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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Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Description This package implements functions to retrieve the nearest genes around the peak, annotate genomic region of the peak, statistical methods for estimate the significance of overlap among ChIP peak data sets, and incorporate GEO database for user to compare the own dataset with those deposited in database. The comparison can be used to infer cooperative regulation and thus can be used to generate hypotheses. Several visualization functions are implemented to summarize the coverage of the peak experiment, average profile and heatmap of peaks binding to TSS regions, genomic annotation, distance to TSS, and overlap of peaks or genes.

Depends R (>= 3.3.0)

Imports AnnotationDbi, BiocGenerics, boot, DOSE, IRanges, GenomInfoDb, 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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</thead>
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<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.5.1</td>
</tr>
<tr>
<td>Date</td>
<td>27-04-2015</td>
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<tr>
<td>License</td>
<td>Artistic-2.0</td>
</tr>
</tbody>
</table>

**Author(s)**

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

**Description**

capture name of variable

**Usage**

```
.(...) .env = parent.frame()
```

**Arguments**

```
... expression
.env  environment
```

**Value**

expression

**Examples**

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

Description
Annotate peaks

Usage
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 re-
port 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 anno-
tated by 5'UTR. Possible annotation is Promoter-TSS, Exon, 5' UTR, 3' UTR, Intron, and Intergen-ic.
as.data.frame.csAnno

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)

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

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

downloadGEObedFiles

**Description**

download all BED files of a particular genome version

**Usage**

downloadGEObedFiles(genome, destDir = getwd())

**Arguments**

- genome: genome version
- destDir: destination folder

**Author(s)**

G Yu

---

downloadGSMbedFiles

downloadGSMbedFiles

**Description**

download BED supplementary files of a list of GSM accession numbers

**Usage**

downloadGSMbedFiles(GSM, destDir = getwd())

**Arguments**

- GSM: GSM accession numbers
- destDir: destination folder

**Author(s)**

G Yu
dropAnno

Description

dropAnno

Usage

dropAnno(csAnno, distanceToTSS_cutoff = 10000)

Arguments

csAnno: output of annotatePeak
distanceToTSS_cutoff: distance to TSS cutoff

Details

drop annotation exceeding distanceToTSS_cutoff

Value

csAnno object

Author(s)

Guangchuang Yu

enrichAnnoOverlap

Description

calculate overlap significant of ChIP experiments based on their nearest gene annotation

Usage

enrichAnnoOverlap(queryPeak, targetPeak, TxDb = NULL, pAdjustMethod = "BH", chainFile = NULL, distanceToTSS_cutoff = NULL)

Arguments

queryPeak: query bed file
targetPeak: target bed file(s) or folder containing bed files
TxDb: TxDb
pAdjustMethod: pvalue adjustment method
chainFile: chain file for liftOver
distanceToTSS_cutoff: restrict nearest gene annotation by distance cutoff
Value
data.frame

Author(s)
G Yu

---

description

calculate overlap significant of ChIP experiments based on the genome coordinations

Usage

enrichPeakOverlap(queryPeak, targetPeak, TxDb = NULL, pAdjustMethod = "BH", nShuffle = 1000, chainFile = NULL, pool = TRUE, mc.cores = detectCores() - 1, verbose = TRUE)

Arguments

queryPeak query bed file or GRanges object
targetPeak target bed file(s) or folder that containing bed files or a list of GRanges objects
TxDb TxDb
pAdjustMethod pvalue adjustment method
nShuffle shuffle numbers
chainFile chain file for liftOver
pool logical, whether pool target peaks
mc.cores number of cores, see mclapply
verbose logical

Value
data.frame

Author(s)
G Yu
getBioRegion

Description
prepare a region center on start site of selected feature

Usage
getBioRegion(TxDB = NULL, upstream = 1000, downstream = 1000, by = "gene")

Arguments
<table>
<thead>
<tr>
<th>TxDB</th>
<th>TxDb</th>
</tr>
</thead>
<tbody>
<tr>
<td>upstream</td>
<td>upstream from start site</td>
</tr>
<tr>
<td>downstream</td>
<td>downstream from start site</td>
</tr>
<tr>
<td>by</td>
<td>one of 'gene', 'transcript', 'exon', 'intron'</td>
</tr>
</tbody>
</table>

Value
GRanges object

Author(s)
Guangchuang Yu

getGeneAnno

Description
get gene annotation, symbol, gene name etc.

Usage
geneAnno(annoDb, geneID, type)

Arguments
<table>
<thead>
<tr>
<th>annoDb</th>
<th>annotation package</th>
</tr>
</thead>
<tbody>
<tr>
<td>geneID</td>
<td>query geneID</td>
</tr>
<tr>
<td>type</td>
<td>gene ID type</td>
</tr>
</tbody>
</table>

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
getPromoters

Description
prepare the promoter regions

Usage
getPromoters(TxDB = NULL, upstream = 1000, downstream = 1000, by = "gene")
**getSampleFiles**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TxDB</td>
<td>TxDB</td>
</tr>
<tr>
<td>upstream</td>
<td>upstream from TSS site</td>
</tr>
<tr>
<td>downstream</td>
<td>downstream from TSS site</td>
</tr>
<tr>
<td>by</td>
<td>one of gene or transcript</td>
</tr>
</tbody>
</table>

**Value**

GRanges object

---

**getTagMatrix**

**Description**

calculate the tag matrix

**Usage**

getTagMatrix(peak, weightCol = NULL, windows)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>peak</td>
<td>peak file or GRanges object</td>
</tr>
<tr>
<td>weightCol</td>
<td>column name of weight, default is NULL</td>
</tr>
<tr>
<td>windows</td>
<td>a collection of region with equal size, eg. promoter region.</td>
</tr>
</tbody>
</table>

**Value**

tagMatrix
**Info**

**Information Datasets**

**Description**
- ucsc genome version, precalculated data and gsm information

**Overlap**

**Description**
- calculate the overlap matrix, which is useful for vennplot

**Usage**

```r
overlap(Sets)
```

**Arguments**

- **Sets**
  - a list of objects

**Value**

- data.frame

**Author(s)**

- G Yu

**peakHeatmap**

**Description**
- plot the heatmap of peaks align to flank sequences of TSS

**Usage**

```r
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

---

**Description**

plotAnnoBar method generics

plotAnnoBar method for list of csAnno instances

plotAnnoBar method for csAnno instance

**Usage**

```r
plotAnnoBar(x, xlab = "", ylab = "Percentage(%)", title = "Feature Distribution", ...)
```

```r
## S4 method for signature 'list'
plotAnnoBar(x, xlab = "", ylab = "Percentage(%)", title = "Feature Distribution", ...)
```

```r
plotAnnoBar(x, xlab="", ylab='Percentage(%)',title="Feature Distribution", ...)
```

Arguments

- **x**: csAnno instance
- **xlab**: xlab
- **ylab**: ylab
- **title**: title
- **...**: additional parameter
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 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, ...)
```

Arguments

- `x` csAnno instance
- `ndigit` number of digit to round
- `cex` label cex
- `col` color
- `legend.position` topright or other.
- `pie3D` plot in 3D or not
- `...` extra parameter

Value

plot

Author(s)

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

---

plotAnnoPie.csAnno

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)
```

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tagMatrix</td>
<td>tagMatrix or a list of tagMatrix</td>
</tr>
<tr>
<td>xlim</td>
<td>xlim</td>
</tr>
<tr>
<td>xlab</td>
<td>x label</td>
</tr>
<tr>
<td>ylab</td>
<td>y label</td>
</tr>
<tr>
<td>conf</td>
<td>confidence interval</td>
</tr>
<tr>
<td>facet</td>
<td>one of 'none', 'row' and 'column'</td>
</tr>
<tr>
<td>free_y</td>
<td>if TRUE, y will be scaled by AvgProf</td>
</tr>
<tr>
<td>...</td>
<td>additional parameter</td>
</tr>
</tbody>
</table>

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 = "Read Count Frequency", conf, facet = "none", free_y = TRUE,
            verbose = TRUE, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>peak</td>
<td>peak file or GRanges object</td>
</tr>
<tr>
<td>weightCol</td>
<td>column name of weight</td>
</tr>
<tr>
<td>TxDb</td>
<td>TxDb object</td>
</tr>
<tr>
<td>upstream</td>
<td>upstream position</td>
</tr>
<tr>
<td>downstream</td>
<td>downstream position</td>
</tr>
<tr>
<td>xlab</td>
<td>xlab</td>
</tr>
<tr>
<td>ylab</td>
<td>ylab</td>
</tr>
<tr>
<td>conf</td>
<td>confidence interval</td>
</tr>
<tr>
<td>facet</td>
<td>one of 'none', 'row' and 'column'</td>
</tr>
<tr>
<td>free_y</td>
<td>if TRUE, y will be scaled by AvgProf</td>
</tr>
<tr>
<td>verbose</td>
<td>print message or not</td>
</tr>
<tr>
<td>...</td>
<td>additional parameter</td>
</tr>
</tbody>
</table>
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
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 label
  title     figure title
  categoryColumn category column

Value

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

Author(s)

Guangchuang Yu http://ygc.name

See Also

annotatePeak

Examples

## Not run:
require(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
peakfile <- system.file("extdata", "sample_peaks.txt", package="ChIPseeker")
peakAnno <- annotatePeak(peakfile, TxDb=txdb)
plotDistToTSS(peakAnno)

## End(Not run)
**readPeakFile**

**Description**
read peak file and store in data.frame or GRanges object

**Usage**
readPeakFile(peakfile, as = "GRanges", ...)

**Arguments**
- `peakfile`: peak file
- `as`: output format, one of GRanges or data.frame
- `...`: additional parameter

**Value**
peak information, in GRanges or data.frame object

**Author(s)**
G Yu

**Examples**
peakfile <- system.file("extdata", "sample_peaks.txt", package="ChIPseeker")
peak.gr <- readPeakFile(peakfile, as="GRanges")
peak.gr

**seq2gene**

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

**Usage**
seq2gene(seq, tssRegion, flankDistance, TxDb, sameStrand = FALSE)

**Arguments**
- `seq`: genomic regions in GRanges object
- `tssRegion`: TSS region
- `flankDistance`: flanking search radius
- `TxDb`: TranscriptDb object
- `sameStrand`: logical whether find nearest/overlap gene in the same strand
### show

**Value**  
gene vector

**Author(s)**  
Guangchuang Yu

---

#### Description

show method for csAnno instance

#### Usage

```
show(object)
```

#### Arguments

- **object**  
  A csAnno instance

---

### 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
**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

---

**Description**

upsetplot method generics

**Usage**

`upsetplot(x, ...)`

**Arguments**

- `x`: A csAnno instance
- `...`: additional parameter

**Value**

plot
vennpie

Description
vennpie method generics
vennpie method generics

Usage
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

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 Vennonable
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

Venn plot 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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