NormqPCR

March 24, 2012

`Bladder` *Data set of Andersen et al (2004)*

Description

This data set was used in Andersen et al (2004) to demonstrate normalization of real-time quantitative RT-PCR data by geometric averaging of housekeeping genes.

Usage

```
data(Bladder)
```

Format

A qPCRBatch object which contains an expression matrix with 28 observations on the following 14 variables which stand for expression data potential reference/housekeeping genes

`Grade` Grade of bladder cancer.

`Sample.no.` sample number.

`ATP5B` ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypetide.

`HSPCB` Heat shock 90-kDa protein 1, beta.

`S100A6` S100 calcium-binding protein A6 (calcylin).

`FLOT2` Flotillin 2.

`TEGT` Testis enhanced gene transcript (BAX inhibitor 1).

`UBB` Ubiquitin B.

`TPT1` Tumor protein, translationally controlled 1.

`CFL1` Cofilin 1 (non-muscle).

`ACTB` Actin, beta.

`RPS13` Ribosomal protein S13.

`RPS23` Ribosomal protein S23.

`GAPD` Glyceraldehyde-3-phosphate dehydrogenase.

`UBC` Ubiquitin C.

`FLJ20030` Hypothetical protein FLJ20030.

It also contains a "group" column in the pData slot, which gives information on the different sample classes, necessary for the NormFinder algorithm

Details

The genes included in this data set were selected by screening 99 bladder sample expression profiles.

Source

The data set was obtained from http://www.mdl.dk/Publications_sup1.htm

References

Claus Lindbjerg Andersen, Jens Ledet Jensen and Torben Falck Orntoft (2004). Normalization of Real-Time Quantitative Reverse Transcription-PCR Data: A Model-Based Variance Estimation Approach to Identify Genes Suited for Normalization, Applied to Bladder and Colon Cancer Data Sets. CANCER RESEARCH 64, 5245-5250, August 1, 2004. http://cancerres.aacrjournals.org/cgi/content/full/64/15/5245

Examples

```
data(Bladder)
head(exprs(Bladder.qPCRBatch))
pData(Bladder.qPCRBatch)
```

BladderRepro *Data set of Andersen et al (2004)*

Description

This data set was used in Andersen et al (2004) to demonstrate normalization of real-time quantitative RT-PCR data by geometric averaging of housekeeping genes.

Usage

```
data(BladderRepro)
```

Format

A qPCRBatch object which contains an expression matrix with 28 observations on the following 14 variables which stand for expression data potential reference/housekeeping genes

`Grade` Grade of bladder cancer.

`Sample.no.` sample number.

`CD14` CD14 molecule.

`FCN1` Ficolin (collagen/fibrinogen domain containing) 1.

`CCNG2` Cyclin G2.

`NPAS2` Neuronal PAS domain protein 2.

`UBC` Ubiquitin C.

`CFL1` Cofilin 1 (non-muscle).

`ACTB` Actin, beta.

`GAPD` Glyceraldehyde-3-phosphate dehydrogenase.

It also contains a "group" column in the pData slot, which gives information on the different sample classes, necessary for the NormFinder algorithm

Details

This data set was used to check the reproducibility of the results obtained in Andersen et al (2004).

Source

The data set was obtained from http://www.mdl.dk/Publications_sup1.htm

References

Claus Lindbjerg Andersen, Jens Ledet Jensen and Torben Falck Orntoft (2004). Normalization of Real-Time Quantitative Reverse Transcription-PCR Data: A Model-Based Variance Estimation Approach to Identify Genes Suited for Normalization, Applied to Bladder and Colon Cancer Data Sets. CANCER RESEARCH 64, 5245-5250, August 1, 2004. http://cancerres.aacrjournals.org/cgi/content/full/64/15/5245

Examples

```
data(BladderRepro)
head(exprs(BladderRepro.qPCRBatch))
pData(BladderRepro.qPCRBatch)
```

Colon *Data set of Andersen et al (2004)*

Description

This data set was used in Andersen et al (2004) to demonstrate normalization of real-time quantitative RT-PCR data by geometric averaging of housekeeping genes.

Usage

```
data(Colon)
```

Format

A qPCRBatch object which contains an expression matrix with 40 observations on the following 13 variables

`UBC` Ubiquitin C.

`UBB` Ubiquitin B.

`SUI1` Putative translation initiation factor.

`NACA` Nascent-polypeptide-associated complex alpha polypeptide.

`FLJ20030` Hypothetical protein FLJ20030.

`CFL1` Cofilin 1 (non-muscle).

`ACTB` Actin, beta.

`CLTC` Clathrin, heavy polypeptide (Hc).

`RPS13` Ribosomal protein S13.

`RPS23` Ribosomal protein S23.

`GAPD` Glyceraldehyde-3-phosphate dehydrogenase.

`TPT1` Tumor protein, translationally controlled 1.

`TUBA6` Tubulin alpha 6.

It also contains a "group" column in the pData slot, which gives information on the different sample classes, necessary for the NormFinder algorithm

Details

The genes included in this data set were selected by screening 161 colon sample expression profiles.

Source

The data set was obtained from http://www.mdl.dk/Publications_sup1.htm

References

Claus Lindbjerg Andersen, Jens Ledet Jensen and Torben Falck Orntoft (2004). Normalization of Real-Time Quantitative Reverse Transcription-PCR Data: A Model-Based Variance Estimation Approach to Identify Genes Suited for Normalization, Applied to Bladder and Colon Cancer Data Sets. CANCER RESEARCH 64, 5245-5250, August 1, 2004. http://cancerres.aacrjournals.org/cgi/content/full/64/15/5245

Examples

```
data(Colon)
head(exprs(Colon.qPCRBatch))
pData(Colon.qPCRBatch)
```

`NormqPCR-package` *Functions for normalisation of RT-qPCR data.*

Description

Functions for normalisation of real-time quantitative PCR data.

Details

Package:	NormqPCR
Type:	Package
Version:	0.99.3
Date:	2011-07-15
Depends:	R(>= 2.10.0), stats, RColorBrewer, Biobase, methods, ReadqPCR
License:	LGPL-3
LazyLoad:	yes
LazyData:	yes

require(NormqPCR)

Author(s)

Matthias Kohl, James Perkins

Maintainer: Matthias Kohl <Matthias.Kohl@stamats.de>

References

Jo Vandesompele, Katleen De Preter, Filip Pattyn et al. (2002). Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biology 2002. 3(7):research0034.1-0034.11. http://genomebiology.com/2002/3/7/research/0034/

Claus Lindbjerg Andersen, Jens Ledet Jensen and Torben Falck Orntoft (2004). Normalization of Real-Time Quantitative Reverse Transcription-PCR Data: A Model-Based Variance Estimation Approach to Identify Genes Suited for Normalization, Applied to Bladder and Colon Cancer Data Sets. CANCER RESEARCH 64, 5245-5250, August 1, 2004. http://cancerres.aacrjournals.org/cgi/content/full/64/15/5245

Kenneth Livak, Thomase Schmittgen (2001). Analysis of Relative Gene Expression Data Using Real-Time Quantitative PCR and the 2^ddCt Method. Methods 25, 402-408, 2001 http://www.ncbi.nlm.nih.gov/pubmed/11846609

Examples

```
## some examples are given in the vignette
## Not run:
library(NormqPCR)
vignette("NormqPCR")

## End(Not run)
```

---

combineTechReps *Combines Technical Replicates*

Description

Takes expression set of qPCR values containing technical replicates and combines them.

Usage

```
combineTechReps(qPCRBatch, ...)

## S4 method for signature 'qPCRBatch'
combineTechReps(qPCRBatch, calc="arith")
```

Arguments

qPCRBatch	Expression set containing qPCR data, read in by a ReadqPCR function and containing technical reps, denoted by _TechRep.n suffix.
...	Extra arguments, detailed below
calc	use median, arithmetic or geometric mean for combining the values

Details

Takes `exprs` of qPCR values containing technical replicates and combines them using a specified centrality measure.

Value

`qPCRBatch` with same number of samples, but with less features, since all technical replicates are replaced with a single value of their means.

Author(s)

James Perkins `<jperkins@biochem.ucl.ac.uk>`

Examples

```
path <- system.file("exData", package = "NormqPCR")
qPCR.example.techReps <- file.path(path, "qPCR.techReps.txt")
qPCRBatch.qPCR.techReps <- read.qPCR(qPCR.example.techReps)
rownames(exprs(qPCRBatch.qPCR.techReps))
combinedTechReps <- combineTechReps(qPCRBatch.qPCR.techReps)
rownames(exprs(combinedTechReps))
```

`deltaCt` *Perform normalization with a given housekeeping gene*

Description

Normalise qPCR eset using a given housekeeping gene as control, then perform differential expression analysis using the delta delta Ct method

Usage

```
deltaCt(qPCRBatch, ...)

## S4 method for signature 'qPCRBatch'
deltaCt(qPCRBatch, hkgs, combineHkgs=FALSE, calc="arith")
```

Arguments

`qPCRBatch`	qPCR-specific expression set, containing qPCR data.
`...`	Extra arguments, detailed below
`hkgs`	String containing the name of the name of the housekeeping gene which will be used to normalise the rest of the genes.
`combineHkgs`	Logical - if TRUE, then as long as more than one housekeeper given for argument hkgs, it will combine the housekeepers by finding the geometric mean. Housekeepers can be found using geNorm or NormFinder algorithms.
`calc`	use arithmetic or geometric mean.

Details

Takes expression set of qPCR values and normalises them using a housekeeping gene. Returns a qPCRBatch with exprs set of the same dimensions but with the given hkg value subtracted.

Value

qPCRBatch with exprs set of the same dimensions but with the given hkg value subtracted.

Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

References

Kenneth Livak, Thomase Schmittgen (2001). Analysis of Relative Gene Expression Data Using Real-Time Quantitative PCR and the 2^DDCt Method. Methods 25, 402-408, 2001 http://www.ncbi.nlm.nih.gov/pubmed/11846609

See Also

selectHKs, deltaDeltaCt

Examples

```
path <- system.file("exData", package = "NormqPCR")
taqman.example <- file.path(path, "example.txt")
qPCRBatch.taqman <- read.taqman(taqman.example)
hkgs<-"Actb-Rn00667869_m1"
qPCRBatch.norm <- deltaCt(qPCRBatch =  qPCRBatch.taqman, hkgs = hkgs, calc="arith")
head(exprs(qPCRBatch.norm))
```

---

deltaDeltaCt *Perform normalization and differential expression with given housekeeping gene*

Description

Normalise qPCR eset using housekeeping genes as control, then perform differential expression analysis using the delta delta Ct method. Differs from the deltaDeltaAvgCt method in that the hkg values are subtracted and the sd is calculated on the differences (i.e. paired). Suitable when housekeeping genes are from same wells/sample as the other detectors

Usage

```
deltaDeltaCt(qPCRBatch,...)

## S4 method for signature 'qPCRBatch'
deltaDeltaCt(qPCRBatch, maxNACase=0, maxNAControl=0, hkgs, contrastM,
             case, control, paired=TRUE, hkgCalc="arith", statCalc="arith")
```

Arguments

qPCRBatch	qPCR-specific expression set, containing qPCR data.
...	Extra arguments, detailed below
maxNACase	Maximum number of NA values allowed before a detector's reading is discarded for samples designated as case.

maxNAControl	Maximum number of NA values allowed before a detector's reading is discarded for samples designated as control.
hkgs	String containing the name of th name of the housekeeping gene which will be used to normalise the rest of the genes.
contrastM	A binary matrix which designates case and control samples.
case	The name of the column in contrastM that corresponds to the case samples.
control	The name of the column in contrastM that corresponds to the control samples.
paired	Logical - if TRUE the detectors and housekeepers in the same sample will be paired for calculating standard deviation, effectively meaning we will be calculating standard deviation of the differences. If FALSE, there will be no pairing, and standard deviation will be pooled between the detector and housekeepers.
hkgCalc	String - either "arith" or "geom", details how the different housekeeper genes should be combined - either by using the arithmetic or geometric mean.
statCalc	String - either "arith" or "geom", details how genes should be combined - either by using the arithmetic or geometric mean.

Details

Takes expression set of qPCR values and normalises them using different housekeeping genes. Returns seperate sets of values for each housekeeping gene given.

Value

matrix with columns containing the detector ids, 2^delta Ct values for the sample of interest and the callibrator sample, alongside their respective standard deviations, the 2^delta delta Ct values and the minimum and maximum values (ie the values that are 1 sd away)

Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

References

Kenneth Livak, Thomase Schmittgen (2001). Analysis of Relative Gene Expression Data Using Real-Time Quantitative PCR and the 2^DDCt Method. Methods 25, 402-408, 2001 http://www.ncbi.nlm.nih.gov/pubmed/11846609

See Also

selectHKs, deltaCt

Examples

```
path <- system.file("exData", package = "NormqPCR")
taqman.example <- file.path(path, "example.txt")
qPCRBatch.taqman <- read.taqman(taqman.example)
hkg <- "Actb-Rn00667869_m1"

contM <- cbind(c(0,0,1,1,0,0,1,1),c(1,1,0,0,1,1,0,0))
colnames(contM) <- c("interestingPhenotype","wildTypePhenotype")
rownames(contM) <- sampleNames(qPCRBatch.taqman)

ddCt.taqman <- deltaDeltaCt(qPCRBatch = qPCRBatch.taqman, maxNACase=1, maxNAControl=1,
head(ddCt.taqman)
```

geNorm *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(geNorm)
```

Format

A qPCRBatch object which contains an expression matrix with 85 observations on the following 10 variables which stand for expression data of ten potential reference/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

References

Jo Vandesompele, Katleen De Preter, Filip Pattyn et al. (2002). Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biology 2002. 3(7):research0034.1-0034.11. http://genomebiology.com/2002/3/7/research/0034/

Examples

```
data(geNorm)
str(exprs(geNorm.qPCRBatch))
sampleNames(geNorm.qPCRBatch)
```

`geomMean` *Geometric Mean*

Description

Computation of the geometric mean.

Usage

```
geomMean(x, na.rm = TRUE)
```

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))`.

Value

geometric mean

Note

A first version of this function appeared in package SLqPCR.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

Examples

```
x <- rlnorm(100)
geomMean(x)
```

makeAllNAs *Make all Ct values NA*

Description

Make all Ct values for a given detector NA when the number of NAs for that detector is above a given threshold

Usage

```
makeAllNAs(qPCRBatch, ...)

## S4 method for signature 'qPCRBatch'
makeAllNAs(qPCRBatch, contrastM, sampleMaxM)
```

Arguments

qPCRBatch	Expression set containing qPCR data.
...	Extra arguments, detailed below
contrastM	Contrast Matrix like that used in limma. Columns represent the different samples types, rows are the different samples, with a 1 or 0 in the matrix indicating which sample types the different samples belong to.
sampleMaxM	Sample Max Matrix. Columns represent the different sample types. There is one value per column, which represents the max number of NAs allowed for that sample type.

Details

Make all NAs when number of NAs above a given threshold

Value

qPCRBatch object with a new exprs slot, everything else equal

Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

Examples

```
# read in the data
path <- system.file("exData", package = "NormqPCR")
taqman.example <- file.path(path, "example.txt")
qPCRBatch.taqman <- read.taqman(taqman.example)
exprs(qPCRBatch.taqman)["Ccl20.Rn00570287_m1",] # values before

# make contrastM
a <- c(0,0,1,1,0,0,1,1) # one for each sample type, with 1 representing
b <- c(1,1,0,0,1,1,0,0) # position of sample type in the samplenames vector
contM <- cbind(a,b)
colnames(contM) <- c("case","control") # then give the names of each sample type
rownames(contM) <- sampleNames(qPCRBatch.taqman) # and the rows of the matrix
```

```
contM

# make sampleMaxM
sMaxM <- t(as.matrix(c(3,3))) # now make the sample max matrix
colnames(sMaxM) <- c("case","control") # make sure these line up with samples
sMaxM

# function
qPCRBatch.taqman.replaced <- makeAllNAs(qPCRBatch.taqman, contM, sMaxM)
exprs(qPCRBatch.taqman.replaced)["Ccl20.Rn00570287_m1",]
```

`replaceAboveCutOff` *Replace Ct values with new value*

Description

Replace Ct values above a given threshold with a new value

Usage

```
replaceAboveCutOff(qPCRBatch, ...)

## S4 method for signature 'qPCRBatch'
replaceAboveCutOff(qPCRBatch, newVal=NA, cutOff=38)
```

Arguments

`qPCRBatch`	Expression set containing qPCR data.
`...`	Extra arguments, detailed below
`newVal`	The new value with which to replace the values above the cutoff
`cutOff`	the minimal threshold above which the values will be replaced

Details

Replaces values in the exprs slot of the `qPCRBatch` object that are above a threshold value with a new number

Value

`qPCRBatch` object with a new exprs slot

Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

Examples

```
path <- system.file("exData", package = "NormqPCR")
taqman.example <- file.path(path, "example.txt")
qPCRBatch.taqman <- read.taqman(taqman.example)
exprs(qPCRBatch.taqman)["Ccl20.Rn00570287_m1",]
qPCRBatch.taqman.replaced <- replaceAboveCutOff(qPCRBatch.taqman, newVal = NA, cutOff =
exprs(qPCRBatch.taqman.replaced)["Ccl20.Rn00570287_m1",]
```

`replaceNAs` *Replace NAs with a given value*

Description

Replace NAs with a given value

Usage

```
replaceNAs(qPCRBatch, ...)

## S4 method for signature 'qPCRBatch'
replaceNAs(qPCRBatch, newNA)
```

Arguments

`qPCRBatch`	Expression set containing qPCR data.
`...`	Extra arguments, detailed below
`newNA`	The new value to replace the NAs with

Details

Replaces NA values in the exprs slot of the qPCRBatch object with a given number

Value

qPCRBatch object with a new exprs slot

Author(s)

James Perkins <jperkins@biochem.ucl.ac.uk>

Examples

```
path <- system.file("exData", package = "NormqPCR")
taqman.example <- file.path(path, "example.txt")
qPCRBatch.taqman <- read.taqman(taqman.example)
qPCRBatch.taqman.replaced <- replaceNAs(qPCRBatch.taqman, newNA = 40)
exprs(qPCRBatch.taqman.replaced)["Ccl20.Rn00570287_m1",]
```

`selectHKs` *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

```
selectHKs(qPCRBatch, ...)

## S4 method for signature 'qPCRBatch'
selectHKs(qPCRBatch, group, method = "geNorm", minNrHKs = 2, log = TRUE, Symbols
      trace = TRUE, na.rm = TRUE)
```

Arguments

`qPCRBatch`	qPCRBatch, containing the data (expression matrix) in the exprs slot
`...`	Extra arguments, detailed below
`group`	optional factor not used by all methods, hence may be missing
`method`	method to compute most stable genes
`minNrHKs`	minimum number of HK genes that should be considered
`log`	logical: is data on log-scale
`Symbols`	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 `"geNorm"` was proposed by Vandesompele et al. (2002).

Currently, the geNorm method by Vandesompele et al. (2002) and the NormFinder method of Andersen et al. (2004) are 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 = "geNorm"` 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

If `method = "NormFinder"` 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
rho	stability measure rho of Andersen et al. (2004)

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References

Jo Vandesompele, Katleen De Preter, Filip Pattyn et al. (2002). Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biology 2002. 3(7):research0034.1-0034.11. http://genomebiology.com/2002/3/7/research/0034/

Claus Lindbjerg Andersen, Jens Ledet Jensen and Torben Falck Orntoft (2004). Normalization of Real-Time Quantitative Reverse Transcription-PCR Data: A Model-Based Variance Estimation Approach to Identify Genes Suited for Normalization, Applied to Bladder and Colon Cancer Data Sets. CANCER RESEARCH 64, 5245-5250, August 1, 2004. http://cancerres.aacrjournals.org/cgi/content/full/64/15/5245

Examples

```
data(geNorm)
tissue <- as.factor(c(rep("BM", 9), rep("FIB", 20), rep("LEU", 13),
  rep("NB", 34), rep("POOL", 9)))

  res.BM <- selectHKs(geNorm.qPCRBatch[,tissue == "BM"], method = "geNorm",
Symbols = featureNames(geNorm.qPCRBatch), minNrHK = 2, log = FALSE)
```

---

stabMeasureM *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

```
stabMeasureM(x, log = TRUE, na.rm = TRUE)
```

Arguments

x	matrix or data.frame containing real-time quantitative RT-PCR data
log	logical: is data on log-scale
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). Note this dispatches on a transposed expression matrix, not a qPCRBatch object since it is only called from within the selectHKs method.

Value

numeric vector with gene expression stability values

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References

Jo Vandesompele, Katleen De Preter, Filip Pattyn et al. (2002). Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biology 2002. 3(7):research0034.1-0034.11. http://genomebiology.com/2002/3/7/research/0034/

See Also

selectHKs

Examples

```
data(geNorm)
tissue <- as.factor(c(rep("BM", 9),  rep("FIB", 20), rep("LEU", 13),
                  rep("NB", 34), rep("POOL", 9)))
res.BM <- selectHKs(geNorm.qPCRBatch[,tissue == "BM"], method = "geNorm",
                  Symbols = featureNames(geNorm.qPCRBatch), minNrHK = 2, log = FALSE)
```

---

stabMeasureRho *Gene expression stability value rho*

Description

Computation of the gene expression stability value rho for real-time quantitativ RT-PCR data. For more details we refer to Andersen et al. (2004).

Usage

```
stabMeasureRho(x,...)

## S4 method for signature 'x'
stabMeasureRho(x, group, log = TRUE, na.rm = TRUE, returnAll = FALSE)
```

Arguments

x	matrix containing real-time quantitative RT-PCR data, or qPCRBatch object
...	Extra arguments, detailed below
group	grouping factor, either a factor vector or a phenoData column called "Group"
log	logical: is data on log-scale
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
returnAll	logical, return additional information.

Details

The gene expression stability value rho is computed. For more details see Andersen et al. (2004).

Value

numeric vector with gene expression stability values

If returnAll == TRUE a list with the following components is returned

rho	stability measure rho of Andersen et al. (2004)
d	used by selectHKs
v	used by selectHKs

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References

Claus Lindbjerg Andersen, Jens Ledet Jensen and Torben Falck Orntoft (2004). Normalization of Real-Time Quantitative Reverse Transcription-PCR Data: A Model-Based Variance Estimation Approach to Identify Genes Suited for Normalization, Applied to Bladder and Colon Cancer Data Sets. CANCER RESEARCH 64, 5245-5250, August 1, 2004. http://cancerres.aacrjournals.org/cgi/content/full/64/15/5245

See Also

selectHKs

Examples

```
data(Colon)
group <- pData(Colon.qPCRBatch)[,"Group"]
res.Colon <- stabMeasureRho(Colon.qPCRBatch, group = group,
                            log = FALSE)
sort(res.Colon) # cf. Table 3 in Andersen et al (2004)
```

Index