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 columes of figure.

Author(s)

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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"]]
```

`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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