

# 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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**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

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`nature2008`*The qPCR data from McMurray et al. Nature 2008.*

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**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)
```

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`oncogene2013`*The qPCR data from Sampson et al. Oncogene 2013.*

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**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)
```

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|            |                                        |
|------------|----------------------------------------|
| qpcrImpute | <i>Impute Non-detects in qPCR data</i> |
|------------|----------------------------------------|

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## 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"))
```

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sagmb2011

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

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**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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