Package ‘miRcomp’

April 11, 2024

Version 1.32.0
Date 2017-03-04
Title Tools to assess and compare miRNA expression estimation methods
Description Based on a large miRNA dilution study, this package provides tools to read in the raw amplification data and use these data to assess the performance of methods that estimate expression from the amplification curves.
Author Matthew N. McCall <mccallm@gmail.com>, Lauren Kemperm-an <lkemperm@u.rochester.edu>
Maintainer Matthew N. McCall <mccallm@gmail.com>
Depends R (>= 3.2), Biobase (>= 2.22.0), miRcompData
Imports utils, methods, graphics, KernSmooth, stats
VignetteBuilder knitr
Suggests BiocStyle, knitr, rmarkdown, RUnit, BiocGenerics, shiny
License GPL-3 | file LICENSE
biocViews Software, qPCR, Preprocessing, QualityControl
NeedsCompilation no
git_url https://git.bioconductor.org/packages/miRcomp
git_branch RELEASE_3_18
git_last_commit a13561f
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-04-10

R topics documented:

accuracy ................................................................. 2
completeFeatures ...................................................... 3
expressionComp ....................................................... 4
### Accuracy

Assess the accuracy of the expression estimates

#### Description

This function assesses the signal detect slope (a measure of accuracy) for each feature.

#### Usage

```r
accuracy(object1, qcThreshold1, object2=NULL, qcThreshold2=NULL,
commonFeatures=TRUE, bins=3, label1=NULL, label2=NULL)
```

#### Arguments

- **object1**: a list containing two elements: `ct` (the expression estimates) and `qc` (quality scores).
- **qcThreshold1**: a numeric threshold corresponding to `object1$qc` below which values are considered low quality.
- **object2**: an optional second list of the same format as object1, used to compare two methods.
- **qcThreshold2**: a numeric threshold corresponding to `object2$qc` below which values are considered low quality.
- **commonFeatures**: if TRUE and `object2` is non-NULL, only high quality non-NA features in common between both objects are used.
- **bins**: the number of bins to divide the data into.
- **label1**: optional label corresponding to object 1 to be used in plotting.
- **label2**: optional label corresponding to object 2 to be used in plotting.

#### Value

A plot of signal detect slopes stratified by difference in pure sample expression is produced, and a summary (median and MAD) of the signal detect slopes in each bin is returned.
completeFeatures

Author(s)
Matthew N. McCall

Examples

data(lifetech)
accuracy(object1=lifetech,qcThreshold1=1.25)
data(qpcRdefault)
accuracy(object1=lifetech,qcThreshold1=1.25,
    object2=qpcRdefault,qcThreshold2=0.99)

Determine the Number of Completely Observed Features

Description
This function determines the number of features that are good quality and non-NA across all samples using a given quality threshold.

Usage

completeFeatures(object1, qcThreshold1, object2=NULL, qcThreshold2=NULL,
    label1=NULL, label2=NULL)

Arguments

object1 a list containing two elements: ct (the expression estimates) and qc (quality scores)
qcThreshold1 a numeric threshold corresponding to object1$qc below which values are considered low quality.
object2 an optional second list of the same format as object1, used to compare two methods.
qcThreshold2 a numeric threshold corresponding to object2$qc below which values are considered low quality.
label1 optional label corresponding to object 1 to be used in plotting.
label2 optional label corresponding to object 2 to be used in plotting.

Value
The function generates a table of the number of complete, partial, and absent features.

Author(s)
Matthew N. McCall
expressionComp

Examples

```r
data(lifetech)
completeFeatures(object1=lifetech,qcThreshold1=1.25)
data(qpcRdefault)
completeFeatures(object1=lifetech,qcThreshold1=1.25,
    object2=qpcRdefault,qcThreshold2=0.99)
```

expressionComp | Compare expression estimates between two methods

Description

This function allows one to easily compare the expression estimates generated by two different algorithms. Feature / sample combinations that differ above a given threshold can be easily highlighted.

Usage

```r
expressionComp(object1, qcThreshold1,
    object2, qcThreshold2,
    label1=NULL, label2=NULL,
    diffThreshold=2,
    plotType=c("scatterplot","MAplot"))
```

Arguments

- `object1`: a list containing two elements: ct (the expression estimates) and qc (quality scores)
- `qcThreshold1`: a numeric threshold corresponding to object1$qc below which values are considered low quality.
- `object2`: a list containing two elements: ct (the expression estimates) and qc (quality scores)
- `qcThreshold2`: a numeric threshold corresponding to object2$qc below which values are considered low quality.
- `label1`: an optional label for plotting on the x-axis
- `label2`: an optional label for plotting on the y-axis
- `diffThreshold`: feature / sample combinations for which the expression estimates differ by more than this value are returned by the function and highlighted in the plot.
- `plotType`: scatterplot or MA-plot

Value

This function plots the expression estimates produced by two different methods. Feature / sample combinations for which the expression estimates differ by more than `diffThreshold` are returned by the function and highlighted in the plot.
Author(s)
Matthew N. McCall

Examples
data(lifetech)
data(qpcRdefault)
tmp <- expressionComp(object1=lifetech, qcThreshold1=1.25, object2=qpcRdefault, qcThreshold2=0.99, plotType="scatter")

lifetech

The processed data generated using the LifeTech software.

Description
These data are also used to demonstrate the functionality of the miRcomp package.

Usage
data(lifetech)

Format
A list with two elements.

ct a miRNA x sample matrix of expression estimates
qc a miRNA x sample matrix of quality scores (here AmpScores)

Examples
data(lifetech)

limitOfDetection

Assess the limit of detection of a given method

Description
This function assesses the limit of detection in one of two ways: (1) the distribution of expression estimates stratified by the proportion of poor quality values within replicates, (2) the average vs expected expression for the two most diluted sample types.

Usage
limitOfDetection(object, qcThreshold, plotType=c("boxplot","scatterplot","MAplot"))
Arguments

object: a list containing two elements: ct (the expression estimates) and qc (quality scores)
qcThreshold: a numeric threshold corresponding to object$qc below which values are considered low quality.
plotType: the desired output type – boxplot is option (1); scatterplot is option (2), an MA-plot is option (3).

Value

This function assesses the limit of detection in several ways. If plotType is boxplot, then boxplots of expression estimates stratified by the proportion of poor quality values within replicates is displayed. If plotType is scatterplot, then the average within replicate expression vs expected expression (based on pure sample expression) is displayed for the 0.1/0.1 dilution and 0.01/0.01 dilution. If plotType is MAplot, then the difference in expression (average within replicate expression - expected expression) is displayed for the 0.1/0.1 dilution and 0.01/0.01 dilution. For both plotTypes, scatterplot and MAplot, the function outputs a matrix containing estimates of the limit of detection for four different tolerances. Specifically, the two columns correspond to the two dilutions (0.1/0.1 and 0.01/0.01) and rows correspond to the median difference between the observed and expected values. The values in the matrix are the expected expression values such that the median absolute difference of all larger expected expression values is approximately equal to the given tolerance.

Author(s)

Matthew N. McCall

Examples

data(lifetech)
tmp <- limitOfDetection(object=lifetech,qcThreshold=1.25)
data(qpcRdefault)
limitOfDetection(object=qpcRdefault,qcThreshold=0.99,plotType="scatter")

miRcompShinyApp

Launch a Shiny app to use the miRcomp package interactively

Description

This function launches the miRcomp Shiny app locally.

Usage

miRcompShinyApp()

Author(s)

Matthew N. McCall and Lauren Kemperman
**precision**

**Examples**

```r
## miRcompShinyApp()
```

### Assess the precision of the expression estimates

**Description**

This function assesses the within-replicate precision for each feature.

**Usage**

```r
precision(object1, qcThreshold1, object2=NULL, qcThreshold2=NULL,
commonFeatures=TRUE, statistic=c("sd","cv"),
scale=c("none","log","log10"), bins=3,
label1=NULL, label2=NULL)
```

**Arguments**

- `object1`: a list containing two elements: ct (the expression estimates) and qc (quality scores)
- `qcThreshold1`: a numeric threshold corresponding to object1$qc below which values are considered low quality.
- `object2`: an optional second list of the same format as object1, used to compare two methods.
- `qcThreshold2`: a numeric threshold corresponding to object2$qc below which values are considered low quality.
- `commonFeatures`: if TRUE and object2 is non-NULL, only high quality non-NA features in common between both objects are used.
- `statistic`: whether to compute the standard deviation (sd) or coefficient of variation (cv).
- `scale`: optional scaling of the values. This can help with visualizing the distributions.
- `bins`: the number of bins to divide the data into.
- `label1`: optional label corresponding to object 1 to be used in plotting.
- `label2`: optional label corresponding to object 2 to be used in plotting.

**Value**

A boxplot of either the standard deviation or coefficient of variation stratified by expression is produced. The values plotted in each box of the boxplot are returned.

**Author(s)**

Matthew N. McCall
**Examples**

```r
data(lifetech)
tmp1 <- precision(object1=lifetech, qcThreshold1=1.25)
data(qpcRdefault)
tmp2 <- precision(object1=lifetech, qcThreshold1=1.25,
                   object2=qpcRdefault, qcThreshold2=0.99)
```

---

**qpcRb4**

*The processed data generated using the 4 parameter sigmoidal method from the qpcR software.*

---

**Description**

These data are also used to demonstrate the functionality of the miRcomp package.

**Usage**

```r
data(qpcRb4)
```

**Format**

A list with two elements.

- ct  a miRNA x sample matrix of expression estimates
- qc  a miRNA x sample matrix of quality scores (here R-squared values)

**Examples**

```r
data(qpcRb4)
```

---

**qpcRb5**

*The processed data generated using the 5 parameter sigmoidal method from the qpcR software.*

---

**Description**

These data are also used to demonstrate the functionality of the miRcomp package.

**Usage**

```r
data(qpcRb5)
```
Format

A list with two elements.

\[ \text{ct} \quad \text{a miRNA x sample matrix of expression estimates} \]

\[ \text{qc} \quad \text{a miRNA x sample matrix of quality scores (here R-squared values)} \]

Examples

data(qpcRb5)

qpcRdefault

The processed data generated using the default method (4 parameter log-logistic) implemented in the qpcR software package.

Description

These data are also used to demonstrate the functionality of the miRcomp package.

Usage

data(qpcRdefault)

Format

A list with two elements.

\[ \text{ct} \quad \text{a miRNA x sample matrix of expression estimates} \]

\[ \text{qc} \quad \text{a miRNA x sample matrix of quality scores (here R-squared values)} \]

Examples

data(qpcRdefault)

qpcRl5

The processed data generated using the 5 parameter log-logistic method from the qpcR software.

Description

These data are also used to demonstrate the functionality of the miRcomp package.

Usage

data(qpcRl5)
qualityAssessment

Format
A list with two elements.

ct a miRNA x sample matrix of expression estimates
qc a miRNA x sample matrix of quality scores (here R-squared values)

Examples

data(qpcR15)

qpcRlinexp  The processed data generated using the linear-exponential method implemented in the qpcR software package.

Description
These data are also used to demonstrate the functionality of the miRcomp package.

Usage
data(qpcRlinexp)

Format
A list with two elements.

ct a miRNA x sample matrix of expression estimates
qc a miRNA x sample matrix of quality scores (here R-squared values)

Examples

data(qpcRlinexp)

qualityAssessment  Quality Assessment for MicroRNA Expression Estimates

Description
This function produces several figures to examine quality scores.

Usage

qualityAssessment(object1, object2=NULL, cloglog1=FALSE, cloglog2=FALSE, na.rm=FALSE, plotType=c("scatterplot","boxplot"), label1=NULL, label2=NULL)
Arguments

object1  a list containing two elements: ct (the expression estimates) and qc (quality scores)
object2  an optional second list of the same format as object1, used to compare two methods.
cloglog1 if TRUE, the -log(-log(object1$qqc)) is plotted. This is useful to visualize certain quality scores such as R-squared.
cloglog2 if TRUE, the -log(-log(object2$qqc)) is plotted. This is useful to visualize certain quality scores such as R-squared.
na.rm  if TRUE, quality scores corresponding to NA expression estimates are removed from analysis. This is only used if plotType=="boxplot".
plotType  type of plot to return. Options are a scatterplot or a boxplot.
label1  optional label corresponding to object 1 to be used in plotting.
label2  optional label corresponding to object 2 to be used in plotting.

Value

The function generates a plot of the desired type.

Author(s)

Matthew N. McCall

Examples

data(lifetech)
qualityAssessment(lifetech, plotType="boxplot")

data(qpcRdefault)
qualityAssessment(object1=lifetech,object2=qpcRdefault,cloglog2=TRUE)

Description

This function determines

Usage

titrationResponse(object1, qcThreshold1, object2=NULL, qcThreshold2=NULL,
  commonFeatures=TRUE, label1=NULL, label2=NULL)
Arguments

object1 a list containing two elements: ct (the expression estimates) and qc (quality scores)

qcThreshold1 a numeric threshold corresponding to object1$qc below which values are considered low quality.

object2 an optional second list of the same format as object1, used to compare two methods.

qcThreshold2 a numeric threshold corresponding to object2$qc below which values are considered low quality.

commonFeatures if TRUE and object2 is non-NULL, only high quality non-NA features in common between both objects are used.

label1 optional label corresponding to object 1 to be used in plotting.

label2 optional label corresponding to object 2 to be used in plotting.

Value

A table listing the number of features showing a monotone titration response and a figure showing the proportion of features showing a monotone titration response vs the difference in pure sample expression.

Author(s)

Matthew N. McCall

Examples

data(lifetech)
titrationResponse(object1=lifetech,qcThreshold1=1.25)
data(qpcRdefault)
titrationResponse(object1=lifetech,qcThreshold1=1.25,object2=qpcRdefault,qcThreshold2=0.99)
Index

* datasets
  lifetech, 5
  qpcRb4, 8
  qpcRb5, 8
  qpcRdefault, 9
  qpcRl5, 9
  qpcRlinexp, 10

* manip
  accuracy, 2
  completeFeatures, 3
  expressionComp, 4
  limitOfDetection, 5
  miRcompShinyApp, 6
  precision, 7
  qualityAssessment, 10
  titrationResponse, 11

accuracy, 2
completeFeatures, 3
expressionComp, 4
lifetech, 5
limitOfDetection, 5
miRcompShinyApp, 6
precision, 7
qpcRb4, 8
qpcRb5, 8
qpcRdefault, 9
qpcRl5, 9
qpcRlinexp, 10
qualityAssessment, 10
titrationResponse, 11