Package ‘ChIPseeker’

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Type Package

Title ChIPseeker for ChIP peak Annotation, Comparison, and Visualization

Version 1.10.2

Author Guangchuang Yu <guangchuangyu@gmail.com> with contributions from Yun Yan, Herve Pages, Michael Kluge and Thomas Schwarzl.

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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, GenomInfoDb, GenomicRanges, GenomicFeatures, ggplot2, gplots, graphics, grDevices, grid, gridBase, tools, 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
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**Description**

This package is designed for chip-seq data analysis.

**Details**

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</tr>
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<td>Date:</td>
<td>27-04-2015</td>
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**Author(s)**

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

**Usage**

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

**Arguments**

- `...` expression
- `.env` environment

**Value**

expression

**Examples**

```r
x <- 1
eval.(.(x)[[1]])
```
**Description**

Annotate peaks

**Usage**

```r
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, Intronic, and Intergenic.
geneChr: Chromosome of the nearest gene
geneStart: gene start
geneEnd: gene end
geneLength: gene length
geneStrand: gene strand
geneId: entrezgene ID
distanceToTSS: distance from peak to gene TSS
if annoDb is provided, extra column will be included:
ENSEMBL: ensembl ID of the nearest gene
SYMBOL: gene symbol
GENENAME: full gene name

Author(s)
G Yu

See Also
plotAnnoBar plotAnnoPie plotDistToTSS

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, tssRegion=c(-3000, 3000), TxDB=txdb)
peakAnno
## End(Not run)
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

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
tlevel 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
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  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**: pvalue adjustment method
- **chainFile**: chain file for liftOver
- **distanceToTSS_cutoff**: restrict nearest gene annotation by distance cutoff
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**
getGeneAnno(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
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
getPromoters(TxDB = NULL, upstream = 1000, downstream = 1000,
by = "gene")
getSampleFiles

Arguments

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></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

Description

get filenames of sample files

Usage

getSampleFiles()

Value

list of file names

Author(s)

G Yu

getTagMatrix

Description

calculate the tag matrix

Usage

getTagMatrix(peak, weightCol = NULL, windows)

Arguments

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></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
**info**

*Information Datasets*

**Description**

ucsc genome version, precalculated data and gsm information

**overlap**

**Description**

calculate the overlap matrix, which is useful for vennplot

**Usage**

```r
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**

```r
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

---

**plotAnnoBar method generics**

**Description**

plotAnnoBar method generics

plotAnnoBar method for list of csAnno instances

plotAnnoBar method for csAnno instance

**Usage**

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**

**Description**

plotAnnoPie method generics

plotAnnoPie method for `csAnno` instance

**Usage**

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

```r
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](https://guangchuangyu.github.io)

---

**plotAnnoPie.csAnno**

**Description**

pieplot from peak genomic annotation

**Usage**

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

Description

plot the profile of peaks

Usage

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**: xlab
- **xlab**: ylab
- **ylab**: confidence interval
- **conf**: one of 'none', 'row' and 'column'
- **facet**: if TRUE, y will be scaled by AvgProf
- **free_y**: additional parameter

Value

ggplot object

Author(s)

G Yu; Y Yan

---

plotAvgProf2  plotAvgProf

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

---

**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](https://guangchuangyu.github.io)

---

**Description**

vennpie method generics

**Usage**

```r
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](https://guangchuangyu.github.io)

---

### vennplot

**Description**

plot the overlap of a list of object

**Usage**

```r
vennplot(Sets, by = "gplots")
```

**Arguments**

- `Sets`: a list of object, can be vector or GRanges object
- `by`: one of gplots or Vennerable
**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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