

Package ‘ChIPseeker’

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Type Package

Title ChIPseeker for ChIP peak Annotation, Comparison, and Visualization

Version 1.32.1

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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 (>= 3.5.0)

Imports AnnotationDbi, BiocGenerics, boot, enrichplot, IRanges, GenomeInfoDb, GenomicRanges, GenomicFeatures, ggplot2, ggVennDiagram, gplots, graphics, grDevices, gtools, methods, plotrix, dplyr, parallel, magrittr, RColorBrewer, rtracklayer, S4Vectors, stats, TxDb.Hsapiens.UCSC.hg19.knownGene, utils

Suggests clusterProfiler, 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 7.2.1

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ChIPseeker-package	<i>ChIP-SEQ Annotation, Visualization and Comparison</i>
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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

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 or EnsDb annotation 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 Inter-genic.

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 *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 *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>

check_upstream_and_downstream

check upstream and downstream parameter

Description

check_upstream_and_downstream

Usage

check_upstream_and_downstream(upstream, downstream)

Arguments

upstream	upstream
downstream	downstream

combine_csAnno

combine_csAnno

Description

Combine csAnno Object

Usage

combine_csAnno(x, ...)

Arguments

x	csAnno object
...	csAnno objects

Details

<https://github.com/YuLab-SMU/ChIPseeker/issues/157>

Value

csAnno object

`covplot`*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

<code>peak</code>	peak file or GRanges object
<code>weightCol</code>	weight column of peak
<code>xlab</code>	xlab
<code>ylab</code>	ylab
<code>title</code>	title
<code>chrs</code>	selected chromosomes to plot, all chromosomes by default
<code>xlim</code>	ranges to plot, default is whole chromosome
<code>lower</code>	lower cutoff of coverage signal

Value

ggplot2 object

Author(s)

G Yu

csAnno-class	<i>Class "csAnno" This class represents the output of ChIPseeker Annotation</i>
--------------	---

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>

See Also

[annotatePeak](#)

downloadGEObedFiles	<i>downloadGEObedFiles</i>
---------------------	----------------------------

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 *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 *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

Value

data.frame

Author(s)

G Yu

enrichPeakOverlap *enrichPeakOverlap*

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

<code>getBioRegion</code>	<i>getBioRegion</i>
---------------------------	---------------------

Description

prepare a bioregion of selected feature

Usage

```
getBioRegion(  
  TxDb = NULL,  
  upstream = 1000,  
  downstream = 1000,  
  by = "gene",  
  type = "start_site"  
)
```

Arguments

<code>TxDb</code>	<code>TxDb</code>
<code>upstream</code>	upstream from start site
<code>downstream</code>	downstream from start site
<code>by</code>	one of 'gene', 'transcript', 'exon', 'intron', '3UTR', '5UTR'
<code>type</code>	one of "start_site", "end_site", "body"

Details

this function combined previous functions `getPromoters()`, `getBioRegion()`, `getGeneBody()` <https://github.com/GuangchuangYu/ChIPseeker/issues/87>

Value

GRanges object

Author(s)

Guangchuang Yu, Ming L

getGeneAnno	<i>getGeneAnno</i>
-------------	--------------------

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	<i>getGenomicAnnotation</i>
----------------------	-----------------------------

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` *getGEOgenomeVersion*

Description

get genome version statistics collecting from GEO ChIPseq data

Usage

```
getGEOgenomeVersion()
```

Value

data.frame

Author(s)

G Yu

getGEOInfo	<i>getGEOInfo</i>
------------	-------------------

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	<i>getGEOspecies</i>
---------------	----------------------

Description

accessing species statistics collecting from GEO database

Usage

```
getGEOspecies()
```

Value

data.frame

Author(s)

G Yu

`getNearestFeatureIndicesAndDistances`*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	<i>getPromoters</i>
--------------	---------------------

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	<i>getSampleFiles</i>
----------------	-----------------------

Description

get filenames of sample files

Usage

```
getSampleFiles()
```

Value

list of file names

Author(s)

G Yu

`getTagMatrix`*getTagMatrix*

Description

calculate the tag matrix

Usage

```
getTagMatrix(  
  peak,  
  upstream,  
  downstream,  
  windows,  
  type,  
  by,  
  TxDb = NULL,  
  weightCol = NULL,  
  nbin = NULL,  
  verbose = TRUE,  
  ignore_strand = FALSE  
)
```

Arguments

peak	peak peak file or GRanges object
upstream	the distance of upstream extension
downstream	the distance of downstream extension
windows	a collection of region
type	one of "start_site", "end_site", "body"
by	one of 'gene', 'transcript', 'exon', 'intron', '3UTR', '5UTR'
TxDb	TxDb
weightCol	column name of weight, default is NULL
nbin	the amount of nbins
verbose	print message or not
ignore_strand	ignore the strand information or not

Value

tagMatrix

```
getTagMatrix.binning.internal
    getTagMatrix.binning.internal
```

Description

calculate the tagMatrix by binning the idea was derived from the function of deeptools <https://deeptools.readthedocs.io/en/dev>

Usage

```
getTagMatrix.binning.internal(
    peak,
    weightCol = NULL,
    windows,
    nbin = 800,
    upstream = NULL,
    downstream = NULL,
    ignore_strand = FALSE
)
```

Arguments

peak	peak peak file or GRanges object
weightCol	weightCol column name of weight, default is NULL
windows	windows a collection of region with equal or not equal size, eg. promoter region, gene region.
nbin	the amount of nbines needed to be splited and it should not be more than min_body_length
upstream	rel object, NULL or actual number
downstream	rel object, NULL or actual number
ignore_strand	ignore the strand information or not

Value

tagMatrix

```
getTagMatrix.internal getTagMatrix.internal
```

Description

calculate the tag matrix

peakHeatmap	<i>peakHeatmap</i>
-------------	--------------------

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 paramter

Value

plot

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

`plotAnnoBar.data.frame`
plotAnnoBar.data.frame

Description

plot feature distribution based on their chromosome region

Usage

```
plotAnnoBar.data.frame(  
  anno.df,  
  xlab = "",  
  ylab = "Percentage%",  
  title = "Feature Distribution",  
  categoryColumn  
)
```

Arguments

<code>anno.df</code>	annotation stats
<code>xlab</code>	xlab
<code>ylab</code>	ylab
<code>title</code>	plot title
<code>categoryColumn</code>	category column

Details

plot chromosome region features

Value

bar plot that summarize genomic features of peaks

Author(s)

Guangchuang Yu <https://yulab-smu.top>

See Also

[annotatePeak](#) [plotAnnoPie](#)

`plotAnnoPie`*plotAnnoPie method generics*

Description

`plotAnnoPie` method for `csAnno` instance

Usage

```
plotAnnoPie(  
  x,  
  ndigit = 2,  
  cex = 0.9,  
  col = NA,  
  legend.position = "rightside",  
  pie3D = FALSE,  
  radius = 0.8,  
  ...  
)
```

```
plotAnnoPie(x, ndigit=2, cex=0.9, col=NA, legend.position="rightside", pie3D=FALSE, radius=0.8, ...)
```

Arguments

<code>x</code>	<code>csAnno</code> instance
<code>ndigit</code>	number of digit to round
<code>cex</code>	label cex
<code>col</code>	color
<code>legend.position</code>	topright or other.
<code>pie3D</code>	plot in 3D or not
<code>radius</code>	radius of the pie
<code>...</code>	extra parameter

Value

plot

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

plotAnnoPie.csAnno *plotAnnoPie*

Description

pieplot from peak genomic annotation

Usage

```
plotAnnoPie.csAnno(  
  x,  
  ndigit = 2,  
  cex = 0.8,  
  col = NA,  
  legend.position = "rightside",  
  pie3D = FALSE,  
  radius = 0.8,  
  ...  
)
```

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
radius	radius of Pie
...	extra parameter

Value

pie plot of peak genomic feature annotation

Author(s)

Guangchuang Yu <https://yulab-smu.top>

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

plotAvgProf

Description

plot the profile of peaks

Usage

```
plotAvgProf(
  tagMatrix,
  xlim,
  xlab = "Genomic Region (5'→3')",
  ylab = "Peak Count Frequency",
  conf,
  facet = "none",
  free_y = TRUE,
  origin_label = "TSS",
  verbose = 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
origin_label	label of the center
verbose	print message or not
...	additional parameter

Value

ggplot object

Author(s)

G Yu; Y Yan

plotAvgProf.binning *plotAvgProf.binning*

Description

plot the profile of peaks by binning

Usage

```
plotAvgProf.binning(
  tagMatrix,
  xlab = "Genomic Region (5'→3')",
  ylab = "Peak Count Frequency",
  conf,
  facet = "none",
  free_y = TRUE,
  upstream = NULL,
  downstream = NULL,
  label,
  ...
)
```

Arguments

tagMatrix	tagMatrix or a list of tagMatrix
xlab	x label
ylab	y label
conf	confidence interval
facet	one of 'none', 'row' and 'column'
free_y	if TRUE, y will be scaled
upstream	rel object reflects the percentage of flank extension, e.g rel(0.2) integer reflects the actual length of flank extension or TSS region NULL reflects the gene body with no extension
downstream	rel object reflects the percentage of flank extension, e.g rel(0.2) integer reflects the actual length of flank extension or TSS region NULL reflects the gene body with no extension
label	label
...	additional parameter

Value

ggplot object

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 = "Peak Count Frequency",
  conf,
  facet = "none",
  free_y = TRUE,
  verbose = TRUE,
  ignore_strand = FALSE,
  ...
)
```

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
ignore_strand	ignore the strand information or not
...	additional parameter

Value

ggplot object

Author(s)

G Yu, Ming L

plotDistToTSS

*plotDistToTSS method generics***Description**

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>

plotDistToTSS.data.frame

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 lable
title	figure title
categoryColumn	category column

Value

bar plot that summarize distance from peak to TSS of the nearest gene.

Author(s)

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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)
```

plotPeakProf

plotPeakProf

Description

plot the profile of peaks

Usage

```
plotPeakProf(
  tagMatrix,
  conf,
  xlab = "Genomic Region (5'→3')",
  ylab = "Peak Count Frequency",
  facet = "none",
  free_y = TRUE,
  ...
)
```

Arguments

tagMatrix	tagMatrix or a list of tagMatrix
conf	confidence interval
xlab	x label
ylab	y label
facet	one of 'none', 'row' and 'column'
free_y	if TRUE, y will be scaled by AvgProf
...	additional parameter

Details

this function combined previous function plotAvgProf()

Value

ggplot object

plotPeakProf2

plotAvgProf2

Description

plot the profile of peaks automatically

Usage

```
plotPeakProf2(
  peak,
  upstream,
  downstream,
  conf,
  by,
  type,
  weightCol = NULL,
  TxDb = NULL,
  xlab = "Genomic Region (5'->3')",
  ylab = "Peak Count Frequency",
  facet = "none",
  free_y = TRUE,
  verbose = TRUE,
  nbin = NULL,
  ignore_strand = FALSE,
  ...
)
```

Arguments

peak	peak file or GRanges object
upstream	upstream position
downstream	downstream position
conf	confidence interval
by	one of 'gene', 'transcript', 'exon', 'intron', '3UTR', '5UTR'
type	one of "start_site", "end_site", "body"
weightCol	column name of weight
TxDb	TxDb object
xlab	xlab
ylab	ylab
facet	one of 'none', 'row' and 'column'
free_y	if TRUE, y will be scaled by AvgProf
verbose	print message or not

nbin the amount of nbins
ignore_strand ignore the strand information or not
... additional parameter

Value

ggplot object

Author(s)

G Yu, Ming Li

readPeakFile *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`*seq2gene*

Description

annotate genomic regions to genes in many-to-many mapping

Usage

```
seq2gene(seq, tssRegion, flankDistance, Txdb, sameStrand = FALSE)
```

Arguments

<code>seq</code>	genomic regions in GRanges object
<code>tssRegion</code>	TSS region
<code>flankDistance</code>	flanking search radius
<code>Txdb</code>	TranscriptDb object
<code>sameStrand</code>	logical whether find nearest/overlap gene in the same strand

Details

This function associates genomic regions with coding genes in a many-to-many mapping. It first maps genomic regions to host genes (either located in exon or intron), proximal genes (located in promoter regions) and flanking genes (located in upstream and downstream within user specify distance).

Value

gene vector

Author(s)

Guangchuang Yu

Examples

```
library(Txdb.Hsapiens.UCSC.hg19.knownGene)
Txdb <- Txdb.Hsapiens.UCSC.hg19.knownGene
file <- getSampleFiles()[[1]] # a bed file
gr <- readPeakFile(file)
genes <- seq2gene(gr, tssRegion=c(-1000, 1000), flankDistance = 3000, Txdb)
```

show	<i>show method</i>
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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	<i>shuffle</i>
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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	<i>tagHeatmap</i>
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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	<i>upsetplot method</i>
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Description

upsetplot method generics

Usage

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

Arguments

x	A csAnno instance
...	additional parameter

Value

plot

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

`vennpie`*vennpie method generics*

Description

vennpie method generics

Usage`vennpie(x, r = 0.2, ...)``vennpie(x, r=0.2, ...)`**Arguments**

<code>x</code>	A csAnno instance
<code>r</code>	initial radius
<code>...</code>	additional parameter

Value

plot

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

vennplot

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, ggVennDiagram or Vennerable
...	extra parameters using ggVennDiagram. Details see ggVennDiagram

Details

There are two ways to plot, which users can specify through 'by'.

The first way is to use 'gplots' packages, by setting 'by = gplots'. This method is default method. The venn plot produced through this way has no color.

The second way is to use 'ggVennDiagram' packages, by setting 'by = ggVennDiagram'. The venn plot produced through this way has colors which can be defined by users using ggplot2 grammar e.g.(scale_fill_distiller()). And users can specify any details, like digital number, text size and showing percentage or not, by inputting '...' extra parameters.

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)
```

`vennplot.peakfile` *vennplot.peakfile*

Description

vennplot for peak files

Usage

```
vennplot.peakfile(files, labels = NULL)
```

Arguments

<code>files</code>	peak files
<code>labels</code>	labels for peak files

Value

figure

Author(s)

G Yu

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