

Package ‘PICS’

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Type Package

Title Probabilistic inference of ChIP-seq

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Suggests rtracklayer, parallel, knitr

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URL <https://github.com/SRenan/PICS>

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| | |
|--------|------------------------------|
| bam2gr | <i>Pre-process bam files</i> |
|--------|------------------------------|

Description

Reads a bam file using Rsamtools and extract the reads for each chromosome.

Usage

```
bam2gr(bamFile, chr = NULL, PE = FALSE, verbose = FALSE)
```

Arguments

| | |
|---------|---|
| bamFile | A character. The name of the .bam file to read. |
| chr | A character. An optional character string. If specified, only the selected chromosome will be returned. Speed up the computation. |
| PE | A logical. Set to TRUE for paired-end sequencing data. |
| verbose | A logical. Print additional information about the data. |

Value

A GRanges of all the reads for each chromosome.

Note

The user might encounter a memory allocation error when using bam files of bigger sizes. Splitting the file by chromosome before calling bam2gr will solve this issue.

For Paired-End data, non matched reads are discarded.

See Also

segmentPICS

| | |
|------------------|-----------------------------------|
| candidate.region | <i>Identify candidate regions</i> |
|------------------|-----------------------------------|

Description

Identify candidate regions from paired-end sequencing data.

Usage

```
candidate.region(PE.RD, islandDepth, min_cut, max_cut)
```

Arguments

| | |
|-------------|--|
| PE.RD | A character. File including sequenced pairs. |
| islandDepth | A numeric. The minimum depth of candidate regions. |
| min_cut | A numeric. The minimum region length. |
| max_cut | A numeric. The maximum region length. |

| | |
|-------------------|--|
| makeGRangesOutput | <i>Export a PICS object to GRanges</i> |
|-------------------|--|

Description

Export a PICS object to GRanges

Usage

```
makeGRangesOutput(
  obj,
  type = "fixed",
  length = 100,
  filter = list(delta = c(0, Inf), se = c(0, Inf), sigmaSqF = c(0, Inf), sigmaSqR = c(0,
    Inf), score = c(0, Inf))
)
```

Arguments

| | |
|--------|---|
| obj | A PICS object. The output of the PICS function. |
| type | A character. One of "fixed", "bed", "ci" or "wig". |
| length | A numeric. The length of the region around the center (μ). Only used when type = "fixed". |
| filter | A list. Additional filtering options. |

Value

A GRanges object.

See Also

PICS

PICS *Estimation of binding site positions*

Description

This object contains Estimation of binding site positions and has the following slots: segReadsList, dataType.

Usage

```
PICS(
  segReadsList,
  dataType = NULL,
  paraEM = NULL,
  paraPrior = NULL,
  nCores = 1
)
```

Arguments

| | |
|--------------|--|
| segReadsList | This object contains segmentation of Genome |
| dataType | A character. The type of data you are processing: 'TF' for transcription factor. |
| paraEM | A list of parameters for the EM algorithm as returned by the setParaEM function. The default parameters should be good enough for most usages. |
| paraPrior | A list of parameters for the priors as returned by setParaPrior. |
| nCores | An integer. The number of cores that should be used in parallel by the function. |

Value

An object of class picList containing the estimated binding site positions.

pics-class

PICS class

Description

This object is used to gather all parameters from fitting PICS to a single candidate region.

Usage

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

```
## S4 method for signature 'pics'  
minRange(x)
```

```
## S4 method for signature 'pics'  
maxRange(x)
```

```
## S4 method for signature 'pics'  
score(x)
```

```
## S4 method for signature 'pics'  
scoreReverse(x)
```

```
## S4 method for signature 'pics'  
scoreForward(x)
```

```
## S4 method for signature 'pics'  
chromosome(x)
```

```
## S4 method for signature 'pics'  
se(x)
```

```
## S4 method for signature 'pics'  
seF(x)
```

```
## S4 method for signature 'pics'  
seR(x)
```

```
## S4 method for signature 'pics'  
sigmaSqF(x)
```

```
## S4 method for signature 'pics'  
sigmaSqR(x)
```

```
## S4 method for signature 'pics'  
delta(x)
```

```
## S4 method for signature 'pics'  
mu(x)  
  
## S4 method for signature 'pics'  
w(x)  
  
## S4 method for signature 'pics'  
K(x)  
  
## S4 method for signature 'pics'  
code(x)  
  
## S4 method for signature 'pics'  
summary(object)
```

Arguments

object, x A pics object.

Functions

- show,pics-method: show method
- minRange,pics-method: Get start of range
- maxRange,pics-method: Get end of range
- score,pics-method: Score accessor.
- scoreReverse,pics-method: Reverse score accessor.
- scoreForward,pics-method: Forward score accessor.
- chromosome,pics-method: Chromosome accessor
- se,pics-method: se accessor
- seF,pics-method: Forward se accessor
- seR,pics-method: Reverse se accessor
- sigmaSqF,pics-method: sigmaSqF accessor
- sigmaSqR,pics-method: sigmaSqR accessor
- delta,pics-method: delta accessor
- mu,pics-method: mu accessor
- w,pics-method: w accessor
- K,pics-method: K accessor
- code,pics-method: Error code accessor
- summary,pics-method: Summary of the object

Slots

`estimates` A list containing all parameters estimates as well as standard errors.
`Nmerged` The number of binding events that were merged; binding events that overlap are merged.
`converge` A logical value indicating whether the EM algorithm has converged.
`chr` The candidate region's chromosome.
`score` Score of the binding event
`scoreF` Forward score of the binding event.
`scoreR` Reverse score of the binding event.
`range` Genomic ranges.

pics-generics

Generics associated with pics classes

Description

These generics are used in methods of `pics`, `picsError` and `picsList` classes. See class help pages for method documentation.

Usage

`minRange(x, ...)`

`maxRange(x, ...)`

`score(x, ...)`

`scoreReverse(x, ...)`

`scoreForward(x, ...)`

`chromosome(x, ...)`

`se(x, ...)`

`seF(x, ...)`

`seR(x, ...)`

`sigmaSqF(x, ...)`

`sigmaSqR(x, ...)`

`delta(x, ...)`

```
mu(x, ...)  
w(x, ...)  
K(x, ...)  
code(x, ...)  
  
## S4 method for signature 'data.frame'  
score(x)  
  
## S4 method for signature 'data.frame'  
scoreReverse(x)  
  
## S4 method for signature 'data.frame'  
scoreForward(x)  
  
## S4 method for signature 'data.frame'  
chromosome(x)  
  
## S4 method for signature 'data.frame'  
se(x)  
  
## S4 method for signature 'data.frame'  
seF(x)  
  
## S4 method for signature 'data.frame'  
seR(x)  
  
## S4 method for signature 'data.frame'  
sigmaSqF(x)  
  
## S4 method for signature 'data.frame'  
sigmaSqR(x)  
  
## S4 method for signature 'data.frame'  
delta(x)  
  
## S4 method for signature 'data.frame'  
mu(x)
```

Arguments

`x, ...` Object and arguments passed to the methods.

Functions

- `minRange`: Start accessor
- `maxRange`: End accessor

- score: Score accessor
- scoreReverse: Reverse score accessor
- scoreForward: Forward score accessor
- chromosome: Chromosome accessor
- se: se accessor
- seF: Forward se accessor
- seR: Reverse se accessor
- sigmaSqF: sigmaSqF accessor
- sigmaSqR: sigmaSqR accessor
- delta: delta accessor
- mu: mu accessor
- w: w accessor
- K: K accessor
- code: Return error codes
- score, data.frame-method: Score accessor
- scoreReverse, data.frame-method: Reverse score accessor
- scoreForward, data.frame-method: Forward score accessor
- chromosome, data.frame-method: chromosome accessor
- se, data.frame-method: se accessor
- seF, data.frame-method: seF accessor
- seR, data.frame-method: seR accessor
- sigmaSqF, data.frame-method: sigmaSqF accessor
- sigmaSqR, data.frame-method: sigmaSqR accessor
- delta, data.frame-method: delta accessor
- mu, data.frame-method: mu accessor

picsError-class

picsError class

Description

This class is used in cases when the algorithm does not converge.

Usage

```
## S4 method for signature 'picsError'  
show(object)  
  
## S4 method for signature 'picsError'  
minRange(x)  
  
## S4 method for signature 'picsError'  
maxRange(x)  
  
## S4 method for signature 'picsError'  
score(x)  
  
## S4 method for signature 'picsError'  
scoreReverse(x)  
  
## S4 method for signature 'picsError'  
scoreForward(x)  
  
## S4 method for signature 'picsError'  
chromosome(x)  
  
## S4 method for signature 'picsError'  
se(x)  
  
## S4 method for signature 'picsError'  
seF(x)  
  
## S4 method for signature 'picsError'  
seR(x)  
  
## S4 method for signature 'picsError'  
sigmaSqF(x)  
  
## S4 method for signature 'picsError'  
sigmaSqR(x)  
  
## S4 method for signature 'picsError'  
delta(x)  
  
## S4 method for signature 'picsError'  
mu(x)  
  
## S4 method for signature 'picsError'  
w(x)  
  
## S4 method for signature 'picsError'  
K(x)
```

```
## S4 method for signature 'picsError'
code(x)
```

Arguments

object, x A picsError object.

Functions

- show,picsError-method: show method
- minRange,picsError-method: Get start of range
- maxRange,picsError-method: Get end of range
- score,picsError-method: Score accessor.
- scoreReverse,picsError-method: Reverse score accessor.
- scoreForward,picsError-method: Forward score accessor.
- chromosome,picsError-method: Chromosome accessor
- se,picsError-method: se accessor
- seF,picsError-method: Forward se accessor
- seR,picsError-method: Reverse se accessor
- sigmaSqF,picsError-method: sigmaSqF accessor
- sigmaSqR,picsError-method: sigmaSqR accessor
- delta,picsError-method: delta accessor
- mu,picsError-method: mu accessor
- w,picsError-method: w accessor
- K,picsError-method: K accessor
- code,picsError-method: Error code accessor

Slots

errorCode The error code for debugging.

picsFDR

Estimate the FDR

Description

Estimate the false detection rate for an object of class pics or picsList.

Usage

```

picsFDR(
  picsIP,
  picsCont,
  filter = list(delta = c(0, Inf), se = c(0, Inf), sigmaSqF = c(0, Inf), sigmaSqR = c(0,
    Inf))
)

```

Arguments

| | |
|-----------------------|--|
| <code>picsIP</code> | An object of class <code>pics</code> or <code>picsList</code> containing the informations for the IP reads. |
| <code>picsCont</code> | An object of class <code>pics</code> or <code>picsList</code> containing the informations for the control reads |
| <code>filter</code> | A list of ranges for filtering regions based on PICS parameters. By default filter is set to NULL and all regions are used. <ul style="list-style-type: none"> • <code>delta</code>: Length of the binding sites • <code>se</code>: Standard error • <code>sigmaSqF</code>: Forward peak variance • <code>sigmaSqR</code>: Reverse peak variance |

Value

A data.frame with the following columns: FDR, score, N

See Also

`picsList` `pics`

`picsList-class`

List of PICS objects

Description

List of PICS objects

Usage

```

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

## S4 method for signature 'picsList'
minRange(x)

## S4 method for signature 'picsList'
maxRange(x)

```

```
## S4 method for signature 'picsList'  
score(x)  
  
## S4 method for signature 'picsList'  
scoreReverse(x)  
  
## S4 method for signature 'picsList'  
scoreForward(x)  
  
## S4 method for signature 'picsList'  
chromosome(x)  
  
## S4 method for signature 'picsList'  
se(x)  
  
## S4 method for signature 'picsList'  
seF(x)  
  
## S4 method for signature 'picsList'  
seR(x)  
  
## S4 method for signature 'picsList'  
sigmaSqF(x)  
  
## S4 method for signature 'picsList'  
sigmaSqR(x)  
  
## S4 method for signature 'picsList'  
delta(x)  
  
## S4 method for signature 'picsList'  
mu(x)  
  
## S4 method for signature 'picsList'  
w(x)  
  
## S4 method for signature 'picsList'  
K(x)  
  
## S4 method for signature 'picsList'  
code(x)  
  
## S4 method for signature 'picsList'  
length(x)  
  
## S4 method for signature 'picsList'  
summary(object)
```

```
## S4 method for signature 'picsList,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'picsList,ANY,ANY'
x[[i, j, ..., exact = TRUE]]
```

Arguments

object, x A pics object.
i, j, ..., drop, exact
 Arguments passed to subset functions

Functions

- show,picsList-method: show method
- minRange,picsList-method: Get start of range
- maxRange,picsList-method: Get end of range
- score,picsList-method: Score accessor.
- scoreReverse,picsList-method: Reverse score accessor.
- scoreForward,picsList-method: Forward score accessor.
- chromosome,picsList-method: Chromosome accessor
- se,picsList-method: se accessor
- seF,picsList-method: Forward se accessor
- seR,picsList-method: Reverse se accessor
- sigmaSqF,picsList-method: sigmaSqF accessor
- sigmaSqR,picsList-method: sigmaSqR accessor
- delta,picsList-method: delta accessor
- mu,picsList-method: mu accessor
- w,picsList-method: w accessor
- K,picsList-method: K accessor
- code,picsList-method: Error code accessor
- length,picsList-method: Return the length of the object
- summary,picsList-method: Summary of the object
- [,picsList,ANY,ANY,ANY-method: Subset list
- [[,picsList,ANY,ANY-method: Subset element

plot-FDR

Plot PICS FDR

Description

This method plots a curve showing the FDR as a function of the PICS scores.

Usage

```
## S4 method for signature 'picsList,picsList'
plot(x, y, filter = NULL, h = 0.1, ...)
```

Arguments

| | |
|--------|---|
| x | A <code>picsList</code> object as returned by the function PICS run on the treatment data. |
| y | A <code>picsList</code> object as returned by the function PICS run on the control data. |
| filter | A list of ranges for filtering regions based on PICS parameters. By default filter is set to 'NULL' and all regions are used. |
| h | A value between 0 and 1, representing the desired FDR. This simply draws a horizontal line at the given value. |
| ... | Further graphical parameters passed to the generic function plot. |

See Also

PICS

plot-pics

Plot methods for PICS objects

Description

Methods to plot `pics` and `segReads` objects and derived classes.

Usage

```
## S4 method for signature 'pics,segReads'
plot(
  x,
  y,
  addKernel = FALSE,
  addNucleosome = FALSE,
  addSe = TRUE,
  main = NULL,
  ...)
```

```

)

## S4 method for signature 'picsError,segReads'
plot(x, y, addKernel = FALSE, main = NULL, ...)

## S4 method for signature 'picsList,segReadsList'
plot(
  x,
  y,
  regionIndex = NULL,
  addKernel = FALSE,
  addNucleosome = FALSE,
  addSe = TRUE,
  main = NULL,
  ...
)

```

Arguments

| | |
|----------------------------|--|
| <code>x, y</code> | Objects |
| <code>addKernel</code> | Add kernel density estimate to the plot. |
| <code>addNucleosome</code> | Add a nucleosome track to the plot. |
| <code>addSe</code> | Add standard error to the plot. |
| <code>main</code> | Main title. |
| <code>...</code> | Arguments to be passed to the plot method. |
| <code>regionIndex</code> | Add region index to the plot. |

Functions

- `plot,pics,segReads-method`: Plot method for `pics` and `segReads`
- `plot,picsError,segReads-method`: Plot method for `picsError` and `segReads`
- `plot,picsList,segReadsList-method`: Plot method for `picsList` and `segReadsList`

segChrRead

Segmentation of paired-end sequencing data

Description

These two functions are part of the segmentation step for paired-end sequencing data and are exported to be used in PING package.

segmentPICS

*Segment the genome into candidate regions***Description**

Pre-process bidirectional aligned reads data from a single ChIP-Seq experiment to detect candidate regions with a minimum number of forward and reverse reads. These candidate regions will then be processed by PICS.

Usage

```
segmentPICS(
  data,
  dataC = NULL,
  map = NULL,
  minReads = 2,
  minReadsInRegion = 3,
  jitter = FALSE,
  dataType = "TF",
  maxLregion = 0,
  minLregion = 100
)
```

Arguments

| | |
|------------------|--|
| data | A GRanges object containing the IP reads. See details for more information on how to set up the data. |
| dataC | A GRanges object containing the control reads. Set to NULL by default, i.e. no control. |
| map | A GRanges object containing the mappability profiles. Set to NULL by default, i.e. no profiles. |
| minReads | A numeric. The minimum number of F/R reads to be present in the sliding window. |
| minReadsInRegion | A numeric. The minimum number of F/R reads to be present in the region. |
| jitter | A logical value stating whether some noise should be added to the read locations. This is recommended if the read positions have lots of duplicates. |
| dataType | A character. Type of experiment. "TF" or "H". |
| maxLregion | A numeric. The maximum length. |
| minLregion | A numeric. The minimum length. |

Value

An object of class `segReadsList` containing the results for all pre-processed regions.

References

X. Zhang, G. Robertson, M. Krzywinski, K. Ning, A. Droit, S. Jones, and R. Gottardo, "PICS: Probabilistic Inference for ChIP-seq" arXiv, 0903.3206, 2009.

See Also

segReadsList

Examples

```
# Read data
path<-system.file("extdata",package="PICS")
## Note that the col name for the chromosome needs to be space and not chr
dataIP <- read.table(file.path(path, "Treatment_tags_chr21_sort.bed"), header=TRUE,
                    colClasses = c("factor","integer","integer","factor"))
dataIP <- as(dataIP, "GRanges")

dataCont <- read.table(file.path(path, "Input_tags_chr21_sort.bed"), header=TRUE,
                    colClasses = c("factor","integer","integer","factor"))
dataCont <- as(dataCont, "GRanges")

map <- read.table(file.path(path, "mapProfileShort"), header=TRUE,
                colClasses = c("factor","integer","integer","NULL"))
map <- as(map, "GRanges")
seg <- segmentPICS(dataIP, dataC = dataCont, map = map, minReads = 1)
```

segReads-class

Classes and functions to segment the genome in candidate regions

Description

Pre-process bidirectional aligned reads data from a single ChIP-Seq experiment to detect candidate regions with a minimum number of forward and reverse reads. These candidate regions will then be processed by PICS.

Usage

```
segReads(yF, yR, cF, cR, map, chr)

segReadsList(List, paraSW, N, Nc)

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

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

```

map(x, ...)

## S4 method for signature 'segReads'
map(x)

## S4 method for signature 'segReadsList'
map(x)

## S4 method for signature 'segReadsList'
length(x)

## S4 method for signature 'segReadsList'
summary(object)

## S4 method for signature 'segReads'
summary(object)

## S4 method for signature 'segReadsList,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'segReadsList,ANY,ANY'
x[[i, j, ..., exact = TRUE]]

```

Arguments

| | |
|------------------------|---|
| yF | A numeric vector. Forward reads. |
| yR | A numeric vector. Reverse reads. |
| cF | A numeric vector. Forward reads for the controls. |
| cR | A numeric vector. Reverse reads for the controls. |
| map | A matrix. The mappability profile. |
| chr | A character. Chromosome name. |
| List | A list of segReads objects. |
| paraSW | A list of parameters for the genomic regions. |
| N | A numeric. The number of reads in the data. |
| Nc | A numeric. The number of reads in the control. |
| object, x | A segReads object. |
| i, j, ..., exact, drop | Additional arguments passed to subset methods. |

Functions

- segReads: segReads Constructor
- segReadsList: segReadsList Constructor
- show, segReads-method: show method
- show, segReadsList-method: show method

- map: map generic
- map, segReads-method: map method
- map, segReadsList-method: map method
- length, segReadsList-method: Return length of segReadsList
- summary, segReadsList-method: Summary method
- summary, segReads-method: Summary method
- [, segReadsList, ANY, ANY, ANY-method: Subset methods
- [[, segReadsList, ANY, ANY-method: Subset methods

Note

segReads and segReadsList objects are not meant to be built via the constructors. The constructors are used in segmentPICS.

| | |
|-----------------|--|
| segReadsGeneric | <i>Perform genome segmentation depending</i> |
|-----------------|--|

Description

Perform genome segmentation depending

Usage

```
segReadsGeneric(
  data,
  dataC = NULL,
  map = NULL,
  minReads = 2,
  minReadsInRegion = 3,
  jitter = FALSE,
  maxLregion = 0,
  minLregion = 100,
  step = 20,
  width = 250,
  package = "PICS"
)
```

Arguments

| | |
|-------|---|
| data | A GRanges object containing the IP reads. See details for more information on how to set up the data. |
| dataC | A GRanges object containing the control reads. Set to NULL by default, i.e. no control. |
| map | A GRanges object containing the mappability profiles. Set to NULL by default, i.e. no profiles. |

| | |
|------------------|--|
| minReads | A numeric. The minimum number of F/R reads to be present in the sliding window. |
| minReadsInRegion | A numeric. The minimum number of F/R reads to be present in the region. |
| jitter | A logical value stating whether some noise should be added to the read locations. This is recommended if the read positions have lots of duplicates. |
| maxLregion | A numeric. The maximum length. |
| minLregion | A numeric. The minimum length. |
| step | A numeric. The increment of the sliding window. |
| width | A numeric. The width of the region. |
| package | A character. "PICS" or "PING" |

segReadsListPE-class *Class and methods for list of candidate regions from paired-end data*

Description

Class and methods for list of candidate regions from paired-end data

Usage

```
segReadsListPE(List, paraSW, N, NFm, NRm, Nc, NcFm, NcRm)
```

```
## S4 method for signature 'segReadsListPE,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]
```

```
## S4 method for signature 'segReadsListPE,ANY,ANY'
x[[i, j, ..., exact = TRUE]]
```

Arguments

| | |
|---------------------------|---|
| List | A list of segReadsPE objects. |
| paraSW | A list of parameters for the genomic regions. |
| N, NFm, NRm | Read counts in the data. |
| Nc, NcFm, NcRm | Read counts in the control. |
| x, i, j, ..., drop, exact | Arguments passed to subset methods |

Functions

- segReadsListPE: segReadsListPE constructor.
- [, segReadsListPE, ANY, ANY, ANY-method: subset method
- [[, segReadsListPE, ANY, ANY-method: subset method

segReadsPE-class *Classe and methods for candidate regions from paired-end data*

Description

A segReadsPE object represents a single candidate region, including all its informative reads and mappability profile.

Usage

```
segReadsPE(yF, yR, yFm, yRm, cF, cR, cFm, cRm, map, chr)
```

Arguments

| | |
|-----|---|
| yF | A numeric vector. Forward reads. |
| yR | A numeric vector. Reverse reads. |
| yFm | A numeric vector. Forward reads on paired end. |
| yRm | A numeric vector. Reverse reads on paired end. |
| cF | A numeric vector. Forward reads for the controls. |
| cR | A numeric vector. Reverse reads for the controls. |
| cFm | A numeric vector. Forward reads on paired end for the controls. |
| cRm | A numeric vector. Reverse reads on paired end for the controls. |
| map | A matrix. The mappability profile. |
| chr | A character. Chromosome name. |

Functions

- segReadsPE: segReadsPE constructor.

Note

segReadsPE objects are not meant to be built via the constructors. The constructors are used in segmentPICS.

| | |
|-----------|---|
| setParaEM | <i>List of parameters for the EM algorithm that can be used as an argument of PICS.</i> |
|-----------|---|

Description

This function takes from 0 to 7 EM algorithm parameters as argument, check if they are valid and returns a list to be used in a call to PICS.

Usage

```
setParaEM(  
  minK = 1,  
  maxK = 15,  
  tol = 1e-04,  
  B = 100,  
  mSelect = "BIC",  
  mergePeaks = TRUE,  
  mapCorrect = TRUE,  
  dataType = NULL  
)
```

Arguments

| | |
|------------|--|
| minK | An integer. The minimum number of binding events per region. If the value is 0, the minimum number is automatically calculated. |
| maxK | An integer. The maximum number of binding events per region. If the value is 0, the maximum number is automatically calculated. |
| tol | A numeric. The tolerance for the EM algorithm. |
| B | An integer. The maximum number of iterations to be used. |
| mSelect | A character. specifying the information criteria to be used when selecting the number of binding events. |
| mergePeaks | A logical stating whether overlapping binding events should be picked. |
| mapCorrect | A logical stating whether mappability profiles should be incorporated in the estimation, i.e: missing reads estimated. |
| dataType | A character. If a dataType is set, the algorithm will use the default parameters for this type of data (all the previous arguments will be ignored). |

Value

A list of parameters to be used in PICS.

See Also

PICS setParaPrior

setParaPrior *List of parameters that can be used as an argument of PICS.*

Description

This function takes from 0 to 6 parameters as argument, check if they are valid and returns a list to be used in a call to PICS.

Usage

```
setParaPrior(
  xi = 200,
  rho = 1,
  alpha = 20,
  beta = 40000,
  lambda = 0,
  dMu = 0,
  dataType = NULL,
  PExi = 0
)
```

Arguments

| | |
|----------|---|
| xi | An integer. The average DNA fragment size. |
| rho | An integer. A variance parameter for the average DNA fragment size distribution. |
| alpha | An integer. First hyperparameter of the inverse Gamma distribution for σ^2 in the PICS model. |
| beta | An integer. Second hyperparameter of the inverse Gamma distribution for σ^2 in the PICS model. |
| lambda | An integer. The precision of the prior for mu used for histone data. |
| dMu | An integer. Our best guess for the distance between two neighboring nucleosomes. |
| dataType | A character string. If a valid dataType is specified, use our suggested parameters. "MNase" or "sonicated" |
| PExi | A numeric. With paired end data, 'xi' can be calculated directly from the reads. If PExi is set, it will overwrite the xi determined by the dataType. |

Value

A list of 6 parameters to be used in PICS.

See Also

setParaEM PICS

Examples

```
# set prior for PICS data
paraPrior <- setParaPrior()
# set prior for sonicated data using our selected default parameters
paraPrior <- setParaPrior(dataType="sonicated")
```

| | |
|------------|--------------------------------------|
| summarySeg | <i>Summarize segmentList objects</i> |
|------------|--------------------------------------|

Description

Summarize segmentList objects into a data.frame

Usage

```
summarySeg(seg)
```

Arguments

seg A segmentList object as returned by segmentPICS.

Value

A data.frame. With

- chr: Chromosome id
- NF: Number of forward reads
- NR: Number of reverse reads
- L: Length of segment
- min: Start location of segments
- max: End location of segments

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