Package ‘NanoStringDiff’

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Description This Package utilizes a generalized linear model (GLM) of the negative binomial family to characterize count data and allows for multi-factor design. NanoStrongDiff incorporate size factors, calculated from positive controls and housekeeping controls, and background level, obtained from negative controls, in the model framework so that all the normalization information provided by NanoString nCounter Analyzer is fully utilized.
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NanoStringDiff-package

Description

A more detailed description of what the package does. A length of about one to five lines is recommended.

Details

This section should provide a more detailed overview of how to use the package, including the most important functions.

Author(s)

Your Name, email optional.

Maintainer: Your Name <your@email.com>

References

This optional section can contain literature or other references for background information.

See Also

Optional links to other man pages
estNormalizationFactors

Examples

## Not run:
## Optional simple examples of the most important functions
## These can be in \dontrun{} and \donttest{} blocks.

## End(Not run)

estNormalizationFactors

estimate normalization factors, include positive size factors, background noise, housekeeping size factors.

Description

This function estimates positive size factors, background noise and housekeeping size factors for the input "NanoStringSet" object and return the same object with positiveFactor, negativeFactor and housekeepingFactor slots filled or replaced.

Usage

estNormalizationFactors(NanoStringData)

Arguments

NanoStringData An object of "NanoStringSet" class.

Value

The same "NanoStringSet" object with positiveFactor, negativeFactor and housekeepingFactor field filled or replaced.

Author(s)

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Examples

data(NanoStringData)
NanoStringData=estNormalizationFactors(NanoStringData)
pf=positiveFactor(NanoStringData)
nf=negativeFactor(NanoStringData)
hf=housekeepingFactor(NanoStringData)
glm.LRT

**perform gene-wise likelihood ratio test for NanoString Data**

**Description**

The method considers a generalized linear model of the negative binomial family to characterize count data and allows for multi-factor design. The method propose an empirical Bayes shrinkage approach to estimate the dispersion parameter and use likelihood ratio test to obtain p-value.

**Usage**

```r
glm.LRT(NanoStringData, design.full, Beta=ncol(design.full), contrast=NULL)
```

**Arguments**

- **NanoStringData**: An object of "NanoStringSet" class.
- **design.full**: numeric matrix giving the design matrix for the generalized linear models under full model. must be of full column rank.
- **Beta**: integer or character vector indicating which coefficients of the linear model are to be tested equal to zero. Values must be columns or column names of design. Defaults to the last coefficient. Ignored if contrast is specified.
- **contrast**: numeric vector or matrix specifying one or more contrasts of the linear model coefficients to be tested equal to zero.

**Value**

A list

- **table**: A data frame with each row corresponding to a gene. Rows are sorted according to likelihood ratio test statistics. The columns are: logFC: log fold change between two groups. lr: likelihood ratio test statistics. pvalue: p-value. qvalue: adjust p-value using the procedure of Benjamini and Hochberg.
- **dispersion**: a vector of dispersion
- **log.dispersion**: a vector of log dispersion: log.dispersion=log(dispersion)
- **design.full**: numeric matrix giving the design matrix under full generalized linear model.
- **design.reduce**: numeric matrix giving the design matrix under reduced generalized linear model.
- **Beta.full**: coefficients under full model.
- **mean.full**: mean value under full model.
- **Beta.reduce**: coefficients under reduced model.
- **mean.reduce**: mean value under reduced model.
- **m0**: hyper-parameter: mean value of the prior distribution of log dispersion
- **sigma**: hyper-parameter: standard deviation of the prior distribution of log dispersion
**housekeepingControl**

**Author(s)**

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**Examples**

```r
data(NanoStringData)
NanoStringData=estNormalizationFactors(NanoStringData)
group=pData(NanoStringData)
design.full=model.matrix(~0+factor(group$group))
contrast=c(1,-1)
result=glm.LRT(NanoStringData,design.full,
  Beta=ncol(design.full),contrast=contrast)
head(result$table)
```

**Description**

User-defined housekeeping control genes can be used to estimate housekeeping factors to adjust variation caused by different sample input.

**Usage**

```r
## S4 method for signature 'NanoStringSet'
housekeepingControl(object)
## S4 replacement method for signature 'NanoStringSet,matrix'
housekeepingControl(object) <- value
```

**Arguments**

- `object` A NanoStringSet object.
- `value` A matrix with housekeeping control genes.

**Details**

NanoString nCounter analyzer also contains probes for a set of species-specific mRNA housekeeping(reference) genes that are not spike-in the system. Nanostring recommends at least three housekeeping genes, but the more that are included, the more accurate the normalization will be. Housekeeping control genes are expected consistent in their expression levels.

**Value**

A matrix contain housekeeping control genes
Author(s)
Hong Wang <hong.wang@uky.edu> chi wang <chi.wang@uky.edu>

See Also
housekeepingFactor

Examples
```r
data(NanoStringData)
## obtain housekeeping control genes
housekeepingControl(NanoStringData)

## assign a matrix
n=ncol(exprs(NanoStringData))
r=nrow(housekeepingControl(NanoStringData))
housekeeping=matrix(rpois(r*n,1000),ncol=n)
housekeepingControl(NanoStringData)=housekeeping
```

Description
Housekeeping size factors can be used to adjust the variance caused by different sample input.

Usage
```r
## S4 method for signature 'NanoStringSet'
housekeepingFactor(object)
## S4 replacement method for signature 'NanoStringSet,numeric'
housekeepingFactor(object) <- value
```

Arguments
- **object** A NanoStringSet object.
- **value** A vector of housekeeping size factors.

Details
Housekeeping gene normalization corrects for different in sample input between assays, since reference genes are supposed to have the same expression rate between samples. So the read counts from housekeeping genes, after subtracting background noise and adjusting by positive size factors, that are not expected to vary between samples. If there exists a difference, which should be caused by sample input variation.
NanoStringData

Value

A vector containing housekeeping factors

Author(s)

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See Also

housekeepingControl

Examples

data(NanoStringData)

## obtain housekeeping factors
housekeepingFactor(NanoStringData)

## assign a vector
n = ncol(exprs(NanoStringData))
housekeepingFactor(NanoStringData) = rep(1, n)

NanoStringData  A real 'NanoStringSet' object.

Description

The object is created based on Mori Data with normal and tumor groups and 2 samples in each group. The object contains 599 endogenes, 6 positive control, 6 negative control and 4 housekeeping control.

Usage

data(NanoStringData)

Value

An object of NanoStringSet

Examples

data(NanoStringData)
NanoStringData
NanoStringDataNormalization

*Normalize NanoStringData*

**Description**

This function is used to get Normalized NanoString Data after adjusting for positive size factors, background noise and housekeeping size factors. Note that the normalized data values should only be used for data exploration / visualization purposes, e.g. drawing a heatmap. To perform differential expression analysis, we recommend users to follow the procedure described in the package vignette.

**Usage**

```
NanoStringDataNormalization(path=path, header=TRUE, designs)
```

**Arguments**

- `path` 
  the path of the file which the data are to be read from.

- `header` 
  a logical value indicating whether the file contains the names of the variables as its first line. If missing, the value is determined from the file format: header is set to TRUE if and only if the first row contains one fewer field than the number of columns.

- `designs` 
  a data frame in which the length of vector matches the column number of NanoStringData

**Author(s)**

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**Examples**

```
##path="/Users/NanoStringdiff-Rcode/Data/horbinski.csv"
##designs=data.frame(control=c(0,0,0,1,1,1))
##NanoStringDataNormalization(path=path, header=TRUE, designs)
```

---

NanoStringSet-class

*NanoStringSet object and constructors*

**Description**

The NanoStringSet is a s4 class used to store data from NanoString nCounter analyzer. This class a subclass of ExpressionSet, with six more slots: positiveControl, negativeControl, housekeepingControl, positiveFactor, negativeFactor and housekeepingFactor. The constructor functions `createNanoStringSet` and `createNanoStringSetFromCsv` create a NanoStringSet object from two types of input: separate matrix or csv files. See the vignette for examples of construction from these two input types.
Usage

createNanoStringSet(endogenous, positiveControl, negativeControl, housekeepingControl, designs)
createNanoStringSetFromCsv(path, header=TRUE, designs)

Arguments

endogenous for matrix input: a matrix of non-negative integers of endogenes
positiveControl for matrix input: a matrix of non-negative integers of positive control genes. There must have 6 positive control genes order by concentrations form high to low
negativeControl for matrix input: a matrix of non-negative integers of negative control genes
housekeepingControl for matrix input: a matrix of non-negative integers of housekeeping control genes
designs for data.frame input: phenotype data for NanoString nCounter data with at least one column. Each row is one sample, that is the number of rows must equal number of samples or replicates in the data.
path path to the csv file.
header a logical value indicating whether the file contains the names of the variables as its first line. The default value is TRUE.

Value

A NanoStringSet object.

Methods

positiveControl, positiveControl<- : Access and set positive control genes.
negativeControl, negativeControl<- : Access and set negative control genes.
housekeepingControl, housekeepingControl<- : Access and set housekeeping control genes.
positiveFactor, positiveFactor<- : Access and set positive factors.
negativeFactor, negativeFactor<- : Access and set negative factors.
housekeepingFactor, housekeepingFactor<- : Access and set housekeeping factors.

Author(s)

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See Also

positiveControl, negativeControl, housekeepingControl, positiveFactor, negativeFactor, housekeepingFactor
Negative control genes are provided by nCounter Analyzer which can be used to estimate background noise for each sample.

Usage

```r
## S4 method for signature 'NanoStringSet'
negativeControl(object)
## S4 replacement method for signature 'NanoStringSet,matrix'
negativeControl(object) <- value
```

Arguments

- `object` A NanoStringSet object.
- `value` A matrix with negative control genes.

Details

Each code set in the nCounter Analyzer includes several negatives control genes for which no transcript is expected to be present. We use these spike-in negative control genes to estimate background noise for each sample.

Value

A matrix contain negative control genes

Author(s)

Hong Wang <hong.wang@uky.edu> chi wang <chi.wang@uky.edu>
See Also

negativeFactor

Examples

data(NanoStringData)
## obtain negative control genes
negativeControl(NanoStringData)

## assign a matrix
m=ncol(exprs(NanoStringData))
r=nrow(negativeControl(NanoStringData))
negative=matrix(rpois(r*n,10),ncol=n)
negativeControl(NanoStringData)=negative

Description

Negative size factors can be used to adjust background noise for each sample.

Usage

## S4 method for signature 'NanoStringSet'
negativeFactor(object)
## S4 replacement method for signature 'NanoStringSet,numeric'
negativeFactor(object) <- value

Arguments

object A NanoStringSet object.
value A vector of background noise.

Details

Accurate estimation of system background is essential for DE detection analysis. Each code set
in the nCounter Analyzer includes several negative control genes for which no transcript is
expected to be present. We use these spike-in negative control genes to estimate background noise
for each sample.

Value

A vector contain background noise

Author(s)

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See Also
negativeControl

Examples

data(NanoStringData)
## obtain negative factors
negativeFactor(NanoStringData)

## assign a vector
n=ncol(exprs(NanoStringData))
lamda=rpois(n,10)
negativeFactor(NanoStringData)=lamda

PlotsPositiveHousekeeping

Plots of positive controls and housekeeping genes

Description
This function is used to pre-check the expressions of positive controls and housekeeping genes before data analysis. Linear regression plot of positive controls and variation analysis of housekeeping genes are available. The expressions of positive controls are supposed to be linearly related to the concentration of input sample materials, and the expressions of housekeeping genes are supposed to have relatively low variation. Nanostring recommends at least three housekeeping genes, but the more that are included, the more accurate the normalization will be.

Usage

PlotsPositiveHousekeeping(path=path, header=TRUE)

Arguments

path the path of the file which the data are to be read from.

header a logical value indicating whether the file contains the names of the variables as its first line. If missing, the value is determined from the file format: header is set to TRUE if and only if the first row contains one fewer field than the number of columns.

Author(s)

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Examples

##path="/Users/NanoStringdiff-Rcode/Data/horbinski.csv"
#PlotsPositiveHousekeeping(path=path, header=TRUE)
**positiveControl**

**Acessor functions for the ’positiveControl’ slot in a NanoStringSet object.**

---

**Description**

*ncounter* Analyzer has positive spike-in RNA hybridization controls for each sample which can be used to estimate the overall efficiency of hybridization and recovery for each sample.

**Usage**

```r
## S4 method for signature 'NanoStringSet'
positiveControl(object)
## S4 replacement method for signature 'NanoStringSet,matrix'
positiveControl(object) <- value
```

**Arguments**

- `object`: A NanoStringSet object.
- `value`: A matrix with six positive control genes.

**Details**

Positive control genes are provided by NanoString nCounter technology. For each sample, nCounter provide six positive controls corresponding to six different concentrations in the 30 ul hybridization: 128fM, 32fM, 8fM, 2fM, 0.5fM, and 0.125fM. Six positive control genes must be order by concentrations from high to low.

**Value**

A matrix contain positive control genes

**Author(s)**

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**See Also**

positiveFactor

**Examples**

```r
data(NanoStringData)
## obtain positive control genes
positiveControl(NanoStringData)
## assign a matrix
n=ncol(exprs(NanoStringData))
```
\begin{verbatim}
x=matrix(c(128,32,8,2,0.5,0.125)*80,nrow=1)
positive=matrix(rpois(6*n,x),ncol=n)
positiveControl(NanoStringData)=positive
\end{verbatim}

\section*{positiveFactor}

\textit{Accessor functions for the 'positiveFactor' slot in a NanoStringSet object.}

\subsection*{Description}

Positive size factors can be used to adjust all platform associated sources of variation.

\subsection*{Usage}

\begin{verbatim}
## S4 method for signature 'NanoStringSet'
positiveFactor(object)
## S4 replacement method for signature 'NanoStringSet,numeric'
positiveFactor(object) <- value
\end{verbatim}

\subsection*{Arguments}

\begin{itemize}
  \item \textbf{object} \hspace{1cm} A NanoStringSet object.
  \item \textbf{value} \hspace{1cm} A vector of positive size factors.
\end{itemize}

\subsection*{Details}

The observed counts including negative control genes and housekeeping control genes might be effect by some experimental factors like hybridization and binding efficiency. In order to get the true rate of gene expression, these variations must be normalized. Positive size factors can normalize this kind of variation.

\subsection*{Value}

A vector contain positive size factors

\subsection*{Author(s)}

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\subsection*{See Also}

positiveControl
Examples

```r
data(NanoStringData)
## obtain positive factors
positiveFactor(NanoStringData)

## assign a vector
n=ncol(exprs(NanoStringData))
positiveFactor(NanoStringData)=rep(1,n)
```
Index

* Plots, Positive Controls, Housekeeping Genes
  PlotsPositiveHousekeeping, 12
  * classes
    NanoStringSet-class, 8
  * datasets
    NanoStringData, 7
  * models
    glm.LRT, 4
  * normalization
    estNormalizationFactors, 3
    NanoStringDataNormalization, 8
  * package
    NanoStringDiff-package, 2
createNanoStringSet
  (NanoStringSet-class), 8
createNanoStringSetFromCsv
  (NanoStringSet-class), 8
estNormalizationFactors, 3
estNormalizationFactors, estNormalizationFactors-method
  (estNormalizationFactors), 3
glm.LRT, 4
glm.LRT, NanoStringSet-method (glm.LRT), 4

housekeepingControl, 5
housekeepingControl, NanoStringSet-method
  (housekeepingControl), 5
housekeepingControl<- (housekeepingControl), 5
housekeepingControl<-, NanoStringSet, matrix-method
  (housekeepingControl), 5
housekeepingFactor, 6
housekeepingFactor, NanoStringSet-method
  (housekeepingFactor), 6
housekeepingFactor<-
  (housekeepingFactor), 6

housekeepingFactor<-, NanoStringSet, numeric-method
  (housekeepingFactor), 6

NanoStringData, 7
NanoStringDataNormalization, 8
NanoStringDataNormalization, NanoStringDataNormalization-method
  (NanoStringDataNormalization), 8
NanoStringDiff
  (NanoStringDiff-package), 2
NanoStringDiff-package, 2
NanoStringSet (NanoStringSet-class), 8
NanoStringSet-class, 8
negativeControl, 10
negativeControl, NanoStringSet-method
  (negativeControl), 10
negativeControl<-
  (negativeControl), 10
negativeControl<-, NanoStringSet, matrix-method
  (negativeControl), 10
negativeFactor, 11
negativeFactor, NanoStringSet-method
  (negativeFactor), 11
negativeFactor<-
  (negativeFactor), 11
negativeFactor<-, NanoStringSet, numeric-method
  (negativeFactor), 11

PlotsPositiveHousekeeping, 12
PlotsPositiveHousekeeping, PlotsPositiveHousekeeping-method
  (PlotsPositiveHousekeeping), 12
positiveControl, 13
positiveControl, NanoStringSet-method
  (positiveControl), 13
positiveControl<-
  (positiveControl), 13
positiveControl<-, NanoStringSet, matrix-method
  (positiveControl), 13
positiveFactor, 14
positiveFactor, NanoStringSet-method
  (positiveFactor), 14
positiveFactor<-
  (positiveFactor), 14
positiveFactor<-,NanoStringSet,numeric-method
  (positiveFactor), 14