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, 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"]]
```

`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 colums 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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