Package 'ctrlGene'

October 12, 2022

Title Assess the Stability of Candidate Housekeeping Genes

Version 1.0.1

Description A simple way to assess the stability of candidate housekeeping genes is implemented in this package.

Depends R (>= 3.2.3)

Imports psych,stats,graphics

License GPL (>= 2)

LazyData true

RoxygenNote 6.1.1

URL <http://www.bioinf.com.cn/>

NeedsCompilation no

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Repository CRAN

Date/Publication 2019-07-04 09:40:28 UTC

R topics documented:

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bestKeeper   *Determines stability of genes*

Description

This function combines the results of cpSta(), pearsonCor() and bki().

Usage

```
bestKeeper(expression, ctVal = TRUE)
```

Arguments

expression   a matrix of expression levels. Each row corresponds to a sample and each col-
               umn to a gene.

ctVal   a logical value indicating data type. If ct-values are input, ctVal=TRUE, other-
               wise, ctVal=FALSE.

Value

A list containing CP.statistics, pair.Wise.cor and HKG.vs.BestKeeper, which are returned by cp-
Sta(), pearsonCor() and bki(), respectively.

References

Pfaffl MW, Tichopad A, Prgomet C, Neuvians TP. Biotechnol Lett (2004) <doi: 10.1023/B:BILE.0000019559.84305.47>

Examples

```
FIBct
bestKeeper(FIBct)
```

---

bki   *Analyzes genes versus BestKeeper index*

Description

All genes are combined into an index. Then, correlation between each genes and the index is
calculated, describing the relation between the index and the contributing gene by the Pearson
correlation coefficient (r), coefficient of determination (r2) and the p-value.

Usage

```
bki(expression, ctVal = TRUE)
```

Arguments

expression a matrix of expression levels. Each row corresponds to a sample and each column to a gene.

ctVal a logical value indicating data type. If ct-values are input, ctVal=TRUE, otherwise, ctVal=FALSE.

Value

A matrix of the Pearson correlation coefficient (r), coefficient of determination (r2) and the p-value.

References

Pfaffl MW, Tichopad A, Prgomet C, Neuvians TP. Biotechnol Lett (2004) <doi: 10.1023/B:BILE.0000019559.84305.47>

Examples

```
FIBct
bki(FIBct)
```

---

cpSta   *Calculates descriptive statistics*

Description

This function calculates descriptive statistics of genes.

Usage

```
cpSta(expression, ctVal = TRUE)
```

Arguments

expression a matrix of expression levels. Each row corresponds to a sample and each column to a gene.

ctVal a logical value indicating data type. If ct-values are input, ctVal=TRUE, otherwise, ctVal=FALSE.

Value

A matrix of descriptive statistics:

N: number of samples;

GM[CP]: the geometric mean of CP;

AM[CP]: the arithmetic mean of CP;

Min[CP] and Max [CP]: the extreme values of CP;

SD[+/- CP]: the standard deviation of the CP;

CV[CP]: the coefficient of variance expressed as a percentage on the CP level;

Min[x-fold] and Max [x-fold]: the extreme values of expression levels expressed as an absolute x-fold over- or under-regulation coefficient;

SD[+/- x-fold]: standard deviation of the absolute regulation coefficients.

References

Pfaffl MW, Tichopad A, Prgomet C, Neuvians TP. Biotechnol Lett (2004) <doi: 10.1023/B:BILE.0000019559.84305.47>

Examples

```
FIBct
cpSta(FIBct)
```

FIB   *Reload Saved Datasets*

Description

The normalized expression level of the ten housekeeping genes in fibroblast cells

Details

The normalized expression level of the ten housekeeping genes in fibroblast cells

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi: 10.1186/gb-2002-3-7-research0034>.

FIBct   *Reload Saved Datasets*

Description

The CT values of the ten housekeeping genes in fibroblast cells

Details

The CT values of the ten housekeeping genes in fibroblast cells

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi: 10.1186/gb-2002-3-7-research0034>.

geNorm	*Ranks genes*

Description

Uses the geNorm algorithm to determine the most stably expressed genes.

Usage

```
geNorm(expression, genes = data.frame(Genes = character(0), Avg.M =
  numeric(0)), ctVal = TRUE)
```

Arguments

expression   a matrix of expression levels. Each row corresponds to a sample and each column to a gene.

genes   a data frame to output the result of the function

ctVal   a logical value indicating data type. If ct-values are input, ctVal=TRUE, otherwise, ctVal=FALSE.

Value

A sorted dataframe with two columns, 'Genes' and 'Avg.M'. The last two genes are the two most stable control genes.

Avg.M is average expression stability values (M) of remaining control genes during stepwise exclusion of the least stable control gene.

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi: 10.1186/gb-2002-3-7-research0034>.

Examples

```
FIB
geNorm(FIB,ctVal=FALSE)
FIBct
geNorm(FIBct)
```

---

geNorm2   *Ranks genes*

Description

Uses the geNorm algorithm to determine the most stably expressed genes.

Usage

```
geNorm2(expression, genes = data.frame(Genes = character(0), Avg.M =
  numeric(0)), ctVal = TRUE)
```

Arguments

expression   a matrix of expression levels. Each row corresponds to a sample and each col-
               umn to a gene.

genes   a data frame to output the result of the function

ctVal   a logical value indicating data type. If ct-values are input, ctVal=TRUE, other-
               wise, ctVal=FALSE.

Value

A sorted dataframe with two columns, 'Genes' and 'Avg.M'. The last two genes are the two most
stable control genes.

Avg.M is average expression stability values (M) of remaining control genes during stepwise ex-
clusion of the least stable control gene.

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi:
10.1186/gb-2002-3-7-research0034>.

Examples

```
FIB
geNorm2(FIB,ctVal=FALSE)
FIBct
geNorm2(FIBct)
```

---

measureM   *Calculates measure M*

Description

This function calculates measure M according to algorithm of geNorm

Usage

```
measureM(expression, ctVal = TRUE)
```

Arguments

expression   a matrix of expression levels. Each row corresponds to a sample and each col-
                umn to a gene.

ctVal   a logical value indicating data type. If ct-values are input, ctVal=TRUE, other-
                wise, ctVal=FALSE.

Value

A sorted dataframe with two columns, 'Genes' and 'M' (the relative stability; lower means more
stable).

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi:
10.1186/gb-2002-3-7-research0034>.

Examples

```
FIB
measureM(FIB,ctVal=FALSE)
FIBct
measureM(FIBct)
```

---

pairwiseV   *Calculates V(n+1/n) values*

Description

Useful for establishing the quality of your normalization regime. See Vandesompele 2002 for advice
on interpretation.

Usage

```
pairwiseV(expression, ctVal = TRUE)
```

Arguments

expression	a matrix of expression levels. Each row corresponds to a sample and each column to a gene.
ctVal	a logical value indicating data type. If ct-values are input, ctVal=TRUE, otherwise, ctVal=FALSE.

Value

A Series of values [V2/3, V3/V4, V4/V5, ...].

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi: 10.1186/gb-2002-3-7-research0034>.

Examples

```
FIB
pairwiseV(FIB,ctVal=FALSE)
FIBct
pairwiseV(FIBct)
```

---

pearsonCor	*Analyzes pair-wise correlation*

Description

This function performs numerous pair-wise correlation analyses of genes. Within each such correlation the Pearson correlation coefficient (r) and the probability p value are calculated.

Usage

```
pearsonCor(expression, ctVal = TRUE)
```

Arguments

expression	a matrix of expression levels. Each row corresponds to a sample and each column to a gene.
ctVal	a logical value indicating data type. If ct-values are input, ctVal=TRUE, otherwise, ctVal=FALSE.

Value

A matrix of the Pearson correlation coefficient (r) and the probability p value.

References

Pfaffl MW, Tichopad A, Prgomet C, Neuvians TP. Biotechnol Lett (2004) <doi: 10.1023/B:BILE.0000019559.84305.47>

Examples

```
FIBct
pearsonCor(FIBct)
```

---

plotM	*Plots average M of remaining genes*

Description

This function plots the average expression stability values of remaining control genes.

Usage

```
plotM(Mrem)
```

Arguments

Mrem   the result returned by function of geNorm()

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi: 10.1186/gb-2002-3-7-research0034>.

Examples

```
FIB
x=geNorm(FIB,ctVal=FALSE)
plotM(x)

FIBct
y=geNorm(FIBct)
plotM(y)
```

---

plotV	*Plots V(n+1/n) values*

Description

This function plots the average expression stability values of remaining control genes.

Usage

```
plotV(Vs)
```

Arguments

Vs   the result returned by function of pairwiseV()

References

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F (2002) <doi: 10.1186/gb-2002-3-7-research0034>.

Examples

```
FIB
Vs1=pairwiseV(FIB,ctVal=F)
plotV(Vs1)

FIBct
Vs2=pairwiseV(FIBct)
plotV(Vs2)
```

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