

Package ‘CexoR’

May 17, 2024

Version 1.42.0

Date 2022-05-28

Type Package

Title An R package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates

Description Strand specific peak-pair calling in ChIP-exo replicates. The cumulative Skellam distribution function is used to detect significant normalised count differences of opposed sign at each DNA strand (peak-pairs). Then, irreproducible discovery rate for overlapping peak-pairs across biological replicates is computed.

Depends R (>= 4.2.0), S4Vectors, IRanges

Imports Rsamtools, GenomeInfoDb, GenomicRanges, rtracklayer, idr, RColorBrewer, genomation

Suggests RUnit, BiocGenerics, BiocStyle, knitr, rmarkdown

License Artistic-2.0 | GPL-2 + file LICENSE

biocViews FunctionalGenomics, Sequencing, Coverage, ChIPSeq, PeakDetection

git_url <https://git.bioconductor.org/packages/CexoR>

git_branch RELEASE_3_19

git_last_commit af27fa1

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-17

Author Pedro Madrigal [aut, cre] (<<https://orcid.org/0000-0003-1959-8199>>)

Maintainer Pedro Madrigal <pmadrigal@ebi.ac.uk>

Contents

| | |
|-------------------------|---|
| CexoR-package | 2 |
| CexoR | 3 |
| cexor | 3 |
| plotcexor | 5 |

| | |
|--------------|----------|
| Index | 7 |
|--------------|----------|

| | |
|---------------|--|
| CexoR-package | <i>An R package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates</i> |
|---------------|--|

Description

Strand specific peak-pair calling in ChIP-exo replicates. The cumulative Skellam distribution function (package 'skellam') is used to detect significant normalised count differences of opposed sign at each DNA strand (peak-pairs). Irreproducible discovery rate for overlapping peak-pairs across biological replicates is estimated using the package 'idr'.

Details

| | |
|-----------|-------------------------------------|
| Package: | CexoR |
| Type: | Package |
| Version: | 1.35.1 |
| Date: | 2022-05-28 |
| License: | Artistic-2.0 GPL-2 + file LICENSE |
| LazyLoad: | yes |

Author(s)

Pedro Madrigal,
 Maintainer: Pedro Madrigal <pmadrigal@ebi.ac.uk>

References

Madrigal P (2015) CexoR: an R/Bioconductor package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates. *EMBnet.journal* 21: e837.
 Skellam JG (1946) The frequency distribution of the difference between two Poisson variates belonging to different populations. *J R Stat Soc Ser A* 109: 296.
 Li Q, Brown J, Huang H, Bickel P (2011) Measuring reproducibility of high-throughput experiments. *Ann Appl Stat* 5: 1752-1779.
 Rhee HS, Pugh BF (2011) Comprehensive genome-wide protein-DNA interactions detected at single-nucleotide resolution. *Cell* 147: 1408-1419.

Examples

```
## hg19. chr2:1-1,000,000. CTCF data from Rhee and Pugh (2011)
owd <- setwd( tempdir() )

rep1 <- "CTCF_rep1_chr2_1-1e6.bam"
rep2 <- "CTCF_rep2_chr2_1-1e6.bam"
rep3 <- "CTCF_rep3_chr2_1-1e6.bam"
r1 <- system.file( "extdata", rep1, package="CexoR",mustWork = TRUE )
r2 <- system.file( "extdata", rep2, package="CexoR",mustWork = TRUE )
r3 <- system.file( "extdata", rep3, package="CexoR",mustWork = TRUE )

chipexo <- cexor( bam=c(r1,r2,r3), chrN="chr2", chrL=1e6, idr=0.01, p=1e-12, N=3e4 )

plotcexor( bam=c(r1,r2,r3), peaks=chipexo, EXT=500 )

setwd( owd )
```

CexoR

*CexoR internal functions***Description**

Internal undocumentation functions

cexor

*ChIP-exo peak-pair calling with replicates***Description**

ChIP-exo peak-pair calling with replicates.

Usage

```
cexor(bam, chrN, chrL, p=1e-9, dpeaks=c(0,150), dpairs=100, idr=0.01,
N=5e6, bedfile=TRUE, mu=2.6, sigma=1.3, rho=0.8, prop=0.7)
```

Arguments

| | |
|------|--|
| bam | BAM alignment files of biological replicates. |
| chrN | Vector of chromosome names. |
| chrL | Vector of chromosome sizes (bp). |
| p | P-value cutoff (should be relaxed, e.g. 1e-3, to allow the correct estimation of the irreproducible discovery rate (idr). However, this depends on the sequencing depth. For datasets with high number of tag counts, 1e-9 can be appropriate. See the vignette for more information.) |

| | |
|---------|---|
| dpeaks | Min. and max. allowed distance between peak pairs located at opposed strands in a replicate (bp). |
| dpairs | Max. allowable distance between peak-pair centres across replicates (bp). |
| idr | Irreproducible discovery rate cutoff [0-1]. |
| N | Genome is divided in blocks of N bp. for processing. N must be not higher than the size of the smallest chromosome. |
| bedfile | Generate BED files of ChIP-exo reproducible peak pairs. |
| mu | A starting value for the mean of the reproducible component (see 'idr' package). |
| sigma | A starting value for the standard deviation of the reproducible component (see 'idr' package). |
| rho | A starting value for the correlation coefficient of the reproducible component (see 'idr' package). |
| prop | A starting value for the proportion of reproducible component (see 'idr' package). |

Details

Strand specific peak-pair calling in ChIP-exo replicates. The cumulative Skellam distribution function (package 'skellam') is used to detect significant normalized count differences of opposed sign at each DNA strand (peak-pairs). Irreproducible discovery rate for overlapping peak-pairs across biological replicates is estimated using the package 'idr'. The internal functions `pskellam` and `pskellam.sp` from the Jerry W. Lewis' 'skellam' R package (version 0.0-8-7) are used to calculate the cumulative Skellam distribution (see LICENSE file).

Value

A list containing the following elements:

| | |
|-----------------|---|
| bindingEvents | A GRanges object with reproducible peak pair locations. The metadata 'value' indicates the Irreproducible discovery rate (IDR) estimated at this region, while 'repI.neg.log10pvalue' indicates $-\log_{10}(\text{p-value})$ for the replicate I. 'Stouffer.pvalue' and 'Fisher.pvalue' report the combined p-value considering they come from independent significance tests. |
| bindingCentres | A GRanges object with centre position of reproducible peak pair locations. The metadata 'value' indicates the Irreproducible discovery rate (IDR) estimated at this region, while 'repI.neg.log10pvalue' indicates $-\log_{10}(\text{p-value})$ for the replicate I. 'Stouffer.pvalue' and 'Fisher.pvalue' report the combined p-value considering they come from independent significance tests. |
| pairedPeaksRep1 | A GRangesList object with the location of peak pairs retrieved at each replicate. The metadata 'score' indicates $-\log_{10}(\text{p-value})$. |

Author(s)

Pedro Madrigal, <pmadrigal@ebi.ac.uk>

References

Madrigal P (2015) CexoR: an R/Bioconductor package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates. *EMBnet.journal* 21: e837.

See Also

[CexoR-package](#)

Examples

```
## hg19. chr2:1-1,000,000. CTCF data from Rhee and Pugh (2011)
owd <- setwd(tempdir())

rep1 <- "CTCF_rep1_chr2_1-1e6.bam"
rep2 <- "CTCF_rep2_chr2_1-1e6.bam"
rep3 <- "CTCF_rep3_chr2_1-1e6.bam"
r1 <- system.file("extdata", rep1, package="CexoR", mustWork = TRUE)
r2 <- system.file("extdata", rep2, package="CexoR", mustWork = TRUE)
r3 <- system.file("extdata", rep3, package="CexoR", mustWork = TRUE)

chipexo <- cexor(bam=c(r1,r2,r3), chrN="chr2", chrL=1e6, idr=0.01, p=1e-12, N=3e4)

plotcexor(bam=c(r1,r2,r3), peaks=chipexo, EXT=500)

setwd(owd)
```

plotcexor

Visualization of ChIP-exo peak-pair calling with replicates

Description

Visualization of ChIP-exo peak-pair calling with replicates.

Usage

```
plotcexor(bam, peaks, EXT=500)
```

Arguments

| | |
|-------|---|
| bam | BAM alignment files of biological replicates. |
| peaks | Object (list) output of the function 'cexor'. |
| EXT | Extension (bp) upstream and downstream the central position of reproducible peak pair locations for visualization purposes. |

Details

Visualization of ChIP-exo peak-pair calling with replicates.

Value

R plot.

Author(s)

Pedro Madrigal, <pmadrigal@ebi.ac.uk>

References

Madrigal P (2015) CexoR: an R/Bioconductor package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates. *EMBNet.journal* 21: e837.

See Also

[CexoR-package](#)

Examples

```
## hg19. chr2:1-1,000,000. CTCF data from Rhee and Pugh (2011)
owd <- setwd(tempdir())

rep1 <- "CTCF_rep1_chr2_1-1e6.bam"
rep2 <- "CTCF_rep2_chr2_1-1e6.bam"
rep3 <- "CTCF_rep3_chr2_1-1e6.bam"
r1 <- system.file("extdata", rep1, package="CexoR", mustWork = TRUE)
r2 <- system.file("extdata", rep2, package="CexoR", mustWork = TRUE)
r3 <- system.file("extdata", rep3, package="CexoR", mustWork = TRUE)

chipexo <- cexor(bam=c(r1,r2,r3), chrN="chr2", chrL=1e6, idr=0.01, p=1e-12, N=3e4)

plotcexor(bam=c(r1,r2,r3), peaks=chipexo, EXT=500)

setwd(owd)
```

Index

* **internal**

CexoR, [3](#)

CexoR, [3](#)

CexoR (CexoR-package), [2](#)

cexor, [3](#)

CexoR-package, [2](#)

plotcexor, [5](#)

pskellam (CexoR), [3](#)