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

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Author(s)

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

Description

capture name of variable

Usage

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

Arguments

\ldots
.expression

.env
.environment

Value

.expression

Examples

x <- 1
.eval(.x[[1]])
annotatePeak

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.
as.data.frame.csAnno

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)
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)

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

---

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

gene   genome version
destDir destination folder

Author(s)

G Yu

downloadGSMbedFiles
downloadGSMbedFiles

download GSM 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
enrichPeakOverlap

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**
```
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**

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

**Value**

GRanges object

---

**getDescription**

getfilenames of sample files

**Usage**

getsamplefiles()

**Value**

list of file names

**Author(s)**

G Yu

---

**getTagMatrix**

calculate the tag matrix

**Usage**

getagmatrix(peak, weightCol = NULL, windows)

**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

**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

**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

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

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 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, ...)
```

```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

---

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, ...)
```
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

```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)
```

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

Value

ggplot object

Author(s)

G Yu

plotDistToTSS method generics

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**
```r
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**
```r
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**
```r
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**

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<thead>
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**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**

<table>
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<th>Description</th>
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</thead>
<tbody>
<tr>
<td>peak.gr</td>
<td>GRanges object</td>
</tr>
<tr>
<td>TxDb</td>
<td>TxDb</td>
</tr>
</tbody>
</table>

**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
### vennpie

**Description**

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
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

## 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

vennplot.peakfile(files, labels = NULL)

Arguments

files peak files
labels labels for peak files

Value

figure

Author(s)

G Yu
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