Package ‘ChIPseeker’

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Type Package

Title ChIPseeker for ChIP peak Annotation, Comparison, and Visualization

Version 1.12.0

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 (>= 3.3.2)

Imports AnnotationDbi, BiocGenerics, boot, DOSE (>= 3.0.0), IRanges, GenomeInfoDb, GenomicRanges, GenomicFeatures, ggplot2 (>= 2.2.0), gplots, graphics, grDevices, grid, gridBase, gtools, methods, plotrix, dplyr, parallel, magrittr, RCColorBrewer, rtracklayer, S4Vectors, 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:

Author Guangchuang Yu [aut, cre],
        Yun Yan [ctb],
        Herve Pages [ctb],
        Michael Kluge [ctb],
        Thomas Schwarzl [ctb]

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ChIPseeker-package  

ChIP-SEQ Annotation, Visualization and Comparison

Description

This package is designed for chip-seq data analysis

Details

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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]])
```
**annotatePeak**

**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, Introne, and Intergenic.
geneChr: Chromosome of the nearest gene
geneStart: gene start
geneEnd: gene end
geneLength: gene length
geneStrand: gene strand
genId: 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)
taxdb <- 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)

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

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

---

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  

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  

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
Value
data.frame

Author(s)
G Yu

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**
```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'

**Value**
GRanges object

**Author(s)**
Guangchuang Yu

**getGeneAnno**

**Description**
get gene annotation, symbol, gene name etc.

**Usage**
```r
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
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
g GEOspecies()

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**

<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

---

### 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)
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

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 paramter
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**

**plotAnnoPie method generics**

**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, ...)
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**

**plotAnnoPie**

**Description**

pieplot from peak genomic annotation

**Usage**

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

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

pie plot of peak genomic feature annotation

Author(s)

G Yu

See Also

annotatePeak plotAnnoBar

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)
plotAnnoPie(peakAnno)
## End(Not run)

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` 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

```r
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
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", ...)

## S4 method for signature 'csAnno'
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)
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
xlab
ylab
title
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
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](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.

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

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