

# Package: r3Cseq (via r-universe)

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

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**Depends** GenomicRanges, Rsamtools, rtracklayer, VGAM, qvalue

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BSgenome.Hsapiens.UCSC.hg18.masked,  
BSgenome.Hsapiens.UCSC.hg19.masked,  
BSgenome.Rnorvegicus.UCSC.rm5.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>, <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

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/r3Cseq>

**RemoteRef** HEAD

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---

calculateBatchRPM	<i>calculate read per million (RPM) for replicates analysis</i>
-------------------	---

---

**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	<i>calculate read per million (RPM)</i>
--------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

Author(s)

S. Thongjuea

See Also

[contrRPM](#), [expRPM](#), [calculateBatchRPM](#)

Examples

#See the vignette

---

contrCoverage	<i>This method has been removed.</i>
---------------	--------------------------------------

---

Description

This method has been removed.

---

contrInteractionRegions	<i>get interaction regions from the control</i>
-------------------------	---

---

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	<i>Accessors for the 'contrRawData' slot of a r3Cseq object.</i>
--------------	--

---

## Description

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

## Usage

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

## Arguments

object	r3Cseq object
value	a GRanges object of aligned reads

## Author(s)

S. Thongjuea

## See Also

[expRawData](#)

## Examples

```
#See the vignette
```

---

contrReadCount	<i>get read count per region for the control</i>
----------------	--

---

**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	<i>get read per million (RPM) for the control</i>
----------	---

---

**Description**

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

**Usage**

```
contrRPM(object)
```

**Arguments**

object	r3Cseq or r3CseqInBatch object
--------	--------------------------------

**Author(s)**

S. Thongjuea

**See Also**[calculateRPM](#), [expRPM](#)**Examples**

#See the vignette

---

enzymeDb*Rebase The Restriction Enzyme Database*

---

**Description**

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

**References**

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

---

expCoverage*This method has been removed.*

---

**Description**

This method has been removed.

---

expInteractionRegions *get interaction regions from the experiment*

---

**Description**

get identified interaction regions from the experiment

**Usage**

expInteractionRegions(object)

**Arguments**

object            r3Cseq or r3CseqInBatch object

**Value**

The candidate interaction regions show in the IRange object

**Author(s)**

S. Thongjuea

**See Also**

[getInteractions](#), [contrInteractionRegions](#)

**Examples**

```
#See the vignette
```

---

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

---

**Description**

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

**Usage**

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

**Arguments**

object	r3Cseq object, The object might contain the interaction regions generated by function <a href="#">getInteractions</a>
datatype	read_count : read count per restriction fragment rpm : normalized read per million per restriction fragment

**Value**

The text file in 'bedGraph' format

**Author(s)**

S. Thongjuea

**See Also**

[exportInteractions2text](#)

**Examples**

```
#See the vignette
```



---

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

---

**Description**

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

**Usage**

```
export3CseqRawReads2bedGraph(object)
```

**Arguments**

object                    r3Cseq object

**Value**

The text file in 'bedGraph' format

**Author(s)**

S. Thongjuea

**See Also**

[exportInteractions2text](#), [export3Cseq2bedGraph](#),

**Examples**

```
#See the vignette
```

---

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

---

**Description**

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

**Usage**

```
exportBatchInteractions2text(object)
```

**Arguments**

object                    r3CseqInBatch object

**Value**

The text file in the tab separated format

**Author(s)**

S. Thongjuea

**See Also**

[export3Cseq2bedGraph](#), [exportInteractions2text](#)

**Examples**

```
#See the vignette
```

---

```
exportInteractions2text
```

*export identified interaction regions to the tab separated format*

---

**Description**

export interaction regions from RagedData to the tab separated format

**Usage**

```
exportInteractions2text(object)
```

**Arguments**

object                    r3Cseq object

**Value**

The text file in the tab separated format

**Author(s)**

S. Thongjuea

**See Also**

[export3Cseq2bedGraph](#)

**Examples**

```
#See the vignette
```

---

expRawData	<i>Accessors for the 'expRawData' slot of a r3Cseq object.</i>
------------	--

---

**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	<i>get read count per region for the experiment</i>
--------------	---

---

**Description**

get the read count per region for the experiment

**Usage**

```
expReadCount(object)
```

**Arguments**

object	r3Cseq
--------	--------

**Author(s)**

S. Thongjuea

**See Also**

[contrReadCount](#), [getReadCountPerRestrictionFragment](#)

**Examples**

```
#See the vignette
```

---

expRPM

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

---

**Description**

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

**Usage**

```
expRPM(object)
```

**Arguments**

object            r3Cseq or r3CseqInBatch

**Author(s)**

S. Thongjuea

**See Also**

[calculateRPM](#), [contrRPM](#)

**Examples**

```
#See the vignette
```

---

generate3CseqReport	<i>generate reports for analysis results from r3Cseq</i>
---------------------	--

---

**Description**

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

**Usage**

```
generate3CseqReport(obj)
```

**Arguments**

obj                      r3Cseq or r3CseqInBatch object

**Value**

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

**Author(s)**

S. Thongjuea

**See Also**

[exportInteractions2text](#) [plotOverviewInteractions](#), [plotInteractionsPerChromosome](#), [plotInteractionsNearViewpoint](#)

**Examples**

```
#See the vignette
```

---

getBatchInteractions	<i>calculate z-score, assign p-value and q-value for each interaction region for replicates data sets</i>
----------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

The interaction regions show in the RangedData

**Author(s)**

S. Thongjuea

**See Also**

[getInteractions vsmooth.spline](#)

**Examples**

```
#See the vignette
```

---

getBatchRawReads	<i>Get aligned reads from the replicates BAM files</i>
------------------	--

---

**Description**

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

**Usage**

```
getBatchRawReads(object)
```

**Arguments**

object	r3CseqInBatch object
--------	----------------------

**Value**

The GRangedData represents the aligned reads from the BAM file

**Author(s)**

S. Thongjuea

**See Also**

[getRawReads](#),

**Examples**

#See the vignette

---

```
getBatchReadCountPerRestrictionFragment
      count reads for replicates analysis
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

The RangedData represents the number of reads per each restriction fragment

**Author(s)**

S. Thongjuea

**See Also**

[getReadCountPerWindow](#), [getReadCountPerRestrictionFragment](#)

**Examples**

#See the vignette

---

getBatchReadCountPerWindow

*count reads per window size for replicates analysis*


---

## Description

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

## Usage

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

## Arguments

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

## Value

The RangedData represents the number of reads per each window size

## Author(s)

S. Thongjuea

## See Also

[getReadCountPerRestrictionFragment](#), [getBatchReadCountPerRestrictionFragment](#), [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**

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

**Value**

List of identified genes, which contain strong interaction signals

**Author(s)**

S. Thongjuea

**See Also**

[getContrInteractionsInRefseq](#)

**Examples**

```
# See the vignette
```

---

getCoverage                    *This method has been removed.*

---

**Description**

This method has been removed.

---

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

---

**Description**

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

**Usage**

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

**Arguments**

<code>obj</code>	<code>obj</code> is <code>r3Cseq</code> or <code>r3CseqInBatch</code> object
<code>cutoff.qvalue</code>	Numeric. The cutoff q-value (default=0.05)
<code>expanded_upstream</code>	Numeric. The expanded distance from the upstream of a gene start (default=50e3)
<code>expanded_downstream</code>	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	<i>calculate z-score, assign p-value and q-value for each interaction region</i>
-----------------	--

---

## 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	<i>Get aligned reads from the BAM file</i>
-------------	--

---

**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	<i>count reads per resitrcition fragment</i>
------------------------------------	--

---

**Description**

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

**Usage**

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

**Arguments**

object            r3Cseq object

getReadsMethod   character. To count all reads found in the particular restriction fragment uses wholeReads option. To count reads found around the edge of restriction fragment both 5'utr and 3'utr uses adjacentFragmentEndsReads option (default=wholeReads)

nFragmentExcludedReadsNearViewpoint  
                       Numeric. The number of excluded fragments around the viewpoint, reads found in these fragments will be removed from the analysis (default=2)

**Value**

The RangedData represents the number of reads per each restriction fragment

**Author(s)**

S. Thongjuea

**See Also**

[getReadCountPerWindow](#), [getBatchReadCountPerRestrictionFragment](#)

**Examples**

```
#See the vignette
```

---

getReadCountPerWindow   *count reads per window size*

---

**Description**

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

**Usage**

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

**Arguments**

object            r3Cseq object

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

nFragmentExcludedReadsNearViewpoint  
                       Numeric. The number of excluded fragments around the viewpoint, reads found in these fragments will be removed from the analysis (default=2)

mode               character. The window-based modes analysis (default="non-overlapping")

**Value**

The RangedData represents the number of reads per each window size

**Author(s)**

S. Thongjuea

**See Also**

[getReadCountPerRestrictionFragment](#),

**Examples**

```
#See the vignette
```

---

getViewpoint	<i>get the viewpoint of 3C-seq data</i>
--------------	---

---

**Description**

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

**Usage**

```
getViewpoint(obj)
```

**Arguments**

obj	r3Cseq or r3CseqInBatch object
-----	--------------------------------

**Value**

The viewpoint shows in the IRanges

**Author(s)**

S. Thongjuea

**Examples**

```
#See the vignette
```

---

hg18refGene	<i>hg18's refGenes</i>
-------------	------------------------

---

**Description**

The human (hg18) reference genes from UCSC

---

hg19refGene	<i>hg19's refGenes</i>
-------------	------------------------

---

**Description**

The human (hg19) reference genes from UCSC

---

mm10refGene	<i>mm10's refGenes</i>
-------------	------------------------

---

**Description**

The mouse (mm10) reference genes from UCSC

---

mm9refGene	<i>mm9's refGenes</i>
------------	-----------------------

---

**Description**

The mouse (mm9) reference genes from UCSC

---

Myb_prom_FB	<i>Myb_prom_FB a data set for the example of r3Cseq analysis</i>
-------------	--

---

**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	<i>Myb_prom_FL a data set for the example of r3Cseq analysis</i>
-------------	--

---

**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	<i>This method has been removed.</i>
------------	--------------------------------------

---

**Description**

This method has been removed.

---

plotDomainogramNearViewpoint	<i>Plot domainogram of interaction regions near the viewpoint</i>
------------------------------	---

---

**Description**

Plot domainogram of interaction regions near the viewpoint

**Usage**

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

**Arguments**

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

**Value**

Plots of domainogram for interaction regions close to the viewpoint



**Author(s)**

S. Thongjuea

**See Also**

[plotOverviewInteractions](#), [plotInteractionsPerChromosome](#), [plotInteractionsNearViewpoint](#)

**Examples**

```
# See the vignette
```

---

`plotInteractionsNearViewpoint`

*Plot identified interaction regions near the viewpoint*

---

**Description**

Plot identified interaction regions near the viewpoint

**Usage**

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

**Arguments**

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

**Value**

Plots of identified interaction regions close to the viewpoint

**Author(s)**

S. Thongjuea

**See Also**

[plotOverviewInteractions](#), [plotInteractionsPerChromosome](#), [plotDomainogramNearViewpoint](#)

**Examples**

```
# See the vignette
```

---

`plotInteractionsPerChromosome`*Plot interaction regions per each chromosome of interest*

---

**Description**

Plot the distribution of interaction regions per each chromosome

**Usage**

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

**Arguments**

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

**Value**

Plots of interaction regions per chromosome.

**Author(s)**

S. Thongjuea

**See Also**

[plotInteractionsNearViewpoint](#), [plotOverviewInteractions](#), [plotDomainogramNearViewpoint](#)

**Examples**

```
# See the vignette
```

---

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

---

**Description**

Plot the distribution of identified interaction regions across genome

**Usage**

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

**Arguments**

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

**Value**

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

**Author(s)**

S. Thongjuea

**See Also**

[plotInteractionsNearViewpoint](#), [plotInteractionsPerChromosome](#), [plotDomainogramNearViewpoint](#)

**Examples**

```
# See the vignette
```

---

r3Cseq-class

*r3Cseq objects*


---

**Description**

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

**Extends**

Class r3CseqCommon, directly.

**Slots**

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

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

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

viewpoint\_primer\_forward    Object of class "character" the forward primer DNA sequences for the viewpoint amplification

viewpoint\_primer\_reverse Object of class "character" the reverse primer DNA sequences for the viewpoint amplification

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

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

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

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

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

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

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

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

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

expLabel Object of class "character" the experiment name

contrLabel Object of class "character" the control name

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

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

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

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

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

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

### Author(s)

S. Thongjuea

### See Also

[r3CseqCommon](#), [r3CseqInBatch](#)

### Examples

```
# See the vignette
```

---

r3CseqCommon-class	<i>r3CseqCommon objects</i>
--------------------	-----------------------------

---

## 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 view-point 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	<i>r3CseqInBatch objects</i>
---------------------	------------------------------

---

## 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 view-point located eg. chr10, chrX etc.

**viewpoint\_primer\_forward** Object of class "character" the forward primer DNA sequences for the viewpoint amplification

**viewpoint\_primer\_reverse** Object of class "character" the reverse primer DNA sequences for the viewpoint amplification

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

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

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

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

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

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

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

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

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

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

**expBatchLabel** Object of class "vector" the labeled experiment names

**contrBatchLabel** Object of class "vector" the labeled control names

readCountTable Object of class "RangedData" the read count table  
RPMsTable Object of class "RangedData" the normalized read per million table  
expBatchLibrarySize Object of class "vector" the library size of each experiment  
contrBatchLibrarySize Object of class "vector" the library size of each control  
expBatchReadLength Object of class "vector" the read length of experiments  
contrBatchReadLength Object of class "vector" the read length of controls

**Author(s)**

S. Thongjuea

**See Also**

[r3CseqCommon](#), [r3CseqInBatch](#)

**Examples**

```
# See the vignette
```

---

rn5refGene

*rn5's refGenes*

---

**Description**

The rat (rn5) reference genes from UCSC

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