

# ReadqPCR

March 24, 2012

---

ReadqPCR-package    *Read qPCR data*

---

## Description

The package provides functions to read raw RT-qPCR data of different platforms.

## Details

Package:	ReadqPCR
Type:	Package
Version:	0.99.3
Date:	2011-06-30
Depends:	R(>= 2.10.0), Biobase, ReadqPCR, methods, RColorBrewer
License:	LGPL-3
LazyLoad:	yes

```
library(ReadqPCR)
```

## Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

Matthias Kohl <Matthias.Kohl@stamats.de>

Maintainer: James Perkins <jperkins@biochem.ucl.ac.uk>

## Examples

```
## some examples are given in the vignette
## Not run:
library(ReadqPCR)
vignette("ReadqPCR")

## End(Not run)
```

---

qPCRBatch-class      *Class qPCRBatch*

---

### Description

Class to Contain and Describe raw and normalised qPCR Data, as Ct or delta-Ct values. Extends eSet

### Creating Objects

```
new("qPCRBatch")
```

### Slots

**assayData:** Object of class AssayData containing the raw data, which will be at minimum a matrix of Ct values. This slot can also hold a matrix of well.info values if these are present in the input file read in by `read.qPCR` or `read.taqman`

**phenoData:** Object of class AnnotatedDataFrame containing phenotypic data for the samples.

**annotation** A character string identifying the annotation that may be used for the ExpressionSet instance.

**protocolData:** Object of class AnnotatedDataFrame containing protocol data for the samples.

**featureData** Object of class AnnotatedDataFrame containing feature-level (e.g., probeset-level) information.

**experimentData:** Object of class "MIAME" containing experiment-level information.

**.\_\_classVersion\_\_:** Object of class Versions describing the R and Biobase version number used to create the instance. Intended for developer use.

### Methods

**exprs** signature(object = "qPCRBatch"): extracts the Ct expression matrix.

**exprs<-** signature(object = "qPCRBatch", value = "matrix"): replaces the Ct expression matrix.

**exprs.well.order** signature(object = "qPCRBatch"): extracts the Ct well order matrix (if it exists).

**exprs.well.order<-** signature(object = "qPCRBatch", value = "matrix"): replaces the Ct well order matrix.

### Note

This class is better described in the vignette.

### Author(s)

James Perkins

### See Also

[eSet](#)

---

`read.qPCR`*Read user formatted qPCR data and produce a qPCRBatch*

---

## Description

Reads RT-qPCR data in format specified in the ReadqPCR vignette and uses the data to populate an object of class "qPCRBatch".

## Usage

```
read.qPCR(filename = character(0),
          phenoData = new("AnnotatedDataFrame"),
          notes = "",
          verbose = FALSE)
```

## Arguments

<code>filename</code>	file name (must be formatted as shown in vignette).
<code>phenoData</code>	an <code>AnnotatedDataFrame</code> object, a character of length one, or a <code>data.frame</code> .
<code>notes</code>	notes.
<code>verbose</code>	verbosity flag. If true more messages are given to the user on the processing steps

## Details

Permits the user to read in qPCR Ct value data in a predefined format (more details on this format in the ReadqPCR package vignette), alongside phenotypic data and further notes about the data. If `phenoData` is a `data.frame`, it is converted to an `AnnotatedDataFrame`. If it is `NULL` then a default object of class `AnnotatedDataFrame` is created, whose `pData` is a `data.frame` with rownames being the names of the samples, and with one column `sample` with an integer index. More details on how technical replicates are handled in the ReadqPCR package vignette

## Value

Object of class "qPCRBatch".

## Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

## See Also

[ExpressionSet-class](#)

## Examples

```
path <- system.file("exData", package = "ReadqPCR")
qPCR.example <- file.path(path, "qPCR.example.txt")
qPCRBatch.qPCR <- read.qPCR(qPCR.example)
```

---

read.taqman	<i>Read Taqman qPCR data and produce a qPCRBatch</i>
-------------	--

---

## Description

Reads Taqman RT-qPCR data and uses the data to populate an object of class "qPCRBatch".

## Usage

```
read.taqman(...,  
             filenames = character(0),  
             phenoData = new("AnnotatedDataFrame"),  
             notes = "",  
             verbose = FALSE)
```

## Arguments

...	file names separated by comma.
filenames	file names in a character vector.
phenoData	an <a href="#">AnnotatedDataFrame</a> object, a character of length one, or a <code>data.frame</code> .
notes	notes.
verbose	verbosity flag. If true more messages are given to the user on the processing steps

## Details

Permits the user to read in qPCR Ct value data from an sds output file, alongside phenotypic data and further notes about the data. If `phenoData` is a `data.frame`, it is converted to an `AnnotatedDataFrame`. If it is `NULL` then a default object of class `AnnotatedDataFrame` is created, whose `pData` is a `data.frame` with rownames being the names of the , and with one column `sample` with an integer index. More details on how technical replicates are handled in the `ReadqPCR` package vignette

## Value

Object of class "qPCRBatch".

## Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

## See Also

[ExpressionSet-class](#)



# Index

## \*Topic classes

qPCRBatch-class, 2

read.qPCR, 3

read.taqman, 4

## \*Topic package

ReadqPCR-package, 1

AnnotatedDataFrame, 3, 4

checkValidqPCRFilename

(read.qPCR), 3

checkValidTaqmanFileNames

(read.taqman), 4

class:qPCRBatch

(qPCRBatch-class), 2

eSet, 2

ExpressionSet-class, 3, 4

exprs.well.order

(qPCRBatch-class), 2

exprs.well.order, qPCRBatch-method

(qPCRBatch-class), 2

exprs.well.order<-

(qPCRBatch-class), 2

exprs.well.order<-, qPCRBatch-method

(qPCRBatch-class), 2

qPCRBatch (qPCRBatch-class), 2

qPCRBatch-class, 2

qSet (qPCRBatch-class), 2

read.qPCR, 3

read.taqman, 4

read\_qPCRBatch (read.qPCR), 3

read\_TaqBatch (read.taqman), 4

ReadqPCR (ReadqPCR-package), 1

ReadqPCR-package, 1