

# Package ‘qpcrNorm’

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**Type** Package

**Title** Data-driven normalization strategies for high-throughput qPCR data.

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**Description** The package contains functions to perform normalization of high-throughput qPCR data. Basic functions for processing raw Ct data plus functions to generate diagnostic plots are also available.

**License** LGPL (>= 2)

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calcCV	<i>Calculates the Average Gene-Specific Coefficient of Variation</i>
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### Description

This function calculates the coefficient of variation for each gene in the qPCR experiment, and returns the average coefficient of variation across all genes.

### Usage

```
calcCV(qBatch)
```

### Arguments

qBatch            A qpcrBatch object.

### Value

A numeric value.

### Author(s)

Jess Mar <jess@jimmy.harvard.edu>

### Examples

```
data(qpcrBatch.object)
mynormRI.data <- normQpcrRankInvariant(qpcrBatch.object, 1)
mynormQuant.data <- normQpcrQuantile(qpcrBatch.object)
barplot(c(calcCV(mynormRI.data), calcCV(mynormQuant.data)), col=c("red", "blue"))
```

**Description**

This function applies a quality control filter to triplicate Ct values before combining them into a single summary Ct measure.

Current implementation can only handle three replicates.

**Usage**

```
ctQc(x)
```

**Arguments**

x                    Matrix with three columns, corresponding to the triplicate Ct values.

**Details**

Applying ctQc is an alternative to averaging the triplicate Ct values. This filter was originally developed by Yasumasa Kimura 1. For each primer, sort Ct values in ascending order so we have [ct1, ct2, ct3]. 2. Take two differences difference1 := ct2 - ct1 difference2 := ct3 - ct2 If either or both have ct 40, we don't calculate the difference and set it to region 4 in the next step. 3. Take an average according to the differences. Here we have 2 thresholds : 0.2 and 1.0. With the thresholds, we classify the 2 differences into the below regions. region1 : difference <= 0.2 region2 : 0.2 < difference <= 1.0 region3 : 1.0 < difference region4 : either or both ct are 40 If the 2 differences are in same region, we take an average of 3 ct values. If the 2 differences are in different regions, we take an average of 2 ct values which are in smaller number region.

**Value**

Numeric vector of Ct values combined over the three replicates according to the QC filter.

**Author(s)**

Yasumasa Kimura  
Jess Mar <jess@jimmy.harvard.edu>

**See Also**

[readQpcr](#), [readQpcrBatch](#)

**Examples**

```
## myQpcrBatch <- readQpcrBatch(qc=T) # reads in data from a batch of qPCR experiments, applies ctQc to raw Ct values
```

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matrixByPlate	<i>Internal function to reorganize qPCR data into a rectangular structure.</i>
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### Description

This function takes a vector of Ct values from a single qPCR experiment and reorganizes it into a matrix structure. Each column in the matrix represents a different plate that was used in the experiment.

### Usage

```
matrixByPlate(xvec, plateIndex)
```

### Arguments

xvec	Numeric vector of Ct values.
plateIndex	Character vector, denoting plate index of each gene or primer pair.

### Details

On the resulting matrix structure:

The number of rows equals the maximum number of genes or primer pairs that were used on a plate in the experiment. For plates with less genes, NA values are padded at the end of the column vector to complete the rectangular structure. Note: these NA values do not affect downstream calculations.

### Value

A matrix object.

### Author(s)

Jess Mar <jess@jimmy.harvard.edu>

### See Also

[normQpcrQuantile](#)

### Examples

```
data(qpcrBatch.object)
mynormQuant.data <- normQpcrQuantile(qpcrBatch.object)
```

---

`normQpcrHouseKeepingGenes`*Function for Housekeeping Gene Normalization of qPCR Data.*

---

**Description**

Implements housekeeping gene normalization for a `qpcrBatch` object.

**Usage**

```
normQpcrHouseKeepingGenes(qBatch, hkeep.genes)
```

**Arguments**

<code>qBatch</code>	A <code>qpcrBatch</code> object to be normalized.
<code>hkeep.genes</code>	Character vector, specifying which housekeeping genes to be used for normalization.

**Details**

The names in `hkeep.genes` must be a subset of the gene or primer pair names slot in the `qpcrBatch` object.

**Value**

A `qpcrBatch` object, the normalized slot is now set at TRUE.

**Author(s)**

Jess Mar <jess@jimmy.harvard.edu>

**See Also**

[normQpcrQuantile](#), [normQpcrRankInvariant](#)

**Examples**

```
data(qpcrBatch.object)
mynormHK.data <- normQpcrHouseKeepingGenes(qpcrBatch.object, c("Gpx4"))
```

---

normQpcrQuantile	<i>Function for Quantile Normalization of qPCR Data.</i>
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---

### Description

Implements quantile normalization for a `qpcrBatch` object. We have adapted this algorithm from the function `normalizeBetweenArrays` from the **limma** package.

Data in a `qpcrBatch` object is normalized such that within an experiment, the expression distributions

across plates are more or less identical, and across experiments, the expression distributions are also now more or less identical.

### Usage

```
normQpcrQuantile(qBatch)
```

### Arguments

`qBatch`            A `link{qpcrBatch}` object.

### Value

A `link{qpcrBatch}` object, the normalized slot is now set at TRUE.

### Author(s)

Jess Mar <jess@jimmy.harvard.edu>

### See Also

[normQpcrRankInvariant](#), [normalizeBetweenArrays](#)

### Examples

```
data(qpcrBatch.object)
mynormQuant.data <- normQpcrQuantile(qpcrBatch.object)
```

---

normQpcrRankInvariant *Function for Rank-Invariant Set Normalization for qPCR Data.*

---

## Description

Implements rank-invariant set normalization for a `qpcrBatch` object. We have adapted this algorithm from the function `normalize.invariantset` from the `affy` package.

## Usage

```
normQpcrRankInvariant(qBatch, refType, rem.highCt = FALSE, thresh.Ct = 30)
```

## Arguments

<code>qBatch</code>	A <code>qpcrBatch</code> object.
<code>refType</code>	Indicates what reference sample should be used, can be an integer or character string. See Details below.
<code>rem.highCt</code>	Logical indicator, TRUE if user wishes to remove genes with high Ct values (very low expression) that may be associated poor data quality.
<code>thresh.Ct</code>	Numerical value indicating the Ct value cutoff threshold, if <code>rem.highCt = FALSE</code> , genes with Ct values > <code>thresh.Ct</code> are removed from the data set.

## Details

The algorithm computes all rank-invariant sets of genes between pairwise comparisons where each experimental sample in the `qpcrBatch` object is paired against a reference. There are several ways to specify what a sensible choice for the reference sample should be.

1. The reference is an experimental sample in the `qpcrBatch` object.  
Specify `refType` as an integer value, corresponding to the index of which experimental sample is the reference.
2. The reference is the sample which is closest to mean of all the experiments.  
Specify `refType = "mean"`.
3. The reference is the sample which is closest to median of all the experiments.  
Specify `refType = "median"`.
4. The reference is the mean of all experiments in the `qpcrBatch` object.  
Specify `refType = "pseudo.mean"`.
5. The reference is the median of all experiments in the `qpcrBatch` object.  
Specify `refType = "pseudo.median"`.

**Value**

A `qpcrBatch` object, the normalized slot is now set at TRUE. The names of the rank-invariant genes used for normalization are stored as a vector in the `normGenes` slot of the `qpcrBatch` object returned. To retrieve the rank-invariant gene names, use `qpcrBatch@normGenes`.

**Author(s)**

Jess Mar <jess@jimmy.harvard.edu>

**See Also**

[normQpcrQuantile](#), [normalize.invariantset](#)

**Examples**

```
data(qpcrBatch.object)
mynormRI.data <- normQpcrRankInvariant(qpcrBatch.object, 1)
mynormRI.data@normGenes # retrieves names of genes in the rank-invariant set
```

---

plotVarMean	<i>Constructs scatter plot to compare the effects of two normalization algorithms on a qPCR dataset.</i>
-------------	--

---

**Description**

This function makes a scatter plot which serves as a useful exploratory tool in evaluating whether one normalization algorithm has been more effective than another on a given qPCR dataset.

**Usage**

```
plotVarMean(qpcrBatch1, qpcrBatch2, normTag1 = "Normalization Type1", normTag2 = "Normalization Type2")
```

**Arguments**

qpcrBatch1	A <a href="#">qpcrBatch</a> object.
qpcrBatch2	A <a href="#">qpcrBatch</a> object.
normTag1	Character string denoting what normalization algorithm was used for this data set.
normTag2	Character string denoting what normalization algorithm was used for this data set.
...	Further arguments can be supplied to the <a href="#">plot</a> function.



## Details

For each gene, the function plots its log-transformed ratio of its expression variance in one normalized dataset versus another normalized dataset, i.e. let  $G_{ij}$  be the variance of the expression values of gene  $i$  that have been normalized with method  $j$ . We plot the natural log-transformed ratio of  $G_{ij}$  to  $G_{ik}$  on the y-axis, and the average expression of gene  $i$  on the x-axis for all genes. The red curve represents a smoothed lowess curve that has been fitted to reflect the overall trend of the data. When the red curve drops below  $y = 0$  (the blue dotted line) we know that method  $j$  effects a greater reduction in the variation of the data over method  $k$ . Similarly, when the red curve is above  $y = 0$ , method  $k$  is more effective in reducing the variation in the data than method  $j$ . If the data from both methods have similar variances then the red curve should remain at  $y = 0$ . Bolstad et al. (2003) originally used these plots for variance comparisons of different normalization methods for high density oligonucleotide array data.

## Value

A plot object.

## Author(s)

Jess Mar <jess@jimmy.harvard.edu>

## References

Bolstad B et al. A comparison of normalization methods for high density oligonucleotide array data based on variance and bias. *Bioinformatics*, 2003.

## See Also

[plot](#)

## Examples

```
# data(qpcrBatch.object)
# mynormRI.data <- normQpcrRankInvariant(qpcrBatch.object, 1)
# mynormQuant.data <- normQpcrQuantile(qpcrBatch.object)
# plotVarMean(mynormRI.data, mynormQuant.data, normTag1="Rank-Invariant", normTag2="Quantile", main="Comparing
```

---

qpcrBatch-class

*Class qpcrBatch*

---

## Description

This is a class representation for qPCR expression data.

## Objects from the Class

Objects can be created using the function [readQpcr](#) or [readQpcrBatch](#) to read in raw data from a text file(s). Objects can also be created by using `new("qpcrBatch", ...)`.

**Slots**

**geneNames:** Character vector denoting gene or primer pair names.  
**plateIndex:** Character vector denoting plate indices.  
**exprs:** Matrix of qPCR expression values, normally these are the Ct values.  
**normalized:** Logical value, TRUE if expression data has been normalized.  
**normGenes:** Character vector of genes used by the normalization algorithm.

**Methods**

No methods have yet been defined with class "qpcrBatch" in the signature.

**Note**

This class is better describe in the vignette.

**Author(s)**

Jess Mar <jess@jimmy.harvard.edu>

**Examples**

```
## load example data
data(qpcrBatch.object)
class(qpcrBatch.object)
```

---

qpcrBatch.object      *qpcrBatch* instance *qpcrBatch.object*

---

**Description**

This is an artificially generated qPCR data set. The data set has been closely simulated from original data for 2396 genes on 13 time points. Each measurement within the one sample was repeated over three replicate wells, across multiple plates.

**Usage**

```
data(qpcrBatch.object)
```

**Format**

A data frame with 2396 observations on the following 41 variables.

**Primers** Character vector of gene or primer pair names.

**Plate\_Index** Numeric vector denoting plate indices.

**Time1\_Rep1** Ct values for first time point, first replicate.

**Time1\_Rep2** Ct values for first time point, second replicate.

**Time1\_Rep3** Ct values for first time point, third replicate.

**Examples**

```
data(qpcrBatch.object)
```

---

readQpcr

*Data Input Function for a Single qPCR Experiment.*


---

**Description**

This function reads in data from a single qPCR experiment. The text file must have the following structure:

1st column = names denoting genes or primer pairs  
 2nd column = plate index of each gene or primer pair  
 remaining columns = (replicate) Ct values.

**Usage**

```
readQpcr(fileName, header = FALSE, qc = FALSE, quote = "\"", dec = ".", fill = TRUE, comment.char = "", ...)
```

**Arguments**

fileName	Character string.
header	Logical value, TRUE if the file contains the names of the variables as its first line.
qc	Logical value, TRUE if a QC filter <code>ctQc</code> should be applied to the data. If qc = F, the replicate Ct values will be averaged.
quote	Set of quoting characters. To disable quoting, set quote = "". See <code>scan</code> for behaviour on quotes embedded in quotes.
dec	Character used for decimal points.
fill	Logical value, TRUE if in case rows have unequal length, blank fields are implicitly added. See <code>read.table</code> .
comment.char	Character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.
...	further arguments to be passed to <code>read.table</code> .

**Details**

Note: the majority of arguments to `readQpcr` are identical to those supplied to `read.table`. These have been included to give the user greater control over data input, should the data deviate from a standard tab-delimited file structure. For a standard tab-delimited text file (without column headings), specifying the `fileName` should be sufficient.

**Value**

A `qpcrBatch` object.

**Author(s)**

Jess Mar <jess@jimmy.harvard.edu>

**See Also**

[readQpcrBatch](#), [ctQc](#)

**Examples**

```
## onerun.data <- readQpcr("singleQpcrRun.txt")
```

---

readQpcrBatch

*Data Input Function for a Batch of qPCR Experiments.*

---

**Description**

This function reads in data from multiple qPCR experiments from the one batch. Each text file in the batch must meet the structure required by [readQpcr](#).

Note: In order to qualify as a batch, it is assumed that the same set of primers are being analyzed in each experiment.

**Usage**

```
readQpcrBatch(..., filenames = character(), header = FALSE, qc = FALSE)
```

**Arguments**

...	Filenames separated by a comma.
filenames	Character vector specifying file names.
header	Logical value, TRUE if the file contains the names of the variables as its first line.
qc	Logical value, TRUE if a QC filter <a href="#">ctQc</a> should be applied to the data. If qc = F, the replicate Ct values will be averaged. See <a href="#">ctQc</a> .

**Details**

If the function is called with no arguments `readQpcrBatch()` all the files in the working directory are read and put into a [qpcrBatch](#) object. All files must conform to the following structure:

1st column = names denoting genes or primer pairs  
 2nd column = plate index of each gene or primer pair  
 remaining columns = (replicate) Ct values

Note: the majority of arguments to `readQpcr` are identical to those supplied to `read.table`. These have been included to give the user greater control over data input, should the data deviate from a standard tab-delimited file structure. For a set of standard tab-delimited text files (without column headers), specifying the `filenames` should be sufficient.

**Value**

A [qpcrBatch](#) object.

**Author(s)**

Jess Mar <jess@jimmy.harvard.edu>

**See Also**

[ctQc](#), [readQpcr](#), [setwd](#)

**Examples**

```
## myBatch <- readQpcrBatch()
```

---

writeQpcr

*Writes qpcrBatch object out to a File.*

---

**Description**

This function writes a [qpcrBatch](#) out to a tab-delimited text file. [writeQpcr](#) can be used to write out the normalized qPCR data out to an external file.

**Usage**

```
writeQpcr(qBatch, fileName, ...)
```

**Arguments**

<code>qBatch</code>	A <a href="#">qpcrBatch</a> object.
<code>fileName</code>	Character string specifying name of the output file.
<code>...</code>	Extra arguments to be passed to <a href="#">write.table</a> .

**Details**

Function creates a tab-delimited text file with three columns,  
1st column = names denoting genes or primer pairs 2nd column = plate index 3rd column = normalized Ct value

**Author(s)**

Jess Mar <jess@jimmy.harvard.edu>

**References**

Mar J et al. Data-driven Normalization Strategies for qPCR Data. Technical Report, 2008.

**See Also**[write.table](#)**Examples**

```
## writeQpcr(qpcrBatch.object, "output1.txt")
```

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