

# Package ‘qPCRhelper’

February 23, 2023

**Type** Package

**Title** qPCR Ct Values to Expression Values

**Version** 0.1.0

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## Description

Computes normalized cycle threshold (Ct) values (delta Ct) from raw quantitative polymerase chain reaction (qPCR) Ct values and conducts test of significance using `t.test()`. Plots expression values based from  $\log_2(2^{-(1 \cdot \Delta \Delta Ct)})$  across groups per gene of interest. Methods for calculation of delta delta Ct and relative expression ( $2^{-(1 \cdot \Delta \Delta Ct)}$ ) values are described in: Livak & Schmittgen, (2001) <[doi:10.1006/meth.2001.1262](https://doi.org/10.1006/meth.2001.1262)>.

**License** GPL-3

**Encoding** UTF-8

**Imports** dplyr (>= 1.0.0), rstatix (>= 0.7.2), ggpubr (>= 0.5.0), ggplot2 (>= 3.4.0), magrittr (>= 2.0.3)

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2023-02-23 14:00:08 UTC

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**Description**

Computes normalized Ct values (delta Ct) from raw qPCR Ct values and conducts test of significance using t.test. Plots expression values based from  $\log_2(2^{-1 \cdot \text{delta Ct}})$  across groups per gene of interest.

**Usage**

```
qPCRhelper(data.dir = NULL, ref.gene = NULL, ref.group = NULL,  
plot.ref.group = NULL, plot.nrow = 1,  
plot.title = NULL)
```

**Arguments**

data.dir	file path.
ref.gene	string: value should be one of column names in input table. Used for delta Ct computation.
ref.group	string: value should be one of 'Group' values in input table. Used for delta delta Ct computation.
plot.ref.group	string: value should be one of 'Group' values in input table. Used to set reference in plotting.
plot.nrow	numeric: optional. Number of rows for plotting n number of plots corresponding to n number of genes.
plot.title	plot title: optional.

**Value**

A dataframe with columns for normalized Ct values (dCt), and gene expression (log2RelExp).

**Note**

If gene names start with a number, e.g. 18S, please precede the gene name with 'X' without space, e.g.:18S -> X18S

**Author(s)**

Wilson Jr. Aala

**Examples**

```
## Create sample table with expected 'Sample', 'Group', and gene Ct columns
Sample <- c("C1", "C2", "T1", "T2") #required column
Group <- c("C", "C", "T", "T") #required column
# Gene Ct values, at least two columns: one reporter, one target gene
GAPDH <- c(18.1,18.2,18.1,18.2) #reporter, ref.gene
IL4 <- c(30.1,30.5,20.1,20.2) #target
a <- data.frame(Sample,Group,GAPDH,IL4) #export using write.table(a,...)

## Write the data frame to a file in a temporary directory
temp_file <- file.path(tempdir(), "a.txt")
write.table(a, file = temp_file, sep = "\t")

## Run qPCRhelper directly on the file
library(qPCRhelper)
b <- qPCRhelper(data.dir=temp_file,
                ref.gene="GAPDH",
                ref.group="C",
                plot.ref.group="C",
                plot.nrow=1,
                plot.title="My cool qPCR data")
```

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