https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich_bar.html (https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich_bar.html).

```
# Get help with command in R console.
# ?TOMicsVis::kegg_enrich_bar
```

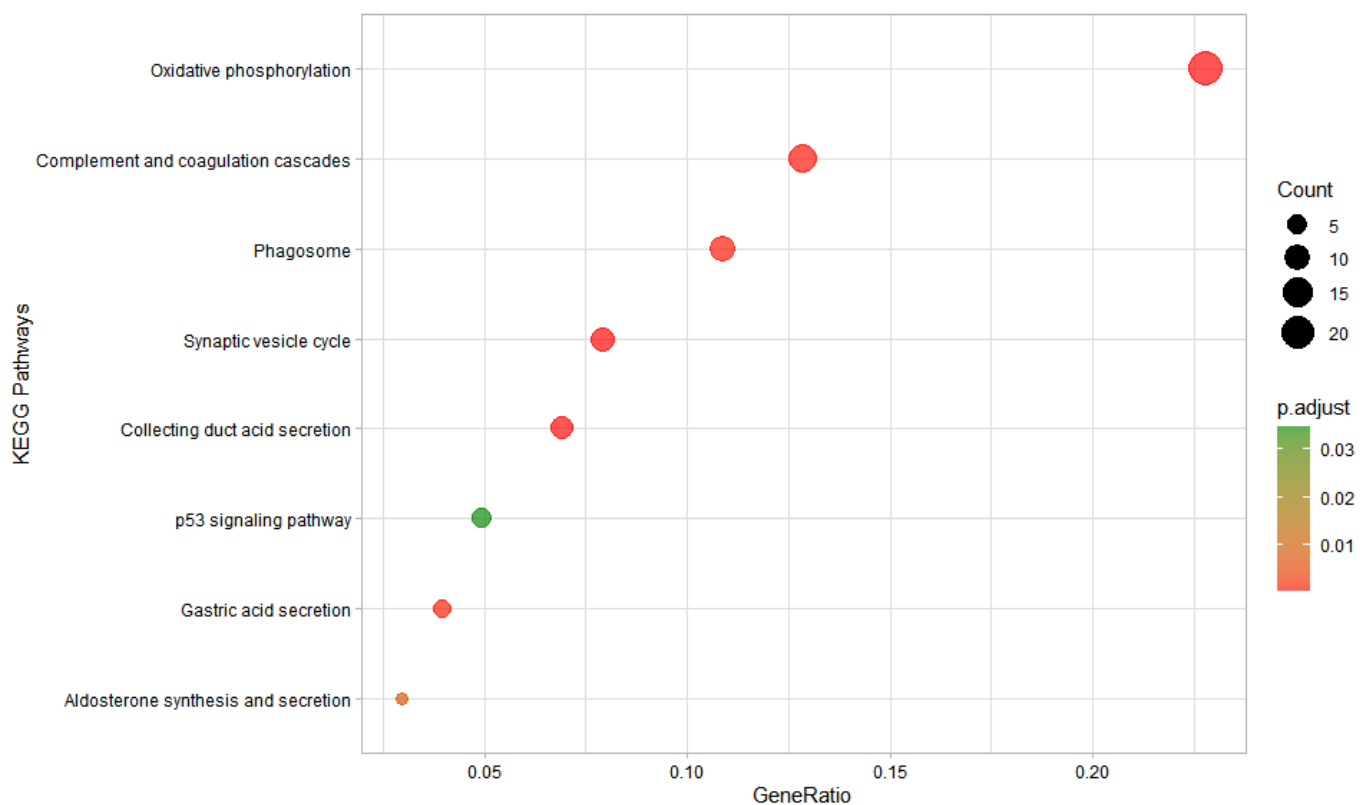
3.5.8 kegg_enrich_dot

Input 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).

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

```
# 1. Load example datasets
data(gene_go_kegg)

# 2. Run kegg_enrich_dot analysis function
kegg_enrich_dot(
  kegg_anno = gene_go_kegg[,c(1,5)],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
#> Scale for colour is already present.
#> Adding another scale for colour, which will replace the existing scale.
```



Get help using command `?TOMicsVis::kegg_enrich_dot` or reference page https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich_dot.html (https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich_dot.html).

```
# Get help with command in R console.
# ?TOMicsVis::kegg_enrich_dot
```

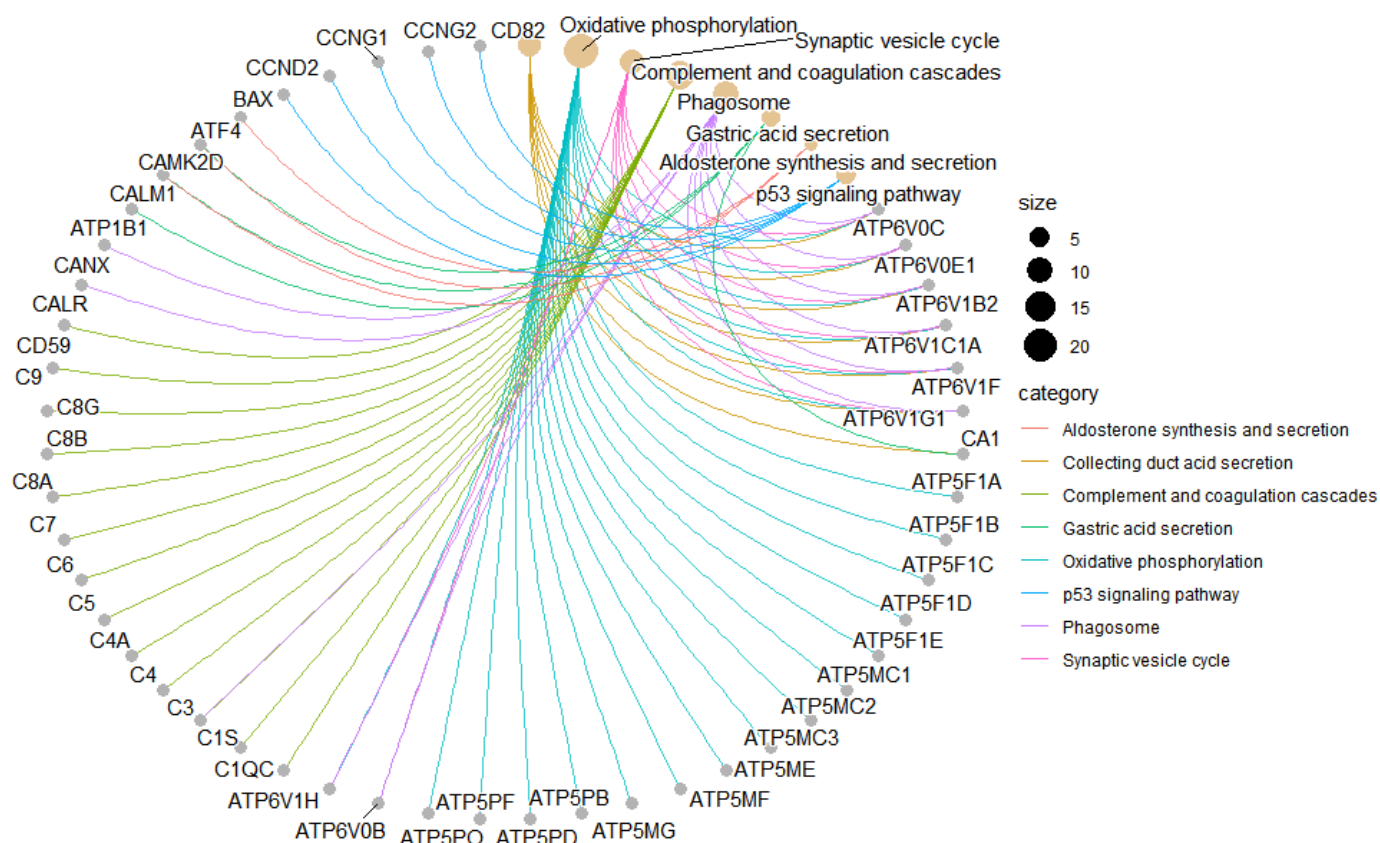
3.5.9 kegg_enrich_net

Input 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).

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

```
# 1. Load example datasets
data(gene_go_kegg)

# 2. Run kegg_enrich_net analysis function
kegg_enrich_net(
  kegg_anno = gene_go_kegg[,c(1,5)],
  degs_list = gene_go_kegg[100:200,1],
  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"
)
```



Get help using command `?TOMicsVis::kegg_enrich_net` or reference page https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich_net.html (https://benben-miao.github.io/TOMicsVis/reference/kegg_enrich_net.html).

```
# Get help with command in R console.
# ?TOMicsVis::kegg_enrich_net
```

3.6 Tables Operations

3.6.1 table_split

Input 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).

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

```

# 1. Load example datasets
data(gene_go_kegg2)
head(gene_go_kegg2)
#>      Genes
#> 1      FN1
#> 2 I4-3-3ZETA
#> 3      A1I3
#> 4      A2M
#> 5      AARS
#> 6      ABAT
#>
kegg_pathway
#> 1                                ko04810(Regulation of actin cytoskeleton);ko04510(Focal a
dhesion);ko04151(PI3K-Akt signaling pathway);ko04512(ECM-receptor interaction)
#> 2 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway -fl
y);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - w
orm)
#> 3                                                                ko0
4610(Complement and coagulation cascades)
#> 4                                                                ko0
4610(Complement and coagulation cascades)
#> 5
ko00970(Aminoacyl-tRNA biosynthesis)
#> 6      ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko006
50(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synaps
e)
#>      go_category
#> 1 biological_process
#> 2 biological_process
#> 3 biological_process
#> 4 biological_process
#> 5 biological_process
#> 6 biological_process
#>
go_term
#> 1 GO:0003181(atrioventricular valve morphogenesis);GO:0003128(heart field specification);GO:0001756(somitogenesis)
#> 2                                <NA>
#> 3                                <NA>
#> 4                                <NA>
#> 5                                GO:0006419(alanyl-tRNA aminoacylation)
#> 6                                GO:0009448(gamma-aminobutyric acid metabolic process)

# 2. Run table_split function
res <- table_split(
  data = gene_go_kegg2,
  grouped_var = "go_category",
  value_var = "go_term",
  miss_drop = TRUE
)
head(res)
#>      Genes
#> 1 I4-3-3ZETA
#> 2      A1I3
#> 3      A2M
#> 4      AARS
#> 5      ABAT

```

```

#> 6 ABCB7
#>
kegg_pathway
#> 1 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway -fly);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - worm)
#> 2 ko0
4610(Complement and coagulation cascades)
#> 3 ko0
4610(Complement and coagulation cascades)
#> 4
ko00970(Aminoacyl-tRNA biosynthesis)
#> 5 ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko00650(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synapse)
#> 6
ko02010(ABC transporters)
#> biological_process
#> 1 <NA>
#> 2 <NA>
#> 3 <NA>
#> 4 GO:0006419(alanyl-tRNA aminoacylation)
#> 5 GO:0009448(gamma-aminobutyric acid metabolic process)
#> 6 <NA>
#> cellular_component
#> 1 <NA>
#> 2 GO:0005615(extracellular space)
#> 3 GO:0005615(extracellular space)
#> 4 GO:0005737(cytoplasm)
#> 5 <NA>
#> 6 GO:0016021(integral component of membrane)
#> molecular_function
#> 1 GO:0019904(protein domain specific binding)
#> 2 GO:0004866(endopeptidase inhibitor activity)
#> 3 GO:0004866(endopeptidase inhibitor activity)
#> 4 GO:0004813(alanine-tRNA ligase activity);GO:0005524(ATP binding);GO:0000049(tRNA binding);GO:0008270(zinc ion binding)
#> 5 GO:0003867(4-aminobutyrate transaminase activity);GO:0030170(pyridoxal phosphate binding)
#> 6 GO:0005524(ATP binding);GO:0016887(ATPase activity);GO:0042626(ATPase-coupled transmembrane transporter activity)

```

Get help using command `?TOMicsVis::table_split` or reference page https://benben-miao.github.io/TOMicsVis/reference/table_split.html (https://benben-miao.github.io/TOMicsVis/reference/table_split.html).

```

# Get help with command in R console.
# ?TOMicsVis::table_split

```

3.6.2 table_merge

Input 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).

Output Table: Table merge used to merge multiple variables to one variable.

```
# 1. Load example datasets
```

```
data(gene_go_kegg)
```

```
head(gene_go_kegg)
```

```
#>      Genes
```

```
#> 1      FN1
```

```
#> 2 14-3-3ZETA
```

```
#> 3      A1I3
```

```
#> 4      A2M
```

```
#> 5      AARS
```

```
#> 6      ABAT
```

```
#>
```

```
      biological_process
```

```
#> 1 GO:0003181(atrioventricular valve morphogenesis);GO:0003128(heart field specification);GO:0001756(somitogenesis)
```

```
#> 2                                     <NA>
```

```
#> 3                                     <NA>
```

```
#> 4                                     <NA>
```

```
#> 5                                     GO:0006419(alanyl-tRNA aminoacylation)
```

```
#> 6                                     GO:0009448(gamma-aminobutyric acid metabolic process)
```

```
#>
```

```
      cellular_component
```

```
#> 1 GO:0005576(extracellular region)
```

```
#> 2                                     <NA>
```

```
#> 3 GO:0005615(extracellular space)
```

```
#> 4 GO:0005615(extracellular space)
```

```
#> 5      GO:0005737(cytoplasm)
```

```
#> 6                                     <NA>
```

```
#>
```

```
      molecular_function
```

```
#> 1                                     <NA>
```

```
#> 2      GO:0019904(protein domain specific binding)
```

```
#> 3      GO:0004866(endopeptidase inhibitor activity)
```

```
#> 4      GO:0004866(endopeptidase inhibitor activity)
```

```
#> 5 GO:0004813(alanine-tRNA ligase activity);GO:0005524(ATP binding);GO:0000049(tRNA binding);GO:0008270(zinc ion binding)
```

```
#> 6      GO:0003867(4-aminobutyrate transaminase activity);GO:0030170(pyridoxal phosphate binding)
```

```
#>
```

```
kegg_pathway
```

```
#> 1      ko04810(Regulation of actin cytoskeleton);ko04510(Focal adhesion);ko04151(PI3K-Akt signaling pathway);ko04512(ECM-receptor interaction)
```

```
#> 2 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway - fly);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - worm)
```

```
#> 3      ko04610(Complement and coagulation cascades) ko0
```

```
4610(Complement and coagulation cascades)
```

```
#> 4      ko04610(Complement and coagulation cascades) ko0
```

```
4610(Complement and coagulation cascades)
```

```
#> 5
```

```
ko00970(Aminoacyl-tRNA biosynthesis)
```

```
#> 6      ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko00650(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synapse)
```

```
# 2. Run function
```

```
res <- table_merge(
```

```
  data = gene_go_kegg,
```

```
  merge_vars = c("biological_process", "cellular_component", "molecular_function"),
```

```
  new_var = "go_category",
```

```
  new_value = "go_term",
```

```

na_remove = FALSE
)
head(res)
#>      Genes
#> 1      FN1
#> 2 14-3-3ZETA
#> 3      A1I3
#> 4      A2M
#> 5      AARS
#> 6      ABAT
#>
kegg_pathway
#> 1      ko04810(Regulation of actin cytoskeleton);ko04510(Focal a
dhesion);ko04151(PI3K-Akt signaling pathway);ko04512(ECM-receptor interaction)
#> 2 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway -fl
y);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - w
orm)
#> 3      ko04610(Complement and coagulation cascades)
#> 4      ko04610(Complement and coagulation cascades)
#> 5      ko00970(Aminoacyl-tRNA biosynthesis)
#> 6      ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko006
50(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synaps
e)
#>      go_category
#> 1 biological_process
#> 2 biological_process
#> 3 biological_process
#> 4 biological_process
#> 5 biological_process
#> 6 biological_process
#>      go_term
#> 1 GO:0003181(atrioventricular valve morphogenesis);GO:0003128(heart field specification);GO:0001756(somitogenesis)
#> 2      <NA>
#> 3      <NA>
#> 4      <NA>
#> 5      GO:0006419(alanyl-tRNA aminoacylation)
#> 6      GO:0009448(gamma-aminobutyric acid metabolic process)

```

Get help using command `?TOMicsVis::table_merge` or reference page https://benben-miao.github.io/TOMicsVis/reference/table_merge.html (https://benben-miao.github.io/TOMicsVis/reference/table_merge.html).

```

# Get help with command in R console.
# ?TOMicsVis::table_merge

```

3.6.3 table_filter

Input 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).

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


```

# 1. Load example datasets
data(traits_sex)
head(traits_sex)
#>   Value Traits Sex
#> 1 36.74 Weight Female
#> 2 38.54 Weight Female
#> 3 44.91 Weight Female
#> 4 43.53 Weight Female
#> 5 39.03 Weight Female
#> 6 26.01 Weight Female

# 2. Run function
res <- table_filter(
  data = traits_sex,
  Sex == "Male" & Traits == "Weight" & Value > 40
)
head(res)
#>   Value Traits Sex
#> 1 48.06 Weight Male
#> 2 42.74 Weight Male
#> 3 45.25 Weight Male
#> 4 44.95 Weight Male
#> 5 43.21 Weight Male
#> 6 40.02 Weight Male

```

Get help using command `?TomicsVis::table_filter` or reference page https://benben-miao.github.io/TomicsVis/reference/table_filter.html (https://benben-miao.github.io/TomicsVis/reference/table_filter.html).

```

# Get help with command in R console.
# ?TomicsVis::table_filter

```

3.6.4 table_cross

Input Data1: Dataframe: Shared DEGs of all paired comparisons in all samples expression dataframe of RNA-Seq. (1st-col: Genes, 2nd-col~: Samples).

Input 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).

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

```
# 1. Load example datasets
```

```
data(gene_expression2)
```

```
head(gene_expression2)
```

```
#> Genes CT_1 CT_2 CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2 LT15_3 LT12_1
```

```
#> 1 ACAA2 24.50 39.83 55.38 114.11 159.32 96.88 169.56 464.84 182.66 116.08
```

```
#> 2 ACAN 14.97 18.71 10.30 71.23 142.67 213.54 253.15 320.80 104.15 174.02
```

```
#> 3 ADH1 1.54 1.56 2.04 14.95 13.60 15.87 12.80 17.74 6.06 10.97
```

```
#> 4 AHSB 0.00 1911.99 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
```

```
#> 5 ALDH2 2.07 2.86 2.54 0.85 0.49 0.47 0.42 0.13 0.26 0.00
```

```
#> 6 AP1S3 6.62 14.59 9.30 24.90 33.94 23.19 24.00 36.08 27.40 24.06
```

```
#> LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3
```

```
#> 1 497.29 464.48 471.43 693.62 229.77
```

```
#> 2 305.81 469.48 1291.90 991.90 966.77
```

```
#> 3 10.71 30.95 9.84 10.91 7.28
```

```
#> 4 0.00 0.00 0.00 0.00 0.00
```

```
#> 5 0.28 0.11 0.37 0.15 0.11
```

```
#> 6 38.74 34.54 62.72 41.36 28.75
```

```
data(gene_go_kegg)
```

```
head(gene_go_kegg)
```

```
#> Genes
```

```
#> 1 FNI
```

```
#> 2 14-3-3ZETA
```

```
#> 3 AII3
```

```
#> 4 A2M
```

```
#> 5 AARS
```

```
#> 6 ABAT
```

```
#>
```

```
biological_process
```

```
#> 1 GO:0003181(atrioventricular valve morphogenesis);GO:0003128(heart field specification);GO:0001756(somitogenesis)
```

```
#> 2 <NA>
```

```
#> 3 <NA>
```

```
#> 4 <NA>
```

```
#> 5 GO:0006419(alanyl-tRNA aminoacylation)
```

```
#> 6 GO:0009448(gamma-aminobutyric acid metabolic process)
```

```
#> cellular_component
```

```
#> 1 GO:0005576(extracellular region)
```

```
#> 2 <NA>
```

```
#> 3 GO:0005615(extracellular space)
```

```
#> 4 GO:0005615(extracellular space)
```

```
#> 5 GO:0005737(cytoplasm)
```

```
#> 6 <NA>
```

```
#>
```

```
molecular_function
```

```
#> 1 <NA>
```

```
#> 2 GO:0019904(protein domain specific binding)
```

```
#> 3 GO:0004866(endopeptidase inhibitor activity)
```

```
#> 4 GO:0004866(endopeptidase inhibitor activity)
```

```
#> 5 GO:0004813(alanine-tRNA ligase activity);GO:0005524(ATP binding);GO:0000049(tRNA binding);GO:0008270(zinc ion binding)
```

```
#> 6 GO:0003867(4-aminobutyrate transaminase activity);GO:0030170(pyridoxal phosphate binding)
```

```
#>
```

```
kegg_pathway
```

```
#> 1 ko04810(Regulation of actin cytoskeleton);ko04510(Focal adhesion);ko04151(PI3K-Akt signaling pathway);ko04512(ECM-receptor interaction)
```

```
#> 2 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway - fly);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - w
```

```

orm)
#> 3 ko0
4610(Complement and coagulation cascades)
#> 4 ko0
4610(Complement and coagulation cascades)
#> 5
ko00970(Aminoacyl-tRNA biosynthesis)
#> 6 ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko006
50(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synaps
e)

# 2. Run function
res <- table_cross(
  data1 = gene_expression2,
  data2 = gene_go_kegg,
  inter_var = "Genes",
  left_index = TRUE,
  right_index = TRUE
)
head(res)
#> Genes CT_1 CT_2 CT_3 LT20_1 LT20_2 LT20_3 LT15_1 LT15_2 LT15_3 LT12_1
#> 1 14-3-3ZETA NA NA NA NA NA NA NA NA NA NA
#> 2 A1I3 NA NA NA NA NA NA NA NA NA NA
#> 3 A2M NA NA NA NA NA NA NA NA NA NA
#> 4 AARS NA NA NA NA NA NA NA NA NA NA
#> 5 ABAT NA NA NA NA NA NA NA NA NA NA
#> 6 ABCB7 NA NA NA NA NA NA NA NA NA NA
#> LT12_2 LT12_3 LT12_6_1 LT12_6_2 LT12_6_3
#> 1 NA NA NA NA NA
#> 2 NA NA NA NA NA
#> 3 NA NA NA NA NA
#> 4 NA NA NA NA NA
#> 5 NA NA NA NA NA
#> 6 NA NA NA NA NA
#> biological_process
#> 1 <NA>
#> 2 <NA>
#> 3 <NA>
#> 4 GO:0006419(alanyl-tRNA aminoacylation)
#> 5 GO:0009448(gamma-aminobutyric acid metabolic process)
#> 6 <NA>
#> cellular_component
#> 1 <NA>
#> 2 GO:0005615(extracellular space)
#> 3 GO:0005615(extracellular space)
#> 4 GO:0005737(cytoplasm)
#> 5 <NA>
#> 6 GO:0016021(integral component of membrane)
#> molecular_function
#> 1 GO:0019904(protein domain specific binding)
#> 2 GO:0004866(endopeptidase inhibitor activity)
#> 3 GO:0004866(endopeptidase inhibitor activity)
#> 4 GO:0004813(alanine-tRNA ligase activity);GO:0005524(ATP binding);GO:0000049(tRNA binding);GO:0008270(zinc io
n binding)
#> 5 GO:0003867(4-aminobutyrate transaminase activity);GO:0030170(pyridoxal phosphate binding)
#> 6 GO:0005524(ATP binding);GO:0016887(ATPase activity);GO:0042626(ATPase-coupled transmembrane transporter

```

```

activity)
#>
kegg_pathway
#> 1 ko04110(Cell cycle);ko04114(Oocyte meiosis);ko04390(Hippo signaling pathway);ko04391(Hippo signaling pathway -fly);ko04013(MAPK signaling pathway - fly);ko04151(PI3K-Akt signaling pathway);ko04212(Longevity regulating pathway - worm)
#> 2 ko04610(Complement and coagulation cascades)
#> 3 ko04610(Complement and coagulation cascades)
#> 4 ko00970(Aminoacyl-tRNA biosynthesis)
#> 5 ko00250(Alanine, aspartate and glutamate metabolism);ko00280(Valine, leucine and isoleucine degradation);ko00650(Butanoate metabolism);ko00640(Propanoate metabolism);ko00410(beta-Alanine metabolism);ko04727(GABAergic synapse)
#> 6 ko02010(ABC transporters)

```

Get help using command `?TOMicsVis::table_cross` or reference page https://benbenmiao.github.io/TOMicsVis/reference/table_cross.html (https://benbenmiao.github.io/TOMicsVis/reference/table_cross.html).

```

# Get help with command in R console.
# ?TOMicsVis::table_cross

```