SLqPCR
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SLqPCR-package

Functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH

Description

Functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH

Details

Package: SLqPCR
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Depends: R(>= 2.4.0), stats, RColorBrewer
License: GPL (version 2 or later)

require(SLqPCR)

Author(s)

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References


SLqPCRdata

SIRS-Lab inhouse qPCR data
geneStabM

Description
This data is part of a SIRS-Lab inhouse real-time quantitative PCR experiment.

Usage
data(SLqPCRdata)

Format
A data frame with 16 observations on the following 4 variables.

Gene1  a numeric vector, average take-off values of gene 1
Gene2  a numeric vector, average take-off values of gene 2
HK1    a numeric vector, average take-off values of housekeeper 1
HK2    a numeric vector, average take-off values of housekeeper 2

Details
The row names of this data set indicate the probes which were investigated. The take-off values are mean values of three replicates.

Source
www.sirs-lab.com

References
www.sirs-lab.com

Examples
data(SLqPCRdata)
SLqPCRdata

geneStabM  Gene expression stability value M

Description
Computation of the gene expression stability value M for real-time quantitativ RT-PCR data. For more details we refer to Vandesompele et al. (2002).

Usage
geneStabM(relData, na.rm = FALSE)

Arguments
relData  matrix or data.frame containing real-time quantitative RT-PCR data
na.rm   a logical value indicating whether NA values should be stripped before the computation proceeds.
The gene expression stability value $M$ is defined as the average pairwise normalization factor; i.e., one needs to specify data from at least two genes. For more details see Vandesompele et al. (2002).

**Value**

numeric vector with gene expression stability values

**Author(s)**

Dr. Matthias Kohl (SIRS-Lab GmbH) (kohl@sirs-lab.com)

**References**


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**geomMean**

**Geometric Mean**

**Description**

Computation of the geometric mean.

**Usage**

```r
geomMean(x, na.rm = FALSE)
```

**Arguments**

- `x` numeric vector of non-negative Reals
- `na.rm` a logical value indicating whether NA values should be stripped before the computation proceeds.

**Details**

The computation of the geometric mean is done via $\prod(x)^{1/\text{length}(x)}$.

**Value**

geometric mean

**Author(s)**

Dr. Matthias Kohl (SIRS-Lab GmbH) (kohl@sirs-lab.com)
**normPCR**

*Normalization of real-time quantitative RT-PCR data*

**Description**

This function can be used to normalize real-time quantitative RT-PCR data.

**Usage**

```r
normPCR(relData, HKs, method = "Vandesompele", na.rm = FALSE)
```

**Arguments**

- `relData`: matrix or data.frame containing relative quantities (genes in columns)
- `HKs`: integer, column numbers of housekeeping genes
- `method`: method for the computation
- `na.rm`: a logical value indicating whether NA values should be stripped before the computation proceeds.

**Details**

This function can be used to normalize real-time quantitative RT-PCR data. The default method "Vandesompele" was proposed by Vandesompele et al. (2002). Currently, only the method by Vandesompele et al. (2002) is implemented.

**Value**

Normalized expression data

**Author(s)**

Dr. Matthias Kohl (SIRS-Lab GmbH) (kohl@sirs-lab.com)

**References**


**Examples**

```r
data(SLqPCRdata)
relData <- apply(SLqPCRdata, 2, relQuantPCR)
geneStabM(relData[, c(3, 4)])
exprData <- normPCR(SLqPCRdata, c(3, 4))
```
**relQuantPCR**

*Compute relative expression values for realtime quantitative RT-PCR data*

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**Description**

Compute relative expression values for realtime quantitative RT-PCR data based on Ct or take-off values, respectively. The computations use the PCR efficiency.

**Usage**

```r
relQuantPCR(x, E = 2, na.rm = FALSE)
```

**Arguments**

- `x`: numeric vector containing raw data
- `E`: PCR efficiency
- `na.rm`: a logical value indicating whether NA values should be stripped before the computation proceeds.

**Value**

vector of relative expression values w.r.t. specified PCR efficiency.

**Author(s)**

Dr. Matthias Kohl (SIRS-Lab GmbH) ⟨kohl@sirs-lab.com⟩

**References**


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**selectHKgenes**

*Selection of reference/housekeeping genes*

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**Description**

This function can be used to determine a set of reference/housekeeping (HK) genes for gene expression experiments.

**Usage**

```r
selectHKgenes(relData, method = "Vandesompele", minNrHK = 2, geneSymbol, trace = TRUE, na.rm = FALSE)
```
selectHKgenes

Arguments

relData matrix or data.frame containing relative expression values
method method to compute most stable genes
minNrHK minimum number of HK genes that should be considered
geneSymbol gene symbols
trace logical, print additional information
na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.

Details

This function can be used to determine a set of reference/housekeeping (HK) genes for gene expression experiments. The default method "Vandesompele" was proposed by Vandesompele et al. (2002).

Currently, only the method by Vandesompele et al. (2002) is implemented.

Vandesompele et al. (2002) propose a cut-off value of 0.15 for the pairwise variation. Below this value the inclusion of an additional housekeeping gene is not required.

Value

If method = "Vandesompele" a list with the following components is returned

ranking ranking of genes from best to worst where the two most stable genes cannot be ranked
variation pairwise variation during stepwise selection
meanM average expression stability M

Author(s)

Dr. Matthias Kohl (SIRS-Lab GmbH) (kohl@sirs-lab.com)

References


Examples

data(vandesompele)
res.BM <- selectHKgenes(vandesompele[1:9,], method = "Vandesompele", geneSymbol = names(vandesompele))
**vandesompele**

**Data set of Vandesompele et al (2002)**

**Description**

This data set was used in Vandesompele et al (2002) to demonstrate normalization of real-time quantitative RT-PCR data by geometric averaging of housekeeping genes.

**Usage**

```r
data(vandesompele)
```

**Format**

A data frame with 85 observations on the following 10 variables which stand for expression data of ten commonly used housekeeping genes

- **ACTB**: actin, beta
- **B2M**: beta-2-microglobulin
- **GAPD**: glyceraldehyde-3-phosphate dehydrogenase
- **HMBS**: hydroxymethylbilane synthase
- **HPRT1**: hypoxanthine phosphoribosyltransferase 1
- **RPL13A**: ribosomal protein L13a
- **SDHA**: succinate dehydrogenase complex subunit A
- **TBP**: TATA box binding protein
- **UBC**: ubiquitin C
- **YWHAZ**: tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide

**Details**

The row names of this data set indicate the various human tissues which were investigated.

- **BM**: 9 normal bone-marrow samples
- **POOL**: 9 normal human tissues from pooled organs (heart, brain, fetal brain, lung, trachea, kidney, mammary gland, small intestine and uterus)
- **FIB**: 20 short-term cultured normal fibroblast samples from different individuals
- **LEU**: 13 normal leukocyte samples
- **NB**: 34 neuroblastoma cell lines (independently prepared in different labs from different patients)

**Source**

The data set was obtained from [http://genomebiology.com/content/supplementary/gb-2002-3-7-research0034-s1.txt](http://genomebiology.com/content/supplementary/gb-2002-3-7-research0034-s1.txt)
References


Examples

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