## Package ‘ChIPseeker’

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**Type** Package  
**Title** ChIPseeker for ChIP peak Annotation, Comparison, and Visualization  
**Version** 1.24.0  
**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 (>= 3.5.0)  
**Imports** AnnotationDbi, BiocGenerics, boot, enrichplot, IRanges, GenomeInfoDb, GenomicRanges, GenomicFeatures, ggplot2, gplots, graphics, grDevices, gtools, methods, plotrix, dplyr, parallel, magrittr, RColorBrewer, rtracklayer, S4Vectors, stats, TxDb.Hsapiens.UCSC.hg19.knownGene, utils  
**Suggests** clusterProfiler (>= 3.15.4), ggimage, ggplotify, ggupset, ReactomePA, org.Hs.eg.db, knitr, rmarkdown, testthat, tibble  
**Remotes** GuangchuangYu/enrichplot  
**URL** https://guangchuangyu.github.io/software/ChIPseeker  
**BugReports** https://github.com/YuLab-SMU/ChIPseeker/issues  
**Encoding** UTF-8  
**VignetteBuilder** knitr  
**ByteCompile** true  
**License** Artistic-2.0  
**biocViews** Annotation, ChIPSeq, Software, Visualization, MultipleComparison  
**RoxygenNote** 7.0.2  
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Author  Guangchuang Yu [aut, cre] (<https://orcid.org/0000-0002-6485-8781>),
         Yun Yan [ctb],
         Hervé Pagès [ctb],
         Michael Kluge [ctb],
         Thomas Schwarzl [ctb],
         Zhougeng Xu [ctb]

R topics documented:

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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
```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
annotatePeak

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.
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.data.frame.csAnno

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

Value
data.frame

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

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
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
downloadGEObedFiles

csAnno-class

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

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
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

Value

data.frame

Author(s)

G Yu

Description

calculate overlap significant of ChIP experiments based on the genome coordinations
**Usage**

```r
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

---

**Description**

prepare a region center on start site of selected feature

**Usage**

```r
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`
getGenomicAnnotation

**Value**
GRanges object

**Author(s)**
Guangchuang Yu

---

getGeneAnno  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  getGenomicAnnotation

**Description**
get Genomic Annotation of peaks

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

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

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
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")

Arguments

- **TxDb**: TxDb
- **upstream**: upstream from TSS site
- **downstream**: downstream from TSS site
- **by**: one of gene or transcript

Value

GRanges object

getSampleFiles

Description

get filenames of sample files

Usage

getSampleFiles()

Value

list of file names

Author(s)

G Yu
**getTagMatrix**

Description

calculate the tag matrix

Usage

```r
getTagMatrix(peak, weightCol = NULL, windows, flip_minor_strand = TRUE)
```

Arguments

- `peak` peak file or GRanges object
- `weightCol` column name of weight, default is NULL
- `windows` a collection of region with equal size, eg. promoter region.
- `flip_minor_strand` whether flip the orientation of minor strand

Value

tagMatrix

---

**info**

**Information Datasets**

Description

ucsc genome version, precalculated data and gsm information

---

**overlap**

**overlap**

Description

calculate the overlap matrix, which is useful for vennplot

Usage

```r
overlap(Sets)
```

Arguments

- `Sets` a list of objects

Value

data.frame
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
)

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

plotAnnoBar method generics

Description
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

Value

plot

Author(s)

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

plot feature distribution based on their chromosome region

Usage

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 https://guangchuangyu.github.io

See Also

annotatePeak plotAnnoPie
**Description**

plotAnnoPie method for csAnno instance

**Usage**

```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)
Description

Pieplot from peak genomic annotation

Usage

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

Arguments

x            csAnno object
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

Pieplot of peak genomic feature annotation

Author(s)

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

See Also

annotatePeak plotAnnoBar

Examples

```r
## 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)
plotAnnoPie(peakAnno)
## End(Not run)
```
Description

plot the profile of peaks

Usage

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

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
plotAvgProf2

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 = "Peak 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

Value

ggplot object

Author(s)

G Yu
Description

`plotDistToTSS` method for `csAnno` instance

Usage

```r
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'

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

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

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

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
Value

gene vector

Author(s)

Guangchuang Yu

show

show method

Description

show method for csAnno instance

Usage

show(object)

Arguments

object A csAnno instance

Value

message

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

shuffle

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

```r
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

```r
upsetplot(x, ...)
```

### Arguments

- `x` 
  A csAnno instance
- `...` 
  additional parameter

### Value

plot

### Author(s)

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

Description

vennpie method generics

Usage

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

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.
**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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