Package 'tinyarray'

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Type Package

Title Expression Data Analysis and Visualization

Version 2.3.0

Maintainer Xiaojie Sun <18763899370@163.com>

Description Gene Expression Omnibus(GEO) and The Cancer Genome Atlas(TCGA) are common bioinformatics public databases. We integrate the regular analysis and charts for expression data, to analyze and display the data concisely and intuitively.

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Encoding UTF-8

LazyData true

Imports BiocManager, clusterProfiler, dplyr, limma, org.Hs.eg.db, stringr, tibble, pheatmap, ggplot2, survival, survminer, patchwork, magrittr

Suggests testthat, AnnoProbe, GEOquery, Biobase, VennDiagram, FactoMineR, factoextra, knitr, rmarkdown, cowplot, ggpubr, ggplotify, tidyr, labeling, Rtsne, scatterplot3d, ComplexHeatmap, circlize

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BugReports https://github.com/xjsun1221/tinyarray/issues

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NeedsCompilation no

Author Xiaojie Sun [aut, cre]

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R topics documented:

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box_surv *box_surv*

Description

draw box plot for a hub gene expression matrix

Usage

```
box_surv(exp_hub, exprSet_hub, meta)
```

Arguments

exp_hub	an expression matrix for hubgenes
exprSet_hub	a tumor expression set for hubgenes
meta	meta data corresponds to expression set

Value

patchwork result for hub genes boxplot and survival plot

Author(s)

Xiaojie Sun

See Also

exp_boxplot;exp_surv

Examples

```
k = box_surv(log2(exp_hub1+1),exprSet_hub1,meta1);k[[1]]
```

cod *cod*

Description

An expression matrix form TCGA

Usage

```
cod
```

Format

An object of class `matrix` (inherits from `array`) with 100 rows and 512 columns.

Examples

```
cod
```

cor.full *cor.test for all variables*

Description

cor.test for all variables(each two columns)

Usage

```
cor.full(x, drop = min(x) - 0.001, min.obs = 10)
```

Arguments

`x`	A numeric matrix or data.frame
`drop`	drop values
`min.obs`	minimum number of observations after dropping

Value

a data.frame with cor.test p.value and estimate

Author(s)

Xiaojie Sun

See Also

`cor.one`

Examples

```
x = iris[,-5]
cor.full(x)
```

`cor.one` *cor.test for one variable with all variables*

Description

cor.test for all variables(each two columns)

Usage

```
cor.one(
  x,
  var,
  drop.var = min(x[, var]) - 0.001,
  drop.other = min(x[, -which(colnames(x) == var)]) - 0.001,
  min.obs = 10
)
```

Arguments

`x`	A numeric matrix or data.frame
`var`	your chosen variable,only one.
`drop.var`	drop values in var
`drop.other`	drop values in other columns
`min.obs`	minimum number of observations after dropping

Value

A data.frame with cor.test p.value and estimate

Author(s)

Xiaojie Sun

See Also

`cor.full`

Examples

```
x = iris[,-5]
cor.one(x,"Sepal.Width")
```

deg *deg*

Description

limma differential analysis result for GSE42872

Usage

```
deg
```

Format

An object of class `data.frame` with 18591 rows and 10 columns.

Examples

```
head(deg)
```

deseq_data *deseq_data*

Description

DEseq2 differential analysis result

Usage

```
deseq_data
```

Format

An object of class `data.frame` with 552 rows and 6 columns.

Examples

```
head(deseq_data)
```

double_enrich *draw enrichment bar plots for both up and down genes*

Description

draw enrichment bar plots for both up and down genes,for human only.

Usage

```
double_enrich(deg, n = 10, color = c("#2874C5", "#f87669"))
```

Arguments

deg	a data.frame contains at least two columns:"ENTREZID" and "change"
n	how many terms will you perform for up and down genes respectively
color	color for bar plot

Value

a list with kegg and go bar plot according to up and down genes enrichment result.

Author(s)

Xiaojie Sun

See Also

quick_enrich

Examples

```
double_enrich(deg)
```

draw_boxplot *draw boxplot for expression*

Description

draw boxplot for expression

Usage

```
draw_boxplot(
  exp,
  group_list,
  method = "kruskal.test",
  sort = TRUE,
  drop = FALSE,
  width = 0.5,
  pvalue_cutoff = 0.05,
  xlab = "Gene",
  ylab = "Expression",
  grouplab = "Group",
  p.label = FALSE,
  add_error_bar = FALSE,
 color = c("#2874C5", "#f87669", "#e6b707", "#868686", "#66C2A5", "#FC8D62", "#8DA0CB",
    "#E78AC3", "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  ...
)
```

Arguments

exp	A numeric matrix
group_list	A factor with duplicated character or factor
method	one of kruskal.test,aov,t.test and wilcox.test
sort	whether the boxplot will be sorted
drop	whether to discard insignificant values
width	width of boxplot and error bar
pvalue_cutoff	if drop = TRUE,genes with p-values below the threshold will be drawn
xlab	title of the x axis
ylab	title of the y axis
grouplab	title of group legend
p.label	whether to show p value in the plot
add_error_bar	whether to add error bar
color	color vector
...	other parameters from stat_compare_means

Value

a boxplot according to exp and grouped by group.

Author(s)

Xiaojie Sun

See Also

draw_heatmap;draw_volcano;draw_venn

Examples

```
draw_boxplot(t(iris[,1:4]),iris$Species)
exp <-  matrix(rnorm(60),nrow = 10)
colnames(exp) <- paste0("sample",1:6)
rownames(exp) <- paste0("gene",1:10)
exp[,4:6] = exp[,4:6] +10
exp[1:4,1:4]
group_list <- factor(rep(c("A","B"),each = 3))
draw_boxplot(exp,group_list)
draw_boxplot(exp,group_list,color = c("grey","red"))
```

---

draw_heatmap *draw a heatmap plot*

Description

print a heatmap plot for expression matrix and group by group_list praramter, exp will be scaled.

Usage

```
draw_heatmap(
  n,
  group_list,
  scale_before = FALSE,
  n_cutoff = 3,
  legend = FALSE,
  show_rownames = FALSE,
  annotation_legend = FALSE,
  split_column = FALSE,
  show_column_title = FALSE,
  color = (grDevices::colorRampPalette(c("#2fa1dd", "white", "#f87669")))(100),
  color_an = c("#2fa1dd", "#f87669", "#e6b707", "#868686", "#92C5DE", "#F4A582",
    "#66C2A5", "#FC8D62", "#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F", "#E5C494",
    "#B3B3B3"),
  scale = TRUE,
  main = NA,
  ...
)
```

Arguments

n	A numeric matrix
group_list	A factor with duplicated character or factor

scale_before	deprecated parameter
n_cutoff	3 by defalut , scale before plot and set a cutoff,usually 2 or 1.6
legend	logical,show legend or not
show_rownames	logical,show rownames or not
annotation_legend	logical,show annotation legend or not
split_column	split column by group_list
show_column_title	show column title or not
color	color for heatmap
color_an	color for column annotation
scale	logical,scale the matrix or not
main	the title of the plot
...	other parameters from pheatmap

Value

a heatmap plot according to exp and grouped by group.

Author(s)

Xiaojie Sun

See Also

draw_pca;draw_volcano;draw_venn

Examples

```
#example data
exp = matrix(abs(rnorm(60,sd = 16)),nrow = 10)
exp[,4:6] <- exp[,4:6]+20
colnames(exp) <- paste0("sample",1:6)
rownames(exp) <- paste0("gene",1:10)
exp[1:4,1:4]
group_list = factor(rep(c("A","B"),each = 3))
draw_heatmap(exp,group_list)
#use iris
n = t(iris[,1:4]);colnames(n) = 1:150
group_list = iris$Species
draw_heatmap(n,group_list)
draw_heatmap(n,group_list,color = colorRampPalette(c("green","black","red"))(100),
             color_an = c("red","blue","pink") )
```

draw_heatmap2 *draw heatmap plots*

Description

print heatmap plots for expression matrix and group by group_list paramter

Usage

```
draw_heatmap2(exp, group_list, deg, my_genes = NULL, heat_union = TRUE, ...)
```

Arguments

exp	A numeric matrix
group_list	A factor with duplicated character or factor
deg	a data.frame created by Differential analysis
my_genes	genes for pheatmap
heat_union	logical ,use union or intersect DEGs for heatmap
...	other parameters from draw_heatmap

Value

a heatmap plot according to exp and grouped by group.

Author(s)

Xiaojie Sun

See Also

draw_pca;draw_volcano;draw_venn

Examples

```
## Not run:
gse = "GSE474"
geo = geo_download(gse,destdir=tempdir())
geo$exp[1:4,1:4]
geo$exp=log2(geo$exp+1)
group_list=ifelse(stringr::str_detect(geo$pd$title,"MObese"),"MObese",
ifelse(stringr::str_detect(geo$pd$title,"NonObese"),"NonObese","Obese"))
group_list=factor(group_list,levels = c("NonObese","Obese","MObese"))
find_anno(geo$gpl)
ids <- AnnoProbe::idmap(geo$gpl,destdir = tempdir())
deg = multi_deg(geo$exp,group_list,ids,adjust = FALSE)
draw_heatmap2(geo$exp,group_list,deg)

## End(Not run)
```

draw_KM *draw_KM*

Description

draw KM-plot with two or more group

Usage

```
draw_KM(
  meta,
  group_list,
  time_col = "time",
  event_col = "event",
  legend.title = "Group",
  legend.labs = levels(group_list),
 color = c("#2874C5", "#f87669", "#e6b707", "#868686", "#92C5DE", "#F4A582", "#66C2A5",
   "#FC8D62", "#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  ...
)
```

Arguments

meta	survival data with time and event column
group_list	A factor with duplicated character or factor
time_col	colname of time
event_col	colname of event
legend.title	legend title
legend.labs	character vector specifying legend labels
color	color vector
...	other parameters from ggsurvplot

Value

a KM-plot

Author(s)

Xiaojie Sun

Examples

```
require("survival")
x = survival::lung
draw_KM(meta = x,
       group_list = x$sex,event_col = "status")
```

draw_pca *draw PCA plots*

Description

do PCA analysis and print a PCA plot

Usage

```
draw_pca(
  exp,
  group_list,
 color = c("#2874C5", "#f87669", "#e6b707", "#868686", "#92C5DE", "#F4A582", "#66C2A5",
   "#FC8D62", "#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  addEllipses = TRUE,
  style = "default",
  color.label = "Group",
  title = "",
  ...
)
```

Arguments

exp	A numeric matrix
group_list	A factor with duplicated character or factor
color	color vector
addEllipses	logical,add ellipses or not
style	plot style,"default","ggplot2"and "3D"
color.label	color legend label
title	plot title
...	other paramters from fviz_pca_ind

Value

a pca plot according to exp and grouped by group.

Author(s)

Xiaojie Sun

See Also

draw_heatmap;draw_volcano;draw_venn

Examples

```
draw_pca(t(iris[,1:4]),iris$Species)
draw_pca(t(iris[,1:4]),iris$Species,style = "ggplot2")
draw_pca(t(iris[,1:4]),iris$Species,style = "3D")
#change color
draw_pca(t(iris[,1:4]),iris$Species,color = c("#E78AC3", "#A6D854", "#FFD92F"))
```

`draw_tsne` *draw_tsne*

Description

draw tsne plot with annotation by ggplot2

Usage

```
draw_tsne(
  exp,
  group_list,
  perplexity = 30,
 color = c("#2874C5", "#f87669", "#e6b707", "#868686", "#92C5DE", "#F4A582", "#66C2A5",
   "#FC8D62", "#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  color.label = "group",
  addEllipses = TRUE
)
```

Arguments

`exp`	A numeric matrix
`group_list`	A factor with duplicated character or factor
`perplexity`	numeric; perplexity parameter for Rtsne
`color`	color vector
`color.label`	color legend label
`addEllipses`	logical,add ellipses or not

Value

a ggplot object

Author(s)

Xiaojie Sun

Examples

```
exp <-  matrix(rnorm(10000),nrow = 50)
colnames(exp) <- paste0("sample",1:200)
rownames(exp) <- paste0("gene",1:50)
exp[1:4,1:4]
exp[,1:100] = exp[,1:100]+10
group_list <- factor(rep(c("A","B"),each = 100))
draw_tsne(exp,group_list)
```

---

draw_venn *draw a venn plot*

Description

print a venn plot for deg result created by three packages

Usage

```
draw_venn(
  x,
  main,
 color = c("#2874C5", "#f87669", "#e6b707", "#868686", "#66C2A5", "#FC8D62", "#8DA0CB",
    "#E78AC3", "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  imagetype = "png",
  filename = NULL,
  lwd = 1,
  lty = 1,
  col = color[1:length(x)],
  fill = color[1:length(x)],
  cat.col = color[1:length(x)],
  cat.cex = 1,
  cat.dist = -0.15,
  rotation.degree = 0,
  main.cex = 1,
  cex = 1,
  alpha = 0.1,
  reverse = TRUE,
  ...
)
```

Arguments

x	a list for plot
main	Character giving the main title of the diagram
color	color vector
imagetype	Specification of the image format (e.g. tiff, png or svg)

filename	Filename for image output, or if NULL returns the grid object itself
lwd	width of the circle's circumference
lty	dash pattern of the circle's circumference
col	Colour of the circle's circumference
fill	Colour of the circle's area
cat.col	Colour of the category name
cat.cex	size of the category name
cat.dist	The distance (in npc units) of the category name from the edge of the circle (can be negative)
rotation.degree	Number of degrees to rotate the entire diagram
main.cex	Number giving the cex (font size) of the main title
cex	size of the area label
alpha	Alpha transparency of the circle's area
reverse	logical,reflect the three-set Venn diagram along its central vertical axis of symmetry. Use in combination with rotation to generate all possible set orders
...	other parameters from venn.diagram

Value

a venn plot according to x, y and.z named "name" paramter

Author(s)

Xiaojie Sun

See Also

draw_pca;draw_volcano;draw_heatmap

Examples

```
x = list(Deseq2=sample(1:100,30),edgeR = sample(1:100,30),limma = sample(1:100,30))
draw_venn(x,"test")
draw_venn(x,"test",color = c("darkgreen", "darkblue", "#B2182B"))
```

draw_volcano *draw a volcano plot*

Description

print a volcano plot for Differential analysis result in data.frame format.

Usage

```
draw_volcano(
  deg,
  lab = NA,
  xlab.package = TRUE,
  pvalue_cutoff = 0.05,
  logFC_cutoff = 1,
  pkg = 1,
  adjust = FALSE,
  symmetry = FALSE,
  color = c("#2874C5", "grey", "#f87669")
)
```

Arguments

deg	a data.frame created by Differential analysis
lab	label for x axis in volcano plot, if NA , x axis names by package
xlab.package	whether to use the package name as the x axis name
pvalue_cutoff	Cutoff value of pvalue,0.05 by default.
logFC_cutoff	Cutoff value of logFC,1 by default.
pkg	a integer ,means which Differential analysis packages you used,we support three packages by now, 1,2,3,4 respectively means "DESeq2","edgeR","limma(voom)","limma"
adjust	a logical value, would you like to use adjusted pvalue to draw this plot,FAlSE by default.
symmetry	a logical value ,would you like to get your plot symmetrical
color	color vector

Value

a volcano plot according to logFC and P.value(or adjust P.value)

Author(s)

Xiaojie Sun

See Also

draw_heatmap;draw_pca;draw_venn

Examples

```
head(deseq_data)
draw_volcano(deseq_data)
draw_volcano(deseq_data,pvalue_cutoff = 0.01,logFC_cutoff = 2)
draw_volcano(deseq_data,color = c("darkgreen", "darkgrey", "#B2182B"))
```

`draw_volcano2` *draw_volcano2*

Description

print one or more volcano plot for Differential analysis result in data.frame fomat.

Usage

```
draw_volcano2(deg, pkg = 4, lab, ...)
```

Arguments

deg	a data.frame created by Differential analysis
pkg	a integer ,means which Differential analysis packages you used,we support three packages by now, 1,2,3,4 respectively means "DESeq2","edgeR","limma(voom)","limma"
lab	label for x axis in volcano plot, if NA , x axis names by package
...	other parameters from draw_volcano

Value

one or more volcano plot

Author(s)

Xiaojie Sun

See Also

geo_download;draw_volcano;draw_venn

Examples

```
## Not run:
#two group
gse = "GSE42872"
geo = geo_download(gse,destdir=tempdir())
group_list = rep(c("A","B"),each = 3)
ids = AnnoProbe::idmap('GPL6244',destdir = tempdir())
deg = get_deg(geo$exp,group_list,ids)
draw_volcano2(deg)
#multigroup
```

```
gse = "GSE474"
geo = geo_download(gse,destdir=tempdir())
geo$exp[1:4,1:4]
geo$exp=log2(geo$exp+1)
group_list=ifelse(stringr::str_detect(geo$pd$title,"MObese"),"MObese",
ifelse(stringr::str_detect(geo$pd$title,"NonObese"),"NonObese","Obese"))
group_list=factor(group_list,levels = c("NonObese","Obese","MObese"))
find_anno(geo$gpl)
ids <- AnnoProbe::idmap(geo$gpl,destdir = tempdir())
deg = multi_deg(geo$exp,group_list,ids,adjust = FALSE)
draw_volcano2(deg)
draw_volcano2(deg,color = c("darkgreen","grey","darkred"))

## End(Not run)
```

---

dumd *count unique values in every columns for data.frame*

Description

in geo analysis,this function can help you simplify pdata, delete columns with unique values,which can't be used as group vector

Usage

```
dumd(x)
```

Arguments

x	A data.frame.

Value

The simple data.frame of columns unique values count in x

Examples

```
dumd(iris)
data(ToothGrowth)
x = ToothGrowth
dumd(ToothGrowth)
```

edges_to_nodes *edges_to_nodes*

Description

get nodes from edges

Usage

```
edges_to_nodes(edges)
```

Arguments

edges	data.frame

Value

nodes data.frame

Author(s)

Xiaojie Sun

See Also

interaction_to_edges

Examples

```
df = data.frame(a = c("gene1","gene2","gene3"),
b = c("d,f,a,b",
"c,e,g",
"a,b,d"))
edges = interaction_to_edges(df)
nodes = edges_to_nodes(edges)
```

exists_anno_list *exists_anno_list*

Description

AnnoProbe supported GPLs

Usage

```
exists_anno_list
```

Format

An object of class `character` of length 175.

Examples

```
exists_anno_list
```

`exprSet_hub1` *exprSet_hub1*

Description

An cpm expression matrix from TCGA,tumor samples only

Usage

```
exprSet_hub1
```

Format

An object of class `matrix` (inherits from `array`) with 8 rows and 177 columns.

Examples

```
exprSet_hub1[1:4,1:4]
```

`exp_boxplot` *exp_boxplot*

Description

draw box plot for a hub gene expression matrix

Usage

```
exp_boxplot(exp_hub, color = c("grey", "red"))
```

Arguments

`exp_hub`	an expression matrix for hubgenes
`color`	color for boxplot

Value

box plots list for all genes in the matrix

Author(s)

Xiaojie Sun

See Also

exp_surv;box_surv

Examples

```
k = exp_boxplot(log2(exp_hub1+1));k[[1]]
```

---

exp_hub1 *exp_hub1*

Description

An expression matrix from TCGA and Gtex

Usage

```
exp_hub1
```

Format

An object of class `matrix` (inherits from `array`) with 8 rows and 350 columns.

Examples

```
exp_hub1[1:4,1:4]
```

---

exp_surv *exp_surv*

Description

draw surv plot for a hub gene expression matrix for tumor samples

Usage

```
exp_surv(exprSet_hub, meta, cut.point = FALSE, color = c("#2874C5", "#f87669"))
```

Arguments

exprSet_hub	a tumor expression set for hubgenes
meta	meta data corresponds to expression set
cut.point	logical , use cut_point or not, if FALSE,use median by defult
color	color for boxplot

Value

survival plots list for all genes

Author(s)

Xiaojie Sun

See Also

exp_boxplot;box_surv;draw_venn

Examples

```
tmp = exp_surv(exprSet_hub1,meta1)
patchwork::wrap_plots(tmp)+patchwork::plot_layout(guides = "collect")
tmp2 = exp_surv(exprSet_hub1,meta1,cut.point = TRUE)
patchwork::wrap_plots(tmp2)+patchwork::plot_layout(guides = "collect")
```

---

find_anno *find annotation package or files*

Description

find gpl annotation package or files

Usage

```
find_anno(gpl, install = FALSE, update = FALSE)
```

Arguments

gpl	a gpl accession
install	whether to install and library the package
update	whether to update the package

Value

a list with deg data.frame, volcano plot and a list with DEGs.

Author(s)

Xiaojie Sun

See Also

geo_download

Examples

```
find_anno("GPL570")
```

genes *genes*

Description

some gene entriz ids

Usage

```
genes
```

Format

An object of class `character` of length 511.

Examples

```
genes
```

geo_download *geo_download*

Description

download gse data and get informations

Usage

```
geo_download(
  gse,
  by_annopbrobe = TRUE,
  simpd = TRUE,
  colon_remove = FALSE,
  destdir = getwd()
)
```

Arguments

gse	gse assession number
by_annopbrobe	getGEO or geoChina
simpd	get simplified pdata,drop out columns with all same values
colon_remove	whether to remove duplicated columns with colons
destdir	The destination directory for data downloads.

Value

a list with exp,pd and gpl

Author(s)

Xiaojie Sun

See Also

find_anno

Examples

```
## Not run:
gse = "GSE42872"
a = geo_download(gse,destdir=tempdir())

## End(Not run)
```

---

get_cgs *get_cgs*

Description

extract DEGs from deg data.frame

Usage

```
get_cgs(deg)
```

Arguments

deg	a data.frame created by Differential analysis

Value

a list with upgenes,downgenes,diffgenes.

Author(s)

Xiaojie Sun

See Also

geo_download;draw_volcano;draw_venn

Examples

```
## Not run:
#two group
gse = "GSE42872"
geo = geo_download(gse,destdir=tempdir())
group_list = rep(c("A","B"),each = 3)
ids = AnnoProbe::idmap('GPL6244',destdir=tempdir())
deg = get_deg(geo$exp,group_list,ids)
cgs = get_cgs(deg)
#mutigroup
gse = "GSE474"
geo = geo_download(gse,destdir=tempdir())
geo$exp[1:4,1:4]
geo$exp=log2(geo$exp+1)
group_list=ifelse(stringr::str_detect(geo$pd$title,"MObese"),"MObese",
ifelse(stringr::str_detect(geo$pd$title,"NonObese"),"NonObese","Obese"))
group_list=factor(group_list,levels = c("NonObese","Obese","MObese"))
find_anno(geo$gpl)
ids = AnnoProbe::idmap(geo$gpl,destdir = tempdir())
deg = multi_deg(geo$exp,group_list,ids,adjust = FALSE)
cgs = get_cgs(deg)

## End(Not run)
```

---

get_deg *get_deg*

Description

do differential analysis according to expression set and group information

Usage

```
get_deg(
  exp,
  group_list,
  ids,
  logFC_cutoff = 1,
  pvalue_cutoff = 0.05,
  adjust = FALSE,
  entriz = TRUE
)
```

Arguments

exp	A numeric matrix
group_list	A factor with duplicated character or factor
ids	a data.frame with 2 columns,including probe_id and symbol

logFC_cutoff	Cutoff value of logFC,1 by default.
pvalue_cutoff	Cutoff value of pvalue,0.05 by default.
adjust	a logical value, would you like to use adjusted pvalue to draw this plot,FAlSE by default.
entriz	whether convert symbols to entriz ids

Value

a deg data.frame with 10 columns

Author(s)

Xiaojie Sun

See Also

multi_deg;get_deg_all

Examples

```
## Not run: gse = "GSE42872"
geo = geo_download(gse,destdir=tempdir())
Group = rep(c("control","treat"),each = 3)
Group = factor(Group)
find_anno(geo$gpl)
ids <- AnnoProbe::idmap(geo$gpl,destdir = tempdir())
deg = get_deg(geo$exp,Group,ids)
head(deg)

## End(Not run)
```

---

get_deg_all *get_deg_all*

Description

do diffiencial analysis according to exprission set and group information

Usage

```
get_deg_all(
  exp,
  group_list,
  ids,
  pkg = 4,
  my_genes = NULL,
  show_rownames = FALSE,
  entriz = TRUE,
```

```
  adjust = FALSE,
  logFC_cutoff = 1,
  pvalue_cutoff = 0.05,
  n_cutoff = 2,
  cluster_cols = TRUE,
  annotation_legend = FALSE,
  lab = NA,
  symmetry = FALSE,
  ...
)
```

Arguments

exp	A numeric matrix
group_list	A factor with duplicated character or factor
ids	a data.frame with 2 columns,including probe_id and symbol
pkg	a integer ,means which Differential analysis packages you used,we support three packages by now, 1,2,3,4 respectively means "DESeq2","edgeR","limma(voom)","limma"
my_genes	genes for pheatmap
show_rownames	logical,show rownames or not
entriz	logical , if TRUE ,convert symbol to entriz id.
adjust	a logical value, would you like to use adjusted pvalue to draw this plot,FAlSE by default.
logFC_cutoff	Cutoff value of logFC,1 by default.
pvalue_cutoff	Cutoff value of pvalue,0.05 by default.
n_cutoff	3 by defalut , scale before plot and set a cutoff,usually 2 or 1.6
cluster_cols	boolean values determining if columns should be clustered or `hclust` object.
annotation_legend	logical,show annotation legend or not
lab	label for x axis in volcano plot, if NA , x axis names by package
symmetry	a logical value ,would you like to get your plot symmetrical
...	other parameters from get_deg

Value

a list with deg data.frame, volcano plot ,pca plot ,heatmap and a list with DEGs.

Author(s)

Xiaojie Sun

See Also

get_deg;multi_deg_all

Examples

```
## Not run:
gse = "GSE42872"
geo = geo_download(gse,destdir=tempdir())
group_list = rep(c("A","B"),each = 3)
group_list = factor(group_list)
find_anno(geo$gpl)
ids <- AnnoProbe::idmap(geo$gpl,destdir = tempdir())
dcp = get_deg_all(geo$exp,group_list,ids)
head(dcp$deg)
dcp$plots

## End(Not run)
```

---

ggheat *ggheat*

Description

draw heatmap plot with annotation by ggplot2

Usage

```
ggheat(
  dat,
  group,
  cluster = FALSE,
  color = c("#2874C5", "white", "#f87669"),
 legend_color = c("#2874C5", "#f87669", "#e6b707", "#868686", "#66C2A5", "#FC8D62",
    "#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  show_rownames = TRUE,
  show_colnames = TRUE,
  cluster_rows = FALSE,
  cluster_cols = FALSE,
  groupname = "group",
  expname = "exp",
  fill_mid = TRUE
)
```

Arguments

dat	expression matrix for plot
group	group for expression colnames
cluster	logical,cluster in both rows and column or not, default F,now replaced by cluster_rows and cluster_cols.
color	color for heatmap

legend_color	color for legend
show_rownames	logical,show rownames in plot or not, default T
show_colnames	logical,show colnames in plot or not, default T
cluster_rows	logical, if rows (on the plot) should be clustered, default F
cluster_cols	logical, if column (on the plot) should be clustered, default F
groupname	name of group legend
expname	name of exp legend
fill_mid	use median value as geom_tile fill midpoint

Value

a ggplot object

Author(s)

Xiaojie Sun

Examples

```
exp_dat = matrix(sample(100:1000,40),ncol = 4)
exp_dat[1:(nrow(exp_dat)/2),] =  exp_dat[1:(nrow(exp_dat)/2),]-1000
rownames(exp_dat) = paste0("sample",1:nrow(exp_dat))
colnames(exp_dat) = paste0("gene",1:ncol(exp_dat))
group = rep(c("A","B"),each = nrow(exp_dat)/2)
group = factor(group,levels = c("A","B"))
ggheat(exp_dat,group)
ggheat(exp_dat,group,cluster_rows = TRUE)
ggheat(exp_dat,group,cluster_rows = TRUE,show_rownames = FALSE,
       show_colnames = FALSE,groupname = "risk",expname = "expression")
```

---

hypertest *hypertest*

Description

make hypertest for given lncRNA and mRNA common miRNAs

Usage

```
hypertest(lnc, pc, deMIR = NULL, lnctarget, pctarget)
```

Arguments

lnc	lncRNA names
pc	mRNA names
deMIR	miRNA names , default NULL
lnctarget	a data.frame with two column,lncRNA in the first column ,miRNA in the second column
pctarget	a data.frame with two column,mRNA in the first column ,miRNA in the second column

Value

a data.frame with hypertest result

Author(s)

Xiaojie Sun

See Also

plcortest

Examples

```
# to update
```

---

interaction_to_edges *interaction_to_edges*

Description

split interactions by sep paramter,return edges data.frame

Usage

```
interaction_to_edges(df, a = 1, b = 2, sep = ",")
```

Arguments

df	interactions data.frame
a	column to replicate
b	column to split
sep	a character string to separate b column

Value

a new data.frame with two column ,one interaction by one rows

Author(s)

Xiaojie Sun

See Also

edges_to_nodes

Examples

```
df = data.frame(a = c("gene1","gene2","gene3"),
b = c("d,f,a,b",
"c,e,g",
"a,b,d"))
interaction_to_edges(df)
```

---

intersect_all *intersect_all*

Description

calculate intersect set for two or more elements

Usage

```
intersect_all(...)
```

Arguments

...	some vectors or a list with some vectors

Value

vector

Author(s)

Xiaojie Sun

See Also

union_all

Examples

```
x1 = letters[1:4]
x2 = letters[3:6]
x3 = letters[3:4]
re =intersect_all(x1,x2,x3)
re2 = intersect_all(list(x1,x2,x3))
re3 = union_all(x1,x2,x3)
```

lnc_anno *lnc_anno*

Description

annotation for TCGA expression matrix(lncRNA),form genecode v22 gtf file.

Usage

```
lnc_anno
```

Format

An object of class `data.frame` with 14826 rows and 3 columns.

Examples

```
head(lnc_anno)
```

lnc_annov23 *lnc_annov23*

Description

annotation for TCGA and gtex expression matrix(lncRNA),form genecode v23 gtf file.

Usage

```
lnc_annov23
```

Format

An object of class `data.frame` with 14852 rows and 3 columns.

Examples

```
head(lnc_annov23)
```

make_tcga_group *make_tcga_group*

Description

make tcga group for given tcga expression matrix

Usage

```
make_tcga_group(exp)
```

Arguments

exp	TCGA or TCGA_Gtex expression set from gdc or xena

Value

a group factor with normal and tumor ,correspond to colnames for expression matrix

Author(s)

Xiaojie Sun

See Also

sam_filter;match_exp_cl

Examples

```
k = make_tcga_group(exp_hub1);table(k)
```

match_exp_cl *match_exp_cl*

Description

match exp and clinical data from TCGA

Usage

```
match_exp_cl(exp, cl, id_column = "id", sample_centric = TRUE)
```

Arguments

exp	TCGA expression set
cl	TCGA clinical data.frame
id_column	which column contains patient ids, column number or colnmn name.
sample_centric	logical,deault T,keep all samples from the same patients.if FALSE,keep only one tumor sample for one patient.

Value

a transformed clinical data.frame with sample ids.

Author(s)

Xiaojie Sun

See Also

make_tcga_group;sam_filter

Examples

```
a = match_exp_cl(exp_hub1,meta1[,2:4],"X_PATIENT")
exp_matched = a[[1]]
cl_matched = a[[2]]
b = match_exp_cl(exp_hub1,meta1[,2:4],"X_PATIENT",sample_centric = FALSE)
exp_matched = b[[1]]
cl_matched = b[[2]]
```

---

meta1 *meta1*

Description

clinical messages for some TCGA patients,correspond to exprSet_hub1

Usage

```
meta1
```

Format

An object of class `data.frame` with 177 rows and 4 columns.

Examples

```
head(meta1)
```

mRNA_anno *mRNA_anno*

Description

annotation for TCGA and gtex expression matrix(mRNA),form genecode v22 gtf file.

Usage

```
mRNA_anno
```

Format

An object of class `data.frame` with 19814 rows and 3 columns.

Examples

```
head(mRNA_anno)
```

mRNA_annov23 *mRNA_annov23*

Description

annotation for TCGA and gtex expression matrix(mRNA),form genecode v23 gtf file.

Usage

```
mRNA_annov23
```

Format

An object of class `data.frame` with 19797 rows and 3 columns.

Examples

```
head(mRNA_annov23)
```

multi_deg *multi_deg*

Description

do diffiential analysis according to expression set and group information

Usage

```
multi_deg(
  exp,
  group_list,
  ids,
  logFC_cutoff = 1,
  pvalue_cutoff = 0.05,
  adjust = FALSE,
  entriz = TRUE
)
```

Arguments

exp	A numeric matrix
group_list	A factor with duplicated character or factor
ids	a data.frame with 2 columns,including probe_id and symbol
logFC_cutoff	Cutoff value of logFC,1 by default.
pvalue_cutoff	Cutoff value of pvalue,0.05 by default.
adjust	a logical value, would you like to use adjusted pvalue to draw this plot,FAlSE by default.
entriz	whether convert symbols to entriz ids

Value

a deg data.frame with 10 columns

Author(s)

Xiaojie Sun

See Also

get_deg;multi_deg_all

Examples

```
## Not run:
gse = "GSE474"
geo = geo_download(gse,destdir=tempdir())
geo$exp[1:4,1:4]
geo$exp=log2(geo$exp+1)
group_list=ifelse(stringr::str_detect(geo$pd$title,"MObese"),
"MObese",ifelse(stringr::str_detect(geo$pd$title,"NonObese"),
"NonObese","Obese"))
group_list=factor(group_list,levels = c("NonObese","Obese","MObese"))
find_anno(geo$gpl)
ids <- AnnoProbe::idmap(geo$gpl,destdir = tempdir())
deg = multi_deg(geo$exp,group_list,ids,adjust = FALSE)
names(deg)
head(deg[[1]])
head(deg[[2]])
head(deg[[3]])

## End(Not run)
```

`multi_deg_all` *multi_deg_all*

Description

do diffiencial analysis according to exprission set and group information

Usage

```
multi_deg_all(
  exp,
  group_list,
  ids,
  pkg = 4,
  symmetry = TRUE,
  my_genes = NULL,
  show_rownames = FALSE,
  cluster_cols = TRUE,
  color_volcano = c("#2874C5", "grey", "#f87669"),
  ...
)
```

Arguments

`exp`	A numeric matrix
`group_list`	A factor with duplicated character or factor
`ids`	a data.frame with 2 columns,including probe_id and symbol

pkg	a integer ,means which Differential analysis packages you used,we support three packages by now, 1,2,3,4 respectively means "DESeq2","edgeR","limma(voom)","limma"
symmetry	a logical value ,would you like to get your plot symmetrical
my_genes	genes for pheatmap
show_rownames	boolean specifying if column names are be shown.
cluster_cols	boolean values determining if columns should be clustered or hclust object.
color_volcano	color for volcano
...	other parameters from multi_deg

Value

a list with deg data.frame, volcano plot and a list with DEGs.

Author(s)

Xiaojie Sun

See Also

geo_download;draw_volcano;draw_venn

Examples

```
## Not run:
gse = "GSE474"
geo = geo_download(gse,destdir=tempdir())
geo$exp[1:4,1:4]
geo$exp=log2(geo$exp+1)
group_list=ifelse(stringr::str_detect(geo$pd$title,"MObese"),"MObese",
ifelse(stringr::str_detect(geo$pd$title,"NonObese"),"NonObese","Obese"))
group_list=factor(group_list,levels = c("NonObese","Obese","MObese"))
find_anno(geo$gpl)
ids = AnnoProbe::idmap(geo$gpl,destdir = tempdir())
dcp = multi_deg_all(geo$exp,
group_list,ids,adjust = FALSE)
dcp[[3]]

## End(Not run)
```

---

pkg_all *pkg_all*

Description

bioconductor annotation packages for GPLs

Usage

```
pkg_all
```

Format

An object of class `data.frame` with 85 rows and 3 columns.

Examples

```
head(pkg_all)
```

`plcortest` *plcortest*

Description

make cor.test for given lncRNA and mRNA

Usage

```
plcortest(lnc_exp, mRNA_exp, cor_cutoff = 0)
```

Arguments

`lnc_exp`	lncRNA expression set
`mRNA_exp`	mRNA expression set which nrow equal to lncRNA_exp
`cor_cutoff`	cor estimate cut_off, default 0

Value

a list with cor.test result,names are lncRNAs, element are mRNAs

Author(s)

Xiaojie Sun

See Also

`hypertest`

Examples

```
# to update
```

point_cut *point_cut*

Description

calculate cut point for multiple genes

Usage

```
point_cut(exprSet_hub, meta)
```

Arguments

exprSet_hub	a tumor expression set for hubgenes
meta	meta data corresponds to expression set

Value

a vector with cutpoint for genes

Author(s)

Xiaojie Sun

See Also

surv_KM;surv_cox

Examples

```
point_cut(exprSet_hub1,meta1)
```

quick_enrich *quick_enrich*

Description

do diffiencial analysis according to exprission set and group information,for human only

Usage

```
quick_enrich(genes, kkgo_file = "kkgo_file.Rdata", destdir = getwd())
```

Arguments

genes	a gene symbol or entrizid vector
kkgo_file	Rdata filename for kegg and go result
destdir	destdir to save kkgofile

Value

enrichment results and dotplots

Author(s)

Xiaojie Sun

See Also

double_enrich

Examples

```
head(genes)
g = quick_enrich(genes,destdir = tempdir())
names(g)
g[[1]][1:4,1:4]
g[[3]]
g[[4]]
```

---

risk_plot *risk_plot*

Description

draw risk plot

Usage

```
risk_plot(
  exprSet_hub,
  meta,
  riskscore,
  cut.point = FALSE,
  color = c("#2fa1dd", "#f87669")
)
```

Arguments

exprSet_hub	a tumor expression set for hubgenes
meta	meta data corresponds to expression set
riskscore	a numeric vector of riskscore
cut.point	logical , use cut_point or not, if FALSE,use median by defult
color	color for boxplot

Value

risk plot

Author(s)

Xiaojie Sun

See Also

exp_boxplot;box_surv;draw_venn

Examples

```
risk_plot(exprSet_hub1,meta1,riskscore = rnorm(nrow(meta1)))
```

---

sam_filter *sam_filter*

Description

drop duplicated samples from the same patients

Usage

```
sam_filter(exp)
```

Arguments

exp	TCGA or TCGA_Gtex expression set from gdc or xena

Value

a transformed expression set without duplicated samples

Author(s)

Xiaojie Sun

See Also

make_tcga_group;match_exp_cl

Examples

```
cod[1:4,1:4]
dim(cod)
cod2 = sam_filter(cod)
dim(cod2)
g = make_tcga_group(cod);table(g)
library(stringr)
table(!duplicated(str_sub(colnames(cod[,g=="tumor"]),1,12)))
```

---

surv_cox *surv_cox*

Description

calculate cox p values and HR for genes

Usage

```
surv_cox(
  exprSet_hub,
  meta,
  cut.point = FALSE,
  pvalue_cutoff = 0.05,
  HRkeep = "all",
  continuous = FALSE,
  min_gn = 0.1
)
```

Arguments

exprSet_hub	a tumor expression set for hubgenes
meta	meta data corresponds to expression set
cut.point	logical , use cut_point or not, if FALSE,use median by defult
pvalue_cutoff	p value cut off ,0.05 by defult
HRkeep	one of "all","protect"or"risk"
continuous	logical, gene expression or gene expression group
min_gn	Depending on the expression of a gene, there may be a large difference in the number of samples between the two groups, and if a smaller group of samples is less than 10 percent (default) of all, the gene will be discarded

Value

a matrix with gene names ,cox p value and HR

Author(s)

Xiaojie Sun

See Also

point_cut;surv_KM

Examples

```
surv_cox(exprSet_hub1,meta1)
surv_cox(exprSet_hub1,meta1,cut.point = TRUE,continuous = TRUE)
surv_cox(exprSet_hub1,meta1,cut.point = TRUE,continuous = TRUE,pvalue_cutoff = 1)
```

---

surv_KM *surv_KM*

Description

calculate log_rank test p values for genes

Usage

```
surv_KM(
  exprSet_hub,
  meta,
  cut.point = FALSE,
  pvalue_cutoff = 0.05,
  min_gn = 0.1
)
```

Arguments

exprSet_hub	a tumor expression set for hubgenes
meta	meta data corresponds to expression set
cut.point	logical , use cut_point or not, if FALSE,use median by defult
pvalue_cutoff	p value cut off ,0.05 by defult
min_gn	Depending on the expression of a gene, there may be a large difference in the number of samples between the two groups, and if a smaller group of samples is less than 10 percent (default) of all, the gene will be discarded

Value

a vector with gene names and log_rank p value

Author(s)

Xiaojie Sun

See Also

point_cut;surv_cox

Examples

```
surv_KM(exprSet_hub1,meta1)
surv_KM(exprSet_hub1,meta1,pvalue_cutoff = 1)
surv_KM(exprSet_hub1,meta1,cut.point = TRUE)
```

---

trans_array *trans_array*

Description

transform rownames for microarray or rnaseq expression matrix

Usage

```
trans_array(exp, ids, from = "probe_id", to = "symbol")
```

Arguments

exp	microarray expression matrix with probe_id as rownames
ids	data.frame with original rownames and new rownames
from	colname for original rownames
to	colname for new rownames

Value

a transformed expression set with new rownames

Author(s)

Xiaojie Sun

See Also

trans_exp

Examples

```
exp = matrix(1:50,nrow = 10)
rownames(exp) = paste0("g",1:10)
ids = data.frame(probe_id = paste0("g",1:10),
                 symbol = paste0("G",c(1:9,9)))
trans_array(exp,ids)
```

trans_exp *trans_exp*

Description

transform rownames of TCGA or TCGA_Gtex expression set from gdc or xena,from ensembl id to gene symbol

Usage

```
trans_exp(exp, mrna_only = FALSE, lncrna_only = FALSE, gtex = FALSE)
```

Arguments

exp	TCGA or TCGA_Gtex expression set from gdc or xena
mrna_only	only keep mrna rows in result
lncrna_only	only keep lncrna rows in result
gtex	logical,whether including Gtex data

Value

a transformed expression set with symbol

Author(s)

Xiaojie Sun

See Also

trans_array

Examples

```
exp = matrix(rnorm(1000),ncol = 10)
rownames(exp) = sample(mRNA_annov23$gene_id,100)
colnames(exp) = c(paste0("TCGA",1:5),paste0("GTEX",1:5))
k  = trans_exp(exp)
```

trans_exp_new *trans_exp_new*

Description

transform rownames of expression set from "ensembl" to"symbol",according to the new information from ensembl database.

Usage

```
trans_exp_new(exp, mrna_only = FALSE, lncrna_only = FALSE)
```

Arguments

exp	expression set with ensembl as rownames
mrna_only	only keep mrna rows in result
lncrna_only	only keep lncrna rows in result

Value

a transformed expression set with symbol

Author(s)

Xiaojie Sun

See Also

trans_exp

Examples

```
exp = matrix(rnorm(1000),ncol = 10)
rownames(exp) = sample(mRNA_annov23$gene_id,100)
colnames(exp) = c(paste0("TCGA",1:5),paste0("GTEX",1:5))
k  = trans_exp_new(exp)
```

t_choose *t_choose*

Description

choose differential expressed genes by simple t.test

Usage

```
t_choose(
  genes,
  exp,
  group_list,
  up_only = FALSE,
  down_only = FALSE,
  pvalue_cutoff = 0.05
)
```

Arguments

genes	a vector with some genes
exp	A numeric matrix
group_list	A factor with duplicated character or factor
up_only	keep up genes in the result only
down_only	keep down genes in the result only
pvalue_cutoff	p value cut off ,0.05 by defult

Value

a vector with differential expressed genes

Author(s)

Xiaojie Sun

Examples

```
exp = matrix(rnorm(1000),ncol = 10)
rownames(exp) = sample(mRNA_annov23$gene_id,100)
colnames(exp) = c(paste0("TCGA",1:5),paste0("GTEX",1:5))
exp2  = trans_exp(exp)
exp2[,1:5] = exp2[,1:5]+10
group_list = rep(c("A","B"),each = 5)
genes = sample(rownames(exp2),3)
t_choose(genes,exp2,group_list)
```

union_all *union_all*

Description

calculate union set for two or more elements

Usage

```
union_all(...)
```

Arguments

...	some vectors or a list with some vectors

Value

vector

Author(s)

Xiaojie Sun

See Also

intersect_all

Examples

```
x1 = letters[1:4]
x2 = letters[3:6]
x3 = letters[3:4]
re =intersect_all(x1,x2,x3)
re2 = intersect_all(list(x1,x2,x3))
re3 = union_all(x1,x2,x3)
```

Index