Package ‘ChIPseeker’

January 14, 2017

Type Package

Title ChIPseeker for ChIP peak Annotation, Comparison, and Visualization

Version 1.10.3

Author Guangchuang Yu <guangchuangyu@gmail.com> with contributions from Yun Yan, Herve Pages, Michael Kluge and Thomas Schwarzl.

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, 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:

- ChIPseeker-package ......................................................... 3
- annotatePeak .............................................................. 4
- as.data.frame.csAnno ..................................................... 5
- as.GRanges ................................................................. 6
- covplot ....................................................................... 6
- csAnno-class ............................................................... 7
- downloadGEObedFiles ..................................................... 8
- downloadGSMbedFiles ..................................................... 8
- dropAnno ................................................................. 9
- enrichAnnoOverlap ........................................................ 9
- enrichPeakOverlap ....................................................... 10
- getBioRegion ............................................................ 11
- getGeneAnno ............................................................. 11
- getGenomicAnnotation .................................................. 12
- getGEOgenomeVersion .................................................... 12
- getGEOInfo ............................................................... 13
- getGEOspecies ........................................................... 13
- getNearestFeatureIndicesAndDistances ................................ 14
- getPromoters ............................................................. 14
- getSampleFiles .......................................................... 15
- getTagMatrix ............................................................. 15
- info ................................................................. 16
- overlap ................................................................. 16
- peakHeatmap ............................................................ 16
- plotAnnoBar .............................................................. 17
- plotAnnoBar.data.frame .................................................. 18
- plotAnnoPie ............................................................. 19
- plotAnnoPie.csAnno ..................................................... 19
- plotAvgProf .............................................................. 20
- plotAvgProf2 ............................................................. 21
- plotDistToTSS ............................................................ 22
- plotDistToTSS.data.frame .............................................. 23
- readPeakFile ............................................................. 24
- seq2gene ................................................................. 24
- show ................................................................. 25
- shuffle ............................................................... 25
- tagHeatmap ............................................................. 26
- upsetplot .............................................................. 26
- vennpie .............................................................. 27
- vennplot .............................................................. 27
- vennplot.peakfile ...................................................... 28

---

**Index** 29
ChIPseeker-package  

ChIP-SEQ Annotation, Visualization and Comparison

Description
This package is designed for chip-seq data analysis

Details

<table>
<thead>
<tr>
<th>Package:</th>
<th>ChIPseeker</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type:</td>
<td>Package</td>
</tr>
<tr>
<td>Version:</td>
<td>1.5.1</td>
</tr>
<tr>
<td>Date:</td>
<td>27-04-2015</td>
</tr>
<tr>
<td>bioViews:</td>
<td>ChIPSeq, Annotation, Software</td>
</tr>
<tr>
<td>Depends:</td>
<td></td>
</tr>
<tr>
<td>Imports:</td>
<td>methods, ggplot2</td>
</tr>
<tr>
<td>Suggests:</td>
<td>clusterProfiler, GOSemSim</td>
</tr>
<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

```
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-
ported 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 Intergenic.
Description
convert csAnno object to data.frame

Usage
## S3 method for class 'csAnno'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

Arguments
x csAnno object
row.names row names
optional should be omitted.
... additional parameters
as.GRanges

Description
convert csAnno object to GRanges

Usage
as.GRanges(x)

Arguments
x csAnno object

Value
GRanges object

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

covplot

Description
plot peak coverage

Usage
covplot(peak, weightCol = NULL, xlab = "Chromosome Size (bp)", ylab = "", title = "ChIP Peaks over Chromosomes", chrs = NULL, xlim = NULL, lower = 1)
Arguments

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

Value

ggplot2 object

Author(s)

G Yu

---

Class "csAnno" This class represents the output of ChIPseeker Annotation

Slots

- `anno`: annotation
- `tssRegion`: TSS region
- `level`: transcript or gene
- `hasGenomicAnnotation`: logical
- `detailGenomicAnnotation`: Genomic Annotation in detail
- `annoStat`: annotation statistics
- `peakNum`: number of peaks

Author(s)

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

See Also

annotatePeak
downloadGEObedFiles

Description

download all BED files of a particular genome version

Usage

downloadGEObedFiles(genome, destDir = getwd())

Arguments

geno

Author(s)

G Yu

downloadGSMbedFiles

Description

download BED supplementary files of a list of GSM accession numbers

Usage

downloadGSMbedFiles(GSM, destDir = getwd())

Arguments

GSM

destDir

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**

calculates 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`: TxB
- `pAdjustMethod`: p-value adjustment method
- `chainFile`: chain file for liftOver
- `distanceToTSS_cutoff`: restrict nearest gene annotation by distance cutoff
enrichPeakOverlap

Value
data.frame

Author(s)
G Yu

Description
calculate overlap significant of ChIP experiments based on the genome coordinations

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

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

Value
data.frame

Author(s)
G Yu
getBioRegion

**Description**
prepare a region center on start site of selected feature

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

**Arguments**
- **TxDb**: TxDb
- **upstream**: upstream from start site
- **downstream**: downstream from start site
- **by**: one of 'gene', 'transcript', 'exon', 'intron'

**Value**
GRanges object

**Author(s)**
Guangchuang Yu

getGeneAnno

**Description**
get gene annotation, symbol, gene name etc.

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

**Arguments**
- **annoDb**: annotation package
- **geneID**: query geneID
- **type**: gene ID type

**Value**
data.frame

**Author(s)**
G Yu
getGenomicAnnotation

Description
get Genomic Annotation of peaks

Usage
getGenomicAnnotation(peaks, distance, tssRegion = c(-3000, 3000), TxDb, level,
genomicAnnotationPriority, sameStrand = FALSE)

Arguments
peaks peaks in GRanges object
distance distance of peak to TSS
tssRegion tssRegion, default is -3kb to +3kb
TxDb TxDb object
level one of gene or transcript
genomicAnnotationPriority genomic Annotation Priority
sameStrand whether annotate gene in same strand

Value
character vector

Author(s)
G Yu

getGEOgenomeVersion

Description
get genome version statistics collecting from GEO ChIPseq data

Usage
getGEOgenomeVersion()

Value
data.frame

Author(s)
G Yu
getGEOInfo

Description
get subset of GEO information by genome version keyword

Usage
getGEOInfo(genome, simplify = TRUE)

Arguments
- genome: genome version
- simplify: simplify result or not

Value
data.frame

Author(s)
G Yu

getGEOspecies

Description
accessing species statistics collecting from GEO database

Usage
getGEOspecies()

Value
data.frame

Author(s)
G Yu
getNearestFeatureIndicesAndDistances

Description

get index of features that closest to peak and calculate distance

Usage

getNearestFeatureIndicesAndDistances(peaks, features, sameStrand = FALSE, ignoreOverlap = FALSE, ignoreUpstream = FALSE, ignoreDownstream = FALSE, overlap = "TSS")

Arguments

- **peaks**: peak in GRanges
- **features**: features in GRanges
- **sameStrand**: logical, whether find nearest gene in the same strand
- **ignoreOverlap**: logical, whether ignore overlap of TSS with peak
- **ignoreUpstream**: logical, if True only annotate gene at the 3' of the peak.
- **ignoreDownstream**: logical, if True only annotate gene at the 5' of the peak.
- **overlap**: one of "TSS" or "all"

Value

list

Author(s)

G Yu

getPromoters

Description

prepare the promoter regions

Usage

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

**Arguments**
- **TxDb**
  - upstream
  - downstream
  - by

**Value**
- GRanges object

**Description**
get filenames of sample files

**Usage**
getSampleFiles()

**Value**
list of file names

**Author(s)**
G Yu

**getTagMatrix**

**Description**
calculate the tag matrix

**Usage**
getTagMatrix(peak, weightCol = NULL, windows)

**Arguments**
- **peak**
- **weightCol**
- **windows**

**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**

`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**

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

```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

- `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 = "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
Value

ggplot object

Author(s)

G Yu

plotDistToTSS

plotDistToTSS method generics

Description

plotDistToTSS method generics
plotDistToTSS method for list of csAnno instances
plotDistToTSS method for csAnno instance

Usage

plotDistToTSS(x, distanceColumn = "distanceToTSS", xlab = ",
ylab = "Binding sites (%) (5'->3')",
title = "Distribution of transcription factor-binding loci relative to TSS",
...)

## S4 method for signature 'list'
plotDistToTSS(x, distanceColumn = "distanceToTSS",
  xlab = ", ylab = "Binding sites (%) (5'->3')",
title = "Distribution of transcription factor-binding loci relative to TSS",
...)

plotDistToTSS(x,distanceColumn="distanceToTSS", xlab="",
ylab="Binding sites (%) (5'->3')",
title="Distribution of transcription factor-binding loci relative to TSS",...)
Description

plot feature distribution based on the distances to the TSS

Usage

plotDistToTSS.data.frame(peakDist, distanceColumn = "distanceToTSS",
                           xlab = "", ylab = "Binding sites (%) (5'->3')",
                           title = "Distribution of transcription factor-binding loci relative to TSS",
                           categoryColumn)

Arguments

peakDist    peak annotation
distanceColumn column name of the distance from peak to nearest gene
xlab        x label
ylab        y label
title       figure title
categoryColumn category column

Value

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

Author(s)

Guangchuang Yu http://ygc.name

See Also

annotatePeak

Examples

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

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

**Description**

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

**Usage**

```r
readPeakFile(peakfile, as = "GRanges", ...)
```

**Arguments**

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

**Value**

peak information, in GRanges or data.frame object

**Author(s)**

G Yu

**Examples**

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

---

**seq2gene**

**Description**

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

**Usage**

```r
seq2gene(seq, tssRegion, flankDistance, TxDb, sameStrand = FALSE)
```

**Arguments**

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

**Value**

gene vector

**Author(s)**

Guangchuang Yu

---

**Description**

show method for csAnno instance

**Usage**

`show(object)`

**Arguments**

- `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

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

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
Index

*Topic classes
  csAnno-class, 7

*Topic datasets
  info, 16

*Topic package
  ChIPseeker-package, 3
  ... 3

annotatePeak, 4, 7, 18, 20, 23
as.data.frame.csAnno, 5
as.GRanges, 6

ChIPseeker (ChIPseeker-package), 3
ChIPseeker-package, 3
coyplot, 6
csvAnno-class, 7

downloadGEObedFiles, 8
downloadGSMbedFiles, 8
dropAnno, 9

enrichAnnoOverlap, 9
enrichPeakOverlap, 10

getBioRegion, 11
getGeneAnno, 11
getGenomicAnnotation, 12
getGEObiogemVersion, 12
getGEOinfo, 13
getGEOspecies, 13
getNearestFeatureIndicesAndDistances, 14
getPromoters, 14
getSampleFiles, 15
getTagMatrix, 15
gsminfo (info), 16

info, 16

mclapply, 10

overlap, 16

peakHeatmap, 16
plotAnnoBar, 5, 17, 20

plotAnnoBar.csAnno, ANY-method
  (plotAnnoBar), 17
plotAnnoBar.csAnno-method
  (csAnno-class), 7
plotAnnoBar.list-method (plotAnnoBar), 17
plotAnnoBar.data.frame, 18
plotAnnoPie, 5, 18, 19
plotAnnoPie.csAnno, ANY-method
  (plotAnnoPie), 19
plotAnnoPie.csAnno-method
  (csAnno-class), 7
plotAnnoPie.csAnno, 19
plotAvgProf, 20
plotAvgProf2, 21
plotDistToTSS, 5, 22
plotDistToTSS.csAnno, ANY-method
  (plotDistToTSS), 22
plotDistToTSS.csAnno-method
  (csAnno-class), 7
plotDistToTSS.list-method
  (plotDistToTSS), 22
plotDistToTSS.data.frame, 23

readPeakFile, 24

seq2gene, 24
show, 25
show, csAnno, ANY-method (show), 25
show, csAnno-method (csAnno-class), 7
shuffle, 25

tagHeatmap, 26
tagMatrixList (info), 16

ucsc_release (info), 16
upsetplot, 26
upsetplot.csAnno-method (csAnno-class), 7

vennipie, 27
vennipie.csAnno-method (csAnno-class), 7
vennplot, 27
vennplot.peakfile, 28