Package 'r3Cseq'

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Title Analysis of Chromosome Conformation Capture and Next-generation Sequencing (3C-seq)

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Depends GenomicRanges, Rsamtools, rtracklayer, VGAM, qvalue

Imports methods, GenomeInfoDb, IRanges, Biostrings, data.table, sqldf, RColorBrewer

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Description
This package is used for the analysis of long-range chromatin interactions from 3C-seq assay.

License GPL-3

URL http://r3cseq.genereg.net,https://github.com/supatt-lab/r3Cseq/

Collate AllClasses.R AllGenerics.R Export.R FunctionInCommon.R FunctionsForBatchAnalysis.R RestrictionEnzymeFunctions.R FunctionsForNoReplicationAnalysis.R Report.R Visualize3Cseq.R Annotation.R

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`calculateBatchRPM` *calculate read per million (RPM) for replicates analysis*

Description

Normalize 3C-Seq data by transforming raw reads to read per million per each region for replication analysis

Usage

```
calculateBatchRPM(object,normalized_method=c("powerlawFittedRPM","normalRPM"))
```

Arguments

`object`	r3CseqInBatch object
`normalized_method`	character. method of normalization (default=powerlawFittedRPM)

Author(s)

S. Thongjuea

See Also

calculateRPM, expRPM contrRPM

Examples

```
#See the vignette
```

`calculateRPM` *calculate read per million (RPM)*

Description

Normalize 3C-Seq data by transforming raw reads to read per million per each region

Usage

```
calculateRPM(object,normalized_method=c("powerlawFittedRPM","normalRPM"))
```

Arguments

`object`	r3Cseq object
`normalized_method`	character. method of normalization (default=powerlawFittedRPM)

Author(s)

S. Thongjuea

See Also

contrRPM, expRPM, calculateBatchRPM

Examples

```
#See the vignette
```

---

contrCoverage *This method has been removed.*

Description

This method has been removed.

---

contrInteractionRegions *get interaction regions from the control*

Description

get all identified interaction regions from the control

Usage

```
contrInteractionRegions(object)
```

Arguments

object	r3Cseq or r3CseqInBatch object

Value

The candidate interaction regions show in the IRange object

Author(s)

S. Thongjuea

See Also

expInteractionRegions, getInteractions

Examples

```
#See the vignette
```

`contrRawData` *Accessors for the 'contrRawData' slot of a r3Cseq object.*

Description

The 'contrRawData' slot of hold the raw aligned reads data in the GRanges object.

Usage

```
## S4 method for signature 'r3Cseq'
contrRawData(object)
## S4 replacement method for signature 'r3Cseq'
contrRawData(object) <- value
```

Arguments

`object`	r3Cseq object
`value`	a GRanges object of aligned reads

Author(s)

S. Thongjuea

See Also

expRawData

Examples

```
#See the vignette
```

contrReadCount *get read count per region for the control*

Description

get the read count per region for the control

Usage

```
contrReadCount(object)
```

Arguments

object	r3Cseq object

Author(s)

S. Thongjuea

See Also

expReadCount, getReadCountPerRestrictionFragment

Examples

```
#See the vignette
```

contrRPM *get read per million (RPM) for the control*

Description

get the normalized 3C-seq data (RPM) for the control

Usage

```
contrRPM(object)
```

Arguments

object	r3Cseq or r3CseqInBatch object

Author(s)

S. Thongjuea

See Also

calculateRPM, expRPM

Examples

```
#See the vignette
```

`enzymeDb` *Rebase The Restriction Enzyme Database*

Description

The database includes all restriction enzyme information from the REBASE database.

References

http://rebase.neb.com/rebase/rebase.html

`expCoverage` *This method has been removed.*

Description

This method has been removed.

`expInteractionRegions` *get interaction regions from the experiment*

Description

get identified interaction regions from the experiment

Usage

```
expInteractionRegions(object)
```

Arguments

`object`	r3Cseq or r3CseqInBatch object

Value

The candidate interaction regions show in the IRange object

Author(s)

S. Thongjuea

See Also

getInteractions, contrInteractionRegions

Examples

```
#See the vignette
```

`export3Cseq2bedGraph` *export interaction regions to the 'bedGraph' format*

Description

export interaction regions from RagedData to the bedGraph format, which suitable for uploading to the UCSC genome browser

Usage

```
export3Cseq2bedGraph(object,datatype=c("rpm","read_count"))
```

Arguments

`object`	r3Cseq object, The object might contain the interaction regions generated by function getInteractions
`datatype`	read_count : read count per restriction fragment rpm : normalized read per million per restriction fragment

Value

The text file in 'bedGraph' format

Author(s)

S. Thongjuea

See Also

exportInteractions2text

Examples

```
#See the vignette
```

`export3CseqRawReads2bedGraph` *export the interaction signal from the raw reads to the 'bedGraph' format*

Description

export interaction regions signal to the bedGraph format, which suitable for uploading to the UCSC genome browser

Usage

```
export3CseqRawReads2bedGraph(object)
```

Arguments

`object`	r3Cseq object

Value

The text file in 'bedGraph' format

Author(s)

S. Thongjuea

See Also

exportInteractions2text, export3Cseq2bedGraph,

Examples

```
#See the vignette
```

`exportBatchInteractions2text` *export identified interaction regions to the tab separated format for replicates analysis*

Description

export interaction regions from RagedData to the tab separated format for replicates analysis

Usage

```
exportBatchInteractions2text(object)
```

Arguments

object	r3CseqInBatch object

Value

The text file in the tab separated format

Author(s)

S. Thongjuea

See Also

export3Cseq2bedGraph, exportInteractions2text

Examples

```
#See the vignette
```

---

exportInteractions2text

export identified interaction regions to the tab separated format

---

Description

export interaction regions from RagedData to the tab separated format

Usage

```
exportInteractions2text(object)
```

Arguments

object	r3Cseq object

Value

The text file in the tab separated format

Author(s)

S. Thongjuea

See Also

export3Cseq2bedGraph

Examples

```
#See the vignette
```

expRawData *Accessors for the 'expRawData' slot of a r3Cseq object.*

Description

The 'expRawData' slot of hold the raw aligned reads data in the GRanges object.

Usage

```
## S4 method for signature 'r3Cseq'
expRawData(object)
## S4 replacement method for signature 'r3Cseq'
expRawData(object) <- value
```

Arguments

object	r3Cseq object
value	a GRanges object of aligned reads

Author(s)

S. Thongjuea

See Also

expRawData

Examples

```
#See the vignette
```

expReadCount *get read count per region for the experiment*

Description

get the read count per region for the experiment

Usage

```
expReadCount(object)
```

Arguments

object	r3Cseq

Author(s)

S. Thongjuea

See Also

contrReadCount, getReadCountPerRestrictionFragment

Examples

```
#See the vignette
```

`expRPM` *get read per million (RPM) for the experiment*

Description

get the normalized 3C-seq data (RPM) for the experiment

Usage

```
expRPM(object)
```

Arguments

`object`	r3Cseq or r3CseqInBatch

Author(s)

S. Thongjuea

See Also

calculateRPM, contrRPM

Examples

```
#See the vignette
```

`generate3CseqReport` *generate reports for analysis results from r3Cseq*

Description

generate reports for analysis results from r3Cseq, the report contains all plots in one pdf file and a text separated out put file.

Usage

```
generate3CseqReport(obj)
```

Arguments

`obj`	r3Cseq or r3CseqInBatch object

Value

The text file in the tab separated format and the pdf file of all plots

Author(s)

S. Thongjuea

See Also

exportInteractions2text plotOverviewInteractions, plotInteractionsPerChromosome, plotInteractionsNearViewpoint

Examples

```
#See the vignette
```

`getBatchInteractions` *calculate z-score, assign p-value and q-value for each interaction region for replicates data sets*

Description

Calculate z-score, assign p-value and q-value to each interaction regions for replicates data sets

Usage

```
getBatchInteractions(object,method=c("union","intersection"),smoothing.parameter=0.1,fdr=0.05)
```

Arguments

`object`	r3Cseq object
`method`	character. The method for combining biological replicates for 3C-Seq analysis (default = "union")
`smoothing.parameter`	A level at which cubic smoothing spline for the spar (see vsmooth.spline) input parameter. Must be in (0.06,0.4] (default=0.1)
`fdr`	A level at which to control the FDR. Must be in (0,1] (default=0.05)

Value

The interaction regions show in the RangedData

Author(s)

S. Thongjuea

See Also

getInteractions vsmooth.spline

Examples

```
#See the vignette
```

`getBatchRawReads` *Get aligned reads from the replicates BAM files*

Description

Reading in the input BAM files from the 3C-Seq replicates analysis and then save files as the local GRanged object .rData files

Usage

```
getBatchRawReads(object)
```

Arguments

`object`	r3CseqInBatch object

Value

The GRangedData represents the aligned reads from the BAM file

Author(s)

S. Thongjuea

See Also

getRawReads,

Examples

```
#See the vignette
```

`getBatchReadCountPerRestrictionFragment`
count reads for replicates analysis

Description

Counts the number of reads from 3C-Seq data per each restriction fragment for replicates analysis

Usage

```
getBatchReadCountPerRestrictionFragment(object,getReadsMethod = c("wholeReads", "adjacentFragmentEnd
   nFragmentExcludedReadsNearViewpoint=2)
```

Arguments

`object`	r3CseqInBatch object
`getReadsMethod`	character. To count all reads found in the particular restriction fragment uses wholeReads option. To count reads found around the edge of restriction fragment both 5'utr and 3'utr uses adjacentFragmentEndsReads option (default=wholeReads)
`nFragmentExcludedReadsNearViewpoint`	Numeric. The number of excluded fragments around the viewpoint, reads found in these fragments will be removed from the analysis (default=2)

Value

The RangedData represents the number of reads per each restriction fragment

Author(s)

S. Thongjuea

See Also

getReadCountPerWindow, getReadCountPerRestrictionFragment

Examples

```
#See the vignette
```

getBatchReadCountPerWindow *count reads per window size for replicates analysis*

Description

Counts the number of reads from 3C-Seq data per each window size for replicates analysis

Usage

```
getBatchReadCountPerWindow(object,windowSize=5e3,nFragmentExcludedReadsNearViewpoint=2,mode=c("non-
```

Arguments

object	r3CseqInBatch object
windowSize	Numeric. non-overlapping window size for counting reads (default=5e3)
nFragmentExcludedReadsNearViewpoint	Numeric. The number of excluded fragments around the viewpoint, reads found in these fragments will be removed from the analysis (default=2)
mode	character. The window-based modes analysis (default="non-overlapping")

Value

The RangedData represents the number of reads per each window size

Author(s)

S. Thongjuea

See Also

getReadCountPerRestrictionFragment, getBatchReadCountPerRestrictionFragment, getReadCount-PerWindow,

Examples

```
#See the vignette
```

getContrInteractionsInRefseq *identified significant interaction regions for RefSeq genes*

Description

Get a list of genes that contain strong interaction signals in the control

Usage

```
getContrInteractionsInRefseq(obj,cutoff.qvalue=0.05,expanded_upstream=50e3,expanded_downstream=10e3
```

Arguments

obj	obj is r3Cseq or r3CseqInBatch object
cutoff.qvalue	Numeric. The cutoff q-value (default=0.05)
expanded_upstream	Numeric. The expanded distance from the upstream of a gene start (default=50e3)
expanded_downstream	Numeric. The expanded distance from the downstream of a gene end (default =10e3)

Value

List of identified genes, which contain strong interaction signals

Author(s)

S. Thongjuea

See Also

getContrInteractionsInRefseq

Examples

```
# See the vignette
```

getCoverage *This method has been removed.*

Description

This method has been removed.

`getExpInteractionsInRefseq` *identified significant interaction regions for RefSeq genes*

Description

Get a list of genes that contain strong interaction signals in the experiment

Usage

```
getExpInteractionsInRefseq(obj,cutoff.qvalue=0.05,expanded_upstream=50e3,expanded_downstream=10e3)
```

Arguments

`obj`	obj is r3Cseq or r3CseqInBatch object
`cutoff.qvalue`	Numeric. The cutoff q-value (default=0.05)
`expanded_upstream`	Numeric. The expanded distance from the upstream of a gene start (default=50e3)
`expanded_downstream`	Numeric. The expanded distance from the downstream of a gene end (default =10e3)

Value

List of identified genes, which contain strong interaction signals

Author(s)

S. Thongjuea

See Also

`getContrInteractionsInRefseq`

Examples

```
# See the vignette
```

getInteractions *calculate z-score, assign p-value and q-value for each interaction region*

Description

Calculate z-score, assign p-value and q-value to each interaction regions

Usage

```
getInteractions(object,smoothing.parameter=0.1,fdr=0.05)
```

Arguments

object	r3Cseq object
smoothing.parameter	A level at which cubic smoothing spline for the spar (see vsmooth.spline) input parameter. Must be in (0.06,0.4] (default=0.1)
fdr	A level at which to control the FDR. Must be in (0,1] (default=0.05)

Value

The interaction regions show in the RangedData

Author(s)

S. Thongjuea

See Also

getBatchInteractions vsmooth.spline

Examples

```
#See the vignette
```

`getRawReads` *Get aligned reads from the BAM file*

Description

Reading in the input BAM file and then store it in the GRanged object

Usage

```
getRawReads(object)
```

Arguments

`object`	r3Cseq object

Value

The GRangedData represents the aligned reads from the BAM file

Author(s)

S. Thongjuea

See Also

getBatchRawReads,

Examples

```
#See the vignette
```

`getReadCountPerRestrictionFragment` *count reads per resitrcition fragment*

Description

Counts the number of reads from 3C-Seq data per each restriction fragment

Usage

```
getReadCountPerRestrictionFragment(object,getReadsMethod = c("wholeReads", "adjacentFragmentEndsRead
   nFragmentExcludedReadsNearViewpoint=2)
```

Arguments

object	r3Cseq object
getReadsMethod	character. To count all reads found in the particular restriction fragment uses wholeReads option. To count reads found around the edge of restriction fragment both 5'utr and 3'utr uses adjacentFragmentEndsReads option (default=wholeReads)
nFragmentExcludedReadsNearViewpoint	Numeric. The number of excluded fragments around the viewpoint, reads found in these fragments will be removed from the analysis (default=2)

Value

The RangedData represents the number of reads per each restriction fragment

Author(s)

S. Thongjuea

See Also

getReadCountPerWindow, getBatchReadCountPerRestrictionFragment

Examples

```
#See the vignette
```

---

getReadCountPerWindow *count reads per window size*

Description

Counts the number of reads from 3C-Seq data per each window size

Usage

```
getReadCountPerWindow(object,windowSize=5e3,nFragmentExcludedReadsNearViewpoint=2,mode=c("non-overl
```

Arguments

object	r3Cseq object
windowSize	Numeric. non-overlapping window size for counting reads (default=5e3)
nFragmentExcludedReadsNearViewpoint	Numeric. The number of excluded fragments around the viewpoint, reads found in these fragments will be removed from the analysis (default=2)
mode	character. The window-based modes analysis (default="non-overlapping")

Value

The RangedData represents the number of reads per each window size

Author(s)

S. Thongjuea

See Also

getReadCountPerRestrictionFragment,

Examples

```
#See the vignette
```

`getViewpoint` *get the viewpoint of 3C-seq data*

Description

The viewpoint is the bait of 3C method, which can be a promoter region of an interested gene, an enhancer, and a transcrition factor binding region.

Usage

```
getViewpoint(obj)
```

Arguments

`obj`	r3Cseq or r3CseqInBatch object

Value

The viewpoint shows in the IRanges

Author(s)

S. Thongjuea

Examples

```
#See the vignette
```

hg18refGene *hg18's refGenes*

Description

The human (hg18) reference genes from UCSC

hg19refGene *hg19's refGenes*

Description

The human (hg19) reference genes from UCSC

mm10refGene *mm10's refGenes*

Description

The mouse (mm10) reference genes from UCSC

mm9refGene *mm9's refGenes*

Description

The mouse (mm9) reference genes from UCSC

Myb_prom_FB *Myb_prom_FB a data set for the example of r3Cseq analysis*

Description

The example aligned reads generated by 3C-Seq protocol from fetal brain. The promoter region of the Myb's gene was selected as the viewpoint. This data was transformed from aligned reads shown in the BAM file to GRanged object by using Rsamtools.

Myb_prom_FL *Myb_prom_FL a data set for the example of r3Cseq analysis*

Description

The example aligned reads generated by 3C-Seq protocol from fetal liver. The promoter region of the Myb's gene was selected as the viewpoint. This data was transformed from aligned reads shown in the BAM file to GRanged object by using Rsamtools.

plot3Cecdf *This method has been removed.*

Description

This method has been removed.

plotDomainogramNearViewpoint
Plot domainogram of interaction regions near the viewpoint

Description

Plot domainogram of interaction regions near the viewpoint

Usage

```
plotDomainogramNearViewpoint(object,smoothing.parameter=0.1,distance=5e5,maximum_window=25e3,view=c
```

Arguments

object	r3Cseq or r3CseqInBatch object
smoothing.parameter	A level at which cubic smoothing spline for the spar (see vsmooth.spline) input parameter. Must be in (0.06,0.4] (default=0.1)
distance	Numeric. The distance relative to the viewpoint (default=5e5)
maximum_window	Numeric. The maximum windowing (default=25e3). We normally compute the interaction regions per window starting from 2Kb to maximum window (default=25kb) to make the interaction matrix for visualizing the domainogram.
view	character. The selected view of data (default="experiment")

Value

Plots of domainogram for interaction regions close to the viewpoint

Author(s)

S. Thongjuea

See Also

plotOverviewInteractions, plotInteractionsPerChromosome, plotInteractionsNearViewpoint

Examples

```
# See the vignette
```

---

plotInteractionsNearViewpoint

Plot identified interaction regions near the viewpoint

Description

Plot identified interaction regions near the viewpoint

Usage

```
plotInteractionsNearViewpoint(obj,distance=5e5,log2fc_cutoff=1,yLim=0)
```

Arguments

obj	obj is r3Cseq or r3CseqInBatch object
distance	Numeric. The distance relative to the viewpoint (default=5e5)
log2fc_cutoff	Numeric. The log2 cutoff ratio between the experiment and control (default=1)
yLim	Numeric. The limited height of y-axis (default=0)

Value

Plots of identified interaction regions close to the viewpoint

Author(s)

S. Thongjuea

See Also

plotOverviewInteractions, plotInteractionsPerChromosome, plotDomainogramNearViewpoint

Examples

```
# See the vignette
```

plotInteractionsPerChromosome

Plot interaction regions per each chromosome of interest

Description

Plot the distribution of interaction regions per each chromosome

Usage

```
plotInteractionsPerChromosome(obj, chromosomeName)
```

Arguments

obj	obj is r3Cseq or r3CseqInBatch object.
chromosomeName	Character. The input chromosome name (e.g. "chr1")

Value

Plots of interaction regions per chromosome.

Author(s)

S. Thongjuea

See Also

plotInteractionsNearViewpoint, plotOverviewInteractions, plotDomainogramNearViewpoint

Examples

```
# See the vignette
```

plotOverviewInteractions

Plot overview of identified interaction regions for genome-wide

Description

Plot the distribution of identified interaction regions across genome

Usage

```
plotOverviewInteractions(obj, cutoff.qvalue=0.05)
```

Arguments

obj	obj is r3Cseq or r3CseqInBatch object
cutoff.qvalue	Numeric. The cutoff q-value (default=0.05)

Value

Plots of identified 3C-Seq interaction regions genome-wide

Author(s)

S. Thongjuea

See Also

plotInteractionsNearViewpoint, plotInteractionsPerChromosome, plotDomainogramNearViewpoint

Examples

```
# See the vignette
```

---

r3Cseq-class *r3Cseq objects*

Description

The r3Cseq class is the extended class from r3CseqCommon class. It is a general container for storing and manipulating a set of input parameters, RangeData of interactions regions from r3Cseq analysis , and the raw reads GRanged data of the genome-wide interaction signal generated by next-generation sequencing.

Extends

Class r3CseqCommon, directly.

Slots

organismName Object of class "character" the version of particular assembly genome from UCSC (e.g. mm9, hg18, hg19) . The package supports three genome assemblies consisting of mouse (mm9), and human (hg18, hg19).

restrictionEnzyme Object of class "character" this is the primary restriction enzyme name using in 3C-Seq experiment

viewpoint_chromosome Object of class "character" chromosome name of where is the viewpoint located eg. chr10, chrX etc.

viewpoint_primer_forward Object of class "character" the forward primer DNA sequences for the viewpoint amplification

`viewpoint_primer_reverse` Object of class `"character"` the reverse primer DNA sequences for the viewpoint amplification

`expReadCount` Object of class `"RangedData"` the read count in experiment

`contrReadCount` Object of class `"RangedData"` the read count in control

`expRPM` Object of class `"RangedData"` the normalized read read per million in experiment

`contrRPM` Object of class `"RangedData"` the normalized read read per million in control

`expInteractionRegions` Object of class `"RangedData"` the identified interaction regions in experiment

`contrInteractionRegions` Object of class `"RangedData"` the identified interaction regions in control

`isControlInvolved` Object of class `"logical"` the logical to ask whether the control is involved in the analysis or not

`alignedReadsBamExpFile` Object of class `"character"` the file name of experiment in BAM format

`alignedReadsBamContrFile` Object of class `"character"` the file name of control in BAM format

`expLabel` Object of class `"character"` the experiment name

`contrLabel` Object of class `"character"` the control name

`expLibrarySize` Object of class `"integer"` the library size of experiment

`contrLibrarySize` Object of class `"integer"` the library size of control

`expReadLength` Object of class `"integer"` the read length of experiment

`contrReadLength` Object of class `"integer"` the read length of experiment

`expRawData` Object of class `"GRanges"` the raw reads found in experiment

`contrRawData` Object of class `"GRanges"` the raw reads found in control

Author(s)

S. Thongjuea

See Also

r3CseqCommon, r3CseqInBatch

Examples

```
# See the vignette
```

`r3CseqCommon-class` *r3CseqCommon objects*

Description

The r3CseqCommon class is a general container for storing and manipulating a set of input parameters, RangeData of interactions regions from r3Cseq analysis. It is a root class for r3Cseq and r3CseqInBatch classes.

Slots

`organismName` Object of class `"character"` the version of particular assembly genome from UCSC (e.g. mm9, hg18, hg19) . The package supports three genome assemblies consisting of mouse (mm9), and human (hg18, hg19).

`restrictionEnzyme` Object of class `"character"` this is the primary restriction enzyme name using in 3C-Seq experiment

`viewpoint_chromosome` Object of class `"character"` chromosome name of where is the viewpoint located eg. chr10, chrX etc.

`viewpoint_primer_forward` Object of class `"character"` the forward primer DNA sequences for the viewpoint amplification

`viewpoint_primer_reverse` Object of class `"character"` the reverse primer DNA sequences for the viewpoint amplification

`expReadCount` Object of class `"RangedData"` the read count in experiment

`contrReadCount` Object of class `"RangedData"` the read count in control

`expRPM` Object of class `"RangedData"` the normalized read read per million in experiment

`contrRPM` Object of class `"RangedData"` the normalized read read per million in control

`expInteractionRegions` Object of class `"RangedData"` the identified interaction regions in experiment

`contrInteractionRegions` Object of class `"RangedData"` the identified interaction regions in control

`isControlInvolved` Object of class `"logical"` the logical to ask whether the control is involved in the analysis or not

Author(s)

S. Thongjuea

See Also

r3Cseq, r3CseqInBatch

Examples

```
# See the vignette
```

r3CseqInBatch-class *r3CseqInBatch objects*

Description

The r3CseqInBatch class is the extended class from r3CseqCommon class. It is a general container for storing and manipulating a set of input parameters, RangeData of interactions regions from r3Cseq analysis for replicates data sets.

Extends

Class r3CseqCommon, directly.

Slots

organismName Object of class "character" the version of particular assembly genome from UCSC (e.g. mm9, hg18, hg19) . The package supports three genome assemblies consisting of mouse (mm9), and human (hg18, hg19).

restrictionEnzyme Object of class "character" this is the primary restriction enzyme name using in 3C-Seq experiment

viewpoint_chromosome Object of class "character" chromosome name of where is the viewpoint located eg. chr10, chrX etc.

viewpoint_primer_forward Object of class "character" the forward primer DNA sequences for the viewpoint amplification

viewpoint_primer_reverse Object of class "character" the reverse primer DNA sequences for the viewpoint amplification

expReadCount Object of class "RangedData" the read count in experiment

contrReadCount Object of class "RangedData" the read count in control

expRPM Object of class "RangedData" the normalized read read per million in experiment

contrRPM Object of class "RangedData" the normalized read read per million in control

expInteractionRegions Object of class "RangedData" the identified interaction regions in experiment

contrInteractionRegions Object of class "RangedData" the identified interaction regions in control

isControlInvolved Object of class "logical" the logical to ask whether the control is involved in the analysis or not

bamFilesDirectory Object of class "character" the path name of directory that contains BAM files

BamExpFiles Object of class "vector" the file names of BAM files in the experiment

BamContrFiles Object of class "vector" the file names of BAM files in the control

expBatchLabel Object of class "vector" the labeled experiment names

contrBatchLabel Object of class "vector" the labeled control names

`readCountTable` Object of class `"RangedData"` the read count table

`RPMsTable` Object of class `"RangedData"` the normalized read per million table

`expBatchLibrarySize` Object of class `"vector"` the library size of each experiment

`contrBatchLibrarySize` Object of class `"vector"` the library size of each control

`expBatchReadLength` Object of class `"vector"` the read length of experiments

`contrBatchReadLength` Object of class `"vector"` the read length of controls

Author(s)

S. Thongjuea

See Also

r3CseqCommon, r3CseqInBatch

Examples

```
# See the vignette
```

`rn5refGene` *rn5's refGenes*

Description

The rat (rn5) reference genes from UCSC

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