

# Package ‘qsmooth’

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**Title** Smooth quantile normalization

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

**Depends** R (>= 4.0)

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

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**License** GPL-3

**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



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`qsmoothData`*Generic function that returns the qsmooth normalized data*

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**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)
```

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`qsmoothGC`*qsmoothGC*

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**Description**

This function applies smoothed quantile normalization separately for groups of features that are binned according to their GC-content.

**Usage**

```
qsmoothGC(object, group_factor, gc, nGroups = 50, round = TRUE, ...)
```

**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.
gc	GC-content of the features, ordered according to the features in object.
nGroups	The number of equally-sized bins used to group the GC-content values. Groups are created using Hmisc::cut2.
round	Should normalized values be rounded to integers?
...	(Optional) Additional arguments passed to qsmooth.

**Value**

A matrix of normalized counts.

**References**

Van den Berge K., Chou H., Roux de Bézieux H., Street K., Risso D., Ngai J., Dudoit S. Normalization benchmark of ATAC-seq datasets shows the importance of accounting for GC-content effects. <https://www.biorxiv.org/content/10.1101/2021.01.26.428252v2>

**Examples**

```
dat <- cbind(matrix(rnorm(1000), nrow=100, ncol=10),
             matrix(rnorm(1000, .1, .7), nrow=100, ncol=10))
gc <- runif(n=100, min=0.2, max=0.9)
dat_qs <- qsmoothGC(object = dat,
                   gc = gc,
                   group_factor = rep(c(0,1), each=10))
```

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qsmoothPlotWeights      *Plot weights from qsmooth function.*

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**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)
```

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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)
```

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qstats

*qstats*


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**Description**

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

**Usage**

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

**Arguments**

object	an object which is a data frame or matrix with observations (e.g. probes or genes) on the rows and samples as the columns.
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.
window	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

Q	sample quantiles
Qref	reference quantile
Qhat	linear model fit at each quantile
SST	total sum of squares
SSB	between sum of squares
SSE	within sum of squares
roughWeights	SSE / SST
smoothWeights	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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