Package ‘r3Cseq’

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**Version** 1.49.0

**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

**Suggests** BSgenome.Musculus.UCSC.mm9.masked,
BSgenome.Musculus.UCSC.mm10.masked,
BSgenome.Hsapiens.UCSC.hg18.masked,
BSgenome.Hsapiens.UCSC.hg19.masked,
BSgenome.Rnorvegicus.UCSC.rn5.masked

**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](http://r3cseq.genereg.net), [https://github.com/supatt-lab/r3Cseq/](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

**biocViews** Preprocessing, Sequencing

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calculateBatchRPM  

**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  

**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)
contrInteractionRegions

Author(s)
S. Thongjuea

See Also
contrRPM, expRPM, calculateBatchRPM

Examples

# See the vignette

contrCoverage

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

\textit{Accessors for the 'contrRawData' slot of a r3Cseq object.}

Description

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

Usage

\begin{verbatim}
## S4 method for signature 'r3Cseq'
contrRawData(object)
## S4 replacement method for signature 'r3Cseq'
contrRawData(object) <- value
\end{verbatim}

Arguments

- \texttt{object} r3Cseq object
- \texttt{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

---

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
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

Description

export identified interaction regions 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

importInteractions2text

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
ccontrReadCount, getReadCountPerRestrictionFragment

Examples
#See the vignette

## 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 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, plotInteractionNearViewpoint

Examples

# See the vignette

getchInteractions  

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

getchInteractions(object, method=c("union", "intersection"), smoothing.parameter=0.1, fdr=0.05)
**getBatchRawReads**

**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
getBatchReadCountPerRestrictionFragment

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", "adjacentFragmentEndsReads"), 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

getCodeCountPerWindow, 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

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.

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

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

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
getchBatchRawReads

Examples
#See the vignette

getReadCountPerRestrictionFragment

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

Usage
getReadCountPerRestrictionFragment(object, getReadsMethod = c("wholeReads", "adjacentFragmentEndsReads"), nFragmentExcludedReadsNearViewpoint=2)
getReadCountPerWindow

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

```r
#See the vignette
```

---

**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"))
```

**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")
getViewpoint

Value
The RangedData represents the number of reads per each window size

Author(s)
S. Thongjuea

See Also
getReadCountPerRestrictionFragment,

Examples
#See the vignette

---

g 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
g getViewpoint(obj)

Arguments
obj r3Cseq or r3CseqInBatch object

Value
The viewpoint shows in the IRanges

Author(s)
S. Thongjuea

Examples
#See the vignette
<table>
<thead>
<tr>
<th>Reference</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>hg18refGene</td>
<td>The human (hg18) reference genes from UCSC</td>
</tr>
<tr>
<td>hg19refGene</td>
<td>The human (hg19) reference genes from UCSC</td>
</tr>
<tr>
<td>mm10refGene</td>
<td>The mouse (mm10) reference genes from UCSC</td>
</tr>
<tr>
<td>mm9refGene</td>
<td>The mouse (mm9) reference genes from UCSC</td>
</tr>
<tr>
<td>Myb_prom_FB</td>
<td>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.</td>
</tr>
</tbody>
</table>
**plotDomainogramNearViewpoint**

<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.

**plot3 Cecdf**

This method has been removed.

**Description**

This method has been removed.

**plotDomainogramNearViewpoint**

Plot domainogram of interaction regions near the viewpoint

**Usage**

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

**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**

```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)
```
r3Cseq-class

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
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
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)
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See Also
r3CseqCommon, r3CseqInBatch

Examples
# See the vignette

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Description
The rat (rn5) reference genes from UCSC
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