Package ‘SPsimSeq’

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Title  Semi-parametric simulation tool for bulk and single-cell RNA sequencing data

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Description  SPsimSeq uses a specially designed exponential family for density estimation to constructs the distribution of gene expression levels from a given real RNA sequencing data (single-cell or bulk), and subsequently simulates a new dataset from the estimated marginal distributions using Gaussian-copulas to retain the dependence between genes. It allows simulation of multiple groups and batches with any required sample size and library size.

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SPsimSeq-package

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SPsimSeq-package SPsimSeq package

Description

SPsimSeq uses a specially designed exponential family for density estimation to constructs the distribution of gene expression levels from a given real RNA sequencing data (single-cell or bulk), and subsequently, simulates a new dataset from the estimated marginal distributions using Gaussian-copulas to retain the dependence between genes. It allows simulation of multiple groups and batches with any required sample size and library size.
buildXmat

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References

**buildXmat**  
An auxialiary function to quickly construct the polynomial matrix, using Horner’s rule

**Usage**

```
buildXmat(x, nc)
```

**Arguments**

- `x`  
The base
- `nc`  
the number of columns

**Value**

A matrix with increasing powers of x in the columns

**calculateCPM**  
Calculates counts per millions of reads, possibly with log-transform

**Description**

Calculates counts per millions of reads, possibly with log-transform

**Usage**

```
calculateCPM(X, const.mult, prior.count)
```

**Arguments**

- `X`  
raw data matrix
- `const.mult`  
a constant to multiply with
- `prior.count`  
prior count to be added to the zeroes
chooseCandGenes

Value

a normalized data matrix

checkInputValidity  

Check for data validity

Description

Check for data validity

Usage

checkInputValidity(
  s.data,
  group,
  batch,
  group.config,
  batch.config,
  w,
  log.CPM.transform,
  prior.count,
  pDE,
  lib.size.params,
  llStat.thrld,
  result.format
)

Arguments

s.data, group, batch, group.config, batch.config, w, log.CPM.transform, prior.count, pDE, lib.size.params, llStat.thrld, result.format

see ?SPsimSeq

Value

Throws errors where needed, otherwise returns invisible

chooseCandGenes  

Select candidate genes

Description

This function can be used to independently select candidate genes from a given real RNA-seq data (bulk/single) for the SPsimSeq simulation. It chooses genes with various characteristics, such as log-fold-change above a certain threshold.
chooseCandGenes

Usage

chooseCandGenes(
  cpm.data,
  group,
  lfc.thrld,
  l1Stat.thrld,
  t.thrld,
  w = w,
  max.frac.zeror.diff = Inf,
  pDE,
  n.genes,
  prior.count
)

Arguments

cpm.data logCPM transformed matrix (if log.CPM.transform=FALSE, then it is the source
  gene expression data)

group a grouping factor

lfc.thrld a positive numeric value for the minimum absolute log-fold-change for selecting
  candidate DE genes in the source data (when group is not NULL and pDE>0)

l1Stat.thrld a positive numeric value for the minimum squared test statistics from the log-
  linear model to select candidate DE genes in the source data (when group is not
  NULL and pDE>0) containing X as a covariate to select DE genes

t.thrld a positive numeric value for the minimum absolute t-test statistic for the log-
  fold-changes of genes for selecting candidate DE genes in the source data (when
  group is not NULL and pDE>0)

w a numeric value between 0 and 1. The number of classes to construct the prob-
  ability distribution will be round(w*n), where n is the total number of sam-
  ples/cells in a particular batch of the source data

max.frac.zeror.diff a numeric value >=0 indicating the maximum absolute difference in the fraction
  of zero counts between the groups for DE genes.

pDE fraction of DE genes

n.genes total number of genes

prior.count a positive constant to be added to the CPM before log transformation, to avoid
  log(0). The default is 1.

Value

a list object containing a set of candidate null and non-null genes and additional results
configExperiment  

Configure experiment

Description

Configure experiment

Usage

configExperiment(batch.config, group.config, tot.samples, batch, group)

Arguments

- **batch.config**: a numerical vector for the marginal fraction of samples in each batch. The number of batches to be simulated is equal to the size of the vector. All values must sum to 1.
- **group.config**: a numerical vector for the marginal fraction of samples in each group. The number of groups to be simulated is equal to the size of the vector. All values must sum to 1.
- **tot.samples**: total number of samples to be simulated.
- **batch, group**: batch and grouping vectors

Value

a list object containing the number of groups and batches to be simulated, and the experiment configuration

Examples

```r
batch = sample(LETTERS[1:3], 20, replace = TRUE)
group = sample(1:3, 20, replace = TRUE)
#---- a design with a total of 10 samples/cells from 1 batch and 1 group
configExperiment(batch.config=1, group.config=1, tot.samples=10,
batch = batch, group = group)

#---- a design with a total of 20 samples/cells from 1 group and 2 batches with
# batch 1 has 15 samples/cells and batch 2 has 5
configExperiment(batch.config = c(15/20, 5/20), group.config = 1,
tot.samples = 20, batch = batch, group = group)

#---- a design with a total of 20 samples/cells from 1 batch and 2 groups with
# group 1 has 10 samples/cells and batch 2 has 10
configExperiment(batch.config=1, group.config=c(0.5, 0.5), tot.samples=20,
batch = batch, group = group)

#---- a design with a total of 30 samples/cells from 2 groups with group 1 has 15 samples
# and group 2 has 15, and three batches with batch 1,2, and 3 have 5, 10, and 15 samples/cells,
# respectively.
```
constructDens

```r
cfgExperiment(batch.config = c(5/30, 10/30, 15/30), group.config = c(0.5, 0.5),
tot.samples = 30, batch = batch, group = group)
```

**constructDens**

*Construct the cumulative density*

**Description**

Construct the cumulative density

**Usage**

```r
constructDens(densList.ii, exprmt.design, DE.ind.ii, returnDens = FALSE)
```

**Arguments**

- `densList.ii`: the estimated density parameters
- `exprmt.design`: experiment configuration
- `DE.ind.ii`: a boolean, is the gene to be DE?
- `returnDens`: A boolean, should densities rather than cumulative densities be returned?

**Value**

The cumulative density

---

estLibSizeDistr

*Estimate log-normal distribution for the library sizes*

**Description**

Estimate log-normal distribution for the library sizes

**Usage**

```r
estLibSizeDistr(LS, batch)
```

**Arguments**

- `LS`: observed library sizes
- `batch`: batches

**Value**

Estimated log-normal parameter library sizes
evaluateDensities  Evaluate the densities in the estimated SPsimSeq object

Description

Evaluate the densities in the estimated SPsimSeq object

Usage

evaluateDensities(SPobj, newData = names(SPobj$detailed.results$densList))

Arguments

SPobj The SPsimSeq object, with details retained
newData A character vector of gene names

Value

a list of estimated densities, breaks and midpoints, one for every gene in newData

Examples

data("zhang.data.sub")
# filter genes with sufficient expression (important step to avoid bugs)
zhang.counts <- zhang.data.sub$counts
MYCN.status <- zhang.data.sub$MYCN.status
# simulate data
sim.data.bulk <- SPsimSeq(n.sim = 1, s.data = zhang.counts,
    group = MYCN.status, n.genes = 2000, batch.config = 1,
    group.config = c(0.5, 0.5), tot.samples = 20,
    pDE = 0.1, lfc.thrld = 0.5, result.format = "list",
    return.details = TRUE)
outDens = evaluateDensities(sim.data.bulk)
select.genes <- sample(names(outDens), 4)
select.sample = sample(
    seq_along(sim.data.bulk$detailed.results$exprmt.design$sub.groups), 1)
par(mfrow=c(2, 2))
for(i in select.genes){
    plot(outDens[[i]][[select.sample]]$mids, outDens[[i]][[select.sample]]$gy, type = "l",
        xlab = "Outcome", ylab = "Density", main = paste("Gene", i))
}
expit

Evaluate the expit function

Description
Evaluate the expit function

Usage
expit(x)

Arguments
x the argument

Value
the expit of the argument

extractMat
A function with S4 dispatching to extract the count matrix

Description
A function with S4 dispatching to extract the count matrix

Usage
extractMat(Y, ...)

## S4 method for signature 'SingleCellExperiment'
extractMat(Y, ...)

## S4 method for signature 'matrix'
extractMat(Y, ...)

## S4 method for signature 'data.frame'
extractMat(Y, ...)

## S4 method for signature 'phyloseq'
extractMat(Y, ...)

Arguments
Y a matrix, data frame, phyloseq object or SingleCellExperiment
... additional arguments, currently ignored
Value

A data matrix with samples in the columns and genes in the rows.

---

**fitLLmodel**  
*Fit log linear model for each gene*

**Description**

Fit log linear model for each gene.

**Usage**

```r
fitLLmodel(yy, mu.hat, sig.hat, n)
```

**Arguments**

- `yy` a list object containing a result from `obtCount()` function for a single gene
- `mu.hat, sig.hat` Carrier density estimators
- `n` number of observations

**Value**

A list object containing the fitted log linear model and carrier density.

---

**fitPoisGlm**  
*Fast fit Poisson regression*

**Description**

Fast fit Poisson regression.

**Usage**

```r
fitPoisGlm(Ny, x, degree, offset)
```

**Arguments**

- `Ny` vector of counts
- `x` regressor
- `degree` degree of the polynomial
- `offset` offset

**Value**

see `glm.fit`
fracZeroLogitModel

Description
Extract data and iterate over batches to estimate zero probability models

Usage
fracZeroLogitModel(s.data, batch, cpm.data, n.mean.class, minFracZeroes)

Arguments
- s.data, cpm.data: raw and transformed data
- batch: the batch vector
- n.mean.class: see zeroProbModel
- minFracZeroes: minimum fraction of zeroes before zero-inflation is applied

Value
a list of binomial regression parameters

---

genCopula

Description
Generate a copula instance

Usage
genCopula(corMats, exprmt.design)

Arguments
- corMats: List of correlation matrices
- exprmt.design: Number of batches, and batch vector

Value
a list of copula instances
geneParmEst

Description

Gene level param estimates for density estimation

Usage

geneParmEst(
  cpm.data.i, 
  batch, 
  group,
  prior.count = prior.count, 
  de.ind,
  model.zero.prob, 
  w
)

Arguments

cpm.data.i full vector of genewise observation
batch, group batch and grouping vectors
prior.count the prior count for the cpm transofrm
de.ind a boolean, is the gene to be DE?
model.zero.prob a boolean, should zero-density be modelled?
w weight

Value

list of density estimates

genLibSizes

Generate library sizes from log-normal

Description

Generate library sizes from log-normal

Usage

genLibSizes(fit.ln, exprmt.design)
**matchCopula**

**Arguments**

- `fit.ln`: the library size model
- `exprmt.design`: the design

**Value**

The generated library sizes per batch and group

---

**Description**

Match copulas to estimated SP distribution

**Usage**

`matchCopula(cumDens, exprmt.design, copSam, sel.genes.ii)`

**Arguments**

- `cumDens`: The cumulative densities evaluated
- `exprmt.design`: the design
- `copSam`: the sampled copula
- `sel.genes.ii`: the gene

**Value**

the outcome values as a vector

---

**obtCorMatsBatch**

_A function to obtain copulas or uniform random variables_

**Description**

A function to obtain copulas or uniform random variables

**Usage**

`obtCorMatsBatch(cpm.data, batch)`

**Arguments**

- `cpm.data`: the transformed data matrix
- `batch`: the batch indicators
**obtCount**

*Calculates height and mid points of a distribution*

**Description**

Calculates height and mid points of a distribution

**Usage**

```r
obtCount(Y, w)
```

**Arguments**

- `Y`: a vector of gene expression data for a particular gene (in log CPM)
- `w`: a numeric value between 0 and 1 or NULL refering the number of classes to be created

**Value**

a list object containing class breaks, mid points and counts

---

**parmEstDensVec**

*Density estimation on a single vector*

**Description**

Density estimation on a single vector

**Usage**

```r
c parmEstDensVec(
  Y0,
  model.zero.prob,
  min.val,
  w,
  prev.min.val = 0.25,
  min.countnonnull = 3
)
```

**Value**

The estimated correlation matrices per batch
**prepareSPsimOutputs**

**Arguments**

- Y0: the vector of observations
- model.zero.prob, min.val, w: see geneParmEst()
- prev.min.val: minimum prevalence of minimum values
- min.countnonnull: minimum count for estimation

**Value**

density estimates

---

**prepareSPsimOutputs**  
*A function to prepare outputs*

---

**Description**

A function to prepare outputs

**Usage**

```r
prepareSPsimOutputs(sim.dat, exprmt.design, DE.ind, result.format, LL)
```

**Arguments**

- sim.dat: The simulated data
- exprmt.design: the design
- DE.ind: the differential abundance indicator
- result.format: the desired output format
- LL: simulated library sizes

**Value**

the data in the desired format
scNGP.data

samZeroID

Return ID for observations to be set to zero

Description
Return ID for observations to be set to zero

Usage
samZeroID(fracZero.logit.list, logLL, gene)

Arguments
fracZero.logit.list
The estimated zero model

logLL
the logged library sizes

gene
the gene name

Value
A boolean, should a zero be introduced or not?

scNGP.data

Neuroblastoma NGP cells single-cell RNA-seq.

Description
It was retrieved from [1] (GEO accession GSE119984): This dataset is generated for a cellular perturbation experiment on the C1 instrument (SMARTer protocol) [1]. This total RNA-seq dataset contains 83 NGP neuroblastoma cells, of which 31 were treated with nutlin-3 and the other 52 cells were treated with vehicle (controls).

Usage
scNGP.data

Format
A SingleCellExperiment object

Source
GEO accession GSE119984
selectGenes

References


**SingleCellExperiment**  counts + gene info + cell info

Examples

```r
data("scNGP.data")
scNGP.data
```

---

```r
selectGenes(pDE, exprmt.design, n.genes, null.genes0, nonnull.genes0)
```

Description

Sample genes from candidate genes

Usage

```r
selectGenes(pDE, exprmt.design, n.genes, null.genes0, nonnull.genes0)
```

Arguments

- `pDE`  fraction of genes to be made DE
- `exprmt.design`  the experiment design
- `n.genes`  the total number of genes required
- `null.genes0`, `nonnull.genes0`  Candidate null and non-null genes

Value

a vector of selected genes
SPsimPerGene

A function that generates the simulated data for a single gene

**Description**

A function that generates the simulated data for a single gene

**Usage**

```r
SPsimPerGene(
  cumDens,
  exprmt.design,
  sel.genes.ii,
  log.CPM.transform,
  prior.count,
  LL,
  copSam,
  model.zero.prob,
  fracZero.logit.list,
  const.mult
)
```

**Arguments**

- `cumDens` cumulative density
- `exprmt.design` the experiment design
- `sel.genes.ii` selected gene
- `log.CPM.transform` a boolean, is log-CPM transform required?
- `prior.count` the prior count
- `LL` the library sizes
- `copSam` the generated copula
- `model.zero.prob` a boolean, should the zeroes be modelled separately
- `fracZero.logit.list` The zero model
- `const.mult` a large constant for the CPM transform, normally 1e6

**Value**

Simulated cpm values
SPsimSeq

A function to simulate bulk or single cell RNA sequencing data

Description

This function simulates (bulk/single cell) RNA-seq dataset from semi-parametrically estimated distributions of gene expression levels in a given real source RNA-seq dataset.

Usage

SPsimSeq(
  n.sim = 1,
  s.data,
  batch = rep(1, ncol(s.data)),
  group = rep(1, ncol(s.data)),
  n.genes = 1000,
  batch.config = 1,
  group.config = 1,
  pDE = 0.1,
  cand.DE.genes = NULL,
  lfc.thrld = 0.5,
  t.thrld = 2.5,
  llStat.thrld = 5,
  tot.samples = ncol(s.data),
  model.zero.prob = FALSE,
  genewiseCor = TRUE,
  log.CPM.transform = TRUE,
  lib.size.params = NULL,
  variable.lib.size = FALSE,
  w = NULL,
  result.format = "SCE",
  return.details = FALSE,
  verbose = TRUE,
  prior.count = 1,
  const.mult = 1e+06,
  n.mean.class = 0.2,
  minFracZeroes = 0.25
)

Arguments

n.sim an integer for the number of simulations to be generated
s.data a real source dataset (a SingleCellExperiment class or a matrix/data.frame of counts with genes in rows and samples in columns)
batch NULL or a vector containing batch indicators for each sample/cell in the source data
group
n.genes
batch.config
group.config
pDE
cand.DE.genes
lfc.thrld
t.thrld
llStat.thrld
tot.samples
model.zero.prob
genewiseCor
log.CPM.transform
lib.size.params

NULL or a vector containing group indicators for each sample/cell in the source data

a numeric value for the total number of genes to be simulated

a numerical vector containing fractions for the composition of samples/cells per batch. The fractions must sum to 1. The number of batches to be simulated is equal to the size of the vector. (Example, batch.config=c(0.6, 0.4) means simulate 2 batches with 60% of the simulated samples/cells in batch 1 and the rest 40% in the second batch. Another example, batch.config=c(0.3, 0.35, 0.25) means simulate 3 batches with the first, second and third batches contain 30%, 35% and 25% of the samples/cells, respectively).

da numerical vector containing fractions for the composition of samples/cells per group. Similar definition to 'batch.config'. The number of groups to be simulated is equal to the size of the vector. The fractions must sum to 1.

a numeric value between 0 and 1 indicating the desired fraction of DE genes in the simulated data

a list object containing candidate null and non-null (DE/predictor) genes. If NULL (the default), an internal function determines candidate genes based on log-fold-change and other statistics. The user can also pass a list of candidate null and non-null genes (they must be disjoint). In particular, the list should contain two character vectors (for the name of the features/genes in the source data) with names 'null.genes' and 'nonnull.genes'. For example, cand.DE.genes=list(null.genes=c('A', 'B'), nonnull.genes=c('C', 'D')).

a positive numeric value for the minimum absolute log-fold-change for selecting candidate DE genes in the source data (when group is not NULL, pDE>0 and cand.DE.genes is NULL)

a positive numeric value for the minimum absolute t-test statistic for the log-fold-changes of genes for selecting candidate DE genes in the source data (when group is not NULL, pDE>0 and cand.DE.genes is NULL)

a positive numeric value for the minimum squared test statistics from the log-linear model to select candidate DE genes in the source data (when group is not NULL, pDE>0 and cand.DE.genes is NULL)

a numerical value for the total number of samples/cells to be simulated.

a logical value whether to model the zero expression probability separately (suitable for simulating of single-cell RNA-seq data or zero-inflated data)

a logical value, if TRUE (default) the simulation will retain the gene-to-gene correlation structure of the source data using Gaussian-copulas . Note that if it is TRUE, the program will be slow or it may fail for a limited memory size.

a logical value. If TRUE, the source data will be transformed into log-(CPM+const) before estimating the probability distributions

NULL or a named numerical vector containing parameters for simulating library sizes from log-normal distribution. If lib.size.params =NULL (default), then the package will fit a log-normal distribution for the library sizes in the source data
to simulate new library sizes. If the user would like to specify the parameters of the log-normal distribution for the desired library sizes, then the log-mean and log-SD params of \texttt{rlnorm()} functions can be passed using this argument. Example, \texttt{lib.size.params = c(meanlog=10, sdlog=0.2)}. See also \texttt{?rlnorm}.

\textbf{variable.lib.size}

a logical value. If FALSE (default), then the expected library sizes are simulated once and remains the same for every replication (if \texttt{n.sim}>1).

\textbf{result.format}

a character value for the type of format for the output. Choice can be 'SCE' for \texttt{SingleCellExperiment} class or "list" for a list object that contains the simulated count, column information and row information.

\textbf{return.details}

a logical value. If TRUE, detailed results including estimated parameters and densities will be returned

\textbf{verbose}

a logical value, if TRUE a message about the status of the simulation will be printed on the console

\textbf{prior.count}

a positive constant to be added to the CPM before log transformation, to avoid log(0). The default is 1.

\textbf{const.mult}

A constant by which the count are scaled. Usually 1e6 to get CPM

\textbf{n.mean.class}

a fraction of the number of genes for the number of groups to be created for the mean log CPM of genes

\textbf{minFracZeroes}

minimum fraction of zeroes before a zero inflation model is fitted

\section*{Details}

This function uses a specially designed exponential family for density estimation to constructs the distribution of gene expression levels from a given real gene expression data (e.g. single-cell or bulk sequencing data), and subsequently, simulates a new from the estimated distributions.

For simulation of single-cell RNA-seq data (or any zero inflated gene expression data), the programm involves an additional step to explicitly account for the high abundance of zero counts (if required). This step models the probability of zero counts as a function the mean expression of the gene and the library size of the cell (both in log scale) to add excess zeros. This can be done by using \texttt{model.zero.prob=TRUE}. Note that, for extremely large size data, it is recemmended to use a random sample of cells to reduce computation time. To enable this, add the argument \texttt{subset.data=TRUE} and you can specify the number of cells to be used using \texttt{n.samples} argument. For example \texttt{n.samples=400}. Given known groups of samples/cells in the source data, DGE is simulated by independently sampling data from distributions constructed for each group separately. In particular, this procedure is applied on a set of genes with absolute log-fold-change in the source data more than a given threshold (lfc.thrld). Moreover, when the source dataset involves samples/cells processed in different batches, our simulation procedure incorporates this batch effect in the simulated data, if required. Different experimental designs can be simulated using the group and batch configuration arguments to simulate biological/experimental conditions and batches, respectively. Also, it is important to filter the source data so that genes with suficient expression will be used to estimate the probability distributions.

\section*{Value}

a list of \texttt{SingleCellExperiment/list} objects each containing simulated counts (not normalized), simple/cell level information in \texttt{colData}, and gene/feature level information in \texttt{rowData}.
References


Examples

```r
# Example 1: simulating bulk RNA-seq

data("zhang.data.sub")

zhang.counts <- zhang.data.sub$counts
MYCN.status <- zhang.data.sub$MYCN.status

# We simulate only a single data (n.sim = 1) with the following property
# - 1000 genes (n.genes = 1000)
# - 40 samples (tot.samples = 40)
# - the samples are equally divided into 2 groups each with 90 samples
# (group.config = c(0.5, 0.5))
# - all samples are from a single batch (batch = NULL, batch.config = 1)
# - we add 10% DE genes (pDE = 0.1)
# - the DE genes have a log-fold-change of at least 0.5 in
# the source data (lfc.thrld = 0.5)
# - we do not model the zeroes separately, they are the part of density
# estimation (model.zero.prob = FALSE)

# simulate data
set.seed(6452)
sim.data.bulk <- SPsimSeq(n.sim = 1, s.data = zhang.counts,
                          group = MYCN.status, n.genes = 1000, batch.config = 1,
                          group.config = c(0.5, 0.5), tot.samples = 40,
                          pDE = 0.1, lfc.thrld = 0.5, result.format = "list")

head(sim.data.bulk$counts[[1]][, seq_len(5)])  # count data
head(sim.data.bulk$colData)  # sample info
head(sim.data.bulk$rowData)  # gene info
```

```
# Example 2: simulating single cell RNA-seq from a single batch (read-counts)
# we simulate only a single scRNA-seq data (n.sim = 1) with the following property
# - 2000 genes (n.genes = 2000)
# - 100 cells (tot.samples = 100)
# - the cells are equally divided into 2 groups each with 50 cells
# (group.config = c(0.5, 0.5))
# - all cells are from a single batch (batch = NULL, batch.config = 1)
# - we add 10% DE genes (pDE = 0.1)
# - the DE genes have a log-fold-change of at least 0.5
# - we model the zeroes separately (model.zero.prob = TRUE)
# - the output will be in SingleCellExperiment class object (result.format = "SCE")
```

```r
# simulate data
set.seed(6452)
sim.data.sc <- SPsimSeq(n.sim = 1, s.data = zhang.counts,
                        group = MYCN.status, n.genes = 2000, batch.config = 1,
                        group.config = c(0.5, 0.5), tot.samples = 100,
                        pDE = 0.1, lfc.thrld = 0.5, result.format = "SCE")
```

head(sim.data.sc$counts[[1]][, seq_len(5)])  # count data
head(sim.data.sc$colData)  # sample info
head(sim.data.sc$rowData)  # gene info
library(SingleCellExperiment)

# load the NGP nutlin data (availabl with the package, processed with
# SMARTer/C1 protocol, and contains read-counts)
data("scNGP.data")

# filter genes with sufficient expression (important step to avoid bugs)
treatment <- ifelse(scNGP.data$characteristics..treatment=="nutlin",2,1)
set.seed(654321)

# simulate data (we simulate here only a single data, n.sim = 1)
sim.data.sc <- SPsimSeq(n.sim = 1, s.data = scNGP.data, group = treatment,
  n.genes = 2000, batch.config = 1, group.config = c(0.5, 0.5),
  tot.samples = 100, pDE = 0.1, lfc.thrld = 0.5, model.zero.prob = TRUE,
  result.format = "SCE")
sim.data.sc1 <- sim.data.sc[[1]]
class(sim.data.sc1)
head(counts(sim.data.sc1)[, seq_len(5)])
colData(sim.data.sc1)
rowData(sim.data.sc1)

zeroProbModel

Predict zero probability using logistic regression

Description

Predict zero probability using logistic regression

Usage

zeroProbModel(cpm.data, logL, zeroMat, n.mean.class)

Arguments

cpm.data log CPM matrix

logL log library size of the source data

zeroMat the matrix of zero indicators

n.mean.class a fraction of the number of genes for the number of groups to be created for the
  mean log CPM of genes

Value

The coefficients of the estimated logistic regression
Description

The data contains 498 neuroblastoma tumors. In short, unstranded poly(A)+ RNA sequencing was performed on the HiSeq 2000 instrument (Illumina). Paired-end reads with a length of 100 nucleotides were obtained. To quantify the full transcriptome, raw fastq files were processed with Kallisto v0.42.4 (index build with GRCh38-Ensembl v85). The pseudo-alignment tool Kallisto was chosen above other quantification methods as it is performing equally good but faster. For this study, a subset of 172 tumors (samples) with high-risk disease were selected, forming two groups: the MYCN amplified ($n_1$ = 91) and MYCN non-amplified ($n_2$ = 81) tumours. Sometimes we refer this dataset to us the Zhang data or the Zhang neuroblastoma data. In this package, a subset of 5000 genes (randomly selected) are made available for illustration purpose only.

Usage

```r
data(zhang.data.sub)
```

Format

A list object

Source

GEO accession GSE49711

References


```r
counts
gene counts
group MYCN (0 for MYCN non-amplified and 1 for MYCN amplified)
```

Examples

```r
data("zhang.data.sub")
str(zhang.data.sub)
```
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