

Package ‘qsmooth’

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Title Smooth quantile normalization

Version 1.8.0

Imports SummarizedExperiment, utils, sva, stats, methods, graphics

Depends R (>= 4.0)

Suggests bodymapRat, quantro, knitr, rmarkdown, BiocStyle, testthat

VignetteBuilder knitr

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Description Smooth quantile normalization is a generalization of quantile normalization, which is average of the two types of assumptions about the data generation process: quantile normalization and quantile normalization between groups.

biocViews Normalization, Preprocessing, MultipleComparison, Microarray, Sequencing, RNASeq, BatchEffect

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qsmooth	<i>qsmooth</i>
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Description

This function applies a generalization of quantile normalization called smoothed quantile normalization. This function defines the qsmooth class and constructor.

Usage

```
qsmooth(object, group_factor, batch = NULL, norm_factors = NULL, window = 0.05)
```

Arguments

object	an object which is a matrix or data.frame with observations (e.g. probes or genes) on the rows and samples as the columns. Alternatively, a user can provide a SummarizedExperiment object and the assay(object, "counts") will be used as input for the qsmooth normalization.
group_factor	a group level continuous or categorical covariate associated with each sample or column in the object. The order of the group_factor must match the order of the columns in object.
batch	(Optional) batch covariate (multiple batches are not allowed). If batch covariate is provided, Combat() from sva is used prior to qsmooth normalization to remove batch effects. See Combat() for more details.
norm_factors	optional normalization scaling factors.
window	window size for running median which is a fraction of the number of rows in object. Default is 0.05.

Details

Quantile normalization is one of the most widely used normalization tools for data analysis in genomics. Although it was originally developed for gene expression microarrays it is now used across many different high-throughput applications including RNAseq and ChIPseq. The methodology relies on the assumption that observed changes in the empirical distribution of samples are due to unwanted variability. Because the data is transformed to remove these differences it has the potential to remove interesting biologically driven global variation. Therefore, applying quantile

qsmoothData *Generic function that returns the qsmooth normalized data*

Description

Given a qsmooth object, this function returns the qsmooth normalized data
 Accessors for the 'qsmoothData' slot of a qsmooth object.

Usage

```
qsmoothData(object)

## S4 method for signature 'qsmooth'
qsmoothData(object)
```

Arguments

object an object of class qsmooth.

Value

The normalized data after applying smoothed quantile normalization.

Examples

```
dat <- cbind(matrix(rnorm(1000), nrow=100, ncol=10),
             matrix(rnorm(1000, .1, .7), nrow=100, ncol=10))
dat_qs <- qsmooth(object = dat,
                 group_factor = rep(c(0,1), each=10))
qsmoothData(dat_qs)
```

qsmoothPlotWeights *Plot weights from qsmooth function.*

Description

This function plots a scatterplot showing the qsmoothWeights along the y-axis and the quantiles on the x-axis.

Usage

```
qsmoothPlotWeights(
  object,
  xLab = "quantiles",
  yLab = "weights",
  mainLab = "qsmooth weights"
)
```

Arguments

object	a qsmooth object from qsmooth
xLab	label for x-axis. Default is "quantiles"
yLab	label for y-axis. Default is "weights"
mainLab	title of plot. Default is "qsmooth weights"

Value

A scatterplot will be created showing the qsmoothWeights along the y-axis and the quantiles on the x-axis.

Examples

```
dat <- cbind(matrix(rnorm(1000), nrow=100, ncol=10),
             matrix(rnorm(1000, .1, .7), nrow=100, ncol=10))
dat_qs <- qsmooth(object = dat,
                 group_factor = rep(c(0,1), each=10))
qsmoothPlotWeights(dat_qs)
```

qsmoothWeights	<i>Generic function that returns the qsmooth weights</i>
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Description

Given a qsmooth object, this function returns the qsmooth weights

Accessors for the 'qsmoothWeights' slot of a qsmooth object.

Usage

```
qsmoothWeights(object)

## S4 method for signature 'qsmooth'
qsmoothWeights(object)
```

Arguments

object	an object of class qsmooth.
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Value

The weights calculated for each feature after applying smoothed quantile normalization.

Examples

```
dat <- cbind(matrix(rnorm(1000), nrow=100, ncol=10),
              matrix(rnorm(1000, .1, .7), nrow=100, ncol=10))
dat_qs <- qsmooth(object = dat,
                  group_factor = rep(c(0,1), each=10))
qsmoothWeights(dat_qs)
```

qstats

qstats

Description

This function is a helper function that computes quantile statistics for the function `qsmooth`.

Usage

```
qstats(object, group_factor, window = 0.05)
```

Arguments

<code>object</code>	an object which is a data frame or matrix with observations (e.g. probes or genes) on the rows and samples as the columns.
<code>group_factor</code>	a group level continuous or categorical covariate associated with each sample or column in the object. The order of the <code>group_factor</code> must match the order of the columns in object.
<code>window</code>	window size for running median which is a fraction of the number of rows in object. Default is 0.05.

Value

A list of quantile statistics including

<code>Q</code>	sample quantiles
<code>Qref</code>	reference quantile
<code>Qhat</code>	linear model fit at each quantile
<code>SST</code>	total sum of squares
<code>SSB</code>	between sum of squares
<code>SSE</code>	within sum of squares
<code>roughWeights</code>	SSE / SST
<code>smoothWeights</code>	smoothed weights computed using a running median with a given window size.

Examples

```
dat <- cbind(matrix(rnorm(1000), nrow=100, ncol=10),  
             matrix(rnorm(1000, .1, .7), nrow=100, ncol=10))  
qs <- qstats(object = dat,  
             group_factor = rep(c(0,1), each=10),  
             window = 0.05)
```

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