Package ‘tidybulk’

March 28, 2024

Type  Package
Title  Brings transcriptomics to the tidyverse
Version  1.14.3
Description  This is a collection of utility functions that allow to perform exploration of and calculations to RNA sequencing data, in a modular, pipe-friendly and tidy fashion.
License  GPL-3
Depends  R (>= 4.1.0), ttservice (>= 0.3.6)
Imports  tibble, readr, dplyr (>= 1.1.0), magrittr, tidyr, stringr, stringr, purrr, tidyselect, preprocessCore, stats, parallel, utils, lifecycle, scales, SummarizedExperiment, GenomicRanges, methods, S4Vectors, crayon, Matrix
Suggests  BiocStyle, testthat, vctrs, AnnotationDbi, BiocManager, Rsutherford, e1071, edgeR, limma, org.Hs.eg.db, org.Mm.eg.db, sva, GGally, knitr, qpdf, covr, Seurat, KernSmooth, Rtsne, ggplot2, widyr, clusterProfiler, msignr, DESeq2, broom, survival, boot, betareg, tidyHeatmap, pasilla, ggrepel, devtools, functional, survminer, tidySummarizedExperiment, markdown, uwot, matrixStats, igraph, EGSEA, IRanges, here, glmnet, pbapply, pbmcapply, lme4, glmmTMB, MASS, pkgconfig
VignetteBuilder  knitr
RdMacros  lifecycle
Biarch  true
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**adjust_abundance**

Adjust transcript abundance for unwanted variation

**Description**

`adjust_abundance()` takes as input a `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with an additional adjusted abundance column. This method uses scaled counts if present.
adjust_abundance

Usage

adjust_abundance(
  .data,
  .formula = NULL,
  .factor_unwanted = NULL,
  .factor_of_interest = NULL,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "combat_seq",
  action = "add",
  ...
)

## S4 method for signature 'spec_tbl_df'
adjust_abundance(
  .data,
  .formula = NULL,
  .factor_unwanted = NULL,
  .factor_of_interest = NULL,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "combat_seq",
  action = "add",
  ...
)

## S4 method for signature 'tbl_df'
adjust_abundance(
  .data,
  .formula = NULL,
  .factor_unwanted = NULL,
  .factor_of_interest = NULL,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "combat_seq",
  action = "add",
  ...
)
### S4 method for signature 'tidybulk'

```r
adjust_abundance(
  .data,
  .formula = NULL,
  .factor_unwanted = NULL,
  .factor_of_interest = NULL,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "combat_seq",
  action = "add",
  ...
)
```

### S4 method for signature 'SummarizedExperiment'

```r
adjust_abundance(
  .data,
  .formula = NULL,
  .factor_unwanted = NULL,
  .factor_of_interest = NULL,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "combat_seq",
  action = "add",
  ...
)
```

### S4 method for signature 'RangedSummarizedExperiment'

```r
adjust_abundance(
  .data,
  .formula = NULL,
  .factor_unwanted = NULL,
  .factor_of_interest = NULL,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "combat_seq",
  action = "add",
  inverse_transform = NULL
)
```
adjust_abundance

log_transform = NULL,
transform = NULL,
inverse_transform = NULL)

Arguments

.data               A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
.formula            DEPRECATED - A formula with no response variable, representing the desired linear model where the first covariate is the factor of interest and the second covariate is the unwanted variation (of the kind ~ factor_of_interest + batch)
.factor_unwanted    A tidy select, e.g. column names without double quotation. c(batch, country) These are the factor that we want to adjust for, including unwanted batch effect, and unwanted biological effects.
.factor_of_interest A tidy select, e.g. column names without double quotation. c(treatment) These are the factor that we want to preserve.
.sample             The name of the sample column
.transcript         The name of the transcript/gene column
.abundance          The name of the transcript/gene abundance column
.method             A character string. Methods include combat_seq (default), combat and limma_remove_batch_effect.
.action             A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).
...                  Further parameters passed to the function sva::ComBat
.log_transform      DEPRECATED - A boolean, whether the value should be log-transformed (e.g., TRUE for RNA sequencing data)
.transform          DEPRECATED - A function that will transform the counts, by default it is log1p for RNA sequencing data, but for avoiding transformation you can use identity
.inverse_transform  DEPRECATED - A function that is the inverse of transform (e.g. expm1 is inverse of log1p). This is needed to transform back the counts after analysis.

Details

`r lifecycle::badge("maturing")`

This function adjusts the abundance for (known) unwanted variation. At the moment just an unwanted covariate is allowed at a time using Combat (DOI: 10.1093/bioinformatics/bts034)

Underlying method: sva::ComBat(data, batch = my_batch, mod = design, prior.plots = FALSE, ...)
**aggregate_duplicates**

**Value**

A consistent object (to the input) with additional columns for the adjusted counts as `<COUNT COLUMN>_adjusted`

A consistent object (to the input) with additional columns for the adjusted counts as `<COUNT COLUMN>_adjusted`

A consistent object (to the input) with additional columns for the adjusted counts as `<COUNT COLUMN>_adjusted`

A consistent object (to the input) with additional columns for the adjusted counts as `<COUNT COLUMN>_adjusted`

A ‘SummarizedExperiment’ object

A ‘SummarizedExperiment’ object

**Examples**

```r
cm = tidybulk::se_mini
cm$batch = 0
cm$batch[colnames(cm) %in% c("SRR1740035", "SRR1740043") = 1

cm |> identify_abundant() |> adjust_abundance(.factor_unwanted = batch, .factor_of_interest = condition, method="combat"
```

---

**aggregate_duplicates**  
*Aggregates multiple counts from the same samples (e.g., from isoforms), concatenates other character columns, and averages other numeric columns*

---

**Description**

`aggregate_duplicates()` takes as input a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with aggregated transcripts that were duplicated.

**Usage**

```r
aggregate_duplicates(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
```
aggregate_duplicates

    aggregation_function = sum,
    keep_integer = TRUE
)

## S4 method for signature 'spec_tbl_df'
aggregate_duplicates(
    .data,
    .sample = NULL,
    .transcript = NULL,
    .abundance = NULL,
    aggregation_function = sum,
    keep_integer = TRUE
)

## S4 method for signature 'tbl_df'
aggregate_duplicates(
    .data,
    .sample = NULL,
    .transcript = NULL,
    .abundance = NULL,
    aggregation_function = sum,
    keep_integer = TRUE
)

## S4 method for signature 'tidybulk'
aggregate_duplicates(
    .data,
    .sample = NULL,
    .transcript = NULL,
    .abundance = NULL,
    aggregation_function = sum,
    keep_integer = TRUE
)

## S4 method for signature 'SummarizedExperiment'
aggregate_duplicates(
    .data,
    .sample = NULL,
    .transcript = NULL,
    .abundance = NULL,
    aggregation_function = sum,
    keep_integer = TRUE
)

## S4 method for signature 'RangedSummarizedExperiment'
aggregate_duplicates(
    .data,
    .sample = NULL,
aggregate_duplicates

```r
data = NULL,
transcript = NULL,
abundance = NULL,
aggregation_function = sum,
keep_integer = TRUE
```

Arguments

- `.data` A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
- `.sample` The name of the sample column
- `.transcript` The name of the transcript/gene column
- `.abundance` The name of the transcript/gene abundance column
- `aggregation_function` A function for counts aggregation (e.g., sum, median, or mean)
- `keep_integer` A boolean. Whether to force the aggregated counts to integer

Details

`r lifecycle::badge("maturing")`

This function aggregates duplicated transcripts (e.g., isoforms, ensembl). For example, we often have to convert ensembl symbols to gene/transcript symbol, but in doing so we have to deal with duplicates. `aggregate_duplicates` takes a tibble and column names (as symbols; for `.sample`, `.transcript` and `.count`) as arguments and returns a tibble with aggregate transcript with the same name. All the rest of the column are appended, and factors and boolean are appended as characters.

Underlying custom method: `data |> filter(n_aggr > 1) |> group_by(!.sample,!!.transcript) |> dplyr::mutate(!!.abundance := !!.abundance |> aggregation_function())`

Value

- A consistent object (to the input) with aggregated transcript abundance and annotation
- A consistent object (to the input) with aggregated transcript abundance and annotation
- A consistent object (to the input) with aggregated transcript abundance and annotation
- A consistent object (to the input) with aggregated transcript abundance and annotation
- A `SummarizedExperiment` object
- A `SummarizedExperiment` object

Examples

```r
# Create a aggregation column
se_mini = tidybulk::se_mini
SummarizedExperiment::rowData(se_mini )$gene_name = rownames(se_mini )
aggregate_duplicates(
  se_mini,
)
.transcript = gene_name
)

---

**arrange**

*Arrange rows by column values*

**Description**

`arrange()` order the rows of a data frame rows by the values of selected columns.

Unlike other dplyr verbs, `arrange()` largely ignores grouping; you need to explicit mention grouping variables (or use `by_group = TRUE`) in order to group by them, and functions of variables are evaluated once per data frame, not once per group.

**Arguments**

- **.data** A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See *Methods*, below, for more details.
- **...** `<[\`tidy-eval\'][dpolyr_tidy_eval]> Variables, or functions or variables. Use `desc()` to sort a variable in descending order.
- **.by_group** If TRUE, will sort first by grouping variable. Applies to grouped data frames only.

**Details**

### Locales

The sort order for character vectors will depend on the collating sequence of the locale in use: see `[locales()]`.  

### Missing values

Unlike base sorting with `sort()`, ‘NA’ are:  
* always sorted to the end for local data, even when wrapped with `desc()`.  
* treated differently for remote data, depending on the backend.

**Value**

An object of the same type as `.data`.

* All rows appear in the output, but (usually) in a different place. * Columns are not modified. * Groups are not modified. * Data frame attributes are preserved.

A tibble

**Methods**

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages:
as_matrix

See Also

Other single table verbs: `filter()`, `mutate()`, `rename()`, `summarise()`

Examples

```r
arrange(mtcars, cyl, disp)
```

---

as_matrix  Get matrix from tibble

Description

Get matrix from tibble

Usage

```r
as_matrix(tbl, rownames = NULL, do_check = TRUE)
```

Arguments

- `tbl` A tibble
- `rownames` The column name of the input tibble that will become the rownames of the output matrix
- `do_check` A boolean

Value

A matrix

Examples

```r
tibble(.feature = "CD3G", count=1) |> as_matrix(rownames=.feature)
```
Description

`as_SummarizedExperiment()` creates a ‘SummarizedExperiment’ object from a ‘tbl’ or ‘tidybulk’
tbl formatted as | <SAMPLE> | <TRANSCRIPT> | <COUNT> | <...> |

Usage

```r
as_SummarizedExperiment(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL
)
```

```r
## S4 method for signature 'spec_tbl_df'
as_SummarizedExperiment(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL
)
```

```r
## S4 method for signature 'tbl_df'
as_SummarizedExperiment(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL
)
```

```r
## S4 method for signature 'tidybulk'
as_SummarizedExperiment(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL
)
```

Arguments

- `.data` A tibble
- `.sample` The name of the sample column
.transcript    The name of the transcript/gene column
.abundance    The name of the transcript/gene abundance column

**Value**

A `SummarizedExperiment` object
A `SummarizedExperiment` object
A `SummarizedExperiment` object
A `SummarizedExperiment` object
A `SummarizedExperiment` object

---

### bind_cols

**Description**

Left join datasets

**Arguments**

- **x** tibs to join. (See dplyr)
- **y** tibs to join. (See dplyr)
- **by** A character vector of variables to join by. (See dplyr)
- **copy** If x and y are not from the same data source, and copy is TRUE, then y will be copied into the same src as x. (See dplyr)
- **suffix** If there are non-joined duplicate variables in x and y, these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2. (See dplyr)
- **...** Data frames to combine (See dplyr)

**Value**

A tt object

**Examples**

```r
annotation = tidybulk::se_mini |> tidybulk() |> as_tibble() |> distinct(.sample) |> mutate(source = "AU")
tidybulk::se_mini |> tidybulk() |> as_tibble() |> left_join(annotation)
```
bind_rows

Efficiently bind multiple data frames by row and column

Description

This is an efficient implementation of the common pattern of 'do.call(rbind, dfs)' or 'do.call(cbind, dfs)' for binding many data frames into one.

Arguments

... Data frames to combine.
Each argument can either be a data frame, a list that could be a data frame, or a list of data frames.
When row-binding, columns are matched by name, and any missing columns will be filled with NA.
When column-binding, rows are matched by position, so all data frames must have the same number of rows. To match by value, not position, see mutate-joins.
.id Data frame identifier.
When '.id' is supplied, a new column of identifiers is created to link each row to its original data frame. The labels are taken from the named arguments to 'bind_rows()'. When a list of data frames is supplied, the labels are taken from the names of the list. If no names are found a numeric sequence is used instead.
.add.cell.ids from Seurat 3.0 A character vector of length(x = c(x, y)). Appends the corresponding values to the start of each objects' cell names.

Details

The output of 'bind_rows()' will contain a column if that column appears in any of the inputs.

Value

'bind_rows()' and 'bind_cols()' return the same type as the first input, either a data frame, 'tbl_df', or 'grouped_df'.

Examples

data(se_mini)

se_mini_tidybulk = se_mini |> tidybulk()
bind_rows( se_mini_tidybulk, se_mini_tidybulk )

tt_bind = se_mini_tidybulk |> select(time, condition)
se_mini_tidybulk |> bind_cols(tt_bind)


**breast_tcga_mini_SE**

Needed for vignette breast_tcga_mini_SE

---

**Description**

Needed for vignette breast_tcga_mini_SE

**Usage**

breast_tcga_mini_SE

**Format**

An object of class SummarizedExperiment with 500 rows and 251 columns.

---

**check_if_counts_is_na**

*Check whether there are NA counts*

---

**Description**

Check whether there are NA counts

**Usage**

check_if_counts_is_na(.data, .abundance)

**Arguments**

- `.data` A tibble of read counts
- `.abundance` A character name of the read count column

**Value**

A tbl
check_if_duplicated_genes

Check whether there are duplicated genes/transcripts

Description
Check whether there are duplicated genes/transcripts

Usage
check_if_duplicated_genes(
  .data,
  .sample = sample,
  .transcript = transcript,
  .abundance = `read count`
)

Arguments
.data A tibble of read counts
.sample A character name of the sample column
.transcript A character name of the transcript/gene column
.abundance A character name of the read count column

Value
A tbl

check_if_wrong_input
Check whether there are NA counts

Description
Check whether there are NA counts

Usage
check_if_wrong_input(.data, list_input, expected_type)

Arguments
.data A tibble of read counts
.list_input A list
.expected_type A character string
Value

A tbl

cluster_elements

Get clusters of elements (e.g., samples or transcripts)

Description

cluster_elements() takes as input a 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and identify clusters in the data.

Usage

cluster_elements(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  transform = log1p,
  action = "add",
  ...,
  log_transform = NULL
)

## S4 method for signature 'spec_tbl_df'
cluster_elements(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  transform = log1p,
  action = "add",
  ...,
  log_transform = NULL
)

## S4 method for signature 'tbl_df'
cluster_elements(
  .data,
  .element = NULL,
  .feature = NULL,
cluster_elements

.abundance = NULL,
method,
of_samples = TRUE,
transform = log1p,
action = "add",
...
log_transform = NULL
)

## S4 method for signature 'tidybulk'
cluster_elements(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
of_samples = TRUE,
transform = log1p,
action = "add",
...
log_transform = NULL
)

## S4 method for signature 'SummarizedExperiment'
cluster_elements(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
of_samples = TRUE,
transform = log1p,
action = "add",
...
log_transform = NULL
)

## S4 method for signature 'RangedSummarizedExperiment'
cluster_elements(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
of_samples = TRUE,
transform = log1p,
action = "add",
...
)
log_transform = NULL

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
.element The name of the element column (normally samples).
.feature The name of the feature column (normally transcripts/genes)
.abundance The name of the column including the numerical value the clustering is based on (normally transcript abundance)
.method A character string. The cluster algorithm to use, at the moment k-means is the only algorithm included.
of_samples A boolean. In case the input is a tidybulk object, it indicates Whether the element column will be sample or transcript column
.transform A function that will transform the counts, by default it is log1p for RNA sequencing data, but for avoiding transformation you can use identity
.action A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).
... Further parameters passed to the function kmeans
.log_transform DEPRECATED - A boolean, whether the value should be log-transformed (e.g., TRUE for RNA sequencing data)

Details

‘r lifecycle::badge("maturing")’

identifies clusters in the data, normally of samples. This function returns a tibble with additional columns for the cluster annotation. At the moment only k-means (DOI: 10.2307/2346830) and SNN clustering (DOI:10.1016/j.cell.2019.05.031) is supported, the plan is to introduce more clustering methods.

Underlying method for kmeans do.call(kmeans(.data, iter.max = 1000, ...)

Underlying method for SNN .data Seurat::CreateSeuratObject() Seurat::ScaleData(display.progress = TRUE,num.cores = 4, do.par = TRUE) Seurat::FindVariableFeatures(selection.method = "vst") Seurat::RunPCA(npcs = 30) Seurat::FindNeighbors() Seurat::FindClusters(method = "igraph", ...)

Value

A tbl object with additional columns with cluster labels
A tbl object with additional columns with cluster labels
A tbl object with additional columns with cluster labels
A tbl object with additional columns with cluster labels
A ‘SummarizedExperiment’ object
A ‘SummarizedExperiment’ object
Examples

```r
cluster_elements(tidybulk::se_mini, centers = 2, method="kmeans")
```

## counts_ensembl

### Counts with ensembl annotation

## Description

Counts with ensembl annotation

### Usage

```r
counts_ensembl
```

### Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 119 rows and 6 columns.

---

## deconvolve_cellularity

### Get cell type proportions from samples

### Description

`deconvolve_cellularity()` takes as input a `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with the estimated cell type abundance for each sample.

### Usage

```r
decovolve_cellularity(
  .data,  
  .sample = NULL,  
  .transcript = NULL,  
  .abundance = NULL,  
  reference = NULL,  
  method = "cibersort",  
  prefix = ",",  
  action = "add",  
  ...)
```
## S4 method for signature 'spec_tbl_df'

deconvolve_cellularity(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  reference = NULL,
  method = "cibersort",
  prefix = "",
  action = "add",
  ...
)

## S4 method for signature 'tbl_df'

deconvolve_cellularity(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  reference = NULL,
  method = "cibersort",
  prefix = "",
  action = "add",
  ...
)

## S4 method for signature 'tidybulk'

deconvolve_cellularity(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  reference = NULL,
  method = "cibersort",
  prefix = "",
  action = "add",
  ...
)

## S4 method for signature 'SummarizedExperiment'

deconvolve_cellularity(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  reference = NULL,
  method = "cibersort",
  prefix = "",
  ...
deconvolve_cellularity

    action = "add",
    ...
)

## S4 method for signature 'RangedSummarizedExperiment'
deconvolve_cellularity(
    .data,
    .sample = NULL,
    .transcript = NULL,
    .abundance = NULL,
    reference = NULL,
    method = "cibersort",
    prefix = "",
    action = "add",
    ...
)

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

.sample The name of the sample column

.transcript The name of the transcript/gene column

.abundance The name of the transcript/gene abundance column

reference A data frame. The methods cibersort and llsr can accept a custom rectangular dataframe with genes as rows names, cell types as column names and gene-transcript abundance as values. For example tidybulk::X_cibersort. The transcript/cell_type data frame of integer transcript abundance. If NULL, the default reference for each algorithm will be used. For llsr will be LM22.

method A character string. The method to be used. At the moment Cibersort (default, can accept custom reference), epic (can accept custom reference) and llsr (linear least squares regression, can accept custom reference), mcp_counter, quantiseq, xcell are available.

.prefix A character string. The prefix you would like to add to the result columns. It is useful if you want to reshape data.

.action A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).

... Further parameters passed to the function Cibersort

Details

`r lifecycle::badge("maturing")`

This function infers the cell type composition of our samples (with the algorithm Cibersort; Newman et al., 10.1038/nmeth.3337).

Underlying method: CIBERSORT(Y = data, X = reference, ...)
`describe_transcript`

**Value**

A consistent object (to the input) including additional columns for each cell type estimated

**Examples**

```r
# Subsetting for time efficiency
tidybulk::se_mini |> deconvolve_cellularity(cores = 1)
```

**Description**

Get DESCRIPTION from gene SYMBOL for Human and Mouse

**Usage**

```r
describe_transcript(.data, .transcript = NULL)
```

## S4 method for signature 'spec_tbl_df'
```r
describe_transcript(.data, .transcript = NULL)
```

## S4 method for signature 'tbl_df'
```r
describe_transcript(.data, .transcript = NULL)
```

## S4 method for signature 'tidybulk'
```r
describe_transcript(.data, .transcript = NULL)
```

`.describe_transcript_SE(.data, .transcript = NULL)`
## S4 method for signature 'SummarizedExperiment'
describe_transcript(.data, .transcript = NULL)

## S4 method for signature 'RangedSummarizedExperiment'
describe_transcript(.data, .transcript = NULL)

### Arguments
- `.data` A tt or tbl object.
- `.transcript` A character. The name of the gene symbol column.

### Value
- A tbl
- A consistent object (to the input) including additional columns for transcript symbol
- A consistent object (to the input) including additional columns for transcript symbol
- A consistent object (to the input) including additional columns for transcript symbol
- A ‘SummarizedExperiment’ object
- A consistent object (to the input) including additional columns for transcript symbol
- A consistent object (to the input) including additional columns for transcript symbol

### Examples

```
describe_transcript(tidybulk::se_mini)
```

---

## distinct

### Description

distinct

### Arguments
- `.data` A tbl. (See dplyr)
- `...` Data frames to combine (See dplyr)
- `.keep_all` If TRUE, keep all variables in `.data`. If a combination of `...` is not distinct, this keeps the first row of values. (See dplyr)

### Value

A tt object
**Examples**

```r
tidybulk::se_mini |> tidybulk() |> distinct()
```

---

**Data set**

**Description**

Data set

**Usage**

```r
ensembl_symbol_mapping
```

**Format**

An object of class `spec_tbl_df` (inherits from `tbl_df`, `tbl`, `data.frame`) with 291249 rows and 3 columns.

---

**Add transcript symbol column from ensembl id for human and mouse data**

**Description**

`ensembl_to_symbol()` takes as input a `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with the additional transcript symbol column

**Usage**

```r
ensembl_to_symbol(.data, .ensembl, action = "add")
```

```r
## S4 method for signature 'spec_tbl_df'
ensembl_to_symbol(.data, .ensembl, action = "add")
```

```r
## S4 method for signature 'tbl_df'
ensembl_to_symbol(.data, .ensembl, action = "add")
```

```r
## S4 method for signature 'tidybulk'
ensembl_to_symbol(.data, .ensembl, action = "add")
```
fill_missing_abundance

Arguments

.data a 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
.ensembl A character string. The column that represents ensembl gene ID
.action A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).

Details

[Questioning] This is useful since different resources use ensembl IDs while others use gene symbol IDs. At the moment this works for human (genes and transcripts) and mouse (genes) data.

Value

A consistent object (to the input) including additional columns for transcript symbol
A consistent object (to the input) including additional columns for transcript symbol
A consistent object (to the input) including additional columns for transcript symbol
A consistent object (to the input) including additional columns for transcript symbol

Examples

# This function was designed for data.frame
# Convert from SummarizedExperiment for this example. It is NOT recommended.

 tidybulk::se_mini |> tidybulk() |> as_tibble() |> ensembl_to_symbol(.feature)

fill_missing_abundance

Fill transcript abundance if missing from sample-transcript pairs

Description

fill_missing_abundance() takes as input a 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with new observations
Usage

```r
fill_missing_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  fill_with
)
```

## S4 method for signature 'spec_tbl_df'
```r
fill_missing_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  fill_with
)
```

## S4 method for signature 'tbl_df'
```r
fill_missing_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  fill_with
)
```

## S4 method for signature 'tidybulk'
```r
fill_missing_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  fill_with
)
```

Arguments

- `.data` A `tbl` formatted as `SAMPLE | TRANSCRIPT | COUNT | ...`
- `.sample` The name of the sample column
- `.transcript` The name of the transcript column
- `.abundance` The name of the transcript abundance column
- `fill_with` A numerical abundance with which fill the missing data points

Details

[Questioning]
This function fills the abundance of missing sample-transcript pair using the median of the sample group defined by the formula

**Value**

A consistent object (to the input) non-sparse abundance
A consistent object (to the input) with filled abundance
A consistent object (to the input) with filled abundance
A consistent object (to the input) with filled abundance

**Examples**

```r
print("Not run for build time.")

# tidybulk::se_mini |> fill_missing_abundance( fill_with = 0)
```

---

**filter**

*Subset rows using column values*

**Description**

`filter()` retains the rows where the conditions you provide a ‘TRUE’. Note that, unlike base sub-setting with `[`, rows where the condition evaluates to ‘NA’ are dropped.

**Arguments**

- `.data` A tbl. (See dplyr)
- `...` Logical predicates defined in terms of the variables in `.data`. Multiple conditions are combined with ‘&’. Only rows where the condition evaluates to ‘TRUE’ are kept.
- `.preserve` when ‘FALSE’ (the default), the grouping structure is recalculated based on the resulting data, otherwise it is kept as is.

**Details**

dplyr is not yet smart enough to optimise filtering optimisation on grouped datasets that don’t need grouped calculations. For this reason, filtering is often considerably faster on [ungroup()]ed data.

**Value**

An object of the same type as `.data`.

* Rows are a subset of the input, but appear in the same order. * Columns are not modified. * The number of groups may be reduced (if `.preserve` is not ‘TRUE’). * Data frame attributes are preserved.
Useful filter functions

* ['=='], ['>'], ['>='] etc * ['&'], ['|'], ['~'], [xor()] * [is.na()] * [between()], [near()]

Grouped tibbles

Because filtering expressions are computed within groups, they may yield different results on grouped tibbles. This will be the case as soon as an aggregating, lagging, or ranking function is involved. Compare this ungrouped filtering:

The former keeps rows with 'mass' greater than the global average whereas the latter keeps rows with 'mass' greater than the gender average.

Methods

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages:

See Also

[filter_all()], [filter_if()] and [filter_at()].

Other single table verbs: arrange(), mutate(), rename(), summarise()

Examples

data(se)

se |> tidybulk() |> filter(dex=="unttr")

# Learn more in ?dplyr_tidy_eval

flybaseIDs

<table>
<thead>
<tr>
<th>flybaseIDs</th>
</tr>
</thead>
<tbody>
<tr>
<td>flybaseIDs</td>
</tr>
</tbody>
</table>

Description

flybaseIDs

Usage

flybaseIDs

Format

An object of class character of length 14599.
get_bibliography  

*Produces the bibliography list of your workflow*

---

**Description**

get_bibliography() takes as input a 'tidybulk'

**Usage**

get_bibliography(.data)

```r
## S4 method for signature 'tbl'
get_bibliography(.data)
```

```r
## S4 method for signature 'tbl_df'
get_bibliography(.data)
```

```r
## S4 method for signature 'spec_tbl_df'
get_bibliography(.data)
```

```r
## S4 method for signature 'tidybulk'
get_bibliography(.data)
```

```r
## S4 method for signature 'SummarizedExperiment'
get_bibliography(.data)
```

```r
## S4 method for signature 'RangedSummarizedExperiment'
get_bibliography(.data)
```

**Arguments**

.data  
A 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

**Details**

'r lifecycle::badge("maturing")'

This methods returns the bibliography list of your workflow from the internals of a tidybulk object (attr(., "internals"))

**Value**

NULL. It prints a list of bibliography references for the software used through the workflow. A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).
A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

Examples

```r
get_bibliography(tidybulk::se_mini)
```

### Description

Get UMAP

### Usage

```r
get_reduced_dimensions_UMAP_bulk(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  .dims = 2,
  top = 500,
  of_samples = TRUE,
  transform = log1p,
  scale = TRUE,
  calculate_for_pca_dimensions = min(20, top),
  ...
)
```

### Arguments

- `.data` A tibble
- `.element` A column symbol. The column that is used to calculate distance (i.e., normally samples)
- `.feature` A column symbol. The column that represents entities to cluster (i.e., normally genes)
- `.abundance` A column symbol with the value the clustering is based on (e.g., ‘count’)
- `.dims` A integer vector corresponding to principal components of interest (e.g., 1:6)
- `top` An integer. How many top genes to select
- `of_samples` A boolean
calculate_for_pca_dimensions
   An integer of length one. The number of PCA dimensions to based the UMAP
   calculation on. If NULL all variable features are considered
   ...
   Further parameters passed to the function uwot
log_transform A boolean, whether the value should be log-transformed (e.g., TRUE for RNA
   sequencing data)

Value
   A tibble with additional columns

get_reduced_dimensions_UMAP_bulk_SE
   Get UMAP

Description
   Get UMAP

Usage
   get_reduced_dimensions_UMAP_bulk_SE(
     .data,
     .dims = 2,
     top = 500,
     of_samples = TRUE,
     transform = log1p,
     scale = NULL,
     calculate_for_pca_dimensions = min(20, top),
     ...
   )

Arguments
   .data A tibble
   .dims A integer vector corresponding to principal components of interest (e.g., 1:6)
   top An integer. How many top genes to select
   of_samples A boolean
   transform A function that will transform the counts, by default it is log1p for RNA sequencing data, but for avoiding transformation you can use identity
   calculate_for_pca_dimensions
      An integer of length one. The number of PCA dimensions to based the UMAP calculation on. If NULL all variable features are considered
   ...
   Further parameters passed to the function uwot
   .abundance A column symbol with the value the clustering is based on (e.g., ‘count’)
group_by

.feature A column symbol. The column that represents entities to cluster (i.e., normally genes)
.element A column symbol. The column that is used to calculate distance (i.e., normally samples)

Value
A tibble with additional columns

group_by

Group by one or more variables

Description
Most data operations are done on groups defined by variables. ‘group_by()’ takes an existing tbl and converts it into a grouped tbl where operations are performed "by group". ‘ungroup()’ removes grouping.

Arguments
.data A tbl. (See dplyr)
... In ‘group_by()’, variables or computations to group by. In ‘ungroup()’, variables to remove from the grouping.
.add When ‘FALSE’, the default, ‘group_by()’ will override existing groups. To add to the existing groups, use ‘.add = TRUE’.
This argument was previously called ‘add’, but that prevented creating a new grouping variable called ‘add’, and conflicts with our naming conventions.
.drop When ‘.drop = TRUE’, empty groups are dropped. See [group_by_drop_default()] for what the default value is for this argument.

Value
A [grouped data frame][grouped_df()], unless the combination of ‘...’ and ‘add’ yields a non empty set of grouping columns, a regular (ungrouped) data frame otherwise.

Methods
These function are **generic**s, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

Examples
by_cyl <- mtcars |> group_by(cyl)
identify_abundant

Description

identify_abundant() takes as input A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional columns for the statistics from the hypothesis test.

Usage

identify_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

## S4 method for signature 'spec_tbl_df'
identify_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

## S4 method for signature 'tbl_df'
identify_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

## S4 method for signature 'tidybulk'
identify_abundant(
  .data,
identify_abundant

```r
.identify_abundant = NULL,
.transcript = NULL,
.abundance = NULL,
.factor_of_interest = NULL,
.minimum_counts = 10,
.minimum_proportion = 0.7
)

## S4 method for signature 'SummarizedExperiment'
identify_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  .factor_of_interest = NULL,
  .minimum_counts = 10,
  .minimum_proportion = 0.7
)

## S4 method for signature 'RangedSummarizedExperiment'
identify_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  .factor_of_interest = NULL,
  .minimum_counts = 10,
  .minimum_proportion = 0.7
)
```

Arguments

- `.data` A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
- `.sample` The name of the sample column
- `.transcript` The name of the transcript/gene column
- `.abundance` The name of the transcript/gene abundance column
- `factor_of_interest` The name of the column of the factor of interest. This is used for defining sample groups for the filtering process. It uses the filterByExpr function from edgeR.
- `minimum_counts` A real positive number. It is the threshold of count per million that is used to filter transcripts/genes out from the scaling procedure.
- `minimum_proportion` A real positive number between 0 and 1. It is the threshold of proportion of samples for each transcripts/genes that have to be characterised by a cmp bigger than the threshold to be included for scaling procedure.
Details

'r lifecycle::badge("maturing")'  
At the moment this function uses edgeR (DOI: 10.1093/bioinformatics/btp616)

Underlying method: edgeR::filterByExpr(data, min.count = minimum_counts, group = string_factor_of_interest, min.prop = minimum_proportion )

Value

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A 'SummarizedExperiment' object

A 'SummarizedExperiment' object

Examples

```
identify_abundant(
tidybulk::se_mini
)
```

---

`impute_missing_abundance`

`impute transcript abundance if missing from sample-transcript pairs`

Description

`impute_missing_abundance()` takes as input A 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional sample-transcript pairs with imputed transcript abundance.
Usage

```r
impute_missing_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  suffix = "",
  force_scaling = FALSE
)
```

```r
## S4 method for signature 'spec_tbl_df'
impute_missing_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  suffix = "",
  force_scaling = FALSE
)
```

```r
## S4 method for signature 'tbl_df'
impute_missing_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  suffix = "",
  force_scaling = FALSE
)
```

```r
## S4 method for signature 'tidybulk'
impute_missing_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  suffix = "",
  force_scaling = FALSE
)
```

```r
## S4 method for signature 'SummarizedExperiment'
impute_missing_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  suffix = "",
  force_scaling = FALSE
)
```
impute_missing_abundance

```
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  suffix = "",
  force_scaling = FALSE
)
```

## S4 method for signature 'RangedSummarizedExperiment'
impute_missing_abundance(
  .data, 
  .formula, 
  .sample = NULL, 
  .transcript = NULL, 
  .abundance = NULL, 
  suffix = "",
  force_scaling = FALSE
)

### Arguments

- **.data**
  - A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

- **.formula**
  - A formula with no response variable, representing the desired linear model where the first covariate is the factor of interest and the second covariate is the unwanted variation (of the kind `~ factor_of_interest + batch`)

- **.sample**
  - The name of the sample column

- **.transcript**
  - The name of the transcript/gene column

- **.abundance**
  - The name of the transcript/gene abundance column

- **suffix**
  - A character string. This is added to the imputed count column names. If empty the count column are overwritten

- **force_scaling**
  - A boolean. In case a abundance-containing column is not scaled (columns with _scale suffix), setting force_scaling = TRUE will result in a scaling by library size, to compensating for a possible difference in sequencing depth.

### Details

`r lifecycle::badge("maturing")`

This function imputes the abundance of missing sample-transcript pair using the median of the sample group defined by the formula

### Value

- A consistent object (to the input) non-sparse abundance
- A consistent object (to the input) with imputed abundance
- A consistent object (to the input) with imputed abundance
inner_join

A consistent object (to the input) with imputed abundance
A `SummarizedExperiment` object
A `SummarizedExperiment` object

Examples

```r
res =
impute_missing_abundance(
tidybulk::se_mini,
  ~ condition
)
```

inner_join | Inner join datasets

Description

Inner join datasets
Right join datasets
Full join datasets

Arguments

- **x**: tbls to join. (See dplyr)
- **y**: tbls to join. (See dplyr)
- **by**: A character vector of variables to join by. (See dplyr)
- **copy**: If x and y are not from the same data source, and copy is TRUE, then y will be copied into the same src as x. (See dplyr)
- **suffix**: If there are non-joined duplicate variables in x and y, these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2. (See dplyr)
- **...**: Data frames to combine (See dplyr)

Value

- A tt object
- A tt object
- A tt object
Examples

```r
annotation = tidybulk::se_mini |> tidybulk() |> as_tibble() |> distinct(.sample) |> mutate(source = "AU")
tidybulk::se_mini |> tidybulk() |> as_tibble() |> inner_join(annotation)

annotation = tidybulk::se_mini |> tidybulk() |> as_tibble() |> distinct(.sample) |> mutate(source = "AU")
tidybulk::se_mini |> tidybulk() |> as_tibble() |> right_join(annotation)

annotation = tidybulk::se_mini |> tidybulk() |> as_tibble() |> distinct(.sample) |> mutate(source = "AU")
tidybulk::se_mini |> tidybulk() |> as_tibble() |> full_join(annotation)
```

### keep_abundant

**Description**

`keep_abundant()` takes as input A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional columns for the statistics from the hypothesis test.

**Usage**

```r
keep_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)
```

```r
## S4 method for signature 'spec_tbl_df'
keep_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)
```

```r
## S4 method for signature 'tbl_df'
```

---

**Keep abundant transcripts**

---
keep_abundant

keep_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

## S4 method for signature 'tidybulk'
keep_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

## S4 method for signature 'SummarizedExperiment'
keep_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

## S4 method for signature 'RangedSummarizedExperiment'
keep_abundant(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  factor_of_interest = NULL,
  minimum_counts = 10,
  minimum_proportion = 0.7
)

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
The name of the sample column

The name of the transcript/gene column

The name of the transcript/gene abundance column

The name of the column of the factor of interest. This is used for defining sample groups for the filtering process. It uses the filterByExpr function from edgeR.

A real positive number. It is the threshold of count per million that is used to filter transcripts/genes out from the scaling procedure.

A real positive number between 0 and 1. It is the threshold of proportion of samples for each transcripts/genes that have to be characterised by a cmp bigger than the threshold to be included for scaling procedure.

At the moment this function uses edgeR (DOI: 10.1093/bioinformatics/btp616)

Underlying method: edgeR::filterByExpr( data, min.count = minimum_counts, group = string_factor_of_interest, min.prop = minimum_proportion )

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A ‘SummarizedExperiment’ object

Examples

```r
keep_abundant(
  tidybulk::se_mini
)
```
**Description**

`keep_variable()` takes as input a 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional columns for the statistics from the hypothesis test.

**Usage**

```r
keep_variable(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  top = 500,
  transform = log1p,
  log_transform = TRUE
)
```

```r
## S4 method for signature 'spec_tbl_df'
keep_variable(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  top = 500,
  transform = log1p,
  log_transform = TRUE
)
```

```r
## S4 method for signature 'tbl_df'
keep_variable(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  top = 500,
  transform = log1p,
  log_transform = NULL
)
```

```r
## S4 method for signature 'tidybulk'
keep_variable(
  .data,
```
.sample = NULL,
.transcript = NULL,
.abundance = NULL,
  top = 500,
(transform = log1p,
  log_transform = NULL)
)

## S4 method for signature 'SummarizedExperiment'
keep_variable(.data, top = 500, transform = log1p)

## S4 method for signature 'RangedSummarizedExperiment'
keep_variable(.data, top = 500, transform = log1p)

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

.sample The name of the sample column

.transcript The name of the transcript/gene column

.abundance The name of the transcript/gene abundance column

top Integer. Number of top transcript to consider

.transform A function that will transform the counts, by default it is log1p for RNA sequencing data, but for avoiding transformation you can use identity

.log_transform DEPRECATED - A boolean, whether the value should be log-transformed (e.g., TRUE for RNA sequencing data)

Details

‘r lifecycle::badge("maturing")’

At the moment this function uses edgeR https://doi.org/10.1093/bioinformatics/btp616

Value

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

Underlying method: s <- rowMeans((x - rowMeans(x))^2) o <- order(s, decreasing = TRUE) x <- x[o[1L:top] , drop = FALSE] variable.transcripts = rownames(x)

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).
log10_reverse_trans

A ‘SummarizedExperiment’ object
A ‘SummarizedExperiment’ object

Examples

```r
keep_variable(tidybulk::se_mini, top = 500)
```

Description

It performs log scaling and reverses the axis. Useful to plot negative log probabilities. To not be used directly but with `ggplot` (e.g. `scale_y_continuous(trans = "log10_reverse")`)

Usage

```r
log10_reverse_trans()
```

Details

'\texttt{r lifecycle::badge("maturing")}'

Value

A scales object

Examples

```r
library(ggplot2)
library(tibble)
tibble(pvalue = c(0.001, 0.05, 0.1), fold_change = 1:3) %>%
  ggplot(aes(fold_change , pvalue)) +
  geom_point() +
  scale_y_continuous(trans = "log10_reverse")
```
logit_trans  

Description

it perform logit scaling with right axis formatting. To not be used directly but with ggplot (e.g. 
\texttt{scale_y_continuous(trans = "log10_reverse")})

Usage

\texttt{logit_trans()}

Details

\texttt{r lifecycle::badge("maturing")}

Value

A scales object

Examples

\begin{verbatim}
library(ggplot2)
library(tibble)
tibble(pvalue = c(0.001, 0.05, 0.1), fold_change = 1:3) %>%
  ggplot(aes(fold_change, pvalue)) +
  geom_point() +
  scale_y_continuous(trans = "log10_reverse")
\end{verbatim}

mutate  

Create, modify, and delete columns

Description

‘\texttt{mutate()}‘ adds new variables and preserves existing ones; ‘\texttt{transmute()}‘ adds new variables and 
drops existing ones. New variables overwrite existing variables of the same name. Variables can be 
removed by setting their value to ‘\texttt{NULL}‘.
**mutate**

**Arguments**

- `.data` A tbl. (See dplyr)

  `<[‘tidy-eval’][dplyr_tidy_eval]>` Name-value pairs. The name gives the name of the column in the output.
  
  The value can be:
  
  * A vector of length 1, which will be recycled to the correct length.
  * A vector the same length as the current group (or the whole data frame if ungrouped).
  * ‘NULL’, to remove the column.
  * A data frame or tibble, to create multiple columns in the output.

**Value**

An object of the same type as `.data`.

For `mutate()`:

* Rows are not affected. * Existing columns will be preserved unless explicitly modified. * New columns will be added to the right of existing columns. * Columns given value ‘NULL’ will be removed * Groups will be recomputed if a grouping variable is mutated. * Data frame attributes are preserved.

For `transmute()`:

* Rows are not affected. * Apart from grouping variables, existing columns will be remove unless explicitly kept. * Column order matches order of expressions. * Groups will be recomputed if a grouping variable is mutated. * Data frame attributes are preserved.

**Useful mutate functions**

* `[‘+’], [‘-’], [log()], etc., for their usual mathematical meanings
* `[lead()], [lag()]
* `[dense_rank()], [min_rank()], [percent_rank()], [row_number()], [cume_dist()], [ntile()]
* `[cumsum()],[cummean()], [cummin()],[cummax()],[cumany()],[cumall()]
* `[na_if()], [coalesce()]
* `[if_else()], [recode()],[case_when()]

**Grouped tibbles**

Because mutating expressions are computed within groups, they may yield different results on grouped tibbles. This will be the case as soon as an aggregating, lagging, or ranking function is involved. Compare this ungrouped mutate:

With the grouped equivalent:

The former normalises ‘mass’ by the global average whereas the latter normalises by the averages within gender levels.
Methods

These functions are **generic**s, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

See Also

Other single table verbs: `arrange()`, `filter()`, `rename()`, `summarise()`

Examples

# Newly created variables are available immediately
mtcars |> as_tibble() |> mutate(
  cyl2 = cyl * 2,
  cyl4 = cyl2 * 2
)

pivot_sample

Extract sample-wise information

Description

`pivot_sample()` takes as input a `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a `tbl` with only sample-related columns

Usage

```
pivot_sample(.data, .sample = NULL)
## S4 method for signature 'spec_tbl_df'
pivot_sample(.data, .sample = NULL)
## S4 method for signature 'tbl_df'
pivot_sample(.data, .sample = NULL)
## S4 method for signature 'tidybulk'
pivot_sample(.data, .sample = NULL)
## S4 method for signature 'SummarizedExperiment'
pivot_sample(.data, .sample = NULL)
## S4 method for signature 'RangedSummarizedExperiment'
pivot_sample(.data, .sample = NULL)
```
pivot_transcript

Arguments

<table>
<thead>
<tr>
<th>.data</th>
<th>A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))</th>
</tr>
</thead>
<tbody>
<tr>
<td>.sample</td>
<td>The name of the sample column</td>
</tr>
</tbody>
</table>

Details

‘r lifecycle::badge("maturing")’

This function extracts only sample-related information for downstream analysis (e.g., visualisation). It is disruptive in the sense that it cannot be passed anymore to tidybulk function.

Value

A ‘tbl’ with transcript-related information

Examples

```r
pivot_sample(tidybulk::se_mini)
```

Description

pivot_transcript() takes as input a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a ‘tbl’ with only transcript-related columns

Usage

```r
pivot_transcript(.data, .transcript = NULL)
```

```r
# S4 method for signature 'spec_tbl_df'
pivot_transcript(.data, .transcript = NULL)
```

```r
# S4 method for signature 'tbl_df'
pivot_transcript(.data, .transcript = NULL)
```

```r
# S4 method for signature 'tidybulk'
pivot_transcript(.data, .transcript = NULL)
```
quantile_normalise_abundance

Normalise by quantiles the counts of transcripts/genes

Description

quantile_normalise_abundance() takes as input A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and Scales transcript abundance compensating for sequencing depth (e.g., with TMM algorithm, Robinson and Oshlack doi.org/10.1186/gb-2010-11-3-r25).
Usage

quantile_normalise_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "limma_normalize_quantiles",
  action = "add"
)

## S4 method for signature 'spec_tbl_df'
quantile_normalise_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "limma_normalize_quantiles",
  action = "add"
)

## S4 method for signature 'tbl_df'
quantile_normalise_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "limma_normalize_quantiles",
  action = "add"
)

## S4 method for signature 'tidybulk'
quantile_normalise_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "limma_normalize_quantiles",
  action = "add"
)

## S4 method for signature 'SummarizedExperiment'
quantile_normalise_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "limma_normalize_quantiles",
  action = NULL
)
## S4 method for signature 'RangedSummarizedExperiment'
quantile_normalise_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "limma_normalize_quantiles",
  action = NULL
)

### Arguments
- `.data` A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
- `.sample` The name of the sample column
- `.transcript` The name of the transcript/gene column
- `.abundance` The name of the transcript/gene abundance column
- `.method` A character string. Either "limma_normalize_quantiles" for limma::normalizeQuantiles or "preprocesscore_normalize_quantiles_use_target" for preprocessCore::normalize.quantiles.use.target for large-scale dataset, where limma could not be compatible.
- `.action` A character string between "add" (default) and "only". "add" joins the new information to the input tbl (default), "only" return a non-redundant tbl with the just new information.

### Details
`
't lifecycle::badge("maturing")'

Scales transcript abundance compensating for sequencing depth (e.g., with TMM algorithm, Robinson and Oshlack doi.org/10.1186/gb-2010-11-3-r25). Lowly transcribed transcripts/genes (defined with minimum_counts and minimum_proportion parameters) are filtered out from the scaling procedure. The scaling inference is then applied back to all unfiltered data.

Underlying method edgeR::calcNormFactors(.data, method = c("TMM","TMMwsp","RLE","upperquartile"))

### Value
A tbl object with additional columns with scaled data as `<NAME OF COUNT COLUMN>_scaled`
A tbl object with additional columns with scaled data as `<NAME OF COUNT COLUMN>_scaled`
A tbl object with additional columns with scaled data as `<NAME OF COUNT COLUMN>_scaled`
A tbl object with additional columns with scaled data as `<NAME OF COUNT COLUMN>_scaled`
A ‘SummarizedExperiment’ object
A ‘SummarizedExperiment’ object
reduce_dimensions

Examples

```r
tidybulk::se_mini |>
  quantile_normalise_abundance()
```

---

**reduce_dimensions**  

*Dimension reduction of the transcript abundance data*

**Description**

reduce_dimensions() takes as input A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and calculates the reduced dimensional space of the transcript abundance.

**Usage**

```r
reduce_dimensions(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  .dims = 2,
  top = 500,
  of_samples = TRUE,
  transform = log1p,
  scale = TRUE,
  action = "add",
  ...
)
```

## S4 method for signature 'spec_tbl_df'
reduce_dimensions(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  .dims = 2,
  top = 500,
  of_samples = TRUE,
  transform = log1p,
)
reduce_dimensions

scale = TRUE,
action = "add",
...,
log_transform = NULL)

## S4 method for signature 'tbl_df'
reduce_dimensions(
.data,
.element = NULL,
.feature = NULL,
.abundance = NULL,
.method,
.dims = 2,
top = 500,
of_samples = TRUE,
.transform = log1p,
scale = TRUE,
.action = "add",
...,
.log_transform = NULL)

## S4 method for signature 'tidybulk'
reduce_dimensions(
.data,
.element = NULL,
.feature = NULL,
.abundance = NULL,
.method,
.dims = 2,
top = 500,
of_samples = TRUE,
.transform = log1p,
scale = TRUE,
.action = "add",
...,
.log_transform = NULL)

## S4 method for signature 'SummarizedExperiment'
reduce_dimensions(
.data,
.element = NULL,
.feature = NULL,
.abundance = NULL,
.method,
.dims = 2,
reduce_dimensions

    top = 500,
    of_samples = TRUE,
    transform = log1p,
    scale = TRUE,
    action = "add",
    ...
    log_transform = NULL

## S4 method for signature 'RangedSummarizedExperiment'
reduce_dimensions(
    .data,
    .element = NULL,
    .feature = NULL,
    .abundance = NULL,
    method,
    .dims = 2,
    top = 500,
    of_samples = TRUE,
    transform = log1p,
    scale = TRUE,
    action = "add",
    ...
    log_transform = NULL
)

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

.element The name of the element column (normally samples).

.feature The name of the feature column (normally transcripts/genes)

.abundance The name of the column including the numerical value the clustering is based on (normally transcript abundance)

.method A character string. The dimension reduction algorithm to use (PCA, MDS, tSNE).

.dims An integer. The number of dimensions you are interested in (e.g., 4 for returning the first four principal components).

top An integer. How many top genes to select for dimensionality reduction

.of_samples A boolean. In case the input is a tidybulk object, it indicates Whether the element column will be sample or transcript column

.transform A function that will transform the counts, by default it is log1p for RNA sequencing data, but for avoiding tranformation you can use identity

.scale A boolean for method="PCA", this will be passed to the 'prcomp' function. It is not included in the ... argument because although the default for 'prcomp' if FALSE, it is advisable to set it as TRUE.
reduce_dimensions

action     A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).

...     Further parameters passed to the function prcomp if you choose method="PCA" or Rtsne if you choose method="tSNE"

log_transform     DEPRECATED - A boolean, whether the value should be log-transformed (e.g., TRUE for RNA sequencing data)

Details

`r lifecycle::badge("maturing")`

This function reduces the dimensions of the transcript abundances. It can use multi-dimensional scaling (MDS; DOI.org/10.1186/gb-2010-11-3-r25), principal component analysis (PCA), or tSNE (Jesse Krijthe et al. 2018)

Underlying method for PCA: prcomp(scale = scale, ...)
Underlying method for MDS: limma::plotMDS(ndim = .dims, plot = FALSE, top = top)
Underlying method for tSNE: Rtsne::Rtsne(data, ...)
Underlying method for UMAP:

`df_source = .data |>
  # Filter NA symbol filter(!!.feature |> is.na() |> not()) |>
  # Prepare data frame distinct(!!.feature,!!.element,!!.abundance) |>
  # Filter most variable genes keep_variable_transcripts(top) |> reduce_dimensions(method="PCA", .dims = calculate_for_pca_dimensions, action="get") |> as_matrix(rownames = quo_name(.element)) |> uwot::tumap(...)

Value

A tbl object with additional columns for the reduced dimensions
A tbl object with additional columns for the reduced dimensions
A tbl object with additional columns for the reduced dimensions
A tbl object with additional columns for the reduced dimensions
A `SummarizedExperiment` object
A `SummarizedExperiment` object

Examples

counts.MDS =
tidybulk::se_mini |>
tidybulk::se_mini |>

counts.PCA =
tidybulk::se_mini |>
```r
 identify_abundant() |> 
 reduce_dimensions(method="PCA", .dims = 3)
```

---

**Objects exported from other packages**

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

`dplyr` `do, select`

`tibble` `as_tibble, tibble`

---

**remove_redundancy**

*Drop redundant elements (e.g., samples) for which feature (e.g., transcript/gene) abundances are correlated*

**Description**

`remove_redundancy()` takes as input A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) for correlation method or `<DIMENSION 1> | <DIMENSION 2> | <...>` for reduced_dimensions method, and returns a consistent object (to the input) with dropped elements (e.g., samples).

**Usage**

```r
remove_redundancy(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  correlation_threshold = 0.9,
  top = Inf,
  transform = identity,
  Dim_a.column,
  Dim_b.column,
  log_transform = NULL
)
```
## S4 method for signature 'spec_tbl_df'
remove_redundancy(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  correlation_threshold = 0.9,
  top = Inf,
  transform = identity,
  Dim_a_column = NULL,
  Dim_b_column = NULL,
  log_transform = NULL
)

## S4 method for signature 'tbl_df'
remove_redundancy(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  correlation_threshold = 0.9,
  top = Inf,
  transform = identity,
  Dim_a_column = NULL,
  Dim_b_column = NULL,
  log_transform = NULL
)

## S4 method for signature 'tidybulk'
remove_redundancy(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  correlation_threshold = 0.9,
  top = Inf,
  transform = identity,
  Dim_a_column = NULL,
  Dim_b_column = NULL,
  log_transform = NULL
)
## S4 method for signature 'SummarizedExperiment'

```r
remove_redundancy(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  correlation_threshold = 0.9,
  top = Inf,
  transform = identity,
  Dim_a_column = NULL,
  Dim_b_column = NULL,
  log_transform = NULL
)
```

## S4 method for signature 'RangedSummarizedExperiment'

```r
remove_redundancy(
  .data,
  .element = NULL,
  .feature = NULL,
  .abundance = NULL,
  method,
  of_samples = TRUE,
  correlation_threshold = 0.9,
  top = Inf,
  transform = identity,
  Dim_a_column = NULL,
  Dim_b_column = NULL,
  log_transform = NULL
)
```

### Arguments

- **.data** A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
- **.element** The name of the element column (normally samples).
- **.feature** The name of the feature column (normally transcripts/genes)
- **.abundance** The name of the column including the numerical value the clustering is based on (normally transcript abundance)
- **method** A character string. The method to use, correlation and reduced_dimensions are available. The latter eliminates one of the most proximar pairs of samples in PCA reduced dimensions.
- **of_samples** A boolean. In case the input is a tidybulk object, it indicates Whether the element column will be sample or transcript column
- **correlation_threshold** A real number between 0 and 1. For correlation based calculation.
An integer. How many top genes to select for correlation based method.

A function that will transform the counts, by default it is log1p for RNA sequencing data, but for avoiding transformation you can use identity.

A character string. For reduced_dimension based calculation. The column of one principal component.

A character string. For reduced_dimension based calculation. The column of another principal component.

DEPRECATED - A boolean, whether the value should be log-transformed (e.g., TRUE for RNA sequencing data).

This function removes redundant elements from the original data set (e.g., samples or transcripts). For example, if we want to define cell-type specific signatures with low sample redundancy. This function returns a tibble with dropped redundant elements (e.g., samples). Two redundancy estimation approaches are supported: (i) removal of highly correlated clusters of elements (keeping a representative) with method="correlation"; (ii) removal of most proximal element pairs in a reduced dimensional space.

Underlying method for correlation: widyr::pairwise_cor(sample, transcript,count, sort = TRUE, diag = FALSE, upper = FALSE)

Underlying custom method for reduced dimensions: select_closest_pairs = function(df) couples <-
  df |> head(n = 0)

  while (df |> nrow() > 0) pair <-
  df |> arrange(dist) |> head(n = 1) couples <-
  couples |> bind_rows(pair)

  df <-
  df |> filter( !sample 1 | sample 2 )

couples

A tbl object with with dropped redundant elements (e.g., samples).

A tbl object with with dropped redundant elements (e.g., samples).

A tbl object with with dropped redundant elements (e.g., samples).

A tbl object with with dropped redundant elements (e.g., samples).

'\texttt{\texttt{SummarizedExperiment}}' object

'\texttt{\texttt{SummarizedExperiment}}' object

\begin{verbatim}
tidybulk::se_mini |> identify_abundant() |> remove_redundancy(
  .element = sample,
  .feature = transcript,
  .abundance = count,
\end{verbatim}
```r
method = "correlation"
)
counts.MDS =
tidybulk::se_mini |> identify_abundant() |> reduce_dimensions(method="MDS", .dims = 3)
remove_redundancy(
counts.MDS,
Dim_a_column = "Dim1",
Dim_b_column = "Dim2",
.element = sample,
.method = "reduced_dimensions"
)
```

<table>
<thead>
<tr>
<th>rename</th>
<th>Rename columns</th>
</tr>
</thead>
</table>

**Description**

Rename individual variables using `new_name = old_name` syntax.

**Arguments**

- `.data` A tbl. (See dplyr)
- `...` Use `new_name = old_name` to rename selected variables.

**Value**

An object of the same type as `.data`. * Rows are not affected. * Column names are changed; column order is preserved * Data frame attributes are preserved. * Groups are updated to reflect new names.

**Scoped selection and renaming**

Use the three scoped variants ([rename_all()], [rename_if()], [rename_at()]) to renaming a set of variables with a function.

**Methods**

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages:
See Also

Other single table verbs: `arrange()`, `filter()`, `mutate()`, `summarise()`

Examples

```r
iris <- as_tibble(iris) # so it prints a little nicerename(iris, petal_length = Petal.Length)
```

### rotate_dimensions

**Rotate two dimensions (e.g., principal components) of an arbitrary angle**

**Description**

`rotate_dimensions()` takes as input a `tbl` formatted as |

<DIMENSION 1> | <DIMENSION 2> | ... |

and calculates the rotated dimensional space of the transcript abundance.

**Usage**

```r
rotate_dimensions(
  .data, 
  dimension_1_column, 
  dimension_2_column, 
  rotation_degrees, 
  .element = NULL, 
  of_samples = TRUE, 
  dimension_1_column_rotated = NULL, 
  dimension_2_column_rotated = NULL, 
  action = "add"
)
```

```r
## S4 method for signature 'spec_tbl_df'
rotate_dimensions(
  .data, 
  dimension_1_column, 
  dimension_2_column, 
  rotation_degrees, 
  .element = NULL, 
  of_samples = TRUE, 
  dimension_1_column_rotated = NULL, 
  dimension_2_column_rotated = NULL, 
  action = "add"
)
```

```r
## S4 method for signature 'tbl_df'
rotate_dimensions(
  .data, 
  dimension_1_column, 
  dimension_2_column, 
  rotation_degrees, 
  .element = NULL, 
  of_samples = TRUE, 
  dimension_1_column_rotated = NULL, 
  dimension_2_column_rotated = NULL, 
  action = "add"
)
```

```r
## S4 method for signature 'tbl'
rotate_dimensions(
  .data, 
  dimension_1_column, 
  dimension_2_column, 
  rotation_degrees, 
  .element = NULL, 
  of_samples = TRUE, 
  dimension_1_column_rotated = NULL, 
  dimension_2_column_rotated = NULL, 
  action = "add"
)
```
rotate_dimensions

rotate_dimensions(.data,
                   dimension_1_column,
                   dimension_2_column,
                   rotation_degrees,
                   .element = NULL,
                   of_samples = TRUE,
                   dimension_1_column_rotated = NULL,
                   dimension_2_column_rotated = NULL,
                   action = "add")

## S4 method for signature 'tidybulk'
rotate_dimensions(.data,
                   dimension_1_column,
                   dimension_2_column,
                   rotation_degrees,
                   .element = NULL,
                   of_samples = TRUE,
                   dimension_1_column_rotated = NULL,
                   dimension_2_column_rotated = NULL,
                   action = "add")

## S4 method for signature 'SummarizedExperiment'
rotate_dimensions(.data,
                   dimension_1_column,
                   dimension_2_column,
                   rotation_degrees,
                   .element = NULL,
                   of_samples = TRUE,
                   dimension_1_column_rotated = NULL,
                   dimension_2_column_rotated = NULL,
                   action = "add")

## S4 method for signature 'RangedSummarizedExperiment'
rotate_dimensions(.data,
                   dimension_1_column,
                   dimension_2_column,
                   rotation_degrees,
                   .element = NULL,
                   of_samples = TRUE,
                   dimension_1_column_rotated = NULL,
                   dimension_2_column_rotated = NULL,
                   action = "add"
Arguments

.data  A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

dimension_1_column  A character string. The column of the dimension 1

dimension_2_column  A character string. The column of the dimension 2

rotation_degrees  A real number between 0 and 360

.element  The name of the element column (normally samples).

of_samples  A boolean. In case the input is a tidybulk object, it indicates Whether the element column will be sample or transcript column

dimension_1_column_rotated  A character string. The column of the rotated dimension 1 (optional)

dimension_2_column_rotated  A character string. The column of the rotated dimension 2 (optional)

action  A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).

Details

‘r lifecycle::badge("maturing")’

This function to rotate two dimensions such as the reduced dimensions.

Underlying custom method: rotation = function(m, d) // r = the angle // m data matrix r = d * pi / 180 ((bind_rows( c(‘1’ = cos(r), ‘2’ = -sin(r)), c(‘1’ = sin(r), ‘2’ = cos(r))) ) |> as_matrix())

Value

A tbl object with additional columns for the reduced dimensions. additional columns for the rotated dimensions. The rotated dimensions will be added to the original data set as ‘<NAME OF DIMENSION> rotated <ANGLE>’ by default, or as specified in the input arguments.

A tbl object with additional columns for the reduced dimensions. additional columns for the rotated dimensions. The rotated dimensions will be added to the original data set as ‘<NAME OF DIMENSION> rotated <ANGLE>’ by default, or as specified in the input arguments.

A tbl object with additional columns for the reduced dimensions. additional columns for the rotated dimensions. The rotated dimensions will be added to the original data set as ‘<NAME OF DIMENSION> rotated <ANGLE>’ by default, or as specified in the input arguments.

A tbl object with additional columns for the reduced dimensions. additional columns for the rotated dimensions. The rotated dimensions will be added to the original data set as ‘<NAME OF DIMENSION> rotated <ANGLE>’ by default, or as specified in the input arguments.

A ‘SummarizedExperiment’ object

A ‘SummarizedExperiment’ object
Examples

```r
counts.MDS =
tidybulk::se_mini |>
  identify_abundant() |>
  reduce_dimensions( method="MDS", .dims = 3)

counts.MDS.rotated = rotate_dimensions(counts.MDS, "Dim1", "Dim2", rotation_degrees = 45, .element = sample)
```

Description

See [this repository](https://github.com/jennybc/row-oriented-workflows) for alternative ways to perform row-wise operations.

Arguments

- **data**
  - Input data frame.
- **...**
  - Variables to be preserved when calling summarise(). This is typically a set of variables whose combination uniquely identify each row. NB: unlike group_by() you can not create new variables here but instead you can select multiple variables with (e.g.) everything().

Details

`rowwise()` is used for the results of [do()] when you create list-variables. It is also useful to support arbitrary complex operations that need to be applied to each row.

Currently, rowwise grouping only works with data frames. Its main impact is to allow you to work with list-variables in summarise() and mutate() without having to use `[[1]]`. This makes `summarise()` on a rowwise tbl effectively equivalent to `plyr::ldply()`.

Value

A consistent object (to the input)

A `tbl`

Examples

```r
df <- expand.grid(x = 1:3, y = 3:1)
df_done <- df |> rowwise()
```
scale_abundance

Scale the counts of transcripts/genes

Description

scale_abundance() takes as input a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and scales transcript abundance compensating for sequencing depth (e.g., with TMM algorithm, Robinson and Oshlack doi.org/10.1186/gb-2010-11-3-r25).

Usage

scale_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "TMM",
  reference_sample = NULL,
  .subset_for_scaling = NULL,
  action = "add",
  reference_selection_function = NULL
)

## S4 method for signature 'spec_tbl_df'
scale_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "TMM",
  reference_sample = NULL,
  .subset_for_scaling = NULL,
  action = "add",
  reference_selection_function = NULL
)

## S4 method for signature 'tbl_df'
scale_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "TMM",
  reference_sample = NULL,
  .subset_for_scaling = NULL,
  action = "add",
  reference_selection_function = NULL
)
reference_selection_function = NULL

## S4 method for signature 'tidybulk'
scale_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "TMM",
  reference_sample = NULL,
  .subset_for_scaling = NULL,
  action = "add",
  reference_selection_function = NULL
)

## S4 method for signature 'SummarizedExperiment'
scale_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "TMM",
  reference_sample = NULL,
  .subset_for_scaling = NULL,
  action = "add",
  reference_selection_function = NULL
)

## S4 method for signature 'RangedSummarizedExperiment'
scale_abundance(
  .data,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "TMM",
  reference_sample = NULL,
  .subset_for_scaling = NULL,
  action = "add",
  reference_selection_function = NULL
)

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

.sample The name of the sample column
The name of the transcript/gene column

The name of the transcript/gene abundance column

A character string. The scaling method passed to the back-end function (i.e., edgeR::calcNormFactors; "TMM","TMMwsp","RLE","upperquartile")

A character string. The name of the reference sample. If NULL the sample with highest total read count will be selected as reference.

A gene-wise quosure condition. This will be used to filter rows (features/genes) of the dataset. For example

A character string between "add" (default) and "only". "add" joins the new information to the input tbl (default), "only" return a non-redundant tbl with the just new information.

DEPRECATED. please use reference_sample.

Scales transcript abundance compensating for sequencing depth (e.g., with TMM algorithm, Robinson and Oshlack doi.org/10.1186/gb-2010-11-3-r25). Lowly transcribed transcripts/genes (defined with minimum_counts and minimum_proportion parameters) are filtered out from the scaling procedure. The scaling inference is then applied back to all unfiltered data.

Underlying method edgeR::calcNormFactors(.data, method = c("TMM","TMMwsp","RLE","upperquartile"))

A tbl object with additional columns with scaled data as '<NAME OF COUNT COLUMN>_scaled'

A tbl object with additional columns with scaled data as '<NAME OF COUNT COLUMN>_scaled'

A tbl object with additional columns with scaled data as '<NAME OF COUNT COLUMN>_scaled'

A tbl object with additional columns with scaled data as '<NAME OF COUNT COLUMN>_scaled'

A 'SummarizedExperiment' object

A 'SummarizedExperiment' object

```r
tidybulk::se_mini |>
  identify_abundant() |>
  scale_abundance()
```
se

**Description**
SummarizedExperiment

**Usage**
se

**Format**
An object of class RangedSummarizedExperiment with 100 rows and 8 columns.

se_mini

**Description**
SummarizedExperiment mini for vignette

**Usage**
se_mini

**Format**
An object of class SummarizedExperiment with 527 rows and 5 columns.

summarise

**Description**
‘summarise()’ creates a new data frame. It will have one (or more) rows for each combination of grouping variables; if there are no grouping variables, the output will have a single row summarising all observations in the input. It will contain one column for each grouping variable and one column for each of the summary statistics that you have specified.
‘summarise()’ and ‘summarize()’ are synonyms.
Arguments

.data A tbl. (See dplyr)

... <[‘tidy-eval’][dplyr_tidy_eval]> Name-value pairs of summary functions. The name will be the name of the variable in the result.

The value can be:

* A vector of length 1, e.g. ‘min(x)’, ‘n()’, or ‘sum(is.na(y))’. * A vector of length ‘n’, e.g. ‘quantile()’. * A data frame, to add multiple columns from a single expression.

Value

An object _usually_ of the same type as `.data`.

* The rows come from the underlying ‘group_keys()’. * The columns are a combination of the grouping keys and the summary expressions that you provide. * If ‘x’ is grouped by more than one variable, the output will be another [grouped_df] with the right-most group removed. * If ‘x’ is grouped by one variable, or is not grouped, the output will be a [tibble]. * Data frame attributes are **not** preserved, because ‘summarise()’ fundamentally creates a new data frame.

Useful functions

* Center: [mean()], [median()] * Spread: [sd()], [IQR()], [mad()] * Range: [min()], [max()], [quantile()] * Position: [first()], [last()], [nth()] * Count: [n()], [n_distinct()] * Logical: [any()], [all()]

Backend variations

The data frame backend supports creating a variable and using it in the same summary. This means that previously created summary variables can be further transformed or combined within the summary, as in [mutate()]. However, it also means that summary variables with the same names as previous variables overwrite them, making those variables unavailable to later summary variables.

This behaviour may not be supported in other backends. To avoid unexpected results, consider using new names for your summary variables, especially when creating multiple summaries.

Methods

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages:

See Also

Other single table verbs: arrange(), filter(), mutate(), rename()
symbol_to_entrez  

Examples

# A summary applied to ungrouped tbl returns a single row

mtcars |> summarise(mean = mean(disp))

symbol_to_entrez  Get ENTREZ id from gene SYMBOL

Description

Get ENTREZ id from gene SYMBOL

Usage

symbol_to_entrez(.data, .transcript = NULL, .sample = NULL)

Arguments

.data  A tt or tbl object.
.transcript  A character. The name of the gene symbol column.
.sample  The name of the sample column

Value

A tbl

Examples

# This function was designed for data.frame  
# Convert from SummarizedExperiment for this example. It is NOT recomended.

tidybulk::se_mini |> tidybulk() |> as_tibble() |> symbol_to_entrez(.transcript = .feature, .sample = .sample)
test_differential_abundance

Perform differential transcription testing using edgeR quasi-likelihood (QLT), edgeR likelihood-ratio (LR), limma-voom, limma-voom-with-quality-weights or DESeq2

Description

test_differential_abundance() takes as input a `tbl` (with at least three columns for sample, feature and transcript abundance) or a `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional columns for the statistics from the hypothesis test.

Usage

test_differential_abundance(
  .data,  
  .formula,  
  .sample = NULL,  
  .transcript = NULL,  
  .abundance = NULL,  
  contrasts = NULL,  
  method = "edgeR_quasi_likelihood",  
  test_above_log2_fold_change = NULL,  
  scaling_method = "TMM",  
  omit_contrast_in_colnames = FALSE,  
  prefix = "",  
  action = "add",  
  ...,  
  significance_threshold = NULL,  
  fill_missing_values = NULL,  
  .contrasts = NULL
)

## S4 method for signature 'spec_tbl_df'

test_differential_abundance(
  .data,  
  .formula,  
  .sample = NULL,  
  .transcript = NULL,  
  .abundance = NULL,  
  contrasts = NULL,  
  method = "edgeR_quasi_likelihood",  
  test_above_log2_fold_change = NULL,  
  scaling_method = "TMM",  
  omit_contrast_in_colnames = FALSE,  
  prefix = ""
test_differential_abundance

action = "add",
...,
significance_threshold = NULL,
fill_missing_values = NULL,
.contrasts = NULL
)

## S4 method for signature 'tbl_df'
test_differential_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  contrasts = NULL,
  method = "edgeR_quasi_likelihood",
  test_above_log2_fold_change = NULL,
  scaling_method = "TMM",
  omit_contrast_in_colnames = FALSE,
  prefix = "",
  action = "add",
  ...
)

## S4 method for signature 'tidybulk'
test_differential_abundance(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  contrasts = NULL,
  method = "edgeR_quasi_likelihood",
  test_above_log2_fold_change = NULL,
  scaling_method = "TMM",
  omit_contrast_in_colnames = FALSE,
  prefix = "",
  action = "add",
  ...
)

## S4 method for signature 'SummarizedExperiment'
test_differential_abundance(
  .data, 
  .formula, 
  .sample = NULL, 
  .transcript = NULL, 
  .abundance = NULL, 
  contrasts = NULL, 
  method = "edgeR_quasi_likelihood", 
  test_above_log2_fold_change = NULL, 
  scaling_method = "TMM", 
  omit_contrast_in_colnames = FALSE, 
  prefix = "", 
  action = "add", 
  ..., 
  significance_threshold = NULL, 
  fill_missing_values = NULL, 
  .contrasts = NULL
)

## S4 method for signature 'RangedSummarizedExperiment'

## Arguments

- **.data** 
  A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

- **.formula** 
  A formula representing the desired linear model. If there is more than one factor, they should be in the order factor of interest + additional factors.

- **.sample** 
  The name of the sample column

- **.transcript** 
  The name of the transcript/gene column
The name of the transcript/gene abundance column.

This parameter takes the format of the contrast parameter of the method of choice. For edgeR and limma-voom is a character vector. For DESeq2 is a list including a character vector of length three. The first covariate is the one the model is tested against (e.g., ~ factor_of_interest)

A string character. Either "edgeR_quasi_likelihood" (i.e., QLF), "edgeR_likelihood_ratio" (i.e., LRT), "edgeR_robust_likelihood_ratio", "DESeq2", "limma_voom", "limma_voom_sample_weights"

A positive real value. This works for edgeR and limma_voom methods. It uses the ‘treat’ function, which tests that the difference in abundance is bigger than this threshold rather than zero https://pubmed.ncbi.nlm.nih.gov/19176553.

A character string. The scaling method passed to the back-end functions: edgeR and limma-voom (i.e., edgeR::calcNormFactors; "TMM", "TMMwsp", "RLE", "upperquartile"). Setting the parameter to "none" will skip the compensation for sequencing-depth for the method edgeR or limma-voom.

If just one contrast is specified you can choose to omit the contrast label in the colnames.

A character string. The prefix you would like to add to the result columns. It is useful if you want to compare several methods.

A character string. Whether to join the new information to the input tbl (add), or just get the non-redundant tbl with the new information (get).

Further arguments passed to some of the internal functions. Currently, it is needed just for internal debug.

DEPRECATED - A real between 0 and 1 (usually 0.05).

DEPRECATED - A boolean. Whether to fill missing sample/transcript values with the median of the transcript. This is rarely needed.

DEPRECATED - This parameter takes the format of the contrast parameter of the method of choice. For edgeR and limma-voom is a character vector. For DESeq2 is a list including a character vector of length three. The first covariate is the one the model is tested against (e.g., ~ factor_of_interest)

Details

This function provides the option to use edgeR https://doi.org/10.1093/bioinformatics/btp616, limma-voom https://doi.org/10.1186/gb-2014-15-2-r29, limma_voom_sample_weights https://doi.org/10.1093/nar/gkv412 or DESeq2 https://doi.org/10.1186/s13059-014-0550-8 to perform the testing. All methods use raw counts, irrespective of if scale_abundance or adjust_abundance have been calculated, therefore it is essential to add covariates such as batch effects (if applicable) in the formula.

Underlying method for edgeR framework: .data >
# Filter keep_abundant(factor_of_interest = !(as.symbol(parse_formula(.formula)[1])), minimum_counts = minimum_counts, minimum_proportion = minimum_proportion) |> 

# Format select(!.transcript,!.sample,!.abundance) |> spread(!.sample,!.abundance) |> as_matrix(rownames = !.transcript) 

# edgeR edgeR::DGEList(counts = .) |> edgeR::calcNormFactors(method = scaling_method) |> edgeR::estimateDisp(design) |> 

# Fit edgeR::glmQLFit(design) |> or glmFit according to choice edgeR::glmQLFTest(coef = 2, contrast = my_contrasts) // or glmLRT according to choice 

Underlying method for DESeq2 framework: keep_abundant(factor_of_interest = !(as.symbol(parse_formula(.formula)[1])), minimum_counts = minimum_counts, minimum_proportion = minimum_proportion) |> 

# DESeq2 DESeq2::DESeqDataSet(design = .formula) |> DESeq2::DESeq() |> DESeq2::results() 

**Value**

A consistent object (to the input) with additional columns for the statistics from the test (e.g., log fold change, p-value and false discovery rate). 

A consistent object (to the input) with additional columns for the statistics from the test (e.g., log fold change, p-value and false discovery rate). 

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate). 

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate). 

A ‘SummarizedExperiment’ object 

A ‘SummarizedExperiment’ object 

**Examples**

# edgeR 

tidybulk::se_mini |> 
identify_abundant() |> 
test_differential_abundance(~ condition ) 

# The function `test_differential_abundance` operates with contrasts too 

tidybulk::se_mini |> 
identify_abundant(factor_of_interest = condition) |> 
test_differential_abundance(~ 0 + condition, 
contrast = c("conditionTRUE - conditionFALSE") 
) 

# DESeq2 - equivalent for limma-voom 

my_se_mini = tidybulk::se_mini 
my_se_mini$condition = factor(my_se_mini$condition)
# demonstrating with `fitType` that you can access any arguments to DESeq()

```r
my_se_mini |> 
  identify_abundant(factor_of_interest = condition) |> 
  test_differential_abundance(~ condition, method="deseq2", fitType="local")
```

# testing above a log2 threshold, passes along value to lfcThreshold of results()

```r
res <- my_se_mini |> 
  identify_abundant(factor_of_interest = condition) |> 
  test_differential_abundance(~ condition, method="deseq2", 
  fitType="local", 
  test_above_log2_fold_change=4 )
```

# Use random intercept and random effect models - NOT RUN BECAUSE MATRIX PACKAGE HAS A TEMPORARY BUG WITH LLME4

```r
## Not run:
se_mini[1:50,] |> 
  identify_abundant(factor_of_interest = condition) |> 
  test_differential_abundance(~ condition + (1 + condition | time), 
  method = "glmmsq_lme4", cores = 1)

## End(Not run)
```

# confirm that lfcThreshold was used

```r
## Not run:
res |> 
  mcols() |> 
  DESeq2::DESeqResults() |> 
  DESeq2::plotMA()

## End(Not run)
```

# The function `test_differential_abundance` operates with contrasts too

```r
my_se_mini |> 
  identify_abundant() |> 
  test_differential_abundance(~ 0 + condition, 
  contrasts = list(c("condition", "TRUE", "FALSE")), 
  method="deseq2", 
  fitType="local"
)
```

---

test_differential_cellularity

Add differential tissue composition information to a tbl
Description

test_differential_cellularity() takes as input a `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional columns for the statistics from the hypothesis test.

Usage

test_differential_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  significance_threshold = 0.05,
  ...
)

## S4 method for signature 'spec_tbl_df'
test_differential_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  significance_threshold = 0.05,
  ...
)

## S4 method for signature 'tbl_df'
test_differential_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  significance_threshold = 0.05,
  ...
)

## S4 method for signature 'tidybulk'
test_differential_cellularity(}
```r
## S4 method for signature 'SummarizedExperiment'

test_differential_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  significance_threshold = 0.05,
  ...
)
```

```r
## S4 method for signature 'RangedSummarizedExperiment'

test_differential_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  significance_threshold = 0.05,
  ...
)
```

**Arguments**

- `.data` A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

- `.formula` A formula representing the desired linear model. The formula can be of two forms: multivariable (recommended) or univariable Respectively: `factor_of_interest ~ .` or `~ factor_of_interest`. The dot represents cell-type proportions, and it is mandatory. If censored regression is desired (coxph) the formula should be of the form `Surv(y, dead) ~ .`

- `.sample` The name of the sample column
test_differential_cellularity

.flowchart .transcript The name of the transcript/gene column
.flowchart .abundance The name of the transcript/gene abundance column
.flowchart method A string character. Either \"cibersort\", \"epic\" or \"llsr\". The regression method will be chosen based on being multivariable: lm or cox-regression (both on logit-transformed proportions); or univariable: beta or cox-regression (on logit-transformed proportions). See .formula for multi- or univariable choice.
.flowchart reference A data frame. The transcript/cell_type data frame of integer transcript abundance
.flowchart significance_threshold A real between 0 and 1 (usually 0.05).
.flowchart ... Further parameters passed to the method deconvolve_cellularity

Details

\机能 lifecycle::badge("maturing")

This routine applies a deconvolution method (e.g., Cibersort; DOI: 10.1038/nmeth.3337) and passes the proportions inferred into a generalised linear model (DOI:dx.doi.org/10.1007/s11749-010-0189-z) or a cox regression model (ISBN: 978-1-4757-3294-8)

Underlying method for the generalised linear model: data |> deconvolve_cellularity( !!.sample, !!.transcript, !!.abundance, method=method, reference = reference, action="get", ... ) [...] betareg::betareg(.my_formula, .)

Underlying method for the cox regression: data |> deconvolve_cellularity( !!.sample, !!.transcript, !!.abundance, method=method, reference = reference, action="get", ... ) [...] mutate(.proportion_0_corrected = .proportion_0_corrected |> boot::logit()) survival::coxph(.my_formula, .)

Value

A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

A 'SummarizedExperiment' object

A 'SummarizedExperiment' object

Examples

# Regular regression
test_differential_cellularity( tidybulk::se_mini ,
    . ~ condition,
    cores = 1
)

# Cox regression - multiple
tidybulk::se_mini |>

# Test
test_differential_cellularity(
test_gene_enrichment

```
survival::Surv(days, dead) ~ .,
cores = 1
```

---

test_gene_enrichment | analyse gene enrichment with EGSEA

**Description**

test_gene_enrichment() takes as input a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a ‘tbl’ of gene set information.

**Usage**

test_gene_enrichment(
  .data,
  .formula,
  .sample = NULL,
  .entrez,
  .abundance = NULL,
  contrasts = NULL,
  methods = c("camera", "roast", "safe", "gage", "padog", "globaltest", "ora"),
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease",
                "kegg_metabolism", "kegg_signaling"),
  species,
  cores = 10,
  method = NULL,
  .contrasts = NULL
)

# S4 method for signature 'spec_tbl_df'
test_gene_enrichment(
  .data,
  .formula,
  .sample = NULL,
  .entrez,
  .abundance = NULL,
  contrasts = NULL,
  methods = c("camera", "roast", "safe", "gage", "padog", "globaltest", "ora"),
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease",
                "kegg_metabolism", "kegg_signaling"),
  species,
  cores = 10,
test_gene_enrichment

```r
method = NULL,
.contrasts = NULL
)

## S4 method for signature 'tbl_df'
test_gene_enrichment(
  .data,
  .formula,
  .sample = NULL,
  .entrez,
  .abundance = NULL,
  contrasts = NULL,
  methods = c("camera", "roast", "safe", "gage", "padog", "globaltest", "ora"),
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease",
                "kegg_metabolism", "kegg_signaling"),
  species,
  cores = 10,
  method = NULL,
  .contrasts = NULL
)

## S4 method for signature 'tidybulk'
test_gene_enrichment(
  .data,
  .formula,
  .sample = NULL,
  .entrez,
  .abundance = NULL,
  contrasts = NULL,
  methods = c("camera", "roast", "safe", "gage", "padog", "globaltest", "ora"),
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease",
                "kegg_metabolism", "kegg_signaling"),
  species,
  cores = 10,
  method = NULL,
  .contrasts = NULL
)

## S4 method for signature 'SummarizedExperiment'
test_gene_enrichment(
  .data,
  .formula,
  .sample = NULL,
  .entrez,
  .abundance = NULL,
  contrasts = NULL,
  methods = c("camera", "roast", "safe", "gage", "padog", "globaltest", "ora"),
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease",
```
```r
"kegg_metabolism", "kegg_signaling"),
species,
cores = 10,
method = NULL,
.contrasts = NULL
)
```

## S4 method for signature 'RangedSummarizedExperiment'

```r
test_gene_enrichment(.
data,
.formula,
.sample = NULL,
.entrez,
.abundance = NULL,
.contrasts = NULL,
.methods = c("camera", "roast", "safe", "gage", "padog", "globaltest", "ora"),
.gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease", "kegg_metabolism", "kegg_signaling"),
species,
cores = 10,
.method = NULL,
.contrasts = NULL)
```

### Arguments

- `.data` A `tbl` (with at least three columns for sample, feature and transcript abundance) or `SummarizedExperiment` (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
- `.formula` A formula with no response variable, representing the desired linear model
- `.sample` The name of the sample column
- `.entrez` The ENTREZ ID of the transcripts/genes
- `.abundance` The name of the transcript/gene abundance column
- `.contrasts` This parameter takes the format of the contrast parameter of the method of choice. For edgeR and limma-voom is a character vector. For DESeq2 is a list including a character vector of length three. The first covariate is the one the model is tested against (e.g., ~ factor_of_interest)
- `.methods` A character vector. One or 3 or more methods to use in the testing (currently EGSEA errors if 2 are used). Type EGSEA::egsea.base() to see the supported GSE methods.
- `.gene_sets` A character vector or a list. It can take one or more of the following built-in collections as a character vector: c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease", "kegg_metabolism", "kegg_signaling"), to be used with EGSEA buildIdx. c1 is human specific. Alternatively, a list of user-supplied gene sets can be provided, to be used with EGSEA buildCustomIdx. In that case, each gene set is a character vector of Entrez IDs and the names of the list are the gene set names.
species  A character. It can be human, mouse or rat.
cores    An integer. The number of cores available
method   DEPRECATED. Please use methods.
.contrasts DEPRECATED - This parameter takes the format of the contrast parameter of
                the method of choice. For edgeR and limma-voom is a character vector. For
                DESeq2 is a list including a character vector of length three. The first covariate
                is the one the model is tested against (e.g., ~ factor_of_interest)

Details
'r lifecycle::badge("maturing")'
This wrapper execute ensemble gene enrichment analyses of the dataset using EGSEA (DOI:0.12688/f1000research.12544.1)

dge = data |> keep_abundant( factor_of_interest = !!as.symbol(parse_formula(.formula)[[1]]), !!.sample,
                         !!.entrez, !!.abundance )

# Make sure transcript names are adjacent [...] as_matrix(rownames = !!.entrez) edgeR::DGEList(counts = )
idx = buildIdx(entrezIDs = rownames(dge), species = species, msigdb.gsets = msigdb.gsets, kegg.exclude = kegg.exclude)

dge |>  # Calculate weights limma::voom(design, plot = FALSE) |>  
       # Execute EGSEA egsea( contrasts = my_contrasts, baseGSEAs = methods, gs.annots = idx, sort.by = "med.rank", num.threads = cores, report = FALSE )

Value
A consistent object (to the input)
A consistent object (to the input)
A consistent object (to the input)
A consistent object (to the input)
A consistent object (to the input)
A consistent object (to the input)

Examples
## Not run:

library(SummarizedExperiment)
se = tidybulk::se_mini
rowData( se)$entrez = rownames(se )
df_entrez = aggregate_duplicates(se,.transcript = entrez )

library("EGSEA")
test_gene_enrichment(
df_entrez,
test_gene_overrepresentation

analyse gene over-representation with GSEA

Description

test_gene_overrepresentation() takes as input a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a ‘tbl’ with the GSEA statistics

Usage

test_gene_overrepresentation(
  .data,
  .entrez,
  .do_test,
  species,
  .sample = NULL,
  gene_sets = NULL,
  gene_set = NULL
)

## S4 method for signature 'spec_tbl_df'
test_gene_overrepresentation(
  .data,
  .entrez,
  .do_test,
  species,
  .sample = NULL,
  gene_sets = NULL,
  gene_set = NULL
)

## S4 method for signature 'tbl_df'

### Arguments

- **.data**: A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
.entrez The ENTREZ ID of the transcripts/genes
.do_test A boolean column name symbol. It indicates the transcript to check
.species A character. For example, human or mouse. MSigDB uses the latin species names (e.g., "Mus musculus", "Homo sapiens")
.sample The name of the sample column
gene_sets A character vector. The subset of MSigDB datasets you want to test against (e.g. "C2"). If NULL all gene sets are used (suggested). This argument was added to avoid time overflow of the examples.
gene_set DEPRECATED. Use gene_sets instead.

details

Details

`r lifecycle::badge("maturing")`
This wrapper execute gene enrichment analyses of the dataset using a list of transcripts and GSEA. This wrapper uses clusterProfiler (DOI: doi.org/10.1089/omi.2011.0118) on the back-end.
Undelying method: msigdb::msigdb(species = species) |> nest(data = -gs_cat) |> mutate(test = map( data, ~ clusterProfiler::enricher( my_entrez_rank, TERM2GENE=.x |> select(gs_name, entrez_gene), pvalueCutoff = 1 ) |> as_tibble() ))

Value

A consistent object (to the input)
A `spec_tbl_df` object
A `tbl_df` object
A `tidybulk` object
A `SummarizedExperiment` object
A `RangedSummarizedExperiment` object

Examples

print("Not run for build time.")

# se_mini = aggregate_duplicates(tidybulk::se_mini, .transcript = entrez)
# df_entrez = mutate(df_entrez, do_test = feature %in% c("TNFRSF4", "PLCH2", "PADI4", "PAX7"))

## Not run:
test_gene_overrepresentation(
  df_entrez,
  .sample = sample,
  .entrez = entrez,
  .do_test = do_test,
  species="Homo sapiens",
  gene_sets =c("C2")
)

## End(Not run)
test_gene_rank

analyse gene rank with GSEA

Description

test_gene_rank() takes as input a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a ‘tbl’ with the GSEA statistics

Usage

test_gene_rank(
  .data,
  .entrez,
  .arrange_desc,
  species,
  .sample = NULL,
  gene_sets = NULL,
  gene_set = NULL
)

## S4 method for signature 'spec_tbl_df'
test_gene_rank(
  .data,
  .entrez,
  .arrange_desc,
  species,
  .sample = NULL,
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7"),
  gene_set = NULL
)

## S4 method for signature 'tbl_df'
test_gene_rank(
  .data,
  .entrez,
  .arrange_desc,
  species,
  .sample = NULL,
  gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7"),
  gene_set = NULL
)

## S4 method for signature 'tidybulk'
test_gene_rank(
  .data,
  .entrez,
test_gene_rank

```
.data, .entrez, .arrange_desc, species, .sample = NULL, gene_sets = c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7"),
gene_set = NULL
```

```R
## S4 method for signature 'SummarizedExperiment'

test_gene_rank(
  .data, .entrez, .arrange_desc, species, .sample = NULL, gene_sets = NULL, gene_set = NULL)
)
## S4 method for signature 'RangedSummarizedExperiment'

test_gene_rank(
  .data, .entrez, .arrange_desc, species, .sample = NULL, gene_sets = NULL, gene_set = NULL
)
```

Arguments

.data A ‘tbl‘ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment‘ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

.entrez The ENTREZ ID of the transcripts/genes

.arrange_desc A column name of the column to arrange in decreasing order

.species A character. For example, human or mouse. MSigDB uses the latin species names (e.g., "Mus musculus", "Homo sapiens")

.sample The name of the sample column

gene_sets A character vector or a list. It can take one or more of the following built-in collections as a character vector: c("h", "c1", "c2", "c3", "c4", "c5", "c6", "c7", "kegg_disease", "kegg_metabolism", "kegg_signaling"), to be used with EGSEA buildIdx. c1 is human specific. Alternatively, a list of user-supplied gene sets can be provided, to be used with EGSEA buildCustomIdx. In that case, each gene set is a character vector of Entrez IDs and the names of the list are the gene set names.

gene_set DEPRECATED. Use gene_sets instead.
Details

[Maturing]

This wrapper execute gene enrichment analyses of the dataset using a list of transcripts and GSEA. This wrapper uses clusterProfiler (DOI: doi.org/10.1089/omi.2011.0118) on the back-end.

Undelying method:

```r
# Get gene sets signatures
msigdb::msigdb(species = species)

# Filter specific gene_sets if specified. This was introduced to speed up examples execution
!is.null(gene_sets) -> filter(.x) |

# Execute calculation
nest(data = -gs_cat) |> mutate(fit = map(data, ~ clusterProfiler::GSEA(my_entrez_rank, TERM2GENE=.x) |> select(gs_name, entrez_gene), pvalueCutoff = 1 ))
```

Value

A consistent object (to the input)
A ‘spec_tbl_df’ object
A ‘tbl_df’ object
A ‘tidybulk’ object
A ‘SummarizedExperiment’ object
A ‘RangedSummarizedExperiment’ object

Examples

```
print("Not run for build time.")
```

```
## Not run:
df_entrez = tidybulk::se_mini
df_entrez = mutate(df_entrez, do_test = .feature %in% c("TNFRSF4", "PLCH2", "PADI4", "PAX7"))
df_entrez = df_entrez |> test_differential_abundance(~ condition)

test_gene_rank(
df_entrez,
.sample = .sample,
.entrez = entrez,
.species="Homo sapiens",
gene_sets =c("C2"),
.arrange_desc = logFC)
```

## End(Not run)
Test of stratification of biological replicates based on tissue composition, one cell-type at a time, using Kaplan-meier curves.

Description

test_stratification_cellularity() takes as input a 'tbl' (with at least three columns for sample, feature and transcript abundance) or 'SummarizedExperiment' (more convenient if abstracted to tibble with library(tidySummarizedExperiment)) and returns a consistent object (to the input) with additional columns for the statistics from the hypothesis test.

Usage

test_stratification_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  ...
)

## S4 method for signature 'spec_tbl_df'
test_stratification_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  ...
)

## S4 method for signature 'tbl_df'
test_stratification_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  ...
```r
## S4 method for signature 'tidybulk'
test_stratification_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  ...
)

## S4 method for signature 'SummarizedExperiment'
test_stratification_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  ...
)

## S4 method for signature 'RangedSummarizedExperiment'
test_stratification_cellularity(
  .data,
  .formula,
  .sample = NULL,
  .transcript = NULL,
  .abundance = NULL,
  method = "cibersort",
  reference = X_cibersort,
  ...
)

Arguments

.data A ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

.formula A formula representing the desired linear model. The formula can be of two forms: multivariable (recommended) or univariable Respectively: "factor_of_interest ~ ." or ". ~ factor_of_interest". The dot represents cell-type proportions, and it is mandatory. If censored regression is desired (coxph) the formula should be of the form "surv::Surv(y, dead) ~ ."
```
The name of the sample column
The name of the transcript/gene column
The name of the transcript/gene abundance column
A string character. Either "cibersort", "epic" or "llsr". The regression method will be chosen based on being multivariable: lm or cox-regression (both on logit-transformed proportions); or univariable: beta or cox-regression (on logit-transformed proportions). See .formula for multi- or univariable choice.
A data frame. The transcript/cell_type data frame of integer transcript abundance
Further parameters passed to the method deconvolve_cellularity

Details
This routine applies a deconvolution method (e.g., Cibersort; DOI: 10.1038/nmeth.3337) and passes the proportions inferred into a generalised linear model (DOI:dx.doi.org/10.1007/s11749-010-0189-z) or a cox regression model (ISBN: 978-1-4757-3294-8)
Underlying method for the test: data |> deconvolve_cellularity( !.sample, !.transcript, !.abundance, method=method, reference = reference, action="get", ... ) [...] |> mutate(.high_cellularity = .proportion > median(.proportion)) |> survival::survdiff(data = data, .my_formula)

Value
A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).
A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).
A consistent object (to the input) with additional columns for the statistics from the hypothesis test (e.g., log fold change, p-value and false discovery rate).

Examples
tidybulk::se_mini |> test_stratification_cellularity( survival::Surv(days, dead) ~ ., cores = 1 )
tidybulk

Creates an annotated ‘tidybulk’ tibble from a ‘tbl’ or ‘SummarizedExperiment’ object

Description

tidybulk() creates an annotated ‘tidybulk’ tibble from a ‘tbl’ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

Usage

tidybulk(.data, .sample, .transcript, .abundance, .abundance_scaled = NULL)
## S4 method for signature 'spec_tbl_df'
tidybulk(.data, .sample, .transcript, .abundance, .abundance_scaled = NULL)
## S4 method for signature 'tbl_df'
tidybulk(.data, .sample, .transcript, .abundance, .abundance_scaled = NULL)
## S4 method for signature 'SummarizedExperiment'
tidybulk(.data, .sample, .transcript, .abundance, .abundance_scaled = NULL)
## S4 method for signature 'RangedSummarizedExperiment'
tidybulk(.data, .sample, .transcript, .abundance, .abundance_scaled = NULL)

Arguments

.data             A ‘tbl‘ (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))
.sample           The name of the sample column
.transcript       The name of the transcript/gene column
.abundance        The name of the transcript/gene abundance column
.abundance_scaled The name of the transcript/gene scaled abundance column

Details

‘r lifecycle::badge("maturing")’

This function creates a tidybulk object and is useful if you want to avoid to specify .sample, .transcript and .abundance arguments all the times. The tidybulk object have an attribute called internals where these three arguments are stored as metadata. They can be extracted as attr(<object>, "internals").
tidybulk_SAM_BAM

Value
A ‘tidybulk’ object

Examples

```r
tidybulk(tidybulk::se_mini)
```

### Description

tidybulk_SAM_BAM() creates a ‘tt’ object from a list of file names of BAM/SAM (with at least three columns for sample, feature and transcript abundance) or ‘SummarizedExperiment’ (more convenient if abstracted to tibble with library(tidySummarizedExperiment))

#### Usage

```r
tidybulk_SAM_BAM(file_names, genome = "hg38", ...)
```

#### Arguments

- `file_names`: A character vector
- `genome`: A character string specifying an in-built annotation used for read summarization. It has four possible values including "mm10", "mm9", "hg38" and "hg19"
- `...`: Further parameters passed to the function Rsubread::featureCounts

#### Details

'r lifecycle::badge("maturing")`

This function is based on FeatureCounts package (DOI: 10.1093/bioinformatics/btt656). This function creates a tidybulk object and is useful if you want to avoid to specify `.sample`, `.transcript` and `.abundance` arguments all the times. The tidybulk object have an attribute called internals where these three arguments are stored as metadata. They can be extracted as `attr(<object>, "internals")`. Underlying core function Rsubread::featureCounts(annot.inbuilt = genome,nthreads = n_cores, ...)
Value

A ‘tidybulk’ object
A ‘tidybulk’ object

______________________________

**tximeta_summarizeToGene_object**

*Needed for tests tximeta_summarizeToGene_object, It is SummarizedExperiment from tximeta*

______________________________

Description

Needed for tests tximeta_summarizeToGene_object, It is SummarizedExperiment from tximeta

Usage

`tximeta_summarizeToGene_object`

Format

An object of class RangedSummarizedExperiment with 10 rows and 1 columns.

______________________________

unnest

unnest

______________________________

Description

unnest
nest

Arguments

data
A tbl. (See tidyr)
cols
<‘tidy-select’>[tidyr_tidy_select]> Columns to unnest. If you ‘unnest()’ multiple columns, parallel entries must be of compatible sizes, i.e. they’re either equal or length 1 (following the standard tidyverse recycling rules).
names_sep
If ‘NULL’, the default, the names will be left as is. In ‘nest()’, inner names will come from the former outer names; in ‘unnest()’, the new outer names will come from the inner names.

If a string, the inner and outer names will be used together. In ‘nest()’, the names of the new outer columns will be formed by pasting together the outer and the inner column names, separated by ‘names_sep’. In ‘unnest()’, the new inner names will have the outer names (+ ‘names_sep’) automatically stripped. This makes ‘names_sep’ roughly symmetric between nesting and unnesting.
### keep_empty
See tidyr::unnest

### names_repair
See tidyr::unnest

### ptype
See tidyr::unnest

### .drop
See tidyr::unnest

### .id
tidyr::unnest

### .sep
tidyr::unnest

### .preserve
See tidyr::unnest

### .data
A tbl. (See tidyr)

... Name-variable pairs of the form new_col = c(col1, col2, col3) (See tidyr)

### Value

A tidySummarizedExperiment object or a tibble depending on input

A tt object

### Examples

```r
tidybulk::se_mini |> tidybulk() |> nest( data = -.feature) |> unnest(data)

tidybulk::se_mini %>% tidybulk() %>% nest( data = -.feature)
```

---

**Description**

Needed for vignette vignette_manuscript_signature_boxplot

**Usage**

vignette_manuscript_signature_boxplot

**Format**

An object of class tbl_df (inherits from tbl, data.frame) with 899 rows and 12 columns.
vignette_manuscript_signature_tsne

_Needed for vignette vignette_manuscript_signature_tsne_

**Description**

Needed for vignette vignette_manuscript_signature_tsne

**Usage**

`vignette_manuscript_signature_tsne`

**Format**

An object of class `spec_tbl_df` (inherits from `tbl_df`, `tbl`, `data.frame`) with 283 rows and 10 columns.

vignette_manuscript_signature_tsne2

_Needed for vignette vignette_manuscript_signature_tsne2_

**Description**

Needed for vignette vignette_manuscript_signature_tsne2

**Usage**

`vignette_manuscript_signature_tsne2`

**Format**

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 283 rows and 9 columns.

X_cibersort

_Cibersort reference_

**Description**

Cibersort reference

**Usage**

`X_cibersort`

**Format**

An object of class `data.frame` with 547 rows and 22 columns.
Pipe operator

Description

See magrittr::%>% for details.

Usage

lhs %>% rhs

Arguments

lhs  A value or the magrittr placeholder.
rhs  A function call using the magrittr semantics.

Value

The result of calling `rhs(lhs)`.
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