Package ‘r3Cseq’

April 26, 2017

Version 1.22.0
Title Analysis of Chromosome Conformation Capture and Next-generation Sequencing (3C-seq)
Author Supat Thongjuea, MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, University of Oxford, UK
<supat.thongjuea@ndcls.ox.ac.uk>
Maintainer Supat Thongjuea <supat.thongjuea@ndcls.ox.ac.uk>
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
Description This package is an implementation of data analysis for the long-range interactions from 3C-seq assay.
License GPL-3
URL http://r3cseq.genereg.net
biocViews Preprocessing, Sequencing
NeedsCompilation no

R topics documented:
calculateBatchRPM .................................................. 2
calculateRPM .......................................................... 3
contrCoverage ......................................................... 4
contrInteractionRegions ............................................ 4
contrRawData .......................................................... 5
contrReadCount ....................................................... 5
contrRPM ............................................................... 6
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"))
**calculateRPM**

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
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

```r
## 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.

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)
exportBatchInteractions2text

Arguments

object r3Cseq object

Value

The text file in 'bedGraph' format

Author(s)

S. Thongjuea

See Also

exportInteractions2text, export3Cseq2bedGraph,

Examples

#See the vignette

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

Arguments
object r3Cseq object
value a GRanges object of aligned reads
### expReadCount

**Author(s)**

S. Thongjuea

**See Also**

expRawData

**Examples**

```r
#See the vignette
```

---

<table>
<thead>
<tr>
<th>expReadCount</th>
<th>get read count per region for the experiment</th>
</tr>
</thead>
</table>

**Description**

get the read count per region for the experiment

**Usage**

```r
expReadCount(object)
```

**Arguments**

- `object` : r3Cseq

**Author(s)**

S. Thongjuea

**See Also**

contrReadCount, getReadCountPerRestrictionFragment

**Examples**

```r
#See the vignette
```
expRPM

generate read per million (RPM) for the experiment

Description

generate 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 output 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

generateBatchInteractions

Description

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

Usage

generateBatchInteractions(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**

```r
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**

```r
#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**

```r
getBatchReadCountPerRestrictionFragment(object$getReadsMethod = c("wholeReads", "adjacentFragmentEndsReads"), nFragmentExcludedReadsNearViewpoint=2)
```
getBatchReadCountPerWindow

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-overlapping", "overlapping"))

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
getContrInteractionsInRefseq

Author(s)
S. Thongjuea

See Also
getReadCountPerRestrictionFragment, getBatchReadCountPerRestrictionFragment, getReadCountPerWindow.

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>obj</td>
<td>obj is r3Cseq or r3CseqInBatch object</td>
</tr>
<tr>
<td>cutoff.qvalue</td>
<td>Numeric. The cutoff q-value (default=0.05)</td>
</tr>
<tr>
<td>expanded_upstream</td>
<td>Numeric. The expanded distance from the upstream of a gene start (default=50e3)</td>
</tr>
<tr>
<td>expanded_downstream</td>
<td>Numeric. The expanded distance from the downstream of a gene end (default=10e3)</td>
</tr>
</tbody>
</table>

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.

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

*compute 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**

```r
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**

```r
#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**

```r
getRawReads(object)
```

**Arguments**

- `object`: r3Cseq object
getReadCountPerRestrictionFragment

Value
The GRangedData represents the aligned reads from the BAM file

Author(s)
S. Thongjuea

See Also
getBatchRawReads,

Examples
#See the vignette

getAddressPerRestrictionFragment

count reads per restriction fragment

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

Usage
getAddressPerRestrictionFragment(object, getReadsMethod = c("wholeReads", "adjacentFragmentEndsReads"), 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
getAddressPerWindow, 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**
```r
getReadCountPerWindow(object, windowSize=5e3, nFragmentExcludedReadsNearViewpoint=2, mode=c("non-overlapping", "overlapping"))
```

**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**
```r
#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 transcription factor binding region.

**Usage**
```r
getViewpoint(obj)
```
### hg18refGene

**Arguments**

`obj`  
`r3Cseq` or `r3CseqInBatch` object

**Value**

The viewpoint shows in the IRanges

**Author(s)**

S. Thongjuea

**Examples**

```r
#See the vignette
```

<table>
<thead>
<tr>
<th><code>hg18refGene</code></th>
<th><code>hg18's refGenes</code></th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>The human (hg18) reference genes from UCSC</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><code>hg19refGene</code></th>
<th><code>hg19's refGenes</code></th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>The human (hg19) reference genes from UCSC</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><code>mm10refGene</code></th>
<th><code>mm10's refGenes</code></th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>The mouse (mm10) reference genes from UCSC</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><code>mm9refGene</code></th>
<th><code>mm9's refGenes</code></th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>The mouse (mm9) reference genes from UCSC</td>
</tr>
</tbody>
</table>
### plotDomainogramNearViewpoint

#### Description

Plot domainogram of interaction regions near the viewpoint

#### Usage

```r
plotDomainogramNearViewpoint(object, smoothing.parameter=0.1, distance=5e5, maximum_window=25e3, view=c("experiment","control","both"))
```

#### Arguments

- **object**: r3Cseq or r3CseqInBatch object
- **smoothing.parameter**: Cubic smoothing 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")

---

### plot3Cecdf

This method has been removed.

---

<table>
<thead>
<tr>
<th>Myb_prom_FB</th>
<th>Myb_prom_FB a data set for the example of r3Cseq analysis</th>
</tr>
</thead>
</table>

**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.

<table>
<thead>
<tr>
<th>Myb_prom_FL</th>
<th>Myb_prom_FL a data set for the example of r3Cseq analysis</th>
</tr>
</thead>
</table>

**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.
plotInteractionsNearViewpoint

Value

Plots of domainogram for interaction regions close to the viewpoint

Author(s)

S. Thongjuea

See Also

plotOverviewInteractions, plotInteractionsPerChromosome, plotInteractionsNearViewpoint

Examples

# See the vignette

```r
plotInteractionsNearViewpoint
```

Description

Plot identified interaction regions near the viewpoint

Usage

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

Arguments

- `obj` : 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**

```r
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**

```r
# See the vignette
```

plotOverviewInteractions

*Plot overview of identified interaction regions for genome-wide*

**Description**

Plot the distribution of identified interaction regions across genome.

**Usage**

```r
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

---

**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 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

---

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.
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)
S. Thongjuea

See Also
r3CseqCommon, r3CseqInBatch

Examples
# See the vignette

rn5refGene      rn5's refGenes

Description
The rat (rn5) reference genes from UCSC
Index

*Topic classes
  r3Cseq-class, 25
  r3CseqCommon-class, 26
  r3CseqInBatch-class, 27

*Topic datasets
  enzymeDb, 6
  hg19refGene, 21
  mm10refGene, 21
  mm9refGene, 21
  Myb_prom_FB, 22
  Myb_prom_FL, 22
  rn5refGene, 28

calculateBatchRPM, 2, 3
calculateBatchRPM, r3CseqInBatch-method (calculateBatchRPM), 2
calculateRPM, 3, 6, 12
calculateRPM, r3Cseq-method (calculateRPM), 3
contrCoverage, 4
contrCoverage, r3Cseq-method (contrCoverage), 4
contrInteractionRegions, 4, 7
contrInteractionRegions, r3CseqCommon-method (contrInteractionRegions), 4
contrRawData, 5
contrRawData, r3Cseq-method (contrRawData), 5
contrRawData<-(contrRawData), 5
contrRawData<-, r3Cseq-method (contrRawData), 5
contrReadCount, 5, 11
contrReadCount, r3CseqCommon-method (contrReadCount), 5
contrRPM, 3, 6, 12
contrRPM, r3CseqCommon-method (contrRPM), 6

dbmixMix, 6
expCoverage, 7
expCoverage, r3Cseq-method (expCoverage), 7
expInteractionRegions, 4, 7
getBatchReadCountPerWindow, 15
getBatchReadCountPerWindow, r3CseqInBatch-method
  (getBatchReadCountPerWindow), 15
getContrInteractionsInRefseq, 16, 16, 17
getContrInteractionsInRefseq, r3Cseq-method
  (getContrInteractionsInRefseq), 16
getCoverage, 17
getCoverage, r3Cseq-method
  (getCoverage), 17
getExpInteractionsInRefseq, 17
getExpInteractionsInRefseq, r3Cseq-method
  (getExpInteractionsInRefseq), 17
getInteractions, 4, 7, 8, 13, 18
getInteractions, r3Cseq-method
  (getInteractions), 18
getRawReads, 14, 18
getRawReads, r3Cseq-method
  (getRawReads), 18
getReadCountPerRestrictionFragment, 6,
  11, 15, 16, 19, 20
getReadCountPerRestrictionFragment, r3Cseq-method
  (getReadCountPerRestrictionFragment), 19
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
Myb_prom_FB, 22
Myb_prom_FL, 22
plot3Cecdf, 22
plot3Cecdf, r3Cseq-method (plot3Cecdf), 22
plotDomainogramNearViewpoint, 22, 23–25
plotDomainogramNearViewpoint, r3Cseq-method
  (plotDomainogramNearViewpoint), 22
plotInteractionsNearViewpoint, 13, 23,
  23, 24, 25
plotInteractionsNearViewpoint, r3Cseq-method
  (plotInteractionsNearViewpoint), 23
plotOverviewInteractions, 13, 23, 24, 24
plotOverviewInteractions, r3Cseq-method
  (plotOverviewInteractions), 24
r3Cseq, 27
r3Cseq (r3Cseq-class), 25
r3Cseq-class, 25
r3CseqCommon, 26, 28
r3CseqCommon (r3CseqCommon-class), 26
r3CseqCommon-class, 26
r3CseqInBatch, 26–28
r3CseqInBatch (r3CseqInBatch-class), 27
r3CseqInBatch-class, 27
rn5refGene, 28
vsmooth.spline, 13, 18