Package: ReadqPCR (via r-universe)

November 24, 2026

Version 1.60.0

Date 2020-03-20

Title Read qPCR data

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

Author James Perkins, Matthias Kohl, Nor Izayu Abdul Rahman

Maintainer James Perkins <jimrperkins@gmail.com>

Depends R(>= 2.14.0), Biobase, methods

Suggests qpcR

biocViews DataImport, MicrotitrePlateAssay, GeneExpression, qPCR

License LGPL-3

LazyLoad yes

URL http://www.bioconductor.org/packages/release/bioc/html/ReadqPCR.html

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:31:03 UTC

RemoteUrl https://github.com/bioc/ReadqPCR

RemoteRef RELEASE_3_24

RemoteSha 5d44493197b3ea01586c8f937f91baa22c202091

Contents

ReadqPCR-package 2
CyclesSet-class 3
merge 4
qpcR2CyclesSet 6
qPCRBatch-class 7
read.LC480 8
read.LC480SampleInfo 10
read.qPCR 12
read.taqman 13

Index **15**

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:	1.5.3
Date:	2013-03-23
Depends:	R(>= 2.14.0), Biobase, methods, affy
Imports:	Biobase
Suggests:	qpcR
License:	LGPL-3
LazyLoad:	yes

library(ReadqPCR)

Author(s)

James Perkins <jimrperkins@gmail.com>
Matthias Kohl <Matthias.Kohl@stamats.de>
Nor Izayu Abdul Rahman

Maintainer: James Perkins <jimrperkins@gmail.com>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

Examples

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

## End(Not run)
```

CyclesSet-class *Class CyclesSet*

Description

Class to contain and describe raw fluorescence data. Extends eSet

Creating Objects

```
new("CyclesSet")
```

Slots

`assayData`**:** Object of class `AssayData` containing the raw data, which will be a matrix of fluorescence values.

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

`annotation` A character string identifying the annotation that may be used for the `CyclesSet` 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 = "CyclesSet")`: extracts the matrix with the fluorescence values.

exprs<- `signature(object = "CyclesSet", value = "matrix")`: replaces the matrix with the fluorescence values.

Author(s)

Nor Izayu Abdul Rahman, Matthias Kohl <Matthias.Kohl@stamats.de>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

See Also

eSet

merge *Generic Function for Merging eSet and AnnotatedDataFrame*

Description

Generic function for the merging an eSet and an AnnotatedDataFrame; that is, the informatiton given in the AnnotatedDataFrame is merged into the appropriate slot of the given eSet. This can be slot phenoData (default), featureData, or protocolData.

Usage

```
merge(x, y, ...)
## S4 method for signature 'eSet,AnnotatedDataFrame'
merge(x, y, eSet.slot = "phenoData",
                  by = intersect(names(pData(x)), names(pData(y))),
                  by.x = by, by.y = by,
                  all = FALSE, all.x = all, all.y = all,
                  sort = FALSE, suffixes = c(".x",".y"),
                  incomparables = NULL, ...)
## S4 method for signature 'AnnotatedDataFrame,eSet'
merge(x, y, eSet.slot = "phenoData",
                  by = intersect(names(pData(x)), names(pData(y))),
                  by.x = by, by.y = by,
                  all = FALSE, all.x = all, all.y = all,
                  sort = FALSE, suffixes = c(".x",".y"),
                  incomparables = NULL, ...)
```

Arguments

x	object of class eSet or AnnotatedDataFrame
y	object of class eSet or AnnotatedDataFrame
eSet.slot	name of the slot of the given eSet which is merged with the given AnnotatedDataFrame. This can be "phenoData" (default), "featureData", or "protocolData"
by	specifications of the columns used for merging.
by.x	specifications of the columns used for merging.
by.y	specifications of the columns used for merging.
all	logical; all = L is shorthand for all.x = L and all.y = L, where L is either TRUE or FALSE.
all.x	logical; if TRUE, then extra rows will be added to the output, one for each row in x that has no matching row in y. These rows will have NAs in those columns that are usually filled with values from y. The default is FALSE, so that only rows with data from both x and y are included in the output.
all.y	logical; analogous to all.x.
sort	logical. Should the result be sorted on the by columns?

suffixes	a character vector of length 2 specifying the suffixes to be used for making unique the names of columns in the result which not used for merging (appearing in by etc).
incomparables	values which cannot be matched. See match.
...	additional arguments to be passed to or from methods.

Details

For details on the arguments see merge.

Value

Object of class "CyclesSet".

Methods

x = "eSet", y = "AnnotatedDataFrame": merge y into specified slot of x.

x = "AnnotatedDataFrame", y = "eSet": merge x into specified slot of y.

Author(s)

Nor Izayu Abdul Rahman, Matthias Kohl <Matthias.Kohl@stamats.de>

See Also

merge, eSet

Examples

```
path <- system.file("exData", package = "ReadqPCR")

LC480.example <- file.path(path, "LC480_Example.txt")
## Read in the raw qPCR data from file "LC480_Example.txt"
## with maximum cycle to be read in the values is 45 (default).
cycData <- read.LC480(file = LC480.example)

LC480.SamInfo <- file.path(path, "LC480_Example_SampleInfo.txt")
# Read in the sample information data from file "LC480_Example_SampleInfo.txt".
samInfo <- read.LC480SampleInfo(LC480.SamInfo)

cycData1 <- merge(cycData, samInfo)
```

qpcR2CyclesSet *Transform a dataset from qpcR Package into CyclesSet*

Description

Transform a dataset from package **qpcR** into an object of class "CyclesSet".

Usage

```
qpcR2CyclesSet(x, cyc = 1, cycleThreshold)
```

Arguments

x	the name of the dataset from package **qpcR** to be transformed.
cyc	the column number which contains cycle data.
cycleThreshold	maximum number of cycles which the data will be counted and transformed.

Details

Allows the user to transform a dataset from package **qpcR** into an object of class "CyclesSet" class, alongside phenotypic data.

Value

Object of class "CyclesSet".

Author(s)

Nor Izayu Abdul Rahman, Matthias Kohl <Matthias.Kohl@stamats.de>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

See Also

reps, CyclesSet-class

Examples

```
library(qpcR)

## Transform the reps dataset from qpcR Package
## with maximum cycle to be read in the value is 45.
repsdata <- qpcR2CyclesSet(reps, cyc=1, cycleThreshold=45)
```

```
## Transform the batsch1 dataset from qpcR Package
## with maximum cycle to be read in the value is 40.
batsch1data <- qpcR2CyclesSet(batsch1, cyc=1, cycleThreshold=40)
```

---

qPCRBatch-class *Class qPCRBatch*

Description

Class to Contain and Describe raw and normalised qPCR Data, as Cq or delta-Cq 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 Cq 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 `qPCRBatch` 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 Cq expression matrix.

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

se.exprs `signature(object = "qPCRBatch")`: extracts the expression matrix with SDs of Cq values.

se.exprs<- `signature(object = "qPCRBatch", value = "matrix")`: replaces the expression matrix with SDs of Cq values.

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

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

effs `signature(object = "qPCRBatch")`: extracts the efficiency matrix (if it exists).

effs<- `signature(object = "qPCRBatch", value = "matrix")`: replaces the efficiency matrix.

se.effs `signature(object = "qPCRBatch")`: extracts the matrix with the standard errors/deviations of the efficiencies (if it exists).

se.effs<- `signature(object = "qPCRBatch", value = "matrix")`: replaces the matrix with the standard errors/deviations of the efficiencies.

Note

This class is better described in the vignette.

Author(s)

James Perkins <jimrperkins@gmail.com>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

See Also

eSet

`read.LC480` *Read in raw qPCR data of Light Cycler 480*

Description

Reads in raw qPCR data of Light Cycler 480 and uses the data to populate an object of class `"CyclesSet"`.

Usage

```
read.LC480(file, colNames = c("Sample position", "Sample name",
                              "Program number", "Segment number",
                              "Cycle number", "Acquisition time",
                              "Acquisition temperature",
                              "Fluorescence data"),
           cycleThreshold = 45, fileType = "txt", skip = 1,
           header = TRUE, sep = "\t", quote = "\"", dec = ".",
           fill = TRUE, comment.char = "")
```

Arguments

file	the name of the file to be read in.
colNames	a character vector of names to be assumed for the columns.
cycleThreshold	maximum number of cycles which will be read in.
fileType	the type of the file.
skip	integer: the number of lines of the data file to skip before beginning to read data.
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.
sep	the field separator character. Values on each line of the file are separated by this character. If sep = "" (the default for read.table) the separator is 'white space', that is one or more spaces, tabs, newlines or carriage returns.
quote	the set of quoting characters. To disable quoting altogether, use quote = "". See scan for the behaviour on quotes embedded in quotes. Quoting is only considered for columns read as character, which is all of them unless colClasses is specified.
dec	the character used in the file for decimal points.
fill	logical. If TRUE then in case the rows have unequal length, blank fields are implicitly added. See read.table.
comment.char	character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.

Details

Allows the user to read in qPCR fluorescence data from Light Cycler 480 which has been exported to a txt-file, alongside phenotypic data.

Value

Object of class "CyclesSet".

Author(s)

Nor Izayu Abdul Rahman, Matthias Kohl <Matthias.Kohl@stamats.de>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

See Also

read.table

read.LC480SampleInfo for reading in sample information of qPCR data from Light Cycler and produce an object of Class "CyclesSet".

merge for merging the phenodata from read.LC480 and read.LC480SampleInfo and produce an object of Class "CyclesSet".

read.qPCR and read.taqman for reading in the RT-qPCR data consisting of Cq values.

eSet, CyclesSet-class

Examples

```
path <- system.file("exData", package = "ReadqPCR")
LC480.example <- file.path(path, "LC480_Example.txt")

## Read in the raw qPCR data from file "LC480_Example.txt"
## with maximum cycle to be read in the values is 45 (default).
cycData <- read.LC480(file = LC480.example)

## Read in the data from file "LC480_Example.txt"
## with maximum cycle to be read in the values is 50.
rawdata <- read.LC480(file=LC480.example, cycleThreshold=50)
```

---

read.LC480SampleInfo *Read sample information data of a qPCR experiment from Light Cycler 480*

Description

Reads sample information data of a qPCR experiment from Light Cycler 480 which is in txt-file and uses the data to populate an object of Class "AnnotatedDataFrame".

Usage

```
read.LC480SampleInfo(file, removeEmptyCols = TRUE,
                     header = TRUE, sep = "\t", quote = "\"",
                     dec = ".",fill = TRUE, comment.char = "",
                     skip = 0)
```

Arguments

file	the name of the file to be read in.
removeEmptyCols	a logical value which indicates whether the empty column(s) should be removed or not.

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.
sep	the field separator character. Values on each line of the file are separated by this character. If sep = "" (the default for read.table) the separator is 'white space', that is one or more spaces, tabs, newlines or carriage returns.
quote	the set of quoting characters. To disable quoting altogether, use quote = "". See scan for the behaviour on quotes embedded in quotes. Quoting is only considered for columns read as character, which is all of them unless colClasses is specified.
dec	the character used in the file for decimal points.
fill	logical. If TRUE then in case the rows have unequal length, blank fields are implicitly added. See read.table.
comment.char	character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.
skip	integer: the number of lines of the data file to skip before beginning to read data.

Details

Allows the user to read in sample information data of a qPCR experiment from Light Cycler 480 which is in txt-file.

Value

Object of class "AnnotatedDataFrame".

Author(s)

Nor Izayu Abdul Rahman, Matthias Kohl <Matthias.Kohl@stamats.de>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

See Also

read.table

read.LC480 for reading in the qPCR data from Light Cycler and produce an object of Class "CyclesSet".

merge for merging the phenodata from read.LC480 and read.LC480SampleInfo and produce an object of Class "CyclesSet".

read.qPCR and read.taqman for reading in the RT-qPCR data.

AnnotatedDataFrame-class

Examples

```
path <- system.file("exData", package = "ReadqPCR")
LC480.SamInfo <- file.path(path, "LC480_Example_SampleInfo.txt")

# Read in the sample information data from file "LC480_Example_SampleInfo.txt".
samInfo <- read.LC480SampleInfo(LC480.SamInfo)
```

`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

`filename`	file name (must be formatted as shown in vignette).
`phenoData`	an `AnnotatedDataFrame` object, a `character` of length one, or a `data.frame`.
`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 Cq 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 <jimrperkins@gmail.com>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

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` *Read Taqman qPCR data and produce a qPCRBatch*

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 `AnnotatedDataFrame` object, a `character` of length one, or a `data.frame`.
`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 Cq 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 <jimrperkins@gmail.com>

References

Perkins, JR, Dawes, JM, McMahon, SB, Bennett, DL, Orengo, C, Kohl, M (2012). ReadqPCR and NormqPCR: R packages for the reading, quality checking and normalisation of RT-qPCR quantification cycle (Cq) data. *BMC Genomics*, **13**, 1:296.

See Also

ExpressionSet-class

Examples

```
path <- system.file("exData", package = "ReadqPCR")
# read 1 file
taqman.example <- file.path(path, "example.txt")
qPCRBatch.taq <- read.taqman(taqman.example)
# read 2 files
taqman.example.second.file <- file.path(path, "example2.txt")
qPCRBatch.taq.two.files <- read.taqman(taqman.example,
                           taqman.example.second.file)
```

Index

∗ **classes**
  CyclesSet-class, 3
  qpcR2CyclesSet, 6
  qPCRBatch-class, 7
  read.LC480, 8
  read.LC480SampleInfo, 10
  read.qPCR, 12
  read.taqman, 13
∗ **distribution**
  merge, 4
∗ **functional**
  merge, 4
∗ **methods**
  merge, 4
∗ **moment**
  merge, 4
∗ **package**
  ReadqPCR-package, 2
∗ **truncated moment**
  merge, 4

AnnotatedDataFrame, *12, 13*

checkValidqPCRFilename *(*read.qPCR*)*, 12
checkValidTaqmanFilenames *(*read.taqman*)*, 13
class:CyclesSet *(*CyclesSet-class*)*, 3
class:qPCRBatch *(*qPCRBatch-class*)*, 7
CyclesSet *(*CyclesSet-class*)*, 3
CyclesSet-class, 3

effs *(*qPCRBatch-class*)*, 7
effs,qPCRBatch-method *(*qPCRBatch-class*)*, 7
effs<- *(*qPCRBatch-class*)*, 7
effs<-,qPCRBatch-method *(*qPCRBatch-class*)*, 7
eSet, *3*, *5*, *8*, *10*
exprs,CyclesSet-method *(*CyclesSet-class*)*, 3
exprs,qPCRBatch-method *(*qPCRBatch-class*)*, 7
exprs.well.order *(*qPCRBatch-class*)*, 7
exprs.well.order,qPCRBatch-method *(*qPCRBatch-class*)*, 7
exprs.well.order<- *(*qPCRBatch-class*)*, 7
exprs.well.order<-,qPCRBatch-method *(*qPCRBatch-class*)*, 7
exprs<-,CyclesSet-method *(*CyclesSet-class*)*, 3
exprs<-,qPCRBatch-method *(*qPCRBatch-class*)*, 7

match, *5*
merge, 4, *5*, *10, 11*
merge,AnnotatedDataFrame,eSet-method *(*merge*)*, 4
merge,eSet,AnnotatedDataFrame-method *(*merge*)*, 4
merge-methods *(*merge*)*, 4

qpcR2CyclesSet, 6
qPCRBatch *(*qPCRBatch-class*)*, 7
qPCRBatch-class, 7
qSet *(*qPCRBatch-class*)*, 7

read.LC480, 8, *11*
read.LC480SampleInfo, 10, *10*
read.qPCR, *10, 11*, 12
read.table, *9–11*
read.taqman, *10, 11*, 13
read_qPCRBatch *(*read.qPCR*)*, 12
read_TaqBatch *(*read.taqman*)*, 13
ReadqPCR *(*ReadqPCR-package*)*, 2
ReadqPCR-package, 2
reps, *6*

scan, *9*, *11*
se.effs *(*qPCRBatch-class*)*, 7
se.effs,qPCRBatch-method *(*qPCRBatch-class*)*, 7

se.effs<- (qPCRBatch-class), 7
se.effs<-,qPCRBatch-method
        (qPCRBatch-class), 7
se.exprs,qPCRBatch-method
        (qPCRBatch-class), 7
se.exprs<-,qPCRBatch-method
        (qPCRBatch-class), 7