

Package ‘ReadqPCR’

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Title Read qPCR data

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

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Depends R(>= 2.10.0), Biobase, methods, affy

Imports Biobase

biocView DataImport, MicrotitrePlateAssay, GeneExpression, qPCR

License LGPL-3

LazyLoad yes

URL <http://qpcr.r-forge.r-project.org/>

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ReadqPCR-package	<i>Read qPCR data</i>
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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)

```

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```

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 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 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 Cq expression matrix.

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

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.

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

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 <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

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

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