Package ‘scDesign3’

March 30, 2024

Type Package

Title A unified framework of realistic in silico data generation and statistical model inference for single-cell and spatial omics

Version 1.0.1

Description We present a statistical simulator, scDesign3, to generate realistic single-cell and spatial omics data, including various cell states, experimental designs, and feature modalities, by learning interpretable parameters from real data. Using a unified probabilistic model for single-cell and spatial omics data, scDesign3 infers biologically meaningful parameters; assesses the goodness-of-fit of inferred cell clusters, trajectories, and spatial locations; and generates in silico negative and positive controls for benchmarking computational tools.

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LazyData false

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Imports dplyr, tibble, stats, methods, mgcv, gamlss, gamlss.dist, SummarizedExperiment, SingleCellExperiment, mclust, mvtnorm, parallel, pbmcapply, rvinecopulib, umap, ggplot2, irlba, viridis, BiocParallel, matrixStats, Matrix

Suggests mvnfast, igraph, knitr, rmarkdown, testthat (>= 3.0.0), RefManageR, sessioninfo, BiocStyle

biocViews Software, SingleCell, Sequencing, GeneExpression, Spatial


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Description

An additive function to be used while fitting GAMLSS models. The interface for bam() in the mgcv package.

Usage

ba(formula, control = ba.control(...), ...)

Arguments

formula A formula of the model.
control The control of the model fitting.
... Other arguments.

Value

A xvar list.
**construct_data**

```r
construct_data
```

**ba**

```
NA
```

**Examples**

```r
print("No example")
```

---

**construct_data**  
*Construct the input data (covariate matrix and expression matrix)*

---

**Description**

This function constructs the input data for `fit_marginal`.

**Usage**

```r
construct_data(
  sce,
  assay_use = "counts",
  celltype,
  pseudotime,
  spatial,
  other_covariates,
  ncell = dim(sce)[2],
  corr_by,
  parallelization = "mcmapply",
  BPPARAM = NULL
)
```

**Arguments**

- `sce`  
  A SingleCellExperiment object.

- `assay_use`  
  A string which indicates the assay you will use in the sce. Default is 'counts'.

- `celltype`  
  A string of the name of cell type variable in the `colData` of the sce. Default is 'cell_type'.

- `pseudotime`  
  A string or a string vector of the name of pseudotime and (if exist) multiple lineages. Default is NULL.

- `spatial`  
  A length two string vector of the names of spatial coordinates. Defualt is NULL.

- `other_covariates`  
  A string or a string vector of the other covaraites you want to include in the data.

- `ncell`  
  The number of cell you want to simulate. Default is `dim(sce)[2]` (the same number as the input data). If an arbitrary number is provided, the function will use Vine Copula to simulate a new covaraite matrix.
construct_data

corr_by A string or a string vector which indicates the groups for correlation structure. If '1', all cells have one estimated corr. If 'ind', no corr (features are independent). If others, this variable decides the corr structures.

parallelization A string indicating the specific parallelization function to use. Must be one of 'mcmapply', 'bpmapply', or 'pbmcmapply', which corresponds to the parallelization function in the package parallel, BiocParallel, and pbmapply respectively. The default value is 'mcmapply'.

BPPARAM A MulticoreParam object or NULL. When the parameter parallelization = 'mcmapply' or 'pbmcmapply', this parameter must be NULL. When the parameter parallelization = 'bpmapply', this parameter must be one of the MulticoreParam object offered by the package BiocParallel. The default value is NULL.

Details
This function takes a SingleCellExperiment object as the input. Based on users' choice, it constructs the matrix of covaraites (explainary variables) and the expression matrix (e.g., count matrix for scRNA-seq).

Value
A list with the components:

count_mat The expression matrix
dat The original covariate matrix
newCovariate The simulated new covariate matrix, is NULL if the parameter ncell is default
filtered_gene The genes that are excluded in the marginal and copula fitting steps because these genes only express in less than two cells.

Examples

data(example_sce)
my_data <- construct_data(
sce = example_sce,
assay_use = "counts",
celltype = "cell_type",
pseudotime = "pseudotime",
spatial = NULL,
other_covariates = NULL,
corr_by = "1"
)
**example_sce**

| example_sce | A SingelCellExperiment object containing both cell type and pseudotime |

**Description**

A SingelCellExperiment object containing both cell type and pseudotime

**Usage**

```r
data("example_sce")
```

**Format**

A dataset with 10 rows (genes) and 1289 cols (cells)

**Value**

The corresponding SingleCellExperiment object

---

**extract_para**

Extract the parameters of each cell's distribution

**Description**

extract_para generates parameter matrices which determine each cell’s distribution

**Usage**

```r
extract_para(
  sce,
  assay_use = "counts",
  marginal_list,
  n_cores,
  family_use,
  new_covariate,
  parallelization = "mcmapply",
  BPPARAM = NULL,
  data
)
```
Arguments

sce A SingleCellExperiment object.

assay_use A string which indicates the assay you will use in the sce. Default is 'counts'.

marginal_list A list of fitted regression models from fit_marginal for each gene in sce.

n_cores An integer. The number of cores to use.

family_use A string of the marginal distribution. Must be one of 'poisson', 'nb', 'zip', 'zib' or 'gaussian', which represent 'poisson distribution', 'negative binomial distribution', 'zero-inflated poisson distribution', 'zero-inflated negative binomial distribution', and 'gaussian distribution' respectively.

new_covariate A data.frame which contains covaraites of targeted simulated data from construct_data and the correlation group assignment for each cell in the column 'corr_group'.

parallelization A string indicating the specific parallelization function to use. Must be one of 'mcmapply', 'bpmapply', or 'pbmcmapply', which corresponds to the parallelization function in the package parallel, BiocParallel, and pbmcapply respectively. The default value is 'mcmapply'.

BPPARAM A MulticoreParam object or NULL. When the parameter parallelization = 'mcmapply' or 'pbmcmapply', this parameter must be NULL. When the parameter parallelization = 'bpmapply', this parameter must be one of the MulticoreParam object offered by the package BiocParallel. The default value is NULL.

data A dataframe which is used when fitting the gamlss model

Details

The function takes the new covariate (if use) from construct_data and marginal models from fit_marginal.

Value

A list with the components:

mean_mat A cell by feature matrix of the mean parameter.

sigma_mat A cell by feature matrix of the sigma parameter (for Gaussian, the variance; for NB, the dispersion.).

zero_mat A cell by feature matrix of the zero-inflation parameter (only non-zero for ZIP and ZINB).

Examples

data(example_sce)
my_data <- construct_data(
sce = example_sce, assay_use = "counts", celltype = "cell_type", pseudotime = "pseudotime", spatial = NULL, other_covariates = NULL,
my_marginal <- fit_marginal(
data = my_data,
mu_formula = "s(pseudotime, bs = 'cr', k = 10)",
sigma_formula = "1",
family_use = "nb",
n_cores = 1,
usebam = FALSE
)

my_copula <- fit_copula(
sce = example_sce,
assay_use = "counts",
marginal_list = my_marginal,
family_use = c(rep("nb", 5), rep("zip", 5)),
copula = "vine",
n_cores = 1,
input_data = my_data$dat
)

my_para <- extract_para(
sce = example_sce,
marginal_list = my_marginal,
n_cores = 1,
family_use = c(rep("nb", 5), rep("zip", 5)),
new_covariate = my_data$new_covariate,
data = my_data$dat
)

---

### fit_copula

**Fit the copula model**

**Description**

fit_copula fits the copula model.

**Usage**

```r
fit_copula(
sce, assay_use, input_data, empirical_quantile = FALSE, marginal_list, family_use, copula = "gaussian", DT = TRUE, pseudo_obs = FALSE, epsilon = 1e-06,
```
fit_copula

family_set = c("gaussian", "indep"),
important_feature = "all",
n_cores,
parallelization = "mcmapply",
BPPARAM = NULL
)

Arguments

sce | A SingleCellExperiment object.
assay_use | A string which indicates the assay you will use in the sce. Default is 'counts'.
input_data | The input data, which is one of the output from construct_data.
empirical_quantile | Please only use it if you clearly know what will happen! A logic variable. If TRUE, DO NOT fit the copula and use the EMPIRICAL CDF values of the original data; it will make the simulated data fixed (no randomness). Default is FALSE. Only works if ncell is the same as your original data.
marginal_list | A list of fitted regression models from fit_marginal.
family_use | A string or a vector of strings of the marginal distribution. Must be one of 'poisson', 'nb', 'zip', 'zinb' or 'gaussian'.
copula | A string of the copula choice. Must be one of 'gaussian' or 'vine'. Default is 'gaussian'. Note that vine copula may have better modeling of high-dimensions, but can be very slow when features are >1000.
DT | A logic variable. If TRUE, perform the distributional transformation to make the discrete data 'continuous'. This is useful for discrete distributions (e.g., Poisson, NB). Default is TRUE. Note that for continuous data (e.g., Gaussian), DT does not make sense and should be set as FALSE.
pseudo_obs | A logic variable. If TRUE, use the empirical quantiles instead of theoretical quantiles for fitting copula. Default is FALSE.
epsilon | A numeric variable for preventing the transformed quantiles to collapse to 0 or 1.
family_set | A string or a string vector of the bivariate copula families. Default is c("gaussian", "indep").
important_feature | A string or vector which indicates whether a gene will be used in correlation estimation or not. If this is a string, then this string must be either "all" (using all genes) or "auto", which indicates that the genes will be automatically selected based on the proportion of zero expression across cells for each gene. Gene with zero proportion greater than 0.8 will be excluded form gene-gene correlation estimation. If this is a vector, then this should be a logical vector with length equal to the number of genes in sce. TRUE in the logical vector means the corresponding gene will be included in gene-gene correlation estimation and FALSE in the logical vector means the corresponding gene will be excluded from the gene-gene correlation estimation. The default value for is "all".
n_cores | An integer. The number of cores to use.
parallelization  
A string indicating the specific parallelization function to use. Must be one of 'mcmapply', 'bpmapply', or 'pbmcmapply', which corresponds to the parallelization function in the package parallel, BiocParallel, and pbmcapply respectively. The default value is 'mcmapply'.

BPPARAM  
A MulticoreParam object or NULL. When the parameter parallelization = 'mcmapply' or 'pbmcmapply', this parameter must be NULL. When the parameter parallelization = 'bpmapply', this parameter must be one of the MulticoreParam object offered by the package 'BiocParallel. The default value is NULL.

Details  
This function takes the result from fit_marginal as the input and fit the copula model on the residuals.

Value  
A list with the components:

new_mvu  A matrix of the new multivariate uniform distribution from the copula.

copula_list  A list of the fitted copula model. If using Gaussian copula, a list of correlation matrices; if vine, a list of vine objects.

model_aic  A vector of the marginal AIC and the copula AIC.

model_bic  A vector of the marginal BIC and the copula BIC.

Examples  
```r
data(example_sce)
my_data <- construct_data(
sce = example_sce,
assay_use = "counts",
celltype = "cell_type",
pseudotime = "pseudotime",
spatial = NULL,
other_covariates = NULL,
corr_by = "1"
)
my_marginal <- fit_marginal(
data = my_data,
mu_formula = "s(pseudotime, bs = 'cr', k = 10)",
sigma_formula = "1",
family_use = "nb",
n_cores = 1,
usebam = FALSE
)
my_copula <- fit_copula(
sce = example_sce,
assay_use = "counts",
marginal_list = my_marginal,
family_use = c(rep("nb", 5), rep("zip", 5)),
```
copula = "vine",
  n_cores = 1,
  input_data = my_data$dat
)


fit_marginal

Fit the marginal models

Description

fit_marginal fits the per-feature regression models.

Usage

fit_marginal(
  data,
  predictor = "gene",
  mu_formula,  # or mu_param
  sigma_formula,
  family_use,  # or name of distribution
  n_cores,
  usebam,
  parallelization = "mcmapply",
  BPPARAM = NULL,
  trace = FALSE,
  simplify = FALSE
)

Arguments

data An object from construct_data.
predictor A string of the predictor for the gam/gamlss model. Default is gene. This is essentially just a name.
mu_formula A string of the mu parameter formula
sigma_formula A string of the sigma parameter formula
family_use A string or a vector of strings of the marginal distribution. Must be one of 'binomial', 'poisson', 'nb', 'zip', 'zineb' or 'gaussian', which represent 'poisson distribution', 'negative binomial distribution', 'zero-inflated poisson distribution', 'zero-inflated negative binomial distribution', and 'gaussian distribution' respectively.
n_cores An integer. The number of cores to use.
usebam A logic variable. If use bam for acceleration.
**parallelization**

A string indicating the specific parallelization function to use. Must be one of 'mcmapply', 'bpmapply', or 'pbmcmapply', which corresponds to the parallelization function in the package parallel, BiocParallel, and pbmcapply respectively. The default value is 'mcmapply'.

**BPPARAM**

A MulticoreParam object or NULL. When the parameter parallelization = 'mcmapply' or 'pbmcmapply', this parameter must be NULL. When the parameter parallelization = 'bpmapply', this parameter must be one of the MulticoreParam object offered by the package 'BiocParallel'. The default value is NULL.

**trace**

A logic variable. If TRUE, the warning/error log and runtime for gam/gamlss will be returned, FALSE otherwise. Default is FALSE.

**simplify**

A logic variable. If TRUE, the fitted regression model will only keep the essential contains for predict. Default is FALSE.

---

**Details**

The function takes the result from `construct_data` as the input, and fit the regression models for each feature based on users' specification.

**Value**

A list of fitted regression models. The length is equal to the total feature number.

**Examples**

```r
data(example_sce)
my_data <- construct_data(
sce = example_sce,
assay_use = "counts",
celltype = "cell_type",
pseudotime = "pseudotime",
spatial = NULL,
other_covariates = NULL,
corr_by = "1"
)
my_marginal <- fit_marginal(
data = my_data,
mu_formula = "s(pseudotime, bs = 'cr', k = 10)",
sigma_formula = "1",
family_use = "nb",
n_cores = 1,
usebam = FALSE
)```
Functions from gamlss/gamlss.add with bugs fixed

Description
An additive function to be used while fitting GAMLSS models. The interface for `gam()` in the `mgcv` package.

Usage
```
ga(formula, envir, control = ga.control(...), ...)
```

Arguments
- `formula`: A formula of the model.
- `envir`: The environment.
- `control`: The control of the model fitting.
- `...`: Other arguments.

Value
A `xvar` list.

ga
NA

Examples
```
print("No example")
```

Support for Function `ba()`

Description
This is support for the smoother functions `ba()` interfaces for Simon Wood’s `bam()` functions from package `mgcv`. It is not intended to be called directly by users. From `gamlss.add::gamlss.ba`.

Usage
```
gamlss.ba(x, y, w, xeval = NULL, ...)
```
Arguments

x  The explanatory variables
y  Iterative y variable
w  Iterative weights
xeval  If xeval=TRUE then prediction is used
...  Other arguments

Value
Not used

Examples

print("No example")

---

gamlss.ga  Support for Function ga()

Description
This is support for the smoother functions ga() interfaces for Simon Wood's gam() functions from package mgcv. It is not intended to be called directly by users. From gamlss.add::gamlss.ga.

Usage

gamlss.ga(x, y, w, xeval = NULL, ...)

Arguments

x  The explanatory variables
y  Iterative y variable
w  Iterative weights
xeval  If xeval=TRUE then prediction is used
...  Other arguments

Value
Not used

Examples

print("No example")
**perform_lrt**

*Perform the likelihood ratio test*

**Description**

`perform_lrt` performs the likelihood ratio test to compare two lists of marginal models.

**Usage**

```r
perform_lrt(alter_marginal, null_marginal)
```

**Arguments**

- `alter_marginal` A list of marginal models from the alternative hypothesis.
- `null_marginal` A list of marginal models from the null hypothesis. It must be strictly nested in the alternative model.

**Details**

The function takes two lists of marginal models (by default, the first list is the alternative and the second is the null) from `fit_marginal`. Note that LRT only makes sense for NESTED models. This can be quite tricky if you use penalized-splines (e.g., for trajectory data).

**Value**

A data frame of the LRT result.

**Examples**

```r
data(example_sce)
my_data <- construct_data(
  sce = example_sce,
  assay_use = "counts",
  celltype = "cell_type",
  pseudotime = "pseudotime",
  spatial = NULL,
  other_covariates = NULL,
  corr_by = "cell_type"
)

my_data2 <- construct_data(
  sce = example_sce,
  assay_use = "counts",
  celltype = "cell_type",
  pseudotime = "pseudotime",
  spatial = NULL,
  other_covariates = NULL,
  corr_by = "pseudotime",
  ncell = 10000
)```
my_marginal1 <- fit_marginal(
  data = my_data,
  mu_formula = "1",
  sigma_formula = "1",
  family_use = "nb",
  n_cores = 1,
  usebam = FALSE
)
my_marginal2 <- fit_marginal(
  data = my_data,
  mu_formula = "s(pseudotime, bs = 'cr', k = 10)",
  sigma_formula = "1",
  family_use = "nb",
  n_cores = 1,
  usebam = FALSE
)
my_fit1 <- lapply(my_marginal1, function(x)x$fit)
my_fit2 <- lapply(my_marginal2, function(x)x$fit)
my_pvalue <- perform_lrt(my_fit2, my_fit1)

---

**plot_reduceddim**  
*Dimensionality reduction and visualization*

**Description**

*plot_reduceddim* performs the dimensionality reduction

**Usage**

```r
plot_reduceddim(
  ref_sce,  
  sce_list,  
  name_vec,  
  assay_use = "logcounts",  
  pc_umap = TRUE,  
  n_pc = 50,  
  center = TRUE,  
  scale. = TRUE,  
  if_plot = TRUE,  
  shape_by = NULL,  
  color_by,  
  point_size = 1
)
```
scdesign3

The wrapper for the whole scDesign3 pipeline

Description

scdesign3 takes the input data, fits the model and

Usage

scdesign3(
  sce,
  assay_use = "counts",
  celltype,
  pseudotime,
  spatial,
  other_covariates,
  ncell = dim(sce)[2],
)
mu_formula,  
sigma_formula = "1",  
family_use = "nb",  
n_cores = 2,  
usebam = FALSE,  
corr_formula,  
empirical_quantile = FALSE,  
copula = "gaussian",  
fastmvn = FALSE,  
DT = TRUE,  
pseudo_obs = FALSE,  
family_set = c("gauss", "indep"),  
important_feature = "all",  
nonnegative = TRUE,  
nonzerovar = FALSE,  
return_model = FALSE,  
simplify = FALSE,  
parallelization = "mcmapply",  
BPPARAM = NULL,  
trace = FALSE
)

Arguments

sce A SingleCellExperiment object.

assay_use A string which indicates the assay you will use in the sce. Default is 'counts'.

celltype A string of the name of cell type variable in the colData of the sce. Default is 'cell_type'.
pseudotime A string or a string vector of the name of pseudotime and (if exist) multiple lineages. Default is NULL.

spatial A length two string vector of the names of spatial coordinates. Defualt is NULL.

other_covariates A string or a string vector of the other covariates you want to include in the data.

ncell The number of cell you want to simulate. Default is dim(sce)[2] (the same number as the input data).

mu_formula A string of the mu parameter formula

sigma_formula A string of the sigma parameter formula

family_use A string of the marginal distribution. Must be one of 'poisson', 'nb', 'zip', 'zinb' or 'gaussian'.

n_cores An integer. The number of cores to use.

usebam A logic variable. If use bam for acceleration.

corr_formula A string of the correlation structure.

empirical_quantile Please only use it if you clearly know what will happen! A logic variable. If TRUE, DO NOT fit the copula and use the EMPIRICAL CDF values of the
original data; it will make the simulated data fixed (no randomness). Default is FALSE. Only works if ncell is the same as your original data.

copula A string of the copula choice. Must be one of 'gaussian' or 'vine'. Default is 'gaussian'. Note that vine copula may have better modeling of high-dimensions, but can be very slow when features are >1000.

fastmvn An logical variable. If TRUE, the sampling of multivariate Gaussian is done by mvnfast, otherwise by mvtnorm. Default is FALSE. It only matters for Gaussian copula.

DT A logic variable. If TRUE, perform the distributional transformation to make the discrete data 'continuous'. This is useful for discrete distributions (e.g., Poisson, NB). Default is TRUE. Note that for continuous data (e.g., Gaussian), DT does not make sense and should be set as FALSE.

pseudo_obs A logic variable. If TRUE, use the empirical quantiles instead of theoretical quantiles for fitting copula. Default is FALSE.

family_set A string or a string vector of the bivariate copula families. Default is c("gauss", "indep"). For more information please check package rvinecoplib.

important_feature A string or vector which indicates whether a gene will be used in correlation estimation or not. If this is a string, then this string must be either "all" (using all genes) or "auto", which indicates that the genes will be automatically selected based on the proportion of zero expression across cells for each gene. Gene with zero proportion greater than 0.8 will be excluded from gene-gene correlation estimation. If this is a vector, then this should be a logical vector with length equal to the number of genes in sce. TRUE in the logical vector means the corresponding gene will be included in gene-gene correlation estimation and FALSE in the logical vector means the corresponding gene will be excluded from the gene-gene correlation estimation. The default value for is a vector with length equal to the number of inputted genes and every value equals to TRUE.

nonnegative A logical variable. If TRUE, values < 0 in the synthetic data will be converted to 0. Default is TRUE (since the expression matrix is nonnegative).

nonzerovar A logical variable. If TRUE, for any gene with zero variance, a cell will be replaced with 1. This is designed for avoiding potential errors, for example, PCA. Default is FALSE.

return_model A logic variable. If TRUE, the marginal models and copula models will be returned. Default is FALSE.

simplify A logic variable. If TRUE, the fitted regression model will only keep the essential contains for predict, otherwise the fitted models can be VERY large. Default is FALSE.

parallelization A string indicating the specific parallelization function to use. Must be one of 'mcmapply', 'bpmapply', or 'pbmcmapply', which corresponds to the parallelization function in the package parallel,BiocParallel, and pbmcapply respectively. The default value is 'mcmapply'.

BPPARAM A MulticoreParam object or NULL. When the parameter parallelization = 'mcmapply' or 'pbmcmapply', this parameter must be NULL. When the parameter parallelization = 'bpmapply', this parameter must be one of the MulticoreParam object offered by the package BiocParallel. The default value is NULL.
A logic variable. If TRUE, the warning/error log and runtime for gam/gamlss will be returned, FALSE otherwise. Default is FALSE.

Value

A list with the components:

- **new_count** A matrix of the new simulated count (expression) matrix.
- **new_covariate** A data.frame of the new covariate matrix.
- **model_aic** The model AIC.
- **marginal_list** A list of marginal regression models if return_model = TRUE.
- **corr_list** A list of correlation models (conditional copulas) if return_model = TRUE.

Examples

data(example_sce)
my_simu <- scdesign3(
sce = example_sce,
assay_use = "counts",
celltype = "cell_type",
pseudotime = "pseudotime",
spatial = NULL,
other_covariates = NULL,
mu_formula = "s(pseudotime, bs = 'cr', k = 10)",
sigma_formula = "s(pseudotime, bs = 'cr', k = 3)",
family_use = c(rep("nb", 5), rep("zip", 5)),
n_cores = 2,
usebam = FALSE,
corr_formula = "pseudotime",
copula = "vine",
DT = TRUE,
pseudo_obs = FALSE,
ncell = 1000,
return_model = FALSE)

simu_new generates new simulated data based on fitted marginal and copula models.
Usage

```r
simu_new(
  sce,
  assay_use = "counts",
  mean_mat,
  sigma_mat,
  zero_mat,
  quantile_mat = NULL,
  copula_list,
  n_cores,
  fastmvn = FALSE,
  family_use,
  nonnegative = TRUE,
  nonzerovar = FALSE,
  input_data,
  new_covariate,
  important_feature = "all",
  parallelization = "mcmapply",
  BPPARAM = NULL,
  filtered_gene
)
```

Arguments

- **sce**: A `SingleCellExperiment` object.
- **assay_use**: A string which indicates the assay you will use in the sce. Default is 'counts'.
- **mean_mat**: A cell by feature matrix of the mean parameter.
- **sigma_mat**: A cell by feature matrix of the sigma parameter.
- **zero_mat**: A cell by feature matrix of the zero-inflation parameter.
- **quantile_mat**: A cell by feature matrix of the multivariate quantile. If provided, the `quantile_mat` must be NULL.
- **copula_list**: A list of copulas for generating the multivariate quantile matrix. If provided, the `quantile_mat` must be NULL.
- **n_cores**: An integer. The number of cores to use.
- **fastmvn**: A logical variable. If TRUE, the sampling of multivariate Gaussian is done by `mvnfast`, otherwise by `mvtnorm`. Default is FALSE.
- **family_use**: A string of the marginal distribution. Must be one of 'poisson', 'binomial', 'nb', 'zip', 'zinb' or 'gaussian'.
- **nonnegative**: A logical variable. If TRUE, values < 0 in the synthetic data will be converted to 0. Default is TRUE (since the expression matrix is nonnegative).
- **nonzerovar**: A logical variable. If TRUE, for any gene with zero variance, a cell will be replaced with 1. This is designed for avoiding potential errors, for example, PCA.
- **input_data**: A input count matrix.
- **new_covariate**: A data.frame which contains covariates of targeted simulated data from `construct_data`. 
important_feature

A string or vector which indicates whether a gene will be used in correlation estimation or not. If this is a string, then this string must be either "all" (using all genes) or "auto", which indicates that the genes will be automatically selected based on the proportion of zero expression across cells for each gene. Gene with zero proportion greater than 0.8 will be excluded form gene-gene correlation estimation. If this is a vector, then this should be a logical vector with length equal to the number of genes in sce. TRUE in the logical vector means the corresponding gene will be included in gene-gene correlation estimation and FALSE in the logical vector means the corresponding gene will be excluded from the gene-gene correlation estimation. The default value for is "all".

parallelization

A string indicating the specific parallelization function to use. Must be one of 'mcmapply', 'bpmapply', or 'pbmcmapply', which corresponds to the parallelization function in the package parallel, BiocParallel, and pbmcapply respectively. The default value is 'mcmapply'.

BPPARAM

A MulticoreParam object or NULL. When the parameter parallelization = 'mcmapply' or 'pbmcmapply', this parameter must be NULL. When the parameter parallelization = 'bpmapply', this parameter must be one of the MulticoreParam object offered by the package BiocParallel. The default value is NULL.

filtered_gene

A vector or NULL which contains genes that are excluded in the marginal and copula fitting steps because these genes only express in less than two cells. This can be obtain from construct_data

Details

The function takes the new covariate (if use) from construct_data, parameter matrices from extract_para and multivariate Unifs from fit_copula.

Value

A feature by cell matrix of the new simulated count (expression) matrix or sparse matrix.

Examples

data(example_sce)
my_data <- construct_data(
  sce = example_sce,
  assay_use = "counts",
  celltype = "cell_type",
  pseudotime = "pseudotime",
  spatial = NULL,
  other_covariates = NULL,
  corr_by = "1"
)
my_marginal <- fit_marginal(
  data = my_data,
  mu_formula = "s(pseudotime, bs = 'cr', k = 10)",
  sigma_formula = "1"
family_use = "nb",
n_cores = 1,
usebam = FALSE
)
my_copula <- fit_copula(
sce = example_sce,
assay_use = "counts",
marginal_list = my_marginal,
family_use = c(rep("nb", 5), rep("zip", 5)),
copula = "vine",
n_cores = 1,
input_data = my_data$dat
)
my_para <- extract_para(
sce = example_sce,
marginal_list = my_marginal,
n_cores = 1,
family_use = c(rep("nb", 5), rep("zip", 5)),
new_covariate = my_data$new_covariate,
data = my_data$dat
)
my_newcount <- simu_new(
sce = example_sce,
mean_mat = my_para$mean_mat,
sigma_mat = my_para$sigma_mat,
zero_mat = my_para$zero_mat,
quantile_mat = NULL,
copula_list = my_copula$copula_list,
n_cores = 1,
family_use = c(rep("nb", 5), rep("zip", 5)),
input_data = my_data$dat,
new_covariate = my_data$new_covariate,
important_feature = my_copula$important_feature,
filtered_gene = my_data$filtered_gene
)
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