

Package ‘SimBu’

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Title Simulate Bulk RNA-seq Datasets from Single-Cell Datasets

Version 1.11.0

Description SimBu can be used to simulate bulk RNA-seq datasets with known cell type fractions. You can either use your own single-cell study for the simulation or the sfaira database. Different pre-defined simulation scenarios exist, as are options to run custom simulations. Additionally, expression values can be adapted by adding an mRNA bias, which produces more biologically relevant simulations.

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Encoding UTF-8

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Imports basilisk, BiocParallel, data.table, dplyr, ggplot2, tools, Matrix (>= 1.3.3), methods, phyloseq, proxyC, RColorBrewer, RCurl, reticulate, sparseMatrixStats, SummarizedExperiment, tidyr

Suggests curl, knitr, matrixStats, rmarkdown, Seurat (>= 5.0.0), SeuratObject (>= 5.0.0), testthat (>= 3.0.0)

URL <https://github.com/omnideconv/SimBu>

BugReports <https://github.com/omnideconv/SimBu/issues>

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calc_scaling_vector	<i>Calculate scaling factor for a dataset</i>
---------------------	---

Description

Each scaling factor has a default matrix it will try to use (counts or TPM). If the required matrix is not available, the other one is used and a warning is given.

Usage

```
calc_scaling_vector(
  data,
  scaling_factor,
  custom_scaling_vector,
  scaling_factor_single_cell,
  BPPARAM,
  run_parallel
)
```

Arguments

data	dataset object
scaling_factor	name of scaling factor; possible are: census, spike_in, read_number, custom or NONE for no scaling factor
custom_scaling_vector	named vector with custom scaling values for cell-types. Cell-types that do not occur in this vector but are present in the dataset will be set to 1
scaling_factor_single_cell	boolean: decide if a scaling value for each single cell is calculated (default) or the median of all scaling values for each cell type is calculated
BPPARAM	BiocParallel::bpparam() by default; if specific number of threads x want to be used, insert: BiocParallel::MulticoreParam(workers = x)
run_parallel	boolean, decide if multi-threaded calculation will be run. FALSE by default

Value

a named vector with a scaling value for each cell in the dataset

census	<i>Applies the Census count transformation on a count matrix</i>
--------	--

Description

needs a sparse matrix with cells in columns and genes in rows. You can find the detailed explanation here: <http://cole-trapnell-lab.github.io/monocle-release/docs/#census>

Usage

```
census(
  matrix,
  exp_capture_rate = 0.25,
  expr_threshold = 0,
  BPPARAM = BiocParallel::bpparam(),
  run_parallel = FALSE
)
```

Arguments

matrix	sparse count matrix; cells in columns, genes in rows
exp_capture_rate	expected capture rate; default=0.25
expr_threshold	expression threshold; default=0
BPPARAM	BiocParallel::bpparam() by default; if specific number of threads x want to be used, insert: BiocParallel::MulticoreParam(workers = x)
run_parallel	boolean, decide if multi-threaded calculation will be run. FALSE by default

Value

a vector for each cell-type, with a scaling factor which can be used to transform the counts of the matrix

Examples

```
tpm <- Matrix::Matrix(matrix(rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))
cen <- SimBu::census(tpm)
```

census_monocle	<i>Census calculation as implemented in monocle</i>
----------------	---

Description

Implementation taken from Monocle2: <https://github.com/cole-trapnell-lab/monocle-release/blob/master/R/normalization.R>

Usage

```
census_monocle(expr_matrix, exp_capture_rate, expr_threshold)
```

Arguments

```
expr_matrix      TPM matrix
exp_capture_rate expected capture rate; default=0.25
expr_threshold   expression threshold; default=0
```

Value

vector with estimated mRNA values per cell in expr_matrix

check_annotation	<i>check for correct column names in annotation file and replace them if necessary</i>
------------------	--

Description

check for correct column names in annotation file and replace them if necessary

Usage

```
check_annotation(annotation, cell_column = "cell_type", id_column = 1)
```

Arguments

```
annotation      dataframe; annotation dataframe
cell_column     name of cell-type column; default is "cell_type"
id_column       name of cell ID column; default is 1, which uses the rownames
```

Value

annotation dataframe with correct column names

check_if_tpm	<i>Checks, if a matrix is TPM-like (columns sum up to 1e6)</i>
--------------	--

Description

Checks, if a matrix is TPM-like (columns sum up to 1e6)

Usage

```
check_if_tpm(tpm_matrix, lower_limit = 7e+05)
```

Arguments

tpm_matrix	matrix to check
lower_limit	the lowest sum value, a cell may have

Value

boolean

compare_matrix_with_annotation	<i>Check if annotation and matrix have same cells</i>
--------------------------------	---

Description

Otherwise intersection of both is used

Usage

```
compare_matrix_with_annotation(m, annotation)
```

Arguments

m	matrix, column names are cells
annotation	data.frame, rownames are genes, cell names are in ID column

Value

intersected matrix

dataset	Build SummarizedExperiment using local annotation and count matrix R objects
---------	--

Description

Build [SummarizedExperiment](#) using local annotation and count matrix R objects

Usage

```
dataset(
  annotation,
  count_matrix = NULL,
  tpm_matrix = NULL,
  name = "SimBu_dataset",
  spike_in_col = NULL,
  additional_cols = NULL,
  filter_genes = TRUE,
  variance_cutoff = 0,
  type_abundance_cutoff = 0,
  scale_tpm = TRUE
)
```

Arguments

annotation	(mandatory) dataframe; needs columns 'ID' and 'cell_type'; 'ID' needs to be equal with cell_names in count_matrix
count_matrix	(mandatory) sparse count matrix; raw count data is expected with genes in rows, cells in columns
tpm_matrix	sparse count matrix; TPM like count data is expected with genes in rows, cells in columns
name	name of the dataset; will be used for new unique IDs of cells
spike_in_col	which column in annotation contains information on spike_in counts, which can be used to re-scale counts; mandatory for spike_in scaling factor in simulation
additional_cols	list of column names in annotation, that should be stored as well in dataset object
filter_genes	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below variance_cutoff
variance_cutoff	numeric, is only applied if filter_genes is TRUE: removes all genes with variance below the chosen cutoff (default = 0)
type_abundance_cutoff	numeric, remove all cells, whose cell-type appears less then the given value. This removes low abundant cell-types
scale_tpm	boolean, if TRUE (default) the cells in tpm_matrix will be scaled to sum up to 1e6

Value

Return a [SummarizedExperiment](#) object

Examples

```
counts <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell_", rep(1:300))
colnames(tpm) <- paste0("cell_", rep(1:300))
rownames(counts) <- paste0("gene_", rep(1:1000))
rownames(tpm) <- paste0("gene_", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell_", rep(1:300)),
  "cell_type" = c(rep("T cells CD4", 300))
)

ds <- SimBu::dataset(annotation = annotation, count_matrix = counts, tpm_matrix = tpm, name = "test_dataset")
```

dataset_h5ad

Build [SummarizedExperiment](#) using a h5ad file for the counts

Description

Build [SummarizedExperiment](#) using a h5ad file for the counts

Usage

```
dataset_h5ad(
  h5ad_file_counts,
  h5ad_file_tpm = NULL,
  cell_id_col = "ID",
  cell_type_col = "cell_type",
  cells_in_obs = TRUE,
  name = "SimBu_dataset",
  spike_in_col = NULL,
  additional_cols = NULL,
  filter_genes = TRUE,
  variance_cutoff = 0,
  type_abundance_cutoff = 0,
  scale_tpm = TRUE
)
```

Arguments

h5ad_file_counts	(mandatory) h5ad file with raw count data
h5ad_file_tpm	h5ad file with TPM count data
cell_id_col	(mandatory) name of column in Seurat meta.data with unique cell ids; 0 for rownames
cell_type_col	(mandatory) name of column in Seurat meta.data with cell type name

cells_in_obs	boolean, if TRUE, cell identifiers are taken from obs layer in anndata object; if FALSE, they are taken from var
name	name of the dataset; will be used for new unique IDs of cells#’ @param spike_in_col which column in annotation contains information on spike_in counts, which can be used to re-scale counts; mandatory for spike_in scaling factor in simulation
spike_in_col	which column in annotation contains information on spike_in counts, which can be used to re-scale counts; mandatory for spike_in scaling factor in simulation
additional_cols	list of column names in annotation, that should be stored as well in dataset object
filter_genes	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below variance_cutoff
variance_cutoff	numeric, is only applied if filter_genes is TRUE: removes all genes with variance below the chosen cutoff
type_abundance_cutoff	numeric, remove all cells, whose cell-type appears less then the given value. This removes low abundant cell-types
scale_tpm	boolean, if TRUE (default) the cells in tpm_matrix will be scaled to sum up to 1e6

Value

Return a [SummarizedExperiment](#) object

Examples

```
# h5 <- system.file("extdata", "anndata.h5ad", package = "SimBu")
# ds_h5ad <- SimBu::dataset_h5ad(
#   h5ad_file_counts = h5,
#   name = "h5ad_dataset",
#   cell_id_col = "id", # this will use the 'id' column of the metadata as cell identifiers
#   cell_type_col = "group", # this will use the 'group' column of the metadata as cell type info
#   cells_in_obs = TRUE
# ) # in case your cell information is stored in the var layer, switch to FALSE
```

dataset_merge

Merge multiple [SummarizedExperiment](#) datasets into one

Description

The objects need to have the same number of assays in order to work.

Usage

```
dataset_merge(
  dataset_list,
  name = "SimBu_dataset",
  spike_in_col = NULL,
  additional_cols = NULL,
  filter_genes = TRUE,
```

```

    variance_cutoff = 0,
    type_abundance_cutoff = 0,
    scale_tpm = TRUE
  )

```

Arguments

dataset_list	(mandatory) list of SummarizedExperiment objects
name	name of the new dataset
spike_in_col	which column in annotation contains information on spike_in counts, which can be used to re-scale counts; mandatory for spike_in scaling factor in simulation
additional_cols	list of column names in annotation, that should be stored as well in dataset object
filter_genes	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below variance_cutoff
variance_cutoff	numeric, is only applied if filter_genes is TRUE: removes all genes with variance below the chosen cutoff
type_abundance_cutoff	numeric, remove all cells, whose cell-type appears less then the given value. This removes low abundant cell-types
scale_tpm	boolean, if TRUE (default) the cells in tpm_matrix will be scaled to sum up to 1e6

Value

[SummarizedExperiment](#) object

Examples

```

counts <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell_", rep(1:300))
colnames(tpm) <- paste0("cell_", rep(1:300))
rownames(counts) <- paste0("gene_", rep(1:1000))
rownames(tpm) <- paste0("gene_", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell_", rep(1:300)),
  "cell_type" = c(rep("T cells CD4", 300))
)

ds1 <- SimBu::dataset(annotation = annotation, count_matrix = counts, tpm_matrix = tpm, name = "test_dataset1")
ds2 <- SimBu::dataset(annotation = annotation, count_matrix = counts, tpm_matrix = tpm, name = "test_dataset2")
ds_merged <- SimBu::dataset_merge(list(ds1, ds2))

```

dataset_seurat

*Build [SummarizedExperiment](#) using a [Seurat](#) object***Description**

Build [SummarizedExperiment](#) using a [Seurat](#) object

Usage

```
dataset_seurat(
  seurat_obj,
  counts_layer,
  cell_id_col,
  cell_type_col,
  assay = NULL,
  tpm_layer = NULL,
  name = "SimBu_dataset",
  spike_in_col = NULL,
  additional_cols = NULL,
  filter_genes = TRUE,
  variance_cutoff = 0,
  type_abundance_cutoff = 0,
  scale_tpm = TRUE
)
```

Arguments

seurat_obj	(mandatory) Seurat object with TPM counts
counts_layer	(mandatory) name of assay in Seurat object which contains count data in 'counts' slot
cell_id_col	(mandatory) name of column in Seurat meta.data with unique cell ids
cell_type_col	(mandatory) name of column in Seurat meta.data with cell type name
assay	name of the Seurat object assay that should be used. If NULL (default), the currently active assay is used
tpm_layer	name of assay in Seurat object which contains TPM data in 'counts' slot
name	name of the dataset; will be used for new unique IDs of cells
spike_in_col	which column in annotation contains information on spike_in counts, which can be used to re-scale counts; mandatory for spike_in scaling factor in simulation
additional_cols	list of column names in annotation, that should be stored as well in dataset object
filter_genes	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below variance_cutoff
variance_cutoff	numeric, is only applied if filter_genes is TRUE: removes all genes with variance below the chosen cutoff
type_abundance_cutoff	numeric, remove all cells, whose cell-type appears less than the given value. This removes low abundant cell-types
scale_tpm	boolean, if TRUE (default) the cells in tpm_matrix will be scaled to sum up to 1e6

Value

Return a [SummarizedExperiment](#) object

Examples

```
counts <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell-", rep(1:300))
colnames(tpm) <- paste0("cell-", rep(1:300))
rownames(counts) <- paste0("gene-", rep(1:1000))
rownames(tpm) <- paste0("gene-", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell-", rep(1:300)),
  "cell_type" = c(
    rep("T cells CD4", 50),
    rep("T cells CD8", 50),
    rep("Macrophages", 100),
    rep("NK cells", 10),
    rep("B cells", 70),
    rep("Monocytes", 20)
  ),
  row.names = paste0("cell-", rep(1:300))
)

seurat_obj <- Seurat::CreateSeuratObject(counts = counts, assay = "gene_expression", meta.data = annotation)
SeuratObject::LayerData(seurat_obj, assay = "gene_expression", layer = "data") <- tpm

ds_seurat <- SimBu::dataset_seurat(
  seurat_obj = seurat_obj,
  counts_layer = "counts",
  cell_id_col = "ID",
  cell_type_col = "cell_type",
  tpm_layer = "data",
  name = "seurat_dataset"
)
```

dataset_sfaira

Build [SummarizedExperiment](#) using a single sfaira entry ID**Description**

Build [SummarizedExperiment](#) using a single sfaira entry ID

Usage

```
dataset_sfaira(
  sfaira_id,
  sfaira_setup,
  name = "SimBu_dataset",
  spike_in_col = NULL,
```

```

    additional_cols = NULL,
    force = FALSE,
    filter_genes = TRUE,
    variance_cutoff = 0,
    type_abundance_cutoff = 0,
    scale_tpm = TRUE
  )

```

Arguments

<code>sfaira_id</code>	(mandatory) ID of a sfaira dataset
<code>sfaira_setup</code>	(mandatory) the sfaira setup; given by setup_sfaira
<code>name</code>	name of the dataset; will be used for new unique IDs of cells
<code>spike_in_col</code>	which column in annotation contains information on spike_in counts, which can be used to re-scale counts
<code>additional_cols</code>	list of column names in annotation, that should be stored as well in dataset object
<code>force</code>	boolean, if TRUE, datasets without annotation will be downloaded, FALSE otherwise (default)
<code>filter_genes</code>	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below <code>variance_cutoff</code>
<code>variance_cutoff</code>	numeric, is only applied if <code>filter_genes</code> is TRUE: removes all genes with variance below the chosen cutoff
<code>type_abundance_cutoff</code>	numeric, remove all cells, whose cell-type appears less then the given value. This removes low abundant cell-types
<code>scale_tpm</code>	boolean, if TRUE (default) the cells in <code>tpm_matrix</code> will be scaled to sum up to 1e6

Value

dataset object

Examples

```

setup_list <- SimBu::setup_sfaira(tempdir())
ds <- SimBu::dataset_sfaira(
  sfaira_id = "homosapiens_lungparenchyma_2019_10x3v2_madissoon_001_10.1186/s13059-019-1906-x",
  sfaira_setup = setup_list,
  name = "test_dataset"
)

```

dataset_sfaira_multiple

Build [SummarizedExperiment](#) using multiple sfaira entries

Description

You can apply different filters on the whole data-zoo of sfaria; the resulting single-cell datasets will be combined into a single dataset which you can use for simulation Note: only datasets in sfaira with annotation are considered!

Usage

```
dataset_sfaira_multiple(
  organisms = NULL,
  tissues = NULL,
  assays = NULL,
  sfaira_setup,
  name = "SimBu_dataset",
  spike_in_col = NULL,
  additional_cols = NULL,
  filter_genes = TRUE,
  variance_cutoff = 0,
  type_abundance_cutoff = 0,
  scale_tpm = TRUE
)
```

Arguments

organisms	(mandatory) list of organisms (only human and mouse available)
tissues	(mandatory) list of tissues
assays	(mandatory) list of assays
sfaira_setup	(mandatory) the sfaira setup; given by setup_sfaira
name	name of the dataset; will be used for new unique IDs of cells
spike_in_col	which column in annotation contains information on spike_in counts, which can be used to re-scale counts
additional_cols	list of column names in annotation, that should be stored as well in dataset object
filter_genes	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below variance_cutoff
variance_cutoff	numeric, is only applied if filter_genes is TRUE: removes all genes with variance below the chosen cutoff
type_abundance_cutoff	numeric, remove all cells, whose cell-type appears less then the given value. This removes low abundant cell-types
scale_tpm	boolean, if TRUE (default) the cells in tpm_matrix will be scaled to sum up to 1e6

Value

dataset object

Examples

```
setup_list <- SimBu::setup_sfaira(tempdir())
ds_human_lung <- SimBu::dataset_sfaira_multiple(
  sfaira_setup = setup_list,
  organisms = "Homo sapiens",
  tissues = "lung parenchyma",
  assay = "10x 3' v2",
  name = "human_lung"
)
```

dmode

use gaussian kernel to calculate the mode of transcript counts

Description

use gaussian kernel to calculate the mode of transcript counts

Usage

dmode(x)

Arguments

x vector of numeric values

Value

most commonly occurring (log-transformed) TPM value

download_sfaira

download a specific dataset from sfaira by an ID

Description

download a specific dataset from sfaira by an ID

Usage

```
download_sfaira(
  setup_list,
  ids,
  force = FALSE,
  synapse_user = NULL,
  synapse_pw = NULL
)
```

Arguments

setup_list	the sfaira setup; given by setup_sfaira
ids	the IDs of the datasets
force	logical; TRUE if you want to force the download, even though no cell-type annotation exists for this dataset. Default if FALSE
synapse_user	character; username for synapse portal (https://www.synapse.org)
synapse_pw	character; password for synapse portal (https://www.synapse.org)

Value

matrix, gene names and cell IDs

download_sfaira_multiple

download multiple datasets from sfaira using filters for organism, tissue and/or assay

Description

similar to the filters on the sfaira website (<https://theislab.github.io/sfaira-portal/Datasets>)

Usage

```
download_sfaira_multiple(
  setup_list,
  organisms = NULL,
  tissues = NULL,
  assays = NULL,
  force = FALSE
)
```

Arguments

setup_list	the sfaira setup; given by setup_sfaira
organisms	list of organisms (only human and mouse available)
tissues	list of tissues
assays	list of assays
force	logical; TRUE if you want to force to download all datasets, otherwise only the ones with cell-type annotation will be returned. Default if FALSE

Value

annotated data object, contains count matrix and annotation

filter_matrix	<i>filter one (or two) expression matrix by genes</i>
---------------	---

Description

filter one (or two) expression matrix by genes

Usage

```
filter_matrix(m1, m2 = NULL, filter_genes = TRUE, variance_cutoff = 0)
```

Arguments

m1	Matrix 1
m2	Matrix 2 (optional)
filter_genes	boolean
variance_cutoff	numeric, genes below this variance value are removed

Value

filtered matrix

generate_summarized_experiment	<i>Generate SummarizedExperiment using multiple parameters</i>
--------------------------------	--

Description

Generate SummarizedExperiment using multiple parameters

Usage

```
generate_summarized_experiment(
  annotation,
  count_matrix,
  tpm_matrix,
  name,
  spike_in_col,
  additional_cols,
  filter_genes,
  variance_cutoff,
  type_abundance_cutoff,
  scale_tpm
)
```

Arguments

annotation	(mandatory) dataframe; needs columns 'ID' and 'cell_type'; 'ID' needs to be equal with cell_names in count_matrix
count_matrix	(mandatory) sparse count matrix; raw count data is expected with genes in rows, cells in columns
tpm_matrix	sparse count matrix; TPM like count data is expected with genes in rows, cells in columns
name	name of the dataset; will be used for new unique IDs of cells
spike_in_col	which column in annotation contains information on spike_in counts, which can be used to re-scale counts; mandatory for spike_in scaling factor in simulation
additional_cols	list of column names in annotation, that should be stored as well in dataset object
filter_genes	boolean, if TRUE, removes all genes with 0 expression over all samples & genes with variance below variance_cutoff
variance_cutoff	numeric, is only applied if filter_genes is TRUE: removes all genes with variance below the chosen cutoff
type_abundance_cutoff	numeric, remove all cells, whose cell-type appears less then the given value. This removes low abundant cell-types
scale_tpm	boolean, if TRUE (default) the cells in tpm_matrix will be scaled to sum up to 1e6

Value

Return a [SummarizedExperiment](#) object

h5ad_to_adata	<i>Use basilisk environment to read h5ad file and access anndata object</i>
---------------	---

Description

Use basilisk environment to read h5ad file and access anndata object

Usage

```
h5ad_to_adata(h5ad_path, cells_in_obs)
```

Arguments

h5ad_path	path to h5ad file
cells_in_obs	boolean, if TRUE, cell identifiers are taken from obs layer in anndata object; if FALSE, they are taken from var

Value

matrix contained on h5ad file as dgCMatrix

merge_scaling_factor	<i>Create scaling vector from custom or pre-defined scaling factor</i>
----------------------	--

Description

Create scaling vector from custom or pre-defined scaling factor

Usage

```
merge_scaling_factor(data, scaling_factor_values, scaling_factor_name)
```

Arguments

data	dataset
scaling_factor_values	named list of scaling values
scaling_factor_name	name of scaling factor method

Value

scaling vector

merge_simulations	<i>Combine multiple simulations into one result</i>
-------------------	---

Description

we recommend to only merge simulations from the same dataset object, otherwise the count matrices might not correspond on the gene level

Usage

```
merge_simulations(simulation_list)
```

Arguments

simulation_list	a list of simulations
-----------------	-----------------------

Value

named list; bulk a [SummarizedExperiment](#) object, where the assays store the simulated bulk RNAseq datasets. Can hold either one or two assays, depending on how many matrices were present in the dataset cell-fractions is a dataframe with the simulated cell-fractions per sample; scaling_vector scaling value for each cell in dataset

Examples

```

counts <- Matrix::Matrix(matrix(rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell_", rep(1:300))
colnames(tpm) <- paste0("cell_", rep(1:300))
rownames(counts) <- paste0("gene_", rep(1:1000))
rownames(tpm) <- paste0("gene_", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell_", rep(1:300)),
  "cell_type" = c(
    rep("T cells CD4", 50),
    rep("T cells CD8", 50),
    rep("Macrophages", 100),
    rep("NK cells", 10),
    rep("B cells", 70),
    rep("Monocytes", 20)
  )
)

dataset <- SimBu::dataset(
  annotation = annotation,
  count_matrix = counts,
  tpm_matrix = tpm,
  name = "test_dataset"
)

s1 <- SimBu::simulate_bulk(dataset,
  scenario = "even",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 100
)

s2 <- SimBu::simulate_bulk(dataset,
  scenario = "even",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 100
)

s <- SimBu::merge_simulations(list(s1, s2))

```

plot_simulation

*Plot the cell-type fractions in your simulated dataset***Description**

Plot the cell-type fractions in your simulated dataset

Usage

```
plot_simulation(simulation)
```

Arguments

simulation a simulation object generated by `simulate_bulk`

Value

a `ggplot2` barplot

Examples

```
counts <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell_", rep(1:300))
colnames(tpm) <- paste0("cell_", rep(1:300))
rownames(counts) <- paste0("gene_", rep(1:1000))
rownames(tpm) <- paste0("gene_", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell_", rep(1:300)),
  "cell_type" = c(
    rep("T cells CD4", 50),
    rep("T cells CD8", 50),
    rep("Macrophages", 100),
    rep("NK cells", 10),
    rep("B cells", 70),
    rep("Monocytes", 20)
  )
)

dataset <- SimBu::dataset(
  annotation = annotation,
  count_matrix = counts,
  tpm_matrix = tpm,
  name = "test_dataset"
)

s <- SimBu::simulate_bulk(dataset,
  scenario = "even",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 100
)

SimBu::plot_simulation(s)
```

save_simulation

Save the expression matrix of a simulated pseudo-bulk dataset to a file

Description

Save the expression matrix of a simulated pseudo-bulk dataset to a file

Usage

```
save_simulation(simulation, filename, assay = "bulk_counts")
```

Arguments

simulation	the result of simulate_bulk()
filename	the filename where to save the expression matrix to
assay	name of the assay in simulation to save, default to bulk_counts

Value

write a file

Examples

```
counts <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell_", rep(1:300))
colnames(tpm) <- paste0("cell_", rep(1:300))
rownames(counts) <- paste0("gene_", rep(1:1000))
rownames(tpm) <- paste0("gene_", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell_", rep(1:300)),
  "cell_type" = c(
    rep("T cells CD4", 50),
    rep("T cells CD8", 50),
    rep("Macrophages", 100),
    rep("NK cells", 10),
    rep("B cells", 70),
    rep("Monocytes", 20)
  )
)

dataset <- SimBu::dataset(
  annotation = annotation,
  count_matrix = counts,
  tpm_matrix = tpm,
  name = "test_dataset"
)

s <- SimBu::simulate_bulk(dataset,
  scenario = "even",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 100
)

save_simulation(s, tempfile())
```

setup_sfaira	<i>setup the sfaira package</i>
--------------	---------------------------------

Description

If you want to download datasets from Sfaira, you need to specify a directory where the datasets are saved into. Additionally, when this function is called for the first time, a conda environment will be established and sfaira along all of its dependencies are installed. This can take some time but will be only performed one single time, as the environment can be re-used.

Usage

```
setup_sfaira(basedir)
```

Arguments

basedir name of the directory, where the raw files will be downloaded into

Value

list with sfaira file directories; must be used as input for other sfaira based functions

Examples

```
setup_list <- setup_sfaira(basedir = tempdir())
```

sfaira_overview	<i>Gives an overview of the possible datasets you can use from the sfaira database</i>
-----------------	--

Description

Gives an overview of the possible datasets you can use from the sfaira database

Usage

```
sfaira_overview(setup_list)
```

Arguments

setup_list the sfaira setup; given by [setup_sfaira](#)

Value

a dataframe with information on each dataset

Examples

```
setup_list <- setup_sfaira(basedir = tempdir())
# all_datasets <- sfaira_overview(setup_list)
```

SimBu	<i>SimBu: Bias-aware simulation of bulk RNA-seq data with variable cell type composition</i>
-------	--

Description

As complex tissues are typically composed of various cell types, deconvolution tools have been developed to computationally infer their cellular composition from bulk RNA sequencing (RNA-seq) data. To comprehensively assess deconvolution performance, gold-standard datasets are indispensable. The simulation of ‘pseudo-bulk’ data, generated by aggregating single-cell RNA-seq (scRNA-seq) expression profiles in pre-defined proportions, offers a scalable and cost-effective way of generating these gold-standard datasets. SimBu was developed to simulate pseudo-bulk samples based on various simulation scenarios, designed to test specific features of deconvolution methods. A unique feature of SimBu is the modelling of cell-type-specific mRNA bias using experimentally-derived or data-driven scaling factors.

Dataset generation

You will need an annotated scRNA-seq dataset (as matrix file, h5ad file, Seurat object), which is the baseline for the simulations. Use the `dataset_*` functions to generate a `SummarizedExperiment`, that holds all important information. It is also possible to access scRNA-seq datasets through the public database Sfaira, by using the functions `dataset_sfaira()` and `dataset_sfaira_multiple()`.

Simulation

Use the `simulate_bulk()` function to generate multiple pseudo-bulk samples, which will be returned as a `SummarizedExperiment`. You can adapt the cell type fractions in each sample by changing the `scenario` parameter.

Visulaization

Inspect the cell type composition of your simulations with the `plot_simulation()` function.

<code>simulate_bulk</code>	<i>Simulate whole pseudo-bulk RNAseq dataset</i>
----------------------------	--

Description

This function allows you to create a full pseudo-bulk RNAseq dataset. You need to provide a [SummarizedExperiment](#) from which the cells will be sampled for the simulation. Also a `scenario` has to be selected, where you can choose how the cells will be sampled and a `scaling_factor` on how the read counts will be transformed prior to the simulation.

Usage

```
simulate_bulk(
  data,
  scenario = c("even", "random", "mirror_db", "weighted", "pure", "custom"),
  scaling_factor = c("NONE", "census", "spike_in", "custom", "read_number",
    "expressed_genes", "annotation_column", "epic", "abis", "quantiseq"),
  scaling_factor_single_cell = TRUE,
  weighted_cell_type = NULL,
  weighted_amount = NULL,
  pure_cell_type = NULL,
  custom_scenario_data = NULL,
  custom_scaling_vector = NULL,
  balance_even_mirror_scenario = 0.01,
  remove_bias_in_counts = FALSE,
  remove_bias_in_counts_method = "read-number",
  norm_counts = FALSE,
  nsamples = 100,
  ncells = 1000,
  total_read_counts = NULL,
  whitelist = NULL,
  blacklist = NULL,
  seed = NA,
  BPPARAM = BiocParallel::bpparam(),
  run_parallel = FALSE
)
```

Arguments

<code>data</code>	(mandatory) SummarizedExperiment object
<code>scenario</code>	(mandatory) select one of the pre-defined cell-type fraction scenarios; possible are: even, random, mirror_db, pure, weighted; you can also use the custom scenario, where you need to set the custom_scenario_data parameter.
<code>scaling_factor</code>	(mandatory) name of scaling factor; possible are: census, spike_in, read_number, expressed_genes, custom, epic, abis, quantiseq or NONE for no scaling factor
<code>scaling_factor_single_cell</code>	boolean: decide if a scaling value for each single cell is calculated (default) or the median of all scaling values for each cell type is calculated
<code>weighted_cell_type</code>	name of cell-type used for weighted scenario
<code>weighted_amount</code>	fraction of cell-type used for weighted scenario; must be between 0 and 0.99
<code>pure_cell_type</code>	name of cell-type for pure scenario
<code>custom_scenario_data</code>	dataframe; needs to be of size nsamples x number_of_cell_types, where each sample is a row and each entry is the cell-type fraction. Rows need to sum up to 1.
<code>custom_scaling_vector</code>	named vector with custom scaling values for cell-types. Cell-types that do not occur in this vector but are present in the dataset will be set to 1; mandatory for custom scaling factor

balance_even_mirror_scenario	balancing value for the uniform and mirror_db scenarios: increasing it will result in more diverse simulated fractions. To get the same fractions in each sample, set to 0. Default is 0.01.
remove_bias_in_counts	boolean; if TRUE the internal mRNA bias that is present in count data will be <i>removed</i> using the number of reads mapped to each cell. Default to FALSE
remove_bias_in_counts_method	'read-number' (default) or 'gene-number'; method with which the mRNA bias in counts will be removed
norm_counts	boolean; if TRUE the samples simulated with counts will be normalized to CPMs, default is FALSE
nsamples	numeric; number of samples in pseudo-bulk RNAseq dataset (default = 100)
ncells	numeric; number of cells in each dataset (default = 1000)
total_read_counts	numeric; sets the total read count value for each sample
whitelist	list; give a list of cell-types you want to keep for the simulation; if NULL, all are used
blacklist	list; give a list of cell-types you want to remove for the simulation; if NULL, all are used; is applied after whitelist
seed	numeric; specify a seed for RNG. This effects cell sampling; with a fixed seed you will always sample the same cells for each sample (seed value is increased by 1 for each sample). Default = NA (two simulation runs will sample different cells).
BPPARAM	BiocParallel::bpparam() by default; if specific number of threads x want to be used, insert: BiocParallel::MulticoreParam(workers = x)
run_parallel	boolean, decide if multi-threaded calculation will be run. FALSE by default

Value

named list; bulk a [SummarizedExperiment](#) object, where the assays store the simulated bulk RNAseq datasets. Can hold either one or two assays, depending on how many matrices were present in the dataset cell-fractions is a dataframe with the simulated cell-fractions per sample; scaling_vector scaling value for each cell in dataset

Examples

```
# generate sample single-cell data to work with:

counts <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::Matrix(matrix(stats::rpois(3e5, 5), ncol = 300), sparse = TRUE)
tpm <- Matrix::t(1e6 * Matrix::t(tpm) / Matrix::colSums(tpm))

colnames(counts) <- paste0("cell_", rep(1:300))
colnames(tpm) <- paste0("cell_", rep(1:300))
rownames(counts) <- paste0("gene_", rep(1:1000))
rownames(tpm) <- paste0("gene_", rep(1:1000))

annotation <- data.frame(
  "ID" = paste0("cell_", rep(1:300)),
  "cell_type" = c(
```

```

    rep("T cells CD4", 50),
    rep("T cells CD8", 50),
    rep("Macrophages", 100),
    rep("NK cells", 10),
    rep("B cells", 70),
    rep("Monocytes", 20)
  )
)

dataset <- SimBu::dataset(
  annotation = annotation,
  count_matrix = counts,
  tpm_matrix = tpm,
  name = "test_dataset"
)

# this creates a basic pseudo-bulk dataset with uniform cell-type distribution
# and no additional transformation of the data with 10 samples and 2000 cells each

s <- SimBu::simulate_bulk(dataset,
  scenario = "even",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 100
)

# use a blacklist to exclude certain cell-types for the simulation
s <- SimBu::simulate_bulk(dataset,
  scenario = "even",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 2000,
  blacklist = c("Monocytes", "Macrophages")
)

# use the pure scenario to only have B cells
s <- SimBu::simulate_bulk(dataset,
  scenario = "pure",
  scaling_factor = "NONE",
  nsamples = 10,
  ncells = 100,
  pure_cell_type = "B cells"
)

# simulate a dataset with custom cell-type fraction for each of the 3 samples
fractions <- data.frame(
  "B cells" = c(0.2, 0.4, 0.2),
  "T cells CD4" = c(0.4, 0.2, 0.1),
  "Macrophages" = c(0.4, 0.4, 0.7), check.names = FALSE
)
s <- SimBu::simulate_bulk(dataset,
  scenario = "custom",
  scaling_factor = "NONE",
  nsamples = 3,
  ncells = 2000,
  custom_scenario_data = fractions

```

)

simulate_sample

simulate single pseudo-bulk sample

Description

function to sample cells according to given cell-type fractions. This creates a single pseudo-bulk sample by calculating the mean expression value per gene over all sampled cells. Note: if total_read_counts is used, the cell-fractions are applied to the number of counts, not the number of cells!

Usage

```
simulate_sample(
  data,
  scaling_vector,
  simulation_vector,
  total_cells,
  total_read_counts,
  remove_bias_in_counts,
  remove_bias_in_counts_method,
  norm_counts,
  seed
)
```

Arguments

data	SummarizedExperiment object
scaling_vector	vector with scaling values for each cell; calculated by the calc_scaling_vector function
simulation_vector	named vector with wanted cell-types and their fractions
total_cells	numeric; number of total cells for this simulation
total_read_counts	numeric; sets the total read count value for each sample
remove_bias_in_counts	boolean; if TRUE (default) the internal mRNA bias that is present in count data will be <i>removed</i> using the number of reads mapped to each cell
remove_bias_in_counts_method	'read-number' (default) or 'gene-number'; method with which the mRNA bias in counts will be removed
norm_counts	boolean; if TRUE the samples simulated with counts will be normalized to CPMs, default is FALSE
seed	numeric; fix this value if you want the same cells to be sampled

Value

returns two vectors (one based on counts, one based on tpm; depends on which matrices are present in data) with expression values for all genes in the provided dataset

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