Package 'INSPEcT'

April 14, 2017

Type Package

Title Analysis of 4sU-seq and RNA-seq time-course data

Version 1.4.0

Date 2015-12-15

Author Stefano de Pretis

Maintainer Stefano de Pretis <ste.depo@gmail.com>

Description INSPEcT (INference of Synthesis, Processing and
dEgradation rates in Time-Course experiments) analyses 4sU-seq
and RNA-seq time-course data in order to evaluate synthesis,
processing and degradation rates and asses via modeling the
rates that determines changes in mature mRNA levels.

License GPL-2

Depends R (>= 3.2), methods, Biobase, BiocParallel

Imports pROC, deSolve, rootSolve, compiler, preprocessCore,
GenomicFeatures, GenomicRanges, IRanges, BiocGenerics,
GenomicAlignments, Rsamtools, S4Vectors

Suggests BiocStyle, knitr, TxDb.Mmusculus.UCSC.mm9.knownGene

VignetteBuilder knitr

biocViews Sequencing, RNASeq, GeneRegulation, TimeCourse,
SystemsBiology

NeedsCompilation no

RoxygenNote 5.0.1

R topics documented:

AIC-INSPEcT-method	*Akaike information criterion calculated for the models evaluated by INSPEcT*

Description

This method is used to retrieve AIC values for all models tested for all genes.

Usage

```
## S4 method for signature 'INSPEcT_model'
AIC(object, ..., k = 2)

## S4 method for signature 'INSPEcT'
AIC(object, ..., k = 2)
```

Arguments

object	An object of class INSPEcT or INSPEcT_model
...	Additional arguments for the generic
k	Additional parameter for the generic

Value

A matrix of AIC values

Examples

```
data('mycerIds10', package='INSPEcT')
AIC(mycerIds10)
```

---

chisqmodel *Retrieve results of chi-squared test for the selected models*

Description

Retrieve results of chi-squared test for the selected models

This method is used to retrieve the chi-squared test results for the models that have been selected to better represent the behavior of each gene.

Usage

```
chisqmodel(object, ...)

## S4 method for signature 'INSPEcT_model'
chisqmodel(object, ...)

## S4 method for signature 'INSPEcT'
chisqmodel(object, ...)
```

Arguments

object	An object of class INSPEcT or INSPEcT_model
...	Additional arguments for the generic

Value

A vector of chi-squared test results

Examples

```
data('mycerIds10', package='INSPEcT')
chisqmodel(mycerIds10)
```

---

chisqtest   *Retrieve all results of chi-squared test*

Description

Retrieve all results of chi-squared test

This method is used to retrieve all the chi-squared test results for all models tested for all genes.

Usage

```
chisqtest(object, ...)

## S4 method for signature 'INSPEcT_model'
chisqtest(object, ...)

## S4 method for signature 'INSPEcT'
chisqtest(object, ...)
```

Arguments

object	An object of class INSPEcT or INSPEcT_model
...	Additional arguments for the generic

Value

A matrix of chi-squared test results for all the tested models

Examples

```
data('mycerIds10', package='INSPEcT')
chisqtest(mycerIds10)
```

---

combine   *Combine different Objects of Class INSPEcT*

Description

This method combines the information coming from different Objects of INSPEcT class. Requirements for two or more object to be combined together are:

- they must be either modeled or either not modeled
- they must have the same time points
- they must have the same modeling parameters

Usage

```
## S4 method for signature 'INSPEcT,INSPEcT'
combine(x, y, ...)
```

Arguments

x	An object of class INSPEcT
y	An object of class INSPEcT
...	Additional objects of class INSPEcT

Details

In case the same gene is contained in more than one object that the user tries to combine, the information from one object will be used and a warning will be reported

Value

An Object of class INSPEcT

Examples

```
data('mycerIds10', package='INSPEcT')
mycerIds_2genes <- mycerIds10[1:2]
mycerIds_5genes <- mycerIds10[6:10]
mycerIds_7genes <- combine(mycerIds_2genes, mycerIds_5genes)
```

---

compareSteady	*Generate an object of class INSPEcT_diffsteady from two objects of class INSPEcT*

Description

Generate an object of class INSPEcT_diffsteady from two objects of class INSPEcT

This method compares two object of class INSPEcT in order to identify differential usage of synthesis, processing or degradation rates in two different steady-state conditions. The two INSPEcT objects must have been profiled with replicates in order to provide a statistical significance to the differences between their rates.

Usage

```
compareSteady(inspectIds1, inspectIds2)

## S4 method for signature 'INSPEcT,INSPEcT'
compareSteady(inspectIds1, inspectIds2)
```

Arguments

inspectIds1	An object of calss INSPEcT
inspectIds2	A second object of calss INSPEcT

Value

An object of class INSPEcT_diffsteady which contains both the absolute quantification of the rates as well as the comparison with the statistcal significance associated for each gene and rate. (See `INSPEcT_diffsteady-class`)

Examples

```
## load data
data('simRates', package='INSPEcT')
data('simData3rep', package='INSPEcT')
## generate a new data set with 3 replicate to make the comparison
newTpts <- c(0, 1/6)
simData3rep_2 <- makeSimDataset(simRates, newTpts, 3, seed=2)
## compare
diffrates <- compareSteady(simData3rep, simData3rep_2)
## visualize results
diffrates
```

---

dim,INSPEcT-method   *Dimensions of an Object of Class INSPEcT*

Description

A method to obtain the dimension of the object of class INSPEcT reported as a vector containing of the genes and the number of time points

Usage

```
## S4 method for signature 'INSPEcT'
dim(x)
```

Arguments

x   An object of class INSPEcT

Value

A numeric that indicates the number of genes within the object and the number of time points contained the object

See Also

`nGenes`, `nTpts`

Extract   *Extract Parts of an INSPEcT or an INSPEcT_model Object*

Description

Operators acting on INSPEcT or INSPEcT_model objects to extract parts. INSPEcT_model objects can be subsetted only by gene. INSPEcT objects can be subsetted either by gene id or time point. In case of subsetting an INSPEcT object by time point, the model should be empty.

Usage

```
## S4 method for signature 'INSPEcT_model,ANY,ANY'
x[i]

## S4 method for signature 'INSPEcT,ANY,ANY'
x[i, j]
```

Arguments

x	An object of class INSPEcT or INSPEcT_model
i	A numeric, a vector of logicals or a vector of names indicating the features to be extracted
j	A numeric, a vector of logicals indicating the time points to be extracted

Value

An Object of class INSPEcT

See Also

removeModel

Examples

```
data('mycerIds10', package='INSPEcT')
mycerIds_5genes <- mycerIds10[1:5]
## Not run:
## This will turn out into an error:
mycerIds_5genes_5tpts <- mycerIds10[1:5, 1:5]

## End(Not run)
## Before subsetting time points, the model should be removed:
mycerIds_5genes_5tpts <- removeModel(mycerIds10)[1:5, 1:5]
```

```
featureNames,INSPEcT-method
```
                Gene Names Associated with an Object of Class INSPEcT

Description

A method to visualize gene names associated with the object of class INSPEcT

Usage

```
## S4 method for signature 'INSPEcT'
featureNames(object)

## S4 replacement method for signature 'INSPEcT'
featureNames(object) <- value
```

Arguments

object	An object of class INSPEcT
value	A character that will replace the current feature names

Value

A character that contains gene names associated with the object of class INSPEcT

---

geneClass   *Retrieve the regulatory class for each gene*

Description

Retrieve the regulatory class for each gene

This method returns a factor that summarise the gene class (transcriptional regulatory mechanism) that INSPEcT has assigned to each gene. The classification depends on the chi-squared and Brown's method thresholds, that can be both provided as arguments. If the user decides a different thresholding respect to the default, these new values can be permanently set within the object.

Usage

```
geneClass(object, bTsh = NULL, cTsh = NULL)

## S4 method for signature 'INSPEcT_model'
geneClass(object, bTsh = NULL, cTsh = NULL)

## S4 method for signature 'INSPEcT'
geneClass(object, bTsh = NULL, cTsh = NULL)
```

Arguments

object	An object of class INSPEcT or INSPEcT_model
bTsh	A numeric representing the p-value threshold for considering a rate as variable. P-values are calculated through [ratePvals](#)
cTsh	A numeric representing the threshold for the chi-squared test to consider a model as valid

Value

A character containing the regulatory class for each gene

See Also

[ratePvals](#)

Examples

```
data('mycerIds10', package='INSPEcT')
geneClass(mycerIds10)
# see the classification with another threshold for chi-squared test
geneClass(mycerIds10, cTsh=.2)
# set the new threshold permanently within the object
thresholds(mycerIds10)$chisquare <- .2
```

---

getModel   *Get or replace INSPEcT_model object within INSPEcT object*

Description

Get or replace INSPEcT_model object within INSPEcT object

A method to get or set the INSPEcT_model object within an INSPEcT object. This method is particularly useful to get and set testing parameters of the INSPEcT_model object within the INSPEcT object.

Usage

```
getModel(object)

getModel(object) <- value

## S4 method for signature 'INSPEcT'
getModel(object)

## S4 replacement method for signature 'INSPEcT'
getModel(object) <- value
```

Arguments

object	An object of class INSPEcT
value	An object of class INSPEcT model

Value

An object of class INSPEcT model

See Also

[testingParams](#)

Examples

```
data('mycerIds10', package='INSPEcT')
getModel(mycerIds10)
```

---

inHeatmap   *Heatmap that represent the fold changes of all the five features*

Description

Heatmap that represent the fold changes of all the five features

A method to see as an heatmap the logRatios of synthesis, degradation and processing rates and pre-mRNA and total mRNA concentration of a population of genes, either at the level of etimated or modeled rates.

Usage

```
inHeatmap(object, type = "pre-model", breaks = seq(-1, 1, length.out = 51),
  palette = colorRampPalette(c("green", "black", "firebrick3")),
  plot_matureRNA = FALSE, absoluteExpression = TRUE, rowLabels = NULL,
  clustering = TRUE, clustIdx = 3:5)

## S4 method for signature 'INSPEcT'
inHeatmap(object, type = "pre-model", breaks = seq(-1,
  1, length.out = 51), palette = colorRampPalette(c("green", "black",
  "firebrick3")), plot_matureRNA = FALSE, absoluteExpression = TRUE,
  rowLabels = NULL, clustering = TRUE, clustIdx = 3:5)
```

Arguments

object	An object of class INSPEcT
type	Eiher "pre-model" or "model" to switch between pre-modeled or modeled features
breaks	A vector of breaks for the heatmap
palette	A color generating function, output of colorRampPalette
plot_matureRNA	A logical. If set to TRUE, matrue-mRNA is displayed instead of total-mRNA (default: FALSE)
absoluteExpression	
	A logical. If set to FALSE, the plot representing the intensity of expression is omitted. (default=TRUE)
rowLabels	A character that represent the label names that will be shown on the y-axis of the heatmap. If NULL featureNames(object) will be shown (default is NULL)

| clustering | A logical. If set to FALSE, it displys genes the order they are, with no clustering (default: TRUE) |
| clustIdx | A numeric. Indicates which of the features are used for the clustering. 0=absolu-teExpression; 1=total-mRNA/mature-mRNA; 2=preMRNA; 3=synthesis; 4=degra-dation; 5=processing (default=3:5, meaning that synthesis, degradation and processing are used for the clustering) |

Value

A list of matrices containing the logRatios for total mRNA levels, pre-mRNA levels, synthesis rates, degradation rates and processing rates. Matrices are ordered according to the clustering.

Examples

```
data('mycerIds10', package='INSPEcT')
inHeatmap(mycerIds10, 'pre-model')
inHeatmap(mycerIds10, 'model')
```

INSPEcT   *INSPEcT package*

Description

INSPEcT (INference of Synthesis, Processing and dEgradation rates in Time-cousre experiments) is a package that analyse 4sU-seq and RNA-seq time-course data in order to evaluate synthesis, processing and degradation rates and asses via modeling the rates that determines changes in mature mRNA levels.

It implements two classes ([INSPEcT_model](#) and [INSPEcT](#)) and their corresponding methods. To have a detailed description of how the two classes are structured and which methods apply on, type:

```
?'INSPEcT-class'
?'INSPEcT_model-class'
?'INSPEcT_diffsteady-class'
```

To see how the typical workflow of INSPEcT works, type:
```
vignette('INSPEcT')
```

Last but not least, to obtain a citation, type:
```
citation('INSPEcT')
```

INSPEcT-class   *An S4 class to contain all rates and models generated by INSPEcT*

Description

INSPEcT is a class able to store all the estimated rates and concentrations (slot ratesFirstGuess), the modeled rates and concentrations (slot modelRates) and the model themselves (slot model). Within the class INSPEcT other information regarding the experimental design are stored, such as the time points where experiments were collected (slot tpts), the labeling time (slot tL) and the normalization scale fators used for RNA- (totalSF) and 4sU-seq libraries (labeledSF). A list of parameters that will be used during the modeling process is stored within the slot params and can be accessed by [modelingParams](#). A new instance of the class INSPEcT can be generated by the constructor function [newINSPEcT](#).

Usage

```
## S4 method for signature 'INSPEcT'
show(object)
```

Arguments

object   An object of class INSPEcT

Details

Methods that apply to INSPEcT class are

[
AIC
chisqmodel
chisqtest
combine
dim
featureNames
geneClass
getModel<-
getModel
inHeatmap
labeledSF llrtests
logLik
makeModelRates
makeSimModel
modelingParams<-
modelingParams
modelRates
modelSelection
nGenes
nTpts
plotGene
ratePvals
ratesFirstGuessVar
ratesFirstGuess
removeModel
sfPlot
thresholds
totalSF
tpts
viewModelRates

Value

Method show for objects of class INSPEcT displays the main features of the slots ratesFirstGuess, model and modelRates

Slots

params A list of parameters of the modeling part

ratesFirstGuess An object of class ExpressionSet that contains all the rates and concentrations guessed from the first part of INSPEcT analysis (before modeling)

precision A matrix that contains the estimated precision of the rates. Rows represent genes, Columns represent time points.

model An object of class INSPEcT_model that contains the output of the mdoeling

modelRates An object of class ExpressionSet that contains all modeled the rates and concentrations

tpts A numeric vector of the time-points

labeledSF A numeric vector of the scaling factor used for inter time-point normalization of 4sU-seq libraries

totalSF A numeric vector of the scaling factor used for inter time-point normalization of RNA-seq libraries

tL A numeric containing the length of the 4sU pulse

INSPEcT_diffsteady-class

An S4 class to represent comparisons between two steady-state conditions

---

Description

INSPEcT_diffsteady is a class able to store the results of the comparisons between two steady states. An object of class INSPEcT_diffsteady is created with the method "compareSteady" applied on two "INSPEcT" objects (see `compareSteady`).

Usage

```
synthesis(object)

processing(object)

degradation(object)

## S4 method for signature 'INSPEcT_diffsteady'
show(object)

## S4 method for signature 'INSPEcT_diffsteady'
synthesis(object)

## S4 method for signature 'INSPEcT_diffsteady'
processing(object)

## S4 method for signature 'INSPEcT_diffsteady'
degradation(object)
```

Arguments

object   An object of class INSPEcT_model

Details

Methods associated to the class INSPEcT_diffsteady are:

- synthesis: Accessor to the synthesis rates and their comparisons.
- degradation: Accessor to the degradation rates and their comparisons.
- processing: Accessor to the processing rates and their comparisons.
- plotMA: visualization fuction for rates comparisons, see `plotMA`

Value

Method show for objects of class INSPEcT_model returns the number of the genes that have been modeled

Slots

synthesis A data.frame which contains both input data and comparisons results regarding synthesis rates

degradation A data.frame which contains both input data and comparisons results regarding degradation rates

processing A data.frame which contains both input data and comparisons results regarding processing rates

Examples

```
data('simData3rep', package='INSPEcT')
data('simData3rep_2', package='INSPEcT')
diffrates <- compareSteady(simData3rep, simData3rep_2)
head(synthesis(diffrates))
head(processing(diffrates))
head(degradation(diffrates))
```

INSPEcT_model-class   *An S4 class to represent models generated by INSPEcT*

Description

INSPEcT_model is a class able to store all the results of the modeling of synthesis, processing and degradation rates made via the method `modelRates` (slot ratesSpecs). It also stores the criteria (slot parameter) to choose between the many models tested for each gene the one that better describes the data and the results. The slot simple is a flag that distinguish wheter the model contains the information of the introns or not. In case not, the flag simple is set to TRUE. Also the method `makeSimModel` of class `INSPEcT-class` creates an object of class INSPEcT_model. This object will be used by `makeSimDataset` to generate a complete simulated data-set, whose classification performance can be tested.

Usage

```
## S4 method for signature 'INSPEcT_model'
show(object)
```

Arguments

object   An object of class INSPEcT_model

Details

Methods that apply to INSPEcT_model class are

[
AIC
chisqmodel
chisqtest
geneClass
llrtests
logLik
makeModelRates
makeSimDataset
modelSelection
ratePvals
rocCurve
rocThresholds
thresholds

Value

Method show for objects of class INSPEcT_model returns the number of the genes that have been modeled

Slots

params A list that defines thresholds and how to perform log likelihood ratio tests

ratesSpecs A list containing the modeling output

simple A logical that indicates whether the mode of INSPEcT is simple (no pre-mRNA and degradation rates) or not.

---

labeledSF   *Accessor to the slot labeledSF of an INSPEcT object*

Description

Accessor to the slot labeledSF of an INSPEcT object

Accessor to obtain the labeledSF slot associated with the object of class INSPEcT

Usage

```
labeledSF(object)

## S4 method for signature 'INSPEcT'
labeledSF(object)
```

Arguments

object   An object of class INSPEcT

Value

A numeric that indicates the scaling factors applied between time points of the data coming from 4sU-seq library (applies directly to synthesis rates and indirectly to degradation rates)

Examples

```
data('mycerIds10')
labeledSF(mycerIds10)
```

---

logLik   *Retrieve results of log likelihood test*

Description

Retrieve results of log likelihood test

This method is used to retrieve all the log likelihood ratio test results for all pairs tested for all genes.

Usage

```
logLik(object, ...)

## S4 method for signature 'INSPEcT_model'
logLik(object, ...)

## S4 method for signature 'INSPEcT'
logLik(object, ...)
```

Arguments

object   An object of class INSPEcT or INSPEcT_model
...   Additional arguments for the generic

Value

A matrix of log likelihood test results for all the tested model comparisons

Examples

```
data('mycerIds10', package='INSPEcT')
logLik(mycerIds10)
```

makeModelRates   *Calculate modeled rates and concentrations*

Description

Calculate modeled rates and concentrations

This function is used to evaluate rates and concentrations after modeling of the rates has been run with modelRates. The modeled rates are in functional form and can be evaluated at any time points.

This method can be used to regenerate the rates assiciated to the modeling, in case some testing parameters has changed.

Usage

```
makeModelRates(object, ...)

## S4 method for signature 'INSPEcT_model'
makeModelRates(object, ...)

## S4 method for signature 'INSPEcT'
makeModelRates(object, ...)
```

Arguments

object	An object of class INSPEcT_model
...	additional arguments tpts : A vector of time points where rates and concentrations have to be evaluated

Value

An object of class ExpressionSet containing the modeled rates and concentrations

Examples

```
data('mycerIds10', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
eSet <- makeModelRates(getModel(mycerIds10), tpts=tpts)
exprs(eSet)
data('mycerIds10', package='INSPEcT')
viewModelRates(mycerIds10, 'degradation')
## force every degradation rate to be accepted as variable
thresholds(getModel(mycerIds10))$brown <- c(synthesis=.01, degradation=1, processing=.01)
mycerIds10 <- makeModelRates(mycerIds10)
viewModelRates(mycerIds10, 'degradation')
```

---

makeRPKMs | *Calculate RPKM and count values on introns and exons from bam/sam files*

Description

Given a TranscriptDb object and a list of bam/sam files for 4su and total RNA experiments, "makeRPKMs" function calculates read counts and RPKM on exonic and intronic features per each gene. Reads that fall where intronic and exonic features overlaps are univoquely assigned to exons.

Usage

```
makeRPKMs(txdb, paths_foursu, paths_total, by = c("gene", "tx"),
  countMultiMappingReads = FALSE, allowMultiOverlap = FALSE,
  strandSpecific = FALSE, isPairedEnd = FALSE)
```

Arguments

txdb	A TranscriptDB object
paths_foursu	A vector of paths of 4sU-seq sam files
paths_total	A vector of paths of RNA-seq sam files
by	A character, either "gene" or "tx", indicating if rpkms and counts should be summarized at the levels of genes or transcripts. "gene" by default
countMultiMappingReads	
	A logical, if multimapping reads should be counted, FALSE by default. Multimap reads are identified using the tag "NH" in the bam/sam file.
allowMultiOverlap	
	A logical, indicating if a read is allowed to be assigned to more than one feature, FALSE by default
strandSpecific	A logical, if strand-specific read counting should be performed, FALSE by default
isPairedEnd	A logical, if paired-end reads are used, FALSE by default

Value

A list containing rpkms, counts and the annotation extracted from TxDB for exons and introns

Examples

```
require(TxDb.Mmusculus.UCSC.mm9.knownGene)
txdb <- TxDb.Mmusculus.UCSC.mm9.knownGene
files4su <- system.file('extdata', '4sURNA_0h.bam', package="INSPEcT")
filesTotal <- system.file('extdata', 'totalRNA_0h.bam', package="INSPEcT")
makeRPKMsOut <- makeRPKMs(txdb, files4su, filesTotal)
rpkms <- makeRPKMsOut$rpkms
counts <- makeRPKMsOut$counts
annotation <- makeRPKMsOut$annotation
```

---

makeSimDataset   *Generate synthetic rates and concentrations*

Description

Generate synthetic rates and concentrations

This method generates rates and concentrations where noise is added according to the desired number of replicates that the user set as an arguments from the INSPEcT_model object that has been created by the method of the class INSPEcT makeSimModel. Rates and concentrations can be generated at the time-points of interest. This method generates an INSPEcT object that can be modeled and the performance of the modeling can be tested directly aginst the INSPEcT_model object created by makeSimModel.

Usage

```
makeSimDataset(object, tpts, nRep, seed = NULL)

## S4 method for signature 'INSPEcT_model'
makeSimDataset(object, tpts, nRep, seed = NULL)
```

Arguments

object	An object of class INSPEcT_model, usually the output of makeSimModel
tpts	A numeric vector of time points where rates and concentrations have to be evaluated
nRep	Number of replicates to simulate
seed	A numeric to obtain reproducible results

Value

An object of the class ExpressionSet containing rates and concentrations

See Also

makeSimModel

Examples

```
## generate a synthtic data-set of 10 genes based on the real data-set
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
simRates <- makeSimModel(mycerIds, 10)
simData <- makeSimDataset(simRates, tpts, 1)
## load simulated datasets
data('simRates', package='INSPEcT')
data('simData3rep', package='INSPEcT')
## measure sensitivity/sensibility of synthesis, degradation and processing
## rates identification
```

```
dev.new()
rocCurve(simRates, simData3rep)
## measure classification with a different threshold for the chi-squared
## test acceptance of models
rocCurve(simRates, simData3rep, cTsh=.2)
```

---

makeSimModel   *Build the synthetic rates shaped on a dataset*

Description

Build the synthetic rates shaped on a dataset

This method allow the creation of synthesis, degradation and processing rates for a certain number of genes. The rates are created according to the distributions of the real data-set which is given as an input of the method. Different proportions of constant varying rates can be set and a new vector of time points can be provided. This method has to be used before the makeSimDataset method.

Usage

```
makeSimModel(object, nGenes, newTpts = NULL, probs = c(constant = 0.5,
  sigmoid = 0.3, impulse = 0.2), na.rm = TRUE, seed = NULL)

## S4 method for signature 'INSPEcT'
makeSimModel(object, nGenes, newTpts = NULL,
  probs = c(constant = 0.5, sigmoid = 0.3, impulse = 0.2), na.rm = TRUE,
  seed = NULL)
```

Arguments

object	An object of class INSPEcT
nGenes	A numeric with the number of synthtic genes to be created
newTpts	A numeric verctor with time points of the synthtic dataset, if NULL the time points of the real dataset will be used
probs	A numeric vector wich describes the probability of a rate to be constant, shaped like a sigmoid or like an impulse model
na.rm	A logical that set whether missing values in the real dataset should be removed
seed	A numeric to obtain reproducible results

Details

The method makeSimModel generates an object of class INSPEcT_model that stores the parametric functions to genrate clean rates of a time-course. To any of the rates also a noise variance is associate but not used yet. In a typical workflow the output of makeSimModel is the input of the method makeSimDataset, that build the noisy rates and concentrations, given a specified number of replicates.

Value

An object of class INSPEcT_model with synthetic rates

See Also

[makeSimDataset](#)

Examples

```
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
## generate a synthtic data-set of 10 genes based on the real data-set
simRates <- makeSimModel(mycerIds, 10)
simData <- makeSimDataset(simRates, tpts, 1)
## measure sensitivity/sensibility of synthesis, degradation and processing
## rates identification
data('simRates', package='INSPEcT')
data('simData3rep', package='INSPEcT')
rocCurve(simRates, simData3rep)
## measure classification with a different threshold for the chi-suared
## test acceptance of models
rocCurve(simRates, simData3rep, cTsh=.2)
## generate a synthtic data-set of 10 genes based on the real data-set
## with more replicates and more time points
## Not run:
newTpts <- c(0, 1/6, 1/3, 1/2, 1, 1.5, 2, 4, 8, 12, 16, 24)
simRates <- makeSimModel(mycerIds, 10, newTpts=newTpts)
simData <- makeSimDataset(simRates, newTpts, 3)

## End(Not run)
```

---

modelingParams	*Get and set number parameters for the modeling*

Description

Get and set number parameters for the modeling

A method to get and set the parameters that will be used in the modeling of estimated rates and concentrations by the method [modelRates](#)

Usage

```
modelingParams(object)

modelingParams(object) <- value

## S4 method for signature 'INSPEcT'
modelingParams(object)

## S4 replacement method for signature 'INSPEcT'
modelingParams(object) <- value
```

Arguments

object	An object of class INSPEcT
value	A list with new parameters

Value

List of parameters and their values

- nInit number of optimization to find the best functional representation of each rate (by default 10)

- nIter number of max iteration during optimization (default is 300)

- na.rm A logical wheter missing values should be removed from estimated rates (default is TRUE)

- verbose A logical wheter to be verbose or not (default is TRUE)

- estimateRatesWith Either "int" or "der". With "int" the degradation and processing rates are estimated integrating the system between one time point and the following. With "der" degradation and processing rates are estimated using the derivative of total and pre mRNA. (default is "int")

- useSigmoidFun A logical, whether to choose between sigmoid and impulse function to fit rates and concentrations. In case not, always impulse function is used. (default is TRUE)

- testOnSmooth A logical, wheter models should be tested on smoothed pre-mRNA, total mRNA and synthesis rates or not. (default is TRUE)

See Also

[modelRates](#)

Examples

```
data('mycerIds10', package='INSPEcT')
modelingParams(mycerIds10)
data('mycerIds10', package='INSPEcT')
mycerIds10 <- removeModel(mycerIds10)
modelingParams(mycerIds10)$useSigmoidFun <- FALSE
```

---

modelRates	*Launch the modeling process*

Description

Launch the modeling process with parameters set with [modelingParams](#)

This method model the synthesis, degradation and processign rates after their estimation by the constructor function [newINSPEcT](#). Estimated rates are not guaranteed to optimally describes provided input data yet. To this purpose, modeled rates can be generated and genes can be assigned to a transcriptional regulatory mechanism. Modeled rates can be accessed via the method [viewModelRates](#) and gene classification according to the regulatory mechanism can be accessed by [geneClass](#). The modeling procedure can be set by the user by modyging the parameters via [modelingParams](#)

Usage

```
modelRates(object, seed = NULL, BPPARAM = bpparam(), verbose = NULL)

## S4 method for signature 'INSPEcT'
modelRates(object, seed = NULL, BPPARAM = bpparam(),
  verbose = NULL)
```

Arguments

object	An object of class INSPEcT
seed	A numeric, indicatindg the seed to be set for reproducible results
BPPARAM	Parallelization parameters for bplapply. By default bpparam()
verbose	Either NULL or logical. If logical indicates whether to output some text during computation or not, if NULL it takes the information from the object (see modelingParams) (Default: NULL) used for parallelization (if nCores=1 doesn't parallelize). If NULL takes the information from the object (see modelingParams) (Default: NULL)

Details

When modeling many genes, parallelization is strongly suggested to reduce computational time. Since all genes run independently, the computational time is diveded by the number of cores used/available. However, when modeling more than 500 genes, it may happen that a single gene returns an error that escapes the try/catch controls of INSPEcT. With the parallel mode, the error will propagate on all genes that have been computed with the same processor (or core). To avoid this, the computation could be splitted in chunks and the whole data set can be obtaied by combining the chunks (see Examples).

Value

An object of class INSPEcT with modeled rates

See Also

viewModelRates, geneClass, modelingParams

Examples

```
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
mycerIdsOneGene <- mycerIds[5]
## View modeling parameters
modelingParams(mycerIdsOneGene)
## Run the modeling in a reproducible way (setting seed)
mycerIdsOneGene <- modelRates(mycerIdsOneGene, seed=1, BPPARAM=SerialParam())
## view modeled synthesis rates
viewModelRates(mycerIdsOneGene, 'synthesis')
## view gene classes
geneClass(mycerIdsOneGene)
```

```
## Divide a parallel computation into chunks
## Not run:
nCores(mycerIds) <- parallel::detectCores()
chunkSize <- 100
splitIdx <- ceiling(c(1:nGenes(mycerIds))/chunkSize)
chunks <- lapply(split(mycerIds, splitIdx), modelRates)
mycerIdsModeled <- do.call('combine', chunks)

## End(Not run)
```

---

modelSelection   *Get or set parameters for model test and selection*

Description

With this methods the user can personalize the criteria by which INSPEcT selects a rate to be variable or constant. In particular, the model selection criteria can be selected between log-likelihood ratio test and Akaike's information criterion. In case log-likelihood ratio test is selected, the thresholds of chi-squared and Brown's method can be set (see Details section).

Usage

```
modelSelection(object)

modelSelection(object) <- value

thresholds(object)

thresholds(object) <- value

llrtests(object)

llrtests(object) <- value

## S4 method for signature 'INSPEcT'
modelSelection(object)

## S4 replacement method for signature 'INSPEcT'
modelSelection(object) <- value

## S4 method for signature 'INSPEcT_model'
modelSelection(object)

## S4 replacement method for signature 'INSPEcT_model'
modelSelection(object) <- value

## S4 method for signature 'INSPEcT'
thresholds(object)

## S4 replacement method for signature 'INSPEcT'
thresholds(object) <- value
```

```
## S4 method for signature 'INSPEcT_model'
thresholds(object)

## S4 replacement method for signature 'INSPEcT_model'
thresholds(object) <- value

## S4 method for signature 'INSPEcT'
llrtests(object)

## S4 replacement method for signature 'INSPEcT'
llrtests(object) <- value

## S4 method for signature 'INSPEcT_model'
llrtests(object)

## S4 replacement method for signature 'INSPEcT_model'
llrtests(object) <- value
```

Arguments

object   An object of class INSPEcT or INSPEcT_model

value   A list or a character that will substitute the set of parameters

- modelSelection: A character, either "llr" to test whether a rate is varying using log-likelihood testing framework or "aic" to choose the best model via Akaike Information Criterion (Default: "llr").
- thresholds: A named list containing the threshold that is used to consider a model as accepted in terms of the chi-squared test and three thresholds (one per each rate) that are used to consider a rate as variable using the Brown's method on the log-likelihood ratio tests
- llrtests: A list of three elements that represent, for each rate, the pairs of models that will be compared via log likelihood ratio test to assess whether the rate is variable or not

Details

When log-likelihood is chosen as a criterion for model selection, different nested models can be compared to assess wheter a single rate is varying or constant. For example, in case we want to establish whether synthesis rate is constant or not we can test the null hypothesis "all the rates are constant" against the alternative hypothesis "synthesis rate is changing". The null hypothesis is a special case of the alternative hypothesis, therefore the models are nested. We can also assess whether synthesis rate is constant or not by comparing the null hypothesis "degradation rate is changing" against the alternative hypothesis "degradation and synthesis are changing". The method [llrtests](#) set the models that are compared to assess the variability of eache rate. Different comparisons will be combined using Brown's method for combinig p-values. Models are named with a short notation where synthesis is "a", degradation is "b" and processing is "c". "0" is the model where all genes are kept constant and "ab", for example is the model where synthesis rate and degradation rate are changing. The user can also set the thresholds for Brown's p-value and chi-suqared p-value. While the former set the threshold to assess whether a rate is variable or not over time, the latter set the chi-squared threshold for a pair of model to be used via the log-likelihood ratio test. In order for a pair to be used, at least one model of the pair should have a chi-squared p-value (goodness of fit) below the threshold. The construction of a synthetic data-set can help in the choice of the correct parameters for the test ([makeSimModel](#), [makeSimDataset](#)).

Value

See "value"

See Also

[makeSimModel](#), [makeSimDataset](#)

Examples

```
data('mycerIds10', package='INSPEcT')
modelSelection(mycerIds10)
modelSelection(mycerIds10) <- 'aic'
thresholds(mycerIds10)
thresholds(mycerIds10)$chisquare <- 1e-3
thresholds(mycerIds10)$brown['synthesis'] <- 1e-3
llrtests(mycerIds10)
llrtests(mycerIds10)$synthesis <- list(c('0','a'), c('b','ab'))
```

---

mycerIds10   *An INSPEcT object with evaluated and modeled rates and concentrations*

Description

This INSPEcT object contains the evaluated and modeled rates and concentrations of the very first 10 genes of the dataset rpkms

Format

An INSPEcT object

---

newINSPEcT   *Create a new INSPEcT object*

Description

The function newINSPEcT creates a new instance of the class INSPEcT, provided the intronic and exonic RPKMs of RNA- and 4sU-seq experiments at different time points, the time points, the labeling time and optionally the scaling factor to normalize the libraries. The scaling factor to normalize the 4sU-seq libraries can be calculated by the function itself and this way of calulating the scaling factors gives robustness to the estimation of sythesis, degradation and processing rates. In case only exonic RPKMs are provided, only synthesis and degradation rates can be estimated by the function newINSPEcT and the scaling factors to normalize 4sU-seq libraries cannot be caluculated. To provide robustness to the procedure the argument labeledSF is strongly suggested in this case.

Usage

```
newINSPEcT(tpts, labeling_time, rpkms_4su_exons, rpkms_total_exons,
  rpkms_4su_introns = NULL, rpkms_total_introns = NULL,
  BPPARAM = bpparam(), totalMedianNorm = TRUE, labeledMedianNorm = FALSE,
  totalSF = NULL, labeledSF = NULL, totalQuantileNorm = FALSE,
  labeledQuantileNorm = FALSE, simulatedData = FALSE,
  degDuringPulse = FALSE)
```

Arguments

tpts	A vector of time points
labeling_time	A number, lenght of the 4sU pulse
rpkms_4su_exons	A matrix containing expression levels of 4su exons
rpkms_total_exons	A matrix containing expression levels of total exons
rpkms_4su_introns	A matrix containing expression levels of 4su introns
rpkms_total_introns	A matrix containing expression levels of total introns
BPPARAM	Configuration for BiocParallel parallelization. By default is set to bpparam()
totalMedianNorm	A logical to perform median normalization over total RNA exons rpkms, it will apply also on introns
labeledMedianNorm	A logical to perform median normalization over 4sU RNA exons rpkms, it will apply also on introns
totalSF	A vector storing user defined normalization scale over Total RNA exons and introns rpkms
labeledSF	A vector storing user defined normalization scale over 4sU RNA exons and introns rpkms
totalQuantileNorm	A logical to perform to perform median normalization over total RNA exons rpkms, it will apply also on introns
labeledQuantileNorm	A logical to perform to perform median normalization over 4sU RNA exons rpkms, it will apply also on introns
simulatedData	A logical, set to TRUE in case the analysis is on simulated data
degDuringPulse	A logical, set to TRUE in case of a long labelling time. Also degradation of newly synthesized transcripts will be taken into account

Value

An object of class INSPEcT with rates guessed, rates can be accessed by [ratesFirstGuess](#) method.

Examples

```
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
```

---

nGenes   *Get the number of genes within the INSPEcT object*

Description

Get the number of genes within the INSPEcT object

A method to obtain the number of the genes associated with the object of class INSPEcT

Usage

```
nGenes(object)

## S4 method for signature 'INSPEcT'
nGenes(object)
```

Arguments

object   An object of class INSPEcT

Value

A numeric that indicates the number of genes within the object

Examples

```
data('mycerIds10')
nGenes(mycerIds10)
```

---

nTpts   *Get the number of time points within the INSPEcT object*

Description

Get the number of time points within the INSPEcT object

A method to obtain the number of the tpts associated with the object of class INSPEcT

Usage

```
nTpts(object)

## S4 method for signature 'INSPEcT'
nTpts(object)
```

Arguments

object	An object of class INSPEcT

Value

A numeric that indicates the number of time points contained the object

Examples

```
data('mycerIds10')
nTpts(mycerIds10)
```

---

plotGene	*Plot the pre-modeled and modeled profiles for one gene*

Description

Plot the pre-modeled and modeled profiles for one gene

A method to see the shapes of the estimated synthesis, degradation and processing rates, pre-mRNA and total mRNA concentrations (solid thin lines) their variances (dashed lines) and the modeled rates and concentrations (ticker solid line) of a single gene.

Usage

```
plotGene(object, ix, fix.yaxis = FALSE)

## S4 method for signature 'INSPEcT'
plotGene(object, ix, fix.yaxis = FALSE)
```

Arguments

object	An object of class INSPEcT
ix	Eiher a rowname or a row number to select one single gene
fix.yaxis	A logical, indicating whether the limits for y-axis of degradation and processing rates should be fixed relative to their distributions

Value

A list containing total mRNA levels and their confidence interval (levels plus and minus one standard deviation), pre-mRNA lelevs and their confidence intervals, synthsis rates and their confidence intervals, degradation rates and processing rates of the selected gene.

Examples

```
data('mycerIds10', package='INSPEcT')
plotGene(mycerIds10, 1)
```

plotMA   *MA-plot from base means and log fold changes*

Description

Visualize the comparison between the rates calculated from two different INSPEcT objects profiled in steady-state conditions.

Usage

```
## S4 method for signature 'INSPEcT_diffsteady'
plotMA(object, ...)
```

Arguments

object   An object of calss INSPEcT_diffsteady

...   Additional parameters, see Details section

Details

Possible arguments to "plotMA":

- "rate" - A character, which represent the rate to be visualized, either "synthesis", "processing" or "degradation". By default, "synthesis" is chosen.

- "alpha" - A numeric, The confidence interval for significance (FDR), by default 0.1

- "xlim" - A numeric vector of length 2, limits of x-axis, by default the range of the data.

- "xlab" - A character, the label of x-axis, by default "log2 geometric mean"

- "ylim" - A numeric vector of length 2, limits of y-axis, by default the range of the data.

- "ylab" - A character, the label of y-axis, by default "log2 fold change"

- "main" - A character, the title of the plot, by default the name of the visualized rate.

See Also

http://en.wikipedia.org/wiki/MA_plot

Examples

```
data('simData3rep', package='INSPEcT')
data('simData3rep_2', package='INSPEcT')
diffrates <- compareSteady(simData3rep, simData3rep_2)
plotMA(diffrates, alpha=.5)
```

---

ratePvals *Retrieve a single p-value for each rate*

Description

Retrieve a single p-value for each rate

This method is used to retrieve all the p-values combined with Brown's method that combines the results of the log likelihood ratio test results for all pairs tested for each rate and all genes. P-values will change according to the threshold set for the chi-squared test because it influences the model that will be taken into consideration to perform log likelihood ratio tests. To have a sense of the best parameter to choose, a sythetic data-set can be built and tested (makeSimModel, makeSimDataset) In case 'aic' has been selected via modelSelection method, this method assigns the chi-squared test result of the model selected by AIC to the respective variable rates

Usage

```
ratePvals(object, cTsh = NULL)

## S4 method for signature 'INSPEcT_model'
ratePvals(object, cTsh = NULL)

## S4 method for signature 'INSPEcT'
ratePvals(object, cTsh = NULL)
```

Arguments

object   An object of class INSPEcT or INSPEcT_model

cTsh   A numeric representing the threshold for the chi-squared test to consider a model as valid

Details

ratePvlas retrieve a single p-value for each rate thanks to multiple log likelihood tests performed on nested models that has a chi-squared test below the selected threshold. Among the many p-values that log likelihood ratio test calculate, a single p-value is obtaied applying Brown's method for combining dependent p-values.

Value

A matrix containing p-values calculated for each rate

See Also

makeSimModel, makeSimDataset

Examples

```
data('mycerIds10', package='INSPEcT')
ratePvals(mycerIds10)
# calculate agin the p-values with Brown with a different threshold
# for considering a model valid for the log likelihood ratio test
```

```
ratePvals(mycerIds10, cTsh=.2)
# Set permaenently the chi-squared threshold at .2 for mycerIds10 object
thresholds(mycerIds10)$chisquare <- .2
```

---

ratesFirstGuess *Retrieve pre-modeling rates and concentrations*

Description

Retrieve pre-modeling rates and concentrations

This method allow to access to the estimated synthesis, degradation, processing rates and pre mRNA and total mRNA concentrations the way they were calculated by the constructor function newINSPEcT.

Usage

```
ratesFirstGuess(object, feature)

## S4 method for signature 'INSPEcT'
ratesFirstGuess(object, feature)
```

Arguments

object   An object of class INSPEcT

feature   A character indicating the feature to retireve, "synthesis", "degradation", "pro-
              cessing" for rates, "total" for total mRNA concentrations or "preMRNA" for
              premature mRNA concentrations

Value

A numeric matrix containing the values for the selected feature

See Also

newINSPEcT, ratesFirstGuessVar

Examples

```
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
# get estimated synthesis rates
ratesFirstGuess(mycerIds, 'synthesis')
```

---

ratesFirstGuessVar   *Retrieve pre-modeling rates and concentrations variance*

Description

Retrieve pre-modeling rates and concentrations variance

This method allow to access to the estimated variance of synthesis rates and pre mRNA and total mRNA concentrations the way they were calculated by the constructor function newINSPEcT.

Usage

```
ratesFirstGuessVar(object, feature)

## S4 method for signature 'INSPEcT'
ratesFirstGuessVar(object, feature)
```

Arguments

object   An object of class INSPEcT

feature   A character indicating the feature to retireve, "synthesis", "degradation", "processing" for rates, "total" for total mRNA concentrations or "preMRNA" for premature mRNA concentrations

Value

A numeric vector containing the values for the selected feature

See Also

newINSPEcT, ratesFirstGuess

Examples

```
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
ratesFirstGuessVar(mycerIds, 'synthesis')
```

---

removeModel   *remove modelling information from INSPEcT object*

Description

remove modelling information from INSPEcT object

Remove the model from an INSPEcT object. It is required when subsetting an INSPEcT object per time points because when removing time points the modeling is not valid anymore.

Usage

```
removeModel(object)

## S4 method for signature 'INSPEcT'
removeModel(object)
```

Arguments

object   An Object of class INSPEcT

Value

An Object of class INSPEcT

Examples

```
data('mycerIds10', package='INSPEcT')
mycerIds_5genes <- mycerIds10[1:5]

## This will turn out into an error:
## Not run: mycerIds_5genes_5tpts <- mycerIds10[1:5, 1:5]


## Before subsetting time points, the model should be removed:
mycerIds_5genes_5tpts <- removeModel(mycerIds10)[1:5, 1:5]

## Also this will turn out into an error:
## Not run: mycerIds10 <- modelRates(mycerIds10)

## Before running the model again, or changing modeling parameters,
## the previous model should be removed:
mycerIds10_old <- mycerIds10
mycerIds10_new <- removeModel(mycerIds10)
modelingParams(mycerIds10_new)$useSigmoidFun <- FALSE
## Not run: mycerIds10_new <- modelRates(mycerIds10_new)
```

---

rocCurve   *Display rate classification performance*

Description

Display rate classification performance

A method to visualize the performance in the classification of synthesis, degradation and processing rates based on the comparison of the original simulated rates and the one obtained by the function [modelRates](). For each rate, classification performance is measured in terms of sensitivity and specificity using a ROC curve analysis. False negatives (FN) represent cases where the rate is identified as constant while it was simulated as varying. False positives (FP) represent cases where INSPEcT identified a rate as varying while it was simulated as constant. On the contrary, true positives (TP) and negatives (TN) are cases of correct classification of varying and constant rates, respectively. Consequently, sensitivity and specificity are computed using increasing thresholds for the brown p-values, and the ability of correctly classifying a rate is measured through the area under the curve (AUC) for each rate.

Usage

```
rocCurve(object, object2, cTsh = NULL, plot = TRUE)

## S4 method for signature 'INSPEcT_model,INSPEcT_model'
rocCurve(object, object2, cTsh = NULL,
  plot = TRUE)

## S4 method for signature 'INSPEcT_model,INSPEcT'
rocCurve(object, object2, cTsh = NULL,
  plot = TRUE)
```

Arguments

object	An object of class INSPEcT_model, with true rates
object2	An object of class INSPEcT or INSPEcT_model, with modeled rates
cTsh	A numeric representing the threshold for the chi-squared test to consider a model as valid; if NULL the value is taken from the INSPEcT_model object
plot	A logical indicating whether ROC curves should be plotted or not

Value

A list of objects of class pROC with summary of each roc curve

See Also

[makeSimModel](), [makeSimDataset](), [rocThresholds]()

Examples

```
data('simRates', package='INSPEcT')
data('simData3rep', package='INSPEcT')
rocCurve(simRates, simData3rep)
```

---

rocThresholds	*Display rate classification performance with thresholds visible at x-axis*

Description

Display rate classification performance with thresholds visible at x-axis

A method to visualize the performance in the classification of synthesis, degradation and processing rates based on the comparison of the original simulated rates and the one obtained by the function [modelRates](). For each rate, classification performance is measured in terms of sensitivity and specificity using a ROC curve analysis. False negatives (FN) represent cases where the rate is identified as constant while it was simulated as varying. False positives (FP) represent cases where INSPEcT identified a rate as varying while it was simulated as constant. On the contrary, true positives (TP) and negatives (TN) are cases of correct classification of varying and constant rates, respectively. Consequently, at increasing brown p-values different sensitivity and specificity can be achieved.

Usage

```
rocThresholds(object, object2, cTsh = NULL, bTsh = NULL, xlim = c(1e-05,
  1))

## S4 method for signature 'INSPEcT_model,INSPEcT_model'
rocThresholds(object, object2,
  cTsh = NULL, bTsh = NULL, xlim = c(1e-05, 1))

## S4 method for signature 'INSPEcT_model,INSPEcT'
rocThresholds(object, object2, cTsh = NULL,
  bTsh = NULL, xlim = c(1e-05, 1))
```

Arguments

object	An object of class INSPEcT_model, with true rates
object2	An object of class INSPEcT or INSPEcT_model, with modeled rates
cTsh	A numeric representing the threshold for the chi-squared test to consider a model as valid
bTsh	A numeric representing the threshold for the Brown's method to consider a rate as varying
xlim	A numeric representing limits for the x-axis (default is c(1-e-5,1))

Value

None

See Also

[makeSimModel](#), [makeSimDataset](#), [rocCurve](#)

Examples

```
data('simRates', package='INSPEcT')
data('simData3rep', package='INSPEcT')
rocThresholds(simRates, simData3rep)
# Increase the Brown threshold for all rates (be more relaxed)
thresholds(simData3rep)$brown <- c(alpha=.05, beta=.05, gamma=.05)
rocThresholds(simRates, simData3rep)
```

---

rpkms   *intron, exons RPKM values of 500 genes from 4sU-seq and RNA-seq experiments*

Description

A dataset containing the values of exonic and intronic RPKMs of 500 genes both in 4sU-seq and RNA-seq experiments. The variables are as follows:

Format

A list of 4 matrices with 500 rows and 9 columns

Details

- rpkms_4su_exons

- rpkms_4su_introns

- rpkms_total_exons

- rpkms_total_introns

---

sfPlot	*A nice plot to see scaling factors used for RNA-seq and 4sU-seq libraries*

Description

A nice plot to see scaling factors used for RNA-seq and 4sU-seq libraries

This method generates a plot that immediately shows the scaling factors used to scale RNA- and 4sU-seq libraries and the possible relations between them. The ratio between the RNA- and the 4sU-seq scaling can be in fact considered as a yield of the synthesis within the cells.

Usage

```
sfPlot(object)

## S4 method for signature 'INSPEcT'
sfPlot(object)
```

Arguments

object   An object of class INSPEcT

Value

None

Examples

```
data('rpkms', package='INSPEcT')
tpts <- c(0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16)
tL <- 1/6
mycerIds <- newINSPEcT(tpts, tL, rpkms$foursu_exons, rpkms$total_exons,
rpkms$foursu_introns, rpkms$total_introns, BPPARAM=SerialParam())
sfPlot(mycerIds)
```

simData1rep	*An INSPEcT object with 1000 simulated rates and concentration and their modeled rates*

Description

A dataset containing the rates and concentrations obtained from the dataset simRates with 1 replicates and time points corresponding to: 0, 1/6, 1/3, 1/2, 1, 2, 4, 8, 16 hours. On this dataset rates and concentrations have been modeled with the method modelRates

Format

An INSPEcT object

simData3rep	*An INSPEcT object with 1000 simulated rates and concentration and their modeled rates*

Description

A dataset containing the rates and concentrations obtained from the dataset simRates with 3 replicates and time points corresponding to: 0, 1/6, 1/3, 1/2, 1, 1.5, 2, 4, 8, 12, 16 and 24 hours. On this dataset rates and concentrations have been modeled with the method modelRates

Format

An INSPEcT object

simRates	*An INSPEcT_model object of 1000 simulated rates*

Description

The INSPEcT_model object contains 1000 simulated rates that were obtained using the dataset rpkms as reference

Format

An INSPEcT_model object

---

split   *Divide an INSPEcT Object into groups*

Description

Divides the INSPEcT object into the groups defined by 'f',

Usage

```
## S4 method for signature 'INSPEcT,ANY'
split(x, f, drop = FALSE, ...)
```

Arguments

x	An object of class INSPEcT
f	A vector of length equal to the number of genes in x which defines the groups
drop	A logical belonging to the generic funciton, useless in this context.
...	Additional arguments to match the generic function

Value

A list containing objects of class INSPEcT

Examples

```
data('mycerIds10')
splitIdx <- c(1,1,1,2,2,2,3,3,3,4)
mycerIds10Split <- split(mycerIds10, splitIdx)
```

---

totalSF   *Accessor to the slot totalSF of an INSPEcT object*

Description

Accessor to the slot totalSF of an INSPEcT object

Accessor to obtain the totalSF slot associated with the object of class INSPEcT

Usage

```
totalSF(object)

## S4 method for signature 'INSPEcT'
totalSF(object)
```

Arguments

object	An object of class INSPEcT

Value

A numeric that indicates the scaling factors applied between time points of the data coming from
RNA-seq library (applies to total-mRNAs and pre-mRNAs concentrations)

Examples

```
data('mycerIds10')
totalSF(mycerIds10)
```

---

tpts   *Accessor to the slot tpts of an INSPEcT object*

Description

Accessor to the slot tpts of an INSPEcT object

Accessor to obtain the tpts associated with the object of class INSPEcT

Usage

```
tpts(object)

## S4 method for signature 'INSPEcT'
tpts(object)
```

Arguments

object   An object of class INSPEcT

Value

A numeric that indicates time points contained the object

Examples

```
data('mycerIds10')
tpts(mycerIds10)
```

UCSC_mm9_genes_exons   *A Gtf file containing exons definition of 100 genes*

Description

A Gtf file containing exons definition of 100 genes

Format

A tab separated file

UCSC_mm9_genes_introns

A Gtf file containing introns definition of 100 genes

Description

A Gtf file containing introns definition of 100 genes

Format

A tab separated file

viewModelRates *Retrieve the modeled rates and concentrations*

Description

Retrieve the modeled rates and concentrations

A method to access the modeld rates via the method modelRates

Usage

```
viewModelRates(object, feature)

## S4 method for signature 'INSPEcT'
viewModelRates(object, feature)
```

Arguments

object   An object of class INSPEcT

feature   A character indicating the feature to retireve, "synthesis", "degradation", "processing" for rates, "total" for total mRNA concentrations or "preMRNA" for premature mRNA concentrations

Value

A numeric matrix containing the values for the selected feature

Examples

```
data('mycerIds10', package='INSPEcT')
viewModelRates(mycerIds10, 'synthesis')
```

Index