Package ‘miRcomp’

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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.

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Depends R (>= 3.2), Biobase (>= 2.22.0), miRcompData
Imports utils, methods, graphics, KernSmooth, stats
VignetteBuilder knitr
Suggests BiocStyle, knitr, rmarkdown, RUnit, BiocGenerics, shiny
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Assess the accuracy of the expression estimates

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 `object1` to be used in plotting.
- `label2`: optional label corresponding to `object2` 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**

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

**completeFeatures**  
*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**

```r
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)
```

**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.

c t  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"))
miRcompShinyApp

Launch a Shiny app to use the miRcomp package interactively

miRcompShinyApp

Description

This function launches the miRcomp Shiny app locally.

Usage

miRcompShinyApp()

Author(s)

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

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

**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 `object1` to be used in plotting.
- `label2`: optional label corresponding to `object2` 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

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

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

data(qpcRb5)
**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(qpcRdefault)

---

**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.

- ct  a miRNA x sample matrix of expression estimates
- qc  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**

```r
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**

```r
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**

```r
data(qpcRlinexp)
```

```
qualityAssessment  Quality Assessment for MicroRNA Expression Estimates
```

**Description**

This function produces several figures to examine quality scores.

**Usage**

```r
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 $-\log(-\log(object1\$qc))$ is plotted. This is useful to visualize certain quality scores such as R-squared.
- **cloglog2**: if `TRUE`, the $-\log(-\log(object2\$qc))$ 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 `object1` to be used in plotting.
- **label2**: optional label corresponding to `object2` to be used in plotting.

**Value**

The function generates a plot of the desired type.

**Author(s)**

Matthew N. McCall

**Examples**

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

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

---

**titrationResponse**  
**Assess monotone signal across titration**

**Description**

This function determines

**Usage**

```r
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)
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