Package 'qPCRtools'

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Version 0.1.1

Title Tools for qPCR

Description qPCR is a widely used method to detect the expression level of genes in biological research. A crucial step in processing qPCR data is to calculate the amplification efficiency of genes to determine which method should be used to calculate expression level of genes. This Package can do it easily.
In addition to that, this package can calculate the expression level of genes based on three methods.

URL https://github.com/lixiang117423/qPCRtools

BugReports https://github.com/lixiang117423/qPCRtools/issues

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Imports broom, data.table, dplyr, ggplot2, ggpmisc, ggthemes, magrittr, multcomp, readxl, reshape2, rstatix, sjmisc, stringr, tibble, tidyr, xlsx

RoxygenNote 7.2.0

NeedsCompilation no

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R topics documented:

CalCurve *Standard Curve Calculation.*

Description

The function can calculate the standard curve. At the same time, it can get the amplification efficiency of primer(s). Based on the amplification efficiency, we can know which method can be used to calculate the expression level.

Arguments

cq.table	The data frame of the position and Cq value.
concen.table	The data frame of the position and concentration.
highest.concen	The highest concentration for calculation.
lowest.concen	The lowest concentration for calculation.
dilution	Dilution factor of cDNA template. The default value is 4.
by.mean	Calculation by mean Cq value or not. The default value is TRUE.

Value

A list.

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Examples

```
df.1.path <- system.file("examples", "calsc.cq.txt", package = "qPCRtools")
df.2.path <- system.file("examples", "calsc.info.txt", package = "qPCRtools")
df.1 <- data.table::fread(df.1.path)
df.2 <- data.table::fread(df.2.path)
CalCurve(
  cq.table = df.1,
  concen.table = df.2,
  lowest.concen = 4,
  highest.concen = 4096,
  dilu = 4,
  by = "mean"
) -> p

p[["table"]]
p[["figure"]]
```

CalExp2ddCt *Calculate expression using standard curve.*

Description

Calculate expression using standard curve.

Arguments

cq.table	The data frame of the position and cq value.
design.table	The data frame of the position and corresponding information.
correction	Correct expression value by reference gene.
ref.gene	The name of reference gene.
ref.group	The name of reference group.
stat.method	Statistical method.
fig.type	Calculation by mean cq value or not.
fig.ncol	Number of columes of figure.

Value

A list contain a table and a figure.

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Examples

```
df1.path = system.file("examples", "ddct.cq.txt", package = "qPCRtools")
df2.path = system.file("examples", "ddct.design.txt", package = "qPCRtools")

cq.table = data.table::fread(df1.path)
design.table = data.table::fread(df2.path)

CalExp2ddCt(cq.table,
            design.table,
            ref.gene = "OsUBQ",
            ref.group = "CK",
            stat.method = "t.test",
            fig.type = "box",
            fig.ncol = NULL) -> res

res[["table"]]
res[["figure"]]
```

CalExpCurve *Calculate expression using standard curve.*

Description

Calculate expression using standard curve.

Arguments

cq.table	The data frame of the position and Cq value.
design.table	The data frame of the position and corresponding information.
correction	Correct expression value by reference gene.
ref.gene	The name of reference gene.
stat.method	Statistical method.
ref.group	The name of reference group.
fig.type	Calculation by mean Cq value or not.
fig.ncol	Number of columes of figure.

Value

A list contain a table and a figure.

Author(s)

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Examples

```
df1.path = system.file("examples", "cal.exp.curve.cq.txt", package = "qPCRtools")
df2.path = system.file("examples", "cal.expre.curve.sdc.txt", package = "qPCRtools")
df3.path = system.file("examples", "cal.exp.curve.design.txt", package = "qPCRtools")

cq.table = data.table::fread(df1.path)
curve.table = data.table::fread(df2.path)
design.table = data.table::fread(df3.path)

CalExpCurve(
  cq.table,
  curve.table,
  design.table,
  correction = TRUE,
  ref.gene = "OsUBQ",
  stat.method = "t.test",
  ref.group = "CK",
  fig.type = "box",
  fig.ncol = NULL) -> res

res[["table"]]
res[["figure"]]
```

`CalExpRqPCR` *Calculate expression using standard curve.*

Description

Calculate expression using standard curve.

Arguments

`cq.table`	The data frame of the position and cq value.
`design.table`	The data frame of the position and corresponding information.
`correction`	Correct expression value by reference gene.
`ref.gene`	The name of reference gene.
`ref.group`	The name of reference group.
`stat.method`	Statistical method.
`fig.type`	Calculation by mean cq value or not.
`fig.ncol`	Number of colums of figure.

Value

A list contain a table and a figure.

Author(s)

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Examples

```
df1.path <- system.file("examples", "cal.expre.rqpcr.cq.txt", package = "qPCRtools")
df2.path <- system.file("examples", "cal.expre.rqpcr.design.txt", package = "qPCRtools")

cq.table <- data.table::fread(df1.path, header = TRUE)
design.table <- data.table::fread(df2.path, header = TRUE)

CalExpRqPCR(cq.table,
            design.table,
            ref.gene = NULL,
            ref.group = "CK",
            stat.method = "t.test",
            fig.type = "box",
            fig.ncol = NULL
            ) -> res

res[["table"]]
res[["figure"]]
```

CalRTable *Calculate RNA volume for reverse transcription.*

Description

The first step of qPCR is usually the preparation of cDNA. We need to calculate the column of RNA for reverse transcription to cDNA. So, if we have the concentration of RNA, we can use the function 'CalRTable' to do that.

Arguments

data	A data.frame contained the sample names and the concentration value. The default unit of concentration is ng/uL.
template	A data.frame contained the information of reverse transcription.
RNA.weight	RNA weight required for reverse transcription. Default is 1 ug.

Value

A list contain a table and a figure.

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Examples

```
df.1.path <- system.file("examples", "crtv.data.txt", package = "qPCRtools")
df.2.path <- system.file("examples", "crtv.template.txt", package = "qPCRtools")
df.1 <- data.table::fread(df.1.path)
df.2 <- data.table::fread(df.2.path)
result <- CalRTable(data = df.1, template = df.2, RNA.weight = 2)
head(result)
```

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