Package: mastR (via r-universe)

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Title Markers Automated Screening Tool in R

Version 1.14.0

Description mastR is an R package designed for automated screening of signatures of interest for specific research questions. The package is developed for generating refined lists of signature genes from multiple group comparisons based on the results from edgeR and limma differential expression (DE) analysis workflow. It also takes into account the background noise of tissue-specificity, which is often ignored by other marker generation tools. This package is particularly useful for the identification of group markers in various biological and medical applications, including cancer research and developmental biology.

biocViews Software, GeneExpression, Transcriptomics, DifferentialExpression, Visualization

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Depends R (>= 4.3.0)

Suggests BiocManager, BiocStyle, clusterProfiler, ComplexHeatmap, depmap, enrichplot, ggrepel, ggvenn, Glimma, gridExtra, jsonlite, knitr, rmarkdown, RobustRankAggreg, rvest, scuttle, singscore, splatter, testthat (>= 3.0.0), UpSetR

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Imports AnnotationDbi, Biobase, dplyr, edgeR, ggplot2, ggpubr, graphics, grDevices, GSEABase, limma, Matrix, methods, msigdb, org.Hs.eg.db, patchwork, SeuratObject (> 5.0.0), SingleCellExperiment, stats, SummarizedExperiment, tidyr, utils

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'get_panglao_sig.R' 'gls2gsc-methods.R' 'gsc_plot.R'
'list_panglao_organs.R' 'list_panglao_types.R'
'mastR-package.R' 'merge_markers.R' 'pca_matrix_plot-methods.R'
'pseudo_samples-methods.R' 'remove_bg_exp-methods.R'
'sig_boxplot-methods.R' 'sig_gseaplot-methods.R'
'sig_heatmap-methods.R' 'sig_rankdensity_plot-methods.R'
'sig_scatter_plot-methods.R' 'subset_sig_by_step.R'

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`ccle_2_wide` *Convert CCLE data from long data to wide data.*

Description

Convert CCLE data downloaded by `depmap::depmap_TPM()` from long data into wide matrix, with row names are gene names and column names are depmap IDs.

Usage

```
ccle_2_wide(ccle)
```

Arguments

`ccle`	CCLE data downloaded by `depmap::depmap_TPM()`

Value

a matrix

Examples

```
data("ccle_crc_5")
ccle <- data.frame(
  gene_name = rownames(ccle_crc_5),
  ccle_crc_5$counts
) |>
  tidyr::pivot_longer(
    -gene_name,
    names_to = "depmap_id",
    values_to = "rna_expression"
  )
ccle_wide <- ccle_2_wide(ccle)
```

ccle_crc_5 *RNA-seq TPM data of 5 CRC cell line samples from CCLE.*

Description

A test DGEList object with RNA-seq RSEM quantified TPM data of 5 CRC cell line samples from CCLE `depmap::depmap_TPM()`.

Usage

```
data(ccle_crc_5)
```

Format

A DGEList of 19177 genes * 5 samples.

Value

DGEList

Source

`depmap::depmap_TPM()`

de_analysis *DE analysis pipeline*

Description

Standard DE analysis by using edgeR and limma::voom pipeline

Usage

```
de_analysis(
  dge,
  group_col,
  target_group,
  normalize = TRUE,
  group = FALSE,
  filter = c(10, 10),
  plot = FALSE,
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  slot = "counts",
```

```
  batch = NULL,
  summary = TRUE,
  ...
)
```

Arguments

dge	DGEList object for DE analysis, including expr and samples info
group_col	character, column name of coldata to specify the DE comparisons
target_group	pattern, specify the group of interest, e.g. NK
normalize	logical, if the expr in data is raw counts needs to be normalized
group	logical, TRUE to separate samples into only 2 groups: 'target_group" and 'Others'; FALSE to set each level as a group
filter	a vector of 2 numbers, filter condition to remove low expression genes, the 1st for min.counts (if normalize = TRUE) or CPM/TPM (if normalize = FALSE), the 2nd for samples size 'large.n'
plot	logical, if to make plots to show QC before and after filtration
lfc	num, cutoff of logFC for DE analysis
p	num, cutoff of p value for DE analysis and permutation test if feature_selection = "rankproduct"
markers	vector, a vector of gene names, listed the gene symbols to be kept anyway after filtration. Default 'NULL' means no special genes need to be kept.
gene_id	character, specify the gene ID target_group of rownames of expression data when markers is not NULL, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'
slot	character, specify which slot to use for DGEList, default 'counts'
batch	vector of character, column name(s) of coldata to be treated as batch effect factor, default NULL
summary	logical, if to show the summary of DE analysis
...	omitted

Value

MArrayLM object generated by `limma::treat()`

Examples

```
data("im_data_6")
dge <- edgeR::DGEList(
  counts = Biobase::exprs(im_data_6),
  samples = Biobase::pData(im_data_6)
)
de_analysis(dge, group_col = "celltype.ch1", target_group = "NK")
```

DEGs_Group *return DEGs UP and DOWN list based on intersection or union of comparisons*

Description

return DEGs UP and DOWN list based on intersection or union of comparisons

Usage

```
DEGs_Group(
  tfit,
  lfc = NULL,
  p = 0.05,
  assemble = "intersect",
  Rank = "adj.P.Val",
  keep.top = NULL,
  keep.group = NULL,
  ...
)
```

Arguments

tfit	MArrayLM object generated by limma::treat()
lfc	num, cutoff of logFC for DE analysis
p	num, cutoff of p value for DE analysis
assemble	'intersect' or 'union', whether to select intersected or union genes of different comparisons, default 'intersect'
Rank	character, the variable for ranking DEGs, can be 'logFC', 'adj.P.Val'..., default 'adj.P.Val'
keep.top	NULL or num, whether to keep top n DEGs of specific comparison
keep.group	NULL or pattern, specify the top DEGs of which comparison or group to be kept
...	omitted

Value

A list of "UP" and "DOWN" genes

DEGs_RP *return DEGs UP and DOWN list based on Rank Product*

Description

return DEGs UP and DOWN list based on Rank Product

Usage

```
DEGs_RP(
  tfit,
  lfc = NULL,
  p = 0.05,
  assemble = "intersect",
  Rank = "adj.P.Val",
  nperm = 1e+05,
  thres = 0.05,
  keep.top = NULL,
  keep.group = NULL,
  ...
)
```

Arguments

tfit	MArrayLM object generated by limma::treat()
lfc	num, cutoff of logFC for DE analysis
p	num, cutoff of p value for DE analysis
assemble	'intersect' or 'union', whether to select intersected or union genes of different comparisons, default 'intersect'
Rank	character, the variable for ranking DEGs, can be 'logFC', 'adj.P.Val'..., default 'adj.P.Val'
nperm	num, permutation runs of simulating the distribution
thres	num, cutoff for rank product permutation test if feature_selection = "rankproduct", default 0.05
keep.top	NULL or num, whether to keep top n DEGs of specific comparison
keep.group	NULL or pattern, specify the top DEGs of which comparison or group to be kept
...	omitted

Value

A list of "UP" and "DOWN" genes

`filter_subset_sig` *Filter specific cell type signature genes against other subsets.*

Description

Specify the signature of the subset matched 'target_group' against other subsets, either "union", "intersect" or "RRA" can be specified when input is a list of datasets to integrate the signatures into one.

Usage

```
filter_subset_sig(
  data,
  group_col,
  target_group,
  markers = NULL,
  normalize = TRUE,
  dir = "UP",
  gene_id = "SYMBOL",
  feature_selection = c("auto", "rankproduct", "none"),
  comb = union,
  filter = c(10, 10),
  s_thres = 0.05,
  ...
)

## S4 method for signature 'list'
filter_subset_sig(
  data,
  group_col,
  target_group,
  markers = NULL,
  normalize = TRUE,
  dir = "UP",
  gene_id = "SYMBOL",
  feature_selection = c("auto", "rankproduct", "none"),
  comb = union,
  filter = c(10, 10),
  s_thres = 0.05,
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'DGEList'
filter_subset_sig(
  data,
```

```
  group_col,
  target_group,
  markers = NULL,
  normalize = TRUE,
  dir = "UP",
  gene_id = "SYMBOL",
  feature_selection = c("auto", "rankproduct", "none"),
  comb = union,
  filter = c(10, 10),
  s_thres = 0.05,
  ...
)

## S4 method for signature 'ANY'
filter_subset_sig(
  data,
  group_col,
  target_group,
  markers = NULL,
  normalize = TRUE,
  dir = "UP",
  gene_id = "SYMBOL",
  feature_selection = c("auto", "rankproduct", "none"),
  comb = union,
  filter = c(10, 10),
  s_thres = 0.05,
  ...
)
```

Arguments

data	An expression data or a list of expression data objects
group_col	vector or character, specify the group factor or column name of coldata for DE comparisons
target_group	pattern, specify the group of interest, e.g. NK
markers	vector, a vector of gene names, listed the gene symbols to be kept anyway after filtration. Default 'NULL' means no special genes need to be kept.
normalize	logical, if the expr in data is raw counts needs to be normalized
dir	character, could be 'UP' or 'DOWN' to use only up- or down-expressed genes
gene_id	character, specify the gene ID target_group of rownames of expression data when markers is not NULL, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'
feature_selection	one of "auto" (default), "rankproduct" or "none", choose if to use rank product or not to select DEGs from multiple comparisons of DE analysis, 'auto' uses 'rankproduct' but change to 'none' if final genes < 5 for both UP and DOWN

comb	'RRA' or Fun for combining sigs from multiple datasets, keep all passing genes or only intersected genes, could be union or intersect or setdiff or customized Fun, or could be 'RRA' to use Robust Rank Aggregation method for integrating multi-lists of sigs, default 'union'
filter	(list of) vector of 2 numbers, filter condition to remove low expression genes, the 1st for min.counts (if normalize = TRUE) or CPM/TPM (if normalize = FALSE), the 2nd for samples size 'large.n'
s_thres	num, threshold of score if comb = 'RRA'
...	other params for get_degs()
slot	character, specify which slot to use only for DGEList, sce or seurat object, optional, default 'counts'
batch	vector of character, column name(s) of coldata to be treated as batch effect factor, default NULL

Value

a vector of gene symbols

Examples

```
data("im_data_6", "nk_markers")
sigs <- filter_subset_sig(im_data_6, "celltype:ch1", "NK",
  markers = nk_markers$HGNC_Symbol,
  gene_id = "ENSEMBL"
)
```

---

get_de_table *Get DE analysis result table(s) with statistics*

Description

This function uses edgeR and limma to get DE analysis results lists for multiple comparisons. Filter out low expressed genes and obtain DE statistics by using limma::voom and limma::treat, and also create an object proc_data to store processed data.

Usage

```
get_de_table(data, group_col, target_group, slot = "counts", ...)

## S4 method for signature 'DGEList,character,character'
get_de_table(data, group_col, target_group, slot = "counts", ...)

## S4 method for signature 'matrix,vector,character'
get_de_table(data, group_col, target_group, slot = "counts", ...)
```

```
## S4 method for signature 'Matrix,vector,character'
get_de_table(data, group_col, target_group, slot = "counts", ...)

## S4 method for signature 'ExpressionSet,character,character'
get_de_table(data, group_col, target_group, slot = "counts", ...)

## S4 method for signature 'SummarizedExperiment,character,character'
get_de_table(data, group_col, target_group, slot = "counts", ...)

## S4 method for signature 'Seurat,character,character'
get_de_table(data, group_col, target_group, slot = "counts", ...)
```

Arguments

data	expression object
group_col	vector or character, specify the group factor or column name of coldata for DE comparisons
target_group	pattern, specify the group of interest, e.g. NK
slot	character, specify which slot to use only for DGEList, sce or seurat object, optional, default 'counts'
...	params for function de_analysis()

Value

A list of DE result table of all comparisons.

Examples

```
data("im_data_6")
DE_tables <- get_de_table(im_data_6, group_col = "celltype:ch1", target_group = "NK")
```

---

get_degs *Get differentially expressed genes by comparing specified groups*

Description

This function uses edgeR and limma to get 'UP' and 'DOWN' DEG lists, for multiple comparisons, DEGs can be obtained from intersection of all DEGs or by using product of p value ranks for multiple comparisons. Filter out low expressed genes and extract DE genes by using limma::voom and limma::treat, and also create an object proc_data to store processed data.

Usage

```
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'DGEList,character,character'
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'matrix,vector,character'
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'Matrix,vector,character'
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)
```

```
## S4 method for signature 'ExpressionSet,character,character'
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'SummarizedExperiment,character,character'
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'Seurat,character,character'
get_degs(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  feature_selection = c("auto", "rankproduct", "none"),
  slot = "counts",
  batch = NULL,
  ...
)
```

Arguments

data	expression object
group_col	vector or character, specify the group factor or column name of coldata for DE comparisons
target_group	pattern, specify the group of interest, e.g. NK
normalize	logical, if the expr in data is raw counts needs to be normalized
feature_selection	one of "auto" (default), "rankproduct" or "none", choose if to use rank product or not to select DEGs from multiple comparisons of DE analysis, 'auto' uses 'rankproduct' but change to 'none' if final genes < 5 for both UP and DOWN

slot	character, specify which slot to use only for DGEList, sce or seurat object, optional, default 'counts'
batch	vector of column name(s) or dataframe, specify the batch effect factor(s), default NULL
...	params for process_data() and select_sig()

Value

A list of 'UP', 'DOWN' gene set of all differentially expressed genes, and a DGEList 'proc_data' containing data after process (filtration, normalization and voom fit). Both 'UP' and 'DOWN' are ordered by rank product or 'Rank' variable if keep.top is NULL

Examples

```
data("im_data_6")
DEGs <- get_degs(im_data_6,
  group_col = "celltype:ch1",
  target_group = "NK", gene_id = "ENSEMBL"
)
```

---

get_gsc_sig *Collect genes from MSigDB or provided GeneSetCollection.*

Description

Collect gene sets from MSigDB or given GeneSetCollection, of which the gene-set names are matched to the given regex pattern by using grep() function. By setting cat and subcat, matching can be constrained in the union of given categories and subcategories if gsc = 'msigdb'.

Usage

```
get_gsc_sig(
  gsc = "msigdb",
  pattern,
  cat = NULL,
  subcat = NULL,
  species = c("hs", "mm"),
  id = c("SYM", "EZID"),
  version = msigdb::getMsigdbVersions(),
  ...
)

## S4 method for signature 'GeneSetCollection,character'
get_gsc_sig(
  gsc = "msigdb",
  pattern,
```

```
  cat = NULL,
  subcat = NULL,
  species = c("hs", "mm"),
  id = c("SYM", "EZID"),
  version = msigdb::getMsigdbVersions(),
  ...
)

## S4 method for signature 'character,character'
get_gsc_sig(
  gsc = "msigdb",
  pattern,
  cat = NULL,
  subcat = NULL,
  species = c("hs", "mm"),
  id = c("SYM", "EZID"),
  version = msigdb::getMsigdbVersions(),
  ...
)
```

Arguments

gsc	'msigdb' or GeneSetCollection to be searched
pattern	pattern pass to grep(), to match the MsigDB gene-set name of interest, e.g. 'NATURAL_KILLER_CELL_MEDIATED'
cat	character, stating the category(s) to be retrieved. The category(s) must be one from msigdb::listCollections(), see details in msigdb::subsetCollection()
subcat	character, stating the sub-category(s) to be retrieved. The sub-category(s) must be one from msigdb::listSubCollections(), see details in msigdb::subsetCollection()
species	character, species of interest, can be 'hs' or 'mm'
id	a character, representing the ID type to use ("SYM" for gene SYMBOLs and "EZID" for ENTREZ IDs)
version	a character, stating the version of MSigDB to be retrieved (should be >= 7.2). See msigdb::getMsigdbVersions().
...	params for grep(), used to match pattern to gene-set names

Value

A GeneSet object containing all matched gene-sets in MSigDB

Examples

```
data("msigdb_gobp_nk")
get_gsc_sig(
  gsc = msigdb_gobp_nk,
  pattern = "natural_killer_cell_mediated",
  subcat = "GO:BP",
  ignore.case = TRUE
```

```
)
```

`get_lm_sig` *Extract specific subset markers from LM7 or/and LM22*

Description

Extract markers for subsets matched to the given pattern from LM7/LM22, and save the matched genes in 'GeneSet' class object, if both pattern are provided, the output would be a 'GeneSetCollection' class object with setName: LM7, LM22.

Usage

```
get_lm_sig(lm7.pattern, lm22.pattern, ...)
```

Arguments

`lm7.pattern`	character string containing a regular expression, to be matched in the given subsets in LM7
`lm22.pattern`	character string containing a regular expression, to be matched in the given subsets in LM22
`...`	params for function `grep()`

Value

A GeneSet or GeneSetCollection for matched subsets in LM7 and/or LM22

Examples

```
data("lm7", "lm22")
get_lm_sig(lm7.pattern = "NK", lm22.pattern = "NK cells")
```

`get_panglao_sig` *Extract immune subset markers from PanglaoDB website.*

Description

Extract specific immune subset markers for 'Hs' or 'Mm', the markers are retrieved from up-to-date PanglaoDB website.

Usage

```
get_panglao_sig(type, species = c("Hs", "Mm", "Mm Hs"))
```

Arguments

type	character vector, cell type name(s) of interest, available subsets could be listed by list_panglao_types()
species	character, default 'Hs', could be 'Hs', 'Mm' or 'Mm Hs', specify the species of interest

Value

a 'GeneSet' class object containing genes of given type(s)

Examples

```
get_panglao_sig(type = "NK cells")
get_panglao_sig(type = c("NK cells", "T cells"))
```

---

gls2gsc *Convert gene-set list into GeneSetCollection*

Description

Convert gene-set list into GeneSetCollection

Usage

```
gls2gsc(...)

## S4 method for signature 'list'
gls2gsc(...)

## S4 method for signature 'vector'
gls2gsc(...)
```

Arguments

...	vector of genes or list of genes

Value

GeneSetCollection

Examples

```
data("msigdb_gobp_nk")
gls2gsc(GSEABase::geneIds(msigdb_gobp_nk[1:3]))
```

gsc_plot *Make upset plot for given gene sets*

Description

Plot upset diagram for overlapping genes among given gene-sets.

Usage

```
gsc_plot(...)
```

Arguments

...	GeneSet or GeneSetCollection

Value

upset plot object

Examples

```
data("msigdb_gobp_nk")
gsc_plot(msigdb_gobp_nk[1:3])
```

im_data_6 *RNA-seq TMM normalized counts data of 6 sorted immune subsets.*

Description

An ExpressionSet objects containing 6 immune subsets (B-cells, CD4, CD8, Monocytes, Neutrophils, NK) from healthy individuals.

Usage

```
data(im_data_6)
```

Format

An ExpressionSet objects of 6*4 samples.

Value

ExpressionSet

Source

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE60424

list_panglao_organs *Show the summary info of available organs in PanglaoDB.*

Description

Show the name of organs available in PanglaoDB. Help users know which organs could be retrieved by PanglaoDB.

Usage

```
list_panglao_organs()
```

Value

a vector of available organ types or cell types in PanglaoDB

Examples

```
list_panglao_organs()
```

list_panglao_types *Show the summary info of available cell types in PanglaoDB.*

Description

Show the name and number of each cell type in PanglaoDB. Help users know which subset(s) marker list(s) could be retrieved by PanglaoDB.

Usage

```
list_panglao_types(organ)
```

Arguments

organ	character, specify the tissue or organ label to list cell types

Value

a vector of available cell types of the organ in PanglaoDB

Examples

```
list_panglao_types(organ = "Immune system")
```

`lm22` *LM22 matrix for CIBERSORT.*

Description

A dataset containing 547 marker genes expression of 22 immune subsets which is generated for CIBERSORT.

Usage

```
data(lm22)
```

Format

A data frame with 547 rows 23 variables:

Gene gene symbols

B cells naive 0 or 1, represents if the gene is significantly up-regulated in the subset

B cells memory 0 or 1

Plasma cells 0 or 1

T cells CD8 0 or 1

T cells CD4 naive 0 or 1

T cells CD4 memory resting 0 or 1

T cells CD4 memory activated 0 or 1

T cells follicular helper 0 or 1

T cells regulatory (Tregs) 0 or 1

T cells gamma delta 0 or 1

NK cells resting 0 or 1

NK cells activated 0 or 1

Monocytes 0 or 1

Macrophages M0 0 or 1

Macrophages M1 0 or 1

Macrophages M2 0 or 1

Dendritic cells resting 0 or 1

Dendritic cells activated 0 or 1

Mast cells resting 0 or 1

Mast cells activated 0 or 1

Eosinophils 0 or 1

Neutrophils 0 or 1

Value

data frame

Source

https://cibersort.stanford.edu/

`lm7` *LM7 matrix for CIBERSORT.*

Description

A dataset containing 375 marker genes expression of 7 immune subsets which is generated for CIBERSORT.

Usage

```
data(lm7)
```

Format

A data frame with 375 rows 9 variables:

Gene gene symbols

Subset immune subset of the marker gene

B cells gene median expression in B cells

T CD4 gene median expression in T CD4 cells

T CD8 gene median expression in T CD8 cells

T gamma delta gene median expression in T gamma delta cells

NK gene median expression in NK cells

MoMaDC gene median expression in MoMaDC cells

granulocytes gene median expression in granulocytes

Value

data frame

Source

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5384348/

merge_markers *Merge markers list into one.*

Description

Merge markers collected from different DB into one 'GeneSet' object, saved a data.frame in json format under `longDescription` with 'TRUE' and '-' to indicate which DB each gene is from, this can be shown via `jsonlite::fromJSON()`.

Usage

```
merge_markers(...)
```

Arguments

...	GeneSet or GeneSetCollection object to be merged

Value

A GeneSet class of union genes in the given list

Examples

```
data("msigdb_gobp_nk")
Markers <- merge_markers(msigdb_gobp_nk[1:3])
jsonlite::fromJSON(GSEABase::longDescription(Markers))
```

msigdb_gobp_nk *Sub-collection of MSigDB gene sets.*

Description

A small GeneSetCollection object, contains gene sets with gene set name matched to 'NATURAL_KILLER' from GO:BP MSigDB v7.4 database.

Usage

```
data(msigdb_gobp_nk)
```

Format

A GeneSetCollection of 55 gene sets.

Value

GeneSetCollection

Source

msigdb::getMsigdb()

---

nk_markers *NK cell markers combination.*

Description

A dataset containing 114 NK cell markers from LM22, LM7 and human orthologs in mice.

Usage

```
data(nk_markers)
```

Format

A data frame with 114 rows and at least 4 variables:

HGNC_Symbol gene symbols

LM22 if included in LM22

LM7 if included in LM7

Huntington if included in orthologs

Value

data frame

Source

https://cancerimmunolres.aacrjournals.org/content/7/7/1162.long

---

pca_matrix_plot *Make a matrix plot of PCA with top PCs*

Description

Make a matrix plot of PCA with top PCs

Usage

```
pca_matrix_plot(
  data,
  features = "all",
  slot = "counts",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)

## S4 method for signature 'matrix'
pca_matrix_plot(
  data,
  features = "all",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)

## S4 method for signature 'Matrix'
pca_matrix_plot(
  data,
  features = "all",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)

## S4 method for signature 'data.frame'
pca_matrix_plot(
  data,
  features = "all",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)
```

```
## S4 method for signature 'ExpressionSet'
pca_matrix_plot(
  data,
  features = "all",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)

## S4 method for signature 'DGEList'
pca_matrix_plot(
  data,
  features = "all",
  slot = "counts",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)

## S4 method for signature 'SummarizedExperiment'
pca_matrix_plot(
  data,
  features = "all",
  slot = "counts",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)

## S4 method for signature 'Seurat'
pca_matrix_plot(
  data,
  features = "all",
  slot = "counts",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
```

```
  n_loadings = 10,
  gene_id = "SYMBOL"
)
```

Arguments

data	expression data, can be matrix, eSet, seurat...
features	vector of gene symbols or 'all', specify the genes used for PCA, default 'all'
slot	character, specify the slot name of expression to be used, optional
group_by	character, specify the column to be grouped and colored, default NULL
scale	logical, if to scale data for PCA, default TRUE
n	num, specify top n PCs to plot
loading	logical, if to plot and label loadings of PCA, default 'FALSE'
n_loadings	num, top n loadings to plot; or a vector of gene IDs; only work when loading = TRUE
gene_id	character, specify which column of IDs used to calculate TPM, also indicate the ID type of expression data's rowname, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'

Value

matrix plot of PCA

Examples

```
data("im_data_6")
pca_matrix_plot(data = im_data_6, scale = FALSE)
```

---

pca_matrix_plot_init *Make a matrix plot of PCA with top PCs*

Description

Make a matrix plot of PCA with top PCs

Usage

```
pca_matrix_plot_init(
  data,
  features = "all",
  group_by = NULL,
  scale = TRUE,
  n = 4,
  loading = FALSE,
  n_loadings = 10,
  gene_id = "SYMBOL"
)
```

Arguments

data	expression matrix
features	vector of gene symbols or 'all', specify the genes used for PCA, default 'all'
group_by	character, specify the column to be grouped and colored, default NULL
scale	logical, if to scale data for PCA, default TRUE
n	num, specify top n PCs to plot
loading	logical, if to plot and label loadings of PCA, default 'FALSE'
n_loadings	num, top n loadings to plot; or a vector of gene IDs; only work when loading = TRUE
gene_id	character, specify which column of IDs used to calculate TPM, also indicate the ID type of expression data's rowname, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'

Value

matrix plot of PCA

---

plot_diagnostics *plot diagnostics before and after* process_data()

Description

plot diagnostics before and after process_data()

Usage

```
plot_diagnostics(expr1, expr2, group_col, abl = 2)
```

Arguments

expr1	expression matrix 1 for original data
expr2	expression matrix 2 for processed data
group_col	vector of group of samples
abl	num, cutoff line

Value

multiple plots

Examples

```
data("im_data_6")
dge <- edgeR::DGEList(
  counts = Biobase::exprs(im_data_6),
  samples = Biobase::pData(im_data_6)
)
dge$logCPM <- edgeR::cpm(dge, log = TRUE)
proc_data <- process_data(dge,
  group_col = "celltype.ch1",
  target_group = "NK"
)
plot_diagnostics(proc_data$logCPM, proc_data$vfit$E,
  group_col = proc_data$samples$group
)
```

---

plot_mean_var *plot Mean-variance trend after voom and after final linear fit*

Description

plot Mean-variance trend after voom and after final linear fit

Usage

```
plot_mean_var(proc_data, span = 0.5)
```

Arguments

proc_data	processed data returned by process_data()
span	num, span for lowess()

Value

comparison plot of mean-variance of voom and final model

Examples

```
data("im_data_6")
proc_data <- process_data(
  im_data_6,
  group_col = "celltype:ch1",
  target_group = "NK"
)
plot_mean_var(proc_data)
```

`plotPCAbiplot` *Single PCA plot function*

Description

Single PCA plot function

Usage

```
plotPCAbiplot(
  prcomp,
  loading = FALSE,
  n_loadings = 10,
  dims = c(1, 2),
  group_by = NULL
)
```

Arguments

`prcomp`	prcomp object generated by `stats::prcomp()`
`loading`	logical, if to plot and label loadings of PCA, default 'FALSE'
`n_loadings`	num, top n loadings to plot; or a vector of gene IDs; only work when `loading = TRUE`
`dims`	a vector of 2 elements, specifying PCs to plot
`group_by`	character, specify the column to be grouped and colored, default NULL

Value

ggplot of PCA

`process_data` *process data*

Description

filter low expression genes, normalize data by 'TMM' and apply `limma::voom()`, `limma::lmFit()` and `limma::treat()` on normalized data

Usage

```
process_data(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  slot = "counts",
  ...
)

## S4 method for signature 'DGEList,character,character'
process_data(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  slot = "counts",
  ...
)

## S4 method for signature 'matrix,vector,character'
process_data(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  batch = NULL,
  ...
)

## S4 method for signature 'Matrix,vector,character'
process_data(
  data,
```

```
  group_col,
  target_group,
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  batch = NULL,
  ...
)

## S4 method for signature 'ExpressionSet,character,character'
process_data(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  batch = NULL,
  ...
)

## S4 method for signature 'SummarizedExperiment,character,character'
process_data(
  data,
  group_col,
  target_group,
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  slot = "counts",
  batch = NULL,
  ...
)

## S4 method for signature 'Seurat,character,character'
process_data(
  data,
  group_col,
  target_group,
```

```
  normalize = TRUE,
  filter = c(10, 10),
  lfc = 0,
  p = 0.05,
  markers = NULL,
  gene_id = "SYMBOL",
  slot = "counts",
  batch = NULL,
  ...
)
```

Arguments

data	expression object
group_col	character, column name of coldata to specify the DE comparisons
target_group	pattern, specify the group of interest, e.g. NK
normalize	logical, if the expr in data is raw counts needs to be normalized
filter	a vector of 2 numbers, filter condition to remove low expression genes, the 1st for min.counts (if normalize = TRUE) or CPM/TPM (if normalize = FALSE), the 2nd for samples size 'large.n'
lfc	num, cutoff of logFC for DE analysis
p	num, cutoff of p value for DE analysis and permutation test if feature_selection = "rankproduct"
markers	vector, a vector of gene names, listed the gene symbols to be kept anyway after filtration. Default 'NULL' means no special genes need to be kept.
gene_id	character, specify the gene ID target_group of rownames of expression data when markers is not NULL, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'
slot	character, specify which slot to use only for DGEList, sce or seurat object, optional, default 'counts'
...	params for `voom_fit_treat()`
batch	vector of character, column name(s) of coldata to be treated as batch effect factor, default NULL

Value

A DGEList containing vfit by `limma::voom()` (if normalize = TRUE) and tfit by `limma::treat()`

Examples

```
data("im_data_6")
proc_data <- process_data(
  im_data_6,
  group_col = "celltype:ch1",
  target_group = "NK"
)
```

`pseudo_sample_list` *Split cells according to specific factors*

Description

Gathering cells to make the pool according to specific factors, and randomly assign the cells from the pool to pseudo-sample with the randomized cell size. (min.cells <= size <= max.cells)

Usage

```
pseudo_sample_list(data, by, min.cells = 0, max.cells = Inf)
```

Arguments

`data`	matrix or data.frame or other single cell expression object
`by`	a vector or data.frame contains factor(s) for aggregation
`min.cells`	num, default 0, the minimum size of cells aggregating to each pseudo-sample
`max.cells`	num, default Inf, the maximum size of cells aggregating to each pseudo-sample

Value

A list of cell names for each pseudo-sample

Examples

```
counts <- matrix(abs(rnorm(10000, 10, 10)), 100)
rownames(counts) <- 1:100
colnames(counts) <- 1:100
meta <- data.frame(
  subset = rep(c("A", "B"), 50),
  level = rep(1:4, each = 25)
)
rownames(meta) <- 1:100
scRNA <- SeuratObject::CreateSeuratObject(counts = counts, meta.data = meta)
pseudo_sample_list(scRNA,
  by = c("subset", "level"),
  min.cells = 10, max.cells = 20
)
```

pseudo_samples *Aggregate single cells to pseudo-samples according to specific factors*

Description

Gather cells for each group according to specified factors, then randomly assign and aggregate cells to each pseudo-samples with randomized cell size. (min.cells <= size <= max.cells)

Usage

```
pseudo_samples(
  data,
  by,
  fun = c("sum", "mean"),
  scale = NULL,
  min.cells = 0,
  max.cells = Inf,
  slot = "counts"
)

## S4 method for signature 'matrix,data.frame'
pseudo_samples(
  data,
  by,
  fun = c("sum", "mean"),
  scale = NULL,
  min.cells = 0,
  max.cells = Inf,
  slot = "counts"
)

## S4 method for signature 'matrix,vector'
pseudo_samples(
  data,
  by,
  fun = c("sum", "mean"),
  scale = NULL,
  min.cells = 0,
  max.cells = Inf,
  slot = "counts"
)

## S4 method for signature 'Seurat,character'
pseudo_samples(
  data,
  by,
  fun = c("sum", "mean"),
```

```
  scale = NULL,
  min.cells = 0,
  max.cells = Inf,
  slot = "counts"
)

## S4 method for signature 'SummarizedExperiment,character'
pseudo_samples(
  data,
  by,
  fun = c("sum", "mean"),
  scale = NULL,
  min.cells = 0,
  max.cells = Inf,
  slot = "counts"
)
```

Arguments

data	a matrix or Seurat/SCE object containing expression and metadata
by	a vector of group names or dataframe for aggregation
fun	chr, methods used to aggregate cells, could be 'sum' or 'mean', default 'sum'
scale	a num or NULL, if to multiply a scale to the average expression
min.cells	num, default 300, the minimum size of cells aggregating to each pseudo-sample
max.cells	num, default 600, the maximum size of cells aggregating to each pseudo-sample
slot	chr, specify which slot of seurat object to aggregate, can be 'counts', 'data', 'scale.data'..., default is 'counts'

Value

An expression matrix after aggregating cells on specified factors

Examples

```
counts <- matrix(abs(rnorm(10000, 10, 10)), 100)
rownames(counts) <- 1:100
colnames(counts) <- 1:100
meta <- data.frame(
  subset = rep(c("A", "B"), 50),
  level = rep(1:4, each = 25)
)
rownames(meta) <- 1:100
scRNA <- SeuratObject::CreateSeuratObject(counts = counts, meta.data = meta)
pseudo_samples(scRNA,
  by = c("subset", "level"),
  min.cells = 10, max.cells = 20
)
```

remove_bg_exp *Remove markers with high signal in background data.*

Description

Specify signatures against specific tissues or cell lines by removing genes with high expression in the background.

Usage

```
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'matrix,matrix,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)
```

```
## S4 method for signature 'DGEList,matrix,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,DGEList,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,ExpressionSet,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
```

```
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,SummarizedExperiment,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,Seurat,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,character,vector'
```

```
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,missing,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)

## S4 method for signature 'ANY,ANY,vector'
remove_bg_exp(
  sig_data,
  bg_data = "CCLE",
  markers,
  s_group_col = NULL,
  s_target_group = NULL,
  b_group_col = NULL,
  b_target_group = NULL,
  snr = 1,
  ...,
```

```
  filter = NULL,
  gene_id = "SYMBOL",
  s_slot = "counts",
  b_slot = "counts",
  ccle_tpm = NULL,
  ccle_meta = NULL
)
```

Arguments

sig_data	log-transformed expression object, can be matrix or DGEList, as signal data
bg_data	'CCLE' or log-transformed expression object as background data
markers	vector, a vector of gene names, listed the gene symbols to be filtered. Must be gene SYMBOLs
s_group_col	vector or character, to specify the group of signal target_groups, or column name of group, default NULL
s_target_group	pattern, specify the target group of interest in sig_data, default NULL
b_group_col	vector or character, to specify the group of background target_groups, or column name of depmap::depmap_metadata(), e.g. 'primary_disease', default NULL
b_target_group	pattern, specify the target_group of interest in bg_data, e.g. 'colorectal', default NULL
snr	num, the cutoff of SNR to screen markers which are not or lowly expressed in bg_data
...	params for grep() to find matched cell lines in bg_data
filter	NULL or a vector of 2 num, filter condition to remove low expression genes in bg_data, the 1st for logcounts, the 2nd for samples size
gene_id	character, specify the gene ID type of rownames of expression data, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'
s_slot	character, specify which slot to use of DGEList, sce or seurat object for sig_data, optional, default 'counts'
b_slot	character, specify which slot to use of DGEList, sce or seurat object for bg_data, optional, default 'counts'
ccle_tpm	ccle_tpm data from depmap::depmap_TPM(), only used when data = 'CCLE', default NULL
ccle_meta	ccle_meta data from depmap::depmap_metadata(), only used when data = 'CCLE', default NULL

Value

a vector of genes after filtration

Examples

```
data("im_data_6", "nk_markers", "ccle_crc_5")
remove_bg_exp(
  sig_data = Biobase::exprs(im_data_6),
  bg_data = ccle_crc_5,
  im_data_6$`celltype:ch1`, "NK", ## for sig_data
  "cancer", "CRC", ## for bg_data
  markers = nk_markers$HGNC_Symbol[40:50],
  filter = c(1, 2),
  gene_id = c("ENSEMBL", "SYMBOL")
)
```

---

remove_bg_exp_mat *Remove genes show high signal in the background expression data from markers.*

Description

Remove genes show high signal in the background expression data from markers.

Usage

```
remove_bg_exp_mat(sig_mat, bg_mat, markers, snr = 1, gene_id = "SYMBOL")
```

Arguments

sig_mat	log-transformed expression matrix of interested signal data
bg_mat	log-transformed expression matrix of interested background data
markers	vector, a vector of gene names, listed the gene symbols to be filtered. Must be gene SYMBOLs.
snr	num, the cutoff of SNR to screen markers which are not or lowly expressed in bg_data
gene_id	character, specify the gene ID types of row names of sig_mat and bg_mat data, could be one of 'ENSEMBL', 'SYMBOL', 'ENTREZ'..., default 'SYMBOL'

Value

a vector of genes after filtration

Examples

```
data("im_data_6", "nk_markers", "ccle_crc_5")
remove_bg_exp_mat(
  sig_mat = Biobase::exprs(im_data_6),
  bg_mat = ccle_crc_5$counts,
  markers = nk_markers$HGNC_Symbol[30:40],
  gene_id = c("ENSEMBL", "SYMBOL")
)
```

select_sig *select DEGs from multiple comparisons*

Description

select DEGs from multiple comparisons

Usage

```
select_sig(tfit, feature_selection = c("auto", "rankproduct", "none"), ...)
```

Arguments

tfit	processed tfit by `limma::treat()` or processed data returned by `process_data()`
feature_selection	one of "auto" (default), "rankproduct" or "none", choose if to use rank product or not to select DEGs from multiple comparisons of DE analysis, 'auto' uses 'rankproduct' but change to 'none' if final genes < 5 for both UP and DOWN
...	params for `DEGs_RP()` or `DEGs_Group()`

Value

GeneSetCollection contains UP and DOWN gene sets

Examples

```
data("im_data_6")
proc_data <- process_data(
  im_data_6,
  group_col = "celltype:ch1",
  target_group = "NK"
)
select_sig(proc_data$tfit)
```

sig_boxplot *Boxplot of median expression or scores of signature*

Description

Make boxplot and show expression or score level of signature across subsets.

Usage

```
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'matrix,vector,vector,character'
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  gene_id = "SYMBOL"
)

## S4 method for signature 'Matrix,vector,vector,character'
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  gene_id = "SYMBOL"
)

## S4 method for signature 'data.frame,vector,vector,character'
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  gene_id = "SYMBOL"
)

## S4 method for signature 'DGEList,vector,character,character'
sig_boxplot(
  data,
```

```
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'ExpressionSet,vector,character,character'
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  gene_id = "SYMBOL"
)

## S4 method for signature 'Seurat,vector,character,character'
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'SummarizedExperiment,vector,character,character'
sig_boxplot(
  data,
  sigs,
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'list,vector,character,character'
sig_boxplot(
  data,
  sigs,
```

```
  group_col,
  target_group,
  type = c("score", "expression"),
  method = "t.test",
  slot = "counts",
  gene_id = "SYMBOL"
)
```

Arguments

data	expression data, can be matrix, DGEList, eSet, seurat, sce...
sigs	a vector of signature (Symbols)
group_col	character or vector, specify the column name to compare in coldata
target_group	pattern, specify the group of interest as reference
type	one of "score" and "expression", to plot score or expression of the signature
method	a character string indicating which method to be used for `stat_compare_means()` to compare the means across groups, could be "t.test", 'wilcox.test', 'anova'..., default "t.test"
slot	character, indicate which slot used as expression, optional
gene_id	character, indicate the ID type of rowname of expression data's , could be one of 'ENSEMBL', 'SYMBOL', ... default 'SYMBOL'

Value

patchwork or ggplot of boxplot

Examples

```
data("im_data_6", "nk_markers")
p <- sig_boxplot(
  im_data_6,
  sigs = nk_markers$HGNC_Symbol[1:30],
  group_col = "celltype:ch1", target_group = "NK",
  gene_id = "ENSEMBL"
)
```

---

sig_gseaplot *Visualize GSEA result with input list of gene symbols.*

Description

Visualize GSEA result with multiple lists of genes by using `clusterProfiler`.

Usage

```
sig_gseaplot(
  data,
  sigs,
  group_col,
  target_group,
  gene_id = "SYMBOL",
  slot = "counts",
  method = c("dotplot", "gseaplot"),
  col = "-log10(p.adjust)",
  size = "enrichmentScore",
  pvalue_table = FALSE,
  digits = 2,
  rank_stat = "logFC",
  ...
)

## S4 method for signature 'MArrayLM,vector'
sig_gseaplot(
  data,
  sigs,
  group_col,
  target_group,
  gene_id = "SYMBOL",
  slot = "counts",
  method = c("dotplot", "gseaplot"),
  col = "-log10(p.adjust)",
  size = "enrichmentScore",
  pvalue_table = FALSE,
  digits = 2,
  rank_stat = "logFC",
  ...
)

## S4 method for signature 'MArrayLM,list'
sig_gseaplot(
  data,
  sigs,
  group_col,
  target_group,
  gene_id = "SYMBOL",
  slot = "counts",
  method = c("dotplot", "gseaplot"),
  col = "-log10(p.adjust)",
  size = "enrichmentScore",
  pvalue_table = FALSE,
  digits = 2,
  rank_stat = "logFC",
```

```
  ...
)

## S4 method for signature 'DGEList,ANY'
sig_gseaplot(
  data,
  sigs,
  group_col,
  target_group,
  gene_id = "SYMBOL",
  slot = "counts",
  method = c("dotplot", "gseaplot"),
  col = "-log10(p.adjust)",
  size = "enrichmentScore",
  pvalue_table = FALSE,
  digits = 2,
  rank_stat = "logFC",
  ...
)

## S4 method for signature 'ANY,ANY'
sig_gseaplot(
  data,
  sigs,
  group_col,
  target_group,
  gene_id = "SYMBOL",
  slot = "counts",
  method = c("dotplot", "gseaplot"),
  col = "-log10(p.adjust)",
  size = "enrichmentScore",
  pvalue_table = FALSE,
  digits = 2,
  rank_stat = "logFC",
  ...
)

## S4 method for signature 'list,ANY'
sig_gseaplot(
  data,
  sigs,
  group_col,
  target_group,
  gene_id = "SYMBOL",
  slot = "counts",
  method = c("dotplot", "gseaplot"),
  col = "-log10(p.adjust)",
  size = "enrichmentScore",
```

```
  pvalue_table = FALSE,
  digits = 2,
  rank_stat = "logFC",
  ...
)
```

Arguments

data	expression data, can be matrix, DGEList, eSet, seurat, sce...
sigs	a vector of signature (Symbols) or a list of signatures
group_col	character or vector, specify the column name to compare in coldata
target_group	pattern, specify the group of interest as reference
gene_id	character, indicate the ID type of rowname of expression data's , could be one of 'ENSEMBL', 'SYMBOL', ... default 'SYMBOL'
slot	character, indicate which slot used as expression, optional
method	one of "gseaplot" and "dotplot", how to plot GSEA result
col	column name of `clusterProfiler::GSEA()` result, used for dot col when method = "dotplot"
size	column name of `clusterProfiler::GSEA()` result, used for dot size when method = "dotplot"
pvalue_table	logical, if to add p value table if method = "gseaplot"
digits	num, specify the number of significant digits of pvalue table
rank_stat	character, specify which metric used to rank for GSEA, default "logFC"
...	params for function `get_de_table()` and function `enrichplot::gseaplot2()`

Value

patchwork object for all comparisons

Examples

```
data("im_data_6", "nk_markers")
sig_gseaplot(
  sigs = list(
    A = nk_markers$HGNC_Symbol[1:15],
    B = nk_markers$HGNC_Symbol[20:40],
    C = nk_markers$HGNC_Symbol[60:75]
  ),
  data = im_data_6, group_col = "celltype:ch1",
  target_group = "NK", gene_id = "ENSEMBL"
)
```

sig_heatmap *Heatmap original markers and screened signature*

Description

Compare the heatmap before and after screening.

Usage

```
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'matrix,character,vector,missing'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'matrix,character,vector,vector'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)
```

```
## S4 method for signature 'matrix,list,vector,missing'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'Matrix,ANY,vector,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'data.frame,ANY,vector,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'DGEList,ANY,character,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = "none",
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
```

```
  slot = "counts",
  ...
)

## S4 method for signature 'ExpressionSet,ANY,character,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = c("none", "row", "column"),
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'Seurat,ANY,character,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = "none",
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'SummarizedExperiment,ANY,character,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
  markers,
  scale = "none",
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)

## S4 method for signature 'list,ANY,character,ANY'
sig_heatmap(
  data,
  sigs,
  group_col,
```

```
  markers,
  scale = "none",
  gene_id = "SYMBOL",
  ranks_plot = FALSE,
  slot = "counts",
  ...
)
```

Arguments

data	expression data, can be matrix, DGEList, eSet, seurat, sce...
sigs	a vector of signature (Symbols) or a list of signatures
group_col	character or vector, specify the column name to compare in coldata
markers	a vector of gene names, listed the gene symbols of original markers pool
scale	could be one of 'none' (default), 'row' or 'column'
gene_id	character, indicate the ID type of rowname of expression data's , could be one of 'ENSEMBL', 'SYMBOL', ... default 'SYMBOL'
ranks_plot	logical, if to use ranks instead of expression of genes to draw heatmap
slot	character, indicate which slot used as expression, optional
...	params for ComplexHeatmap::Heatmap()

Value

patchwork object of heatmap

Examples

```
data("im_data_6", "nk_markers")
sig_heatmap(
  data = im_data_6, sigs = nk_markers$HGNC_Symbol[1:10],
  group_col = "celltype:ch1",
  gene_id = "ENSEMBL"
)
```

---

sig_rankdensity_plot *Plot rank density*

Description

Show the rank density of given signature in the given comparison.

Usage

```
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'matrix,vector,vector'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  gene_id = "SYMBOL"
)

## S4 method for signature 'Matrix,vector,vector'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  gene_id = "SYMBOL"
)

## S4 method for signature 'data.frame,vector,vector'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  gene_id = "SYMBOL"
)

## S4 method for signature 'DGEList,vector,character'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'ExpressionSet,vector,character'
```

```
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  gene_id = "SYMBOL"
)

## S4 method for signature 'Seurat,vector,character'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'SummarizedExperiment,vector,character'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  slot = "counts",
  gene_id = "SYMBOL"
)

## S4 method for signature 'list,vector,character'
sig_rankdensity_plot(
  data,
  sigs,
  group_col,
  aggregate = FALSE,
  slot = "counts",
  gene_id = "SYMBOL"
)
```

Arguments

data	expression data, can be matrix, DGEList, eSet, seurat, sce...
sigs	a vector of signature (Symbols)
group_col	character or vector, specify the column name to compare in coldata
aggregate	logical, if to aggregate expression according to group_col, default FALSE
slot	character, indicate which slot used as expression, optional
gene_id	character, indicate the ID type of rowname of expression data's , could be one of 'ENSEMBL', 'SYMBOL', ... default 'SYMBOL'

Value

ggplot or patchwork

Examples

```
data("im_data_6", "nk_markers")
sig_rankdensity_plot(
  data = im_data_6, sigs = nk_markers$HGNC_Symbol[1:10],
  group_col = "celltype:ch1", gene_id = "ENSEMBL"
)
```

---

sig_scatter_plot *Scatter plot of signature for specific subset vs others*

Description

Scatter plot depicts mean expression for each signature gene in the specific subset against other cell types.

Usage

```
sig_scatter_plot(
  data,
  sigs,
  group_col,
  target_group,
  slot = "counts",
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'matrix,vector,vector,character'
sig_scatter_plot(
  data,
  sigs,
  group_col,
  target_group,
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'Matrix,vector,vector,character'
sig_scatter_plot(
  data,
```

```
  sigs,
  group_col,
  target_group,
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'DGEList,vector,character,character'
sig_scatter_plot(
  data,
  sigs,
  group_col,
  target_group,
  slot = "counts",
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'ExpressionSet,vector,character,character'
sig_scatter_plot(
  data,
  sigs,
  group_col,
  target_group,
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'Seurat,vector,character,character'
sig_scatter_plot(
  data,
  sigs,
  group_col,
  target_group,
  slot = "counts",
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'SummarizedExperiment,vector,character,character'
sig_scatter_plot(
  data,
  sigs,
  group_col,
```

```
  target_group,
  slot = "counts",
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)

## S4 method for signature 'list,vector,character,character'
sig_scatter_plot(
  data,
  sigs,
  group_col,
  target_group,
  slot = "counts",
  xint = 1,
  yint = 1,
  gene_id = "SYMBOL"
)
```

Arguments

data	expression data, can be matrix, DGEList, eSet, seurat, sce...
sigs	a vector of signature (Symbols)
group_col	character or vector, specify the column name to compare in coldata
target_group	pattern, specify the group of interest as reference
slot	character, indicate which slot used as expression, optional
xint	intercept of vertical dashed line, default 1
yint	intercept of horizontal dashed line, default 1
gene_id	character, indicate the ID type of rowname of expression data's , could be one of 'ENSEMBL', 'SYMBOL', ... default 'SYMBOL'

Value

patchwork or ggplot of scatter plot of median expression

Examples

```
data("im_data_6", "nk_markers")
sig_scatter_plot(
  sigs = nk_markers$HGNC_Symbol, data = im_data_6,
  group_col = "celltype:ch1", target_group = "NK",
  gene_id = "ENSEMBL"
)
```

`voom_fit_treat` *return DGEList containing vfit by limma::voom (if normalize = TRUE) and tfit by limma::treat*

Description

return DGEList containing vfit by limma::voom (if normalize = TRUE) and tfit by limma::treat

Usage

```
voom_fit_treat(
  dge,
  group_col,
  target_group,
  normalize = TRUE,
  group = FALSE,
  lfc = 0,
  p = 0.05,
  batch = NULL,
  summary = TRUE,
  ...
)
```

Arguments

`dge`	DGEList object for DE analysis, including expr and samples info
`group_col`	character, column name of coldata to specify the DE comparisons
`target_group`	pattern, specify the group of interest, e.g. NK
`normalize`	logical, if the expr in data is raw counts needs to be normalized
`group`	logical, TRUE to separate samples into only 2 groups: 'target_group" and 'Others'; FALSE to set each level as a group
`lfc`	num, cutoff of logFC for DE analysis
`p`	num, cutoff of p value for DE analysis and permutation test if feature_selection = "rankproduct"
`batch`	vector of character, column name(s) of coldata to be treated as batch effect factor, default NULL
`summary`	logical, if to show the summary of DE analysis
`...`	omitted

Value

A DGEList containing vfit and tfit

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