

Package ‘nondetects’

November 29, 2024

Version 2.36.0

Date 2017-12-07

Title Non-detects in qPCR data

Description Methods to model and impute non-detects in the results of qPCR experiments.

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Depends R (>= 3.2), Biobase (>= 2.22.0)

Imports limma, mvtnorm, utils, methods, arm, HTqPCR (>= 1.16.0)

VignetteBuilder knitr

Suggests knitr, rmarkdown, BiocStyle (>= 1.0.0), RUnit, BiocGenerics (>= 0.8.0)

biocViews Software, AssayDomain, GeneExpression, Technology, qPCR, WorkflowStep, Preprocessing

License GPL-3

Encoding UTF-8

LazyData true

git_url <https://git.bioconductor.org/packages/nondetects>

git_branch RELEASE_3_20

git_last_commit f1bfb66

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-11-28

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nature2008

The qPCR data from McMurray et al. Nature 2008.

Description

A study of the effect of p53 and/or Ras mutations on gene expression. The third dataset is a comparison between four cell types – YAMC cells, mutant-p53 YAMC cells, activated-Ras YAMC cells, and p53/Ras double mutant YAMC cells. Three replicates were performed for the untransformed YAMC cells, and four replicates were performed for each of the other cell types.

Usage

```
data(nature2008)
```

Format

A qPCRset object.

Examples

```
data(nature2008)  
show(nature2008)
```

oncogene2013

The qPCR data from Sampson et al. Oncogene 2013.

Description

Two cell types – young adult mouse colon (YAMC) cells and mutant-p53/activated-Ras transformed YAMC cells – in combination with three treatments – untreated, sodium butyrate, or valproic acid. Four replicates were performed for each cell-type/treatment combination.

Usage

```
data(oncogene2013)
```

Format

A qPCRset object.

Examples

```
data(oncogene2013)  
show(oncogene2013)
```

qpcrImpute

*Impute Non-detects in qPCR data***Description**

This function models the missing data mechanism and uses an EM algorithm to impute the non-detect values in qPCR data.

Usage

```
qpcrImpute(object, dj=NULL, pyfit=NULL, groupVars=NULL,
           batch=NULL, tol=1, iterMax=100,
           outform=c("Single", "Param", "Multy"),
           vary_fit=TRUE, vary_model=TRUE, add_noise=TRUE,
           formula=NULL, numsam=5,
           linkglm = c("logit", "probit", "cloglog"))
```

Arguments

| | |
|------------|--|
| object | a qPCRset |
| dj | normalization values. If NULL, features with "control" in featureType(object) are used to normalize the data. If no control features are found, the data are not normalized. |
| pyfit | initial estimate of the relationship between the probability of a non-detect and average expression. If NULL, this relationship is estimated from the data. |
| groupVars | which columns in pData(object) should be used to determine replicate samples. If NULL, all columns are used. |
| batch | amatrix with control samples for each batch, if NULL, batch effect is not taken into account. |
| tol | likelihood convergence criterion of the EM algorithm. |
| iterMax | maximum number of iterations of the EM algorithm. |
| outform | the form of the output requested. If "Single" performs a single imputation of missing values. If "Param" returns estimated model parameters: mean and variance. If "Multy" performs a multiple imputation of missing values, and creates multiple data sets with imputed values. |
| vary_fit | if outform="Multy", includes the model uncertainty due to the logit of the probability of being missing. The default value is "TRUE". |
| vary_model | if outform="Multy", includes the model uncertainty due to the estimating mean of the data. The default value is "TRUE". |
| add_noise | if outform="Multy", introduces the variance component due to the random noise. The default value is "TRUE". |
| formula | specifies the model. |
| numsam | number of the datasets to be created if outform="Multy". The default value is 5. |
| linkglm | a link used for estimation of the missing data mechanism. |

Value

The function returns a qPCRset object with non-detects replaced by their imputed values.

Author(s)

Valeriia Sherina

Examples

```
data(sagmb2011)
tst <- qpcrImpute(sagmb2011, groupVars="sampleType",
                 outform=c("Single"), batch=NULL, linkglm = c("logit"))
```

`sagmb2011`*The qPCR data from Almudevar et al. SAGMB 2011.*

Description

Cells transformed to malignancy by mutant p53 and activated Ras are perturbed with the aim of restoring gene expression to levels found in non-transformed parental cells via retrovirus-mediated re-expression of corresponding cDNAs or shRNA-dependent stable knock-down. The data contain 4-6 replicates for each perturbation, and each perturbation has a corresponding control sample in which only the vector has been added.

Usage

```
data(sagmb2011)
```

Format

A qPCRset object.

Examples

```
data(sagmb2011)
show(sagmb2011)
```

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