

Package ‘segRNAcountings’

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Type Package

Title Using Criteria To Choose A Segmentation of Counts From RNA-seq

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Description Containing some criteria to choose an appropriate segmentation from criteria based on penalty value, such as mse or nid.

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counts.per.seg	<i>The average countings per segments for each replica</i>
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Description

The average countings per segments for each replica

Usage

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

Arguments

list.tau	list of changepoints for each replica, for a given penalty value.
list.data	list of dataset for each replica.

Value

a matrix containing the average count for each segment (column), for each replica(row).

Examples

```
l.d1 <- log.transform(dataset1)
seg_rob1 <- Rob_seg.std(x = l.d1, loss = "Outlier", lambda = 25*log(length(l.d1)), lthreshold=3)
tau1 <- seg_rob1$t.est
l.d2 <- log.transform(dataset2)
seg_rob2 <- Rob_seg.std(x = l.d2, loss = "Outlier", lambda = 25*log(length(l.d1)), lthreshold=3)
tau2 <- seg_rob2$t.est
l.d3 <- log.transform(dataset3)
seg_rob3 <- Rob_seg.std(x = l.d3, loss = "Outlier", lambda = 25*log(length(l.d1)), lthreshold=3)
tau3 <- seg_rob3$t.est
l.data <- list(dataset1,dataset2,dataset3)
l.tau <- list(tau1,tau2,tau3)
cps <- counts.per.seg(list.tau=l.tau,list.data=l.data)
```

CROPS.RFPOP_	<i>Segmenting a dataset using rob_seg, over a penalty range scanned by a CROPS algorithm</i>
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Description

Segmenting a dataset using rob_seg, over a penalty range scanned by a CROPS algorithm

Usage

```
CROPS.RFPOP_(data, min_pen = 5, max_pen = 20, lthreshold = 3)
```

Arguments

data	The dataset, a vector
min_pen	minimum value of the penalty range
max_pen	maximum value of the penalty range
lthreshold	the threshold used to detect and rescale the outliers among the dataset (3 by default)

Value

A list: respectively a matrix of penalties (the 2nd line contains the intermediate penalties), a list of segmentations for each intermediate lambda and a list of smt for each intermediate lambda (they are obviously all the same...)

Examples

```
log.t1 <- log.transform(dataRNA[,1])
crops.out <- CROPS.RFPOP_(log.t1,min_pen = 5,max_pen = 10,lthreshold = 3)
View(crops.out)
```

getIndexLambda	<i>returning the index of a penalty among a vector of intermediate penalties</i>
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Description

returning the index of a penalty among a vector of intermediate penalties

Usage

```
getIndexLambda(lambda, o.crops)
```

Arguments

lambda	a penalty value
o.crops	the output object from CROPS.RFPOP_

Value

the index of the penalty, an integer

Examples

```
log.t1 <- log.transform(dataRNA[,1])
crops.out <- CROPS.RFPOP_(log.t1,min_pen = 5,max_pen = 10,lthreshold = 3)
getInd <- getIndex(lambda = 10*log(n), o.crops = crops.out)
getInd
```

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")
```

mse.penalties	<i>Computing MSE depending on penalty</i>
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Description

Computing MSE depending on penalty

Usage

```
mse.penalties(list.seg)
```

Arguments

list.seg a "SEGMENTATIONS" object

Value

a matrix of results: the lines represent the observations (the replicas), the "avant-dernière" line: the mean of them. The last line: the intermediate penalties. The columns represent the mse value for each penalty.

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)
list.res <- seg.func(func="rob_seg",list.rna.data=l.data,penalty_range=c(10,100))
mse.res <- mse.penalties(list.res)

```

nid.penalties	<i>Computing NID depending on penalty</i>
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Description

Computing NID depending on penalty

Usage

```
nid.penalties(list.seg)
```

Arguments

list.seg an "SEGMENTATIONS" object

Value

a matrix of results: the lines represent the observations (the replicas), the "avant-dernière" line: the mean of them. The last line: the intermediate penalties. The columns represent the nid value for each penalty.

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)
list.res <- seg.func(func="rob_seg",list.rna.data=l.data,penalty_range=c(10,100))
nid.res <- nid.penalties(list.res)

```

plot.MSE	<i>Ploting the mse depending on the penalties</i>
----------	---

Description

Ploting the mse depending on the penalties

Usage

```
## S3 method for class 'MSE'  
plot(mse.res)
```

Arguments

mse.res a "MSE" object

Value

a graph...

Examples

```
plot(mse.res)
```

plot.NID	<i>Ploting the nid depending on the penalties</i>
----------	---

Description

Ploting the nid depending on the penalties

Usage

```
## S3 method for class 'NID'  
plot(nid.res)
```

Arguments

mse.res a "NID" object

Value

a graph...

Examples

```
plot(nid.res)
```

seg.criteria

*Computing different criterion for RNAs segmentations***Description**

Computing different criterion for RNAs segmentations

Usage

```
seg.criteria(list.seg, criterion)
```

Arguments

`list.seg` A "SEGMENTATIONS" object
`criterion` A string indicating the selected criterion: "MSE" or "NID" so far

Value

the selected criterion and a plot

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)
list.res <- seg.func(func="rob_seg",list.rna.data=l.data,penalty_range=c(10,100))
crit.res <- seg.criteria(list.res, criterion="MSE")
crit.res2 <- seg.criteria(list.res, criterion="NID")
```

seg.func

*Segmenting a list of dataset for a given segmentation algo and a penalty range***Description**

Segmenting a list of dataset for a given segmentation algo and a penalty range

Usage

```
seg.func(list.rna.data, penalty_range, mc.cores = 1)
```

Arguments

`list.rna.data` a list of dataset
`penalty_range` a vector of length 2. Respectively. The min and max penalties
`mc.cores` a parameter for `mclapply`, 1 by default... (CF the appropriate documentation about `mclapply`...)

Value

a list of values: a list of tau for each beta, a list of smt for each dataset, a list of intermediate penalties.

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)
list.res <- seg.func(list.rna.data=l.data,penalty_range=c(10,100),mc.cores = 1)
View (list.res)
```


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