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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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]])
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, Intr, and Intergenic.
Description

class 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

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**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
downloadGEObedFiles

downloadGSMbedFiles
downloadGSMbedFiles

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
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**

```r
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

gPromoters

description
prepare the promoter regions

Usage
gPromoters(TxDb = NULL, upstream = 1000, downstream = 1000,
by = "gene")
**getSampleFiles**

**Arguments**

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

**Value**

- Description: GRanges object

**Usage**

```r
getSampleFiles()
```

**Value**

- Description: list of file names

**Author(s)**

G Yu

---

**getTagMatrix**

**Description**

- Description: calculate the tag matrix

**Usage**

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

**Arguments**

- **peak**
  - Description: peak file or GRanges object
- **weightCol**
  - Description: column name of weight, default is NULL
- **windows**
  - Description: a collection of region with equal size, eg. promoter region.

**Value**

- Description: 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**
overal(Sets)

**Arguments**

- **Sets**
a list of objects

### Value

data.frame

**Author(s)**
G Yu

### peakHeatmap

#### 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

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
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
Description

plotAnnoPie method generics

plotAnnoPie method for csAnno instance

Usage

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

Description

pieplot from peak genomic annotation

Usage

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

plotAnnoPie.csAnno
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, ...)

plotAvgProf

plotAvgProf
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**  
```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**  
`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

vennpie  vennpie method generics

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

vennpplot

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

figure

Author(s)

G Yu
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