Package ‘SLqPCR’

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Description Functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH
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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
- Type: Package
- Version: 1.0.0
- Date: 2007-01-02
- Depends: R(>= 2.4.0), stats, RColorBrewer
- License: GPL (version 2 or later)

require(SLqPCR)

Author(s)

- Dr. Matthias Kohl (SIRS-Lab GmbH) [http://www.sirs-lab.com](http://www.sirs-lab.com)
- Maintainer: Dr. Matthias Kohl <kohl@sirs-lab.com>

References


geneStabM

Gene expression stability value M

Description

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

Usage

geneStabM(relData, na.rm = FALSE)
**geomMean**

**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.

**Details**

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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**Description**

Computation of the geometric mean.

**Usage**

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/length(x)).
normPCR

Value

geometric mean

Author(s)

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

Description

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

Usage

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*

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

selectHKgenes

Selection of reference/housekeeping genes

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)
```

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>
SLqPCRdata

References


Examples
data(vandesompele)
res.BM <- selectHKgenes(vandesompele[1:9,], method = "Vandesompele", geneSymbol = names(vandesompele), minNrHK = 2

---

SLqPCRdata     SIRS-Lab inhouse qPCR data

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
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
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

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACTB</td>
<td>actin, beta</td>
</tr>
<tr>
<td>B2M</td>
<td>beta-2-microglobulin</td>
</tr>
<tr>
<td>GAPD</td>
<td>glyceraldehyde-3-phosphate dehydrogenase</td>
</tr>
<tr>
<td>HMB5</td>
<td>hydroxymethylbilane synthase</td>
</tr>
<tr>
<td>HPRT1</td>
<td>hypoxanthine phosphoribosyltransferase 1</td>
</tr>
<tr>
<td>RPL13A</td>
<td>ribosomal protein L13a</td>
</tr>
<tr>
<td>SDHA</td>
<td>succinate dehydrogenase complex subunit A</td>
</tr>
<tr>
<td>TBP</td>
<td>TATA box binding protein</td>
</tr>
<tr>
<td>UBC</td>
<td>ubiquitin C</td>
</tr>
<tr>
<td>YWHAZ</td>
<td>tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>BM</td>
<td>9 normal bone-marrow samples</td>
</tr>
<tr>
<td>POOL</td>
<td>9 normal human tissues from pooled organs (heart, brain, fetal brain, lung, trachea, kidney, mammary gland, small intestine and uterus)</td>
</tr>
<tr>
<td>FIB</td>
<td>20 short-term cultured normal fibroblast samples from different individuals</td>
</tr>
<tr>
<td>LEU</td>
<td>13 normal leukocyte samples</td>
</tr>
<tr>
<td>NB</td>
<td>34 neuroblastoma cell lines (independently prepared in different labs from different patients)</td>
</tr>
</tbody>
</table>

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


Examples

data(vandesompele)
str(vandesompele)
rownames(vandesompele)
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