Package 'qPCRtools'

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Version 0.1.1

Title Tools for qPCR

Description A set of tools for qPCR data process.

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

Standard Curve Calculation.

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.
`lowest.concen`	The lowest concentration.
`dilution`	Dilution factor of cDNA template.
`by.mean`	Calculation by mean Cq value or not.

Value

A list.

Author(s)

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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 colomes of 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.

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 columes of 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 volume.
```

Description

Calculate RNA and other reagent volume required for reverse transcription.

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 data frame.

Author(s)

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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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