

Package ‘NormExpression’

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Type Package

Title Normalize Gene Expression Data using Evaluated Methods

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Description It provides a framework and a fast and simple way for researchers to evaluate methods (particularly some data-driven methods or their own methods) and then select a best one for data normalization in the gene expression analysis, based on the consistency of metrics and the consistency of datasets.

Zhenfeng Wu, Weixiang Liu, Xiufeng Jin, Deshui Yu, Hua Wang, Gustavo Glusman, Max Robinson, Lin Liu, Jishou Ruan and Shan Gao (2018) <doi:10.1101/251140>.

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bkRNA18	<i>bkRNA18</i>
---------	----------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

data("bkRNA18")

Format

A data frame with 57955 observations on the following 18 variables.

- col13616_1 a numeric vector
- col13816_3 a numeric vector
- col13916_5 a numeric vector
- col14016_7 a numeric vector
- col14416_9 a numeric vector
- col14516_11 a numeric vector

```
col4716_13 a numeric vector
col4816_97 a numeric vector
col5216_17 a numeric vector
col3616_2  a numeric vector
col3816_4  a numeric vector
col3916_6  a numeric vector
col4016_8  a numeric vector
col4416_10 a numeric vector
col4516_12 a numeric vector
col4716_14 a numeric vector
col4816_98 a numeric vector
col5216_18 a numeric vector
```

Examples

```
data(bkRNA18)
## maybe str(bkRNA18) ; plot(bkRNA18) ...
```

bkRNA18_factors	<i>bkRNA18_factors</i>
-----------------	------------------------

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
data("bkRNA18_factors")
```

Format

A data frame with 18 observations on the following 13 variables.

```
HG7  a numeric vector
ERCC  a numeric vector
TN   a numeric vector
TC   a numeric vector
CR   a numeric vector
NR   a numeric vector
DESeq a numeric vector
UQ   a numeric vector
TMM  a numeric vector
TU   a numeric vector
NCS  a numeric vector
ES   a numeric vector
GAPDH a numeric vector
```

Examples

```
data(bkRNA18_factors)
## maybe str(bkRNA18_factors) ; plot(bkRNA18_factors) ...
```

calcFactorRLE

calcFactorRLE

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
calcFactorRLE(data, p = p)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
p	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, p = p)
{
  gm <- exp(rowMeans(.log(data), na.rm = TRUE))
  apply(data, 2, function(u) quantile((u/gm)[u != 0], na.rm = TRUE,
    p = p))
}
```

calcFactorUpperquartile

calcFactorUpperquartile

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
calcFactorUpperquartile(data, lib.size, p = p)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
lib.size	Please refer to the file /inst/doc/readme.pdf.
p	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, lib.size, p = p)
{
  y <- t(t(data)/lib.size)
  f <- apply(y, 2, function(x) quantile(x[x != 0], p = p))
}
```

calcFactorWeighted	<i>calcFactorWeighted</i>
--------------------	---------------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
calcFactorWeighted(obs, ref, libsize.obs, libsize.ref, logratioTrim,
sumTrim, doWeighting, Acutoff)
```

Arguments

obs	Please refer to the file /inst/doc/readme.pdf.
ref	Please refer to the file /inst/doc/readme.pdf.
libsize.obs	Please refer to the file /inst/doc/readme.pdf.
libsize.ref	Please refer to the file /inst/doc/readme.pdf.
logratioTrim	Please refer to the file /inst/doc/readme.pdf.
sumTrim	Please refer to the file /inst/doc/readme.pdf.
doWeighting	Please refer to the file /inst/doc/readme.pdf.
Acutoff	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (obs, ref, libsize.obs = NULL, libsize.ref = NULL, logratioTrim = 0.3,
        sumTrim = 0.05, doWeighting = TRUE, Acutoff = -1e+10)
{
  if (all(obs == ref))
    return(1)
  obs <- as.numeric(obs)
  ref <- as.numeric(ref)
  if (is.null(libsize.obs))
    n0 <- sum(obs)
  else n0 <- libsize.obs
  if (is.null(libsize.ref))
    nR <- sum(ref)
  else nR <- libsize.ref
  logR <- log2((obs/n0)/(ref/nR))
  absE <- (log2(obs/n0) + log2(ref/nR))/2
  v <- (n0 - obs)/n0/obs + (nR - ref)/nR/ref
  fin <- is.finite(logR) & is.finite(absE) & (absE > Acutoff)
  logR <- logR[fin]
  absE <- absE[fin]
  v <- v[fin]
  n <- length(logR)
  loL <- floor(n * logratioTrim) + 1
  hiL <- n + 1 - loL
  loS <- floor(n * sumTrim) + 1
  hiS <- n + 1 - loS
  keep <- (rank(logR) >= loL & rank(logR) <= hiL) & (rank(absE) >=
    loS & rank(absE) <= hiS)
  if (doWeighting) {
    2^(sum(logR[keep]/v[keep], na.rm = TRUE)/sum(1/v[keep],
      na.rm = TRUE))
  }
  else {
    2^(mean(logR[keep], na.rm = TRUE))
  }
}
```

change_colours

change_colours

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
change_colours(p, palette, type)
```

Arguments

p	Please refer to the file /inst/doc/readme.pdf.
palette	Please refer to the file /inst/doc/readme.pdf.
type	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (p, palette, type)
{
  n <- nlevels(p$data[[deparse(p$mapping$group)]])
  tryCatch(as.character(palette), error = function(e) stop("be vector", call. = FALSE))
  if (n > length(palette))
    stop("Not enough colours in palette.")
  if (missing(type))
    type <- grep("colour|fill", names(p$layers[[1]]$mapping),
      value = TRUE)[1]
  pal <- function(n) palette[seq_len(n)]
  p + discrete_scale(type, "foo", pal)
}
```

CV2AUCVC

CV2AUCVC

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
CV2AUCVC(data, cvResolution = 0.005)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
cvResolution	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, cvResolution = 0.005)
{
  cv_cutoff <- NULL
  uniform_genes_counts <- NULL
  for (i in seq(0, 1, cvResolution)) {
    cv_cutoff <- c(cv_cutoff, i)
    gene_number <- length(which(data <= i))
    uniform_genes_counts <- c(uniform_genes_counts, gene_number)
  }
  getArea(cv_cutoff, uniform_genes_counts)
}
```

```
estimateSizeFactorsForMatrix
```

```
estimateSizeFactorsForMatrix
```

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
estimateSizeFactorsForMatrix(data, p = p)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
p	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, p = p)
{
  loggeomeans <- rowMeans(.log(data), na.rm = TRUE)
  apply(data, 2, function(cnts) exp(quantile(.log(cnts) - loggeomeans,
    na.rm = TRUE, p = p)))
}
```

filteredZero	<i>filteredZero</i>
--------------	---------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
filteredZero(data, nonzeroRatio)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
nonzeroRatio	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, nonzeroRatio)
{
  nonzeroCount <- apply(data, 1, function(x) length(which(x !=
    0)))
  geneIndex <- which(nonzeroCount >= ncol(data) * nonzeroRatio)
  return(geneIndex)
}
```

findGenes	<i>findGenes</i>
-----------	------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
findGenes(g, qlower = NULL, qupper = NULL, pre_ratio = NULL)
```

Arguments

g	Please refer to the file /inst/doc/readme.pdf.
qlower	Please refer to the file /inst/doc/readme.pdf.
qupper	Please refer to the file /inst/doc/readme.pdf.
pre_ratio	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (g, qlower = NULL, qupper = NULL, pre_ratio = NULL)
{
  gene_name <- rownames(g)
  g <- unlist(g)
  seen <- which(g >= qlower & g <= qupper)
  counts <- length(seen)
  if (counts >= pre_ratio * length(g)) {
    gene_name
  }
}
```

gatherCors

gatherCors

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
gatherCors(data, cor_method = c("spearman", "pearson", "kendall"),
HG7 = NULL, ERCC = NULL, TN = NULL, TC = NULL, CR = NULL, NR = NULL,
DESeq = NULL, UQ = NULL, TMM = NULL, TU = NULL, GAPDH = NULL,
pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65, rounds = 1e+06)
```

Arguments

data	Please refer to the file <code>/inst/doc/readme.pdf</code> .
cor_method	Please refer to the file <code>/inst/doc/readme.pdf</code> .
HG7	Please refer to the file <code>/inst/doc/readme.pdf</code> .
ERCC	Please refer to the file <code>/inst/doc/readme.pdf</code> .
TN	Please refer to the file <code>/inst/doc/readme.pdf</code> .
TC	Please refer to the file <code>/inst/doc/readme.pdf</code> .
CR	Please refer to the file <code>/inst/doc/readme.pdf</code> .
NR	Please refer to the file <code>/inst/doc/readme.pdf</code> .
DESeq	Please refer to the file <code>/inst/doc/readme.pdf</code> .
UQ	Please refer to the file <code>/inst/doc/readme.pdf</code> .
TMM	Please refer to the file <code>/inst/doc/readme.pdf</code> .

TU	Please refer to the file /inst/doc/readme.pdf.
GAPDH	Please refer to the file /inst/doc/readme.pdf.
pre_ratio	Please refer to the file /inst/doc/readme.pdf.
lower_trim	Please refer to the file /inst/doc/readme.pdf.
upper_trim	Please refer to the file /inst/doc/readme.pdf.
rounds	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, cor_method = c("spearman", "pearson", "kendall"),
  HG7 = NULL, ERCC = NULL, TN = NULL, TC = NULL, CR = NULL,
  NR = NULL, DESeq = NULL, UQ = NULL, TMM = NULL, TU = NULL,
  GAPDH = NULL, pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65,
  rounds = 1e+06)
{
  methodsList <- list(HG7 = HG7, ERCC = ERCC, TN = TN, TC = TC,
    CR = CR, NR = NR, DESeq = DESeq, UQ = UQ, TMM = TMM,
    TU = TU, GAPDH = GAPDH)
  specifiedMethods <- methodsList[!unlist(lapply(methodsList,
    is.null))]
  numMethod <- length(specifiedMethods)
  method_range <- seq(1, numMethod, 1)
  ubq_genes <- identifyUbq(data, pre_ratio = pre_ratio, lower_trim = lower_trim,
    upper_trim = upper_trim, min_ubq = 100)
  cor_value_method <- NULL
  for (j in method_range) {
    norm.matrix <- getNormMatrix(data, specifiedMethods[[j]])
    dataUse2Cor <- norm.matrix[ubq_genes, ]
    cor.result <- getCor(dataUse2Cor, method = cor_method,
      rounds = rounds)
    cor_vm <- cbind(cor.result, rep(names(specifiedMethods)[j],
      times = round(rounds)))
    cor_value_method <- rbind(cor_value_method, cor_vm)
  }
  colnames(cor_value_method) <- c("Value", "Methods")
  return(cor_value_method)
}
```

gatherCors4Matrices	<i>gatherCors4Matrices</i>
---------------------	----------------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
gatherCors4Matrices(..., raw_matrix, cor_method = c("spearman", "pearson", "kendall"),
pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65, rounds = 1e+06)
```

Arguments

...	Please refer to the file /inst/doc/readme.pdf.
raw_matrix	Please refer to the file /inst/doc/readme.pdf.
cor_method	Please refer to the file /inst/doc/readme.pdf.
pre_ratio	Please refer to the file /inst/doc/readme.pdf.
lower_trim	Please refer to the file /inst/doc/readme.pdf.
upper_trim	Please refer to the file /inst/doc/readme.pdf.
rounds	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (... , raw_matrix, cor_method = c("spearman", "pearson",
      "kendall"), pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65,
      rounds = 1e+06)
{
  matrices <- list(...)
  numMethod <- length(matrices)
  method_range <- seq(1, numMethod, 1)
  ubq_genes <- identifyUbq(raw_matrix, pre_ratio = pre_ratio,
    lower_trim = lower_trim, upper_trim = upper_trim, min_ubq = 100)
  cor_value_method <- NULL
  for (j in method_range) {
    dataUse2Cor <- matrices[[j]][ubq_genes, ]
    cor.result <- getCor(dataUse2Cor, method = cor_method,
      rounds = rounds)
    cor_vm <- cbind(cor.result, rep(names(matrices)[j], times = round(rounds)))
    cor_value_method <- rbind(cor_value_method, cor_vm)
  }
  colnames(cor_value_method) <- c("Value", "Methods")
  return(cor_value_method)
}
```

gatherCVs

*gatherCVs***Description**

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
gatherCVs(data, nonzeroRatio, HG7, ERCC, TN, TC, CR, NR,
           DESeq, UQ, TMM, TU, GAPDH, cvNorm, cvResolution)
```

Arguments

<code>data</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>nonzeroRatio</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>HG7</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>ERCC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TN</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>CR</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>NR</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>DESeq</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>UQ</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TMM</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TU</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>GAPDH</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvNorm</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvResolution</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, nonzeroRatio = NULL, HG7 = NULL, ERCC = NULL,
          TN = NULL, TC = NULL, CR = NULL, NR = NULL, DESeq = NULL,
          UQ = NULL, TMM = NULL, TU = NULL, GAPDH = NULL, cvNorm = TRUE,
          cvResolution = 0.005)
{
  if (is.null(nonzeroRatio)) {
    stop("Please provide nonzeroRatio!")
  }
}
```

```

}
methodsList <- list(HG7 = HG7, ERCC = ERCC, TN = TN, TC = TC,
  CR = CR, NR = NR, DESeq = DESeq, UQ = UQ, TMM = TMM,
  TU = TU, GAPDH = GAPDH)
specifiedMethods <- methodsList[!unlist(lapply(methodsList,
  is.null))]
numMethod <- length(specifiedMethods)
method_range_tmp <- seq(1, numMethod, 1)
cv_range_tmp <- seq(0, 1, cvResolution)
method_range_times <- length(cv_range_tmp)
cv_range_times <- length(method_range_tmp)
method_range <- rep(method_range_tmp, each = round(method_range_times))
cv_range <- rep(cv_range_tmp, times = round(cv_range_times))
nozeroIndex <- filteredZero(data, nonzeroRatio = nonzeroRatio)
for (j in method_range_tmp) {
  norm.matrix <- getNormMatrix(data, specifiedMethods[[j]])
  dataUse2CV <- norm.matrix[nozeroIndex, ]
  cv.result <- getCV(dataUse2CV, cvNorm = cvNorm)
  assign(paste(names(specifiedMethods)[j], ".cv", sep = ""),
    cv.result)
}
cv_uniform <- NULL
cv_uniform_all <- mapply(function(i, j) {
  cv.result <- paste(names(specifiedMethods)[j], ".cv",
    sep = "")
  gene_number <- length(which(get(cv.result) <= i))
  cv_uniform_row <- c(i, gene_number, names(specifiedMethods)[j])
  rbind(cv_uniform, cv_uniform_row)
}, cv_range, method_range)
cv_uniform_all <- t(cv_uniform_all)
colnames(cv_uniform_all) <- c("Cutoff", "Counts", "Methods")
return(cv_uniform_all)
}

```

gatherCVs4Matrices

gatherCVs4Matrices

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
gatherCVs4Matrices(..., raw_matrix, nonzeroRatio , cvNorm , cvResolution = 0.005)
```

Arguments

<code>...</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>raw_matrix</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

nonzeroRatio Please refer to the file /inst/doc/readme.pdf.
 cvNorm Please refer to the file /inst/doc/readme.pdf.
 cvResolution Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (... , raw_matrix, nonzeroRatio = NULL, cvNorm = TRUE,
  cvResolution = 0.005)
{
  if (is.null(nonzeroRatio)) {
    stop("Please provide nonzeroRatio!")
  }
  matrices <- list(...)
  matrices_name <- names(matrices)
  numMethod <- length(matrices)
  method_range_tmp <- seq(1, numMethod, 1)
  cv_range_tmp <- seq(0, 1, cvResolution)
  method_range_times <- length(cv_range_tmp)
  cv_range_times <- length(method_range_tmp)
  method_range <- rep(method_range_tmp, each = round(method_range_times))
  cv_range <- rep(cv_range_tmp, times = round(cv_range_times))
  nozeroIndex <- filteredZero(raw_matrix, nonzeroRatio = nonzeroRatio)
  for (j in method_range_tmp) {
    dataUse2CV <- matrices[[j]][nozeroIndex, ]
    cv.result <- getCV(dataUse2CV, cvNorm = cvNorm)
    assign(paste(matrices_name[j], ".cv", sep = ""), cv.result)
  }
  cv_uniform <- NULL
  cv_uniform_all <- mapply(function(i, j) {
    cv.result <- paste(matrices_name[j], ".cv", sep = "")
    gene_number <- length(which(get(cv.result) <= i))
    cv_uniform_row <- c(i, gene_number, matrices_name[j])
    rbind(cv_uniform, cv_uniform_row)
  }, cv_range, method_range)
  cv_uniform_all <- t(cv_uniform_all)
  colnames(cv_uniform_all) <- c("Cutoff", "Counts", "Methods")
  return(cv_uniform_all)
}
```

gatherFactors

gatherFactors

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
gatherFactors(data,
  methods = c("HG7", "ERCC", "TN", "TC", "CR", "NR", "DESeq", "UQ", "TMM", "TU"),
  HG7.size = NULL, ERCC.size = NULL, TN.size = NULL, TC.size = NULL,
  CR.size = NULL, NR.size = NULL, pre_ratio = 0.5,
  lower_trim = 0.05, upper_trim = 0.65, min_ubq = 100)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
methods	Please refer to the file /inst/doc/readme.pdf.
HG7.size	Please refer to the file /inst/doc/readme.pdf.
ERCC.size	Please refer to the file /inst/doc/readme.pdf.
TN.size	Please refer to the file /inst/doc/readme.pdf.
TC.size	Please refer to the file /inst/doc/readme.pdf.
CR.size	Please refer to the file /inst/doc/readme.pdf.
NR.size	Please refer to the file /inst/doc/readme.pdf.
pre_ratio	Please refer to the file /inst/doc/readme.pdf.
lower_trim	Please refer to the file /inst/doc/readme.pdf.
upper_trim	Please refer to the file /inst/doc/readme.pdf.
min_ubq	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, methods = c("HG7", "ERCC", "TN", "TC", "CR",
  "NR", "DESeq", "UQ", "TMM", "TU"), HG7.size = NULL, ERCC.size = NULL,
  TN.size = NULL, TC.size = NULL, CR.size = NULL, NR.size = NULL,
  pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65, min_ubq = 100)
{
  method1 <- as.list(methods)
  numMethod <- length(method1)
  method_range <- seq(1, numMethod, 1)
  for (i in method_range) {
    if (method1[[i]] == "HG7" || method1[[i]] == "ERCC" ||
      method1[[i]] == "TN" || method1[[i]] == "TC" || method1[[i]] ==
      "CR" || method1[[i]] == "NR") {
      size.name <- paste(method1[[i]], ".size", sep = "")
      out.name1 <- paste(method1[[i]], ".factors", sep = "")
      if (is.null(size.name)) {
        stop("Please provide", size.name, "!")
      }
    }
    else {
```



```

        assign(out.name1, getFactors(data, method = "sizefactor",
                                     lib.size = get(size.name)))
    }
}
if (method1[[i]] == "DESeq" || method1[[i]] == "RLE" ||
    method1[[i]] == "UQ" || method1[[i]] == "TMM") {
    out.name2 <- paste(method1[[i]], ".factors", sep = "")
    assign(out.name2, getFactors(data, method = method1[[i]]))
}
if (method1[[i]] == "TU") {
    TU.factors <- getFactors(data, method = "TU", pre_ratio = pre_ratio,
                             lower_trim = lower_trim, upper_trim = upper_trim,
                             min_ubq = min_ubq)
}
}
factors.list <- NULL
for (m in methods) {
    m.factors <- paste(m, ".factors", sep = "")
    factors.list <- c(factors.list, m.factors)
}
factors.result <- NULL
for (i in method_range) {
    factors.result <- cbind(factors.result, get(factors.list[i]))
}
colnames(factors.result) <- methods
return(factors.result)
}

```

getArea

getArea

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
getArea(x, y)
```

Arguments

x	Please refer to the file <code>/inst/doc/readme.pdf</code> .
y	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

```

```
## The function is currently defined as
function (x, y)
{
  x <- x/max(x)
  y <- y/max(y)
  if (!(is.numeric(x) || is.complex(x)) || !(is.numeric(y) ||
    is.complex(y))) {
    stop("Arguments 'x' and 'y' must be real or complex vectors.")
  }
  if (length(x) != length(y)) {
    stop("The length of two input vectors should be equal!")
  }
  m <- length(x)
  n <- 2 * m
  xp <- c(x, x[m:1])
  yp <- c(numeric(m), y[m:1])
  p1 <- sum(xp[1:(n - 1)] * yp[2:n]) + xp[n] * yp[1]
  p2 <- sum(xp[2:n] * yp[1:(n - 1)]) + xp[1] * yp[n]
  return(0.5 * (p1 - p2))
}
```

getAUCVC

getAUCVC

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
getAUCVC(data, nonzeroRatio = NULL, cvNorm = TRUE, cvResolution = 0.005)
```

Arguments

data	Please refer to the file <code>/inst/doc/readme.pdf</code> .
nonzeroRatio	Please refer to the file <code>/inst/doc/readme.pdf</code> .
cvNorm	Please refer to the file <code>/inst/doc/readme.pdf</code> .
cvResolution	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, nonzeroRatio = NULL, cvNorm = TRUE, cvResolution = 0.005)
{
  nozeroIndex <- filteredZero(data, nonzeroRatio = nonzeroRatio)
```

```

dataUse2CV <- data[nozeroIndex, ]
cv.result <- getCV(dataUse2CV, cvNorm = cvNorm)
CV2AUCVC(cv.result, cvResolution = cvResolution)
}

```

getAUCVCs

getAUCVCs

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
getAUCVCs(..., nonzeroRatio = NULL, cvNorm = TRUE, cvResolution = 0.005)
```

Arguments

...	Please refer to the file /inst/doc/readme.pdf.
nonzeroRatio	Please refer to the file /inst/doc/readme.pdf.
cvNorm	Please refer to the file /inst/doc/readme.pdf.
cvResolution	Please refer to the file /inst/doc/readme.pdf.

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (... , nonzeroRatio = NULL, cvNorm = TRUE, cvResolution = 0.005)
{
  matrices <- list(...)
  numMethod <- length(matrices)
  method_range <- seq(1, numMethod, 1)
  result <- NULL
  for (i in method_range) {
    AUCVC.result <- getAUCVC(matrices[[i]], nonzeroRatio = nonzeroRatio,
                             cvNorm = cvNorm, cvResolution = cvResolution)
    result <- c(result, AUCVC.result)
    names(result)[i] <- names(matrices)[i]
  }
  sorted_AUCVCs <- sort(result, decreasing = TRUE)
  return(sorted_AUCVCs)
}

```

getCor

getCor

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
getCor(data, method = c("spearman", "pearson", "kendall"), rounds = 1e+06)
```

Arguments

<code>data</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>method</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>rounds</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, method = c("spearman", "pearson", "kendall"),
  rounds = 1e+06)
{
  sp_result <- NULL
  method <- match.arg(method)
  for (i in 1:rounds) {
    rg1 <- sample(1:nrow(data), size = 1)
    rg2 <- sample(1:nrow(data), size = 1)
    while (rg1 == rg2) {
      rg2 <- sample(1:nrow(data), size = 1)
    }
    gene1 <- unlist(data[rg1, ])
    gene2 <- unlist(data[rg2, ])
    sp_value <- cor(gene1, gene2, method = method)
    sp_result <- c(sp_result, sp_value)
  }
  return(sp_result)
}
```

getCorMedians	<i>getCorMedians</i>
---------------	----------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
getCorMedians(data)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
------	--

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data)
{
  if (!is.data.frame(data))
    data <- data.frame(data)
  if (is.factor(data$Value))
    data$Value <- as.numeric(as.character(data$Value))
  sorted_result <- sort(tapply(data$Value, data$Methods, median),
    decreasing = FALSE)
  return(sorted_result)
}
```

getCV	<i>getCV</i>
-------	--------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
getCV(data, cvNorm = TRUE)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
cvNorm	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, cvNorm = TRUE)
{
  if (!is.matrix(data))
    data <- as.matrix(data)
  if (cvNorm) {
    rawCV <- apply(data, 1, function(x) {
      sd(log2(x[x != 0]))/mean(log2(x[x != 0]))
    })
    (rawCV - min(rawCV))/(max(rawCV) - min(rawCV))
  }
  else {
    apply(data, 1, function(x) {
      sd(x)/mean(x)
    })
  }
}
```

getFactors

getFactors

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
getFactors(data, method = c("sizefactor", "DESeq", "RLE", "UQ", "TMM", "TU"),
  lib.size = NULL, pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65, min_ubq = 100)
```

Arguments

data	Please refer to the file <code>/inst/doc/readme.pdf</code> .
method	Please refer to the file <code>/inst/doc/readme.pdf</code> .
lib.size	Please refer to the file <code>/inst/doc/readme.pdf</code> .
pre_ratio	Please refer to the file <code>/inst/doc/readme.pdf</code> .
lower_trim	Please refer to the file <code>/inst/doc/readme.pdf</code> .
upper_trim	Please refer to the file <code>/inst/doc/readme.pdf</code> .
min_ubq	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, method = c("sizefactor", "DESeq", "RLE", "UQ",
  "TMM", "TU"), lib.size = NULL, pre_ratio = 0.5, lower_trim = 0.05,
  upper_trim = 0.65, min_ubq = 100)
{
  if (!is.matrix(data))
    data <- as.matrix(data)
  if (any(is.na(data)))
    stop("NA counts not permitted")
  if (is.null(lib.size))
    libsize <- colSums(data)
  else libsize <- lib.size
  if (any(is.na(libsize)))
    stop("NA libsizes not permitted")
  method <- match.arg(method)
  i <- apply(data <= 0, 1, all)
  if (any(i))
    data <- data[!i, , drop = FALSE]
  f <- switch(method, sizefactor = 1e+06/libsize, DESeq = 1/estimateSizeFactorsForMatrix(data,
    p = 0.5), RLE = calcFactorRLE(data, p = 0.5)/libsize,
    UQ = calcFactorUpperquartile(data, lib.size = libsize,
      p = 0.75), TMM = {
      fq <- calcFactorUpperquartile(data = data, lib.size = libsize,
        p = 0.75)
      refColumn <- which.min(abs(fq - mean(fq)))
      if (length(refColumn) == 0 | refColumn < 1 | refColumn >
        ncol(data)) refColumn <- 1
      f <- rep(NA, ncol(data))
      for (i in 1:ncol(data)) {
        f[i] <- calcFactorWeighted(obs = data[, i], ref = data[,
          refColumn], libsize.obs = libsize[i], libsize.ref = libsize[refColumn],
          logratioTrim = 0.3, sumTrim = 0.05, doWeighting = TRUE,
          Acutoff = -1e+10)
      }
      f
    }, TU = {
      if (!is.data.frame(data)) data <- data.frame(data)
      ubq_genes <- identifyUbq(data, lower_trim = lower_trim,
        upper_trim = upper_trim, pre_ratio = pre_ratio,
        min_ubq = min_ubq)
      ubq_sums <- colSums(data[ubq_genes, ])
      mean(ubq_sums)/ubq_sums
    }, )
  if (method == "RLE" || method == "UQ" || method == "TMM") {
    f <- 1e+06/libsize/f
  }
  norm.factors <- f/exp(mean(base::log(f)))
}

```

```
round(norm.factors, digits = 5)
}
```

getNormMatrix	<i>getNormMatrix</i>
---------------	----------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
getNormMatrix(data, norm.factors)
```

Arguments

- data Please refer to the file /inst/doc/readme.pdf.
- norm.factors Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, norm.factors)
{
  data * matrix(rep(norm.factors, dim(data)[1]), nrow = dim(data)[1],
    ncol = length(norm.factors), byrow = T)
}
```

gridAUCVC	<i>gridAUCVC</i>
-----------	------------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
gridAUCVC(data, dataType = c("bk", "sc"), HG7 = NULL, ERCC = NULL, TN = NULL,
TC = NULL, CR = NULL, NR = NULL, DESeq = NULL, UQ = NULL, TMM = NULL, TU = 0,
GAPDH = NULL, nonzeroRatios = c(0.7, 0.8, 0.9, 1), cvNorm = TRUE, cvResolution = 0.005)
```


Arguments

data	Please refer to the file /inst/doc/readme.pdf.
dataType	Please refer to the file /inst/doc/readme.pdf.
HG7	Please refer to the file /inst/doc/readme.pdf.
ERCC	Please refer to the file /inst/doc/readme.pdf.
TN	Please refer to the file /inst/doc/readme.pdf.
TC	Please refer to the file /inst/doc/readme.pdf.
CR	Please refer to the file /inst/doc/readme.pdf.
NR	Please refer to the file /inst/doc/readme.pdf.
DESeq	Please refer to the file /inst/doc/readme.pdf.
UQ	Please refer to the file /inst/doc/readme.pdf.
TMM	Please refer to the file /inst/doc/readme.pdf.
TU	Please refer to the file /inst/doc/readme.pdf.
GAPDH	Please refer to the file /inst/doc/readme.pdf.
nonzeroRatios	Please refer to the file /inst/doc/readme.pdf.
cvNorm	Please refer to the file /inst/doc/readme.pdf.
cvResolution	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, dataType = c("bk", "sc"), HG7 = NULL, ERCC = NULL,
  TN = NULL, TC = NULL, CR = NULL, NR = NULL, DESeq = NULL,
  UQ = NULL, TMM = NULL, TU = 0, GAPDH = NULL, nonzeroRatios = c(0.7,
    0.8, 0.9, 1), cvNorm = TRUE, cvResolution = 0.005)
{
  grid_result <- NULL
  if (length(TU) == 1 && TU == 1) {
    colnames_paraMatrix <- c("nonzeroRatio", "pre_ratio",
      "lower_trim", "upper_trim")
    write.table(t(as.matrix(colnames_paraMatrix)), file = "bestPara.txt",
      sep = "\t", row.names = FALSE, col.names = FALSE)
  }
  for (i in nonzeroRatios) {
    if (dataType == "sc") {
      if ((ncol(data) * i) <= 100) {
        cat("nonzeroRatio:", i, " is too small!\n")
        stop("We suggest that the minimal counts of
          nonzero samples should be greater than 100!")
      }
    }
  }
  result <- nonzeroRatio2AUCVC(data = data, dataType = dataType,
```

```

    HG7 = HG7, ERCC = ERCC, TN = TN, TC = TC, CR = CR,
    NR = NR, DESeq = DESeq, UQ = UQ, TMM = TMM, TU = TU,
    GAPDH = GAPDH, nonzeroRatio = i, cvNorm = cvNorm,
    cvResolution = cvResolution)
  nonzeroM <- matrix(i, 1, 1, TRUE)
  colnames(nonzeroM) <- "NonzeroRatio"
  grid_record <- cbind(nonzeroM, result)
  grid_result <- rbind(grid_result, grid_record)
}
return(grid_result)
}

```

gridAUCVC4Matrices	<i>gridAUCVC4Matrices</i>
--------------------	---------------------------

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
gridAUCVC4Matrices(..., nonzeroRatios = NULL, cvNorm = TRUE, cvResolution = 0.005)
```

Arguments

<code>...</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>nonzeroRatios</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvNorm</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvResolution</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (... , nonzeroRatios = NULL, cvNorm = TRUE, cvResolution = 0.005)
{
  if (is.null(nonzeroRatios)) {
    stop("Please provide nonzeroRatios!")
  }
  matrices <- list(...)
  numMethod <- length(matrices)
  grid_result <- NULL
  for (i in nonzeroRatios) {
    result.sorted <- getAUCVCs(..., nonzeroRatio = i, cvNorm = cvNorm,
      cvResolution = cvResolution)
    grid_record <- c(i, result.sorted)
  }
}

```

```

        names(grid_record)[1] <- "NonzeroRatio"
        grid_result <- c(grid_result, names(grid_record), grid_record)
    }
    grid_result2 <- matrix(grid_result, ncol = numMethod + 1,
        byrow = TRUE)
    return(grid_result2)
}

```

identifyUbq

identifyUbq

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
identifyUbq(data, pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65, min_ubq = 100)
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
pre_ratio	Please refer to the file /inst/doc/readme.pdf.
lower_trim	Please refer to the file /inst/doc/readme.pdf.
upper_trim	Please refer to the file /inst/doc/readme.pdf.
min_ubq	Please refer to the file /inst/doc/readme.pdf.

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, pre_ratio = 0.5, lower_trim = 0.05, upper_trim = 0.65,
    min_ubq = 100)
{
    qlower <- apply(data, 2, function(x) quantile(x[x != 0],
        p = lower_trim))
    qupper <- apply(data, 2, function(x) quantile(x[x != 0],
        p = upper_trim))
    ubq_genes <- NULL
    for (i in 1:nrow(data)) {
        genes_finded <- findGenes(data[i, ], qlower = qlower,
            qupper = qupper, pre_ratio = pre_ratio)
        ubq_genes <- c(ubq_genes, genes_finded)
    }
    if (length(ubq_genes) < min_ubq) {

```

```

        cat("Parameters range", lower_trim, "-", upper_trim,
            "...identified too few ubiquitous genes (", length(ubq_genes),
            "), trying range 5-95 instead", "\n")
        ubq_genes <- identifyUbqRepeat(data, pre_ratioC = pre_ratio,
            lower_trimC = 0.05, upper_trimC = 0.95)
    }
    return(ubq_genes)
}

```

identifyUbqRepeat	<i>identifyUbqRepeat</i>
-------------------	--------------------------

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
identifyUbqRepeat(data, pre_ratioC = NULL, lower_trimC = NULL, upper_trimC = NULL)
```

Arguments

<code>data</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>pre_ratioC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>lower_trimC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>upper_trimC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, pre_ratioC = NULL, lower_trimC = NULL, upper_trimC = NULL)
{
  qlower <- apply(data, 2, function(x) quantile(x[x != 0],
    p = lower_trimC))
  qupper <- apply(data, 2, function(x) quantile(x[x != 0],
    p = upper_trimC))
  ubq_genes <- NULL
  for (i in 1:nrow(data)) {
    genes_finded <- findGenes(data[i, ], qlower = qlower,
      qupper = qupper, pre_ratio = pre_ratioC)
    ubq_genes <- c(ubq_genes, genes_finded)
  }
  return(ubq_genes)
}

```

nonzeroRatio2AUCVC	<i>nonzeroRatio2AUCVC</i>
--------------------	---------------------------

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
nonzeroRatio2AUCVC(data, dataType = c("bk", "sc"),
  HG7 = NULL, ERCC = NULL, TN = NULL, TC = NULL, CR = NULL, NR = NULL, DESeq = NULL,
  UQ = NULL, TMM = NULL, TU = 0, GAPDH = NULL, nonzeroRatio = NULL, cvNorm = TRUE,
  cvResolution = 0.005)
```

Arguments

<code>data</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>dataType</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>HG7</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>ERCC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TN</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TC</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>CR</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>NR</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>DESeq</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>UQ</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TMM</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>TU</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>GAPDH</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>nonzeroRatio</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvNorm</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvResolution</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, dataType = c("bk", "sc"), HG7 = NULL, ERCC = NULL,
  TN = NULL, TC = NULL, CR = NULL, NR = NULL, DESeq = NULL,
  UQ = NULL, TMM = NULL, TU = 0, GAPDH = NULL, nonzeroRatio = NULL,
```

```

cvNorm = TRUE, cvResolution = 0.005)
{
  nonzeroIndex <- filteredZero(data, nonzeroRatio = nonzeroRatio)
  methodsList <- list(HG7 = HG7, ERCC = ERCC, TN = TN, TC = TC,
    CR = CR, NR = NR, DESeq = DESeq, UQ = UQ, TMM = TMM,
    TU = TU, GAPDH = GAPDH)
  specifiedMethods <- methodsList[!unlist(lapply(methodsList,
    is.null)))]
  if (length(TU) == 1 && TU == 0) {
    specifiedMethods$TU <- NULL
  }
  if (length(TU) == 1 && TU == 1) {
    if (dataType == "bk") {
      optimalPara <- optTU(data, nonzeroRatio = nonzeroRatio,
        pre_ratio_range = c(1, 1), prResolution = 0.1,
        lower_range = c(0.05, 0.4), upper_range = c(0.6,
          0.95), qResolution = 0.05, min_ubq = 1000,
        cvNorm = cvNorm, cvResolution = cvResolution)
    }
    else {
      optimalPara <- optTU(data, nonzeroRatio = nonzeroRatio,
        pre_ratio_range = c(0.2, 0.6), prResolution = 0.1,
        lower_range = c(0.05, 0.4), upper_range = c(0.6,
          0.95), qResolution = 0.05, min_ubq = 100, cvNorm = cvNorm,
        cvResolution = cvResolution)
    }
    optimalPara <- as.matrix(optimalPara)
    lower_trim <- optimalPara["lower", 1]
    upper_trim <- optimalPara["upper", 1]
    pre_ratio <- optimalPara["ratio", 1]
    para <- c(nonzeroRatio, pre_ratio, lower_trim, upper_trim)
    names(para)[1] <- "nonzeroRatio"
    paraMatrix <- t(as.matrix(para))
    write.table(paraMatrix, file = "bestPara.txt", sep = "\t",
      row.names = FALSE, col.names = FALSE, append = TRUE)
    TU.factors <- getFactors(data, method = "TU", lower_trim = lower_trim,
      upper_trim = upper_trim, pre_ratio = pre_ratio, min_ubq = 100)
    norm.matrix <- getNormMatrix(data, TU.factors)
    dataUse2CV <- norm.matrix[nonzeroIndex, ]
    cv.result <- getCV(dataUse2CV, cvNorm = cvNorm)
    TU.AUCVC <- CV2AUCVC(cv.result, cvResolution = cvResolution)
    specifiedMethods$TU <- NULL
  }
}
numMethod <- length(specifiedMethods)
if (numMethod >= 1) {
  method_range <- seq(1, numMethod, 1)
  for (i in method_range) {
    norm.matrix <- getNormMatrix(data, specifiedMethods[[i]])
    dataUse2CV <- norm.matrix[nonzeroIndex, ]
    cv.result <- getCV(dataUse2CV, cvNorm = cvNorm)
    assign(names(specifiedMethods)[i], CV2AUCVC(cv.result,
      cvResolution = cvResolution))
  }
}

```

```

AUCVC.result <- NULL
for (i in method_range) {
  AUCVC.result <- cbind(AUCVC.result, get(names(specifiedMethods)[i]))
}
colnames(AUCVC.result) <- names(specifiedMethods)
if (length(TU) == 1 && TU == 1) {
  AUCVC.result <- cbind(AUCVC.result, TU.AUCVC)
  colnames(AUCVC.result) <- c(names(specifiedMethods),
    "TU")
}
}
if (numMethod == 0 && TU == 0)
  stop("Please specify at least one method!")
if (numMethod == 0 && TU == 1) {
  AUCVC.result <- as.matrix(TU.AUCVC)
  colnames(AUCVC.result) <- "TU"
}
return(AUCVC.result)
}

```

optTU

optTU

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```

optTU(data, nonzeroRatio = NULL, pre_ratio_range = c(0.2, 0.6), prResolution = 0.1,
lower_range = c(0.05, 0.4), upper_range = c(0.6, 0.95),
qResolution = 0.05, min_ubq = 100, cvNorm = TRUE, cvResolution = 0.005)

```

Arguments

<code>data</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>nonzeroRatio</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>pre_ratio_range</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>prResolution</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>lower_range</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>upper_range</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>qResolution</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>min_ubq</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvNorm</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>cvResolution</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, nonzeroRatio = NULL, pre_ratio_range = c(0.2,
  0.6), prResolution = 0.1, lower_range = c(0.05, 0.4), upper_range = c(0.6,
  0.95), qResolution = 0.05, min_ubq = 100, cvNorm = TRUE,
  cvResolution = 0.005)
{
  if (is.null(nonzeroRatio)) {
    stop("Please provide nonzeroRatios!")
  }
  pre_ratio_times <- (pre_ratio_range[2] - pre_ratio_range[1] +
    prResolution) * 10
  lower_times <- (upper_range[2] - upper_range[1] + qResolution)/qResolution
  lower_range_tmp <- rep(seq(lower_range[1], lower_range[2],
    qResolution), each = round(lower_times))
  lower_range2 <- rep(lower_range_tmp, times = round(pre_ratio_times))
  upper_times <- (lower_range[2] - lower_range[1] + qResolution)/qResolution
  upper_range_tmp <- rep(seq(upper_range[1], upper_range[2],
    qResolution), times = round(upper_times))
  upper_range2 <- rep(upper_range_tmp, times = round(pre_ratio_times))
  lower_upper_tmp_len <- length(lower_range_tmp)
  pre_ratio_range2 <- rep(seq(pre_ratio_range[1], pre_ratio_range[2],
    0.1), each = round(lower_upper_tmp_len))
  nozeroIndex <- filteredZero(data, nonzeroRatio = nonzeroRatio)
  all_aucvc <- mapply(function(lower_trim, upper_trim, pre_ratio) {
    factors.TU <- getFactors(data, method = "TU", lower_trim = lower_trim,
      upper_trim = upper_trim, pre_ratio = pre_ratio, min_ubq = min_ubq)
    norm.TU <- getNormMatrix(data, factors.TU)
    dataUse2CV <- norm.TU[nozeroIndex, ]
    cv.TU <- getCV(dataUse2CV, cvNorm = cvNorm)
    TU.AUCVC <- CV2AUCVC(cv.TU, cvResolution = cvResolution)
    return(c(TU.AUCVC = TU.AUCVC, lower = lower_trim, upper = upper_trim,
      ratio = pre_ratio))
  }, lower_range2, upper_range2, pre_ratio_range2)
  all_aucvc2 <- t(all_aucvc)
  max_index <- which(max(all_aucvc2[, "TU.AUCVC"]) == all_aucvc2[,
    "TU.AUCVC"])
  return(all_aucvc2[max_index, ])
}
```

plotCors

plotCors

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
plotCors(data, methods = c("None", "HG7", "ERCC", "TN", "TC", "CR", "NR", "DESeq",
"UQ", "TMM", "TU"), legend.position = c(0.15, 0.56))
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
methods	Please refer to the file /inst/doc/readme.pdf.
legend.position	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, methods = c("None", "HG7", "ERCC", "TN", "TC",
"CR", "NR", "DESeq", "UQ", "TMM", "TU"), legend.position = c(0.15,
0.56))
{
  if (!is.data.frame(data))
    data <- data.frame(data)
  if (is.factor(data$Value))
    data$Value <- as.numeric(as.character(data$Value))
  data$Methods <- factor(data$Methods, levels = methods, labels = methods)
  change_colours(ggplot(data = data, aes(x = Value, y = ..count../sum(..count..))) +
    geom_freqpoly(aes(group = Methods, color = Methods),
      size = 3, bins = 50) + xlab("Spearman correlation") +
    ylab("Fraction of gene pairs") + theme_bw() + theme(panel.grid.minor = element_blank(),
      axis.title.x = element_text(size = 48), axis.title.y = element_text(size = 48),
      axis.text.x = element_text(size = 38), axis.text.y = element_text(size = 38),
      legend.text = element_text(size = 39), legend.title = element_text(size = 43),
      legend.position = legend.position, legend.background = element_blank(),
      legend.key = element_blank(), legend.key.height = unit(1.8,
        "cm"), plot.margin = unit(c(0.5, 1, 0.5, 0.5), "cm")) +
    scale_x_continuous(expand = c(0.01, 0.01), breaks = round(seq(-1,
      1, 0.25), 2)) + scale_y_continuous(expand = c(0.01,
      0)) + guides(color = guide_legend(title = NULL), c("olivedrab",
      "blue", "red", "violet", "orange", "yellow", "magenta",
      "peru", "black", "maroon", "lightblue", "darkslateblue",
      "seashell4", "tan2", "darkgreen", "springgreen"))
}
```

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
plotCVs(data, methods = c("None", "HG7", "ERCC", "TN", "TC", "CR", "NR",
"DESeq", "UQ", "TMM", "TU"), legend.position = c(0.85, 0.48))
```

Arguments

<code>data</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>methods</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .
<code>legend.position</code>	Please refer to the file <code>/inst/doc/readme.pdf</code> .

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, methods = c("None", "HG7", "ERCC", "TN", "TC",
"CR", "NR", "DESeq", "UQ", "TMM", "TU"), legend.position = c(0.85,
0.48))
{
  if (!is.data.frame(data))
    data <- data.frame(data)
  if (is.factor(data$Cutoff))
    data$Cutoff <- as.numeric(as.character(data$Cutoff))
  if (is.factor(data$Counts))
    data$Counts <- as.numeric(as.character(data$Counts))
  data$Methods <- factor(data$Methods, levels = methods, labels = methods)
  change_colours(ggplot(data = data, aes(x = Cutoff, y = Counts)) +
    geom_line(aes(group = Methods, color = Methods), size = 3) +
    xlab("Normalized CV cutoff") + ylab("Number of uniform genes") +
    theme_bw() + theme(panel.grid.minor = element_blank(),
    axis.title.x = element_text(size = 48), axis.title.y = element_text(size = 48),
    axis.text.x = element_text(size = 38), axis.text.y = element_text(size = 38),
    legend.text = element_text(size = 39), legend.title = element_text(size = 43),
    legend.position = legend.position, legend.background = element_blank(),
    legend.key = element_blank(), legend.key.height = unit(1.8,
    "cm"), plot.margin = unit(c(0.5, 0.5, 0.5, 0.5),
    "cm")) + scale_x_continuous(breaks = seq(0, 1, 0.2)) +
    scale_y_continuous() + guides(color = guide_legend(title = NULL)),
    c("olivedrab", "blue", "red", "violet", "orange", "yellow",
    "magenta", "peru", "black", "maroon", "lightblue",
    "darkslateblue", "seashell4", "tan2", "darkgreen",
    "springgreen"))
}
```

plotHC	<i>plotHC</i>
--------	---------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
plotHC(data, method = c("spearman", "pearson", "kendall"), mar = c(9, 1, 0, 20))
```

Arguments

data	Please refer to the file /inst/doc/readme.pdf.
method	Please refer to the file /inst/doc/readme.pdf.
mar	Please refer to the file /inst/doc/readme.pdf.

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (data, method = c("spearman", "pearson", "kendall"),
  mar = c(9, 1, 0, 20))
{
  if (!is.data.frame(data))
    data <- data.frame(data)
  method <- match.arg(method)
  hc <- hclust(as.dist(1 - cor(data, method = method)))
  dend <- as.dendrogram(hc)
  dend <- dend %>% set("labels_cex", 6.5) %>% set("branches_lwd",
    6.5)
  par(mar = mar, mgp = c(10, 5, 0), cex.axis = 6)
  plot(dend, horiz = TRUE)
  axis(side = 1, lwd = 8)
}
```

scRNA663	<i>scRNA663</i>
----------	-----------------

Description

Please refer to the file /inst/doc/readme.pdf.

Usage

```
data("scRNA663")
```

Format

A data frame with 57955 observations on the following 663 variables.

col361_1 a numeric vector
col361_2 a numeric vector
col361_3 a numeric vector
col361_4 a numeric vector
col361_5 a numeric vector
col361_6 a numeric vector
col361_7 a numeric vector
col361_8 a numeric vector
col361_9 a numeric vector
col361_10 a numeric vector
col361_11 a numeric vector
col361_12 a numeric vector
col361_13 a numeric vector
col361_14 a numeric vector
col361_15 a numeric vector
col361_16 a numeric vector
col361_17 a numeric vector
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col361_38 a numeric vector
col361_39 a numeric vector
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col361_43 a numeric vector
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col361_45 a numeric vector
col361_46 a numeric vector
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col361_69 a numeric vector

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col4411_94 a numeric vector
col4412_1 a numeric vector
col4412_2 a numeric vector
col4412_3 a numeric vector
col4412_4 a numeric vector
col4412_5 a numeric vector
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col4817_20 a numeric vector
col4817_21 a numeric vector

Examples

```
data(scRNA663)
## maybe str(scRNA663) ; plot(scRNA663) ...
```

scRNA663_factors	<i>scRNA663_factors</i>
------------------	-------------------------

Description

Please refer to the file `/inst/doc/readme.pdf`.

Usage

```
data("scRNA663_factors")
```

Format

A data frame with 663 observations on the following 12 variables.

HG7 a numeric vector
ERCC a numeric vector
TN a numeric vector
TC a numeric vector
CR a numeric vector
NR a numeric vector
DESeq a numeric vector
UQ a numeric vector
TMM a numeric vector
TU a numeric vector
NCS a numeric vector
ES a numeric vector

Examples

```
data(scRNA663_factors)
## maybe str(scRNA663_factors) ; plot(scRNA663_factors) ...
```

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