# Package 'r3Cseq'

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Depends GenomicRanges, Rsamtools, rtracklayer, VGAM, qvalue
Imports methods, GenomeInfoDb, IRanges, Biostrings, data.table, sqldf, RColorBrewer
Suggests BSgenome.Mmusculus.UCSC.mm9.masked, BSgenome.Mmusculus.UCSC.mm10.masked, BSgenome.Hsapiens.UCSC.hg18.masked, BSgenome.Hsapiens.UCSC.hg19.masked, BSgenome.Rnorvegicus.UCSC.rn5.masked
<b>Description</b> This package is an implementation of data analysis for the long-range interactions from 3C-seq assay.
License GPL-3
<pre>URL http://r3cseq.genereg.net</pre>
Collate AllClasses.R AllGenerics.R Export.R FunctionInCommon.R FunctionsForBatchAnalysis.R RestrictionEnzymeFunctions.R FunctionsForNoReplicationAnalysis.R Report.R Visualize3Cseq.R Annotation.R
biocViews Preprocessing, Sequencing
NeedsCompilation no
R topics documented:
calculateBatchRPM calculateRPM contrCoverage contrInteractionRegions contrRawData contrReadCount contrRPM

2 calculateBatchRPM

	enzymeDb	6
	expCoverage	7
	expInteractionRegions	7
	export3Cseq2bedGraph	8
	export3CseqRawReads2bedGraph	8
	exportBatchInteractions2text	9
		10
		10
	expReadCount	11
	expRPM	12
	generate3CseqReport	12
	getBatchInteractions	13
		14
		14
		15
		16
		17
		17
	getInteractions	18
	getRawReads	18
	getReadCountPerRestrictionFragment	19
	getReadCountPerWindow	20
	getViewpoint	20
	hg18refGene	21
	hg19refGene	21
	mm10refGene	21
	mm9refGene	21
	Myb_prom_FB	22
	Myb_prom_FL	22
	plot3Cecdf	22
		22
		23
	I	24
	plotOverviewInteractions	24
	1	25
	<b>1</b>	26
	1	27
	rn5refGene	28
T., J.		20
Index		29

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

 $calculate Batch RPM (object, normalized\_method = c("powerlawFitted RPM", "normal RPM"))$ 

calculateRPM 3

## **Arguments**

```
\begin{tabular}{lll} object & r3CseqInBatch\ object \\ normalized\_method & character.\ method\ of\ normalization\ (default=powerlawFittedRPM) \\ \end{tabular}
```

### 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

```
\begin{tabular}{ll} object & r3Cseq object \\ normalized\_method & character. method of normalization (default=powerlawFittedRPM) \\ \end{tabular}
```

# Author(s)

S. Thongjuea

### See Also

```
contrRPM, expRPM, calculateBatchRPM
```

# Examples

```
#See the vignette
```

 ${\tt contrCoverage}$ 

This method has been removed.

# Description

This method has been removed.

 ${\tt contrInteractionRegions}$ 

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**

contrRawData 5

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</pre>
```

# 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

6 enzymeDb

#### 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 7

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**

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

 ${\tt exportBatchInteractions2text}$ 

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**

10 expRawData

```
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</pre>
```

# Arguments

object r3Cseq object

value a GRanges object of aligned reads

expReadCount 11

# 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**

12 generate3CseqReport

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

getBatchInteractions 13

#### See Also

 $exportInteractions 2 text\ plot Overview Interactions,\ plot Interactions Per Chromosome,\ plot Interactions Near Viewpoint$ 

### **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**

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

# Description

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

# Usage

getBatchReadCountPerRestrictionFragment(object,getReadsMethod = c("wholeReads", "adjacentFragmen'
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 frag-

ment 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

 $get Read Count Per Window, \ get Read Count Per Restriction Fragment$ 

#### **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

 $\tt getBatchReadCountPerWindow(object, windowSize=5e3, nFragmentExcludedReadsNearViewpoint=2, mode=c("range") and the state of the stat$ 

#### **Arguments**

object r3CseqInBatch object

windowSize Numeric. non-overlapping window size for counting reads (default=5e3)

n Fragment Excluded Reads Near Viewpoint

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

get Read Count Per Restriction Fragment, get Batch Read Count Per Restriction Fragment, get Read Count Per Window,

### **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=1

# **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**

getCoverage 17

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

 $\texttt{getExpInteractionsInRefseq(obj,cutoff.qvalue=0.05,expanded\_upstream=50e3,expanded\_downstream=10e3,expanded\_downstream=10e3,expanded\_downstream=10e3,expanded\_upstream=50e3,expanded\_downstream=1$ 

# 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**

18 getRawReads

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", "adjacentFragmentEndslineReads", "adjacentFragmentEnds

## **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 frag-

ment 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**

20 getViewpoint

getReadCountPerWindow count reads per window size

#### **Description**

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

# Usage

 $\tt getReadCountPerWindow(object, windowSize=5e3, nFragmentExcludedReadsNearViewpoint=2, mode=c("non-overlapped and the contraction of the contrac$ 

### **Arguments**

object r3Cseq object

windowSize Numeric. non-overlapping window size for counting reads (default=5e3)

n Fragment Excluded Reads Near Viewpoint

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

get Read Count Per Restriction Fragment,

#### **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)
```

hg18refGene 21

# 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, vie

### **Arguments**

object 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

### **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 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

 $\verb|plotOverviewInteractions| plotInteractions| PerChromosome, \verb|plotDomainogram| NearViewpoint| and \verb|plotOverviewInteractions| plotInteractions| plotInter$ 

# **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

 $\verb|plotInteractions| Near Viewpoint|, \verb|plotOverviewInteractions|, \verb|plotDomainogram| Near Viewpoint|, \verb|plotOverviewInteractions|, \verb|$ 

# **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)
```

r3Cseq-class 25

#### 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

26 r3CseqCommon-class

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.

r3CseqInBatch-class 27

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.

28 rn5refGene

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)

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#### See Also

r3CseqCommon, r3CseqInBatch

#### **Examples**

# See the vignette

rn5refGene

rn5's refGenes

# Description

The rat (rn5) reference genes from UCSC

# Index

*Topic <b>classes</b>	expInteractionRegions,r3CseqCommon-method
r3Cseq-class, 25	(expInteractionRegions), 7
r3CseqCommon-class, 26	export3Cseq2bedGraph, 8, 9, 10
r3CseqInBatch-class, 27	export3Cseq2bedGraph,r3Cseq-method
*Topic datasets	(export3Cseq2bedGraph), 8
enzymeDb, 6	export3CseqRawReads2bedGraph, 8
hg18refGene, 21	export3CseqRawReads2bedGraph,r3Cseq-method
hg19refGene, 21	<pre>(export3CseqRawReads2bedGraph),</pre>
mm10refGene, 21	8
mm9refGene, 21	exportBatchInteractions2text, 9
Myb_prom_FB, 22	<pre>exportBatchInteractions2text,r3CseqInBatch-method</pre>
Myb_prom_FL, 22	<pre>(exportBatchInteractions2text),</pre>
rn5refGene, 28	9
	exportInteractions2text, 8, 9, 10, 13
calculateBatchRPM, $2$ , $3$	exportInteractions2text,r3Cseq-method
calculateBatchRPM,r3CseqInBatch-method	(exportInteractions2text), 10
(calculateBatchRPM), $2$	expRawData, 5, 10, 11
calculateRPM, 3, 3, 6, 12	<pre>expRawData,r3Cseq-method(expRawData),</pre>
calculateRPM,r3Cseq-method	10
(calculateRPM), 3	expRawData<- (expRawData), 10
contrCoverage, 4	expRawData<-,r3Cseq-method
contrCoverage,r3Cseq-method	(expRawData), 10
(contrCoverage), 4	expReadCount, 6, 11
contrInteractionRegions, 4, 7	expReadCount,r3CseqCommon-method
$\verb contrInteractionRegions, r3CseqCommon-method \\$	(expReadCount), 11
(contrInteractionRegions), 4	expRPM, 3, 6, 12
contrRawData, 5	expRPM, r3CseqCommon-method (expRPM), 12
contrRawData,r3Cseq-method	
(contrRawData), 5	generate3CseqReport, 12
<pre>contrRawData&lt;- (contrRawData), 5</pre>	generate3CseqReport,r3Cseq-method
contrRawData<-,r3Cseq-method	(generate3CseqReport), 12
(contrRawData), 5	generate3CseqReport,r3CseqInBatch-method
contrReadCount, 5, 11	(generate3CseqReport), 12
contrReadCount,r3CseqCommon-method	getBatchInteractions, 13, 18
(contrReadCount), 5	<pre>getBatchInteractions,r3CseqInBatch-method</pre>
contrRPM, 3, 6, 12	(getBatchInteractions), 13
contrRPM,r3CseqCommon-method	getBatchRawReads, 14, 19
(contrRPM), 6	<pre>getBatchRawReads,r3CseqInBatch-method</pre>
	(getBatchRawReads), 14
enzymeDb, 6	getBatchReadCountPerRestrictionFragment,
expCoverage, 7	14, 16, 19
expCoverage,r3Cseq-method	getBatchReadCountPerRestrictionFragment,r3CseqInBatc
(expCoverage), 7	(getBatchReadCountPerRestrictionFragment),
expInteractionRegions, 4, 7	14

30 INDEX

```
getBatchReadCountPerWindow, 15
                                                 plotInteractionsPerChromosome, 13, 23,
getBatchReadCountPerWindow,r3CseqInBatch-method
        (getBatchReadCountPerWindow),
                                                 plotInteractionsPerChromosome,r3Cseq-method
        15
                                                         (plotInteractionsPerChromosome),
getContrInteractionsInRefseq, 16, 16, 17
                                                 plotOverviewInteractions, 13, 23, 24, 24
getContrInteractionsInRefseq,r3Cseq-method
                                                 plotOverviewInteractions,r3Cseq-method
        (getContrInteractionsInRefseq),
                                                         (plotOverviewInteractions), 24
getCoverage, 17
                                                 r3Cseq, 27
getCoverage, r3Cseq-method
                                                 r3Cseq(r3Cseq-class), 25
        (getCoverage), 17
                                                 r3Cseq-class, 25
getExpInteractionsInRefseq, 17
                                                 r3CseqCommon, 26, 28
getExpInteractionsInRefseq,r3Cseq-method
                                                 r3CseqCommon (r3CseqCommon-class), 26
        (getExpInteractionsInRefseq),
                                                 r3CseqCommon-class, 26
        17
                                                 r3CseqInBatch, 26-28
getInteractions, 4, 7, 8, 13, 18
                                                 r3CseqInBatch (r3CseqInBatch-class), 27
getInteractions,r3Cseq-method
                                                 r3CseqInBatch-class, 27
        (getInteractions), 18
                                                 rn5refGene, 28
getRawReads, 14, 18
getRawReads,r3Cseq-method
                                                 vsmooth.spline, 13, 18
        (getRawReads), 18
getReadCountPerRestrictionFragment, 6,
         11, 15, 16, 19, 20
getReadCountPerRestrictionFragment,r3Cseq-method
        (getReadCountPerRestrictionFragment),
getReadCountPerWindow, 15, 16, 19, 20
getReadCountPerWindow,r3Cseq-method
        (getReadCountPerWindow), 20
getViewpoint, 20
getViewpoint,r3Cseq-method
        (getViewpoint), 20
hg18refGene, 21
hg19refGene, 21
mm10refGene, 21
mm9refGene, 21
\texttt{Myb\_prom\_FB}, \textcolor{red}{\textbf{22}}
Myb_prom_FL, 22
plot3Cecdf, 22
plot3Cecdf, r3Cseq-method (plot3Cecdf),
plotDomainogramNearViewpoint, 22, 23-25
plotDomainogramNearViewpoint,r3Cseq-method
        (plotDomainogramNearViewpoint),
        22
plotInteractionsNearViewpoint, 13, 23,
        23, 24, 25
plotInteractionsNearViewpoint,r3Cseq-method
        (plotInteractionsNearViewpoint),
        23
```