Package ‘ChIPseeker’

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Type Package

Title ChIPseeker for ChIP peak Annotation, Comparison, and Visualization

Version 1.10.3

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Description This package implements functions to retrieve the nearest genes around the peak, annotate genomic region of the peak, statistical methods for estimate the significance of overlap among ChIP peak data sets, and incorporate GEO database for user to compare the own dataset with those deposited in database. The comparison can be used to infer cooperative regulation and thus can be used to generate hypotheses. Several visualization functions are implemented to summarize the coverage of the peak experiment, average profile and heatmap of peaks binding to TSS regions, genomic annotation, distance to TSS, and overlap of peaks or genes.

Depends R (>= 3.3.0)

Imports AnnotationDbi, BiocGenerics, boot, DOSE, IRanges, GenomeInfoDb, GenomicRanges, GenomicFeatures, ggplot2 (>= 2.2.0), gplots, graphics, grDevices, grid, gridBase, gtools, methods, plotrix, dplyr, parallel, magrittr, RColorBrewer, rtracklayer, S4Vectors (>= 0.9.25), stats, TxDB.Hsapiens.UCSC.hg19.knownGene, UpSetR, utils

Suggests clusterProfiler, ReactomePA, org.Hs.eg.db, knitr, BiocStyle, rmarkdown, testthat

URL https://guangchuangyu.github.io/ChIPseeker

BugReports https://github.com/GuangchuangYu/ChIPseeker/issues

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

biocViews Annotation, ChIPSeq, Software, Visualization, MultipleComparison

RoxygenNote 5.0.1

NeedsCompilation no
R topics documented:

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ChIPseeker-package  

ChIP-SEQ Annotation, Visualization and Comparison

Description

This package is designed for chip-seq data analysis

Details

Package: ChIPseeker
Type: Package
Version: 1.5.1
Date: 27-04-2015
biocViews: ChIPSeq, Annotation, Software
Depends:
Imports: methods, ggplot2
Suggests: clusterProfiler, GOSemSim
License: Artistic-2.0

Author(s)

Guangchuang Yu
Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

Description

capture name of variable

Usage

.(..., .env = parent.frame())

Arguments

... expression
.env environment

Value

expression

Examples

x <- 1
eval(.x[1])
Description
Annotate peaks

Usage
annotatePeak(peak, tssRegion = c(-3000, 3000), TxDb = NULL,
level = "transcript", assignGenomicAnnotation = TRUE,
genomicAnnotationPriority = c("Promoter", "5UTR", "3UTR", "Exon", "Intron",
"Downstream", "Intergenic"), annoDb = NULL, addFlankGeneInfo = FALSE,
flankDistance = 5000, sameStrand = FALSE, ignoreOverlap = FALSE,
ignoreUpstream = FALSE, ignoreDownstream = FALSE, overlap = "TSS",
verbose = TRUE)

Arguments
peak  peak file or GRanges object
tssRegion Region Range of TSS
TxDb  TxDb object
level one of transcript and gene
assignGenomicAnnotation logical, assign peak genomic annotation or not
genomicAnnotationPriority genomic annotation priority
annoDb annotation package
addFlankGeneInfo logical, add flanking gene information from the peaks
flankDistance distance of flanking sequence
sameStrand logical, whether find nearest/overlap gene in the same strand
ignoreOverlap logical, whether ignore overlap of TSS with peak
ignoreUpstream logical, if True only annotate gene at the 3’ of the peak.
ignoreDownstream logical, if True only annotate gene at the 5’ of the peak.
overlap one of ‘TSS’ or ‘all’, if overlap="all", then gene overlap with peak will be reported as nearest gene, no matter the overlap is at TSS region or not.
verbose print message or not

Value
data.frame or GRanges object with columns of:
all columns provided by input.
annotation: genomic feature of the peak, for instance if the peak is located in 5’UTR, it will annotated by 5’UTR. Possible annotation is Promoter-TSS, Exon, 5’ UTR, 3’ UTR, Intron, and Intergenic.
Description

convert csAnno object to data.frame

Usage

## S3 method for class 'csAnno'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

Arguments

x csAnno object
row.names row names
optional should be omitted.
... additional parameters
as.GRanges

Description
convert csAnno object to GRanges

Usage
as.GRanges(x)

Arguments

x csAnno object

Value
GRanges object

Author(s)
Guangchuang Yu https://guangchuangyu.github.io

covplot
covplot

Description
plot peak coverage

Usage
covplot(peak, weightCol = NULL, xlab = "Chromosome Size (bp)", ylab = "", title = "ChIP Peaks over Chromosomes", chrs = NULL, xlim = NULL, lower = 1)
**Arguments**

- `peak`: peak file or GRanges object
- `weightCol`: weight column of peak
- `xlab`: xlab
- `ylab`: ylab
- `title`: title
- `chrs`: selected chromosomes to plot, all chromosomes by default
- `xlim`: ranges to plot, default is whole chromosome
- `lower`: lower cutoff of coverage signal

**Value**

ggplot2 object

**Author(s)**

G Yu

---

**csAnno-class Class "csAnno" This class represents the output of ChIPseeker Annotation**

**Description**

Class "csAnno" This class represents the output of ChIPseeker Annotation

**Slots**

- `anno`: annotation
- `tssRegion`: TSS region
- `level`: transcript or gene
- `hasGenomicAnnotation`: logical
- `detailGenomicAnnotation`: Genomic Annotation in detail
- `annoStat`: annotation statistics
- `peakNum`: number of peaks

**Author(s)**

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

**See Also**

annotatePeak
downloadGEObedFiles

Description

download all BED files of a particular genome version

Usage

downloadGEObedFiles(genome, destDir = getwd())

Arguments

genome genome version
destDir destination folder

Author(s)

G Yu

downloadGSMbedFiles

Description

download BED supplementary files of a list of GSM accession numbers

Usage

downloadGSMbedFiles(GSM, destDir = getwd())

Arguments

GSM GSM accession numbers
destDir destination folder

Author(s)

G Yu
**dropAnno**

---

**Description**

dropAnno

**Usage**
dropAnno(csAnno, distanceToTSS_cutoff = 10000)

**Arguments**

- csAnno: output of annotatePeak
- distanceToTSS_cutoff: distance to TSS cutoff

**Details**

drop annotation exceeding distanceToTSS_cutoff

**Value**

csAnno object

**Author(s)**

Guangchuang Yu

---

**enrichAnnoOverlap**

---

**Description**

calculate overlap significant of ChIP experiments based on their nearest gene annotation

**Usage**
enrichAnnoOverlap(queryPeak, targetPeak, TxDb = NULL, pAdjustMethod = "BH", chainFile = NULL, distanceToTSS_cutoff = NULL)

**Arguments**

- queryPeak: query bed file
- targetPeak: target bed file(s) or folder containing bed files
- TxDb: TxDb
- pAdjustMethod: p-value adjustment method
- chainFile: chain file for liftOver
- distanceToTSS_cutoff: restrict nearest gene annotation by distance cutoff
enrichPeakOverlap

Description

calculate overlap significant of ChIP experiments based on the genome coordinations

Usage

enrichPeakOverlap(queryPeak, targetPeak, TxDb = NULL, pAdjustMethod = "BH",
nShuffle = 1000, chainFile = NULL, pool = TRUE,
mc.cores = detectCores() - 1, verbose = TRUE)

Arguments

queryPeak       query bed file or GRanges object
targetPeak      target bed file(s) or folder that containing bed files or a list of GRanges objects
TxDb            TxDb
pAdjustMethod   pvalue adjustment method
nShuffle        shuffle numbers
chainFile       chain file for liftOver
pool            logical, whether pool target peaks
mc.cores        number of cores, see mclapply
verbose         logical

Value

data.frame

Author(s)

G Yu
**getBioRegion**

Description
prepare a region center on start site of selected feature

Usage
getBioRegion(TxDb = NULL, upstream = 1000, downstream = 1000, by = "gene")

Arguments
- **TxDb**: TxDb
- **upstream**: upstream from start site
- **downstream**: downstream from start site
- **by**: one of 'gene', 'transcript', 'exon', 'intron'

Value
GRanges object

Author(s)
Guangchuang Yu

**getGeneAnno**

Description
get gene annotation, symbol, gene name etc.

Usage
geneAnno(annoDb, geneID, type)

Arguments
- **annoDb**: annotation package
- **geneID**: query geneID
- **type**: gene ID type

Value
data.frame

Author(s)
G Yu
getGenomicAnnotation

Description
get Genomic Annotation of peaks

Usage
getGenomicAnnotation(peaks, distance, tssRegion = c(-3000, 3000), TxDb, level,
genomicAnnotationPriority, sameStrand = FALSE)

Arguments
peaks peaks in GRanges object
distance distance of peak to TSS
tssRegion tssRegion, default is -3kb to +3kb
TxDb TxDb object
level one of gene or transcript
genomicAnnotationPriority genomic Annotation Priority
sameStrand whether annotate gene in same strand

Value
character vector

Author(s)
G Yu

getGEOgenomeVersion

Description
get genome version statistics collecting from GEO ChIPseq data

Usage
getGEOgenomeVersion()

Value
data.frame

Author(s)
G Yu
**getGEOInfo**

**Description**

get subset of GEO information by genome version keyword

**Usage**

getGEOInfo(genome, simplify = TRUE)

**Arguments**

- genome: genome version
- simplify: simplify result or not

**Value**

data.frame

**Author(s)**

G Yu

---

**getGEOspecies**

**Description**

accessing species statistics collecting from GEO database

**Usage**

getGEOspecies()

**Value**

data.frame

**Author(s)**

G Yu
**getNearestFeatureIndicesAndDistances**

**Description**

get index of features that closest to peak and calculate distance

**Usage**

```r
getNearestFeatureIndicesAndDistances(peaks, features, sameStrand = FALSE,
ignoreOverlap = FALSE, ignoreUpstream = FALSE, ignoreDownstream = FALSE,
overlap = "TSS")
```

**Arguments**

- `peaks`: peak in GRanges
- `features`: features in GRanges
- `sameStrand`: logical, whether find nearest gene in the same strand
- `ignoreOverlap`: logical, whether ignore overlap of TSS with peak
- `ignoreUpstream`: logical, if True only annotate gene at the 3' of the peak.
- `ignoreDownstream`: logical, if True only annotate gene at the 5' of the peak.
- `overlap`: one of "TSS" or "all"

**Value**

list

**Author(s)**

G Yu

---

**getPromoters**

**Description**

prepare the promoter regions

**Usage**

```r
getPromoters(TxDB = NULL, upstream = 1000, downstream = 1000,
by = "gene")
```
**getSampleFiles**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TxDB</td>
<td>TxDB</td>
</tr>
<tr>
<td>upstream</td>
<td>upstream from TSS site</td>
</tr>
<tr>
<td>downstream</td>
<td>downstream from TSS site</td>
</tr>
<tr>
<td>by</td>
<td>one of gene or transcript</td>
</tr>
</tbody>
</table>

**Value**

GRanges object

---

**getDescription**

**Usage**

getDescription()

**Value**

list of file names

**Author(s)**

G Yu

---

**getTagMatrix**

**Description**

calculate the tag matrix

**Usage**

getTagMatrix(peak, weightCol = NULL, windows)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>peak</td>
<td>peak file or GRanges object</td>
</tr>
<tr>
<td>weightCol</td>
<td>column name of weight, default is NULL</td>
</tr>
<tr>
<td>windows</td>
<td>a collection of region with equal size, eg. promoter region.</td>
</tr>
</tbody>
</table>

**Value**

tagMatrix
### Information Datasets

**Description**
ucsc genome version, precalculated data and gsm information

### overlap

**Description**
calculate the overlap matrix, which is useful for vennplot

**Usage**
overlap(Sets)

**Arguments**
- **Sets** a list of objects

**Value**
data.frame

**Author(s)**
G Yu

---

### peakHeatmap

**Description**
plot the heatmap of peaks align to flank sequences of TSS

**Usage**
peakHeatmap(peak, weightCol = NULL, TxDb = NULL, upstream = 1000, downstream = 1000, xlab = "", ylab = "", title = NULL, color = NULL, verbose = TRUE)
**plotAnnoBar**

**Arguments**

- **peak**: peak file or GRanges object
- **weightCol**: column name of weight
- **TxDb**: TxDb object
- **upstream**: upstream position
- **downstream**: downstream position
- **xlab**: xlab
- **ylab**: ylab
- **title**: title
- **color**: color
- **verbose**: print message or not

**Value**

figure

**Author(s)**

G Yu

---

**Description**

plotAnnoBar method generics

plotAnnoBar method for list of csAnno instances

plotAnnoBar method for csAnno instance

**Usage**

```r
plotAnnoBar(x, xlab = "", ylab = "Percentage(%)", title = "Feature Distribution", ...)  
## S4 method for signature 'list'
plotAnnoBar(x, xlab = "", ylab = "Percentage(%)", title = "Feature Distribution", ...)  
plotAnnoBar(x, xlab="", ylab='Percentage(%)',title="Feature Distribution", ...)
```

**Arguments**

- **x**: csAnno instance
- **xlab**: xlab
- **ylab**: ylab
- **title**: title
- **...**: additional parameter
plotAnnoBar.data.frame

**Value**

plot

**Author(s)**

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

---

**Description**

plot feature distribution based on their chromosome region

**Usage**

```r
plotAnnoBar.data.frame(anno.df, xlab = "", ylab = "Percentage(%)", title = "Feature Distribution", categoryColumn)
```

**Arguments**

- `anno.df`: annotation stats
- `xlab`: xlab
- `ylab`: ylab
- `title`: plot title
- `categoryColumn`: category column

**Details**

plot chromosome region features

**Value**

bar plot that summarize genomic features of peaks

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

**See Also**

`annotatePeak` `plotAnnoPie`
plotAnnoPie method generics

plotAnnoPie method for csAnno instance

Usage

plotAnnoPie(x, ndigit = 2, cex = 0.9, col = NA,
            legend.position = "rightside", pie3D = FALSE, ...)

Arguments

  x            csAnno instance
  ndigit       number of digit to round
  cex          label cex
  col          color
  legend.position  topright or other.
  pie3D        plot in 3D or not
  ...          extra parameter

Value

plot

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

plotAnnoPie.csAnno  plotAnnoPie

Description

pieplot from peak genomic annotation

Usage

plotAnnoPie.csAnno(x, ndigit = 2, cex = 0.9, col = NA,
                    legend.position = "rightside", pie3D = FALSE, ...)
plotAvgProf

**Description**

plot the profile of peaks

**Usage**

```r
plotAvgProf(tagMatrix, xlim, xlab = "Genomic Region (5'->3')", ylab = "Read Count Frequency", conf, facet = "none", free_y = TRUE, ...)
```
plotAvgProf2

Arguments
- tagMatrix: tagMatrix or a list of tagMatrix
- xlim: xlim
- xlab: x label
- ylab: y label
- conf: confidence interval
- facet: one of 'none', 'row' and 'column'
- free_y: if TRUE, y will be scaled by AvgProf
- ...: additional parameter

Value
- ggplot object

Author(s)
- G Yu; Y Yan

Description
plot the profile of peaks that align to flank sequences of TSS

Usage
plotAvgProf2(peak, weightCol = NULL, TxDb = NULL, upstream = 1000, downstream = 1000, xlab = "Genomic Region (5'-3')", ylab = "Read Count Frequency", conf, facet = "none", free_y = TRUE, verbose = TRUE, ...)

Arguments
- peak: peak file or GRanges object
- weightCol: column name of weight
- TxDb: TxDb object
- upstream: upstream position
- downstream: downstream position
- xlab: xlab
- ylab: ylab
- conf: confidence interval
- facet: one of 'none', 'row' and 'column'
- free_y: if TRUE, y will be scaled by AvgProf
- verbose: print message or not
- ...: additional parameter
plotDistToTSS

Description

plotDistToTSS method generics
plotDistToTSS method for list of csAnno instances
plotDistToTSS method for csAnno instance

Usage

plotDistToTSS(x, distanceColumn = "distanceToTSS", xlab = ",
    ylab = "Binding sites (%) (5'->3')",
    title = "Distribution of transcription factor-binding loci relative to TSS",
    ...
)

## S4 method for signature 'list'
plotDistToTSS(x, distanceColumn = "distanceToTSS",
    xlab = ",
    ylab = "Binding sites (%) (5'->3')",
    title = "Distribution of transcription factor-binding loci relative to TSS",
    ...
)

plotDistToTSS(x, distanceColumn = "distanceToTSS",
    xlab = ",
    ylab = "Binding sites (%) (5'->3')",
    title = "Distribution of transcription factor-binding loci relative to TSS",
    ...
)

Arguments

x                  csAnno instance
distanceColumn    distance column name
xlab               xlab
ylab               ylab
title              title
...                 additional parameter

Value

plot

Author(s)

Guangchuang Yu https://guangchuangyu.github.io
Description

plot feature distribution based on the distances to the TSS

Usage

plotDistToTSS.data.frame(peakDist, distanceColumn = "distanceToTSS",
                          xlab = "", ylab = "Binding sites (%) (5'->3')",
                          title = "Distribution of transcription factor-binding loci relative to TSS",
                          categoryColumn)

Arguments

peakDist     peak annotation
distanceColumn column name of the distance from peak to nearest gene
xlab         x label
ylab         y label
title         figure title
categoryColumn category column

Value

bar plot that summarize distance from peak to TSS of the nearest gene.

Author(s)

Guangchuang Yu http://ygc.name

See Also

annotatePeak

Examples

## Not run:
require(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
peakfile <- system.file("extdata", "sample_peaks.txt", package="ChIPseeker")
peakAnno <- annotatePeak(peakfile, TxDb=txdb)
plotDistToTSS(peakAnno)

## End(Not run)
readPeakFile

Description
read peak file and store in data.frame or GRanges object

Usage
readPeakFile(peakfile, as = "GRanges", ...)

Arguments
- peakfile: peak file
- as: output format, one of GRanges or data.frame
- ...: additional parameter

Value
peak information, in GRanges or data.frame object

Author(s)
G Yu

Examples
peakfile <- system.file("extdata", "sample_peaks.txt", package="ChIPseeker")
peak.gr <- readPeakFile(peakfile, as="GRanges")
peak.gr

seq2gene

Description
annotate genomic regions to genes in many-to-many mapping

Usage
seq2gene(seq, tssRegion, flankDistance, TxDB, sameStrand = FALSE)

Arguments
- seq: genomic regions in GRanges object
- tssRegion: TSS region
- flankDistance: flanking search radius
- TxDB: TranscriptDb object
- sameStrand: logical whether find nearest/overlap gene in the same strand
**show**

**Value**

- gene vector

**Author(s)**

- Guangchuang Yu

---

**Description**

show method for csAnno instance

**Usage**

```
show(object)
```

**Arguments**

- `object` A csAnno instance

**Value**

- message

**Author(s)**

- Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

---

**shuffle**

**Description**

shuffle the position of peak

**Usage**

```
shuffle(peak.gr, TxDb)
```

**Arguments**

- `peak.gr` GRanges object
- `TxDb` TxDb

**Value**

- GRanges object

**Author(s)**

- G Yu
tagHeatmap

Description
plot the heatmap of tagMatrix

Usage
tagHeatmap(tagMatrix, xlim, xlab = "", ylab = "", title = NULL, color = "red")

Arguments
tagMatrix tagMatrix or a list of tagMatrix
xlim xlim
xlab xlab
ylab ylab
title title
color color

Value
figure

Author(s)
G Yu

upsetplot

Description
upsetplot method generics

Usage
upsetplot(x, ...)

Arguments
x A csAnno instance
... additional parameter

Value
plot
vennpie

Author(s)
Guangchuang Yu https://guangchuangyu.github.io

Description
vennpie method generics
vennpie method generics

Usage
vennpie(x, r = 0.2, ...)
vennpie(x, r=0.2, ...)

Arguments
x A csAnno instance
r initial radius
... additional parameter

Value
plot

Author(s)
Guangchuang Yu https://guangchuangyu.github.io

vennplot

Description
plot the overlap of a list of object

Usage
vennplot(Sets, by = "gplots")

Arguments
Sets a list of object, can be vector or GRanges object
by one of gplots or Vennerable
vennplot.peakfile

Value

venn plot that summarize the overlap of peaks from different experiments or gene annotation from different peak files.

Author(s)

G Yu

Examples

```r
## example not run
## require(TxDb.Hsapiens.UCSC.hg19.knownGene)
## txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
## peakfiles <- getSampleFiles()
## peakAnnoList <- lapply(peakfiles, annotatePeak)
## names(peakAnnoList) <- names(peakfiles)
## genes= lapply(peakAnnoList, function(i) as.data.frame(i)$geneId)
## vennplot(genes)
```

---

Description

vennplot for peak files

Usage

```r
vennplot.peakfile(files, labels = NULL)
```

Arguments

- **files**: peak files
- **labels**: labels for peak files

Value

figure

Author(s)

G Yu
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