Package 'epiSeeker'

November 17, 2026

Type Package

Title epiSeeker: an R package for Annotation, Comparison and Visualization of multi-omics epigenetic data

Version 1.1.5

Description This package implements functions to analyze multi-omics epigenetic data.
Data of fragment type and base type are supported by epiSeeker.
It provides functions to retrieve the nearest genes around the peak, annotate genomic region of the peak,
statistical methods to estimate the significance of overlap among peak data sets, and motif analysis.
It incorporates the GEO database for users to compare their own dataset with those deposited in the 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, overlap of peaks or genes, and the single-base resolution epigenetic data by considering the strand, motif, and additional information.

Depends R (>= 4.6.0)

Imports AnnotationDbi, aplot, bsseq, BiocGenerics, Biostrings, boot, dplyr, enrichplot, IRanges, GenomeInfoDb, GenomicRanges, GenomicFeatures, ggplot2, graphics, grDevices, magrittr, methods, plotrix, parallel, RColorBrewer, rlang, RSQLite, rtracklayer, S4Vectors, scales, stats, SummarizedExperiment, tibble, tidyselect, tidyr, utils, yulab.utils (>= 0.2.0), grid

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`epiSeeker-package` *epiSeeker: epiSeeker: an R package for Annotation, Comparison and Visualization of multi-omics epigenetic data*

Description

This package implements functions to analyze multi-omics epigenetic data. Data of fragment type and base type are supported by epiSeeker. It provides functions to retrieve the nearest genes around the peak, annotate genomic region of the peak, statistical methods to estimate the significance of overlap among peak data sets, and motif analysis. It incorporates the GEO database for users to compare their own dataset with those deposited in the 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, overlap of peaks or genes, and the single-base resolution epigenetic data by considering the strand, motif, and additional information.

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See Also

Useful links:

- https://github.com/YuLab-SMU/epiSeeker
- Report bugs at https://github.com/YuLab-SMU/epiSeeker/issues

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. .

Description

capture name of variable

Usage

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

Arguments

...	expression
.env	environment

Value

expression

Examples

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

.epiSeekerEnv *Env function for epiSeeker*

Description

Env function for epiSeeker

Usage

```
.epiSeekerEnv(TxDb, item = "epiSeekerEnv", force = FALSE)
```

Arguments

TxDb	TxDb object
item	item name
force	force to update txdb item in cache or not.

Value

Returns ‘invisible(NULL)‘ invisibly. The primary purpose of this function is to manage the TXDB cache through side effects (creating, updating, or removing cached objects), rather than returning a value.

annotateSeq *annotateSeq*

Description

Annotate peaks

Usage

```
annotateSeq(
  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,
  columns = c("ENTREZID", "ENSEMBL", "SYMBOL", "GENENAME")
)
```

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. The resulting ‘flank_gene_distances‘ column reports 0 when the peak overlaps the feature range (at ‘level = "transcript"‘ this is the whole transcript, so peaks inside a transcript body get 0) and the signed distance to the feature TSS otherwise.
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
columns	names of columns to be obtained from database

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 Intergenic.

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 addFlankGeneInfo is TRUE, extra columns will be included:

flank_geneIds: semicolon-separated gene IDs within 'flankDistance' of the peak

flank_gene_distances: semicolon-separated distances of these genes. A value of 0 means that the peak overlaps the feature range: at level = "transcript" the feature is the whole transcript, so peaks inside a transcript body always get 0 regardless of their distance to the TSS. For non-overlapping features the signed distance to the feature TSS is reported. See https://github.com/YuLab-SMU/ChIPseeker/issues/235

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

```
data(peakAnno)
peakAnno
```

arrange.GRanges *Arrange GRanges object*

Description

Arrange GRanges object

Usage

```
## S3 method for class 'GRanges'
arrange(.data, ..., .by_group = FALSE)
```

Arguments

.data	granges object
...	additional parameters
.by_group	If TRUE, will sort first by grouping variable. Applies to grouped data frames only.

Value

grange object

Examples

```
peakfile <- system.file("extdata", "sample_peaks.txt", package = "epiSeeker")
peak <- readPeakFile(peakfile)
dplyr::arrange(peak, seqnames)
```

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>

Examples

```
data(peakAnno)
as.GRanges(peakAnno)
```

---

bin_vector *bin vector function*

Description

bin vector function

Usage

```
bin_vector(vec, nbin = 800)
```

Arguments

vec	vector.
nbin	number of bin.

Value

bin list

`bmData` *Constructor for bmData objects*

Description

This is constructor fo bmData objects.

Usage

```
bmData(
  value1 = NULL,
  value2 = NULL,
  pos = NULL,
  chr = NULL,
  gr = NULL,
  sampleNames = NULL,
  valueNames = NULL,
  ...
)
```

Arguments

`value1`	the first value to be stored, a matrix-like object
`value2`	the second value to be stored, a matrix-like object
`pos`	A vector of locations
`chr`	A vector of chromosomes
`gr`	An object of type [GenomicRanges::GRanges]
`sampleNames`	A vector of sample names
`valueNames`	the name of value1 or value2 or both. The order maps to the value.
`...`	other parameters from [bsseq::BSseq]

Value

bmData object

Examples

```
data(demo_bmdata)
```

bmData-class *bmData Class*

Description

This class added extra data to [bsseq::BSseq-class]. Change the assays by storing M/Cov to any value1/2

Value

bmData object

See Also

bmData class inherits [SummarizedExperiment::RangedSummarizedExperiment-class], other slots see [SummarizedExperiment::RangedSummarizedExperiment]

check_bin *check bin parameter method*

Description

check bin parameter method

Usage

```
check_bin(nbin, windows, verbose)
```

Arguments

nbin	numbers of bin.
windows	a list of region in granges.
verbose	show details or not

Value

message or nothing

check_extension *check upstream and downstream extension*

Description

check upstream and downstream extension

Usage

```
check_extension(upstream, downstream, type)
```

Arguments

upstream	upstream extension. One of actual number or rel() object.
downstream	downstream extension. One of actual number or rel() object.
type	one of "start_site", "end_site", "body".

Value

message or null

check_windows *check windows function*

Description

check windows function

Usage

```
check_windows(windows)
```

Arguments

windows	windows

Value

message or null

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

Examples

```
data(peakAnno)
combine_csAnno(peakAnno, peakAnno)
```

---

create_regex_patterns_negative
create regex patterns in negative strand

Description

create regex patterns in negative strand

Usage

```
create_regex_patterns_negative(motif)
```

Arguments

motif	the motif(e.g C:CG/CH, A:GAGG/AGG) of the base modification

Value

regex pattern

create_regex_patterns_positive *create regex patterns in positive strand*

Description

create regex patterns in positive strand

Usage

```
create_regex_patterns_positive(motif)
```

Arguments

motif	the motif(e.g C:CG/CH, A:GAGG/AGG) of the base modification

Value

regex pattern

csAnno-class *Class "csAnno" This class represents the output of epiSeeker Annotation*

Description

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

Value

annotation object

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

[annotateSeq()]

demo_bmdata *demo base modification data*

Description

A small example bmData object representing cytosine methylation measurements from Bisulfite-Seq data. This dataset is intended for demonstrating base-modification visualization, regional methylation profiling, and epiSeeker workflows operating on bmData objects. See data-raw/example_data.R

Format

A bmData object containing one sample.

Value

bmData object

Provenance

The example dataset was constructed from publicly available Bisulfite-Seq data (GEO accession: GSM6940395, genome build: hg38). The raw methylation coverage file (*.bismark.cov.gz) was imported using **data.table::fread()**.

A small genomic window on chromosome 22 ([10525991, 10526342]) was selected to create a lightweight example dataset. The data were processed as follows:

1. Filter records where chrom == 22 and positions fall within the chosen window.
2. Convert chromosome name to UCSC style ("chr22").
3. Compute total coverage as: Cov = methylated + unmethylated.
4. Extract columns: chromosome, position, coverage, and methylation percentage.
5. Convert methylation percentage to a fraction.

Data structure

A bmData S4 object containing one sample ("acinar_methyl"). Each entry stores:

chr Chromosome in UCSC format (e.g. "chr22").

pos Genomic coordinate of the cytosine.

Cov Total read coverage at the site.

Methylation Methylation level as a fraction (0–1).

demo_peak *demo peak file*

Description

Peak in Grange object. See data-raw/example_data.R

Format

A GRanges object with 200 rows and 5 metadata columns.

Value

Grange object

Provenance

The demo peaks were extracted from GSM6418464 in the GEO database (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM6418464).

Data structure

A GRanges object with 220 genomic ranges and the following metadata columns:

seqnames chr name

ranges Peak ranges

strand strand information

mcol output from MACS2

---

downloadGEObedFiles *downloadGEObedFiles*

Description

Download all BED files of a particular genome version

Usage

```
downloadGEObedFiles(genome, destDir = getwd())
```

Arguments

genome	genome version
destDir	destination folder

Value

GEO files

Author(s)

G Yu

Examples

```
gse <- "GSE11431"
```

`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

Value

GEO data

Author(s)

G Yu

Examples

```
gsm <- "GSM288348"
```

`dropAnno` *dropAnno*

Description

dropAnno

Usage

```
dropAnno(csAnno, distanceToTSS_cutoff = 10000)
```

Arguments

`csAnno`	output of annotateSeq
`distanceToTSS_cutoff`	distance to TSS cutoff

Details

drop annotation exceeding distanceToTSS_cutoff

Value

csAnno object

Author(s)

Guangchuang Yu

Examples

```
data(peakAnno)
dropAnno(peakAnno)
```

`enrichAnnoOverlap` *enrichAnnoOverlap*

Description

Calculate overlap significance 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

Details

'N_OL' counts overlapping *genes*, not peaks, so it can be larger than the number of input peaks: a peak is annotated to its nearest gene, but the same gene is reported once per peak and a peak region may overlap several target genes (see issue #84 of ChIPseeker).

Value

data.frame

Author(s)

G Yu

Examples

```
if (interactive()) {
    require(TxDb.Hsapiens.UCSC.hg38.knownGene)
    txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
    peakfile <- system.file("extdata", "demo_peak.txt", package = "epiSeeker")
    enrichAnnoOverlap(peakfile, peakfile, txdb)
}
```

`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,
  symmetric = FALSE
)
```

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

symmetric — logical, whether the p-value should be direction free. Default is FALSE, which reports the one-sided test described above. If TRUE, the mirrored direction (query and target exchanged) is computed as well and the two are combined as ‘min(1, 2*min(p, p_rev))‘ (Hedges), so that the result does not depend on the order of the arguments. Note that this doubles the number of permutations and that the smallest reportable p-value becomes ‘2/(nShuffle+1)‘; use a larger ‘nShuffle‘ and ‘set.seed()‘ for a reproducible result (issue #84 of ChIPseeker)

Details

The observed quantity is the fraction of *target* peaks covered by the query peaks (‘N_OL / length(targetPeak)‘) and the null distribution is generated by shuffling the *target* peaks, i.e. the test answers "are the query peaks enriched within the target peaks?". ‘N_OL‘ itself is symmetric (the same number is reported in both directions), but the p-value is not: exchanging ‘queryPeak‘ and ‘targetPeak‘ asks the mirrored question and normalises by the other peak set, so the p-values can differ substantially when the two peak sets differ in size. Even for equally sized sets the two null distributions are sampled independently, which leaves small Monte-Carlo differences (see issue #84 of ChIPseeker). Compare ‘N_OL‘ directly if a direction-free measure is needed, and increase ‘nShuffle‘ to reduce the Monte-Carlo part.

Value

data.frame

Author(s)

G Yu

Examples

```
require(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
peakfile <- system.file("extdata", "demo_peak.txt", package = "epiSeeker")
peak <- readPeakFile(peakfile)[1:10]
enrichPeakOverlap(peak, peakfile, txdb, mc.cores = 1, nShuffle = 20)
```

---

epiSeekerCache *Name of the epiSeeker cache environment (internal static variable)*

Description

Name of the epiSeeker cache environment (internal static variable)

Usage

```
epiSeekerCache
```

Format

character vector

extend_gr *Extend regions functions*

Description

Extend regions functions

Usage

```
extend_gr(regions, upstream, downstream, by, type)
```

Arguments

regions	GRanges object
upstream	upstream extension. One of actual number or rel() object.
downstream	downstream extension. One of actual number or rel() object.
by	one of 'gene', 'transcript', 'exon', 'intron' , '3UTR' , '5UTR', 'UTR'.
type	one of "start_site", "end_site", "body".

Value

GRanges object

filter.GRanges *Extend filter to Peak (GRanges class object)*

Description

Extend filter to Peak (GRanges class object)

Usage

```
## S3 method for class 'GRanges'
filter(.data, ..., .by = NULL, .preserve = FALSE)
```

Arguments

.data	granges object
...	additional parameters
.by	Optional grouping variable(s) (column name or variable expression) specifying which columns to group by when applying filters
.preserve	Logical value indicating whether to preserve the original grouping structure when .by is specified. If TRUE, group order and identities are maintained

Value

A filtered GRanges object containing only rows that meet the specified criteria

grange object

Examples

```
peakfile <- system.file("extdata", "sample_peaks.txt", package = "epiSeeker")
peak <- readPeakFile(peakfile)
dplyr::filter(peak, fold_enrichment > 20)
```

`getAnnoStat` *getAnnoStat*

Description

getting status of annotation

Usage

```
getAnnoStat(x)
```

Arguments

x	csAnno object

Value

data frame

Examples

```
data(peakAnno)
getAnnoStat(peakAnno)
```

`getBioRegion` *Prepare a bioregion of selected feature*

Description

Prepare a bioregion of selected feature

Usage

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

Arguments

TxDb	TxDb object or self-made granges object.
upstream	upstream extension. One of actual number or rel() object.
downstream	downstream extension. One of actual number or rel() object.
by	one of 'gene', 'transcript', 'exon', 'intron' , '3UTR' , '5UTR', 'UTR'.
type	one of "start_site", "end_site", "body".

Details

this function combined previous functions getPromoters(), getBioRegion() and getGeneBody() in order to solve the following issues.

(1) <https://github.com/GuangchuangYu/ChIPseeker/issues/16>

(2) <https://github.com/GuangchuangYu/ChIPseeker/issues/87>

1. function can provide a region of interest from txdb object. 2. function can make region from granges object. txdb object do not contain insulator or enhancer regions. Users can provide these regions through self-made granges object https://github.com/YuLab-SMU/ChIPseeker/issues/189.

There are three kinds of way to extend regions: start_site, end_site and body. We take transcript region to expain the differences of these three regions (tx: chr1 1000 1400).

(1) body region refers to the 1000 ~ 1400 bp.

(2) start_site region with (upstream = upstream = 100) refers to 900-1100bp.

(3) end_site region with (upstream = upstream = 100) refers to 1300-1500bp.

Value

GRanges object

Author(s)

Guangchuang Yu

Examples

```
require(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
getBioRegion(txdb)
```

---

getBmMatrix *getBmMatrix methods generics*

Description

getBmMatrix method for [bsseq::BSseq]

getBmMatrix method for bmData

Usage

```
getBmMatrix(
  region,
  input,
  BSgenome,
  base = NULL,
  motif = NULL,
  position_bias = NULL,
  ...
)

## S4 method for signature 'ANY,BSseq'
getBmMatrix(
  region,
  input,
  BSgenome,
  base = NULL,
  motif = NULL,
  position_bias = NULL,
  cover_depth = TRUE,
  ...
)

## S4 method for signature 'ANY,bmData'
getBmMatrix(
  region,
  input,
  BSgenome,
  base = NULL,
  motif = NULL,
  position_bias = NULL,
  ...
)
```

Arguments

region	base modification region in the form of dataframe, having columns of "chr","start" and "end"
input	the input data stored in BSseq objects or BSseqExtra objects
BSgenome	genome reference
base	one of A/T/G/C/U
motif	the motif(e.g C:CG/CH, A:GAGG/AGG) of the base modification
position_bias	1-base bias. e.g position_bias = 1("C" in "CHH"), position_bias = 2("A" in "GAGG")
...	other parameters
cover_depth	take the depth of cover into account or not

Value

data.frame

dataframe

Examples

```
require(BSgenome.Hsapiens.UCSC.hg38)
data(demo_bmdata)
bmMatrix <- getBmMatrix(
    region = data.frame(chr = "chr22", start = 10525991, end = 10526342),
    BSgenome = BSgenome.Hsapiens.UCSC.hg38,
    input = demo_bmdata,
    base = "C",
    motif = c("CG")
)
```

`getBmMatrix.bmData` *get the information of base modification*

Description

get the information of base modification

Usage

```
getBmMatrix.bmData(
  region,
  input,
  BSgenome,
  base = NULL,
  motif = NULL,
  position_bias = NULL
)
```

Arguments

`region`	base modification region in the form of dataframe, having columns of "chr","start" and "end"
`input`	the input data stored in bmData objects
`BSgenome`	genome reference
`base`	one of A/T/G/C/U
`motif`	the motif(e.g C:CG/CH, A:GAGG/AGG) of the base modification
`position_bias`	1-base bias. e.g position_bias = 1("C" in "CHH"), position_bias = 2("A" in "GAGG")

Details

This function retrieve the information of each base, requiring bmData object as input. Then organized it to dataframe.

Value

dataframe

`getBmMatrix.BSseq` *Get the information of base modification*

Description

Get the information of base modification

Usage

```
getBmMatrix.BSseq(
  region,
  input,
  BSgenome,
  cover_depth = TRUE,
  base = NULL,
  motif = NULL,
  position_bias = NULL
)
```

Arguments

`region`	base modification region in the form of data.frame, having columns of "chr","start" and "end"
`input`	the input data stored in [bsseq::BSseq] objects
`BSgenome`	genome reference
`cover_depth`	take the depth of cover into account or not
`base`	one of A/T/G/C/U
`motif`	the motif(e.g C:CG/CH, A:GAGG/AGG) of the base modification
`position_bias`	1-base bias. e.g position_bias = 1("C" in "CHH"), position_bias = 2("A" in "GAGG")

Details

This function retrieve the information of each base, requiring [bsseq::BSseq] object as input. Then organized it to data.frame.

Value

data.frame

getGeneAnno *getGeneAnno*

Description

Get gene annotation, symbol, gene name etc.

Usage

```
getGeneAnno(annoDb, geneID, type, columns)
```

Arguments

annoDb	annotation package
geneID	query geneID
type	gene ID type
columns	names of columns to be obtained from database

Value

data.frame

Author(s)

G Yu

getGenomicAnnotation *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 *getGEOgenomeVersion*

Description

Get genome version statistics collecting from GEO ChIPseq data

Usage

```
getGEOgenomeVersion()
```

Value

data.frame

Author(s)

G Yu

Examples

```
getGEOgenomeVersion()
```

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

Examples

```
hg19 <- getGEOInfo(genome = "hg19", simplify = TRUE)
```

getGEOspecies *getGEOspecies*

Description

Accessing species statistics collecting from GEO database

Usage

```
getGEOspecies()
```

Value

data.frame

Author(s)

G Yu

Examples

```
getGEOspecies()
```

`getMotifMatrix` *Get the information of motif in a range*

Description

Get the information of motif in a range

Usage

```
getMotifMatrix(region, pwm, ref_obj, by = "name")
```

Arguments

`region`	region object in granges.
`pwm`	PFMatrixList.
`ref_obj`	seq reference object. e.g. BSgenome object.
`by`	show the motif by name or ID.

Value

score matrix

Examples

```
require(BSgenome.Hsapiens.UCSC.hg38)
data(pwm_obj)

region_oi <- GRanges(
    seqnames = "chr22",
    ranges = IRanges(start = 10525891, end = 10525991)
)
motifMatrix <- getMotifMatrix(
    region = region_oi,
    pwm = pwm_obj[c(45, 120, 170)],
    ref_obj = BSgenome.Hsapiens.UCSC.hg38
)
```

`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, both when finding the nearest feature and when detecting overlaps with it. Peaks with ambiguous strand ('*') are compatible with features on any 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 *Get promoter region in GRanges format*

Description

Get promoter region in GRanges format

Usage

```
getPromoters(TxDb = NULL, upstream = 1000, downstream = 1000, by = "gene")
```

Arguments

TxDb	TxDb object
upstream	upstream extension. One of actual number or rel() object.
downstream	downstream extension. One of actual number or rel() object.
by	one of 'gene', 'transcript'.

Value

GRanges object

Author(s)

Guangchuang Yu

Examples

```
require(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
promoters <- getPromoters(TxDb = txdb, upstream = 1000, downstream = 1000)
```

---

getSampleFiles *getSampleFiles*

Description

get filenames of sample files

Usage

```
getSampleFiles()
```

Value

list of file names

Author(s)

G Yu

Examples

```
files <- getSampleFiles()
```

---

getTagMatrix *getTagMatrix*

Description

getTagMatrix

Usage

```
getTagMatrix(
  peak,
  upstream = 0,
  downstream = 0,
  windows = NULL,
  type = NULL,
  by = NULL,
  TxDb = NULL,
  weightCol = NULL,
  nbin = NULL,
  verbose = TRUE,
  ignore_strand = FALSE
)
```

Arguments

peak	(1) a peak file or GRanges object. (2) a list of peak file or GRanges object.
upstream	upstream extension. One of actual number or rel() object.
downstream	downstream extension. One of actual number or rel() object.
windows	a collection of region
type	one of "start_site", "end_site", "body"
by	one of 'gene', 'transcript', 'exon', 'intron', '3UTR' , '5UTR', or specified by users
TxDb	TxDb or self-made granges object, served as txdb
weightCol	column name of weight, default is NULL.This column acts as a weight vaule. Details see https://github.com/YuLab-SMU/ChIPseeker/issues/15
nbin	the amount of nbines. Calculate the tagMatrix by binning method. Idea is derived from the function of deeptools(https://deeptools.readthedocs.io/en/develop/content/tools/compu
verbose	print message or not
ignore_strand	ignore the strand information or not

Details

getTagMatrix() function can produce the matrix for visualization. Matrix represents the peak count in a windows and there are two ways to specify the 'windows':

(1) use getPromoters and getBioRegion to get 'windows' and put it into windows parameter in getTagMatrix().

(2) use getTagMatrix() to call getPromoters()/getBioRegion(). In this way users do not need to input 'windows' parameter but need to input 'TxDb' parameter. 'TxDb' can accept a set of packages contained annotation of regions of different genomes(e.g. TxDb.Hsapiens.UCSC.hg38.knownGene). Users can get the regions of interest through specific functions. These specific functions are built in getPromoters()/getBioRegion().

However, many regions can not be gain through txdb(e.g. insulator and enhancer regions), Users can provide these regions in the form of granges object. These self-made granges object will be passed to 'TxDb' and they will be passed to makeBioRegionFromGranges() to produce the 'windows'.

In a word, 'TxDb' parameter getTagMatrix() is a reference information. Users can pass txdb object or self-made granges into it.

Value

tagMatrix

Author(s)

G Yu

Examples

```
if (interactive()) {
    require(TxDb.Hsapiens.UCSC.hg38.knownGene)
    txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
    data(demo_peak)
    tagMatrix <- getTagMatrix(demo_peak,
        type = "start_site", by = "gene",
        upstream = 500, downstream = 500,
        TxDb = txdb, weightCol = "V7"
    )
}
```

---

getTagMatrix.internal *getTagMatrix internal function*

Description

getTagMatrix internal function

Usage

```
getTagMatrix.internal(
  peak,
  upstream = 0,
  downstream = 0,
  windows = NULL,
  type = NULL,
  by = NULL,
  TxDb = NULL,
  weightCol = NULL,
  nbin = NULL,
  verbose = TRUE,
  ignore_strand = FALSE
)
```

Arguments

peak	peak file or GRanges object
upstream	upstream extension. One of actual number or rel() object.
downstream	downstream extension. One of actual number or rel() object.
windows	a collection of region
type	one of "start_site", "end_site", "body"

by	one of 'gene', 'transcript', 'exon', 'intron', '3UTR' , '5UTR', or specified by users
TxDb	TxDb or self-made granges object, served as txdb
weightCol	column name of weight, default is NULL.
nbin	the amount of nbines.
verbose	print message or not
ignore_strand	ignore the strand information or not

Value

matrix

`getTagMatrix_body` *getTagMatrix function for region of body*

Description

getTagMatrix function for region of body

Usage

```
getTagMatrix_body(
  peak.cov,
  windows,
  nbin,
  verbose = TRUE,
  ignore_strand = FALSE
)
```

Arguments

peak.cov	peak coverage.
windows	a collection of region.
nbin	the amount of nbines
verbose	print message or not
ignore_strand	ignore the strand information or not

Value

tagMatrix

getTagMatrix_body_internal *get tagmatrix internal function*

Description

get tagmatrix internal function

Usage

```
getTagMatrix_body_internal(peak.cov, windows, nbin, chr.idx)
```

Arguments

peak.cov	peak coverage.
windows	a collection of region.
nbin	the amount of nbines.
chr.idx	idx of chr.

Value

matrix

getTagMatrix_site *getTagMatrix function for region of site*

Description

getTagMatrix function for region of site

Usage

```
getTagMatrix_site(
  peak.cov,
  windows,
  chr.idx,
  nbin = NULL,
  verbose = TRUE,
  ignore_strand = FALSE
)
```

Arguments

peak.cov	peak coverage.
windows	a collection of region.
chr.idx	idx of chr.
nbin	the amount of nbines
verbose	print message or not
ignore_strand	ignore the strand information or not

Value

tagMatrix

`grange2mt` *change a list grange object to matrix*

Description

change a list grange object to matrix

Usage

```
grange2mt(gr_list, weightCol = NULL)
```

Arguments

`gr_list`	grange list object
`weightCol`	weight column of peak.

Value

matrix

Examples

```
data(demo_peak)
grange2mt(list(a = demo_peak, b = demo_peak), "V5")
```

`gsminfo` *Information Datasets*

Description

ucsc genome version, precalculated data and gsm information

Format

A data frame with ‘n‘ rows (GSM samples) and 14 columns.

Value

data frame

Provenance

The ‘gsminfo‘ dataset was constructed programmatically from public resources in the NCBI GEO and UCSC Genome Browser databases. The data generation pipeline is implemented in ‘data-raw/‘ (see ‘prepareGSMInfo()‘ in the package source).

Briefly, GEO metadata were retrieved using the ‘GEOmetadb‘ SQLite database and ‘GEOquery‘. The latest GEOmetadb SQLite file was downloaded via ‘getSQLiteFile()‘ or, if unavailable, directly from <http://starbuck1.s3.amazonaws.com/sradb/GEOmetadb.sqlite.gz>. Platform (GPL) records were queried to identify platforms associated with high-throughput sequencing experiments. For each sequencing platform, the corresponding GSM records were obtained using ‘Meta(getGEO())‘. Supplementary BED-like files for each GSM were collected using ‘getGSMsuppFile()‘ and ‘batchGetGSMsuppFile()‘.

Additional metadata fields (title, organism, extract protocol, characteristics, data processing description, submission date, and supplementary file URLs) were extracted from GSM SOFT files downloaded using ‘GEOquery‘. Genome assembly versions for each GSM were inferred using the function ‘getGenomicVersion()‘, which matches UCSC genome labels to either the data processing description or the supplementary file names, using the reference table provided in the internal dataset ‘ucsc_release‘.

PubMed IDs associated with each GEO series (GSE) were obtained from the ‘gse‘ table in GEOmetadb. All GSM-level metadata were merged, cleaned, and converted to ASCII using ‘iconv()‘ to remove non-ASCII characters.

Finally, newly processed GSM entries were appended to any preexisting ‘gsminfo‘ object stored in the package, deduplicated, and saved as ‘gsminfo.rda‘ with ‘compress="xz"‘.

Thus, ‘gsminfo‘ represents a curated, reproducibly constructed metadata table summarizing GEO high-throughput sequencing samples, including organism, platform, experimental descriptions, processing information, genome versions, supplementary BED file locations, and associated PubMed IDs.

Data structure

A data frame with one row per GSM sample and the following columns:

‘series_id‘ GEO series accession (GSE).

‘gsm‘ GEO sample accession (GSM).

‘gpl‘ GEO platform accession (GPL).

‘organism‘ Organism name (e.g., *Mus musculus*).

‘title‘ Sample title as provided in GEO.

‘characteristics‘ Experiment-specific metadata such as cell type, treatment, or antibody.

‘source_name‘ Source material for sequencing, typically cell or tissue type.

‘extract_protocol‘ Detailed wet-lab protocol for chromatin extraction, immunoprecipitation, and library preparation as reported in GEO.

‘description‘ Antibody information or additional sample description.

‘data_processing‘ Bioinformatics processing description including aligner, genome build, peak calling method, and filtering steps.

‘submission_date‘ Date when the sample was submitted to GEO.

‘supplementary_file‘ URL to supplementary processed files (e.g., BED).

‘genomeVersion‘ Genome assembly used in the processed data (e.g., mm8, hg19).

‘pubmed_id‘ PMID of the reference publication associated with the dataset.

loadTxDb *load defaulst txdb*

Description

load defaulst txdb

Usage

```
loadTxDb(TxDb)
```

Arguments

TxDb	txdb.

Value

txdb object

makeBmDataFromData *makeBmDataFromData method generics*

Description

makeBmDataFromData method generics

makeBmDataFromData method for ‘CompressedGRangesList‘ objects

makeBmDataFromData method for ‘GRanges‘ objects

makeBmDataFromData method for ‘list‘ objects

makeBmDataFromData method for `data.frame` objects

Usage

```
makeBmDataFromData(data, sampleNames = NULL)

## S4 method for signature 'CompressedGRangesList'
makeBmDataFromData(data, sampleNames = NULL)

## S4 method for signature 'GRanges'
makeBmDataFromData(data, sampleNames = NULL)

## S4 method for signature 'list'
makeBmDataFromData(data, sampleNames = NULL)

## S4 method for signature 'data.frame'
makeBmDataFromData(data, sampleNames = NULL)
```

Arguments

data	lists object
sampleNames	the name of each samples

Details

The objects in ‘data‘ must have specific forms. Colunms should be features, which should be organized in the order of "chr", "pos", "value1", "value2(optional)". chr stands for chromosome. pos stands for position on chromosome, also known as coordinates. value1/2 stands for the value on each base. The colnames can be any character but must be in the order. Rows stands for each observation.

The objects in data must have specific forms. Colunms should be features, which should be organized in the order of "chr", "pos", "value1", "value2(optional)". chr stands for chromosome. pos stands for position on chromosome, also known as coordinates. value1/2 stands for the value on each base. The colnames can be any character but must be in the order. Rows stands for each observation.

Value

bmData

Examples

```
demo_bisseq_file <- system.file("extdata", "demo_bisseq.txt",
    package = "epiSeeker"
)
demo_bisseq <- read.table(demo_bisseq_file, header = TRUE)
demo_bmdata <- makeBmDataFromData(
    data = list(acinar_methyl = demo_bisseq),
    sampleNames = "acinar_methyl"
)
```

---

makeBmDataFromData.internal *makeBmDataFromData.internal*

Description

make dmData object from data

Usage

```
makeBmDataFromData.internal(data, sampleNames = NULL)
```

Arguments

data	lists object
sampleNames	the name of each samples

Details

This internal function was inspired by DSS::makeBSseqData.

The objects in `data` must have specific forms. Colunms should be features, which should be organized in the order of "chr", "pos", "value1", "value2(optional)". chr stands for chromosome. pos stands for position on chromosome, also known as coordinates. value1/2 stands for the value on each base. The colnames can be any character but must be in the order. Rows stands for each observation.

Value

dmData object

`makeBmDataFromFiles` *make bmData from files*

Description

This function makes bmData object from files. Users can input the name of a file or a file folder.

Usage

```
makeBmDataFromFiles(name, sampleNames = NULL, variablesNames = NULL)
```

Arguments

`name`	the name of files or file folder
`sampleNames`	the name for each file
`variablesNames`	the names of the first two columns will be assigned c("chr","pos"), the names of the following columns will be assigned by variablesNames

Details

bed files and txt files are supported. Bed files can only contain no more than two metadata, as it stands for value1/2. Txt files should organize the columns as chr, pos, value1, value2(optional).

Value

bmData

Examples

```
demo_bisseq_file <- system.file("extdata", "demo_bisseq.txt", package = "epiSeeker")
data <- makeBmDataFromFiles(demo_bisseq_file,
    sampleNames = "acinar_methyl",
    variablesNames = c("Cov", "Methylation")
)
```

`mutate.GRanges` *Extend mutate to Peak (GRanges class object)*

Description

Extend mutate to Peak (GRanges class object)

Usage

```
## S3 method for class 'GRanges'
mutate(
  .data,
  ...,
  .by = NULL,
  .keep = c("all", "used", "unused", "none"),
  .before = NULL,
  .after = NULL
)
```

Arguments

`.data`	granges object
`...`	additional parameters
`.by`	Optional grouping variable(s) (column name or variable expression) specifying which columns to group by for operations
`.keep`	Character vector specifying which columns to retain. Possible values: "all" (retain all columns, default), "used" (retain only columns used in calculations), "unused" (retain only columns not used in calculations), "none" (retain only newly created columns)
`.before`	Column name or position index specifying where to insert new columns before
`.after`	Column name or position index specifying where to insert new columns after

Value

A processed GRanges object containing the added or modified columns

Examples

```
peakfile <- system.file("extdata", "sample_peaks.txt", package = "epiSeeker")
peak <- readPeakFile(peakfile)
dplyr::mutate(peak, score = tags)
```

overlap *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

parse_peak *parse peak str*

Description

parse peak str

Usage

```
parse_peak(peak_str)
```

Arguments

peak_str	peak str

Value

data frame

Examples

```
parse_peak("chr1:150235946-150236624")
```

peakAnno *Example data of peak annotation*

Description

A ‘csAnno‘ object representing the annotation result of the example peak set ‘demo_peak‘. Peaks were annotated using the function ‘annotateSeq()‘ in ‘epiSeeker‘.

Format

A ‘csAnno‘ object containing 220 annotated peaks.

Value

csAnno object

Provenance

Input peaks were taken from the example dataset ‘demo_peak‘. Annotation was generated using ‘epiSeeker::annotateSeq()‘.

Data structure

A ‘csAnno‘ S4 object with the following slots:

‘anno‘ A ‘GRanges‘ object containing the annotated peaks, including peak coordinates, basic peak metrics, and gene-based annotation fields.

‘tssRegion‘ Numeric vector of length two defining the upstream and downstream window used for TSS annotation.

‘level‘ Character string indicating whether annotation was performed at the ‘"transcript"‘ or ‘"gene"‘ level.

‘hasGenomicAnnotation‘ Logical value indicating whether detailed genomic annotation (promoter, exon, intron, etc.) was computed.

‘detailGenomicAnnotation‘ A data frame providing per-peak binary indicators for genomic categories.

‘annoStat‘ A data frame summarizing annotation category frequencies across the annotated peak set.

‘peakNum‘ Total number of annotated peaks.

peakAnnoList *Example data of a list of peak annotation*

Description

A list of csAnno objects obtained by annotating multiple peak files using epiSeeker::annotateSeq(). See data-raw/example_data.R

Format

A a list of csAnno objects.

Value

list of csAnno object

Provenance

The example peak annotation list was generated using several example peak files returned by getSampleFiles(). Each peak file was annotated using epiSeeker::annotateSeq().

Data structure

A named list where each element is a csAnno S4 object produced by annotateSeq().

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>

Examples

```
data(peakAnno)
plotAnnoBar(peakAnno)
```

---

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://yulab-smu.top>

See Also

[annotateSeq()] [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

`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
`radius`	radius of the pie
`...`	extra parameter

Value

plot

Author(s)

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

Examples

```
data(peakAnno)
plotAnnoPie(peakAnno)
```

`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

[annotateSeq()] [plotAnnoBar()]

Examples

```
data(peakAnno)
plotAnnoPie(peakAnno)
```

---

plotBmProf *plotBmProf*

Description

Plot base modification profile

Usage

```
plotBmProf(
  df,
  motif_color = NULL,
  title = NULL,
  xlim = NULL,
  interactive = FALSE,
  width_svg = 10,
  height_svg = 6,
  highlight = NULL,
  highlight_color = "#c6c3c3",
  highlight_alpha = 0.2,
  xlab = "Genomic Region(5'->3')",
  ylab = NULL,
  second_ylab = NULL,
  switch_y_value = TRUE,
  legend_lab_motif = NULL,
  legend_lab_value2 = NULL,
  strip_placement = "outside",
  angle_of_facet_label = 360,
  alpha = 0.6,
  y_ticks_length = 0.25,
  x_ticks_length = 0.25,
  auto_x_axis = TRUE,
  strip_border = FALSE,
  facet_label_text_size = 10,
  axis_title_text_size = 17,
  title_text_size = 20,
  right_y_axis_text_size = 10,
  left_y_axis_text_size = 10,
  x_axis_text_size = 10,
  depth_heatmap = TRUE,
  nrow = NULL,
  ncol = NULL,
  panel_spacing = 1,
```

```
  legend_box_spacing = 3,
  legend_position = "right"
)
```

Arguments

df	the base modification data.frame
motif_color	the color for different motifs(CHH,CHG,CG)
title	the title of the plot, can also be a list of title.
xlim	the specified interval of region, must be the sub-interval of the dmR. list for list df
interactive	produce interactive fig or not.
width_svg	width_svg.
height_svg	height_svg.
highlight	a region or a list of region to highlight.
highlight_color	colors of highlight rect. Default "#c6c3c3"
highlight_alpha	alpha of highlight rect.
xlab	the x label, can also be a list of x label
ylab	the y label, can also be a list of y label
second_ylab	the ylab for second y-axis
switch_y_value	switch the value from left y-axis to right y-axis
legend_lab_motif	the label of legend for motif
legend_lab_value2	the label of legend for the second value(ylab is the label for the first value)
strip_placement	strip.placement
angle_of_facet_label	the angle of facet label, e.g. 0 is horizontal
alpha	transparency for the depth information line
y_ticks_length	the length of y-axis ticks
x_ticks_length	the length of x-axis ticks
auto_x_axis	use auto x axis or not.
strip_border	add border to the facet label or not
facet_label_text_size	the size of facet label text
axis_title_text_size	the size of axis title text
title_text_size	the size of the title text
right_y_axis_text_size	the size of the left y axis text,this work when depth information is taken into account
left_y_axis_text_size	the size of the left y axis text

x_axis_text_size
: the size of x axis text

depth_heatmap
: draw the heatmap of depth information or not

nrow
: the nrow of plotting a list of dmR

ncol
: the ncol of plotting a list of dmR

panel_spacing
: the distance between panels

legend_box_spacing
: the distance between legend and plotting area,"cm"

legend_position
: the position of legend

Value

ggplot object

Examples

```
require(BSgenome.Hsapiens.UCSC.hg38)
data(demo_bmdata)
bmMatrix <- getBmMatrix(
    region = data.frame(chr = "chr22", start = 10525991, end = 10526342),
    BSgenome = BSgenome.Hsapiens.UCSC.hg38,
    input = demo_bmdata,
    #                           base = "C",
    motif = c("CG")
)
plotBmProf(bmMatrix)
```

---

plotCov *plotCov*

Description

plotCov

Usage

```
plotCov(
  peak,
  weightCol = NULL,
  facet_level = NULL,
  highlight = NULL,
  highlight_color = "#c6c3c3",
  highlight_alpha = 0.2,
  xlab = "Chromosome Size (bp)",
  ylab = "",
  interactive = FALSE,
  width_svg = 10,
  height_svg = 6,
  title = "ChIP Peaks over Chromosomes",
  x_text_size = 10,
```

```
  y_text_size = 10,
  facet_label_text_size = 10,
  chrs = NULL,
  xlim = NULL,
  facet_var = NULL,
  facet_scales = "free",
  lower = 1,
  fill_color = "black",
  add_cluster_tree = FALSE,
  cluster_dist_method = "euclidean",
  cluster_hclust_methond = "complete",
  legend_position = NULL,
  add_coaccess = FALSE,
  curvature = 0.3,
  coaccess_top_n = NULL,
  coaccess_cor_threshold = NULL,
  design = NULL,
  coaccess_legend_pos = c(0.9, 0.5),
  coaccess_legend_text_size = 10,
  coaccess_legend_title_size = 12
)
```

Arguments

peak	peak file or GRanges object.
weightCol	weight column of peak.
facet_level	facet_level.
highlight	a region or a list of region to highlight.
highlight_color	colors of highlight rect. Default "#c6c3c3"
highlight_alpha	alpha of highlight rect.
xlab	xlab.
ylab	ylab.
interactive	produce interactive fig or not.
width_svg	width_svg
height_svg	height_svg
title	title.
x_text_size	the size of x text.
y_text_size	the size of y text.
facet_label_text_size	the size of facet label text.
chrs	selected chromosomes to plot, all chromosomes by default.
xlim	ranges to plot, default is whole chromosome.
facet_var	how to facet. one of c("chr~.", ".~ chr", ".~.id", ".id~.", ".id~chr", "chr~.id")
facet_scales	how to scale facet data. Default: "free".
lower	lower cutoff of coverage signal.

`fill_color` specify the color/palette for the plot. Order matters.

`add_cluster_tree`
add cluster tree for samples or not.

`cluster_dist_method`
method for calculate cluster tree. Details see [stats::dist()]

`cluster_hclust_methond`
method for hclust. Details see [stats::hclust()]

`legend_position`
legend_position

`add_coaccess` add co-accessibility or not

`curvature` curvature.

`coaccess_top_n` top n co-accessibility to show, default: 3.

`coaccess_cor_threshold`
co-access peak cor threshold.

`design` the design layout of figure.

`coaccess_legend_pos`
the legend position of co-accessibiliy plot legend.

`coaccess_legend_text_size`
the legend position of co-accessibiliy plot legend text size.

`coaccess_legend_title_size`
the legend position of co-accessibiliy plot legend title size.

Details

Plot peak coverage

Value

ggplot2 object

Author(s)

G Yu

Examples

```
peakfile <- system.file("extdata", "sample_peaks.txt", package = "epiSeeker")
peak <- readPeakFile(peakfile)
plotCov(peak)
```

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",
  distanceBreaks = c(0, 1000, 3000, 5000, 10000, 1e+05),
  palette = NULL,
  ...
)

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
distanceBreaks	breaks of distance, default is ‘c(0, 1000, 3000, 5000, 10000, 100000)‘
palette	palette name for coloring different distances. Run ‘RColorBrewer::display.brewer.all()‘ to see all applicable values.

Value

plot

Author(s)

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

Examples

```
data(peakAnno)
plotDistToTSS(peakAnno)
```

`plotDistToTSS.data.frame` *plotDistToTSS.data.frame*

Description

Plot feature distribution based on the distances to the TSS

Usage

```
plotDistToTSS.data.frame(
  peakDist,
  distanceColumn = "distanceToTSS",
  distanceBreaks = c(0, 1000, 3000, 5000, 10000, 1e+05),
  palette = NULL,
  xlab = "",
  ylab = "Binding sites (%) (5'->3')",
  title = "Distribution of transcription factor-binding loci relative to TSS",
  categoryColumn = ".id"
)
```

Arguments

`peakDist`	peak annotation
`distanceColumn`	column name of the distance from peak to nearest gene
`distanceBreaks`	default is 'c(0, 1000, 3000, 5000, 10000, 100000)'
`palette`	palette name for coloring different distances. Run 'RColorBrewer::display.brewer.all()' to see all applicable values.
`xlab`	x label
`ylab`	y label
`title`	figure title
`categoryColumn`	category column, default is ".id"

Value

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

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

See Also

annotateSeq

---

plotGeneTrack *Plot gene track*

Description

Plot gene track

Usage

```
plotGeneTrack(
  txdb,
  chr,
  start_pos,
  end_pos,
  xlab = "",
  ylab = "",
  x_text_size = 10,
  y_text_size = 10,
  select_gene = "all",
  palette = NULL,
  fromType = "ENTREZID",
  highlight = NULL,
  highlight_color = "#c6c3c3",
  highlight_alpha = 0.2,
  OrgDb = NULL,
  show_legend = FALSE,
  auto_x_axis = TRUE
)
```

Arguments

txdb	TxDb object, providing gene annotation.
chr	chromosome id.
start_pos	start coordinate of windows.
end_pos	end coordinate of windows.
xlab	x lab.
ylab	y lab.
x_text_size	the size of x text.
y_text_size	the size of y text.
select_gene	show all gene or specifc gene. (1)"all", show all genes. (2) gene symbol, e.g. c("SKAP1", "EFCAB13"). (3) gene id, e.g. c(4831, 55316)
palette	palette, default "Set3".
fromType	from which type of gene name to change gene id. Default: ENTREZID. See [clusterProfiler::bitr()]

highlight	a region or a list of region to highlight.
highlight_color	colors of highlight rect. Default "#c6c3c3"
highlight_alpha	alpha of highlight rect.
OrgDb	OrgDb for change gene id to gene symbol.
show_legend	show legend or not.
auto_x_axis	use auto x axis or not.

Value

ggplot object

Examples

```
require(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
plotGeneTrack(txdb = txdb, chr = "chr8", start_pos = 126712193, end_pos = 126712293)
```

---

plotMotifProf *Plot the profile of motif of specific peak*

Description

Plot the profile of motif of specific peak

Usage

```
plotMotifProf(
  df,
  legend_lab = "motif",
  y_lab = "motif score",
  x_lab = NULL,
  interactive = FALSE,
  width_svg = 10,
  height_svg = 6
)
```

Arguments

df	motif information data.frame.
legend_lab	legend lab.
y_lab	y axis label.
x_lab	x axis label.
interactive	produce interactive fig or not.
width_svg	width_svg
height_svg	height_svg

Value

ggplot object

Examples

```
require(BSgenome.Hsapiens.UCSC.hg38)
data(pwm_obj)
region_oi <- GRanges(
    seqnames = "chr22",
    ranges = IRanges(start = 10525891, end = 10525991)
)
motifMatrix <- getMotifMatrix(
    region = region_oi,
    pwm = pwm_obj[c(45, 120, 170)],
    ref_obj = BSgenome.Hsapiens.UCSC.hg38
)
plotMotifProf(motifMatrix)
```

---

plotPeakHeatmap *plotPeakHeatmap function*

Description

plotPeakHeatmap function

Usage

```
plotPeakHeatmap(
  tagMatrix,
  plot_prof = TRUE,
  xlab = "",
  ylab = "",
  palette = NULL,
  title = NULL,
  facet_label_text_size = 12,
  nrow = NULL,
  ncol = NULL,
  conf = NULL,
  statistic_method = "mean",
  missingDataAsZero = TRUE,
  facet = "none",
  free_y = TRUE,
  height_proportion = 4,
  ...
)
```

Arguments

tagMatrix	output from getTagMatrix().
plot_prof	combine prof or not. Default: TRUE
xlab	xlab.

ylab	ylab.
palette	palette to be filled in,details see scale_colour_brewer.
title	title.
facet_label_text_size	the size of facet label text
nrow	nrow to place a number of fig.
ncol	ncol to place a number of fig.
conf	confidence interval.
statistic_method	method to do statistic. one of "mean", "median", "min", "max", "sum", "std"
missingDataAsZero	set missing data as zero or not.
facet	one of 'none', 'row' and 'column'.
free_y	if TRUE, y will be scaled.
height_proportion	the proportion of profiling picture and heatmap
...	additional parameters

Value

ggplot object

Examples

```
data(tagMatrix)
plotPeakHeatmap(tagMatrix)
```

---

plotPeakHeatmap_sub *Plot peak heatmap sub function*

Description

Plot peak heatmap sub function

Usage

```
plotPeakHeatmap_sub(
  tagMatrix,
  xlab = "",
  ylab = "",
  palette = NULL,
  title = NULL,
  facet_label_text_size = 12,
  nrow = NULL,
  ncol = NULL
)
```

Arguments

tagMatrix	output from getTagMatrix().
xlab	xlab.
ylab	ylab.
palette	palette to be filled in,details see [ggplot2::scale_colour_brewer()].
title	title.
facet_label_text_size	the size of facet label text
nrow	nrow to place a number of fig.
ncol	ncol to place a number of fig.

Value

ggplot object

---

plotPeakHeatmap_sub.internal

internal function of plotPeakHeatmap

Description

internal function of plotPeakHeatmap

Usage

```
plotPeakHeatmap_sub.internal(
  tagMatrix,
  xlab = "",
  ylab = "",
  palette = NULL,
  title = NULL,
  facet_label_text_size = 12
)
```

Arguments

tagMatrix	output from getTagMatrix().
xlab	xlab.
ylab	ylab.
palette	palette to be filled in,details see [ggplot2::scale_colour_brewer()].
title	title.
facet_label_text_size	the size of facet label text

Value

ggplot object

plotPeakProf *plot peak profile*

Description

plot peak profile

Usage

```
plotPeakProf(
  tagMatrix,
  xlab = "Genomic Region (5'->3')",
  ylab = "Peak Count Frequency",
  conf = NULL,
  title = "",
  facet = "none",
  free_y = TRUE,
  statistic_method = "mean",
  missingDataAsZero = TRUE,
  ...
)
```

Arguments

tagMatrix	output from getTagMatrix().
xlab	xlab.
ylab	ylab.
conf	confidence interval.
title	title.
facet	one of 'none', 'row' and 'column'.
free_y	if TRUE, y will be scaled.
statistic_method	method to do statistic. one of "mean", "median", "min", "max", "sum", "std"
missingDataAsZero	set missing data as zero or not.
...	additional parameters

Value

ggplot object

Author(s)

G Yu; Y Yan

Examples

```
data(tagMatrix)
plotPeakProf(tagMatrix)
```

pwm_obj *motif reference for Homo sapiens*

Description

A collection of transcription factor position weight matrices (PWMs) retrieved from the JASPAR 2024 database. This dataset is used to demonstrate motif enrichment, motif scanning, and peak–motif association analyses in **epiSeeker**. See data-raw/example_data.R

Format

A `PFMatrixList` object containing PWMs for multiple human transcription factors from the JASPAR 2024 CORE collection.

Value

pwm_obj

Provenance

The PWM set was obtained using the JASPAR 2024 SQLite database bundled in the **JASPAR2024** package. Matrices were retrieved using **TFBSTools** with the following parameters:

- `collection = "CORE"`
- `all_versions = FALSE`
- `species = "Homo sapiens"`
- `tax_group = "vertebrates"`

Data structure

A `TFBSTools::PWMatrixList` (or `PFMatrixList`) object containing one PWM per transcription factor. Each matrix stores nucleotide position weights across the TF binding motif, with rows representing `A, C, G, T` and columns representing motif positions.

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 (pass to 'utils::read.delim()')

Value

peak information, in GRanges or data.frame object

Author(s)

G Yu

Examples

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

---

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

ggplot2 rel()

Value

function

Examples

```
rel(0.2)
```

---

rename.GRanges *Rename columns of a GRanges object*

Description

Rename columns of a GRanges object

Usage

```
## S3 method for class 'GRanges'
rename(.data, ...)
```

Arguments

.data	A GRanges object.
...	Rename expressions in the form new_name = old_name.

Value

A GRanges object with renamed metadata columns.

Examples

```
peakfile <- system.file("extdata", "sample_peaks.txt", package = "episeeker")
peak <- readPeakFile(peakfile)
dplyr::rename(peak, tag = tags)
```

---

seq2gene *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	TxDb object
sameStrand	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-specified distance).

Value

gene vector

Author(s)

Guangchuang Yu

Examples

```
data(seq2gene_result)
seq2gene_result
```

seq2gene_result *Result of seq2gene*

Description

A character vector of gene IDs returned by `seq2gene()`, representing genes associated with a subset of peaks. This dataset is used to illustrate peak-to-gene mapping and regulatory region annotation workflows in **epiSeeker**. See data-raw/example_data.R

Format

A character vector of gene IDs generated by `seq2gene()` from the subset of peaks derived from demo_peak.

Value

vector of gene names

Data structure

A character vector of gene identifiers (ENTREZ IDs) representing genes linked to the example peak set via TSS proximity or flanking-gene search.

Provenance

The example peak set `demo_peak` was constructed by sampling up to 10 peaks per autosome (chr1–chr22) from the ChIP-seq dataset `GSM6418464`. Peaks were imported using `readPeakFile()`, subset by chromosome, and combined into a single `GRanges` object.

The gene-level associations were then computed directly using:

```
seq2gene_result <- seq2gene(
    demo_peak,
    tssRegion = c(-1000, 1000),
    flankDistance = 3000,
    txdb
)
```

The resulting character vector of gene IDs was saved via `data-raw/example_data.R`.

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>

Examples

```
peakfile <- system.file("extdata", "sample_peaks.txt", package = "epiSeeker")
show(peakfile)
```

---

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

Examples

```
require(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
p <- GRanges(
    seqnames = c("chr1", "chr3"),
    ranges = IRanges(start = c(1, 100), end = c(50, 130))
)
shuffle(p, TxDb = txdb)
```

tagMatrix *Example data of tagMatrix*

Description

tagMatrix result used to demonstrate TSS enrichment visualization and tag distribution plotting functions in **epiSeeker**. See data-raw/example_data.R

Format

A numeric matrix with n genes × 500 bins.

Value

matrix

Provenance

The tag matrix was generated using a sample peak file obtained from `getSampleFiles()[[4]]`. Peaks were imported via `readPeakFile()` and processed using `epiSeeker::getTagMatrix()` with the following settings:

- Transcript database: `TxDb.Hsapiens.UCSC.hg19.knownGene`
- Annotation mode: `type = "start_site"`, `by = "gene"`
- TSS window: upstream 3000 bp, downstream 3000 bp
- Peak weight: column `"V5"` of the peak file
- Number of bins: `nbin = 500`

Data structure

A numeric matrix in which:

Rows Represent individual genes contributing tags around their TSS.

Columns Represent evenly spaced bins across the TSS window from -3000 bp to +3000 bp (500 bins total).

upsetplot *upsetplot method*

Description

upsetplot method generics

Usage

```
upsetplot(x, n = 10, type = "boxplot", layer = NULL,
    value = c("score", "abs_score"), core_enrichment = FALSE, ...)
```

Arguments

x	A ‘csAnno‘ instance
n	number of categories to be plotted; only used by methods that support it and ignored by the ‘csAnno‘ method
type	plot type; only used by methods that support it and ignored by the ‘csAnno‘ method
layer	optional layer; only used by methods that support it and ignored by the ‘csAnno‘ method
value	score summary to display for overlapping features; only used by methods that support it and ignored by the ‘csAnno‘ method
core_enrichment	logical indicating whether only core features should be used; only used by methods that support it and ignored by the ‘csAnno‘ method
...	additional parameter

Value

plot

Author(s)

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

Examples

```
data(peakAnno)
upsetplot(peakAnno)
```

---

vennpie *vennpie method generics*

Description

vennpie method generics

Usage

```
vennpie(x, r = 0.2, cex = 1.2, ...)

vennpie(x, r = 0.2, cex=1.2, ...)
```

Arguments

x	A ‘csAnno‘ instance
r	initial radius
cex	value to adjust legend
...	additional parameter

Value

plot

Author(s)

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

Examples

```
data(peakAnno)
vennpie(peakAnno)
```

---

vennplot *vennplot*

Description

Plot the overlap of a list of object

Usage

```
vennplot(Sets, ...)
```

Arguments

Sets	a list of object, can be vector or GRanges object.
...	extra parameters using ggVennDiagram. Details see [ggVennDiagram::ggVennDiagram]

Details

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

```
data(peakAnnoList)
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

files	peak files
labels	labels for peak files

Value

figure

Author(s)

G Yu

Examples

```
files <- list(
    system.file("extdata", "sample_peaks.txt", package = "epiSeeker"),
    system.file("extdata", "sample_peaks.txt", package = "epiSeeker")
)
vennplot.peakfile(files)
```

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