Package 'scMultiSim'

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Title Simulation of Multi-Modality Single Cell Data Guided By Gene Regulatory Networks and Cell-Cell Interactions

Version 1.2.0

Description
scMultiSim simulates paired single cell RNA-seq, single cell ATAC-seq and RNA velocity data, while incorporating mechanisms of gene regulatory networks, chromatin accessibility and cell-cell interactions. It allows users to tune various parameters controlling the amount of each biological factor, variation of gene-expression levels, the influence of chromatin accessibility on RNA sequence data, and so on. It can be used to benchmark various computational methods for single cell multi-omics data, and to assist in experimental design of wet-lab experiments.

License Artistic-2.0

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Contents

`.amplifyOneCell` *This function simulates the amplification, library prep, and the sequencing processes.*

Description

This function simulates the amplification, library prep, and the sequencing processes.

Usage

```
.amplifyOneCell(
  true_counts_1cell,
  protocol,
  rate_2cap,
  gene_len,
  amp_bias,
  rate_2PCR,
  nPCR1,
  nPCR2,
  LinearAmp,
  LinearAmp_coef,
  N_molecules_SEQ
)
```

Arguments

`true_counts_1cell`	the true transcript counts for one cell (one vector)
`protocol`	a string, can be "nonUMI" or "UMI"
`rate_2cap`	the capture efficiency for this cell
`gene_len`	gene lengths for the genes/transcripts, sampled from real human transcript length
`amp_bias`	amplification bias for each gene, a vector of length ngenes
`rate_2PCR`	PCR efficiency, usually very high
`nPCR1`	the number of PCR cycles
`nPCR2`	the number of PCR cycles
`LinearAmp`	if linear amplification is used for pre-amplification step, default is FALSE
`LinearAmp_coef`	the coeficient of linear amplification, that is, how many times each molecule is amplified by
`N_molecules_SEQ`	number of molecules sent for sequencing; sequencing depth

Value

read counts (if protocol="nonUMI") or UMI counts (if protocol="UMI)

.calAmpBias *Simulate technical biases*

Description

Simulate technical biases

Usage

```
.calAmpBias(lenslope, nbins, gene_len, amp_bias_limit)
```

Arguments

lenslope	amount of length bias. This value sould be less than 2*amp_bias_limit[2]/(nbins-1)
nbins	number of bins for gene length
gene_len	transcript length of each gene
amp_bias_limit	range of amplification bias for each gene, a vector of length ngenes

Value

a vector

.continuousCIF *Generates cifs for cells sampled along the trajectory of cell development*

Description

Generates cifs for cells sampled along the trajectory of cell development

Usage

```
.continuousCIF(
  seed,
  N,
  options,
  ncell_key = "cell",
  is_spatial = FALSE,
  spatial_params = NULL,
  .plot = FALSE,
  .plot.name = "cont_cif.pdf"
)
```

Arguments

seed	random seed
N	the number list
options	the option list
ncell_key	the key for the number of cells in N
is_spatial	return a list of cifs for spatial
spatial_params	the spatial parameters
.plot	save the CIF plot
.plot.name	plot name

Value

a list containing the cif and meta data

.divideBatchesImpl *Divide the observed counts into multiple batches by adding batch effect to each batch*

Description

Divide the observed counts into multiple batches by adding batch effect to each batch

Usage

```
.divideBatchesImpl(
  counts,
  meta_cell,
  nbatch,
  batch_effect_size = 1,
  randseed = 0
)
```

Arguments

counts	gene cell matrix
meta_cell	the meta information related to cells, will be combined with technical cell level information and returned
nbatch	number of batches
batch_effect_size	amount of batch effects. Larger values result in bigger differences between batches. Default is 1.
randseed	random seed

Value

a list with two elements: counts and meta_cell

`.expandToBinary` *expand transcript counts to a vector of binaries of the same length of as the number of transcripts*

Description

expand transcript counts to a vector of binaries of the same length of as the number of transcripts

Usage

```
.expandToBinary(true_counts_1cell)
```

Arguments

`true_counts_1cell`	number of transcript in one cell

Value

a list of two vectors, the first vector is a vector of 1s, the second vector is the index of transcripts

`.getCountCorrMatrix` *This function finds the correlation between every pair of genes*

Description

This function finds the correlation between every pair of genes

Usage

```
.getCountCorrMatrix(counts)
```

Arguments

`counts`	rna seq counts

Value

the correlation matrix

.getParams *Get Kineic Parameters for all cells and genes*

Description

Get Kineic Parameters for all cells and genes

Usage

```
.getParams(seed, sim, sp_cell_i = NULL, sp_path_i = NULL)
```

Arguments

seed	random seed
sim	the simulation environment
sp_cell_i	spatial cell index
sp_path_i	the pre-sampled path along the tree for this cell

Value

the kinetic parameters

.normalizeGRNParams *Rename the original gene IDs in the GRN table to integers.*

Description

Rename the original gene IDs in the GRN table to integers.

Usage

```
.normalizeGRNParams(params)
```

Arguments

params	GRN parameters.

Value

list

.rnormTrunc *sample from truncated normal distribution*

Description

sample from truncated normal distribution

Usage

```
.rnormTrunc(n, mean, sd, a, b)
```

Arguments

n	number of values to create
mean	mean of the normal distribution
sd	standard deviation of the normal distribution
a	the minimum value allowed
b	the maximum value allowed

Value

a vector of length n

add_expr_noise *Add experimental noise to true counts*

Description

Add experimental noise to true counts

Usage

```
add_expr_noise(results, ...)
```

Arguments

results	The scMultisim result object
...	randseed: The random seed protocol: UMI or non-UMI gene_len: A vector with lengths of all genes alpha_mean, alpha_sd: rate of subsampling of transcripts during capture step depth_mean, depth_sd: The sequencing depth

Value

none

See Also

The underlying methods True2ObservedCounts and True2ObservedATAC

Examples

```
results <- sim_example(ncells = 10)
add_expr_noise(results)
```

`add_outliers` *Add outliers to the observed counts*

Description

Add outliers to the observed counts

Usage

```
add_outliers(
  res,
  prob = 0.01,
  factor = 2,
  sd = 0.5,
  cell.num = 1,
  max.var = Inf
)
```

Arguments

`res`	The scMultisim result object
`prob`	The probability of adding outliers for each gene
`factor`	The factor of the outliers
`sd`	The standard deviation of the outliers
`cell.num`	For a gene, the number of cells chosen to add outliers
`max.var`	The maximum variance allowed

Value

none

`cci_cell_type_params` *Generate cell-type level CCI parameters*

Description

See the return value if you want to specify the cell-type level ground truth.

Usage

```
cci_cell_type_params(
  tree,
  total.lr,
  ctype.lr = 4:6,
  step.size = 1,
  rand = TRUE,
  discrete = FALSE
)
```

Arguments

tree	Use the same value for sim_true_counts().
total.lr	Total number of LR pairs in the database. Use the same value for sim_true_counts().
ctype.lr	If rand is TRUE, how many LR pairs should be enabled between each cell type pair. Should be a range, e.g. 4:6.
step.size	Use the same value for sim_true_counts().
rand	Whether fill the matrix randomly
discrete	Whether the cell population is discrete. Use the same value for sim_true_counts().

Value

A 3D matrix of (n_cell_type, n_cell_type, n_lr). The value at (i, j, k) is 1 if there exist CCI of LR-pair k between cell type i and cell type j.

Examples

```
cci_cell_type_params(Phyla3(), 100, 4:6, 0.5, TRUE, FALSE)
```

---

dens_nonzero *this is the density function of log(x+1), where x is the non-zero values for ATAC-SEQ data*

Description

this is the density function of log(x+1), where x is the non-zero values for ATAC-SEQ data

Usage

```
data(dens_nonzero)
```

Format

a vector.

Value

a vector.

Examples

```
data(dens_nonzero)
```

`divide_batches` *Divide batches for observed counts*

Description

Divide batches for observed counts

Usage

```
divide_batches(results, nbatch = 2, effect = 3, randseed = 0)
```

Arguments

`results`	The scMultisim result object, after running `addExprNoise()`
`nbatch`	Number of batches
`effect`	Batch effect size, default is 3
`randseed`	Random seed

Value

none

Examples

```
results <- sim_example(ncells = 10)
add_expr_noise(results)
divide_batches(results)
```

`gene_corr_cci` *Plot the ligand-receptor correlation summary*

Description

Plot the ligand-receptor correlation summary

Usage

```
gene_corr_cci(
  results = .getResultsFromGlobal(),
  all.genes = FALSE,
  .pair = NULL,
  .exclude.same.types = TRUE
)
```

Arguments

results	The scMultisim result object
all.genes	Whether to use all genes or only the ligand/receptor genes
.pair	Return the raw data for the given LR pair
.exclude.same.types	Whether to exclude neighbor cells with same cell type

Value

none

Examples

```
results <- sim_example_spatial(ncells = 10)
gene_corr_cci(results)
```

---

gene_corr_regulator *Print the correlations between targets of each regulator*

Description

Print the correlations between targets of each regulator

Usage

```
gene_corr_regulator(results = .getResultsFromGlobal(), regulator)
```

Arguments

results	The scMultisim result object
regulator	The regulator ID in the GRN params

Value

none

Examples

```
results <- sim_example(ncells = 10)
gene_corr_regulator(results, 2)
```

gene_len_pool *a pool of gene lengths to sample from*

Description

a pool of gene lengths to sample from

Usage

```
data(gene_len_pool)
```

Format

a vector.

Value

a vector of gene lengths.

Examples

```
data(gene_len_pool)
```

gen_1branch *Generate true transcript counts for linear structure*

Description

Generate true transcript counts for linear structure

Usage

```
gen_1branch(
  kinet_params,
  start_state,
  start_s,
  start_u,
  randpoints1,
  ncells1,
  ngenes,
  beta_vec,
  d_vec,
  cycle_length_factor,
  cell
)
```

Arguments

kinet_params	kinetic parameters, include k_on, k_off, s and beta
start_state	the starting state: on or off of each gene
start_s	spliced count of the root cell in the branch
start_u	unspliced count of the root cell in the branch
randpoints1	the value which evf mean is generated from
ncells1	number of cells in the branch
ngenes	number of genes
beta_vec	splicing rate of each gene
d_vec	degradation rate of each gene
cycle_length_factor	for generating velocity data, a factor which is multiplied by the expected time to transition from kon to koff and back to to form the the length of a cycle
cell	the cell number currently having counts generated

Value

a list of 4 elements, the first element is true counts, second is the gene level meta information, the third is cell level meta information, including a matrix of evf and a vector of cell identity, and the fourth is the parameters kon, koff and s used to simulation the true counts

---

gen_clutter *generate a clutter of cells by growing from the center*

Description

generate a clutter of cells by growing from the center

Usage

```
gen_clutter(
  n_cell,
  grid_size = NA,
  center = c(0, 0),
  existing_loc = NULL,
  existing_grid = NULL
)
```

Arguments

n_cell	the number of cells
grid_size	the width and height of the grid
center	the center of the grid
existing_loc	only place cells on the specified existing locations
existing_grid	manually specify what locations are in the grid

Value

a matrix of locations

Examples

```
gen_clutter(10, 10, c(5, 5))
```

`Get_1region_ATAC_correlation`

This function gets the average correlation rna seq counts and region effect on genes for genes which are only associated with 1 chromatin region

---

Description

This function gets the average correlation rna seq counts and region effect on genes for genes which are only associated with 1 chromatin region

Usage

```
Get_1region_ATAC_correlation(counts, atacseq_data, region2gene)
```

Arguments

`counts`	rna seq counts
`atacseq_data`	atac seq data
`region2gene`	a 0 1 coupling matrix between regions and genes of shape (nregions) x (num_genes), where a value of 1 indicates the gene is affected by a particular region

Value

the correlation value

Examples

```
results <- sim_example(ncells = 10)
Get_1region_ATAC_correlation(results$counts, results$atacseq_data, results$region_to_gene)
```

`Get_ATAC_correlation` *This function gets the average correlation rna seq counts and chromatin region effect on genes*

Description

This function gets the average correlation rna seq counts and chromatin region effect on genes

Usage

```
Get_ATAC_correlation(counts, atacseq_data, num_genes)
```

Arguments

`counts`	rna seq counts
`atacseq_data`	atac seq data
`num_genes`	number of genes

Value

the correlation value

Examples

```
results <- sim_example(ncells = 10)
Get_ATAC_correlation(results$counts, results$atacseq_data, results$num_genes)
```

`GRN_params_100` *100_gene_GRN is a matrix of GRN params consisting of 100 genes where: # - column 1 is the target gene ID, # - column 2 is the gene ID which acts as a transcription factor for the target (regulated) gene # - column 3 is the effect of the column 2 gene ID on the column 1 gene ID*

Description

100_gene_GRN is a matrix of GRN params consisting of 100 genes where: # - column 1 is the target gene ID, # - column 2 is the gene ID which acts as a transcription factor for the target (regulated) gene # - column 3 is the effect of the column 2 gene ID on the column 1 gene ID

Usage

```
data(GRN_params_100)
```

Format

a data frame.

Value

a data frame with three columns: target gene ID, TF gene ID, and the effect of TF on target gene.

Examples

```
data(GRN_params_100)
```

`GRN_params_1139` *GRN_params_1139 is a matrix of GRN params consisting of 1139 genes where: # - column 1 is the target gene ID, # - column 2 is the gene ID which acts as a transcription factor for the target (regulated) gene # - column 3 is the effect of the column 2 gene ID on the column 1 gene ID*

Description

GRN_params_1139 is a matrix of GRN params consisting of 1139 genes where: # - column 1 is the target gene ID, # - column 2 is the gene ID which acts as a transcription factor for the target (regulated) gene # - column 3 is the effect of the column 2 gene ID on the column 1 gene ID

Usage

```
data(GRN_params_1139)
```

Format

a data frame.

Value

a data frame with three columns: target gene ID, TF gene ID, and the effect of TF on target gene.

Examples

```
data(GRN_params_1139)
```

`len2nfrag` *from transcript length to number of fragments (for the nonUMI protocol)*

Description

from transcript length to number of fragments (for the nonUMI protocol)

Usage

```
data(len2nfrag)
```

Format

a vector.

Value

a vector.

Examples

```
data(len2nfrag)
```

`match_params` *distribution of kinetic parameters learned from the Zeisel UMI cortex datasets*

Description

distribution of kinetic parameters learned from the Zeisel UMI cortex datasets

Usage

```
data(param_realdata.zeisel.imputed)
```

Format

a data frame.

Value

a data frame.

Examples

```
data(param_realdata.zeisel.imputed)
```

`OP` *Get option from an object in the current environment*

Description

Get option from an object in the current environment

Usage

```
OP(..., .name = "options")
```

Arguments

`...`	the parameter name
`.name`	get option from this object

Value

the parameter value

Phyla1 *Creating a linear example tree*

Description

Creating a linear example tree

Usage

```
Phyla1(len = 1)
```

Arguments

len	length of the tree

Value

a R phylo object

Examples

```
Phyla1(len = 1)
```

Phyla3 *Creating an example tree with 3 tips*

Description

Creating an example tree with 3 tips

Usage

```
Phyla3(plotting = FALSE)
```

Arguments

plotting	True for plotting the tree on console, False for no plot

Value

a R phylo object

Examples

```
Phyla3()
```

Phyla5 *Creating an example tree with 5 tips*

Description

Creating an example tree with 5 tips

Usage

```
Phyla5(plotting = FALSE)
```

Arguments

plotting	True for plotting the tree on console, False for no plot

Value

a R phylo object

Examples

```
Phyla5()
```

plot_cell_loc *Plot cell locations*

Description

Plot cell locations

Usage

```
plot_cell_loc(
  results = .getResultsFromGlobal(),
  size = 4,
  show.label = FALSE,
  show.arrows = TRUE,
  lr.pair = 1,
  .cell.pop = NULL,
  .locs = NULL
)
```

Arguments

results	The scMultisim result object
size	Fig size
show.label	Show cell numbers
show.arrows	Show arrows representing cell-cell interactions
lr.pair	The ligand-receptor pair used to plot CCI arrows `results$cci_cell_type_param[lr.pair]`
.cell.pop	Specify the cell population metadata
.locs	Manually specify the cell locations as a 2x`ncells` matrix

Value

none

Examples

```
results <- sim_example_spatial(ncells = 10)
plot_cell_loc(results)
```

`plot_gene_module_cor_heatmap` *Plot the gene module correlation heatmap*

Description

Plot the gene module correlation heatmap

Usage

```
plot_gene_module_cor_heatmap(
  results = .getResultsFromGlobal(),
  seed = 0,
  grn.genes.only = TRUE,
  save = FALSE
)
```

Arguments

`results`	The scMultisim result object
`seed`	The random seed
`grn.genes.only`	Plot the GRN gens only
`save`	save the plot as pdf

Value

none

Examples

```
results <- sim_example(ncells = 10)
plot_gene_module_cor_heatmap(results)
```

plot_grid *Plot the CCI grid*

Description

In normal cases, please use `plotCellLoc` instead.

Usage

```
plot_grid(results = .getResultsFromGlobal())
```

Arguments

`results`	The scMultisim result object

Value

none

Examples

```
results <- sim_example_spatial(ncells = 10)
plot_grid(results)
```

plot_grn *Plot the GRN network*

Description

Plot the GRN network

Usage

```
plot_grn(params)
```

Arguments

`params`	The GRN params data frame

Value

none

Examples

```
data(GRN_params_100, envir = environment())
plot_grn(GRN_params_100)
```

plot_phyla *Plot a R phylogenic tree*

Description

Plot a R phylogenic tree

Usage

```
plot_phyla(tree)
```

Arguments

tree	The tree

Value

none

Examples

```
plot_phyla(Phyla5())
```

plot_rna_velocity *Plot RNA velocity as arrows on tSNE plot*

Description

Plot RNA velocity as arrows on tSNE plot

Usage

```
plot_rna_velocity(
  results = .getResultsFromGlobal(),
  velocity = results$velocity,
  perplexity = 70,
  arrow.length = 1,
  save = FALSE,
  randseed = 0,
  ...
)
```

Arguments

results	The scMultiSim result object
velocity	The velocity matrix, by default using the velocity matrix in the result object
perplexity	The perplexity for tSNE
arrow.length	The length scaler of the arrow
save	Whether to save the plot
randseed	The random seed
...	Other parameters passed to ggplot

Value

The plot

Examples

```
results <- sim_example(ncells = 10, velocity = TRUE)
plot_rna_velocity(results, perplexity = 3)
```

`plot_tsne` *Plot t-SNE visualization of a data matrix*

Description

Plot t-SNE visualization of a data matrix

Usage

```
plot_tsne(
  data,
  labels,
  perplexity = 60,
  legend = "",
  plot.name = "",
  save = FALSE,
  rand.seed = 0,
  continuous = FALSE,
  labels2 = NULL,
  lim = NULL,
  runPCA = FALSE,
  alpha = 1
)
```

Arguments

`data`	The dxn matrix
`labels`	A vector of length n, usually cell clusters
`perplexity`	Perplexity value used for t-SNE
`legend`	A list of colors for the labels
`plot.name`	The plot title
`save`	If `TRUE`, save as `plot.name.pdf`
`rand.seed`	The random seed
`continuous`	Whether `labels` should be treated as continuous, e.g. pseudotime
`labels2`	Additional label
`lim`	Specify the xlim and y lim c(x_min, x_max, y_min, y_max)
`runPCA`	Whether to run PCA before t-SNE
`alpha`	The alpha value for the points

Value

the figure if not save, otherwise save the figure as plot.name.pdf

Examples

```
results <- sim_example(ncells = 10)
plot_tsne(log2(results$counts + 1), results$cell_meta$pop, perplexity = 3)
```

---

run_shiny *Launch the Shiny App to configure the simulation*

Description

Launch the Shiny App to configure the simulation

Usage

```
run_shiny()
```

SampleDen *sample from smoothed density function*

Description

sample from smoothed density function

Usage

```
SampleDen(nsample, den_fun, reduce.mem = FALSE)
```

Arguments

nsample	number of samples needed
den_fun	density function estimated from density() from R default
reduce.mem	use alternative implementation to reduce memory usage

Value

a vector of samples

scmultisim_help *Show detailed documentations of scMultiSim's parameters*

Description

Show detailed documentations of scMultiSim's parameters

Usage

```
scmultisim_help(topic = NULL)
```

Arguments

topic	Can be options, dynamic.GRN, or cci

Value

none

Examples

```
scmultisim_help()
```

sim_example *Simulate a small example dataset with 200 cells and the 100-gene GRN*

Description

Simulate a small example dataset with 200 cells and the 100-gene GRN

Usage

```
sim_example(ncells = 10, velocity = FALSE)
```

Arguments

ncells	number of cells, please increase this number on your machine
velocity	whether to simulate RNA velocity

Value

the simulation result

Examples

```
sim_example(ncells = 10)
```

sim_example_spatial *Simulate a small example dataset with 200 cells and the 100-gene GRN, with CCI enabled*

Description

Simulate a small example dataset with 200 cells and the 100-gene GRN, with CCI enabled

Usage

```
sim_example_spatial(ncells = 10)
```

Arguments

ncells	number of cells, please increase this number on your machine

Value

the simulation result

Examples

```
sim_example_spatial(ncells = 10)
```

sim_true_counts *Simulate true scRNA and scATAC counts from the parameters*

Description

Simulate true scRNA and scATAC counts from the parameters

Usage

```
sim_true_counts(options, return_summarized_exp = FALSE)
```

Arguments

options	See scMultiSim_help().
return_summarized_exp	Whether to return a SummarizedExperiment object.

Value

scMultiSim returns an environment with the following fields:

- counts: Gene-by-cell scRNA-seq counts.
- atac_counts: Region-by-cell scATAC-seq counts.
- region_to_gene: Region-by-gene 0-1 marix indicating the corresponding relationship between chtomatin regions and genes.
- atacseq_data: The "clean" scATAC-seq counts without added intrinsic noise.

- `cell_meta`: A dataframe containing cell type labels and pseudotime information.
- `cif`: The CIF used during the simulation.
- `giv`: The GIV used during the simulation.
- `kinetic_params`: The kinetic parameters used during the simulation.
- `.grn`: The GRN used during the simulation.
- `.grn$regulators`: The list of TFs used by all gene-by-TF matrices.
- `.grn$geff`: Gene-by-TF matrix representing the GRN used during the simulation.
- `.n`: Other metadata, e.g. `.n$cells` is the number of cells.

If `do.velocity` is enabled, it has these additional fields:

- `unspliced_counts`: Gene-by-cell unspliced RNA counts.
- `velocity`: Gene-by-cell RNA velocity ground truth.
- `cell_time`: The pseudotime at which the cell counts were generated.

If dynamic GRN is enabled, it has these additional fields:

- `cell_specific_grn`: A list of length `n_cells`. Each element is a gene-by-TF matrix, indicating the cell's GRN.

If cell-cell interaction is enabled, it has these additional fields:

- `grid`: The grid object used during the simulation.
  - `grid$get_neighbours(i)`: Get the neighbour cells of cell `i`.
- `cci_locs`: A dataframe containing the X and Y coordinates of each cell.
- `cci_cell_type_param`: A dataframe containing the CCI network ground truth: all ligand-receptor pairs between each pair of cell types.
- `cci_cell_types`: For continuous cell population, the sub-divided cell types along the trajectory used when simulating CCI.

If it is a debug session (`debug = TRUE`), a `sim` field is available, which is an environment contains all internal states and data structures.

Examples

```
data(GRN_params_100, envir = environment())
sim_true_counts(list(
  rand.seed = 0,
  GRN = GRN_params_100,
  num.cells = 100,
  num.cifs = 50,
  tree = Phyla5()
))
```

spatialGrid-class *The class for spatial grids*

Description

The class for spatial grids

Value

a spatialGrid object

Fields

`method` the method to generate the cell layout

`grid_size` the width and height of the grid

`ncells` the number of cells

`grid` the grid matrix

`locs` a list containing the locations of all cells

`loc_order` deprecated, don't use; the order of the locations

`cell_types` a map to save the cell type of each allocated cell

`same_type_prob` the probability of a new cell placed next to a cell with the same type

`max_nbs` the maximum number of neighbors for each cell

`nb_map` a list containing the neighbors for each cell

`nb_adj` adjacency matrix for neighbors

`nb_radius` the radius of neighbors

`final_types` the final cell types after the final time step

`pre_allocated_pos` the pre-allocated positions for each cell, if any

`method_param` additional parameters for the layout method

True2ObservedATAC *Simulate observed ATAC-seq matrix given technical noise and the true counts*

Description

Simulate observed ATAC-seq matrix given technical noise and the true counts

Usage

```
True2ObservedATAC(
  atacseq_data,
  randseed,
  observation_prob = 0.3,
  sd_frac = 0.1
)
```

Arguments

atacseq_data	true ATAC-seq data
randseed	(should produce same result if nregions, nevf and randseed are all the same)
observation_prob	for each integer count of a particular region for a particular cell, the probability the count will be observed
sd_frac	the fraction of ATAC-seq data value used as the standard deviation of added normally distrubted noise

Value

a matrix of observed ATAC-seq data

Examples

```
results <- sim_example(ncells = 10)
True2ObservedATAC(results$atac_counts, randseed = 1)
```

True2ObservedCounts *Simulate observed count matrix given technical biases and the true counts*

Description

Simulate observed count matrix given technical biases and the true counts

Usage

```
True2ObservedCounts(
  true_counts,
  meta_cell,
  protocol,
  randseed,
  alpha_mean = 0.1,
  alpha_sd = 0.002,
  alpha_gene_mean = 1,
  alpha_gene_sd = 0,
  gene_len,
  depth_mean,
  depth_sd,
  lenslope = 0.02,
  nbins = 20,
  amp_bias_limit = c(-0.2, 0.2),
  rate_2PCR = 0.8,
  nPCR1 = 16,
  nPCR2 = 10,
  LinearAmp = FALSE,
  LinearAmp_coef = 2000
)
```

Arguments

true_counts	gene cell matrix
meta_cell	the meta information related to cells, will be combined with technical cell level information and returned
protocol	a string, can be "nonUMI" or "UMI"
randseed	(should produce same result if nregions, nevf and randseed are all the same)
alpha_mean	the mean of rate of subsampling of transcripts during capture step, default at 10 percent efficiency
alpha_sd	the std of rate of subsampling of transcripts
alpha_gene_mean	the per-gene scale factor of the alpha parameter, default at 1
alpha_gene_sd	the standard deviation of the per-gene scale factor of the alpha parameter, default at 0
gene_len	a vector with lengths of all genes
depth_mean	mean of sequencing depth
depth_sd	std of sequencing depth
lenslope	amount of length bias
nbins	number of bins for gene length
amp_bias_limit	range of amplification bias for each gene, a vector of length ngenes
rate_2PCR	PCR efficiency, usually very high, default is 0.8
nPCR1	the number of PCR cycles in "pre-amplification" step, default is 16
nPCR2	the number of PCR cycles used after fragmentation.
LinearAmp	if linear amplification is used for pre-amplification step, default is FALSE
LinearAmp_coef	the coeficient of linear amplification, that is, how many times each molecule is amplified by

Value

if UMI, a list with two elements, the first is the observed count matrix, the second is the metadata; if nonUMI, a matrix

Examples

```
results <- sim_example(ncells = 10)
data(gene_len_pool)
gene_len <- sample(gene_len_pool, results$num_genes, replace = FALSE)
True2ObservedCounts(
  results$counts, results$cell_meta, protocol = "nonUMI", randseed = 1,
  alpha_mean = 0.1, alpha_sd = 0.05, gene_len = gene_len, depth_mean = 1e5, depth_sd = 3e3
)
```

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