Package ‘SimBu’

March 21, 2024

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

Version 1.4.3

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  Calculate scaling factor for a dataset

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, 
)
census

  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**

*Applies the Census count transformation on a count matrix*

**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](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
census_monocle

**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**

```r
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  

*Census calculation as implemented in monocle*

**Description**


**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**

**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**

**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

*Check if annotation and matrix have same cells*

**Description**

Otherwise intersection of both is used

**Usage**

```r
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**

```r
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

```r
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**

```r
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
- `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
dataset_merge

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
)
dataset_merge

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 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

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_{\(r\)}", rep(1:300))
colnames(tpm) <- paste0("cell_{\(r\)}", rep(1:300))
rownames(counts) <- paste0(\"gene_{\(r\)}\", rep(1:1000))
rownames(tpm) <- paste0("gene_{\(r\)}", rep(1:1000))

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

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

**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**

```r
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
dataset_sfaira

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

  sfaira_id       (mandatory) ID of a sfaira dataset
  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
  force          boolean, if TRUE, datasets without annotation will be downloaded, FALSE oth-
                  erwise (default)
  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
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

```r
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

Examples

```r
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"
)
```
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

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  

**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  

**Description**

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

**Usage**

```r
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**

filter one (or two) expression matrix by genes

**Description**

filter one (or two) expression matrix by genes

**Usage**

```r
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

Generate SummarizedExperiment using multiple parameters

Description

Generate SummarizedExperiment using multiple parameters

Usage

```r
generate_summarized_experiment(
  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
)
```

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
### h5ad_to_adata

**Value**

Return a `SummarizedExperiment` object

**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

**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  Combine multiple simulations into one result

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,
plot_simulation

```r
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**

```r
plot_simulation(simulation)
```

**Arguments**

- `simulation`: a simulation object generated by `simulate_bulk`

**Value**

a `ggplot2` barplot

**Examples**

```r
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))
```
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
setup_sfaira

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

setup the sfaira package

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 only be 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

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

---

**Description**

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

**Usage**

```r
sfaira_overview(setup_list)
```

**Arguments**

```
setup_list the sfaira setup; given by setup_sfaira
```

**Value**

a dataframe with information on each dataset

**Examples**

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

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

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.

Visualization

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

simulate_bulk

Simulate whole pseudo-bulk RNAseq dataset

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

data (mandatory) SummarizedExperiment object

scenario (mandatory) select on 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.

scaling_factor (mandatory) name of scaling factor; possible are: census, spike_in, read_number, expressed_genes, custom, epic, abis, quantiseq or NONE for no scaling factor

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

weighted_cell_type
  name of cell-type used for weighted scenario

weighted_amount
  fraction of cell-type used for weighted scenario; must be between 0 and 0.99

pure_cell_type
  name of cell-type for pure scenario

custom_scenario_data
  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.
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; 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 removed 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))
simulate_bulk

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

```r
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 removed 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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