

Package ‘segRNAs’

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Type Package

Title Compute MSE and NID for segmentation selection

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Description Robust RNA-seq data segmentation selection criteria: MSE and NID.

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Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

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counts.per.seg	<i>Average count per segment for each replicat</i>
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Description

Average count per segment for each replicat

Usage

```
counts.per.seg(list.tau, list.rna.data)
```

Arguments

list.tau A list of changepoints, for each dataset, for a given penalty.
list.rna.data A list of dataset (RNA countings)

Value

a matrix of average counts per segmentation per replica. The last line is the actual average counts per segment.

Examples

```
library(robseg)
log.d1      <- log.transform(dataset1)
log.d2      <- log.transform(dataset2)
my.list.data <- list(log.d1,log.d2)
rob_seg1    <- Rob_seg.std( x = log.d1 , loss = "Outlier", lambda = 25*log(length(dataset1)), lthreshold=3)
rob_seg2    <- Rob_seg.std( x = log.d2 , loss = "Outlier", lambda = 25*log(length(dataset1)), lthreshold=3)
my.list.tau <- list(rob_seg1$t.est,rob_seg2$t.est)
cps         <- counts.per.seg(list.tau = my.list.tau,list.rna.data = my.list.data)
```

log.transform	<i>log-transformation function for segmentation</i>
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Description

log-transformation function for segmentation

Usage

```
## S3 method for class 'transform'
log(rna.data)
```

Arguments

rna.data : a vector of counts from RNA-sequencing

Value

a vector of log-transformed data

Examples

```
log.data <- log.transform(dataset1)
plot(dataset1, type="l")
plot(log.data, type="l")
```

mean.seg	<i>Segment mean per data</i>
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Description

Segment mean per data

Usage

```
## S3 method for class 'seg'
mean(tau, rna.data)
```

Arguments

tau a vector of changepoints
rna.data a vector of counts

Value

a vector of means per data

Examples

```
library(robseg)
log.trans <- log.transform(dataset1)
seg_rob <- Rob_seg.std(x = log.trans, loss = "Outlier", lambda = beta, lthreshold=3)
tau <- seg_rob$t.est
av.line <- mean.seg(rna.data = data, tau = tau)
plot(av.line)
```

mse.func	<i>Computing the MSE from a pair of datasets, depending on a given penalty</i>
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Description

Computing the MSE from a pair of datasets, depending on a given penalty

Usage

```
mse.func(rna.data1, rna.data2, beta)
```

Arguments

rna.data1	a vector of data
rna.data2	a vector of data, same length as rna.data1
beta	a value of penalty

Value

the value of MSE from two datasets by a given penalty

Examples

```
log.dataset1 <- log.transform(dataset1)
log.dataset2 <- log.transform(dataset2)
mse.val <- mse.func(rna.data1=log.dataset1, rna.data2=log.dataset2, beta=25*log(length(dataset1)))
```

mse.penalties	<i>Segmentation selection on MSE criterion</i>
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Description

Segmentation selection on MSE criterion

Usage

```
mse.penalties(list.rna.data, penalty_range)
```

Arguments

list.rna.data	a list of vector of dataset
penalty_range	a vector of length 2, respectively defining the minimum penalty and the maximum penalty

Value

A list with a vector of penalties and a matrix of mse

Examples

```
l.d1 <- log.transform(dataset1)
l.d2 <- log.transform(dataset2)
l.d3 <- log.transform(dataset3)
l.data <- list(l.d1,l.d2,l.d3)
mse.res <- mse.penalties(list.rna.data=l.data, penalty_range=c(10,100))
```

nid.func

NID computed from two changepoint datasets

Description

NID computed from two changepoint datasets

Usage

```
nid.func(rna.data1, rna.data2, beta)
```

Arguments

rna.data1	a vector of data
rna.data2	a vector of data
beta	penalty value

Value

the NID from the 2 segmentations, a decimal value between 0 and 1.

Examples

```
log.dataset1 <- log.transform(dataset1)
log.dataset2 <- log.transform(dataset2)
nid.val <- nid.func(rna.data1=log.dataset1,rna.data2=log.dataset2,beta=25*log(length(dataset1)))
```

nid.penalties	<i>Segmentation penalty criterion by NID</i>
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Description

Segmentation penalty criterion by NID

Usage

```
nid.penalties(list.rna.data, penalty_range)
```

Arguments

`list.rna.data` a list of datasets with the same length
`penalty_range` a vector of length 2 respectively defining the minimum penalty and the maximum penalty

Value

A list with a vector of penalties and a matrix of nid

Examples

```
l.d1 <- log.transform(dataset1)
l.d2 <- log.transform(dataset2)
l.d3 <- log.transform(dataset3)
l.data <- list(l.d1,l.d2,l.d3)
nid.res <- nid.penalties(list.rna.data=l.data, penalty_range=c(10,100))
```

plot.MSE	<i>Plotting MSE object</i>
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Description

Plotting MSE object

Usage

```
## S3 method for class 'MSE'
plot(mses)
```

Arguments

`mse` : the MSE objet returned by the function mse.penalties

Value

the graph according to the parameters entered in the function

Examples

```
mse.beta <- mse.penalties(list(log.transform(dataset1),log.transform(dataset2),log.transform(dataset3)), penalty_range = c(15,75))  
plot(mse.beta)
```

plot.NID

Plotting NID object

Description

Plotting NID object

Usage

```
## S3 method for class 'NID'  
plot(nids)
```

Arguments

nid : the NID objet returned by the function nid.penalties

Value

the graph according to the parameters entered in the function

Examples

```
nid.beta <- nid.penalties(rna.data1 = dataset1 , rna.data2 = dataset2, penalty_range = c(15,75) )  
plot(nid.beta)
```

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