Package 'nondetects'

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Title Non-detects in qPCR data

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

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VignetteBuilder knitr

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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	maximimum number of iterations of the EM algorithm.
outform	the form of the output requested.If "Single" performes a single imputation of missing values. If "Param" returnes estimated model parameters: mean and variance. If "Multy" performes a multiple imputation of missing values, and creats 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", introduses 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"))
```

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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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