Package ‘r3Cseq’

March 28, 2024

Version 1.48.0
Title Analysis of Chromosome Conformation Capture and Next-generation Sequencing (3C-seq)
Author Supat Thongjuea, MRC WIMM Centre for Computational Biology, Weatherall Institute of Molecular Medicine, University of Oxford, UK
<sapat.thongjuea@imm.ox.ac.uk>
Maintainer Supat Thongjuea <sapat.thongjuea@imm.ox.ac.uk> or <sapat.thongjuea@gmail.com>
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, https://github.com/supatt-lab/r3Cseq/
FunctionsForBatchAnalysis.R RestrictionEnzymeFunctions.R
FunctionsForNoReplicationAnalysis.R Report.R Visualize3Cseq.R
Annotation.R
biocViews Preprocessing, Sequencing
git_url https://git.bioconductor.org/packages/r3Cseq
git_branch RELEASE_3_18
git_last_commit d9ef32a
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-27
R topics documented:

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>calculateBatchRPM</td>
<td>3</td>
</tr>
<tr>
<td>calculateRPM</td>
<td>3</td>
</tr>
<tr>
<td>contrCoverage</td>
<td>4</td>
</tr>
<tr>
<td>contrInteractionRegions</td>
<td>4</td>
</tr>
<tr>
<td>contrRawData</td>
<td>5</td>
</tr>
<tr>
<td>contrReadCount</td>
<td>6</td>
</tr>
<tr>
<td>contrRPM</td>
<td>6</td>
</tr>
<tr>
<td>enzymeDb</td>
<td>7</td>
</tr>
<tr>
<td>expCoverage</td>
<td>7</td>
</tr>
<tr>
<td>expInteractionRegions</td>
<td>7</td>
</tr>
<tr>
<td>export3Cseq2bedGraph</td>
<td>8</td>
</tr>
<tr>
<td>export3CseqRawReads2bedGraph</td>
<td>9</td>
</tr>
<tr>
<td>exportBatchInteractions2text</td>
<td>9</td>
</tr>
<tr>
<td>exportInteractions2text</td>
<td>10</td>
</tr>
<tr>
<td>expRawData</td>
<td>11</td>
</tr>
<tr>
<td>expReadCount</td>
<td>11</td>
</tr>
<tr>
<td>expRPM</td>
<td>12</td>
</tr>
<tr>
<td>generate3CseqReport</td>
<td>13</td>
</tr>
<tr>
<td>getBatchInteractions</td>
<td>13</td>
</tr>
<tr>
<td>getBatchRawReads</td>
<td>14</td>
</tr>
<tr>
<td>getBatchReadCountPerRestrictionFragment</td>
<td>15</td>
</tr>
<tr>
<td>getBatchReadCountPerWindow</td>
<td>16</td>
</tr>
<tr>
<td>getContrInteractionsInRefseq</td>
<td>17</td>
</tr>
<tr>
<td>getCoverage</td>
<td>17</td>
</tr>
<tr>
<td>getExpInteractionsInRefseq</td>
<td>18</td>
</tr>
<tr>
<td>getInteractions</td>
<td>19</td>
</tr>
<tr>
<td>getRawReads</td>
<td>20</td>
</tr>
<tr>
<td>getReadCountPerRestrictionFragment</td>
<td>20</td>
</tr>
<tr>
<td>getReadCountPerWindow</td>
<td>21</td>
</tr>
<tr>
<td>getViewpoint</td>
<td>22</td>
</tr>
<tr>
<td>hg18refGene</td>
<td>23</td>
</tr>
<tr>
<td>hg19refGene</td>
<td>23</td>
</tr>
<tr>
<td>mm10refGene</td>
<td>23</td>
</tr>
<tr>
<td>mm9refGene</td>
<td>23</td>
</tr>
<tr>
<td>Myb_prom_FB</td>
<td>23</td>
</tr>
<tr>
<td>Myb_prom_FL</td>
<td>24</td>
</tr>
<tr>
<td>plot3Cecdf</td>
<td>24</td>
</tr>
<tr>
<td>plotDomainogramNearViewpoint</td>
<td>24</td>
</tr>
<tr>
<td>plotInteractionsNearViewpoint</td>
<td>25</td>
</tr>
<tr>
<td>plotInteractionsPerChromosome</td>
<td>26</td>
</tr>
<tr>
<td>plotOverviewInteractions</td>
<td>26</td>
</tr>
<tr>
<td>r3Cseq-class</td>
<td>27</td>
</tr>
<tr>
<td>r3CseqCommon-class</td>
<td>29</td>
</tr>
<tr>
<td>r3CseqInBatch-class</td>
<td>30</td>
</tr>
<tr>
<td>rn5refGene</td>
<td>31</td>
</tr>
</tbody>
</table>

Index 32
calculateBatchRPM  calculate read per million (RPM) for replicates analysis

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

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

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

Author(s)
S. Thongjuea

See Also
calculateRPM, expRPM contrRPM

Examples
#See the vignette

calculateRPM  calculate read per million (RPM)

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

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

Arguments
object           r3Cseq object
normalized_method character. method of normalization (default=powerlawFittedRPM)
Author(s)
S. Thongjuea

See Also
contrRPM, expRPM, calculateBatchRPM

Examples
# See the vignette

contrInteractionRegions

Description
get 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**

**Description**

The `contrRawData` slot 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**

<table>
<thead>
<tr>
<th>name</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>r3Cseq object</td>
</tr>
<tr>
<td>value</td>
<td>a GRanges object of aligned reads</td>
</tr>
</tbody>
</table>

**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**
```r
contrReadCount(object)
```

**Arguments**
- `object`: r3Cseq object

**Author(s)**
S. Thongjuea

**See Also**
- `expReadCount`, `getReadCountPerRestrictionFragment`

**Examples**
```r
#See the vignette
```

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

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

**Usage**
```r
contrRPM(object)
```

**Arguments**
- `object`: r3Cseq or r3CseqInBatch object

**Author(s)**
S. Thongjuea
enzymeDb

See Also
calculateRPM, expRPM

Examples

#See the vignette

<table>
<thead>
<tr>
<th>enzymeDb</th>
<th>Rebase The Restriction Enzyme Database</th>
</tr>
</thead>
</table>

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)
exportInteractions2text

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**

```r
## 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

**Author(s)**

S. Thongjuea

**See Also**

expRawData

**Examples**

```r
#See the vignette
```

---

**expReadCount**

*get read count per region for the experiment*

**Description**

get the read count per region for the experiment

**Usage**

```r
expReadCount(object)
```

**Arguments**

- `object` r3Cseq
expRPM

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**

**Description**

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

**Usage**

```r
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**

```r
#See the vignette
```

---

**getBatchInteractions**

**Description**

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

**Usage**

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

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

Value

The interaction regions show in the RangedData

Author(s)

S. Thongjuea

See Also

getInteractions vsmooth.spline

Examples

#See the vignette

getBatchRawReads  Get aligned reads from the replicates BAM files

Description

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

Usage

getBatchRawReads(object)

Arguments

object  r3CseqInBatch object

Value

The GRangedData represents the aligned reads from the BAM file

Author(s)

S. Thongjuea
getBatchReadCountPerRestrictionFragment

See Also
getRawReads,

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

Value
List of identified genes, which contain strong interaction signals

Author(s)
S. Thongjuea

See Also
getContrInteractionsInRefseq

Examples
# See the vignette

getCoverage

This method has been removed.

Description
This method has been removed.
getExpInteractionsInRefseq

identified significant interaction regions for RefSeq genes

Description

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

Usage

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

Arguments

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

Value

List of identified genes, which contain strong interaction signals

Author(s)

S. Thongjuea

See Also

getContrInteractionsInRefseq

Examples

# See the vignette
getInteractions

**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
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 restriction fragment

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", "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

---

ggetViewpoint  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

ggetViewpoint(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 Gene</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

Myb_prom_FL  Myb_prom_FL a data set for the example of r3Cseq analysis

Description

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

plot3Cecdf

This method has been removed.

Description

This method has been removed.

plotDomainogramNearViewpoint

Plot domainogram of interaction regions near the viewpoint

Description

Plot domainogram of interaction regions near the viewpoint

Usage

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

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
plotInteractionsNearViewpoint

Author(s)
S. Thongjuea

See Also
plotOverviewInteractions, plotInteractionsPerChromosome, plotInteractionsNearViewpoint

Examples
# See the vignette

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
plotOverviewInteractions

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

---

**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

```r
# See the vignette
```
r3CseqInBatch-class  
r3CseqInBatch objects

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

Extends
Class r3CseqCommon, directly.

Slots
organismName  Object of class "character" the version of particular assembly genome from UCSC (e.g. mm9, hg18, hg19). The package supports three genome assemblies consisting of mouse (mm9), and human (hg18, hg19).
restrictionEnzyme Object of class "character" this is the primary restriction enzyme name using in 3C-Seq experiment
viewpoint_chromosome Object of class "character" chromosome name of where is the viewpoint located eg. chr10, chrX etc.
viewpoint_primer_forward Object of class "character" the forward primer DNA sequences for the viewpoint amplification
viewpoint_primer_reverse Object of class "character" the reverse primer DNA sequences for the viewpoint amplification
expReadCount  Object of class "RangedData" the read count in experiment
contrReadCount Object of class "RangedData" the read count in control
expRPM  Object of class "RangedData" the normalized read read per million in experiment
contrRPM  Object of class "RangedData" the normalized read read per million in control
expInteractionRegions Object of class "RangedData" the identified interaction regions in experiment
contrInteractionRegions Object of class "RangedData" the identified interaction regions in control
isControlInvolved Object of class "logical" the logical to ask whether the control is involved in the analysis or not
bamFilesDirectory Object of class "character" the path name of directory that contains BAM files
BamExpFiles  Object of class "vector" the file names of BAM files in the experiment
BamContrFiles Object of class "vector" the file names of BAM files in the control
expBatchLabel Object of class "vector" the labeled experiment names
contrBatchLabel Object of class "vector" the labeled control names
readCountTable  Object of class "RangedData" the read count table
RPMsTable  Object of class "RangedData" the normalized read per million table
expBatchLibrarySize  Object of class "vector" the library size of each experiment
contrBatchLibrarySize  Object of class "vector" the library size of each control
expBatchReadLength  Object of class "vector" the read length of experiments
contrBatchReadLength  Object of class "vector" the read length of controls

Author(s)
S. Thongjuea

See Also
r3CseqCommon, r3CseqInBatch

Examples

# See the vignette

<table>
<thead>
<tr>
<th>rn5refGene</th>
<th>rn5's refGenes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Description

The rat (rn5) reference genes from UCSC
Index

* classes
  r3Cseq-class, 27
  r3CseqCommon-class, 29
  r3CseqInBatch-class, 30

* datasets
  enzymeDb, 7
  hg18refGene, 23
  hg19refGene, 23
  mm10refGene, 23
  mm9refGene, 23
  Myb_prom_FB, 23
  Myb_prom_FL, 24
  rn5refGene, 31

  calculateBatchRPM, 3, 4
  calculateBatchRPM,r3CseqInBatch-method (calculateBatchRPM), 3
  calculateRPM, 3, 3, 7, 12
  calculateRPM,r3Cseq-method (calculateRPM), 3
  contrCoverage, 4
  contrCoverage,r3Cseq-method (contrCoverage), 4
  contrInteractionRegions, 4, 8
  contrInteractionRegions,r3CseqCommon-method (contrInteractionRegions), 4
  contrRawData, 5
  contrRawData,r3Cseq-method (contrRawData), 5
  contrRawData<-(contrRawData), 5
  contrRawData<-,r3Cseq-method (contrRawData), 5
  contrReadCount, 6, 12
  contrReadCount,r3CseqCommon-method (contrReadCount), 6
  contrRPM, 3, 4, 6, 12
  contrRPM,r3CseqCommon-method (contrRPM), 6

  expCoverage, 7
  expCoverage,r3Cseq-method (expCoverage), 7
  expInteractionRegions, 4, 7
  expInteractionRegions,r3CseqCommon-method (expInteractionRegions), 7
  export3Cseq2bedGraph, 8, 9, 10
  export3Cseq2bedGraph,r3Cseq-method (export3Cseq2bedGraph), 8
  export3CseqRawReads2bedGraph, 9
  export3CseqRawReads2bedGraph,r3Cseq-method (export3CseqRawReads2bedGraph), 9
  exportBatchInteractions2text, 9
  exportBatchInteractions2text,r3CseqInBatch-method (exportBatchInteractions2text), 9
  exportInteractions2text, 8–10, 10, 13
  exportInteractions2text,r3Cseq-method (exportInteractions2text), 10
  exportInteractions2text,r3CseqInBatch-method (exportInteractions2text), 10
  expRawData, 5, 11, 11
  expRawData,r3Cseq-method (expRawData), 11
  expRawData<-(expRawData), 11
  expRawData<-,r3Cseq-method (expRawData), 11
  expReadCount, 6, 11
  expReadCount,r3CseqCommon-method (expReadCount), 11
  expRPM, 3, 4, 7, 12
  expRPM,r3CseqCommon-method (expRPM), 12

  generate3CseqReport, 13
  generate3CseqReport,r3Cseq-method (generate3CseqReport), 13
  generate3CseqReport,r3CseqInBatch-method (generate3CseqReport), 13
  getBatchInteractions, 13, 19
  getBatchInteractions,r3CseqInBatch-method (getBatchInteractions), 13
getBatchRawReads, 14, 20
getBatchRawReads, r3CseqInBatch-method
  (getBatchRawReads), 14
getBatchReadCountPerRestrictionFragment, 15, 16, 21
getBatchReadCountPerRestrictionFragment, r3CseqInBatch-method
  (getBatchReadCountPerRestrictionFragment), 15
getBatchReadCountPerWindow, 16
getBatchReadCountPerWindow, r3CseqInBatch-method
  (getBatchReadCountPerWindow), 16
getContrInteractionsInRefseq, 17, 17, 18
getContrInteractionsInRefseq, r3Cseq-method
  (getContrInteractionsInRefseq), 17
getCoverage, 17
getCoverage, r3Cseq-method
  (getCoverage), 17
getExpInteractionsInRefseq, 18
getExpInteractionsInRefseq, r3Cseq-method
  (getExpInteractionsInRefseq), 18
getInteractions, 4, 8, 14, 19
getInteractions, r3Cseq-method
  (getInteractions), 19
getRawReads, 15, 20
getRawReads, r3Cseq-method
  (getRawReads), 20
getReadCountPerRestrictionFragment, 6, 12, 15, 16, 20, 22
getReadCountPerRestrictionFragment, r3Cseq-method
  (getReadCountPerRestrictionFragment), 20
getReadCountPerWindow, 15, 16, 21, 21
getReadCountPerWindow, r3Cseq-method
  (getReadCountPerWindow), 21
getViewpoint, 22
getViewpoint, r3Cseq-method
  (getViewpoint), 22

hg18refGene, 23
hg19refGene, 23

mm10refGene, 23
mm9refGene, 23
Myb_prom_FB, 23
Myb_prom_FL, 24

plot3Cecdf, 24
plot3Cecdf, r3Cseq-method (plot3Cecdf), 24
plotDomainogramNearViewpoint, 24, 25–27
plotDomainogramNearViewpoint, r3Cseq-method
  (plotDomainogramNearViewpoint), 24
plotInteractionsNearViewpoint, 13, 25, 25, 26, 27
plotInteractionsNearViewpoint, r3Cseq-method
  (plotInteractionsNearViewpoint), 25
plotInteractionsPerChromosome, 13, 25, 26, 27
plotInteractionsPerChromosome, r3Cseq-method
  (plotInteractionsPerChromosome), 26
plotOverviewInteractions, 13, 25, 26, 26
plotOverviewInteractions, r3Cseq-method
  (plotOverviewInteractions), 26
r3Cseq, 29
r3Cseq (r3Cseq-class), 27
r3Cseq-class, 27
r3CseqCommon, 28, 31
r3CseqCommon (r3CseqCommon-class), 29
r3CseqCommon-class, 29
r3CseqInBatch, 28, 29, 31
r3CseqInBatch (r3CseqInBatch-class), 30
r3CseqInBatch-class, 30
rn5refGene, 31
vsmooth.spline, 14, 19