Package: ChIPQC (via r-universe)

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Type Package

Title Quality metrics for ChIPseq data

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License GPL (>= 3)

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`ChIPQC-package` *ChIPQC - Quality metrics for ChIPseq data*

Description

ChIPQC analyzes aligned reads (in .bam format) for ChIP-seq samples and their associated controls, computing a variety of quality control metrics and statistics, and providing reporting and plotting functions to enable assessment of experimental data for further analysis.

Details

Package:	ChIPQC
Type:	Package
Version:	0.1
Date:	2014-03-01
License:	GPL3

`ChIPQC` primarily uses two object classes: `ChIPQCsample`, which encapsulates the information about individual samples, and `ChIPQCexperiment`, which encapsulates information about larger ChIP-seq experiments (consisting of a number of samples). The primary entry point is the constructor function `ChIPQC`, which takes a description of an entire experiment, constructs objects for all the samples, and computes the quality metrics.

Author(s)

Tom Carroll and Rory Stark

Maintainers: Tom Carroll <tc.infomatics@gmail.com> and Rory Stark <rory.stark@cruk.cam.ac.uk>

References

Frontiers?

See Also

`ChIPQC` is designed to work closely with the `DiffBind` package, which provides functionality for analyzing ChIP-seq experiments, including performing differential binding analysis to identify significantly differentially bound peaks.

averagepeaksignal-methods *Retrieve average peak profiles*

Description

Retrieve the average peak profile for a sample or set of samples.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `matrix` of the average peak profiles for all of the samples in an ChIP-seq experiment. Each column represents a sample, and each row a base pair position, centered on peak summits.

`signature(object = "list")` Retrieve a `matrix` of the average peak profiles for all of the samples in a list of ChIPQC samples. Each column represents a sample, and each row a base pair position, centered on peak summits.

`signature(object = "ChIPQCsample")` Retrieve a `vector` representing the average peak profile for a sample. Each column represents a basepair position, centered on the peak summits.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
CTCFprofile = averagepeaksignal(QCsample(exampleExp,1))
length(CTCFprofile)
plot(CTCFprofile,type='l',ylab="mean pileup")

allprofiles = averagepeaksignal(exampleExp)
dim(allprofiles)
for(i in 1:ncol(allprofiles)) lines(allprofiles[,i],col=i)
```

ChIPQC *Construct a* ChIPQCexperiment *object*

Description

Constructs a new ChIPQCexperiment object.

Usage

```
ChIPQC(experiment, annotation, chromosomes, samples,
       consensus=FALSE, bCount=FALSE, mapQCth=15, blacklist=NULL,
       profileWin=400, fragmentLength=125, shifts=1:300, ...)
```

Arguments

`experiment` A specification of the ChIP-seq experiment to evaluate. This can either be a dataframe, a filename for a .csv file, or a DBA-object object as defined in the DiffBind package. Columns names in sample sheet may include:

SampleID: Identifier string for sample

Tissue: Identifier string for tissue type

Factor: Identifier string for factor

Condition: Identifier string for condition

Treatment: Identifier string for treatment

Replicate: Replicate number of sample

bamReads: file path for bam file containing aligned reads for ChIP sample

bamControl: file path for bam file containing aligned reads for control sample

ControlID: Identifier string for control sample

Peaks: path for file containing peaks for sample. Format determined by PeakCaller field or caller parameter

PeakCaller: Identifier string for peak caller used. If Peaks is not a bed file, this will determine how the Peaks file is parsed. If missing, will use default peak caller specified in caller parameter. Possible values:

"raw": text file file; peak score is in fourth column

"bed": .bed file; peak score is in fifth column

"narrow": default peak.format: narrowPeaks file

"macs": MACS .xls file

"swembl": SWEMBL .peaks file

"bayes": bayesPeak file

"fp4": FindPeaks v4

PeakFormat: string indicating format for peak files; see PeakCaller and dba.peakset

ScoreCol: column in peak files that contains peak scores

LowerBetter: logical indicating that lower scores signify better peaks

See the documentation for the sampleSheet parameter of dba for details.

annotation — Either a character string indicating the genome and version to use as a genomic annotation, or a previously defined annotation (obtained using QCannotation on a previously defined ChIPQCexperiment object.) May be left unspecified, in which case no genomic feature analysis is performed. The following annotation specifiers are supported:

"hg19": Human, version 19

"hg18": Human, version 18

"mm10": Mouse, version 10

"mm9" : Mouse, version 19

"rn4" : Rat, version 4

"ce6" : C. Elgans, version 6

"dm3" : D. Melanogaster, version 3

Alternatively, you can construct your own annotation; see the package vignette for more information.

chromosomes — Specification of which chromosomes to use for computing QC statistics. If missing, the first chromosome which has a peak is checked. If NULL, all chromosomes will be checked (which may be time-consuming). This can be a character string (e.g. "chr18") or a vector or list of character strings. If it is an integer or vector of integers, the chromosomes will be checked based on the order that they are listed in a peak set.

samples — list of ChIPCsample objects. If present, the sample objects will be taken directly from this list instead of being computed using the ChIPQCsample constructor.

consensus — If consensus is a GRanges object, all samples will use this peakset when computing peak-based metrics. If consensus=TRUE, a consensus peakset will be generated and used for all samples, derived by merging overlapping peaks in all provided peaksets, keeping any peaks that overlap in at least two samples To avoid this behavior, set consensus=FALSE; this will result in only supplied peaksets being used for calculation of peak-based metrics (and no peak-based metric being computed for samples with no peakset specified, such as controls).

bCount — if TRUE, the peak scores for all samples will be based on read counts using dba.count using a consensus peakset. If consenus is missing, any samples (such as controls) that are not already associated with a peakset will be associated with the consensus peakset (if consensus is not missing, all samples will be associated with the consensus peakset). Note that the re-counting process may be time-consuming.

mapQCth — An integer representing a mapping quality score threshold. Only reads with mapping quality scores above this threshold will be used for some statistics.

blacklist — A GRanges object or filename specifying a bed file containing genomic regions that should be excluded from the analysis. If missing and the annotation is "hg19", a default blacklist, blacklist_hg19 derived from the UCSC list, will be used. No blacklist is used if this is set to NULL, or is left missing and the annotation is not "hg19".

profileWin — An integer indicating the width, in base pairs, of the window to be used for peak profiles. Peaks will be centered on their summits, and include half the window size upstream and half downstream of this point.

fragmentLength	An integer indicating the expected fragment length of the libraries. Optional, as this value will be computed for each library.
shifts	A vector of values to try when computing optimal shift sizes.
...	additional parameters passed to dba.count if bCount=TRUE.

Details

ChIPQC first constructs a new DBA-object object if one is not provided. Next it computes the annotation if one is not provided. The main loop constructs new ChIPQCsample objects for each sample (and unique control sample).

Value

A ChIPQCexperiment object.

Note

ChIPQC uses bplapply from the BiocParallel package to build the ChIPQCsample object in parallel, if supported. Control of the parallelization can be effected using BiocParallel functions, such as register.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample, DiffBind

Examples

```
## Not run: exampleExp = ChIPQC(samples,annotation="hg19")
data(example_QCexperiment)
exampleExp

## Not run: tamoxifen = ChIPQC(samples, ,annotation="hg19", consensus=TRUE, bCounts=T)
data(tamoxifen_QC)
tamoxifen
```

ChIPQC-data *Example data sets for ChIPQC package, each containing a ChIPQCexperiment object, as well as a pre-compiled blacklist for hg19.*

Description

The tamoxifen_QC example data set contains a ChIPQCexperiment object named tamoxifen. This data set, based on Ross-Innes et al (2012), includes 11 ER ChIP libraries, and their input controls, divided into tamoxifen responsive and tamoxifen resistant sample groups. Only data for chromosome 18 (chr18) are included.

The example_QCexperiment data set contains a ChIPQCexperiment object named exampleExp. This data set, derived from ENCODE data, includes 6 ChIP libraries. Only data for chromosome 22 (chr22) are included.

blacklist_hg19 data set includes a GRanges object named blacklist_hg19 containing blacklisted regions for the human genome, derived from the UCSC blacklist.

Usage

```
data(tamoxifen_QC)
data(example_QCexperiment)
data(blacklist_hg19)
```

Format

tamoxifen_QC: A single ChIPQCexperiment object named tamoxifen is loaded. This object is used for the ChIPQC-package examples and vignette. This object can also be used with the DiffBind package (see related data objects tamoxifen).

example_QCexperiment: A single ChIPQCexperiment object named exampleExp is loaded. This object is used for the ChIPQC-package examples and vignette.

blacklist_hg19: A single GRanges object named blacklist.hg19 that is used by default when processing hg19 data sets.

Source

Ross-Innes, C. S., Stark, R., Teschendorff, A. E., Holmes, K. A., Ali, H. R., Dunning, M. J., Brown, G. D., Gojis, O., Ellis, I. O., Green, A. R., Ali, S., Chin, S.-F., Palmieri, C., Caldas, C., and Carroll, J. S. (2012). Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. Nature 481, 389-393.

Examples

```
data(tamoxifen_QC)
tamoxifen
plotRegi(tamoxifen)

data(example_QCexperiment)
exampleExp

data(blacklist_hg19)
blacklist.hg19
```

ChIPQC-deprecated *Deprecated functions in package 'ChIPQC'*

Description

These functions are provided for compatibility with older versions of 'ChIPQC' only, and will be defunct at the next release.

Details

The following functions are deprecated and will be made defunct in the next Bioconductor release cycle:

- `ChIPQCreport`: there is no replacement function. The **Nozzle.R1** CRAN package that `ChIPQCreport` depended on for HTML report generation is no longer available and cannot be installed. ChIP-seq quality metrics are still available through the exported accessor methods (`QCmetrics`, `coveragehistogram`, `crosscoverage`, `flagtagcounts`, `fragmentlength`, `ssd`, `frip`, etc.). For visual ChIP-seq QC reports, the `deeptools` Python package is the de facto standard. The original `ChIPQCreport` source code is preserved in `inst/legacy/report.r` and can be accessed via `system.file("legacy/report.r", package = "ChIPQC")` for reference and possible future revival.

ChIPQCexperiment-class *ChIPQCexperiment instances*

Description

The `ChIPQCexperiment` class is built around a list of `ChIPQCsample` objects, each representing a ChIP or control sample in a ChIP-seq experiment. These objects are created using the `ChIPQC` function.

Slots

`.Data`**:** Object of class `"list"`: internal

`Samples`**:** Object of class `"list"`: List of `ChIPQCsample` objects.

`DBA`**:** Object of class `"DBA"`: `DBA-object` object (from package `DiffBind`)

`annotation`**:** Object of class `"list"` : annotation data

Extends

Class `"list"`.

Methods

QCmetadata signature(object = "ChIPQCexperiment"): see QCmetadata.

QCmetrics signature(object = "ChIPQCexperiment"): see QCmetrics.

QCsample signature(object = "ChIPQCexperiment"): see QCsample.

QCcontrol signature(object = "ChIPQCexperiment"): see QCcontrol.

QCannotation signature(object = "ChIPQCexperiment"): see QCannotation.

QCdba signature(object = "ChIPQCexperiment"): see QCdba.

averagepeaksignal signature(object = "ChIPQCexperiment"): see averagepeaksignal.

coveragehistogram signature(object = "ChIPQCexperiment"): see coveragehistogram.

crosscoverage signature(object = "ChIPQCexperiment"): see crosscoverage.

flagtagcounts signature(object = "ChIPQCexperiment"): see flagtagcounts.

fragmentlength signature(object = "ChIPQCexperiment"): see fragmentlength.

FragmentLengthCrossCoverage signature(object = "ChIPQCexperiment"): see FragmentLengthCrossCoverage.

frip signature(object = "ChIPQCexperiment"): see frip.

mapped signature(object = "ChIPQCexperiment"): see mapped.

reads signature(object = "ChIPQCexperiment"): see reads.

duplicates signature(object = "ChIPQCexperiment"): see duplicates.

duplicateRate signature(object = "ChIPQCexperiment"): see duplicateRate.

Normalisedaveragepeaksignal signature(object = "ChIPQCexperiment"): see Normalisedaveragepeaksignal.

peaks signature(object = "ChIPQCexperiment"):see peaks.

readlength signature(object = "ChIPQCexperiment"): see readlength.

ReadLengthCrossCoverage signature(object = "ChIPQCexperiment"): see ReadLengthCrossCoverage.

RelativeCrossCoverage signature(object = "ChIPQCexperiment"):see RelativeCrossCoverage.

ribl signature(object = "ChIPQCexperiment"): see ribl.

rip signature(object = "ChIPQCexperiment"): see rip.

show signature(object = "ChIPQCexperiment"): see show.

ssd signature(object = "ChIPQCexperiment"): see ssd.

regi signature(object = "ChIPQCexperiment"): see regi.

plotCC signature(object = "ChIPQCexperiment"): see plotCC.

plotCoverageHist signature(object = "ChIPQCexperiment"): see plotCoverageHist.

plotFribl signature(object = "ChIPQCexperiment"): see plotFribl.

plotPeakProfile signature(object = "ChIPQCexperiment"): see plotPeakProfile.

plotRap signature(object = "ChIPQCexperiment"): see plotRap.

plotRegi signature(object = "ChIPQCexperiment"): see plotRegi.

plotCorHeatmap signature(object = "ChIPQCexperiment"): see plotCorHeatmap.

plotPrincomp signature(object = "ChIPQCexperiment"): see plotPrincomp.

ChIPQCreport signature(object = "ChIPQCexperiment"): see ChIPQCreport.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCsample, DiffBind

Examples

```
## Not run: exampleExp = ChIPQC(samples)
data(example_QCexperiment)
exampleExp

## Not run: tamoxifen = ChIPQC(samples, consensus=TRUE, bCounts=T)
data(tamoxifen_QC)
tamoxifen
```

ChIPQCreport-methods *Generate a summary QC report*

Description

Generate an HTML summary QC report.

Methods

`signature(experiment = "ChIPQCexperiment", facet=TRUE, reportName="ChIPQC", reportFolder="ChIPQCreport`

Generates an summary QC report for the experiment in HTML format.

experiment	`ChIPQCexperiment` object
facet	logical indicating whether or not to facet using experimental metadata.
reportName	filename of main report file (.html).
reportFolder	directory name where plot graphics will be saved
facetBy	metadata fields to use for faceting
colourBy	metadata field to color by

`signature(experiment = "list", facet=TRUE, reportName="ChIPQC", reportFolder="ChIPQCreport", facetBy=c`

Generates an summary QC report for a list of ChIPQCsample objects in HTML format.

experiment	`list` object
facet	logical indicating whether or not to facet using experimental metadata.
reportName	filename of main report file (.html).
reportFolder	directory name where plot graphics will be saved
facetBy	metadata fields to use for faceting
colourBy	metadata field to color by

`signature(sample = "ChIPQCsample", reportName="ChIPQC", reportFolder="ChIPQCreport",)`
Generate a summary QC report for a sample in HTML format.

sample	ChIPQCsample object
reportName	filename of main report file (.html).
reportFolder	directory name where plot graphics will be saved

Note

`ChIPQCreport` is deprecated as of ChIPQC 1.49.1. The `Nozzle.R1` CRAN package it depended on for HTML report generation is no longer available. See `?'ChIPQC-deprecated'` for replacements (QC accessor methods; `deeptools` for visual reports). The original implementation is preserved at `system.file("legacy/report.r", package = "ChIPQC")`.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

ChIPQCsample-class *Class* "ChIPQCsample"

Description

Object containing quality metrics computed for a ChIP-seq (or associated control) sample.

Objects from the Class

Objects can be created using the ChIPQCsample function.

Constructor Function

`ChIPQCsample(reads, peaks, annotation, chromosomes = NULL, mapQCth = 15, blacklist, profileWin = 400, fragmentLength = 125, shifts = 1:300, runCrossCor = FALSE,verboseT=FALSE)`

`reads` character string filename of .bam file

`peaks` GRanges object or character string filename of peaks. If present, peak-based metrics will be computed.

`annotation` Either a character string indicating the genome and version to use as a genomic annotation, or a previously defined annotation (obtained using QCannotation on a previously defined ChIPQCexperiment object.) May be left unspecified, in which case no genomic feature analysis is performed. The following annotation specifiers are supported:

"hg20"	Human, version 20
"hg19"	Human, version 19
"hg18"	Human, version 18
"mm10"	Mouse, version 10
"mm9"	Mouse, version 19
"rn4"	Rat, version 4
"ce6"	C. Elgans, version 6
"dm3"	D. Melanogaster, version 3

Alternatively, you can construct your own annotation; see the package Vignette for more information.

`chromosomes` Specification of which chromosomes to use for computing QC statistics. If missing, the first chromosome which has a peak is checked. If NULL, all chromosomes will be checked (which may be time-consuming). This can be a character string (e.g. "chr18") or a vector or list of character strings. If it is an integer or vector of integers, the chromosomes will be checked based on the order that they are listed in a peak set.

`mapQCth` An integer representing a mapping quality score threshold. Only reads with mapping quality scores above this threshold will be used for some statistics.

`blacklist` A `GRanges` object or filename specifying a bed file containing genomic regions that should be excluded from the analysis. If missing and the `annotation` is "hg19", a default blacklist, `blacklist_hg19` derived from the UCSC list, will be used. No blacklist is used if this is set to NULL, or is left missing and the annotation is not "hg19".

`profileWin` An integer indicating the width, in base pairs, of the window to be used for peak profiles. Peaks will be centered on their summits, and include half the window size upstream and half downstream of this point.

`fragmentLength` An integer indicating the expected fragment length of the libraries. Optional, as this value will be computed.

`shifts` A vector of values to try when computing optimal shift sizes.

`runCrossCor` Compute cross-correlation in addition to cross-coverage. This will take more compute time, and is currently not used in the final report.

`verboseT` TRUE or FALSE, specifying whether to report progress. Default is TRUE. When set to FALSE ChIPQC does not report any progress until complete.

Slots

`AveragePeakSignal`: Object of class `"list"`

`CrossCoverage`: Object of class `"numeric"`

`CrossCorrelation`: Object of class `"numeric"`

`SSD`: Object of class `"numeric"`

`SSDBL`: Object of class `"numeric"`

`CountsInPeaks`: Object of class `"numeric"`

`CountsInBlackList`: Object of class `"numeric"`

`CountsInFeatures`: Object of class `"list"`

PropInFeatures: Object of class "list"

CoverageHistogram: Object of class "numeric"

FlagAndTagCounts: Object of class "numeric"

readlength: Object of class "numeric"

seqnames: Object of class "Rle"

ranges: Object of class "IRanges"

strand: Object of class "Rle"

elementMetadata: Object of class "DataFrame"

seqinfo: Object of class "Seqinfo"

metadata: Object of class "list"

Extends

Class "GRanges"

Methods

averagepeaksignal signature(object = "ChIPQCsample"): see averagepeaksignal.

coveragehistogram signature(object = "ChIPQCsample"): see coveragehistogram.

crosscoverage signature(object = "ChIPQCsample"): see crosscoverage.

flagtagcounts signature(object = "ChIPQCsample"): see flagtagcounts.

fragmentlength signature(object = "ChIPQCsample"): see fragmentlength.

FragmentLengthCrossCoverage signature(object = "ChIPQCsample"): see FragmentLengthCrossCoverage.

frip signature(object = "ChIPQCsample"): see frip.

mapped signature(object = "ChIPQCsample"): see mapped.

reads signature(object = "ChIPQCsample"): see reads.

duplicates signature(object = "ChIPQCsample"): see duplicates.

duplicateRate signature(object = "ChIPQCsample"): see duplicateRate.

Normalisedaveragepeaksignal signature(object = "ChIPQCsample"): see Normalisedaveragepeaksignal.

peaks signature(object = "ChIPQCsample"):see peaks.

readlength signature(object = "ChIPQCsample"): see readlength.

ReadLengthCrossCoverage signature(object = "ChIPQCsample"): see ReadLengthCrossCoverage.

RelativeCrossCoverage signature(object = "ChIPQCsample"):see RelativeCrossCoverage.

ribl signature(object = "ChIPQCsample"): see ribl.

rip signature(object = "ChIPQCsample"): see rip.

show signature(object = "ChIPQCsample"): see show.

ssd signature(object = "ChIPQCsample"): see ssd.

regi signature(object = "ChIPQCsample"): see regi.

plotCC signature(object = "ChIPQCsample"): see plotCC.

plotCoverageHist `signature(object = "ChIPQCsample")`: see `plotCoverageHist`.

plotFribl `signature(object = "ChIPQCsample")`: see `plotFribl`.

plotPeakProfile `signature(object = "ChIPQCsample")`: see `plotPeakProfile`.

plotRap `signature(object = "ChIPQCsample")`: see `plotRap`.

plotRegi `signature(object = "ChIPQCsample")`: see `plotRegi`.

Author(s)

Thomas Carroll and Rory Stark

References

Carroll TS, Liang Z, Salama R, Stark R and Santiago Id (in press). Impact of artefact removal on ChIP quality metrics in ChIP-seq and ChIP-exo data. Frontiers in Genetics.

See Also

ChIPQC-package, ChIPQCsample

Examples

```
bamFile <- system.file("extdata", "ex1.bam",
                       package="Rsamtools")
ex1 <- ChIPQCsample(bamFile,annotation=NULL)
readlength(ex1)
fragmentlength(ex1)
```

---

coveragehistogram-methods

Retrieve histogram data representing densities of coverage pileups

---

Description

Retrieve histogram data representing densities of coverage pileups.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `matrix` of coverage histogram data for all samples in a ChIP-seq experiment. Each column represents a sample, and each row a pileup height, with the value representing the number of basepair positions that report this pileup height.

`signature(object = "list")` Retrieve a `matrix` of coverage histogram data for all ChIPQCsamples in a list. Each column represents a sample, and each row a pileup height, with the value representing the number of basepair positions that report this pileup height.

`signature(object = "ChIPQCsample")` Retrieve a `vector` representing coverage histogram data for a sample. Values represent the number of base pairs positions that report the pileup value. The value in position 1 of the vector the contains the number of examined basepair positions that are overlapped by exactly zero reads, while position 2 shows the number of basepair positions overlapped by exactly one read, etc.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
CTCFcoverage = coveragehistogram(QCsample(exampleExp,1))
length(CTCFcoverage)
plot(log10(CTCFcoverage),type='l',ylab="log10 Density",
                          xlab="Pileup")

allcoverages = coveragehistogram(exampleExp)
dim(allcoverages)
for(i in 1:ncol(allcoverages)) lines(log10(allcoverages[,i]),col=i)
```

---

crosscoverage-methods *Retrieve the cross coverage values for a range of shift sizes*

Description

Retrieves the cross-coverage values for a range of shift sizes.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `matrix` of cross-coverage data for all samples in an ChIP-seq experiment. Each column represents a sample, and each row a shift size, with the value representing the cross-coverage using that size read.

`signature(object = "list")` Retrieve a `matrix` of cross-coverage data for all samples in a list of ChIPQCsample objects. Each column represents a sample, and each row a shift size, with the value representing the cross-coverage using that size read.

`signature(object = "ChIPQCsample")` Retrieve a `vector` of cross-coverage data for a sample. Each position in the vector corresponds to a shift size, with the value representing the cross-coverage using that size read.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
CTCFcoverage = crosscoverage(QCsample(exampleExp,1))
length(CTCFcoverage)
plot(CTCFcoverage,type='l',
     ylab="Cross-coverage",
     xlab="Fragment length")

allcoverages = crosscoverage(exampleExp)
dim(allcoverages)
for(i in 1:ncol(allcoverages)) lines(allcoverages[,i],col=i)
```

`duplicateRate-methods` *Retrieve duplication rates*

Description

Retrieve duplication rates.

Methods

`signature(object = "ChIPQCexperiment", bFiltered)` Retrieve a `vector` of the duplication rates for each sample in an experiment. A read is considered duplicated if another read maps to the same genomic location; the duplication rate is the number of duplicated reads divided by the total number of reads for a sample. If `bFiltered=TRUE` (or is missing), only reads that pass the mapping quality filter for each sample are included. if `bFiltered=FALSE`, all reads for each sample will be included.

`signature(object = "list", bFiltered)` Retrieve a `vector` of the duplication rates for each sample in a list of ChIPQCsample objects. A read is considered duplicated if another read maps to the same genomic location; the duplication rate is the number of duplicated reads divided by the total number of reads for a sample. If `bFiltered=TRUE` (or is missing), only reads that pass the mapping quality filter for each sample are included. if `bFiltered=FALSE`, all reads for each sample will be included.

`signature(object = "ChIPQCsample", bFiltered)` Retrieve the duplication rate for a sample. A read is considered duplicated if another read maps to the same genomic location; the duplication rate is the number of duplicated reads divided by the total number of reads for the sample. If `bFiltered=TRUE` (or is missing), only reads that pass the mapping quality filter for the sample are included. if `bFiltered=FALSE`, all reads for the sample will be included.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
duplicateRate(exampleExp)
duplicateRate(QCsample(exampleExp,1))
```

`duplicates-methods` *Retrieve numbers of duplicate reads.*

Description

Retrieve the numbers of duplicate reads.

Methods

`signature(object = "ChIPQCexperiment", bFiltered)` Retrieve a `vector` of the numbers of duplicate reads for each sample in an experiment. A read is considered duplicated if another read maps to the same genomic location. If `bFiltered=TRUE` (or is missing), this will be the number of duplicates that pass the mapping quality filter for each sample. if `bFiltered=FALSE`, it will be the total number of duplicates for each sample.

`signature(object = "list", bFiltered)` Retrieve a `vector` of the numbers of duplicate reads for each sample in a list of ChIPQCsample objects. A read is considered duplicated if another read maps to the same genomic location. If `bFiltered=TRUE` (or is missing), this will be the number of duplicates that pass the mapping quality filter for each sample. if `bFiltered=FALSE`, it will be the total number of duplicates for each sample.

`signature(object = "ChIPQCsample", bFiltered)` Retrieve the number of duplicates for a sample. A read is considered duplicated if another read maps to the same genomic location. If `bFiltered=TRUE` (or is missing), this will be the number of duplicates that pass the mapping quality filter. if `bFiltered=FALSE`, it will be the total number of duplicates for the sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
duplicates(exampleExp)
duplicates(QCsample(exampleExp,1))
```

`flagtagcounts-methods` *Retrieve numbers of reads that pass various filters*

Description

Retrieve numbers of reads that pass various filters

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `matrix` of counts passing various filters for all the samples in an experiment. Each column represents the counts in a sample.

`signature(object = "list")` Retrieve a `matrix` of counts passing various filters for all the samples in a list of ChIPQCsample objects. Each column represents the counts in a sample.

`signature(object = "ChIPQCsample")` Retrieve a `vector` of counts passing various filters. The values are:

UnMapped	Number of reads that are not mapped (aligned)
Mapped	Number of reads that are mapped (aligned)
Duplicates	Number of reads that align to exactly the same place as another read
MapQPass	Number of reads with a mapping quality score greater than or equal to the specified threshold
MapQPassandDup	Number of reads that are mapped (aligned) and not duplicates

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
flagtagcounts(exampleExp)
flagtagcounts(QCsample(exampleExp,1))
```

fragmentlength-methods *Retrieve the estimated fragment length*

Description

Retrieve the estimated fragment length.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of estimated fragments sizes, one for each sample in the experiment.

`signature(object = "list")` Retrieve a `vector` of estimated fragments sizes, one for each sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample", width)` Retrieve the estimated fragment length for a sample. If `width` is missing, the readlength derived from the bam file is used as the read length.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
fragmentlength(exampleExp)
fragmentlength(QCsample(exampleExp,1))
```

frip-methods *Retrieve fraction of reads in peaks*

Description

Retrieve the fraction of reads in peaks

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of values representing the proportion of reads that overlap peaks for each sample in an experiment.

`signature(object = "list")` Retrieve a `vector` of values representing the proportion of reads that overlap peaks for each sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve a value representing the proportion of reads that overlap the peaks for a sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
frip(exampleExp)
frip(QCsample(exampleExp,1))
```

---

mapped-methods *Retrieve numbers of mapped reads*

Description

Retrieve the numbers of mapped reads.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of the numbers of mapped (aligned) reads for each sample in an experiment.

`signature(object = "list")` Retrieve a `vector` of the numbers of mapped (aligned) reads for each sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve the number of mapped (aligned) reads in a sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
mapped(exampleExp)
mapped(QCsample(exampleExp,1))
```

`Normalisedaveragepeaksignal-methods`
Retrieve normalised average peak profiles

Description

Retrieve normalised average peak profiles

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `matrix` of normalised average peak signal data for all samples in a ChIP-seq experiment. Each column represents a sample, and each row a base pair position, centered on peak summits.

`signature(object = "list")` Retrieve a `matrix` of normalised average peak signal data for all samples in a list of ChIPQCsample objects. Each column represents a sample, and each row a base pair position, centered on peak summits.

`signature(object = "ChIPQCsample")` Retrieve a `vector` representing the normalised average peak profile for a sample. Each column represents a basepair position, centered on the peak summits.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
CTCFprofile = Normalisedaveragepeaksignal(QCsample(exampleExp,1))
length(CTCFprofile)
plot(CTCFprofile,type='l',ylab="normalised mean pileup")

allprofiles = Normalisedaveragepeaksignal(exampleExp)
dim(allprofiles)
for(i in 1:ncol(allprofiles)) lines(allprofiles[,i],col=i)
```

peaks-methods *Retrieve peaks*

Description

Retrieve peaks.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `GRangesList` of the peaks associated with all the samples in an experiment.

`signature(object = "list")` Retrieve a `GRangesList` of the peaks associated with all the samples in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve a `GRanges` object containing the peaks associated with a sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
expPeaks = peaks(exampleExp)
length(expPeaks)
peaks(QCsample(exampleExp,1))
```

plotCC-methods *Generate Cross-Coverage plots*

Description

Generate Cross-Coverage plots.

Methods

`signature(object = "ChIPQCexperiment", method)` Generate cross-coverage plots for all the samples in an experiment.

`signature(object = "list", method)` Generate cross-coverage plots for list of samples in an experiment.

`signature(object = "ChIPQCsample", methods)` Generate cross-coverage plots for a sample. Supported methods include:

"Coverage" [default] Coverage plot

Note

plotCC uses `ggplot2` for plotting, and returns a `ggplot2` plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotCC(exampleExp)
plotCC(exampleExp,excludedBox=TRUE)
plotCC(QCsample(exampleExp,1))
plotCC(QCsample(exampleExp)[1:4])
```

---

plotCorHeatmap-methods

Generate Correlation Heatmap for ChIP samples

Description

Generates correlation heatmap for ChIP samples.

Methods

`signature(object = "ChIPQCexperiment", attributes, ...)` Generate correlation heatmap, including clustering dendrogram, for all the samples in an experiment that are associated with a peakset.

attributes	character string, or vector of character strings, representing metadata field names, for use in labeling
...	additional parameters passed to `dba.plotHeatmap`

Note

plotCorHeatmap uses `dba.plotHeatmap` for plotting.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCexperiment, dba.plotHeatmap

Examples

```
data(tamoxifen_QC)
plotCorHeatmap(tamoxifen,attributes=c("Tissue","Condition","Replicate"))
```

---

plotCoverageHist-methods

Generate coverage histogram plot

Description

Generate coverage histogram plot.

Methods

`signature(object = "ChIPQCexperiment")` Generate coverage histogram plots for all the samples in an experiment.

`signature(object = "list")` Generate coverage histogram plots for all the samples in a list of ChIPQCsamples.

`signature(object = "ChIPQCsample")` Generate coverage histogram plots for a sample.

Note

Uses `ggplot2` for plotting, and returns a `ggplot2` plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotCoverageHist(exampleExp,facetBy=c("Tissue","Factor"))
plotCoverageHist(QCsample(exampleExp,1))
```

`plotFribl-methods` *Generate fraction of reads in blacklist plot*

Description

Generate fraction of reads in blacklist plot.

Methods

`signature(object = "ChIPQCexperiment", type="barstacked",facet=T, facetBy=c("Tissue","Factor"),AsPerc`
Generate fraction of reads in blacklist plots for all the samples in an experiment.

`signature(object = "list", type="barstacked",facet=T, facetBy=c("Sample"),AsPercent=TRUE)`
Generate fraction of reads in blacklist plots for all the samples in a list of ChIPQCsample objects..

`signature(object = "ChIPQCsample", type="barstacked",AsPercent=TRUE)` Generate fraction of reads in blacklist plots for a sample.

Note

plotFribl uses `ggplot2` for plotting, and returns a `ggplot2` plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotFribl(exampleExp)
plotFribl(QCsample(exampleExp,1))
```

plotFrip-methods *Generate fraction of reads in peaks plot*

Description

Generate fraction of reads in peaks plot.

Methods

`signature(object = "ChIPQCexperiment", type="barstacked",facet=T, facetBy=c("Tissue","Factor"),AsPerc`
Generate fraction of reads in peaks plots for all the samples in an experiment.

`signature(object = "list", type="barstacked",facet=T, facetBy=c("Sample"),AsPercent=TRUE)`
Generate fraction of reads in peaks plots for all the samples in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample",type="barstacked",facet=T, facetBy=c("Tissue","Factor"),AsPercent=T`
Generate fraction of reads in peaks plots for a sample.

Note

plotFrip usesggplot2 for plotting, and returns a ggplot2 plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotFrip(exampleExp)
plotFrip(QCsample(exampleExp,1))
```

plotPeakProfile-methods *Generate peak profile plots*

Description

Generate peak profile plots.

Methods

`signature(object = "ChIPQCexperiment", method)` Generate peak profile plots for all the samples in an experiment.

`signature(object = "list", method)` Generate peak profile plots for all the samples in a list of ChIPQCsample objects..

`signature(object = "ChIPQCsample", method)` Generate peak profile plots for a sample.

Note

plotPeakProfile uses `ggplot2` for plotting, and returns a `ggplot2` plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotCoverageHist(exampleExp,facetBy=c("Tissue","Factor"))
plotCoverageHist(QCsample(exampleExp,1))
data(tamoxifen_QC)
plotCoverageHist(tamoxifen,facetBy=c("Tissue","Condition"))
```

---

plotPrincomp-methods *Generate Principal Components Analysis plot for ChIP samples*

Description

Generate principal components analysis plot for ChIP samples.

Methods

`signature(object = "ChIPQCexperiment", attributes, ...)` Generate principal components analysis plot, for all the samples in an experiment that are associated with a peakset.

attributes	character string, or vector of character strings, representing metadata field names, for use grouping samples by colo
...	additional parameters passed to `dba.plotPCA`

Note

plotPrincomp uses `dba.plotPCA` for plotting.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCexperiment, dba.plotPCA

Examples

```
data(tamoxifen_QC)
plotPrincomp(tamoxifen,attributes=c("Condition"))
```

---

plotRap-methods *Generate reads in peaks plot*

Description

Generate reads in peaks plot.

Methods

`signature(object = "ChIPQCexperiment", type="barstacked",facet=T, facetBy=c("Tissue","Factor"))`
Generate reads in peaks plots for all the samples in an experiment.

`signature(object = "list", type="barstacked",facet=T, facetBy=c("Sample"))` Generate reads in peaks plots for all the samples in a list of ChIPQCsample objects.

`signature(object = "ChIPQCexperiment", type="barstacked",facet=T, facetBy=c("Tissue","Factor"))`
Generate reads in peaks plots for all the samples in an experiment.

`signature(object = "ChIPQCsample",type="barstacked",facet=T, facetBy=c("Tissue","Factor"))`
Generate reads in peaks plots for a sample.

Note

plotRap uses `ggplot2` for plotting, and returns a `ggplot2` plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotRap(exampleExp,facetBy=c("Tissue","Factor"))
plotRap(QCsample(exampleExp,1))
```

plotRegi-methods *Generate relative enrichment of genomic features plot*

Description

Generate relative enrichment of genomic features plot.

Methods

`signature(object = "ChIPQCexperiment", facet=T, facetBy=c("Tissue","Factor"))` Generate relative enrichment of genomic features plots for all the samples in an experiment.

`signature(object = "list",facet=T, facetBy=c("Sample"))` Generate relative enrichment of genomic features plots for all the samples in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Generate relative enrichment of genomic features plots for a sample.

Note

plotRegi uses `ggplot2` for plotting, and returns a `ggplot2` plot dataframe.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotRegi(exampleExp,facetBy=c("Tissue","Factor"))
plotRegi(QCsample(exampleExp,1))
data(tamoxifen_QC)
plotRegi(tamoxifen,facetBy=c("Tissue","Condition"))
```

plotSSD-methods *Generate SSD plot*

Description

Generate SSD metric plot. If blacklists supplied, will generate SSD prior and post blacklisting

Methods

`signature(object = "ChIPQCexperiment", facet=T, facetBy=c("Tissue","Factor"))` Generate SSD metric plot for all samples in experiment. If blacklists supplied, will generate SSD prior and post blacklisting

`signature(object = "list", facet=T, facetBy=c("Tissue","Factor"))` Generate SSD metric plot for list of samples in experiment. If blacklists supplied, will generate SSD prior and post blacklisting

`signature(object = "ChIPQCsample")` Generate SSD metric plot for single sample. If blacklists supplied, will generate SSD prior and post blacklisting

Note

plotSSD uses `ggplot2` for plotting, and returns a `ggplot2` plot gg object.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
plotSSD(exampleExp,facetBy=c("Tissue","Factor"))
plotSSD(QCsample(exampleExp,1))
plotSSD(QCsample(exampleExp)[1:3])
data(tamoxifen_QC)
plotSSD(tamoxifen,facetBy=c("Tissue","Condition"))
```

QCannotation-methods *Retrieve an annotation description, or a processed annotation*

Description

Retrieve an annotation description, or a processed annotation, from a `ChIPQCexperiment` object.

Methods

`signature(object = "ChIPQCexperiment", bRetrieve=FALSE)` Retrieve the annotation. If `bRetrieve=FALSE` (default), the character string describing the annotation is returned (currently only "hg19" is supported). If `bRetrieve=TRUE`, a processed annotation is returned (in the form of a `list`). This can be used in subsequent calls to `ChIPQC` and/or `ChIPQCsample` for efficiency purposes.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCsample, ChIPQCexperiment

Examples

```
data(example_QCexperiment)
QCannotation(exampleExp)
```

`QCcontrol-methods` *Retrieve control objects associated with a sample*

Description

Retrieve the `ChIPQCsample` objects representing controls, or a specific `ChIPQCsample` representing the control for a specific sample, from a `ChIPQCexperiment` object.

Methods:

`signature(object = "ChIPQCexperiment", sampleID)` Get the control sample (as a `ChIPQCsample` object) associated with a ChIP sample, or, if `sampleID` is missing, a list of all samples used as controls. `sampleID` is a character string or an integer.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCsample, ChIPQCexperiment

Examples

```
data(tamoxifen_QC)
controls = QCcontrol(tamoxifen)
length(controls)
names(controls)
controls[[1]]
bt474control = QCcontrol(tamoxifen,"BT4741")
bt474control
```

QCdba-methods *Retrieve the DBA-object object associated with an experiment*

Description

Retrieve the DBA-object object associated with a ChIPQCexperiment object.

Methods:

signature(object = "ChIPQCexperiment") Retrieves the DBA-object object associated with a ChIPQCexperiment. This object can be used with DiffBind functions to further analyse a ChIP-seq experiment, including performing a differential binding analysis.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCexperiment, DiffBind, dba

Examples

```
data(tamoxifen_QC)
tamoxifenDBA = QCdba(tamoxifen)
## library(DiffBind)
## tamoxifenDBA
```

QCmetadata-methods *Retrieve metadata associated with an experiment*

Description

Retrieve metadata for a ChIPQCexperiment object.

Methods:

signature(object = "ChIPQCexperiment") Retrieve a data frame containing metadata for all the samples in a ChIP-seq experiment represented by a ChIPQCexperiment object.

signature(object = "list") Retrieve a data frame containing metadata for all the samples in a list of ChIPQCsample objects.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCsample, ChIPQCexperiment

Examples

```
data(tamoxifen_QC)
meta = QCmetadata(tamoxifen)
meta
```

`QCmetrics-methods` *Retrieve consolidated set of QC metrics*

Description

Retrieves a consolidated set of QC metrics.

Methods

`signature(object = "ChIPQCexperiment")` Retrieves a `matrix` of QC metrics for all the samples in an experiment, with a column of values for each sample.

`signature(object = "list")` Retrieves a `matrix` of QC metrics for all the samples in a list of ChIPQCsample objects, with a column of values for each sample.

`signature(object = "ChIPQCsample")` Retrieves a `vector` of QC metrics for a sample.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCsample, ChIPQCexperiment

Examples

```
data(example_QCexperiment)
QCmetrics(exampleExp)

data(tamoxifen_QC)
QCmetrics(tamoxifen)

QCmetrics(QCsample(tamoxifen,1))
```

QCsample-methods *Retrieve sample objects associated with an experiment*

Description

Retrieves a list of ChIPQCsample objects, or one specific ChIPQCsample object, from a ChIPQCexperiment object.

Methods

signature(object = "ChIPQCexperiment", sampleID) If sampleID is missing or equal to 0, the full list of ChIPQCsample objects is returned. If sampleID is an integer n, the ChIPQCsample object corresponding to the nth sample is returned. If sampleID is a character string, the ChIPQCsample object corresponding to the sample with that ID is returned.

Author(s)

Rory Stark and Thomas Carroll

See Also

ChIPQC-package, ChIPQCsample, ChIPQCexperiment

Examples

```
data(example_QCexperiment)
samples = QCsample(exampleExp)
length(samples)
names(samples)
samples$CTCF_1
```

readlength-methods *Retrieve read length values*

Description

Retrieve read length values.

Methods

signature(object = "ChIPQCexperiment") Retrieve a vector of read length values, one for each sample in an experiment.

signature(object = "list") Retrieve a vector of read length values, one for each sample in a list of ChIPQCsample objects.

signature(object = "ChIPQCsample") Retrieve the read length value for a sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
readlength(exampleExp)
readlength(QCsample(exampleExp,1))
```

ReadLengthFragmentLengthCrossCoverage-methods

Retrieve the cross coverage values when extending reads to the optimal fragment length.

Description

Retrieve the cross coverage values when extending reads to the optimal fragment length.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of cross-coverage values for all samples in a ChIP-seq experiment, when all reads are shifted by the optimal fragment length (the maximum cross-coverage value).

`signature(object = "list")` Retrieve a `vector` of cross-coverage values for all samples in a list of ChIPQCsample objects, when all reads are shifted by the optimal fragment length (the maximum cross-coverage value).

`signature(object = "ChIPQCsample")` Retrieve the cross-coverage value for a sample, when all reads are shifted by the optimal fragment length (the maximum cross-coverage value).

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
FragmentLengthCrossCoverage(exampleExp)
FragmentLengthCrossCoverage(QCsample(exampleExp,1))
```

`ReadLengthReadLengthCrossCoverage-methods` *Retrieve the cross coverage values without extending reads*

Description

Retrieve the cross coverage values without extending reads.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of cross-coverage values for all samples in a ChIP-seq experiment, with no shift.

`signature(object = "list")` Retrieve a `vector` of cross-coverage values for all samples in a list of ChIPQCsample objects, with no shift.

`signature(object = "ChIPQCsample")` Retrieve the cross-coverage value for a sample, with no shift.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
ReadLengthCrossCoverage(exampleExp)
ReadLengthCrossCoverage(QCsample(exampleExp,1))
```

`reads-methods` *Retrieve numbers of reads*

Description

Retrieve the numbers of reads.

Methods

`signature(object = "ChIPQCexperiment", bFiltered)` Retrieve a `vector` of the numbers of reads for each sample in an experiment. If `bFiltered=TRUE` (or is missing), this will be the number of reads that pass the mapping quality filter for each sample. if `bFiltered=FALSE`, it will be the total number of reads for each sample.

`signature(object = "list", bFiltered)` Retrieve a `vector` of the numbers of reads for each sample in a list of ChIPQCsample objects. If `bFiltered=TRUE` (or is missing), this will be the number of reads that pass the mapping quality filter for each sample. if `bFiltered=FALSE`, it will be the total number of reads for each sample.

`signature(object = "ChIPQCsample", bFiltered)` Retrieve the number of reads for a sample. If `bFiltered=TRUE` (or is missing), this will be the number of reads that pass the mapping quality filter. if `bFiltered=FALSE`, it will be the total number of reads for the sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
reads(exampleExp)
reads(QCsample(exampleExp,1))
```

`regi-methods` *Retrieve genomic profile information*

Description

Retrieve genomic profile information in terms of relative enrichment over background genomic distribution.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `matrix` of relative enrichment values for a variety of genomic features. Each column represents the enrichment values for one sample in the experiment.

`signature(object = "list")` Retrieve a `matrix` of relative enrichment values for a variety of genomic features. Each column represents the enrichment values for one sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve a `vector` of relative enrichment values for a variety of genomic features for a sample. Relative enrichment is computed as the proportion of reads overlapping a genomic feature type compared to the overall proportion of base pairs in the genome comprising those features. Genomic features include:

3UTRs	3' UTRs
5UTRs	5' UTRs
Introns	Intronic (non-coding) portions of gene bodies
Transcripts	Transcribed regions, including exons
Promoters500	500bp regions immediately upstream of annotated TSSs
Promoters2000to500	2500bp regions from 2000bp immediately upstream of annotated TSSs to 500bp downstream
Promoters20000to2000	22000bp regions from 20000bp immediately upstream of annotated TSSs to 2000bp downstream

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
genomicprofile = regi(exampleExp)
heatmap(genomicprofile)
regi(QCsample(exampleExp,1))
```

`RelativeCrossCoverage-methods`

Retrieve the relative cross coverage values for a range of shift sizes

---

Description

Retrieve the relative cross-coverage values for a range of shift sizes

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of relative cross-coverage values for all samples in a ChIP-seq experiment, computed based on the maximal value (when extending the reads to the optimal fragment length) versus the cross-coverage values using non-extended reads.

`signature(object = "list")` Retrieve a `vector` of relative cross-coverage values for all samples in a list of ChIPQCsample objects, computed based on the maximal value (when extending the reads to the optimal fragment length) versus the cross-coverage values using non-extended reads.

`signature(object = "ChIPQCsample")` Retrieve the relative cross-coverage value for a sample, computed based on the maximal value (when extending the reads to the optimal fragment length) versus the cross-coverage values using non-extended reads.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
RelativeCrossCoverage(exampleExp)
RelativeCrossCoverage(QCsample(exampleExp,1))
```

---

ribl-methods *Retrieve numbers of reads overlapping blacklisted regions*

Description

Retrieve the numbers of reads overlapping blacklisted regions.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of the numbers of reads overlapping blacklisted regions for each sample in an experiment.

`signature(object = "list")` Retrieve a `vector` of the numbers of reads overlapping blacklisted regions for each sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve the number of reads overlapping blacklisted regions in a sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
ribl(exampleExp)
ribl(QCsample(exampleExp,1))
```

rip-methods *Retrieve numbers of reads overlapping peaks*

Description

Retrieve the numbers of reads overlapping peaks.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of the numbers of reads overlapping peaks for each sample in an experiment.

`signature(object = "list")` Retrieve a `vector` of the numbers of reads overlapping peaks for each sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve the number of reads overlapping peaks in a sample.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
rip(exampleExp)
rip(QCsample(exampleExp,1))
```

ssd-methods *Retrieve SSD (squared sum of deviations) values of peak coverage*

Description

Retrieve SSD (squared sum of deviations) values of peak coverage density.

Methods

`signature(object = "ChIPQCexperiment")` Retrieve a `vector` of SSD values, one for each sample in an experiment.

`signature(object = "list")` Retrieve a `vector` of SSD values, one for each sample in a list of ChIPQCsample objects.

`signature(object = "ChIPQCsample")` Retrieve the SSD (squared sum of deviations) for a sample, computed from the standard deviation of the `coveragehistogram`.

Note

uses the SSD calculation from the `chipseq` package.

Author(s)

Thomas Carroll and Rory Stark

See Also

ChIPQC-package, ChIPQCexperiment, ChIPQCsample

Examples

```
data(example_QCexperiment)
ssd(exampleExp)
ssd(QCsample(exampleExp,1))
```

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