

# Package ‘ChIPseeker’

March 30, 2021

**Type** Package

**Title** ChIPseeker for ChIP peak Annotation, Comparison, and Visualization

**Version** 1.26.2

**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** 7.1.1

**git\_url** <https://git.bioconductor.org/packages/ChIPseeker>

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ChIPseeker-package      *ChIP-SEQ Annotation, Visualization and Comparison*

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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 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>

---

covplot	<i>covplot</i>
---------	----------------

---

## 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	<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 <a href="#">mclapply</a>
verbose	logical

**Value**

data.frame

**Author(s)**

G Yu

---

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

---

**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

---

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

---

**Description**

get gene annotation, symbol, gene name etc.

**Usage**`getGeneAnno(annoDb, geneID, type)`**Arguments**

<code>annoDb</code>	annotation package
<code>geneID</code>	query geneID
<code>type</code>	gene ID type

**Value**

data.frame

**Author(s)**

G Yu

---

<code>getGenomicAnnotation</code>	<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                      *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                      *getGEOspecies*

---

**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	<i>getTagMatrix</i>
--------------	---------------------

---

**Description**

calculate the tag matrix

**Usage**

```
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	<i>Information Datasets</i>
------	-----------------------------

---

**Description**

ucsc genome version, precalculated data and gsm information

---

overlap	<i>overlap</i>
---------	----------------

---

**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	<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	<i>plotAnnoBar method generics</i>
-------------	------------------------------------

---

## 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

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](#)

---

plotAnnoPie	<i>plotAnnoPie method generics</i>
-------------	------------------------------------

---

## Description

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>

---

plotAnnoPie.csAnno     *plotAnnoPie*

---

### 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

pie plot of peak genomic feature annotation

### Author(s)

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

### 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	<i>plotAvgProf</i>
-------------	--------------------

---

**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,  
  ...  
)
```

**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

*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,
  ...
)
```

**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



---

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)

Guangchuang Yu <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	<i>readPeakFile</i>
--------------	---------------------

---

**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	<i>seq2gene</i>
----------	-----------------

---

**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	<i>tagHeatmap</i>
------------	-------------------

---

**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>
-----------	-------------------------

---

**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**

x	A csAnno instance
r	initial radius
...	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 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**

```
## 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	<i>vennplot.peakfile</i>
-------------------	--------------------------

---

**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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