Package: SPsimSeq (via r-universe)

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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` *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.

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References

- Alemu Takele Assefa, Jo Vandesompele, Olivier Thas. (2020). SPsimSeq: semi-parametric simulation of bulk and single cell RNA sequencing data, *Bioinformatics*, , btaa105, https://doi.org/10.1093/bioinformatic

---

buildXmat — *An auxialiary function to quickly construct the polyomial matrix, using Horner's rule*

Description

An auxialiary function to quickly construct the polyomial 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

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 neede, otherwise returns invisible

chooseCandGenes *Select candidate genes*

Description

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

Usage

```
chooseCandGenes(
  cpm.data,
  group,
  lfc.thrld,
  llStat.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)
llStat.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 probability distribution will be round(w*n), where n is the total number of samples/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 contating 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 contating the number of groups and batches to be simukated, and the experiment configurartion

Examples

```
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 batchs 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 batchs with batch 1,2, and 3 have 5, 10, and 15 samples/cells,
# respectively.
configExperiment(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

```
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

```
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

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

Arguments

`yy`	a list object contating 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

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

Arguments

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

Value

see glm.fit

fracZeroLogitModel *Extract data and iterate over batches to estimate zero probability models*

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 *Generate a copula instance*

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 *Gene level param estimates for density estimation*

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)
```

Arguments

fit.ln	the library size model
exprmt.design	the design

Value

The generated libray sizes per batch and group

---

matchCopula *Match copulas to estimated SP distribution*

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

Value

The estimated correlation matrices per batch

`obtCount` *Calculates height and mid points of a distribution*

Description

Calculates height and mid points of a distribution

Usage

```
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 contating class breaks, mid points and counts

`parmEstDensVec` *Density estimation on a single vector*

Description

Density estimation on a single vector

Usage

```
parmEstDensVec(
  Y0,
  model.zero.prob,
  min.val,
  w,
  prev.min.val = 0.25,
  min.count.nonnull = 3
)
```

Arguments

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

Value

density estimates

`prepareSPsimOutputs` *A function to prepare outputs*

Description

A function to prepare outputs

Usage

```
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

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

References

1 - Verboom, K., Everaert, C., Bolduc, N., Livak, K. J., Yigit, N., Rombaut, D., ... & Speleman, F. (2019). SMARTer single cell total RNA sequencing. Nucleic Acids Research, 47(16), e93-e93.

SingleCellExperiment counts + gene info + cell infro

Examples

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

`selectGenes` *Sample genes from candidate genes*

Description

Sample genes from candidate genes

Usage

```
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

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

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

`batch.config` 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).

`group.config` a 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.

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

`cand.DE.genes` a list object contatining canidiate 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 canidate 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')).

`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, pDE>0 and cand.DE.genes is NULL)

`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, pDE>0 and cand.DE.genes is NULL)

`llStat.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, pDE>0 and cand.DE.genes is NULL)

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

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

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

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

`lib.size.params` 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 rlnorm() functions can be passed using this argument. Example, lib.size.params = c(meanlog=10, sdlog=0.2). See also ?rlnorm.

`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 n.sim>1).

`w` see ?hist

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

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

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

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

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

`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

`minFracZeroes` minimum fraction of zeroes before a zero inflation model is fitted

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 *model.zero.prob=TRUE*. Note that, for extremly large size data, it is recomended to use a random sample of cells to reduce computation time. To enable this, add the argument *subset.data=TRUE* and you can specify the number of cells to be used using *n.samples* argument. For example *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 seprately. 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 biologica/experimental conditions and batchs, respectively. Also, it is important to filter the source data so that genes with suffient expression will be used to estimate the probability distributions.

Value

a list of SingleCellExperiment/list objects each containing simulated counts (not normalized), smple/cell level information in colData, and gene/feature level information in rowData.

References

- Assefa, A. T., Vandesompele, J., & Thas, O. (2020). SPsimSeq: semi-parametric simulation of bulk and single cell RNA sequencing data. *Bioinformatics*, doi: https://doi.org/10.1093/bioinformatics/btaa105.
- Efron, B., & Tibshirani, R. (1996). Using specially designed exponential families for density estimation. *The Annals of Statistics*, 24(6), 2431-2461.

Examples

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

# load the Zhang bulk RNA-seq data (availabl with the package)
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 ouput will be in SingleCellExperiment class object (result.format = "SCE")
```

```
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 rgression*

Description

Predict zero probability using logistic rgression

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

zhang.data.sub *Neuroblastoma bulk RNA-seq data retrieved from Zhang et (2015).*

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

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

Format

A list object

Source

GEOaccessionGSE49711

References

1. Zhang W, Yu Y, Hertwig F, Thierry-Mieg J, Zhang W, Thierry-Mieg D, Wang J, Furlanello C, Devanarayan V, Cheng J, et al. Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biol. 2015;16(133) https://doi.org/10.1186/s13059-015-0694-1 2. Assefa, A. T., De Paepe, K., Everaert, C., Mestdagh, P., Thas, O., & Vandesompele, J. (2018). Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. GENOME BIOLOGY, 19.

counts gene counts

group MYCN (0 for MYCN non-amplified and 1 for MYCN amplified)

Examples

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

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