PICS

April 20, 2011

`makeRangedDataOutput`
Create a RangedData object from a PICS output

Description

Create a list of 'RangedData' objects from a 'pics' object. The resulting RangedData object can then be analyzed with the 'IRanges' packages and/or exported to bed/wig files with the 'rtracklayer' package.

Usage

```
makeRangedDataOutput(obj, type="fixed", filter=list(delta=c(0,Inf),se=c(0,Inf),s
```

Arguments

`obj`	An object of class 'picsList' as returned by 'PICS' when running it on the IP/Control data.
`type`	The type of intervals to be created. The different types are 'bed', 'wig', 'ci' and 'fixed'. See details for more info.
`filter`	A list of filters to be used before computing the FDR. By default all regions are included, see details for more info on how to specify the filters.
`length`	The length to be used for the fixed type 'RangedData', see details.

Details

'bed' will generate intervals from the forward peak max to the reverse peak max. 'wig' will generate a density profile for the forward and reverse reads. 'bed' and 'wig' types should be used to be exported to wig/bed files to be used with the UCSC genome browser. 'ci' corresponds to the binding site estimates +/-3*se, while 'fixed' corresponds to the binding site estimates +/-3*length. 'bed' and 'wig' files can be exported using the 'export' function fo the 'rtracklayer' package.

Value

An object of type 'RangedData'.

Author(s)

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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. To appear in Biometrics.

See Also

export

Examples

```
## Not run:
  rdBed<-makeRangedDataOutput(pics,type="bed",filter=list(delta=c(50,Inf),se=c(0,50),sigm
  export(rbBed,"myfile.bed")
  rdBed<-makeRangedDataOutput(pics,type="wig",filter=list(delta=c(50,Inf),se=c(0,50),sigm
  export(rbBed,"myfile.wig")
## End(Not run)
```

`pics-class` *The pics class*

Description

This object is used to gather all parameters from fitting PICS to a single candidate region. The objet contains the following slots: 'estimates', 'infMat', 'Nmerged', 'converge', 'chr'. 'estimates' is a list containing all parameters estimates as well as standard errors. 'infMat' is the Cholesky decomposition of the information matrix, 'converge' is a logical value indicating whether the EM algorithm has converged, while 'chr' is a character string corresponding to a candidate region's chromosome. 'Nmerged' gives the number of binding events that were merged; binding events that overlap are merged (see the cited paper below for details).

Accessors

The PICS package provide accessors to directly access to most of the parameters/standard errors and chromosome. In the code snippets below, 'x' is a 'pics' object.

'chromosome(x)' Gets the chromosome name of the candidate region.

'mu(x)' Gets the position estimates of all binding sites identified in the region.

'delta(x)' Gets the average fragment lengths of all binding sites identified in the region.

'sigmaSqF(x)' Gets the F peak variances of all binding sites identified in the region.

'sigmaSqR(x)' Gets the R peak variances of all binding sites identified in the region.

'seF(x)' Gets the standard errors of all binding site position estimates identified in the region.

'seF(x)' Gets the standard errors of all F peak modes identified in the region.

'seR(x)' Gets the standard errors of all R peak modes identified in the region.

score `signature(x = "pics")`: return the score for each binding event.

scoreF `signature(x = "pics")`: return the score of the forward (F) for each binding event.

scoreR `signature(x = "pics")`: return the score of the forward (R) for each binding event.

Constructor

newPics(w,mu,delta,sigmaSqF,sigmaSqR,seMu,seMuF,seMuR,score,Nmerged,converge,infMat,chr) construct a new 'pics' object with the following arguments:

w The mixture weights (a vector)

mu The binding site positions (a vector)

delta The DNA fragment lengths (a vector)

sigmaSqF The variance parameters for the forward distribution (vector)

sigmaSqR The variance parameters for the forward distribution (vector)

seMu The standard errors for mu (vector)

seMuF The standard errors for muF (vector)

seMuR The standard errors for muR (vector)

seMuR The standard errors for muR (vector)

score The scores for each binding event (vector)

Nmerged The number of peaks that got merged (integer)

converge A logical value, TRUE, if the EM as converged

infMat The information matrix

chr The chromosome for the region

Author(s)

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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. To appear in Biometrics.

See Also

pics picsError

Examples

```
# Here is an example of how to construct such a region.
# Typically, you would not do this manually, you would use the pics function to return a
w<-1
mu<-10000
delta<-150
sigmaSqF<-5000
sigmaSqR<-5000
seMu<-10
seMuF<-10
seMuR<-10
score<-5
Nmerged<-0
converge<-TRUE
chr<-"chr1"
range<-c(1000,2000)
# Contructor
#myPICS<-newPics(w,mu,delta,sigmaSqF,sigmaSqR,seMu,seMuF,seMuR,score,Nmerged,as.integer(r
```

picsError-class *The pics class*

Description

This object is used to return an error code when the PICS function failed to return a valid set of estimates for a candidate regions. This could be due to non-convergence of the EM algorithm, a singular information matrix, or a number of reads below the limit specified by the user. All of these are typically due to too few reads in the region and do not affect the rest of the analysis, as such regions would most likely be labelled as false positives.

Accessors

All of the accessors defined for a 'pics' object still work for a 'picsError' object but will simply return a NULL pointer.

Constructor

newPicsError(string) where 'string' is the error code.

Constructor

newPicsError<-function(string)

string The mixture weights (a vector)

Author(s)

Xuekui Zhang <<xzhang@stat.ubc.ca>> and Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>>

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. To appear in Biometrics.

See Also

pics

Examples

```
# Here is an example on how to construct such a picsError object
# Typically, you would not do this manually, you would use the pics function to return a
# Contructor
myPicsError<-newPicsError("Singular information matrix")
# Accessors
# Get the standard error of Mu
se(myPicsError)
# Get the standard error of MuF
seF(myPicsError)
# Get the scores
score(myPicsError)
```

picsFDR *Compute the global FDR*

Description

Calculate an estimate of the FDR for PICS. This calculation requires control data (e.g. from an input DNA sample).

Usage

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

Arguments

picsIP	An object of class 'picsList' as returned by 'PICS' when run on IP/Control data.
picsCont	An object of class 'picsList' as returned by 'PICS' when run on Control/IP data.
filter	A list of filters to be used before computing the FDR. By default all regions are included. See details for more info on how to specify the filters.

Value

A dataframe with three columns corresponding to the estimated FDR, the score, and the number of regions.

Author(s)

Xuekui Zhang and Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>>

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. To appear in Biometrics.

See Also

pics

Examples

```
## Not run:
  # Segment the reads in order to identify candidate regions
   segC<-segmentReads(RD, minReads=3,invert=TRUE)
  # Use the serial version of PICS
  picsC<-PICS(segC,dataType='TF')
plot(pics,picsC,xlim=c(0,50),ylim=c(0,.2),filter=list(delta=c(50,300),se=c(0,50),sigmaSqF

## End(Not run)
```

picsList-class *The pics class*

Description

This object is used to gather all parameters from fitting PICS to multiple candidate regions (as returned by the 'segmentReads' function). The objet contains the following slots: 'List', 'paraPrior', 'paraEM', 'minReads', 'N', 'Nc'. 'List' is a list of 'pics' or 'picsError' objects. 'paraPrior' is a list containing the hyperparameters used for the prior, 'paraEM' is a list of convergence parameters for the EM, 'minReads' is a list containing the minimum number of reads used to fit a region with 'PICS', 'N' is the total number of reads in the ChIP samples while 'Nc' is the total number of reads in the control sample.

Arguments

object	An object of class pics.

Accessors

The PICS package provide accessors to directly access to most of the parameters/standard errors and chromosomes. In the code snippets below, 'x' is a 'picsList' object. For all accessors, the 'picsError' objects are omitted, so that the accessors only return values for the 'pics' objects (i.e. all valid binding events).

'chromosome(x)' Gets the chromosome names of all candidate regions.

'mu(x)' Gets the position estimates of all binding sites identified in all candidate regions.

'delta(x)' Gets the average fragment lengths of all binding sites identified in all candidate regions.

'sigmaSqF(x)' Gets the F peak variances of all binding sites identified in all candidate regions.

'sigmaSqR(x)' Gets the R peak variances of all binding sites identified in all candidate regions.

'seF(x)' Gets the standard errors of all binding site position estimates identified in all candidate regions.

'seF(x)' Gets the standard errors of all F peak modes identified in all candidate regions.

'seR(x)' Gets the standard errors of all R peak modes identified in all candidate regions.

'score(x)' Gets the scores of all binding events identified in all candidate regions.

Constructor

newPicsList(List, paraEM, paraPrior, minReads, N, Nc)

List The mixture weights (a vector)

paraEM The binding site positions (a vector)

paraPrior The DNA fragment lengths (a vector)

N The variance parameters for the forward distribution (vector)

Nc The variance parameters for the forward distribution (vector)

Methods

[signature(x = "pics"): subset PICS object.

Methods

length `signature(x = "pics")`: subset PICS object.

Constructor

newPicsList<-function(List, paraEM, paraPrior, minReads, N, Nc) constructs a new 'picsList' object with the following arguments.

newPicsList

w The mixture weights (a vector)

mu The binding site positions (a vector)

delta The DNA fragment lengths (a vector)

sigmaSqF The variance parameters for the forward distribution (vector)

sigmaSqR The variance parameters for the reverse distribution (vector)

seMu The standard errors for mu (vector)

seMuF The standard errors for muF (vector)

seMuR The standard errors for muR (vector)

seMuR The standard errors for muR (vector)

score The scores for each binding event (vector)

Nmerged The number of peaks that were merged (integer)

converge A logical value, TRUE, if the EM as converged

infMat The information matrix

chr The chromosome for the region

Author(s)

Xuekui Zhang <<xzhang@stat.ubc.ca>> and Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>>

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. To appear in Biometrics.

See Also

`pics`

Examples

```
# Here is an example of how to construct such a region
# Typically, you would not do this manually, you would use the pics function to return a
w<-1
mu<-10000
delta<-150
sigmaSqF<-5000
sigmaSqR<-5000
seMu<-10
seMuF<-10
seMuR<-10
score<-5
```

```
Nmerged<-0
converge<-TRUE
infMat<-matrix(0)
chr<-"chr1"
range<-c(1000,2000)
# Contructor
#myPICS1<-newPics(w,mu,delta,sigmaSqF,sigmaSqR,seMu,seMuF,seMuR,score,Nmerged,converge,in
#myPICS2<-newPics(w,mu+1000,delta,sigmaSqF,sigmaSqR,seMu,seMuF,seMuR,score,Nmerged,conver

#minReads<-list(perPeak=2,perRegion=5)
#paraPrior<-list(xi=200,rho=1,alpha=20,beta=40000)
#paraEM<-list(minK=1,maxK=15,tol=10e-6,B=100)
#N<-100
#Nc<-200

#mynewPicsList<-newPicsList(list(myPICS1,myPICS2), paraEM, paraPrior, minReads, as.intege
# Accessors
# Get the standard error of Mu
#se(mynewPicsList)
# Get the standard error of MuF
#seF(mynewPicsList)
# Get the scores
#score(mynewPicsList)
```

`pics` *Estimation of binding site positions*

Description

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

Usage

```
PICS<-pics(segReadsList,dataType="TF")
```

Arguments

`segReadsList`	This object contains segmentation of Genome
`dataType`	The type of data you are processing: specified 'TF' for transcription factor.

Methods

code `signature(x = "pics")`: return the error code for each list element (i.e. candidate region) of a PICS object. If the string is empty, there were no errors.

plot `signature(x = "pics")`: Plot all regions in the PICS object. This might be long, and should only be used to plot a few regions, so subset the object before plotting.

sigmaSqR `signature(x = "pics")`: return the variance parameter of the reverse (R) distribution for each binding event.

sigmaSqF `signature(x = "pics")`: return the variance parameter of the forward (F) distribution for each binding event.

score `signature(x = "pics")`: return the score for each binding event.

scoreF `signature(x = "pics")`: return the score of the forward (F) for each binding event.

scoreR `signature(x = "pics")`: return the score of the forward (R) for each binding event.

maxRange `signature(x = "pics")`: return the range maximum.

minRange `signature(x = "pics")`: return the range minimal.

K `signature(x = "pics")`: subset PICS object.

density `signature(x = "pics")`: return the density for each binding event.

Author(s)

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Arnaud Droit, <arnaud.droit@ircm.qc.ca>

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. To appear in Biometrics.

See Also

`pics`

---

plot-FDR *FDR plot for PICS*

Description

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

Usage

```
## S4 method for signature 'picsList,picsList':
plot(x, y, filter=NULL, h=.1, ...)
```

Arguments

`x`	A `picsList` object as returned by the function `PICS` run on the treatment data.
`y`	A `picsList` 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`.

Author(s)

Raphael Gottardo <<raph@rglab.org>>

References

X. Zhang, G. Robertson, M. Krzywinski, K. Ning, A. Droit, S. Jones, and R. Gottardo, "PICS: Probabilistic Inference for ChIP-seq," Biometrics, iss. In press, 2010.

See Also

PICS

`segmentReads` *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

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

Arguments

`data`	A 'GenomeData' object containing the IP reads. See details for more information on how to set up the data.
`dataC`	A 'GenomeData' object containing the control reads. Set to NULL by default, i.e. no control.
`map`	A 'RangedData' object containing the mappability profiles. Set to NULL by default, i.e. no profiles.
`minReads`	The minimum number of F/R reads to be present in the sliding window.
`minReadsInRegion`	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`	Type of experiment.
`maxLregion`	The maximum length.
`minLregion`	The minimum length.

Value

An object of class 'segmentReadsList' containing the results for all regions pre-processed.

Author(s)

Xuekui Zhang and Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>>

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

segmentReads, picsFDR

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
dataIP<-as(dataIP,"RangedData")
dataIP<-as(dataIP,"GenomeData")

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

map<-read.table(file.path(path,"mapProfileShort"),header=TRUE,colClasses=c("factor","inte
map<-as(map,"RangedData")
## Remove the chrM
map<-map[-23]
seg<-segmentReads(dataIP, dataC=dataCont, map=map, minReads=1)
```

`segReadsList` *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

```
segReadsList<-new(List,paraSW,N,Nc)
```

Arguments

`List`	This object contains an ExpressionSet
`paraSW`	String containing the genome name used (vector).
`N`	String containing the name of chromosome used (vector).
`Nc`	String containing the Position of the sequences (vector).

Methods

[`signature(x = "pics")`: subset gadem object.

[`signature(x = "pics")`: subset gadem object.

Methods

length `signature(x = "pics")`: subset PICS object.

Author(s)

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Arnaud Droit, <arnaud.droit@ircm.qc.ca>

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. To appear in Biometrics.

See Also

`pics`

---

segReads *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

```
segReads<-new(yF, yR, cF, cR, map, chr)
```

Arguments

`yF`	This object contains an ExpressionSet
`yR`	String containing the genome name used (vector).
`cF`	String containing the name of chromosome used (vector).
`cR`	String containing the Position of the sequences (vector).
`map`	String containing the copy number of sequence (vector).
`chr`	String containing the expresion data of enriched region (matrix with n column.

Methods

map `signature(x = "pics")`: subset PICS object.

Author(s)

Charles Cheung, <cykc@interchange.ubc.ca> and Raphael Gottardo, <raphael.gottardo@ircm.qc.ca
Arnaud Droit, <arnaud.droit@ircm.qc.ca>

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. To appear in Biometrics.

See Also

pics

`setParaEM` *Set convergence parameters of the EM algorithm*

Description

This function can be used to change the internal PICS parameters for the EM algorithm. This function should only be called if you really now what you are doing!.

Usage

```
setParaEM(minK=1,maxK=15,tol=1e-4,B=100,mSelect="BIC",mergePeaks=TRUE,mapCorrect
```

Arguments

`minK`	An integer value. The minimum number of binding events per region.
`maxK`	An integer value. The maximum number of binding events per region.
`tol`	The tolerance for the EM algorithm
`B`	An integer value. The maximum number of iterations to be used.
`mSelect`	A character string specifying the information criteria to be used when selecting the number of binding events.
`mergePeaks`	A logical value stating whether overlapping binding events should be picked.
`mapCorrect`	Should mappability profiles be incorporated in the estimation, that is missing reads estimated.
`dataType`	A character string equal to either 'H' or 'TF', 'H' for histone and 'TF' for transcription factors.

Value

No value returned. The function simply modifies the internal variables 'paraEMTF' if dataType='TF' and 'paraEMH' if dataType='H'.

Author(s)

Xuekui Zhang and Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>>

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. To appear in Biometrics.

See Also

setParaPrior

Examples

```
# Using mSelect="BIC"
setParaEM(minK=1,maxK=15,tol=1e-4,B=100,mSelect="BIC",mergePeaks=TRUE,mapCorrect=TRUE,dat
# Using mSelect="AIC"
setParaEM(minK=1,maxK=15,tol=1e-4,B=100,mSelect="AIC",mergePeaks=TRUE,mapCorrect=TRUE,dat
```

---

setParaPrior *Set convergence parameters of the EM algorithm*

Description

This function can be used to change the internal PICS parameters for the prior distribution. This function should only be called if you really now what you are doing! In particular, you may want to specify the average DNA fragment size for your sample by changing the 'xi' parameter.

Usage

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

Arguments

xi	Our best guest for the average DNA fragment size.
rho	A variance parameter for the average DNA fragment size distribution.
alpha	First hyperparameter of the inverse Gamma distribution for sigma^2 in the PICS model.
beta	First hyperparameter of the inverse Gamma distribution for sigma^2 in the PICS model.
lambda	The precision of the prior for mu used for histone data.
dMu	Our best guess for the distance between two neighboring nucleosomes.
dataType	A character string equal to either 'H' or 'TF', 'H' for histone and 'TF' for transcription factors. 'H' is not yet supported

Value

No value returned. The function simply modifies the internal variables 'paraPriorTF' if dataType='TF' and 'paraPriorH' if dataType='H'.

Author(s)

Xuekui Zhang and Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>>

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. To appear in Biometrics.

See Also

setParaEM

Examples

```
# Using xi=200 for the average DNA fragment size
setParaPrior(xi=200,rho=1,alpha=20,beta=40000,lambda=0,dMu=200,dataType="TF")
# Using xi=150 for the average DNA fragment size
setParaPrior(xi=150,rho=1,alpha=20,beta=40000,lambda=0,dMu=200,dataType="TF")
```

---

show *show PICS*

Description

This methods show the objects of PICS

Usage

```
## S4 method for signature 'pics':
show(object)
## S4 method for signature 'picsError':
show(object)
## S4 method for signature 'picsList':
show(object)
## S4 method for signature 'segReads':
show(object)
## S4 method for signature 'segReadsList':
show(object)
```

Arguments

object	Object returned from pics .

Details

List of the slots include in the object

Author(s)

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See Also

summary

summary *summary PICS*

Description

This methods summarized 'pics', 'picsList', 'seg' or 'segList' objects.

Usage

```
## S4 method for signature 'pics':
summary(object)
## S4 method for signature 'picsList':
summary(object)
## S4 method for signature 'segReads':
summary(object)
## S4 method for signature 'segReadsList':
summary(object)
```

Arguments

object	Object returned from pics .

Author(s)

Xuekui Zhang <<xzhang@stat.ubc.ca> Arnaud Droit, <arnaud.droit@ircm.qc.ca> Raphael Gottardo <<raphael.gottardo@ircm.qc.ca>

See Also

show

unique *GenomeData Unique Reads*

Description

This methods select the unique elements in a GenomeData object

Arguments

object	A 'GenomeData' object.

Author(s)

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See Also

segmentReads

Index