

# Package ‘ChIPpeakAnno’

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**Type** Package

**Title** Batch annotation of the peaks identified from either ChIP-seq, ChIP-chip experiments, or any experiments that result in large number of genomic interval data

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**Depends** R (>= 3.5), methods, IRanges (>= 2.13.12), GenomicRanges (>= 1.31.8), S4Vectors (>= 0.17.25)

**Imports** AnnotationDbi, BiocGenerics (>= 0.1.0), Biostrings (>= 2.47.6), palign, DBI, dplyr, GenomeInfoDb, GenomicAlignments, GenomicFeatures, RBGL, Rsamtools, SummarizedExperiment, VennDiagram, biomaRt, ggplot2, grDevices, graph, graphics, grid, InteractionSet, KEGGREST, matrixStats, multtest, regioneR, rtracklayer, stats, utils, universalmotif, stringr, tibble, tidyr, data.table, scales, ensemblldb

**Suggests** AnnotationHub, BSgenome, limma, reactome.db, BiocManager, BiocStyle, BSgenome.Ecoli.NCBI.20080805,

BSgenome.Hsapiens.UCSC.hg19, org.Ce.eg.db, org.Hs.eg.db,  
 BSgenome.Celegans.UCSC.ce10, BSgenome.Drerio.UCSC.danRer7,  
 BSgenome.Hsapiens.UCSC.hg38, DelayedArray, idr, seqinr,  
 EnsDb.Hsapiens.v75, EnsDb.Hsapiens.v79, EnsDb.Hsapiens.v86,  
 TxDb.Hsapiens.UCSC.hg18.knownGene,  
 TxDb.Hsapiens.UCSC.hg19.knownGene,  
 TxDb.Hsapiens.UCSC.hg38.knownGene, GO.db, gplots, UpSetR,  
 knitr, rmarkdown, reshape2, testthat, trackViewer, motifStack,  
 OrganismDbi, BiocFileCache

**Description** The package encompasses a range of functions for identifying the closest gene, exon, miRNA, or custom features—such as highly conserved elements and user-supplied transcription factor binding sites. Additionally, users can retrieve sequences around the peaks and obtain enriched Gene Ontology (GO) or Pathway terms. In version 2.0.5 and beyond, new functionalities have been introduced. These include features for identifying peaks associated with bi-directional promoters along with summary statistics (peaksNearBDP), summarizing motif occurrences in peaks (summarizePatternInPeaks), and associating additional identifiers with annotated peaks or enrichedGO (addGeneIDs). The package integrates with various other packages such as biomaRt, IRanges, Biostrings, BSgenome, GO.db, multtest, and stat to enhance its analytical capabilities.

**License** GPL (>= 2)

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**LazyData** true

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ChIPpeakAnno-package	<i>Batch annotation of the peaks identified from either ChIP-seq or ChIP-chip experiments.</i>
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## Description

The package includes functions to retrieve the sequences around the peak, obtain enriched Gene Ontology (GO) terms, find the nearest gene, exon, miRNA or custom features such as most conserved elements and other transcription factor binding sites leveraging biomaRt, IRanges, Biostrings, BSgenome, GO.db, hypergeometric test phyper and multtest package.

## Details

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Type:	Package
Version:	3.0.0
Date:	2014-10-24
License:	LGPL
LazyLoad:	yes

## Author(s)

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## References

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## Examples

```
if(interactive()){
  data(myPeakList)
  library(ensemblDb)
  library(EnsDb.Hsapiens.v75)
  anno <- annoGR(EnsDb.Hsapiens.v75)
  annotatedPeak <-
    annotatePeakInBatch(myPeakList[1:6], AnnotationData=anno)
```

}

---

addAncestors*Add GO IDs of the ancestors for a given vector of GO ids*

---

## Description

Add GO IDs of the ancestors for a given vector of GO IDs leveraging GO.db

## Usage

```
addAncestors(go.ids, ontology = c("bp", "cc", "mf"))
```

## Arguments

go.ids	A matrix with 4 columns: first column is GO IDs and 4th column is entrez IDs.
ontology	bp for biological process, cc for cellular component and mf for molecular function.

## Value

A vector of GO IDs containing the input GO IDs with the GO IDs of their ancestors added.

## Author(s)

Lihua Julie Zhu

## Examples

```
go.ids = cbind(c("GO:0008150", "GO:0005576", "GO:0003674"),
                c("ND", "IDA", "ND"),
                c("BP", "BP", "BP"),
                c("1", "1", "1"))
library(GO.db)
addAncestors(go.ids, ontology="bp")
```

---

addGeneIDs	<i>Add common IDs to annotated peaks such as gene symbol, entrez ID, ensemble gene id and refseq id.</i>
------------	--

---

## Description

Add common IDs to annotated peaks such as gene symbol, entrez ID, ensemble gene id and refseq id leveraging organism annotation dataset. For example, org.Hs.eg.db is the dataset from orgs.Hs.eg.db package for human, while org.Mm.eg.db is the dataset from the org.Mm.eg.db package for mouse.

## Usage

```
addGeneIDs(
  annotatedPeak,
  orgAnn,
  IDs2Add = c("symbol"),
  feature_id_type = "ensembl_gene_id",
  silence = TRUE,
  mart
)
```

## Arguments

annotatedPeak	GRanges or a vector of feature IDs.
orgAnn	organism annotation dataset such as org.Hs.eg.db.
IDs2Add	a vector of annotation identifiers to be added
feature_id_type	type of ID to be annotated, default is ensembl_gene_id
silence	TRUE or FALSE. If TRUE, will not show unmapped entrez id for feature ids.
mart	mart object, see <a href="#">useMart</a> of biomaRt package for details

## Details

One of orgAnn and mart should be assigned.

- If orgAnn is given, parameter feature\_id\_type should be ensemble\_gene\_id, entrez\_id, gene\_symbol, gene\_alias or refseq\_id. And parameter IDs2Add can be set to any combination of identifiers such as "accnum", "ensembl", "ensemblprot", "ensembltrans", "entrez\_id", "enzyme", "gene-name", "pfam", "pmid", "prosite", "refseq", "symbol", "unigene" and "uniprot". Some IDs are unique to an organism, such as "omim" for org.Hs.eg.db and "mgi" for org.Mm.eg.db.

Here is the definition of different IDs :

- accnum: GenBank accession numbers
- ensembl: Ensembl gene accession numbers
- ensemblprot: Ensembl protein accession numbers

- ensembltrans: Ensembl transcript accession numbers
- entrez\_id: entrez gene identifiers
- enzyme: EC numbers
- genename: gene name
- pfam: Pfam identifiers
- pmid: PubMed identifiers
- prosite: PROSITE identifiers
- refseq: RefSeq identifiers
- symbol: gene abbreviations
- unigene: UniGene cluster identifiers
- uniprot: Uniprot accession numbers
- omim: OMIM(Mendelian Inheritance in Man) identifiers
- mgf: Jackson Laboratory MGI gene accession numbers
- If mart is used instead of orgAnn, for valid parameter feature\_id\_type and IDs2Add parameters, please refer to [getBM](#) in bioMart package. Parameter feature\_id\_type should be one valid filter name listed by [listFilters\(mart\)](#) such as ensemble\_gene\_id. And parameter IDs2Add should be one or more valid attributes name listed by [listAttributes\(mart\)](#) such as external\_gene\_id, entrezgene, wikigene\_name, or mirbase\_transcript\_name.

### Value

GRanges if the input is a GRanges or data frame if input is a vector.

### Author(s)

Jianhong Ou, Lihua Julie Zhu

### References

<http://www.bioconductor.org/packages/release/data/annotation/>

### See Also

[getBM](#), AnnotationDb

### Examples

```
data(annotatedPeak)
library(org.Hs.eg.db)
addGeneIDs(annotatedPeak[1:6,],orgAnn="org.Hs.eg.db",
           IDs2Add=c("symbol","omim"))
##addGeneIDs(annotatedPeak$feature[1:6],orgAnn="org.Hs.eg.db",
##           IDs2Add=c("symbol","genename"))
if(interactive()){
  mart <- useMart("ENSEMBL_MART_ENSEMBL",host="www.ensembl.org",
                  dataset="hsapiens_gene_ensembl")
  ##mart <- useMart(biomart="ensembl",dataset="hsapiens_gene_ensembl")
  addGeneIDs(annotatedPeak[1:6,], mart=mart,
```

```
    IDs2Add=c("hgnc_symbol", "entrezgene"))
}
```

---

**addMetadata**

*Add metadata of the GRanges objects used for findOverlapsOfPeaks*

---

**Description**

Add metadata to overlapping peaks after calling [findOverlapsOfPeaks](#).

**Usage**

```
addMetadata(ol, colNames = NULL, FUN = c, ...)
```

**Arguments**

ol	An object of <a href="#">overlappingPeaks</a> , which is output of <a href="#">findOverlapsOfPeaks</a> .
colNames	Names of metadata column to be added. If it is NULL, addMetadata will guess what to add.
FUN	A function to be called
...	Arguments to the function call.

**Value**

return value is An object of [overlappingPeaks](#).

**Author(s)**

Jianhong Ou

**See Also**

See Also as [findOverlapsOfPeaks](#)

**Examples**

```
peaks1 <- GRanges(seqnames=c(6,6,6,6,5),
                   IRanges(start=c(1543200,1557200,1563000,1569800,167889600),
                           end=c(1555199,1560599,1565199,1573799,167893599),
                           names=c("p1","p2","p3","p4","p5")),
                   strand="+",
                   score=1:5, id=letters[1:5])
peaks2 <- GRanges(seqnames=c(6,6,6,6,5),
                   IRanges(start=c(1549800,1554400,1565000,1569400,167888600),
                           end=c(1550599,1560799,1565399,1571199,167888999),
                           names=c("f1","f2","f3","f4","f5")),
                   strand="+",
                   score=6:10, id=LETTERS[1:5])
```

```
ol <- findOverlapsOfPeaks(peaks1, peaks2)
addMetadata(ol)
```

---

annoGR-class

*Class* annoGR

---

## Description

An object of class annoGR represents the annotation data could be used by annotationPeakInBatch.

## Usage

```
## S4 method for signature 'annoGR'
info(object)

## S4 method for signature 'GRanges'
annoGR(ranges, feature = "group", date, ...)

## S4 method for signature 'TxDb'
annoGR(
  ranges,
  feature = c("gene", "transcript", "exon", "CDS", "fiveUTR", "threeUTR", "tRNAs",
  "geneModel"),
  date,
  source,
  mdata,
  OrganismDb
)

## S4 method for signature 'EnsDb'
annoGR(
  ranges,
  feature = c("gene", "transcript", "exon", "disjointExons"),
  date,
  source,
  mdata
)
```

## Arguments

object	annoGR object.
ranges	an object of <a href="#">GRanges</a> , <a href="#">TxDb</a> or <a href="#">EnsDb</a>
feature	annotation type
date	a <a href="#">Date</a> object
...	could be following parameters

source	character, where the annotation comes from
mdata	data frame, metadata from annotation
OrganismDb	an object of OrganismDb. It is used for extracting gene symbol for geneModel group for <a href="#">TxDb</a>

## Slots

`seqnames, ranges, strand, elementMetadata, seqinfo` slots inherit from [GRanges](#). The ranges must have unique names.

`source` character, where the annotation comes from

`date` a [Date](#) object

`feature` annotation type, could be "gene", "exon", "transcript", "CDS", "fiveUTR", "threeUTR", "microRNA", "tRNAs", "geneModel" for [TxDb](#) object, or "gene", "exon", "transcript" for [EnsDb](#) object

`mdata` data frame, metadata from annotation

## Objects from the Class

Objects can be created by calls of the form `new("annoGR", date, elementMetadata, feature, mdata, ranges, seqinfo, seqnames, source, strand)`

## Author(s)

Jianhong Ou

## Examples

```
if(interactive() || Sys.getenv("USER")=="jou"){
  library(EnsDb.Hsapiens.v79)
  anno <- annoGR(EnsDb.Hsapiens.v79)
}
```

---

## Description

Annotate peaks by annoGR object in the given range.

## Usage

```
annoPeaks(
  peaks,
  annoData,
  bindingType = c("nearestBiDirectionalPromoters", "startSite", "endSite", "fullRange"),
  bindingRegion = c(-5000, 5000),
  ignore.peak.strand = TRUE,
  select = c("all", "bestOne"),
  ...
)
```

## Arguments

peaks	peak list, <a href="#">GRanges</a> object
annoData	annotation data, <a href="#">GRanges</a> object
bindingType	Specifying the criteria to associate peaks with annotation. Here is how to use it together with the parameter bindingRegion <ul style="list-style-type: none"> <li>• To obtain peaks within 5kb upstream and up to 3kb downstream of TSS within the gene body, set bindingType = "startSite" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks up to 5kb upstream within the gene body and 3kb downstream of gene/Exon End, set bindingType = "endSite" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks from 5kb upstream to 3kb downstream of genes/Exons , set bindingType = "fullRange" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks with nearest bi-directional promoters within 5kb upstream and 3kb downstream of TSS, set bindingType = "nearestBiDirectionalPromoters" and bindingRegion = c(-5000, 3000)</li> </ul>
	<b>startSite</b> start position of the feature (strand is considered)
	<b>endSite</b> end position of the feature (strand is considered)
	<b>fullRange</b> whole range of the feature
	<b>nearestBiDirectionalPromoters</b> nearest promoters from both direction of the peaks (strand is considered). It will report bidirectional promoters if there are promoters in both directions in the given region (defined by bindingRegion). Otherwise, it will report the closest promoter in one direction.
bindingRegion	Annotation range used together with bindingType, which is a vector with two integer values, default to c (-5000, 5000). The first one must be no bigger than 0, which means upstream. And the second one must be no less than 1, which means downstream (1 is the site position, 2 is the next base of the site position). For details, see bindingType.
ignore.peak.strand	ignore the peaks strand or not.
select	"all" or "bestOne". Return the annotation containing all or the best one. The "bestOne" is selected by the shortest distance to the sites and then similarity between peak and annotations. Ignored if bindingType is nearestBiDirectionalPromoters.

... Not used.

### Value

Output is a GRanges object of the annotated peaks.

### Author(s)

Jianhong Ou

### See Also

See Also as [annotatePeakInBatch](#)

### Examples

```
library(ensemblDb)
library(EnsDb.Hsapiens.v75)
data("myPeakList")
annoGR <- toGRanges(EnsDb.Hsapiens.v75)
seqlevelsStyle(myPeakList) <- seqlevelsStyle(annoGR)
annoPeaks(myPeakList, annoGR)
```

---

annotatedPeak

*Annotated Peaks*

---

### Description

TSS annotated putative STAT1-binding regions that are identified in un-stimulated cells using ChIP-seq technology (Robertson et al., 2007)

### Usage

annotatedPeak

### Format

GRanges with slot start holding the start position of the peak, slot end holding the end position of the peak, slot names holding the id of the peak, slot strand holding the strands and slot space holding the chromosome location where the peak is located. In addition, the following variables are included.

**list("feature")** id of the feature such as ensembl gene ID

**list("insideFeature")** upstream: peak resides upstream of the feature; downstream: peak resides downstream of the feature; inside: peak resides inside the feature; overlapStart: peak overlaps with the start of the feature; overlapEnd: peak overlaps with the end of the feature; includeFeature: peak include the feature entirely

**list("distancetoFeature")** distance to the nearest feature such as transcription start site

```
list("start_position") start position of the feature such as gene
list("end_position") end position of the feature such as gene
```

### Details

```
obtained by data(TSS.human.GRCh37)
data(myPeakList)
annotatePeakInBatch(myPeakList, AnnotationData = TSS.human.GRCh37, output="b", multiple=F)
```

### Examples

```
data(annotatedPeak)
head(annotatedPeak, 4) # show first 4 ranges
if (interactive() || Sys.getenv("USER")=="jou") {
  y = annotatedPeak$distancetoFeature[!is.na(annotatedPeak$distancetoFeature)]
  hist(as.numeric(as.character(y)),
       xlab="Distance To Nearest TSS", main="", breaks=1000,
       ylim=c(0, 50), xlim=c(min(as.numeric(as.character(y)))-100,
       max(as.numeric(as.character(y)))+100))
}
```

---

annotatePeakInBatch	<i>Obtain the distance to the nearest TSS, miRNA, and/or exon for a list of peaks</i>
---------------------	---

---

### Description

Obtain the distance to the nearest TSS, miRNA, exon et al for a list of peak locations leveraging IRanges and biomaRt package

### Usage

```
annotatePeakInBatch(
  myPeakList,
  mart,
  featureType = c("TSS", "miRNA", "Exon"),
  AnnotationData,
  output = c("nearestLocation", "overlapping", "both", "shortestDistance", "inside",
            "upstream&inside", "inside&downstream", "upstream", "downstream",
            "upstreamORdownstream", "nearestBiDirectionalPromoters"),
  multiple = c(TRUE, FALSE),
  maxgap = -1L,
  PeakLocForDistance = c("start", "middle", "end", "endMinusStart"),
  FeatureLocForDistance = c("TSS", "middle", "start", "end", "geneEnd"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = TRUE,
```

```

bindingRegion = NULL,
...
)

```

## Arguments

myPeakList	A <a href="#">GRanges</a> object
mart	A mart object, used if AnnotationData is not supplied, see useMart of <a href="#">bioMart</a> package for details
featureType	A character vector used with mart argument if AnnotationData is not supplied; choose from "TSS", "miRNA" or "Exon"
AnnotationData	A <a href="#">GRanges</a> or <a href="#">annoGR</a> object. It can be obtained from the function <code>getAnnotation</code> or customized annotation of class <code>GRanges</code> containing additional variable: <code>strand</code> (1 or + for plus strand and -1 or - for minus strand). Pre-compiled annotations, such as <code>TSS.human.NCBI36</code> , <code>TSS.mouse.NCBIM37</code> , <code>TSS.rat.RGSC3.4</code> and <code>TSS.zebrafish.Zv8</code> , are provided by this package (attach them with <code>data()</code> function). Another method to provide annotation data is to obtain through <a href="#">biomaRt</a> in real time by using the <code>mart</code> and <code>featureType</code> option
output	<p><b>nearestLocation (default)</b> will output the nearest features calculated as Peak-Loc - FeatureLocForDistance; when selected, the output can consist of both "strictly nearest features (non-overlapping)" and "overlapping features" as long as they are the nearest</p> <p><b>overlapping</b> will output overlapping features with maximum gap specified as <code>maxgap</code> between peak range and feature range; it is possible for a peak to be annotated with zero ("NA" will be returned) or multiple overlapping features if exist</p> <p><b>both</b> will output all the nearest features as well as any features that overlap with the peak that is not the nearest</p> <p><b>shortestDistance</b> will output the features with the shortest distance; the "shortest distance" is determined from either ends of the feature to either ends of the peak</p> <p><b>upstream&amp;inside</b> will output all upstream and overlapping features with maximum gap</p> <p><b>inside&amp;downstream</b> will output all downstream and overlapping features with maximum gap</p> <p><b>upstream</b> will output all upstream features with maximum gap</p> <p><b>downstream</b> will output all downstream features with maximum gap</p> <p><b>upstreamORdownstream</b> will output all upstream features with maximum gap or downstream with maximum gap</p> <p><b>nearestBiDirectionalPromoters</b> will use <a href="#">annoPeaks</a> to annotate peaks. Nearest promoters from both direction of the peaks (strand is considered). It will report bidirectional promoters if there are promoters in both directions in the given region (defined by <code>bindingRegion</code>). Otherwise, it will report the closest promoter in one direction.</p>
multiple	Not applicable when output is nearest. TRUE: output multiple overlapping features for each peak. FALSE: output at most one overlapping feature for each peak. This parameter is kept for backward compatibility, please use <code>select</code> .

maxgap	The maximum <i>gap</i> that is allowed between 2 ranges for the ranges to be considered as overlapping. The <i>gap</i> between 2 ranges is the number of positions that separate them. The <i>gap</i> between 2 adjacent ranges is 0. By convention when one range has its start or end strictly inside the other (i.e. non-disjoint ranges), the <i>gap</i> is considered to be -1.
PeakLocForDistance	Specify the location of peak for calculating distance,i.e., middle means using middle of the peak to calculate distance to feature, start means using start of the peak to calculate the distance to feature, endMinusStart means using the end of the peak to calculate the distance to features on plus strand and the start of the peak to calculate the distance to features on minus strand. To be compatible with previous version, by default using start
FeatureLocForDistance	Specify the location of feature for calculating distance,i.e., middle means using middle of the feature to calculate distance of peak to feature, start means using start of the feature to calculate the distance to feature, TSS means using start of feature when feature is on plus strand and using end of feature when feature is on minus strand, geneEnd means using end of feature when feature is on plus strand and using start of feature when feature is on minus strand. To be compatible with previous version, by default using TSS
select	"all" may return multiple overlapping peaks, "first" will return the first overlapping peak, "last" will return the last overlapping peak and "arbitrary" will return one of the overlapping peaks.
ignore.strand	When set to TRUE, the strand information is ignored in the annotation. Unless you have stranded peaks and you are interested in annotating peaks to the features in the same strand only, you should just use the default setting ignore.strand = TRUE.
bindingRegion	Annotation range used for <a href="#">annoPeaks</a> , which is a vector with two integer values, default to c (-5000, 5000). The first one must be no bigger than 0. And the second one must be no less than 1. Once bindingRegion is defined, annotation will based on <a href="#">annoPeaks</a> . Here is how to use it together with the parameter output and FeatureLocForDistance. <ul style="list-style-type: none"> <li>• To obtain peaks with nearest bi-directional promoters within 5kb upstream and 3kb downstream of TSS, set output = "nearestBiDirectionalPromoters" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks within 5kb upstream and up to 3kb downstream of TSS within the gene body, set output="overlapping", FeatureLocForDistance="TSS" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks up to 5kb upstream within the gene body and 3kb downstream of gene/Exon End, set output="overlapping", FeatureLocForDistance="geneEnd" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks from 5kb upstream to 3kb downstream of genes/Exons, set output="overlapping", bindingType = "fullRange" and bindingRegion = c(-5000, 3000)</li> </ul>
...	For details, see <a href="#">annoPeaks</a> . Parameters could be passed to <a href="#">annoPeaks</a>

**Value**

An object of **GRanges** with slot start holding the start position of the peak, slot end holding the end position of the peak, slot space holding the chromosome location where the peak is located, slot rownames holding the id of the peak. In addition, the following variables are included.

```
list("feature")
      id of the feature such as ensembl gene ID
list("insideFeature")
      upstream: peak resides upstream of the feature; downstream: peak resides downstream of the feature; inside: peak resides inside the feature; overlapStart: peak overlaps with the start of the feature; overlapEnd: peak overlaps with the end of the feature; includeFeature: peak include the feature entirely
list("distancetoFeature")
      distance to the nearest feature such as transcription start site. By default, the distance is calculated as the distance between the start of the binding site and the TSS that is the gene start for genes located on the forward strand and the gene end for genes located on the reverse strand. The user can specify the location of peak and location of feature for calculating this
list("start_position")
      start position of the feature such as gene
list("end_position")
      end position of the feature such as the gene
list("strand")
      1 or + for positive strand and -1 or - for negative strand where the feature is located
list("shortestDistance")
      The shortest distance from either end of peak to either end the feature.
list("fromOverlappingOrNearest")
      Relevant only when output is set to "both". If "nearestLocation": indicates this feature's start (feature's end for features from minus strand) is the closest to the peak start ("strictly nearest" or "nearest overlapping"); if "Overlapping": indicates this feature overlaps with this peak although it is not the nearest (non-nearest overlapping)
```

**Author(s)**

Lihua Julie Zhu, Jianhong Ou

**References**

1. Zhu L.J. et al. (2010) ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. *BMC Bioinformatics* 2010, 11:237doi:10.1186/1471-2105-11-237
2. Zhu L (2013). "Integrative analysis of ChIP-chip and ChIP-seq dataset." In Lee T and Luk ACS (eds.), Tilling Arrays, volume 1067, chapter 4, pp. -19. Humana Press. [http://dx.doi.org/10.1007/978-1-62703-607-8\\_8](http://dx.doi.org/10.1007/978-1-62703-607-8_8)

**See Also**

[getAnnotation](#), [findOverlappingPeaks](#), [makeVennDiagram](#), [addGeneIDs](#), [peaksNearBDP](#), [summarizePatternInPeaks](#), [annoGR](#), [annoPeaks](#)

## Examples

```

## example 1: annotate myPeakList by TxDb or EnsDb.
data(myPeakList)
library(ensemblDb)
library(EnsDb.Hsapiens.v75)
annoData <- annoGR(EnsDb.Hsapiens.v75)
annotatePeak = annotatePeakInBatch(myPeakList[1:6], AnnotationData=annoData)
annotatePeak

## example 2: annotate myPeakList (GRanges)
## with TSS.human.NCBI36 (Granges)
data(TSS.human.NCBI36)
annotatedPeak = annotatePeakInBatch(myPeakList[1:6],
                                   AnnotationData=TSS.human.NCBI36)
annotatedPeak

## example 3: you have a list of transcription factor biding sites from
## literature and are interested in determining the extent of the overlap
## to the list of peaks from your experiment. Prior calling the function
## annotatePeakInBatch, need to represent both dataset as GRanges
## where start is the start of the binding site, end is the end of the
## binding site, names is the name of the binding site, space and strand
## are the chromosome name and strand where the binding site is located.

myexp <- GRanges(seqnames=c(6,6,6,6,5,4,4),
                  IRanges(start=c(1543200,1557200,1563000,1569800,
                            167889600,100,1000),
                            end=c(1555199,1560599,1565199,1573799,
                            167893599,200,1200),
                            names=c("p1","p2","p3","p4","p5","p6", "p7")),
                            strand="+")
literature <- GRanges(seqnames=c(6,6,6,6,5,4,4),
                      IRanges(start=c(1549800,1554400,1565000,1569400,
                            167888600,120,800),
                            end=c(1550599,1560799,1565399,1571199,
                            167888999,140,1400),
                            names=c("f1","f2","f3","f4","f5","f6", "f7")),
                            strand=rep(c("+", "-"), c(5, 2)))
annotatedPeak1 <- annotatePeakInBatch(myexp,
                                       AnnotationData=literature)
pie(table(annotatedPeak1$insideFeature))
annotatedPeak1
### use toGRanges or rtracklayer::import to convert BED or GFF format
### to GRanges before calling annotatePeakInBatch
test.bed <- data.frame(space=c("4", "6"),
                        start=c("100", "1000"),
                        end=c("200", "1100"),
                        name=c("peak1", "peak2"))
test.GR = toGRanges(test.bed)
annotatePeakInBatch(test.GR, AnnotationData = literature)

```

```

library(testthat)
peak <- GRanges(seqnames = "chr1",
                 IRanges(start = 24736757, end=24737528,
                         names = "testPeak"))

data(TSS.human.GRCh37)
TSS.human.GRCh37[names(TSS.human.GRCh37)== "ENSG00000001461"]
# GRanges object with 1 range and 1 metadata column:
# seqnames      ranges strand |      description
#<Rle>      <IRanges> <Rle> |      <character>
# ENSG00000001461      1 24742285-24799466      + | NIPA-like domain con..
peak
#GRanges object with 1 range and 0 metadata columns:
# seqnames      ranges strand
#<Rle>      <IRanges> <Rle>
# testPeak      chr1 24736757-24737528      *
TSS.human.GRCh37[names(TSS.human.GRCh37)== "ENSG00000001460"]
#GRanges object with 1 range and 1 metadata column:
# seqnames      ranges strand |      description
#<Rle>      <IRanges> <Rle> |      <character>
# ENSG00000001460      1 24683490-24743424      - | UPF0490 protein C1or..
ap <- annotatePeakInBatch(peak, Annotation=TSS.human.GRCh37,
                           PeakLocForDistance = "start")
stopifnot(ap$feature=="ENSG00000001461")
ap <- annotatePeakInBatch(peak, Annotation=TSS.human.GRCh37,
                           PeakLocForDistance = "end")
stopifnot(ap$feature=="ENSG00000001461")
ap <- annotatePeakInBatch(peak, Annotation=TSS.human.GRCh37,
                           PeakLocForDistance = "middle")
stopifnot(ap$feature=="ENSG00000001461")
ap <- annotatePeakInBatch(peak, Annotation=TSS.human.GRCh37,
                           PeakLocForDistance = "endMinusStart")
stopifnot(ap$feature=="ENSG00000001461")
## Let's calculate the distances between the peak and the TSS of the genes
## in the annotation file used for annotating the peaks.
## Please note that we need to compute the distance using the annotation
## file TSS.human.GRCh37.
## If you would like to use TxDb.Hsapiens.UCSC.hg19.knownGene,
## then you will need to annotate the peaks
## using TxDb.Hsapiens.UCSC.hg19.knownGene as well.
#### using start
start(peak) -start(TSS.human.GRCh37[names(TSS.human.GRCh37)==
                      "ENSG00000001461"]) #picked
#[1] -5528
start(peak) -end(TSS.human.GRCh37[names(TSS.human.GRCh37)==
                      "ENSG00000001460"])
#[1] -6667
#### using middle
(start(peak) + end(peak))/2 -
  start(TSS.human.GRCh37[names(TSS.human.GRCh37)== "ENSG00000001461"])
#[1] -5142.5
(start(peak) + end(peak))/2 -
  end(TSS.human.GRCh37[names(TSS.human.GRCh37)== "ENSG00000001460"])
# [1] 49480566

```

```

end(peak) -start(TSS.human.GRCh37[names(TSS.human.GRCh37)==
                  "ENSG00000001461"]) #picked
# [1] -4757
end(peak) -end(TSS.human.GRCh37[names(TSS.human.GRCh37)==
                  "ENSG00000001460"])
# [1] -5896
##### using endMinusStart
end(peak) - start(TSS.human.GRCh37[names(TSS.human.GRCh37)==
                  "ENSG00000001461"]) ## picked
# [1] -4575
start(peak) -end(TSS.human.GRCh37[names(TSS.human.GRCh37)==
                  "ENSG00000001460"])
#[1] -6667
##### using txdb object to annotate the peaks
library(org.Hs.eg.db)
select(org.Hs.eg.db, key="STPG1", keytype="SYMBOL",
       columns=c("ENSEMBL", "ENTREZID", "SYMBOL"))
# SYMBOL      ENSEMBL ENTREZID
# STPG1 ENSG00000001460      90529
select(org.Hs.eg.db, key= "ENSG00000001461", keytype="ENSEMBL",
       columns=c("ENSEMBL", "ENTREZID", "SYMBOL"))
#ENSEMBL ENTREZID SYMBOL
# ENSG00000001461      57185 NIPAL3
require(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb.ann.current <- genes(TxDb.Hsapiens.UCSC.hg19.knownGene)
# note: the annotation of STPG1 shifted from old version
# here we set the old one for the test
txdb.ann <- GRanges('chr1', IRanges(start=c(24683489, 24742245),
                                         end=c(24741587, 24799473)),
                                         strand=c('-', '+'), gene_id=c('90529', '57185'))
names(txdb.ann) <- txdb.ann$gene_id
STPG1 <- select(org.Hs.eg.db, key="STPG1", keytype="SYMBOL",
                 columns=c("SYMBOL", "ENSEMBL", "ENTREZID"))[1,3]
NIPAL3 <- select(org.Hs.eg.db, key="NIPAL3", keytype="SYMBOL",
                 columns=c("SYMBOL", "ENSEMBL", "ENTREZID"))[1,3]
ap <- annotatePeakInBatch(peak, Annotation=txdb.ann,
                           PeakLocForDistance = "start")
expect_equal(ap$feature, STPG1)
ap <- annotatePeakInBatch(peak, Annotation=txdb.ann,
                           PeakLocForDistance = "end")
expect_equal(ap$feature, STPG1)
ap <- annotatePeakInBatch(peak, Annotation=txdb.ann,
                           PeakLocForDistance = "middle")
expect_equal(ap$feature, STPG1)
ap <- annotatePeakInBatch(peak, Annotation=txdb.ann,
                           PeakLocForDistance = "endMinusStart")
expect_equal(ap$feature, NIPAL3)
txdb.ann.current[NIPAL3]
txdb.ann[txdb.ann$gene_id == NIPAL3]
# GRanges object with 1 range and 1 metadata column:
#   seqnames      ranges strand |   gene_id
#   <Rle>      <IRanges>  <Rle> | <character>
#   57185      chr1 24742245-24799473      + |      57185

```

```

#-----
txdb.ann.current[STPG1]
txdb.ann[txdb.ann$gene_id == STPG1]
#   GRanges object with 1 range and 1 metadata column:
#   seqnames      ranges strand |   gene_id
#   <Rle>      <IRanges> <Rle> | <character>
#   90529      chr1 24683489-24741587      - |      90529

```

---

## assignChromosomeRegion

*Summarize peak distribution over exon, intron, enhancer, proximal promoter, 5 prime UTR and 3 prime UTR*

---

### Description

Summarize peak distribution over exon, intron, enhancer, proximal promoter, 5 prime UTR and 3 prime UTR

### Usage

```

assignChromosomeRegion(
  peaks.RD,
  exon,
  TSS,
  utr5,
  utr3,
  proximal.promoter.cutoff = c(upstream = 2000, downstream = 100),
  immediate.downstream.cutoff = c(upstream = 0, downstream = 1000),
  nucleotideLevel = FALSE,
  precedence = NULL,
  TxDb = NULL
)

```

### Arguments

peaks.RD	peaks in GRanges: See example below
exon	exon data obtained from getAnnotation or customized annotation of class GRanges containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). This parameter is for backward compatibility only. <a href="#">TxD</a> b should be used instead.
TSS	TSS data obtained from getAnnotation or customized annotation of class GRanges containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). For example, data(TSS.human.NCBI36),data(TSS.mouse.NCBIM37), data(TSS.rat.RGSC3.4) and data(TSS.zebrafish.Zv8). This parameter is for backward compatibility only. <a href="#">TxD</a> b should be used instead.

utr5	5 prime UTR data obtained from getAnnotation or customized annotation of class GRanges containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). This parameter is for backward compatibility only. <a href="#">TxDb</a> should be used instead.
utr3	3 prime UTR data obtained from getAnnotation or customized annotation of class GRanges containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). This parameter is for backward compatibility only. <a href="#">TxDb</a> should be used instead.
proximal.promoter.cutoff	Specify the cutoff in bases to classify proximal promoter or enhancer. Peaks that reside within proximal.promoter.cutoff upstream from or overlap with transcription start site are classified as proximal promoters. Peaks that reside upstream of the proximal.promoter.cutoff from gene start are classified as enhancers. The default is upstream 2000 bases and downstream 100 bases.
immediate.downstream.cutoff	Specify the cutoff in bases to classify immediate downstream region or enhancer region. Peaks that reside within immediate.downstream.cutoff downstream of gene end but not overlap 3 prime UTR are classified as immediate downstream. Peaks that reside downstream over immediate.downstream.cutoff from gene end are classified as enhancers. The default is upstream 0 bases and downstream 1000 bases.
nucleotideLevel	Logical. Choose between peak centric and nucleotide centric view. Default=FALSE
precedence	If no precedence specified, double count will be enabled, which means that if a peak overlap with both promoter and 5'UTR, both promoter and 5'UTR will be incremented. If a precedence order is specified, for example, if promoter is specified before 5'UTR, then only promoter will be incremented for the same example. The values could be any combinations of "Promoters", "immediateDownstream", "fiveUTRs", "threeUTRs", "Exons" and "Introns", Default=NULL
TxDb	an object of <a href="#">TxDb</a> or similar including <a href="#">EnsDb</a>

### Value

A list of two named vectors: percentage and jaccard (Jaccard Index). The information in the vectors:

```
list("Exons")    Percent or the picard index of the peaks resided in exon regions.
list("Introns")  Percent or the picard index of the peaks resided in intron regions.
list("fiveUTRs") Percent or the picard index of the peaks resided in 5 prime UTR regions.
list("threeUTRs") Percent or the picard index of the peaks resided in 3 prime UTR regions.
list("Promoter")  Percent or the picard index of the peaks resided in proximal promoter regions.
list("ImmediateDownstream") Percent or the picard index of the peaks resided in immediate downstream regions.
```

```
list("Intergenic.Region")
Percent or the picard index of the peaks resided in intergenic regions.
```

The Jaccard index, also known as Intersection over Union. The Jaccard index is between 0 and 1. The higher the index, the more significant the overlap between the peak region and the genomic features in consideration.

### Author(s)

Jianhong Ou, Lihua Julie Zhu

### References

1. Zhu L.J. et al. (2010) ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. *BMC Bioinformatics* 2010, 11:237doi:10.1186/1471-2105-11-237
2. Zhu L.J. (2013) Integrative analysis of ChIP-chip and ChIP-seq dataset. *Methods Mol Biol.* 2013;1067:105-24. doi: 10.1007/978-1-62703-607-8\_8.

### See Also

[genomicElementDistribution](#), [genomicElementUpSetR](#), [binOverFeature](#), [binOverGene](#), [binOverRegions](#)

### Examples

```
if (interactive() || Sys.getenv("USER")=="jou"){
  ##Display the list of genomes available at UCSC:
  #library(rtracklayer)
  #ucscGenomes()[, "db"]
  ## Display the list of Tracks supported by makeTxBFromUCSC()
  #supportedUCSCtables()
  ##Retrieving a full transcript dataset for Human from UCSC
  ##TranscriptDb <-
  ##  makeTxBFromUCSC(genome="hg19", tablename="ensGene")
  if(require(TxDb.Hsapiens.UCSC.hg19.knownGene)){
    TxB <- TxDb.Hsapiens.UCSC.hg19.knownGene
    exons <- exons(TxB, columns=NULL)
    fiveUTRs <- unique(unlist(fiveUTRsByTranscript(TxB)))
    Feature.distribution <-
      assignChromosomeRegion(exons, nucleotideLevel=TRUE, TxB=TxB)
    barplot(Feature.distribution$percentage)
    assignChromosomeRegion(fiveUTRs, nucleotideLevel=FALSE, TxB=TxB)
    data(myPeakList)
    assignChromosomeRegion(myPeakList, nucleotideLevel=TRUE,
      precedence=c("Promoters", "immediateDownstream",
      "fiveUTRs", "threeUTRs",
      "Exons", "Introns"),
      TxB=TxB)
  }
}
```

---

bdp	<i>obtain the peaks near bi-directional promoters</i>
-----	---

---

## Description

Obtain the peaks near bi-directional promoters. Also output percent of peaks near bi-directional promoters.

## Usage

```
bdp(peaks, annoData, maxgap = 2000L, ...)
```

## Arguments

peaks	peak list, <a href="#">GRanges</a> object
annoData	annotation data, <a href="#">annoGR</a> object
maxgap	maxgap between peak and TSS
...	Not used.

## Value

Output is a list of [GRanges](#) object of the peaks near bi-directional promoters.

## Author(s)

Jianhong Ou

## See Also

See Also as [annoPeaks](#), [annoGR](#)

## Examples

```
if(interactive() || Sys.getenv("USER")=="jou"){
  library(ensemblDb)
  library(EnsDb.Hsapiens.v75)
  data("myPeakList")
  annoGR <- annoGR(EnsDb.Hsapiens.v75)
  seqlevelsStyle(myPeakList) <- seqlevelsStyle(annoGR)
  ChIPpeakAnno:::bdp(myPeakList, annoGR)
}
```

---

bindist-class	<i>Class "bindist"</i>
---------------	------------------------

---

## Description

An object of class "bindist" represents the relevant fixed-width range of binding site from the feature and number of possible binding site in each range.

## Objects from the Class

Objects can be created by calls of the form `new("bindist", counts="integer", mids="integer", halfBinSize="integer", bindingType="character", featureType="character")`.

## See Also

[preparePool](#), [peakPermTest](#)

---

binOverFeature	<i>Aggregate peaks over bins from the TSS</i>
----------------	---

---

## Description

Aggregate peaks over bins from the feature sites.

## Usage

```
binOverFeature(
  ...,
  annotationData = GRanges(),
  select = c("all", "nearest"),
  radius = 5000L,
  nbins = 50L,
  minGeneLen = 1L,
  aroundGene = FALSE,
  mbins = nbins,
  featureSite = c("FeatureStart", "FeatureEnd", "bothEnd"),
  PeakLocForDistance = c("all", "end", "start", "middle"),
  FUN = sum,
  errFun = sd,
  xlab,
  ylab,
  main
)
```

**Arguments**

...	Objects of GRanges to be analyzed
annotationData	An object of <a href="#">GRanges</a> or <a href="#">annoGR</a> for annotation
select	Logical: annotate the peaks to all features or the nearest one
radius	The radius of the longest distance to feature site
nbins	The number of bins
minGeneLen	The minimal gene length
aroundGene	Logical: count peaks around features or a given site of the features. Default = FALSE
mbins	if aroundGene set as TRUE, the number of bins intra-feature. The value will be normalized by value * (radius/genelen) * (mbins/nbins)
featureSite	which site of features should be used for distance calculation
PeakLocForDistance	which site of peaks should be used for distance calculation
FUN	the function to be used for score calculation
errFun	the function to be used for errorbar calculation or values for the errorbar.
xlab	titles for each x axis
ylab	titles for each y axis
main	overall titles for each plot

**Value**

A data.frame with bin values.

**Author(s)**

Jianhong Ou

**Examples**

```
bed <- system.file("extdata", "MACS_output.bed", package="ChIPpeakAnno")
gr1 <- toGRanges(bed, format="BED", header=FALSE)
data(TSS.human.GRCh37)
binOverFeature(gr1, annotationData=TSS.human.GRCh37,
               radius=5000, nbins=10, FUN=length, errFun=0)
```

---

binOverGene	<i>coverage of gene body</i>
-------------	------------------------------

---

## Description

calculate the coverage of gene body per gene per bin.

## Usage

```
binOverGene(  
  cvglists,  
  TxDb,  
  upstream.cutoff = 0L,  
  downstream.cutoff = upstream.cutoff,  
  nbinsGene = 100L,  
  nbinsUpstream = 20L,  
  nbinsDownstream = nbinsUpstream,  
  includeIntron = FALSE,  
  minGeneLen = nbinsGene,  
  maxGeneLen = Inf  
)
```

## Arguments

cvglists	A list of <a href="#">SimpleRleList</a> or <a href="#">RleList</a> . It represents the coverage for samples.
TxDb	An object of <a href="#">TxDb</a> . It is used for extracting the annotations.
upstream.cutoff, downstream.cutoff	cutoff length for upstream or downstream of transcript.
nbinsGene, nbinsUpstream, nbinsDownstream	The number of bins for gene, upstream and downstream.
includeIntron	A logical value which indicates including intron or not.
minGeneLen, maxGeneLen	minimal or maximal length of gene.

## Author(s)

Jianhong Ou

## See Also

[binOverRegions](#), [plotBinOverRegions](#)

## Examples

```
if(Sys.getenv("USER")=="jou"){
  path <- system.file("extdata", package="ChIPpeakAnno")
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  library(rtracklayer)
  files <- dir(path, "bigWig")
  if(.Platform$OS.type != "windows"){
    cvglists <- lapply(file.path(path, files), import,
                       format="BigWig", as="RleList")
    names(cvglists) <- sub(".bigWig", "", files)
    d <- binOverGene(cvglists, TxDb.Hsapiens.UCSC.hg19.knownGene)
    plotBinOverRegions(d)
  }
}
```

---

<code>binOverRegions</code>	<i>coverage of chromosome regions</i>
-----------------------------	---------------------------------------

---

## Description

calculate the coverage of 5'UTR, CDS and 3'UTR per transcript per bin.

## Usage

```
binOverRegions(
  cvglists,
  TxDb,
  upstream.cutoff = 1000L,
  downstream.cutoff = upstream.cutoff,
  nbinsCDS = 100L,
  nbinsUTR = 20L,
  nbinsUpstream = 20L,
  nbinsDownstream = nbinsUpstream,
  includeIntron = FALSE,
  minCDSLen = nbinsCDS,
  minUTRLen = nbinsUTR,
  maxCDSLen = Inf,
  maxUTRLen = Inf
)
```

## Arguments

<code>cvglists</code>	A list of <a href="#">SimpleRleList</a> or <a href="#">RleList</a> . It represents the coverage for samples.
<code>TxDb</code>	An object of <a href="#">TxDb</a> . It is used for extracting the annotations.
<code>upstream.cutoff, downstream.cutoff</code>	cutoff length for upstream or downstream of transcript.

```

nbinsCDS, nbinsUTR, nbinsUpstream, nbinsDownstream
  The number of bins for CDS, UTR, upstream and downstream.

includeIntron  A logical value which indicates including intron or not.

minCDSLen, minUTRLen
  minimal length of CDS or UTR of transcript.

maxCDSLen, maxUTRLen
  maximal length of CDS or UTR of transcript.

```

### Author(s)

Jianhong Ou

### See Also

[binOverGene](#), [plotBinOverRegions](#)

### Examples

```

if(Sys.getenv("USER")=="jou"){
  path <- system.file("extdata", package="ChIPpeakAnno")
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  library(rtracklayer)
  files <- dir(path, "bigWig")
  if(.Platform$OS.type != "windows"){
    cvglists <- lapply(file.path(path, files), import,
                       format="BigWig", as="RleList")
    names(cvglists) <- sub(".bigWig", "", files)
    d <- binOverRegions(cvglists, TxDb.Hsapiens.UCSC.hg19.knownGene)
    plotBinOverRegions(d)
  }
}

```

---

### Description

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as the next release.

### Arguments

Peaks1	GRanges: See example below.
Peaks2	GRanges: See example below.

maxgap, minoverlap	Used in the internal call to <code>findOverlaps()</code> to detect overlaps. See <a href="#">?findOverlaps</a> in the <b>IRanges</b> package for a description of these arguments.
multiple	TRUE or FALSE: TRUE may return multiple overlapping peaks in Peaks2 for one peak in Peaks1; FALSE will return at most one overlapping peaks in Peaks2 for one peak in Peaks1. This parameter is kept for backward compatibility, please use <code>select</code> .
NameOfPeaks1	Name of the Peaks1, used for generating column name.
NameOfPeaks2	Name of the Peaks2, used for generating column name.
select	all may return multiple overlapping peaks, first will return the first overlapping peak, last will return the last overlapping peak and arbitrary will return one of the overlapping peaks.
annotate	Include <code>overlapFeature</code> and <code>shortestDistance</code> in the <code>OverlappingPeaks</code> or not. 1 means yes and 0 means no. Default to 0.
ignore.strand	When set to TRUE, the strand information is ignored in the overlap calculations.
connectedPeaks	If multiple peaks involved in overlapping in several groups, set it to "merge" will count it as only 1, while set it to "min" will count it as the minimal involved peaks in any concered groups
...	Objects of <a href="#">GRanges</a> : See also <a href="#">findOverlapsOfPeaks</a> .

## Details

`findOverlappingPeaks` is now deprecated wrappers for [findOverlapsOfPeaks](#)

## See Also

[Deprecated](#), [findOverlapsOfPeaks](#), [toGRanges](#)

---

cntOverlaps	<i>count overlaps</i>
-------------	-----------------------

---

## Description

Count overlaps with max gap.

## Usage

`cntOverlaps(A, B, maxgap = 0L, ...)`

## Arguments

A, B	A <code>GRanges</code> object.
maxgap	A single integer $\geq 0$ .
...	parameters passed to <a href="#">numOverlaps#</a>

---

**condenseMatrixByColnames**

*Condense matrix by colnames*

---

**Description**

Condense matrix by colnames

**Usage**

```
condenseMatrixByColnames(mx, iname, sep = ";", cnt = FALSE)
```

**Arguments**

mx	a matrix to be condensed
iname	the name of the column to be condensed
sep	separator for condensed values, default ;
cnt	TRUE/FALSE specifying whether adding count column or not?

**Value**

dataframe of condensed matrix

**Author(s)**

Jianhong Ou, Lihua Julie Zhu

**Examples**

```
a<-matrix(c(rep(rep(1:5,2),2),rep(1:10,2)),ncol=4)
colnames(a)<-c("con.1","con.2","index.1","index.2")
condenseMatrixByColnames(a,"con.1")
condenseMatrixByColnames(a,2)
```

---

**convert2EntrezID**

*Convert other common IDs to entrez gene ID.*

---

**Description**

Convert other common IDs such as ensemble gene id, gene symbol, refseq id to entrez gene ID leveraging organism annotation dataset. For example, org.Hs.eg.db is the dataset from orgs.Hs.eg.db package for human, while org.Mm.eg.db is the dataset from the org.Mm.eg.db package for mouse.

**Usage**

```
convert2EntrezID(IDs, orgAnn, ID_type = "ensembl_gene_id")
```

**Arguments**

IDs	a vector of IDs such as ensembl gene ids
orgAnn	organism annotation dataset such as org.Hs.eg.db
ID_type	type of ID: can be ensemble_gene_id, gene_symbol or refseq_id

**Value**

vector of entrez ids

**Author(s)**

Lihua Julie Zhu

**Examples**

```
ensemblIDs = c("ENSG00000115956", "ENSG00000071082", "ENSG00000071054",
  "ENSG00000115594", "ENSG00000115594", "ENSG00000115598", "ENSG00000170417")
library(org.Hs.eg.db)
entrezIDs = convert2EntrezID(IDs=ensemblIDs, orgAnn="org.Hs.eg.db",
  ID_type="ensembl_gene_id")
```

countPatternInSeqs      *Output total number of patterns found in the input sequences*

**Description**

Output total number of patterns found in the input sequences

**Usage**

```
countPatternInSeqs(pattern, sequences)
```

**Arguments**

pattern	DNAStringSet object
sequences	a vector of sequences

**Value**

Total number of occurrence of the pattern in the sequences

**Author(s)**

Lihua Julie Zhu

**See Also**

[summarizePatternInPeaks](#), [translatePattern](#)

**Examples**

```
library(Biostrings)
filepath =
  system.file("extdata", "examplePattern.fa", package="ChIPpeakAnno")
dict = readDNAStringSet(filepath = filepath, format="fasta",
  use.names=TRUE)
sequences = c("ACTGGGGGGGGCTGGCCCCAAAT",
  "AAAAAACCCCTTTGCCATCCGGGACGGCCCAT",
  "ATCGAAAATTCC")
countPatternInSeqs(pattern=dict[1], sequences=sequences)
countPatternInSeqs(pattern=dict[2], sequences=sequences)
pattern = DNAStringSet("ATNGMAA")
countPatternInSeqs(pattern=pattern, sequences=sequences)
```

**cumulativePercentage** *Plot the cumulative percentage tag allocation in sample*

**Description**

Plot the difference between the cumulative percentage tag allocation in paired samples.

**Usage**

```
cumulativePercentage(bamfiles, gr, input = 1, binWidth = 1000, ...)
```

**Arguments**

bamfiles	Bam file names.
gr	An object of <a href="#">GRanges</a>
input	Which file name is input. default 1.
binWidth	The width of each bin.
...	parameter for <a href="#">summarizeOverlaps</a> .

**Value**

A list of data.frame with the cumulative percentages.

**Author(s)**

Jianhong Ou

**References**

Normalization, bias correction, and peak calling for ChIP-seq Aaron Diaz, Kiyoub Park, Daniel A. Lim, Jun S. Song Stat Appl Genet Mol Biol. Author manuscript; available in PMC 2012 May 3. Published in final edited form as: Stat Appl Genet Mol Biol. 2012 Mar 31; 11(3): 10.1515/1544-6115.1750 /j/sagmb.2012.11.issue-3/1544-6115.1750/1544-6115.1750.xml. Published online 2012 Mar 31. doi: 10.1515/1544-6115.1750 PMCID: PMC3342857

**Examples**

```
## Not run:
path <- system.file("extdata", "reads", package="MMDiffBamSubset")
files <- dir(path, "bam$", full.names = TRUE)
library(BSgenome.Hsapiens.UCSC.hg19)
gr <- as(seqinfo(Hsapiens)[["chr1"]], "GRanges")
cumulativePercentage(files, gr)

## End(Not run)
```

downstreams

*Get downstream coordinates*

**Description**

Returns an object of the same type and length as x containing downstream ranges. The output range is defined as

**Usage**

```
downstreams(gr, upstream, downstream)
```

**Arguments**

gr	A GenomicRanges object
upstream, downstream	non-negative integers.

**Details**

(end(x) - upstream) to (end(x) + downstream -1)  
 for ranges on the + and \* strand, and as  
 (start(x) - downstream + 1) to (start(x) + downstream)  
 for ranges on the - strand.

Note that the returned object might contain out-of-bound ranges.

**Value**

A GenomicRanges object

**Examples**

```
gr <- GRanges("chr1", IRanges(rep(10, 3), width=6), c("+", "-", "*"))
downstreams(gr, 2, 2)
```

---

egOrgMap

*Convert between the name of the organism annotation package ("OrgDb") and the name of the organism.*

---

**Description**

Give a species name and return the organism annotation package name or give an organism annotation package name then return the species name.

**Usage**

```
egOrgMap(name)
```

**Arguments**

**name** The name of the organism annotation package or the species.

**Value**

A object of character

**Author(s)**

Jianhong Ou

**Examples**

```
egOrgMap("org.Hs.eg.db")
egOrgMap("Mus musculus")
```

enrichedGO

*Enriched Gene Ontology terms used as example***Description**

Enriched Gene Ontology terms used as example

**Usage**

enrichedGO

**Format**

A list of 3 dataframes.

```
list("bp") dataframe described the enriched biological process with 9 columns
  go.id:GO biological process id
  go.term:GO biological process term
  go.Definition:GO biological process description
  Ontology: Ontology branch, i.e. BP for biological process
  count.InDataset: count of this GO term in this dataset
  count.InGenome: count of this GO term in the genome
  pvalue: pvalue from the hypergeometric test
  totaltermInDataset: count of all GO terms in this dataset
  totaltermInGenome: count of all GO terms in the genome

list("mf") dataframe described the enriched molecular function with the following 9 columns
  go.id:GO molecular function id
  go.term:GO molecular function term
  go.Definition:GO molecular function description
  Ontology: Ontology branch, i.e. MF for molecular function
  count.InDataset: count of this GO term in this dataset
  count.InGenome: count of this GO term in the genome
  pvalue: pvalue from the hypergeometric test
  totaltermInDataset: count of all GO terms in this dataset
  totaltermInGenome: count of all GO terms in the genome

list("cc") dataframe described the enriched cellular component the following 9 columns
  go.id:GO cellular component id
  go.term:GO cellular component term
  go.Definition:GO cellular component description
  Ontology: Ontology type, i.e. CC for cellular component
  count.InDataset: count of this GO term in this dataset
  count.InGenome: count of this GO term in the genome
  pvalue: pvalue from the hypergeometric test
  totaltermInDataset: count of all GO terms in this dataset
  totaltermInGenome: count of all GO terms in the genome
```

**Author(s)**

Lihua Julie Zhu

**Examples**

```
data(enrichedGO)
dim(enrichedGO$mf)
dim(enrichedGO$cc)
dim(enrichedGO$bp)
```

---

enrichmentPlot *plot enrichment results*

---

**Description**

Plot the GO/KEGG/reactome enrichment results

**Usage**

```
enrichmentPlot(
  res,
  n = 20,
  strlength = Inf,
  style = c("v", "h"),
  label_wrap = 40,
  label_substring_to_remove = NULL,
  orderBy = c("pvalue", "termId", "none")
)
```

**Arguments**

res	output of <a href="#">getEnrichedGO</a> , <a href="#">getEnrichedPATH</a> .
n	number of terms to be plot.
strlength	shorten the description of term by the number of char.
style	plot vertically or horizontally
label_wrap	soft wrap the labels (i.e. descriptions of the GO or PATHWAY terms), default to 40 characters.
label_substring_to_remove	remove common substring from label, default to NULL. Special characters must be escaped. E.g. if you would like to remove "Homo sapiens (human)" from labels, you must use "Homo sapiens \\( human\\)".
orderBy	order the data by pvalue, termId or none.

**Value**

an object of `ggplot`

**Author(s)**

Jianhong Ou, Kai Hu

**Examples**

```

data(enrichedGO)
enrichmentPlot(enrichedGO)
if (interactive()||Sys.getenv("USER")=="jou") {

  library(org.Hs.eg.db)
  library(GO.db)
  bed <- system.file("extdata", "MACS_output.bed", package="ChIPpeakAnno")
  gr1 <- toGRanges(bed, format="BED", header=FALSE)
  gff <- system.file("extdata", "GFF_peaks.gff", package="ChIPpeakAnno")
  gr2 <- toGRanges(gff, format="GFF", header=FALSE, skip=3)
  library(EnsDb.Hsapiens.v75) ##(hg19)
  annoData <- toGRanges(EnsDb.Hsapiens.v75)
  gr1.anno <- annoPeaks(gr1, annoData)
  gr2.anno <- annoPeaks(gr2, annoData)
  over <- lapply(GRangesList(gr1=gr1.anno, gr2=gr2.anno),
                 getEnrichedGO, orgAnn="org.Hs.eg.db",
                 maxP=.05, minGOterm=10, condense=TRUE)
  enrichmentPlot(over$gr1)
  enrichmentPlot(over$gr2, style = "h")
}

```

---

EnsDb2GR

*EnsDb object to GRanges*

---

**Description**

convert EnsDb object to GRanges

**Usage**

```
EnsDb2GR(ranges, feature)
```

**Arguments**

ranges	an EnsDb object
feature	feature type, could be disjointExons, gene, exon and transcript

---

estFragmentLength	<i>estimate the fragment length</i>
-------------------	-------------------------------------

---

## Description

estimate the fragment length for bam files

## Usage

```
estFragmentLength(
  bamfiles,
  index = bamfiles,
  plot = TRUE,
  lag.max = 1000,
  minFragmentSize = 100,
  ...
)
```

## Arguments

bamfiles	The file names of the 'BAM' ('SAM' for asBam) files to be processed.
index	The names of the index file of the 'BAM' file being processed; this is given without the '.bai' extension.
plot	logical. If TRUE (the default) the acf is plotted.
lag.max	maximum lag at which to calculate the acf. See <a href="#">acf</a>
minFragmentSize	minimal fragment size to avoid the phantom peak.
...	Not used.

## Value

numeric vector

## Author(s)

Jianhong Ou

## Examples

```
if(interactive() || Sys.getenv("USER")=="jou"){
  path <- system.file("extdata", "reads", package="MMDiffBamSubset")
  if(file.exists(path)){
    WT.AB2 <- file.path(path, "WT_2.bam")
    Null.AB2 <- file.path(path, "Null_2.bam")
    Resc.AB2 <- file.path(path, "Resc_2.bam")
    estFragmentLength(c(WT.AB2, Null.AB2, Resc.AB2))
  }
}
```

```
}
```

---

estLibSize	<i>estimate the library size</i>
------------	----------------------------------

---

## Description

estimate the library size of bam files

## Usage

```
estLibSize(bamfiles, index = bamfiles, ...)
```

## Arguments

bamfiles	The file names of the 'BAM' ('SAM' for asBam) files to be processed.
index	The names of the index file of the 'BAM' file being processed; this is given without the '.bai' extension.
...	Not used.

## Value

numeric vector

## Author(s)

Jianhong Ou

## Examples

```
if(interactive() || Sys.getenv("USER")=="jou"){
  path <- system.file("extdata", "reads", package="MMDiffBamSubset")
  if(file.exists(path)){
    WT.AB2 <- file.path(path, "WT_2.bam")
    Null.AB2 <- file.path(path, "Null_2.bam")
    Resc.AB2 <- file.path(path, "Resc_2.bam")
    estLibSize(c(WT.AB2, Null.AB2, Resc.AB2))
  }
}
```

---

**ExonPlusUtr.human.GRCh37**

*Gene model with exon, 5' UTR and 3' UTR information for human sapiens (GRCh37) obtained from biomaRt*

---

**Description**

Gene model with exon, 5' UTR and 3' UTR information for human sapiens (GRCh37) obtained from biomaRt

**Usage**

```
ExonPlusUtr.human.GRCh37
```

**Format**

GRanges with slot start holding the start position of the exon, slot end holding the end position of the exon, slot rownames holding ensembl transcript id and slot space holding the chromosome location where the gene is located. In addition, the following variables are included.

```
list("strand") 1 for positive strand and -1 for negative strand
list("description") description of the transcript
list("ensembl_gene_id") gene id
list("utr5start") 5' UTR start
list("utr5end") 5' UTR end
list("utr3start") 3' UTR start
list("utr3end") 3' UTR end
```

**Details**

used in the examples Annotation data obtained by: `mart = useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl")` `ExonPlusUtr.human.GRCh37 = getAnnotation(mart=human, featureType="ExonPlusUtr")`

**Examples**

```
data(ExonPlusUtr.human.GRCh37)
slotNames(ExonPlusUtr.human.GRCh37)
```

---

**featureAlignedDistribution**  
*plot distribution in given ranges*

---

## Description

plot distribution in the given feature ranges

## Usage

```
featureAlignedDistribution(
  cvglists,
  feature.gr,
  upstream,
  downstream,
  n.tile = 100,
  zeroAt,
  ...
)
```

## Arguments

cvglists	Output of <a href="#">featureAlignedSignal</a> or a list of <a href="#">SimpleRleList</a> or <a href="#">RleList</a>
feature.gr	An object of <a href="#">GRanges</a> with identical width. If the width equal to 1, you can use upstream and downstream to set the range for plot. If the width not equal to 1, you can use zeroAt to set the zero point of the heatmap.
upstream, downstream	upstream or dwonstream from the feature.gr.
n.tile	The number of tiles to generate for each element of feature.gr, default is 100
zeroAt	zero point position of feature.gr
...	any paramters could be used by <a href="#">matplotlib</a>

## Value

invisible matrix of the plot.

## Author(s)

Jianhong Ou

## See Also

See Also as [featureAlignedSignal](#), [featureAlignedHeatmap](#)

## Examples

```
cvglists <- list(A=RleList(chr1=Rle(sample.int(5000, 100),
                                     sample.int(300, 100))),
                  B=RleList(chr1=Rle(sample.int(5000, 100),
                                     sample.int(300, 100))))
feature.gr <- GRanges("chr1", IRanges(seq(1, 4900, 100), width=100))
featureAlignedDistribution(cvglists, feature.gr, zeroAt=50, type="l")
```

### featureAlignedExtendSignal

*extract signals in given ranges from bam files*

## Description

extract signals in the given feature ranges from bam files (DNAseq only). The reads will be extended to estimated fragment length.

## Usage

```
featureAlignedExtendSignal(
  bamfiles,
  index = bamfiles,
  feature.gr,
  upstream,
  downstream,
  n.tile = 100,
  fragmentLength,
  librarySize,
  pe = c("auto", "PE", "SE"),
  adjustFragmentLength,
  gal,
  ...
)
```

## Arguments

bamfiles	The file names of the 'BAM' ('SAM' for asBam) files to be processed.
index	The names of the index file of the 'BAM' file being processed; this is given without the '.bai' extension.
feature.gr	An object of <a href="#">GRanges</a> with identical width.
upstream, downstream	upstream or downstream from the feature.gr.
n.tile	The number of tiles to generate for each element of feature.gr, default is 100
fragmentLength	Estimated fragment length.

librarySize      Estimated library size.  
 pe                Pair-end or not. Default auto.  
 adjustFragmentLength  
                   A numeric vector with length 1. Adjust the fragments/reads length to.  
 gal                A GAlignmentsList object or a list of GAlignmentPairs. If bamfiles is missing,  
                   gal is required.  
 ...                Not used.

## Value

A list of matrix. In each matrix, each row record the signals for corresponding feature.

## Author(s)

Jianhong Ou

## See Also

See Also as [featureAlignedSignal](#), [estLibSize](#), [estFragmentLength](#)

## Examples

```

if(interactive() || Sys.getenv("USER")=="jou"){
  path <- system.file("extdata", package="MMDiffBamSubset")
  if(file.exists(path)){
    WT.AB2 <- file.path(path, "reads", "WT_2.bam")
    Null.AB2 <- file.path(path, "reads", "Null_2.bam")
    Resc.AB2 <- file.path(path, "reads", "Resc_2.bam")
    peaks <- file.path(path, "peaks", "WT_2_Macs_peaks.xls")
    estLibSize(c(WT.AB2, Null.AB2, Resc.AB2))
    feature.gr <- toGRanges(peaks, format="MACS")
    feature.gr <- feature.gr[seqnames(feature.gr)=="chr1" &
      start(feature.gr)>3000000 &
      end(feature.gr)<75000000]
    sig <- featureAlignedExtendSignal(c(WT.AB2, Null.AB2, Resc.AB2),
      feature.gr=reCenterPeaks(feature.gr, width=1),
      upstream = 505,
      downstream = 505,
      n.tile=101,
      fragmentLength=250,
      librarySize=1e9)
    featureAlignedHeatmap(sig, reCenterPeaks(feature.gr, width=1010),
      zeroAt=.5, n.tile=101)
  }
}

```

---

featureAlignedHeatmap *Heatmap representing signals in given ranges*

---

## Description

plot heatmap in the given feature ranges

## Usage

```
featureAlignedHeatmap(
  cvglists,
  feature.gr,
  upstream,
  downstream,
  zeroAt,
  n.tile = 100,
  annoMcols = c(),
  sortBy = names(cvglists)[1],
  color = colorRampPalette(c("yellow", "red"))(50),
  lower.extreme,
  upper.extreme,
  margin = c(0.1, 0.01, 0.15, 0.1),
  gap = 0.01,
  newpage = TRUE,
  gp = gpar(fontsize = 10),
  ...
)
```

## Arguments

cvglists	Output of <a href="#">featureAlignedSignal</a> or a list of <a href="#">SimpleRleList</a> or <a href="#">RleList</a>
feature.gr	An object of <a href="#">GRanges</a> with identical width. If the width equal to 1, you can use upstream and downstream to set the range for plot. If the width not equal to 1, you can use zeroAt to set the zero point of the heatmap.
upstream, downstream	upstream or dwonstream from the feature.gr. It must keep same as <a href="#">featureAlignedSignal</a> . It is used for x-axis label.
zeroAt	zero point position of feature.gr
n.tile	The number of tiles to generate for each element of feature.gr, default is 100
annoMcols	The columns of metadata of feature.gr that specifies the annotations shown of the right side of the heatmap.
sortBy	Sort the feature.gr by columns by annoMcols and then the signals of the given samples. Default is the first sample. Set to NULL to disable sort.
color	vector of colors used in heatmap

lower.extreme, upper.extreme	The lower and upper boundary value of each samples
margin	Margin for of the plot region.
gap	Gap between each heatmap columns.
newpage	Call grid.newpage or not. Default, TRUE
gp	A gpar object can be used for text.
...	Not used.

**Value**

invisible gList object.

**Author(s)**

Jianhong Ou

**See Also**

See Also as [featureAlignedSignal](#), [featureAlignedDistribution](#)

**Examples**

```
cvglists <- list(A=RleList(chr1=Rle(sample.int(5000, 100),
                                      sample.int(300, 100))),
                  B=RleList(chr1=Rle(sample.int(5000, 100),
                                      sample.int(300, 100))))
feature.gr <- GRanges("chr1", IRanges(seq(1, 4900, 100), width=100))
feature.gr$anno <- rep(c("type1", "type2"), c(25, 24))
featureAlignedHeatmap(cvglists, feature.gr, zeroAt=50, annoMcols="anno")
```

`featureAlignedSignal` *extract signals in given ranges*

**Description**

extract signals in the given feature ranges

**Usage**

```
featureAlignedSignal(
  cvglists,
  feature.gr,
  upstream,
  downstream,
  n.tile = 100,
  ...
)
```

**Arguments**

<code>cvglists</code>	List of <a href="#">SimpleRleList</a> or <a href="#">RleList</a>
<code>feature.gr</code>	An object of <a href="#">GRanges</a> with identical width.
<code>upstream, downstream</code>	Set the <code>feature.gr</code> to upstream and dwonstream from the center of the <code>feature.gr</code> if they are set.
<code>n.tile</code>	The number of tiles to generate for each element of <code>feature.gr</code> , default is 100
<code>...</code>	Not used.

**Value**

A list of matrix. In each matrix, each row record the signals for corresponding feature. rownames of the matrix show the seqnames and coordinates.

**Author(s)**

Jianhong Ou

**See Also**

See Also as [featureAlignedHeatmap](#), [featureAlignedDistribution](#)

**Examples**

```

cvglists <- list(A=RleList(chr1=Rle(sample.int(5000, 100),
                                      sample.int(300, 100))),
                    B=RleList(chr1=Rle(sample.int(5000, 100),
                                      sample.int(300, 100))))
feature.gr <- GRanges("chr1", IRanges(seq(1, 4900, 100), width=100))
featureAlignedSignal(cvglists, feature.gr)

```

**Description**

Find possible enhancers by data from chromosome conformation capture techniques such as 3C, 5C or HiC.

## Usage

```
findEnhancers(
  peaks,
  annoData,
  DNAinteractiveData,
  bindingType = c("nearestBiDirectionalPromoters", "startSite", "endSite"),
  bindingRegion = c(-5000, 5000),
  ignore.peak.strand = TRUE,
  ...
)
```

## Arguments

peaks	peak list, <a href="#">GRanges</a> object
annoData	annotation data, <a href="#">GRanges</a> object
DNAinteractiveData	DNA interaction data, <a href="#">GRanges</a> object with interaction blocks informations, <a href="#">GInteractions</a> object, or BEDPE file which could be imported by <a href="#">importGInteractions</a> or <a href="#">BiocIO::import</a> or assembly in following list: hg38, hg19, mm10, danRer10, danRer11.
bindingType	Specifying the criteria to associate peaks with annotation. Here is how to use it together with the parameter bindingRegion. The annotation will be shift to a new position depend on the DNA interaction region. <ul style="list-style-type: none"> <li>• To obtain peaks within 5kb upstream and up to 3kb downstream of shift TSS within the gene body, set bindingType = "startSite" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks up to 5kb upstream within the gene body and 3kb downstream of shift gene/Exon End, set bindingType = "endSite" and bindingRegion = c(-5000, 3000)</li> <li>• To obtain peaks with nearest bi-directional enhancer regions within 5kb upstream and 3kb downstream of shift TSS, set bindingType = "nearestBiDirectionalPromoters" and bindingRegion = c(-5000, 3000)</li> </ul>
	<b>startSite</b> start position of the feature (strand is considered)
	<b>endSite</b> end position of the feature (strand is considered)
	<b>nearestBiDirectionalPromoters</b> nearest enhancer regions from both direction of the peaks (strand is considered). It will report bidirectional enhancer regions if there are enhancer regions in both directions in the given region (defined by bindingRegion). Otherwise, it will report the closest enhancer regions in one direction.
bindingRegion	Annotation range used together with bindingType, which is a vector with two integer values, default to c (-5000, 5000). The first one must be no bigger than 0. And the second one must be no less than 1. For details, see bindingType.
ignore.peak.strand	ignore the peaks strand or not.
...	Not used.

**Value**

Output is a GRanges object of the annotated peaks.

**Author(s)**

Jianhong Ou

**See Also**

See Also as [annotatePeakInBatch](#)

**Examples**

```
bed <- system.file("extdata",
                    "wgEncodeUmassDekker5CGm12878PkV2.bed.gz",
                    package="ChIPpeakAnno")
DNAinteractiveData <- toGRanges(gzfile(bed))
library(EnsDb.Hsapiens.v75)
annoData <- toGRanges(EnsDb.Hsapiens.v75, feature="gene")
data("myPeakList")
findEnhancers(myPeakList[500:1000], annoData, DNAinteractiveData)
```

**findMotifsInPromoterSeqs**

*Find occurrence of input motifs in the promoter regions of the input gene list*

**Description**

Find occurrence of input motifs in the promoter regions of the input gene list

**Usage**

```
findMotifsInPromoterSeqs(
  patternFilePath1,
  patternFilePath2,
  findPairedMotif = FALSE,
  BSGenomeName,
  txdb,
  geneIDs,
  upstream = 5000L,
  downstream = 5000L,
  name.motif1 = "motif1",
  name.motif2 = "motif2",
  max.distance = 100L,
  min.distance = 1L,
  motif.orientation = c("both", "motif1UpstreamOfMotif2", "motif2UpstreamOfMotif1"),
```

```

  ignore.strand = FALSE,
  format = "fasta",
  skip = 0L,
  motif1LocForDistance = "end",
  motif2LocForDistance = "start",
  outfile,
  append = FALSE
)

```

## Arguments

patternFilePath1	File path containing a list of known motifs. Required
patternFilePath2	File path containing a motif required to be in the flanking regions of the motif(s) in the first file, i.e, patternFilePath1. Required if findPairedMotif is set to TRUE
findPairedMotif	Find motifs in paired configuration only or not. Default FALSE
BSgenomeName	A BSgenome object. For a list of existing Bsgenomes, please refer use the function available.genomes in BSgenome package. For example, BSgenome.Hsapiens.UCSC.hg38 is for hg38, BSgenome.Hsapiens.UCSC.hg19 is for hg19, BSgenome.Mmusculus.UCSC.mm10 is for mm10, BSgenome.Celegans.UCSC.ce6 is for ce6 BSgenome.Rnorvegicus.UCSC.rn5 is for rn5, BSgenome.Drerio.UCSC.danRer7 is for Zv9, and BSgenome.Dmelanogaster.UCSC.dm3 is for dm3. Required
txdb	A TxDb object. For creating and using TxDb object, please refer to GenomicFeatures package. For a list of existing TxDb object, please search for annotation package starting with Txdb at <a href="http://www.bioconductor.org/packages/release/BiocViews.html#_Annotation">http://www.bioconductor.org/packages/release/BiocViews.html#_Annotation</a> such as TxDb.Rnorvegicus.UCSC.rn5.refGene for rat, TxDb.Mmusculus.UCSC.mm10.knownGene for mouse, TxDb.Hsapiens.UCSC.hg19.knownGene and TxDb.Hsapiens.UCSC.hg38.knownGene for human, TxDb.Dmelanogaster.UCSC.dm3.ensGene for Drosophila and TxDb.Celegans.UCSC.ce6.ensGene for C.elegans
geneIDs	One or more gene entrez IDs. For example the entrez ID for EWSIR is 2130 <a href="https://www.genecards.org/cgi-bin/carddisp.pl?gene=EWSR1">https://www.genecards.org/cgi-bin/carddisp.pl?gene=EWSR1</a> You can use the addGeneIDs function in ChIPpeakAnno to convert other types of Gene IDs to entrez ID
upstream	Number of bases upstream of the TSS to search for the motifs. Default 5000L
downstream	Number of bases downstream of the TSS to search for the motifs. Default 5000L
name.motif1	Name of the motif in inputFilePath2 for labeling the output file column. Default motif1. used only when searching for motifs in paired configuration
name.motif2	Name of the motif in inputFilePath2 for labeling the output file column. Default motif2 used only when searching for motifs in paired configuration
max.distance	maximum required gap between a paired motifs to be included in the output file. Default 100L
min.distance	Minimum required gap between a paired motifs to be included in the output file. Default 1L

<code>motif.orientation</code>	Required relative orientation between paired motifs: both means any orientation, motif1UpstreamOfMotif2 means motif1 needs to be located on the upstream of motif2, and motif2UpstreamOfMotif1 means motif2 needs to be located on the upstream of motif1. Default both
<code>ignore.strand</code>	Specify whether paired motifs should be located on the same strand. Default FALSE
<code>format</code>	The format of the files specified in <code>inputFilePath1</code> and <code>inputFilePath2</code> . Default fasta
<code>skip</code>	Specify number of lines to skip at the beginning of the input file. Default 0L
<code>motif1LocForDistance</code>	Specify whether to use the start or end of the motif1 location to calculate distance between paired motifs. Only applicable when <code>findPairedMotif</code> is set to TRUE. Default end
<code>motif2LocForDistance</code>	Specify whether to use the start or end of the motif2 location to calculate distance between paired motifs. Only applicable when <code>findPairedMotif</code> is set to TRUE. Default start
<code>outfile</code>	File path to save the search results
<code>append</code>	Specify whether to append the results to the specified output file, i.e., <code>outfile</code> . Default FALSE

## Details

This function outputs the motif occurring locations in the promoter regions of input gene list and input motifs. It also can find paired motifs within specified gap threshold

## Value

A vector of numeric. It is the background corrected log2-transformed ratios, CPMRatios or Odd-Ratios.

An object of GRanges with metadata "tx\_start", "tx\_end tx\_strand", "tx\_id", "tx\_name", "Gene ID", and motif specific information such as motif name, motif found, motif strand etc.

## Author(s)

Lihua Julie Zhu, Kai Hu

## Examples

```
library("BSgenome.Hsapiens.UCSC.hg38")
library("TxDb.Hsapiens.UCSC.hg38.knownGene")

patternFilePath1 =system.file("extdata", "motifIRF4.fa", package="ChIPpeakAnno")
patternFilePath2 =system.file("extdata", "motifAP1.fa", package="ChIPpeakAnno")
pairedMotifs <- findMotifsInPromoterSeqs(patternFilePath1 = patternFilePath1,
  patternFilePath2 = patternFilePath2.
```

```

findPairedMotif = TRUE,
name.motif1 = "IRF4", name.motif2 = "AP1",
BSgenomeName = BSgenome.Hsapiens.UCSC.hg38,
geneIDs = 7486, txdb = TxDb.Hsapiens.UCSC.hg38.knownGene,
outfile = "testPaired.xls")

unPairedMotifs <- findMotifsInPromoterSeqs(patternFilePath1 = patternFilePath1,
                                             BSgenomeName = BSgenome.Hsapiens.UCSC.hg38,
                                             geneIDs = 7486, txdb = TxDb.Hsapiens.UCSC.hg38.knownGene,
                                             outfile = "testUnPaired.xls")

```

---

**findOverlappingPeaks** *Find the overlapping peaks for two peak ranges.*

---

## Description

Find the overlapping peaks for two input peak ranges.

## Usage

```

findOverlappingPeaks(
  Peaks1,
  Peaks2,
  maxgap = -1L,
  minoverlap = 0L,
  multiple = c(TRUE, FALSE),
  NameOfPeaks1 = "TF1",
  NameOfPeaks2 = "TF2",
  select = c("all", "first", "last", "arbitrary"),
  annotate = 0,
  ignore.strand = TRUE,
  connectedPeaks = c("min", "merge"),
  ...
)

```

## Arguments

Peaks1	GRanges: See example below.
Peaks2	GRanges: See example below.
maxgap, minoverlap	Used in the internal call to <code>findOverlaps()</code> to detect overlaps. See <a href="#">?findOverlaps</a> in the <b>IRanges</b> package for a description of these arguments.
multiple	TRUE or FALSE: TRUE may return multiple overlapping peaks in Peaks2 for one peak in Peaks1; FALSE will return at most one overlapping peaks in Peaks2 for one peak in Peaks1. This parameter is kept for backward compatibility, please use select.

NameOfPeaks1	Name of the Peaks1, used for generating column name.
NameOfPeaks2	Name of the Peaks2, used for generating column name.
select	all may return multiple overlapping peaks, first will return the first overlapping peak, last will return the last overlapping peak and arbitrary will return one of the overlapping peaks.
annotate	Include overlapFeature and shortestDistance in the OverlappingPeaks or not. 1 means yes and 0 means no. Default to 0.
ignore.strand	When set to TRUE, the strand information is ignored in the overlap calculations.
connectedPeaks	If multiple peaks involved in overlapping in several groups, set it to "merge" will count it as only 1, while set it to "min" will count it as the minimal involved peaks in any concered groups
...	Objects of <a href="#">GRanges</a> : See also <a href="#">findOverlapsOfPeaks</a> .

## Details

The new function `findOverlapsOfPeaks` is recommended.

Efficiently perform overlap queries with an interval tree implemented in `IRanges`.

## Value

### OverlappingPeaks

a data frame consists of input peaks information with added information: overlapFeature (upstream: peak1 resides upstream of the peak2; downstream: peak1 resides downstream of the peak2; inside: peak1 resides inside the peak2 entirely; overlapStart: peak1 overlaps with the start of the peak2; overlapEnd: peak1 overlaps with the end of the peak2; includeFeature: peak1 include the peak2 entirely) and shortestDistance (shortest distance between the overlapping peaks)

### MergedPeaks

`GRanges` contains merged overlapping peaks

## Author(s)

Lihua Julie Zhu

## References

1. Interval tree algorithm from: Cormen, Thomas H.; Leiserson, Charles E.; Rivest, Ronald L.; Stein, Clifford. *Introduction to Algorithms*, second edition, MIT Press and McGraw-Hill. ISBN 0-262-53196-8
2. Zhu L.J. et al. (2010) ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. *BMC Bioinformatics* 2010, 11:237 doi:10.1186/1471-2105-11-237
3. Zhu L (2013). Integrative analysis of ChIP-chip and ChIP-seq dataset. In Lee T and Luk ACS (eds.), *Tilling Arrays*, volume 1067, chapter 4, pp. -19. Humana Press. [http://dx.doi.org/10.1007/978-1-62703-607-8\\_8](http://dx.doi.org/10.1007/978-1-62703-607-8_8)

## See Also

`findOverlapsOfPeaks`, `annotatePeakInBatch`, `makeVennDiagram`

## Examples

```

if (interactive())
{
  peaks1 =
    GRanges(seqnames=c(6,6,6,6,5),
            IRanges(start=c(1543200,1557200,1563000,1569800,167889600),
                    end=c(1555199,1560599,1565199,1573799,167893599),
                    names=c("p1","p2","p3","p4","p5")),
                    strand=as.integer(1))
  peaks2 =
    GRanges(seqnames=c(6,6,6,6,5),
            IRanges(start=c(1549800,1554400,1565000,1569400,167888600),
                    end=c(1550599,1560799,1565399,1571199,167888999),
                    names=c("f1","f2","f3","f4","f5")),
                    strand=as.integer(1))
  t1 =findOverlappingPeaks(peaks1, peaks2, maxgap=1000,
                           NameOfPeaks1="TF1", NameOfPeaks2="TF2", select="all", annotate=1)
  r = t1$OverlappingPeaks
  pie(table(r$overlapFeature))
  as.data.frame(t1$MergedPeaks)
}

```

---

**findOverlapsOfPeaks** *Find the overlapped peaks among two or more set of peaks.*

---

## Description

Find the overlapping peaks for two or more (less than five) set of peak ranges.

## Usage

```

findOverlapsOfPeaks(
  ...,
  maxgap = -1L,
  minoverlap = 0L,
  ignore.strand = TRUE,
  connectedPeaks = c("keepAll", "min", "merge")
)

```

## Arguments

... Objects of **GRanges**: See example below.

maxgap, minoverlap

Used in the internal call to `findOverlaps()` to detect overlaps. See `?findOverlaps` in the **IRanges** package for a description of these arguments. If  $0 < \text{minoverlap} < 1$ , the function will find overlaps by percentage covered of interval and the filter condition will be set to max covered percentage of overlapping peaks.

`ignore.strand` When set to TRUE, the strand information is ignored in the overlap calculations.

`connectedPeaks` If multiple peaks are involved in any group of connected/overlapping peaks in any input peak list, set it to "merge" will add 1 to the overlapping counts, while set it to "min" will add the minimal involved peaks in each group of connected/overlapped peaks to the overlapping counts. Set it to "keepAll" will add the number of involved peaks for each peak list to the corresponding overlapping counts. In addition, it will output counts as if `connectedPeaks` were set to "min". For examples (<https://support.bioconductor.org/p/133486/#133603>), if 5 peaks in group1 overlap with 2 peaks in group 2, setting `connectedPeaks` to "merge" will add 1 to the overlapping counts; setting it to "keepAll" will add 5 peaks to `count.group1`, 2 to `count.group2`, and 2 to `counts`; setting it to "min" will add 2 to the overlapping counts.

## Details

Efficiently perform overlap queries with an interval tree implemented with GRanges.

## Value

return value is An object of overlappingPeaks.

<code>venn_cnt</code>	an object of VennCounts
<code>peaklist</code>	a list consists of all overlapping peaks or unique peaks
<code>uniquePeaks</code>	an object of GRanges consists of all unique peaks
<code>mergedPeaks</code>	an object of GRanges consists of all merged overlapping peaks
<code>peaksInMergedPeaks</code>	an object of GRanges consists of all peaks in each samples involved in the overlapping peaks
<code>overlappingPeaks</code>	a list of data frame consists of the annotation of all the overlapped peaks
<code>all.peaks</code>	a list of GRanges object which contain the input peaks with formated rownames.

## Author(s)

Jianhong Ou

## References

1. Interval tree algorithm from: Cormen, Thomas H.; Leiserson, Charles E.; Rivest, Ronald L.; Stein, Clifford. Introduction to Algorithms, second edition, MIT Press and McGraw-Hill. ISBN 0-262-53196-8
2. Zhu L.J. et al. (2010) ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. BMC Bioinformatics 2010, 11:237doi:10.1186/1471-2105-11-237
3. Zhu L (2013). "Integrative analysis of ChIP-chip and ChIP-seq dataset." In Lee T and Luk ACS (eds.), Tiling Arrays, volume 1067, chapter 4, pp. -19. Humana Press. [http://dx.doi.org/10.1007/978-1-62703-607-8\\_8](http://dx.doi.org/10.1007/978-1-62703-607-8_8), [http://link.springer.com/protocol/10.1007%2F978-1-62703-607-8\\_8](http://link.springer.com/protocol/10.1007%2F978-1-62703-607-8_8)

**See Also**

[annotatePeakInBatch](#), [makeVennDiagram](#), [getVennCounts](#), [findOverlappingPeaks](#)

**Examples**

```
peaks1 <- GRanges(seqnames=c(6,6,6,6,5),
                    IRanges(start=c(1543200,1557200,1563000,1569800,167889600),
                           end=c(1555199,1560599,1565199,1573799,167893599),
                           names=c("p1","p2","p3","p4","p5")),
                           strand="+")
peaks2 <- GRanges(seqnames=c(6,6,6,6,5),
                    IRanges(start=c(1549800,1554400,1565000,1569400,167888600),
                           end=c(1550599,1560799,1565399,1571199,167888999),
                           names=c("f1","f2","f3","f4","f5")),
                           strand="+")
t1 <- findOverlapsOfPeaks(peaks1, peaks2, maxgap=1000)
makeVennDiagram(t1)
t1$venn_cnt
t1$peaklist
t2 <- findOverlapsOfPeaks(peaks1, peaks2, minoverlap = .5)
makeVennDiagram(t2)

t3 <- findOverlapsOfPeaks(peaks1, peaks2, minoverlap = .90)
makeVennDiagram(t3)
```

---

genomicElementDistribution  
*Genomic Element distribution*

---

**Description**

Plot pie chart for genomic element distribution

**Usage**

```
genomicElementDistribution(
  peaks,
  TxDb,
  seqlev,
  nucleotideLevel = FALSE,
  ignore.strand = TRUE,
  promoterRegion = c(upstream = 2000, downstream = 100),
  geneDownstream = c(upstream = 0, downstream = 1000),
  labels = list(geneLevel = c(promoter = "Promoter", geneDownstream = "Downstream",
                               geneBody = "Gene body", distalIntergenic = "Distal Intergenic"),
                           ExonIntron = c(exon = "Exon", intron = "Intron", intergenic = "Intergenic"),
                           Exons = c(utr5 = "5' UTR", utr3 = "3' UTR", CDS = "CDS", otherExon = "Other exon"),
                           group = c(geneLevel =
```

```

  "Transcript Level", promoterLevel = "Promoter Level", Exons = "Exon level",
  ExonIntron = "Exon/Intron/Intergenic")),
  labelColors = c(promoter = "#E1F114", geneBody = "#9EFF00", geneDownstream = "#57CB1B",
  distalIntergenic = "#066A4B", exon = "#6600FF", intron = "#8F00FF", intergenic =
  "#DA00FF", utr5 = "#00FFDB", utr3 = "#00DFFF", CDS = "#00A0FF", otherExon =
  "#006FFF"),
  plot = TRUE,
  keepExonsInGenesOnly = TRUE,
  promoterLevel
)

```

## Arguments

peaks	peak list, <a href="#">GRanges</a> object or a <a href="#">GRangesList</a> .
TxDb	an object of <a href="#">TxDb</a>
seqlev	sequence level should be involved. Default is all the sequence levels in intersect of peaks and TxDb.
nucleotideLevel	Logical. Choose between peak centric and nucleotide centric view. Default=FALSE
ignore.strand	logical. Whether the strand of the input ranges should be ignored or not. Default=TRUE
promoterRegion	numeric. The upstream and downstream of genes to define promoter region.
geneDownstream	numeric. The upstream and downstream of genes to define gene downstream region.
labels	list. A list for labels for the genomic elements.
labelColors	named character vector. The colors for each labels.
plot	logic. Plot the pie chart for the genomic elements or not.
keepExonsInGenesOnly	logic. Keep the exons within annotated gene only.
promoterLevel	list. The breaks, labels, and colors for divided range of promoters. The breaks must be from 5' -> 3' and the percentage will use the fixed precedence 3' -> 5'

## Details

The distribution will be calculated by geneLevel, ExonIntron, and Exons. The geneLevel will be categorized as promoter region, gene body, gene downstream and distal intergenic region. The ExonIntron will be categorized as exon, intron and intergenic. The Exons will be categorized as 5' UTR, 3'UTR and CDS. The precedence will follow the order of labels definition. For example, for ExonIntron, if a peak overlap with both exon and intron, and exon is specified before intron, then only exon will be incremented for the same example.

## Value

Invisible list of data for plot.

## Examples

```

if (interactive() || Sys.getenv("USER")=="jou"){
  data(myPeakList)
  if(require(TxDb.Hsapiens.UCSC.hg19.knownGene)){
    seqinfo(myPeakList) <-
      seqinfo(TxDb.Hsapiens.UCSC.hg19.knownGene)[seqlevels(myPeakList)]
    myPeakList <- GenomicRanges::trim(myPeakList)
    myPeakList <- myPeakList[width(myPeakList)>0]
    genomicElementDistribution(myPeakList,
      TxDb.Hsapiens.UCSC.hg19.knownGene)
    genomicElementDistribution(myPeakList,
      TxDb.Hsapiens.UCSC.hg19.knownGene,
      nucleotideLevel = TRUE)
    genomicElementDistribution(myPeakList,
      TxDb.Hsapiens.UCSC.hg19.knownGene,
      promoterLevel=list(
        #from 5' -> 3', fixed precedence 3' -> 5'
        breaks = c(-2000, -1000, -500, 0, 100),
        labels = c("upstream 1-2Kb", "upstream 0.5-1Kb",
          "upstream <500b", "TSS - 100b"),
        colors = c("#FFE5CC", "#FFCA99",
          "#FFAD65", "#FF8E32"))))
  }
}

```

---

genomicElementUpSetR    *Genomic Element data for upset plot*

---

## Description

Prepare data for upset plot for genomic element distribution

## Usage

```

genomicElementUpSetR(
  peaks,
  TxDb,
  seqlev,
  ignore.strand = TRUE,
  breaks = list(distal_upstream = c(-1e+05, -10000, -1, 1), proximal_upstream = c(-10000,
  -5000, -1, 1), distal_promoter = c(-5000, -2000, -1, 1), proximal_promoter = c(-2000,
  200, -1, 0), `5'UTR` = fiveUTRsByTranscript, `3'UTR` = threeUTRsByTranscript, CDS =
  cds, exon = exons, intron = intronsByTranscript, gene_body = genes,
  immediate_downstream = c(0, 2000, 1, 1), proximal_downstream = c(2000, 5000, 1, 1),
  distal_downstream = c(5000, 1e+05, 1, 1))
)

```

### Arguments

peaks	peak list, <a href="#">GRanges</a> object or a <a href="#">GRangesList</a> .
TxDb	an object of <a href="#">TxDb</a>
seqlev	sequence level should be involved. Default is all the sequence levels in intersect of peaks and TxDb.
ignore.strand	logical. Whether the strand of the input ranges should be ignored or not. Default=TRUE
breaks	list. A list for labels and sets for the genomic elements. The element could be an S4 method for signature 'TxDb' or a numeric vector with length of 4. The three numbers are c(upstream point, downstream point, promoter (-1) or downstream (1), remove gene body or not (1: remove, 0: keep)).

### Details

The data will be calculated by for each breaks. No precedence will be considered.

### Value

list of data for plot.

### Examples

```
if (interactive() || Sys.getenv("USER")=="jou"){
  data(myPeakList)
  if(require(TxDb.Hsapiens.UCSC.hg19.knownGene)){
    seqinfo(myPeakList) <-
      seqinfo(TxDb.Hsapiens.UCSC.hg19.knownGene)[seqlevels(myPeakList)]
    myPeakList <- GenomicRanges::trim(myPeakList)
    myPeakList <- myPeakList[width(myPeakList)>0]
    x <- genomicElementUpSetR(myPeakList,
      TxDb.Hsapiens.UCSC.hg19.knownGene)
    library(UpSetR)
    upset(x$plotData, nsets=13, nintersects=NA)
  }
}
```

---

getAllPeakSequence	<i>Obtain genomic sequences around the peaks</i>
--------------------	--

---

### Description

Obtain genomic sequences around the peaks leveraging the BSgenome and biomaRt package

## Usage

```
getAllPeakSequence(
  myPeakList,
  upstream = 200L,
  downstream = upstream,
  genome,
  AnnotationData
)
```

## Arguments

myPeakList	An object of <a href="#">GRanges</a> : See example below
upstream	upstream offset from the peak start, e.g., 200
downstream	downstream offset from the peak end, e.g., 200
genome	BSgenome object or mart object. Please refer to available.genomes in BSgenome package and useMart in bioMart package for details
AnnotationData	GRanges object with annotation information.

## Value

[GRanges](#) with slot start holding the start position of the peak, slot end holding the end position of the peak, slot rownames holding the id of the peak and slot seqnames holding the chromosome where the peak is located. In addition, the following variables are included:

upstream	upstream offset from the peak start
downstream	downstream offset from the peak end
sequence	the sequence obtained

## Author(s)

Lihua Julie Zhu, Jianhong Ou

## References

Durinck S. et al. (2005) BioMart and Bioconductor: a powerful link between biological biomarts and microarray data analysis. Bioinformatics, 21, 3439-3440.

## Examples

```
#### use Annotation data from BSgenome
peaks <- GRanges(seqnames=c("NC_008253", "NC_010468"),
  IRanges(start=c(100, 500), end=c(300, 600),
  names=c("peak1", "peak2")))
library(BSgenome.Ecoli.NCBI.20080805)
seq <- getAllPeakSequence(peaks, upstream=20, downstream=20, genome=Ecoli)
write2FASTA(seq, file="test.fa")
```

---

getAnnotation	<i>Obtain the TSS, exon or miRNA annotation for the specified species</i>
---------------	---

---

## Description

Obtain the TSS, exon or miRNA annotation for the specified species using the biomaRt package

## Usage

```
getAnnotation(  
  mart,  
  featureType = c("TSS", "miRNA", "Exon", "5utr", "3utr", "ExonPlusUtr", "transcript")  
)
```

## Arguments

mart	A mart object, see useMart of biomaRt package for details.
featureType	TSS, miRNA, Exon, 5'UTR, 3'UTR, transcript or Exon plus UTR. The default is TSS.

## Value

**GRanges** with slot start holding the start position of the feature, slot end holding the end position of the feature, slot names holding the id of the feature, slot space holding the chromosome location where the feature is located. In addition, the following variables are included.

```
list("strand") 1 for positive strand and -1 for negative strand where the feature is located  
list("description")  
description of the feature such as gene
```

## Note

For featureType of TSS, start is the transcription start site if strand is 1 (plus strand), otherwise, end is the transcription start site.

Note that the version of the annotation db must match with the genome used for mapping because the coordinates may differ for different genome releases. For example, if you are using Mus\_musculus.v103 for mapping, you'd best also use EnsDb.Mmusculus.v103 for annotation. See Examples for more info.

## Author(s)

Lihua Julie Zhu, Jianhong Ou, Kai Hu

## References

Durinck S. et al. (2005) BioMart and Bioconductor: a powerful link between biological biomarts and microarray data analysis. Bioinformatics, 21, 3439-3440.

## Examples

```

if (interactive() || Sys.getenv("USER")=="jou" )
{
  library(biomaRt)
  mart <- useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")
  Annotation <- getAnnotation(mart, featureType="TSS")
}

#####
# Below are 3 options to fetch the annotation file. #
#####

if (interactive() || Sys.getenv("USER")=="jou" ){
## Option1: with the AnnotationHub package
library(AnnotationHub)
ah <- AnnotationHub()
EnsDb.Mmusculus <- query(ah, pattern = c("Mus musculus", "EnsDb"))
EnsDb.Mmusculus.v101 <- EnsDb.Mmusculus[[length(EnsDb.Mmusculus)]]
class(EnsDb.Mmusculus.v101)

## Option2: with the getAnnotation() function
library(ChIPpeakAnno)
library(biomaRt)
listMarts()
mart <- useMart(biomart="ENSEMBL_MART_ENSEMBL",
                 dataset="mmusculus_gene_ensembl")
Annotation <- getAnnotation(mart)
# Note that getAnnotation() queries biomart, which is always up-to-date.

## Option3: build your own EnsDb package
## This may need extra effort, and the ?makeEnsmeblDbPackage
## is a good starting point.
}

```

getEnrichedGO

*Obtain enriched gene ontology (GO) terms that near the peaks*

## Description

Obtain enriched gene ontology (GO) terms based on the features near the enriched peaks using GO.db package and GO gene mapping package such as org.Hs.db.eg to obtain the GO annotation and using hypergeometric test (phyper) and multtest package for adjusting p-values

## Usage

```

getEnrichedGO(
  annotatedPeak,
  orgAnn,
  feature_id_type = "ensembl_gene_id",
  maxP = 0.01,

```

```

minGOterm = 10,
multiAdjMethod = NULL,
condense = FALSE,
removeAncestorByPval = NULL,
keepByLevel = NULL,
subGroupComparison = NULL
)

```

### Arguments

annotatedPeak	A GRanges object or a vector of feature IDs
orgAnn	Organism annotation package such as org.Hs.eg.db for human and org.Mm.eg.db for mouse, org.Dm.eg.db for fly, org.Rn.eg.db for rat, org.Sc.eg.db for yeast and org.Dr.eg.db for zebrafish
feature_id_type	The feature type in annotatedPeak such as ensembl_gene_id, refseq_id, gene_symbol or entrez_id
maxP	The maximum p-value to be considered to be significant
minGOterm	The minimum count in a genome for a GO term to be included
multiAdjMethod	The multiple testing procedures, for details, see mt.rawp2adjp in multtest package
condense	Condense the results or not.
removeAncestorByPval	Remove ancestor by p-value. P-value is calculated by fisher exact test. If gene number in all of the children is significant greater than it in parent term, the parent term will be removed from the list.
keepByLevel	If the shortest path from the go term to 'all' is greater than the given level, the term will be removed.
subGroupComparison	A logical vector to split the peaks into two groups. The enrichment analysis will compare the over-present GO terms in TRUE group and FALSE group separately. The analysis will split into two steps: 1. enrichment analysis for TRUE group by hypergeometric test; 2. enrichment analysis for TRUE over FALSE group by Fisher's Exact test for the enriched GO terms. To keep the output same format, if you want to compare FALSE vs TRUE, please repeat the analysis by inverting the parameter. Default is NULL.

### Value

A list with 3 elements

list("bp")	enriched biological process with the following 9 variables go.id:GO biological process id go.term:GO biological process term go.Definition:GO biological process description Ontology: Ontology branch, i.e. BP for biological process
------------	--

```

count.InDataset: count of this GO term in this dataset
count.InGenome: count of this GO term in the genome
pvalue: pvalue from the hypergeometric test
totaltermInDataset: count of all GO terms in this dataset
totaltermInGenome: count of all GO terms in the genome
list("mf")
  enriched molecular function with the following 9 variables
  go.id:GO molecular function id
  go.term:GO molecular function term
  go.Definition:GO molecular function description
  Ontology: Ontology branch, i.e. MF for molecular function
  count.InDataset: count of this GO term in this dataset
  count.InGenome: count of this GO term in the genome
  pvalue: pvalue from the hypergeometric test
  totaltermInDataset: count of all GO terms in this dataset
  totaltermInGenome: count of all GO terms in the genome
list("cc")
  enriched cellular component the following 9 variables
  go.id:GO cellular component id
  go.term:GO cellular component term
  go.Definition:GO cellular component description
  Ontology: Ontology type, i.e. CC for cellular component
  count.InDataset: count of this GO term in this dataset
  count.InGenome: count of this GO term in the genome
  pvalue: pvalue from the hypergeometric test
  totaltermInDataset: count of all GO terms in this dataset
  totaltermInGenome: count of all GO terms in the genome

```

### Author(s)

Lihua Julie Zhu. Jianhong Ou for subGroupComparison

### References

Johnson, N. L., Kotz, S., and Kemp, A. W. (1992) Univariate Discrete Distributions, Second Edition. New York: Wiley

### See Also

phyper, hyperGtest

### Examples

```

data(enrichedGO)
enrichedGO$mf[1:10,]
enrichedGO$bp[1:10,]
enrichedGO$cc
if (interactive()) {

```

```

data(annotatedPeak)
library(org.Hs.eg.db)
library(GO.db)
enriched.GO = getEnrichedGO(annotatedPeak[1:6,],
                           orgAnn="org.Hs.eg.db",
                           maxP=0.01,
                           minGOterm=10,
                           multiAdjMethod= NULL)
dim(enriched.GO$mf)
colnames(enriched.GO$mf)
dim(enriched.GO$bp)
enriched.GO$cc
}

```

---

getEnrichedPATH	<i>Obtain enriched PATH that near the peaks</i>
-----------------	---

---

### Description

Obtain enriched PATH that are near the peaks using path package such as reactome.db and path mapping package such as org.Hs.db.eg to obtain the path annotation and using hypergeometric test (phyper) and multtest package for adjusting p-values

### Usage

```

getEnrichedPATH(
  annotatedPeak,
  orgAnn,
  pathAnn,
  feature_id_type = "ensembl_gene_id",
  maxP = 0.01,
  minPATHterm = 10,
  multiAdjMethod = NULL,
  subGroupComparison = NULL
)

```

### Arguments

annotatedPeak	GRanges such as data(annotatedPeak) or a vector of feature IDs
orgAnn	organism annotation package such as org.Hs.eg.db for human and org.Mm.eg.db for mouse, org.Dm.eg.db for fly, org.Rn.eg.db for rat, org.Sc.eg.db for yeast and org.Dr.eg.db for zebrafish
pathAnn	pathway annotation package such as KEGG.db (deprecated), reactome.db, KEG-GREST
feature_id_type	the feature type in annotatedPeakRanges such as ensembl_gene_id, refseq_id, gene_symbol or entrez_id

**maxP** maximum p-value to be considered to be significant  
**minPATHterm** minimum count in a genome for a path to be included  
**multiAdjMethod** multiple testing procedures, for details, see `mt.rawp2adjp` in `multtest` package  
**subGroupComparison**  
A logical vector to split the peaks into two groups. The enrichment analysis will compare the over-present GO terms in TRUE group and FALSE group separately. The analysis will split into two steps: 1. enrichment analysis for TRUE group by hypergeometric test; 2. enrichment analysis for TRUE over FALSE group by Fisher's Exact test for the enriched GO terms. To keep the output same format, if you want to compare FALSE vs TRUE, please repeat the analysis by inverting the parameter. Default is NULL.

### Value

A dataframe of enriched path with the following variables.

<code>path.id</code>	KEGG PATH ID
<code>EntrezID</code>	Entrez ID
<code>count.InDataset</code>	count of this PATH in this dataset
<code>count.InGenome</code>	count of this PATH in the genome
<code>pvalue</code>	pvalue from the hypergeometric test
<code>totaltermInDataset</code>	count of all PATH in this dataset
<code>totaltermInGenome</code>	count of all PATH in the genome
<code>PATH</code>	PATH name

### Author(s)

Jianhong Ou, Kai Hu

### References

Johnson, N. L., Kotz, S., and Kemp, A. W. (1992) *Univariate Discrete Distributions*, Second Edition. New York: Wiley

### See Also

`phyper`, `hyperGtest`

### Examples

```

if (interactive() || Sys.getenv("USER") == "jou") {
  data(annotatedPeak)
  library(org.Hs.eg.db)
  library(reactome.db)
  enriched.PATH = getEnrichedPATH(annotatedPeak, orgAnn = "org.Hs.eg.db",

```

```

        feature_id_type="ensembl_gene_id",
        pathAnn="reactome.db", maxP=0.01,
        minPATHterm=10, multiAdjMethod=NULL)
head(enriched.PATH)
enrichedKEGG = getEnrichedPATH(annotatedPeak, orgAnn="org.Hs.eg.db",
                               feature_id_type="ensembl_gene_id",
                               pathAnn="KEGGREST", maxP=0.01,
                               minPATHterm=10, multiAdjMethod=NULL)
enrichmentPlot(enrichedKEGG)
}

```

---

getGeneSeq*Get gene sequence using the biomaRt package*

---

**Description**

Get gene sequence using the biomaRt package

**Usage**

```
getGeneSeq(LocationParameters, mart)
```

**Arguments**

LocationParameters	c(ensembl_gene_id, distance from the peak to the transcription start site of the gene with the above ensemblID, upstream offset from the peak, downstream offset from the peak, Gene Start, Gene End)
mart	see useMart of bioMaRt package for details

**Value**

a list with the following items

feature_id	ensemble gene ID
distancetoFeature	distance from the peak to the transcriptionstart site of the gene with the above ensembl gene ID
upstream	upstream offset from the peakStart
downstream	downstream offset from the peakEnd
seq	sequence obtained around the peak with above upstream and downstream offset

**Note**

internal function not intended to be called directly by users

**Author(s)**

Lihua Julie Zhu

**Examples**

```
if (interactive())
{
  mart <- useMart(biomart="ensembl", dataset="drerio_gene_ensembl")
  LocationParameters =c("ENSDARG00000054562",400, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)

  LocationParameters =c("ENSDARG00000054562",752, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)

  LocationParameters =c("ENSDARG00000054562",750, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)

  LocationParameters =c("ENSDARG00000054562",-2, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)

  LocationParameters =c("ENSDARG00000054562",0, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)

  LocationParameters =c("ENSDARG00000054562",2, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)

  LocationParameters =c("ENSDARG00000054562",1000, 750, 750,40454140,40454935)
  getGeneSeq(LocationParameters, mart)
}
```

---

getGO

*Obtain gene ontology (GO) terms for given genes*

---

**Description**

Obtain gene ontology (GO) terms using GO gene mapping package such as org.Hs.db.eg to obtain the GO annotation.

**Usage**

```
getGO(all.genes, orgAnn = "org.Hs.eg.db", writeTo, ID_type = "gene_symbol")
```

**Arguments**

all.genes	A character vector of feature IDs
orgAnn	Organism annotation package such as org.Hs.eg.db for human and org.Mm.eg.db for mouse, org.Dm.eg.db for fly, org.Rn.eg.db for rat, org.Sc.eg.db for yeast and org.Dr.eg.db for zebrafish
writeTo	File path for output table
ID_type	The feature type in annotatedPeak such as ensembl_gene_id, refseq_id, gene_symbol

**Value**

An invisible table with genes and GO terms.

**Author(s)**

Lihua Julie Zhu

**See Also**

getEnrichedGO

**Examples**

```
if (interactive()) {
  data(annotatedPeak)
  library(org.Hs.eg.db)
  getGO(annotatedPeak[1:6]$feature,
        orgAnn="org.Hs.eg.db",
        ID_type="ensembl_gene_id")
}
```

---

getUniqueGOidCount *get the count for each unique GO ID*

---

**Description**

get the count for each unique GO ID

**Usage**

getUniqueGOidCount(goList)

**Arguments**

goList	a set of GO terms as character vector
--------	---------------------------------------

**Value**

a list with 2 variables

GOterm	a vector of GO terms as character vector
GOcount	counts corresponding to the above GOterm as numeric vector

**Note**

internal function not intended to be called directly by users

**Author(s)**

Lihua Julie Zhu

**See Also**

getEnrichedGO

**Examples**

```
goList= c("GO:0000075", "GO:0000082","GO:0000082","GO:0000122","GO:0000122",
        "GO:0000075","GO:0000082","GO:0000082","GO:0000122","GO:0000122",
        "GO:0000122","GO:0000122","GO:0000075", "GO:0000082","GO:000012")  
getUniqueGOidCount(goList)
```

getVennCounts	<i>Obtain Venn Counts for Venn Diagram, internal function for makeVennDiagram</i>
---------------	---

**Description**

Obtain Venn Counts for peak ranges using chromosome ranges or feature field, internal function for makeVennDiagram

**Usage**

```
getVennCounts(  
  ...,  
  maxgap = -1L,  
  minoverlap = 0L,  
  by = c("region", "feature", "base"),  
  ignore.strand = TRUE,  
  connectedPeaks = c("min", "merge", "keepAll")  
)
```

## Arguments

...	Objects of <a href="#">GRanges</a> . See example below.
maxgap, minoverlap	Used in the internal call to <code>findOverlaps()</code> to detect overlaps. See <a href="#">?findOverlaps</a> in the <a href="#">IRanges</a> package for a description of these arguments.
by	region, feature or base, default region. feature means using feature field in the <a href="#">GRanges</a> for calculating overlap, region means using chromosome range for calculating overlap, and base means using calculating overlap in nucleotide level.
ignore.strand	When set to TRUE, the strand information is ignored in the overlap calculations.
connectedPeaks	If multiple peaks involved in overlapping in several groups, set it to "merge" will count it as only 1, while set it to "min" will count it as the minimal involved peaks in any concered groups

## Value

vennCounts	vennCounts objects containing counts for Venn Diagram generation, see details in limma package <code>vennCounts</code>
------------	--

## Author(s)

Jianhong Ou

## See Also

[makeVennDiagram](#), [findOverlappingPeaks](#)

## Examples

```
if(interactive() || Sys.getenv("USER")=="jou"){
  peaks1 = GRanges(seqnames=c("1", "2", "3"),
    IRanges(start = c(967654, 2010897, 2496704),
            end = c(967754, 2010997, 2496804),
            names = c("Site1", "Site2", "Site3")),
    strand=as.integer(1),
    feature=c("a", "b", "c"))

  peaks2 =
  GRanges(seqnames= c("1", "2", "3", "1", "2"),
    IRanges(start=c(967659, 2010898, 2496700, 3075866, 3123260),
            end=c(967869, 2011108, 2496920, 3076166, 3123470),
            names = c("t1", "t2", "t3", "t4", "t5")),
    strand = c(1L, 1L, -1L,-1L,1L),
    feature=c("a", "c", "d", "e", "a"))

  getVennCounts(peaks1,peaks2)
  getVennCounts(peaks1,peaks2, by="feature")
  getVennCounts(peaks1, peaks2, by="base")
}
```

HOT.spots

*High Occupancy of Transcription Related Factors regions***Description**

High Occupancy of Transcription Related Factors regions of human (hg19)

**Usage**

HOT.spots

**Format**

An object of GRangesList

**Details**

How to generated the data:

```
temp <- tempfile()
url <- "http://metatracks.encode.nets.gersteinlab.org"
download.file(file.path(url, "HOT_All_merged.tar.gz"), temp)
temp2 <- tempfile()
download.file(file.path(url, "HOT_intergenic_All_merged.tar.gz"), temp2)
untar(temp, exdir=dirname(temp))
untar(temp2, exdir=dirname(temp))
f <- dir(dirname(temp), "bed$")
HOT.spots <- sapply(file.path(dirname(temp), f), toGRanges, format="BED")
names(HOT.spots) <- gsub("_merged.bed", "", f)
HOT.spots <- sapply(HOT.spots, unname)
HOT.spots <- GRangesList(HOT.spots)
save(list="HOT.spots",
file="data/HOT.spots.rda",
compress="xz", compression_level=9)
```

**Source**

<http://metatracks.encode.nets.gersteinlab.org/>

## References

Yip KY, Cheng C, Bhardwaj N, Brown JB, Leng J, Kundaje A, Rozowsky J, Birney E, Bickel P, Snyder M, Gerstein M. Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. *Genome Biol.* 2012 Sep 26;13(9):R48. doi: 10.1186/gb-2012-13-9-r48. PubMed PMID: 22950945; PubMed Central PMCID: PMC3491392.

## Examples

```
data(HOT.spots)
elementNROWS(HOT.spots)
```

---

hyperGtest

*hypergeometric test*

---

## Description

hypergeometric test with lower.tail = FALSE used by getEnrichedGO

## Usage

```
hyperGtest(alltermcount, thistermcount, totaltermInGenome, totaltermInPeakList)
```

## Arguments

alltermcount a list with two variables: GOterm and GOcount which is GO terms and corresponding counts in the whole genome  
thistermcount a list with two variables: GOterm and GOcount which is GO terms and corresponding counts in the peak list  
totaltermInGenome number of total GO terms in the whole genome  
totaltermInPeakList number of total GO terms in the peak list

## Details

see phyper for details

## Value

a list with 6 variables

thisterm GO term  
thistermcount count of this GO term in the peak list  
thistermtotal count of this GO term in the whole genome

```

pvalue          pvalue of the hypergeometric test
totaltermInPeakList
                  number of total GO terms in the peak list
totaltermInGenome
                  number of total GO terms in the whole genome

```

### Note

internal function not intended to be used directly by users

### Author(s)

Lihua Julie ZHu

### References

Johnson, N. L., Kotz, S., and Kemp, A. W. (1992) Univariate Discrete Distributions, Second Edition. New York: Wiley

### See Also

phyper, getEnrichedGO

### Examples

```

goList= c("GO:0000075", "GO:0000082", "GO:0000082", "GO:0000122",
        "GO:0000122", "GO:0000075", "GO:0000082", "GO:0000082",
        "GO:0000122", "GO:0000122", "GO:0000122", "GO:0000122",
        "GO:0000075", "GO:0000082", "GO:000012")

alltermcount = list(GOterm=c("GO:0000075", "GO:0000082", "GO:000012",
                            "GO:0000122"),
                     GOcount=c(100, 200, 10, 10))
thistermcount = getUniqueGOidCount(goList)
totaltermInPeakList = 15
totaltermInGenome = 1000
hyperGtest(alltermcount,thistermcount, totaltermInGenome, totaltermInPeakList)

```

---

### Description

Using IDR to assess the consistency of replicate experiments and obtain a high-confidence single set of peaks

## Usage

```
IDRfilter(  
  peaksA,  
  peaksB,  
  bamfileA,  
  bamfileB,  
  maxgap = -1L,  
  minoverlap = 0L,  
  singleEnd = TRUE,  
  IDRcutoff = 0.01,  
  ...  
)
```

## Arguments

peaksA, peaksB	peaklist, <a href="#">GRanges</a> object.
bamfileA, bamfileB	file path of bam files.
maxgap, minoverlap	Used in the internal call to <code>findOverlaps()</code> to detect overlaps. See <a href="#">?findOverlaps</a> in the <b>IRanges</b> package for a description of these arguments.
singleEnd	(Default TRUE) A logical indicating if reads are single or paired-end.
IDRcutoff	If the IDR no less than IDRcutoff, the peak will be removed.
...	Not used.

## Value

## An object GRanges

## Author(s)

Jianhong Ou

## References

Li, Qunhua, et al. "Measuring reproducibility of high-throughput experiments." *The annals of applied statistics* (2011): 1752-1779.

## Examples

```

peaksA=toGRanges(WT.AB2.Peaks, format="MACS")
peaksB=toGRanges(Resc.AB2.Peaks, format="MACS")
library(idr)
library(DelayedArray)
IDRfilter(peaksA, peaksB,
           bamfileA, bamfileB)
}
}

```

---

**makeVennDiagram***Make Venn Diagram from a list of peaks*

---

**Description**

Make Venn Diagram from two or more peak ranges, Also calculate p-value to determine whether those peaks overlap significantly.

**Usage**

```

makeVennDiagram(
  Peaks,
  NameOfPeaks,
  maxgap = -1L,
  minoverlap = 0L,
  totalTest,
  by = c("region", "feature", "base"),
  ignore.strand = TRUE,
  connectedPeaks = c("min", "merge", "keepAll", "keepFirstListConsistent"),
  method = c("hyperG", "permutation"),
  TxDb,
  plot = TRUE,
  ...
)

```

**Arguments**

Peaks	A list of peaks in <a href="#">GRanges</a> format: See example below.
NameOfPeaks	Character vector to specify the name of Peaks, e.g., c("TF1", "TF2"). This will be used as label in the Venn Diagram.
maxgap, minoverlap	Used in the internal call to <code>findOverlaps()</code> to detect overlaps. See <a href="#">?findOverlaps</a> in the <a href="#">IRanges</a> package for a description of these arguments.
totalTest	Numeric value to specify the total number of tests performed to obtain the list of peaks. It should be much larger than the number of peaks in the largest peak set.

by	"region", "feature" or "base", default = "region". "feature" means using feature field in the GRanges for calculating overlap, "region" means using chromosome range for calculating overlap, and "base" means calculating overlap in nucleotide level.
ignore.strand	Logical: when set to TRUE, the strand information is ignored in the overlap calculations.
connectedPeaks	If multiple peaks involved in overlapping in several groups, set it to "merge" will count it as only 1, while set it to "min" will count it as the minimal involved peaks in any connected peak group. "keepAll" will show all the orginal counts for each list while the final counts will be same as "min". "keepFirstListConsistent" will keep the counts consistent with first list.
method	method to be used for p value calculation. hyperG means hypergeometric test and permutation means <a href="#">peakPermTest</a> .
TxDb	An object of <a href="#">TxDb</a> .
plot	logical. If TRUE (default), a venn diagram is plotted.
...	Additional arguments to be passed to <a href="#">venn.diagram</a> .

## Details

For customized graph options, please see [venn.diagram](#) in [VennDiagram](#) package.

## Value

A p.value is calculated by hypergeometric test or permutation test to determine whether the overlaps of peaks or features are significant.

## Author(s)

Lihua Julie Zhu, Jianhong Ou

## See Also

[findOverlapsOfPeaks](#), [venn.diagram](#), [peakPermTest](#)

## Examples

```
if (interactive()){
  peaks1 <- GRanges(seqnames=c("1", "2", "3"),
                     IRanges(start=c(967654, 2010897, 2496704),
                             end=c(967754, 2010997, 2496804),
                             names=c("Site1", "Site2", "Site3")),
                     strand="+",
                     feature=c("a", "b", "f"))
  peaks2 = GRanges(seqnames=c("1", "2", "3", "1", "2"),
                   IRanges(start = c(967659, 2010898, 2496700,
                                   3075866, 3123260),
                           end = c(967869, 2011108, 2496920,
                                   3076166, 3123470),
                           names = c("t1", "t2", "t3", "t4", "t5"))),
```

```

strand = c("+", "+", "-", "-", "+"),
feature=c("a","b","c","d","a"))
makeVennDiagram(list(peaks1, peaks2), NameOfPeaks=c("TF1", "TF2"),
               totalTest=100,scaled=FALSE, euler.d=FALSE,
               fill=c("#009E73", "#F0E442"), # circle fill color
               col=c("#D55E00", "#0072B2"), #circle border color
               cat.col=c("#D55E00", "#0072B2"))

makeVennDiagram(list(peaks1, peaks2), NameOfPeaks=c("TF1", "TF2"),
               totalTest=100,
               fill=c("#009E73", "#F0E442"), # circle fill color
               col=c("#D55E00", "#0072B2"), #circle border color
               cat.col=c("#D55E00", "#0072B2"))

##### 4-way diagram using annotated feature instead of chromosome ranges

makeVennDiagram(list(peaks1, peaks2, peaks1, peaks2),
               NameOfPeaks=c("TF1", "TF2", "TF3", "TF4"),
               totalTest=100, by="feature",
               main = "Venn Diagram for 4 peak lists",
               fill=c(1,2,3,4))
}

```

---

mergePlusMinusPeaks     *Merge peaks from plus strand and minus strand*

---

## Description

Merge peaks from plus strand and minus strand within certain distance apart, and output merged peaks as bed format.

## Usage

```

mergePlusMinusPeaks(
  peaks.file,
  columns = c("name", "chromosome", "start", "end", "strand", "count", "count", "count",
             "count"),
  sep = "\t",
  header = TRUE,
  distance.threshold = 100,
  plus.strand.start.gt_MINUS.strand.end = TRUE,
  output.bedfile
)

```

## Arguments

peaks.file	Specify the peak file. The peak file should contain peaks from both plus and minus strand
columns	Specify the column names in the peak file

```

sep           Specify column delimiter, default tab-delimited
header        Specify whether the file has a header row, default TRUE
distance.threshold
              Specify the maximum gap allowed between the plus stranded and the negative
              stranded peak
plus.strand.start.gt.minus.strand.end
              Specify whether plus strand peak start greater than the paired negative strand
              peak end. Default to TRUE
output.bedfile Specify the bed output file name

```

### Value

output the merged peaks in bed file and a data frame of the bed format

### Author(s)

Lihua Julie Zhu

### References

Zhu L.J. et al. (2010) ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. *BMC Bioinformatics* 2010, 11:237doi:10.1186/1471-2105-11-237

### See Also

[annotatePeakInBatch](#), [findOverlappingPeaks](#), [makeVennDiagram](#)

### Examples

```

if (interactive())
{
  data(myPeakList)
  data(TSS.human.NCBI36)
  library(matrixStats)
  peaks <- system.file("extdata", "guide-seq-peaks.txt",
                        package = "ChIPpeakAnno")
  merged.bed <- mergePlusMinusPeaks(peaks.file = peaks,
                                      columns=c("name", "chromosome",
                                                "start", "end", "strand",
                                                "count", "count"),
                                      sep = "\t", header = TRUE,
                                      distance.threshold = 100,
                                      plus.strand.start.gt.minus.strand.end = TRUE,
                                      output.bedfile = "T2test100bp.bed")
}

```

---

metagenePlot	<i>peak distance to features</i>
--------------	----------------------------------

---

## Description

Bar plot for distance to features

## Usage

```
metagenePlot(
  peaks,
  AnnotationData,
  PeakLocForDistance = c("middle", "start", "end"),
  FeatureLocForDistance = c("TSS", "middle", "geneEnd"),
  upstream = 1e+05,
  downstream = 1e+05
)
```

## Arguments

**peaks** peak list, [GRanges](#) object or a [GRangesList](#).

**AnnotationData** A [GRanges](#) object or a [TxDb](#) object.

**PeakLocForDistance**

Specify the location of peak for calculating distance,i.e., middle means using middle of the peak to calculate distance to feature, start means using start of the peak to calculate the distance to feature. To be compatible with previous version, by default using start

**FeatureLocForDistance**

Specify the location of feature for calculating distance,i.e., middle means using middle of the feature to calculate distance of peak to feature, TSS means using start of feature when feature is on plus strand and using end of feature when feature is on minus strand, geneEnd means using end of feature when feature is on plus strand and using start of feature when feature is on minus strand.

**upstream, downstream**

numeric(1). Upstream or downstream region of features to plot.

## Details

the bar heatmap is indicates the peaks around features.

## Examples

```
path <- system.file("extdata", package="ChIPpeakAnno")
files <- dir(path, "broadPeak")
peaks <- sapply(file.path(path, files), toGRanges, format="broadPeak")
peaks <- GRangesList(peaks)
names(peaks) <- sub(".broadPeak", "", basename(names(peaks)))
```

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
metagenePlot(peaks, TxDb.Hsapiens.UCSC.hg19.knownGene)
```

---

**myPeakList***An example GRanges object representing a ChIP-seq peak dataset*

---

## Description

the putative STAT1-binding regions identified in un-stimulated cells using ChIP-seq technology (Robertson et al., 2007)

## Usage

```
myPeakList
```

## Format

GRanges with slot rownames containing the ID of peak as character, slot start containing the start position of the peak, slot end containing the end position of the peak and seqnames containing the chromosome where the peak is located.

## Source

Robertson G, Hirst M, Bainbridge M, Bilenky M, Zhao Y, et al. (2007) Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nat Methods 4:651-7

## Examples

```
data(myPeakList)
slotNames(myPeakList)
```

---

**oligoFrequency***get the oligonucleotide frequency*

---

## Description

Prepare the oligonucleotide frequency for given Markov order.

## Usage

```
oligoFrequency(sequence, MarkovOrder = 3L)
```

## Arguments

sequence	The sequences packaged in DNAStringSet, DNAString object or output of function <a href="#">getAllPeakSequence</a> .
MarkovOrder	Markov order.

**Value**

A numeric vector.

**Author(s)**

Jianhong Ou

**See Also**

See Also as [oligoSummary](#)

**Examples**

```
library(seqinr)
library(Biostrings)
oligoFrequency(DNAString("AATTCGACGTACAGATGACTAGACT"))
```

**oligoSummary**

*Output a summary of consensus in the peaks*

**Description**

Calculate the z-scores of all combinations of oligonucleotide in a given length by Markov chain.

**Usage**

```
oligoSummary(
  sequence,
  oligoLength = 6L,
  freqs = NULL,
  MarkovOrder = 3L,
  quickMotif = FALSE,
  revcomp = FALSE,
  maxsize = 1e+05
)
```

**Arguments**

<code>sequence</code>	The sequences packaged in DNAStringSet, DNAString object or output of function <a href="#">getAllPeakSequence</a> .
<code>oligoLength</code>	The length of oligonucleotide.
<code>freqs</code>	Output of function <a href="#">frequency</a> .
<code>MarkovOrder</code>	The order of Markov chain.
<code>quickMotif</code>	Generate the motif by z-score of not.
<code>revcomp</code>	Consider both the given strand and the reverse complement strand when searching for motifs in a complementable alphabet (ie DNA). Default, FALSE.
<code>maxsize</code>	Maximum allowed dataset size (in length of sequences).

**Value**

A list is returned.

zscores	A numeric vector. The z-scores of each oligonucleotide.
counts	A numeric vector. The counts number of each oligonucleotide.
motifs	a list of motif matrix.

**Author(s)**

Jianhong Ou

**References**

van Helden, Jacques, Marcel li del Olmo, and Jose E. Perez-Ortin. "Statistical analysis of yeast genomic downstream sequences reveals putative polyadenylation signals." Nucleic Acids Research 28.4 (2000): 1000-1010.

**See Also**

See Also as [frequency](#)

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jou"){
  data(annotatedPeak)
  library(BSgenome.Hsapiens.UCSC.hg19)
  library(seqinr)
  seq <- getAllPeakSequence(annotatedPeak[1:100],
                           upstream=20,
                           downstream=20,
                           genome=Hsapiens)
  oligoSummary(seq)
}
```

**Description**

Performs a permutation test to see if there is an association between two given peak lists.

**Usage**

```
peakPermTest(
  peaks1,
  peaks2,
  ntimes = 100,
  seed = as.integer(Sys.time()),
  mc.cores = getOption("mc.cores", 2L),
  maxgap = -1L,
  pool,
  TxDb,
  bindingDistribution,
  bindingType = c("TSS", "geneEnd"),
  featureType = c("transcript", "exon"),
  seqn = NA,
  ...
)
```

**Arguments**

peaks1, peaks2	an object of <a href="#">GRanges</a>
ntimes	number of permutations
seed	random seed
mc.cores	The number of cores to use. see <a href="#">mclapply</a> .
maxgap	See <a href="#">findOverlaps</a> in the <a href="#">IRanges</a> package for a description of these arguments.
pool	an object of <a href="#">permPool</a>
TxDb	an object of <a href="#">TxDb</a>
bindingDistribution	an object of <a href="#">bindist</a>
bindingType	where the peaks should bind, TSS or geneEnd
featureType	what annotation type should be used for detecting the binding distribution.
seqn	default is NA, which means not filter the universe pool for sampling. Otherwise the universe pool will be filtered by the seqnames in seqn.
...	further arguments to be passed to <a href="#">numOverlaps</a> .

**Value**

A list of class [permTestResults](#). See [permTest](#)

**Author(s)**

Jianhong Ou

**References**

Davison, A. C. and Hinkley, D. V. (1997) Bootstrap methods and their application, Cambridge University Press, United Kingdom, 156-160

**See Also**[preparePool](#), [bindist](#)**Examples**

```

path <- system.file("extdata", package="ChIPpeakAnno")
#files <- dir(path, pattern="[12]_WS170.bed", full.names=TRUE)
#peaks1 <- toGRanges(files[1], skip=5)
#peaks2 <- toGRanges(files[2], skip=5)
#peakPermTest(peaks1, peaks2, TxDb=TxDb.Celegans.UCSC.ce6.ensGene)
if(interactive()){
  peaks1 <- toGRanges(file.path(path, "MACS2_peaks.xls"),
                      format="MACS2")
  peaks2 <- toGRanges(file.path(path, "peaks.narrowPeak"),
                      format="narrowPeak")
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  peakPermTest(peaks1, peaks2,
               TxDb=TxDb.Hsapiens.UCSC.hg19.knownGene, min.pctA=10)
}

```

**Peaks.Ste12.Replicate1***Ste12-binding sites from biological replicate 1 in yeast (see reference)***Description**

Ste12-binding sites from biological replicate 1 in yeast (see reference)

**Usage**

Peaks.Ste12.Replicate1

**Format**

GRanges with slot names containing the ID of peak as character, slot start containing the start position of the peak, slot end containing the end position of the peak and space containing the chromosome where the peak is located.

**References**

Philippe Lefrancois, Ghia M Euskirchen, Raymond K Auerbach, Joel Rozowsky, Theodore Gibson, Christopher M Yellman, Mark Gerstein and Michael Snyder (2009) Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing BMC Genomics 10:37

**Examples**

```

data(Peaks.Ste12.Replicate1)
Peaks.Ste12.Replicate1

```

---

**Peaks.Ste12.Replicate2**

*Ste12-binding sites from biological replicate 2 in yeast (see reference)*

---

**Description**

Ste12-binding sites from biological replicate 2 in yeast (see reference)

**Usage**

Peaks.Ste12.Replicate2

**Format**

GRanges with slot names containing the ID of peak as character, slot start containing the start position of the peak, slot end containing the end position of the peak and space containing the chromosome where the peak is located.

**Source**

<http://www.biomedcentral.com/1471-2164/10/37>

**References**

Philippe Lefranois, Ghia M Euskirchen, Raymond K Auerbach, Joel Rozowsky, Theodore Gibson, Christopher M Yellman, Mark Gerstein and Michael Snyder (2009) Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing BMC Genomics 10:37doi:10.1186/1471-2164-10-37

**Examples**

```
data(Peaks.Ste12.Replicate2)
Peaks.Ste12.Replicate2
```

---

**Peaks.Ste12.Replicate3**

*Ste12-binding sites from biological replicate 3 in yeast (see reference)*

---

**Description**

Ste12-binding sites from biological replicate 3 in yeast (see reference)

**Usage**

Peaks.Ste12.Replicate3

**Format**

GRanges with slot names containing the ID of peak as character, slot start containing the start position of the peak, slot end containing the end position of the peak and space containing the chromosome where the peak is located.

**Source**

<http://www.biomedcentral.com/1471-2164/10/37>

**References**

Philippe Lefranois, Ghia M Euskirchen, Raymond K Auerbach, Joel Rozowsky, Theodore Gibson, Christopher M Yellman, Mark Gerstein and Michael Snyder (2009) Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing BMC Genomics 10:37doi:10.1186/1471-2164-10-37

**Examples**

```
data(Peaks.Ste12.Replicate3)
Peaks.Ste12.Replicate3
```

---

peaks1

*An example GRanges object representing a ChIP-seq peak dataset*

---

**Description**

An example GRanges object representing a ChIP-seq peak dataset

**Usage**

```
peaks1
```

**Format**

GRanges

**Examples**

```
data(peaks1)
head(peaks1, n = 2)
```

peaks2

*An example GRanges object representing a ChIP-seq peak dataset*

---

**Description**

An example GRanges object representing a ChIP-seq peak dataset

**Usage**

peaks2

**Format**

GRanges

**Examples**

```
data(peaks2)
head(peaks2, n = 2)
```

peaks3

*An example GRanges object representing a ChIP-seq peak dataset*

---

**Description**

An example GRanges object representing a ChIP-seq peak dataset

**Usage**

peaks3

**Format**

GRanges

**Examples**

```
data(peaks3)
head(peaks3, n = 2)
```

---

peaksNearBDP	<i>obtain the peaks near bi-directional promoters</i>
--------------	---

---

## Description

Obtain the peaks near bi-directional promoters. Also output percent of peaks near bi-directional promoters.

## Usage

```
peaksNearBDP(myPeakList, AnnotationData, MaxDistance = 5000L, ...)
```

## Arguments

myPeakList	<a href="#">GRanges</a> : See example below
AnnotationData	annotation data obtained from <code>getAnnotation</code> or customized annotation of class <a href="#">GRanges</a> containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). For example, <code>data(TSS.human.NCBI36)</code> , <code>data(TSS.mouse.NCBIM37)</code> , <code>data(TSS.rat.RGSC3.4)</code> and <code>data(TSS.zebrafish.Zv8)</code> .
MaxDistance	Specify the maximum gap allowed between the peak and nearest gene
...	Not used

## Value

A list of 4

```
list("peaksWithBDP")
```

annotated Peaks containing bi-directional promoters.

`GRangesList` with slot `start` holding the start position of the peak, slot `end` holding the end position of the peak, slot `space` holding the chromosome location where the peak is located, slot `rownames` holding the id of the peak. In addition, the following variables are included.

`feature`: id of the feature such as ensembl gene ID

`insideFeature`: `upstream`: peak resides upstream of the feature; `downstream`: peak resides downstream of the feature; `inside`: peak resides inside the feature; `overlapStart`: peak overlaps with the start of the feature; `overlapEnd`: peak overlaps with the end of the feature; `includeFeature`: peak include the feature entirely.

`distancetoFeature`: distance to the nearest feature such as transcription start site. By default, the distance is calculated as the distance between the start of the binding site and the TSS that is the gene start for genes located on the forward strand and the gene end for genes located on the reverse strand. The user can specify the location of peak and location of feature for calculating this

`feature_range`: start and end position of the feature such as gene

`feature_strand`: 1 or + for positive strand and -1 or - for negative strand where the feature is located

```

list("percentPeaksWithBDP")
  The percent of input peaks containing bi-directional promoters
list("n.peaks")
  The total number of input peaks
list("n.peaksWithBDP")
  The # of input peaks containing bi-directional promoters

```

### Author(s)

Lihua Julie Zhu, Jianhong Ou

### References

Zhu L.J. et al. (2010) ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. *BMC Bioinformatics* 2010, 11:237doi:10.1186/1471-2105-11-237

### See Also

annotatePeakInBatch, findOverlappingPeaks, makeVennDiagram

### Examples

```

if (interactive() || Sys.getenv("USER")=="jou")
{
  library(GenomeInfoDb)
  data(myPeakList)
  data(TSS.human.NCBI36)
  seqlevelsStyle(TSS.human.NCBI36) <- seqlevelsStyle(myPeakList)
  annotatedBDP = peaksNearBDP(myPeakList[1:6,],
                               AnnotationData=TSS.human.NCBI36,
                               MaxDistance=5000,
                               PeakLocForDistance = "middle",
                               FeatureLocForDistance = "TSS")
  c(annotatedBDP$percentPeaksWithBDP, annotatedBDP$n.peaks,
    annotatedBDP$n.peaksWithBDP)
}

```

---

*permPool-class*      *Class "permPool"*

---

### Description

An object of class "permPool" represents the possible locations to do permutation test.

### Slots

grs object of "GRangesList" The list of binding ranges  
 N vector of "integer", permutation number for each ranges

## Objects from the Class

Objects can be created by calls of the form `new("permPool", grs="GRangesList", N="integer")`.

## See Also

[preparePool](#), [peakPermTest](#)

---

pie1

*Pie Charts*

---

## Description

Draw a pie chart with percentage

## Usage

```
pie1(  
  x,  
  labels = names(x),  
  edges = 200,  
  radius = 0.8,  
  clockwise = FALSE,  
  init.angle = if (clockwise) 90 else 0,  
  density = NULL,  
  angle = 45,  
  col = NULL,  
  border = NULL,  
  lty = NULL,  
  main = NULL,  
  percentage = TRUE,  
  rawNumber = FALSE,  
  digits = 3,  
  cutoff = 0.01,  
  legend = FALSE,  
  legendpos = "topright",  
  legendcol = 2,  
  radius.innerlabel = radius,  
  ...  
)
```

## Arguments

<code>x</code>	a vector of non-negative numerical quantities. The values in <code>x</code> are displayed as the areas of pie slices.
<code>labels</code>	one or more expressions or character strings giving names for the slices. Other objects are coerced by <code>as.graphicsAnnot</code> . For empty or NA (after coercion to character) labels, no label nor pointing line is drawn.

edges	the circular outline of the pie is approximated by a polygon with this many edges.
radius	the pie is drawn centered in a square box whose sides range from -1 to 1. If the character strings labeling the slices are long it may be necessary to use a smaller radius.
clockwise	logical indicating if slices are drawn clockwise or counter clockwise (i.e., mathematically positive direction), the latter is default.
init.angle	number specifying the starting angle (in degrees) for the slices. Defaults to 0 (i.e., "3 o'clock") unless clockwise is true where init.angle defaults to 90 (degrees), (i.e., "12 o'clock").
density	the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn. Non-positive values of density also inhibit the drawing of shading lines.
angle	the slope of shading lines, given as an angle in degrees (counter-clockwise).
col	a vector of colors to be used in filling or shading the slices. If missing a set of 6 pastel colours is used, unless density is specified when par("fg") is used.
border, lty	(possibly vectors) arguments passed to polygon which draws each slice.
main	an overall title for the plot.
percentage	logical. Add percentage in the figure or not. default TRUE.
rawNumber	logical. Instead percentage, add raw number in the figure or not. default FALSE.
digits	When set percentage as TRUE, how many significant digits are to be used for percentage. see <a href="#">format</a> . default 3.
cutoff	When percentage is TRUE, if the percentage is lower than cutoff, it will NOT be shown. default 0.01.
legend	logical. Instead of lable, draw legend for the pie. default, FALSE.
legendpos, legendcol	legend position and legend columns. see <a href="#">legend</a>
radius.innerlabel	position of percentage or raw number label relative to the circle.
...	graphical parameters can be given as arguments to pie. They will affect the main title and labels only.

### Author(s)

Jianhong Ou

### See Also

[pie](#)

### Examples

`pie1(1:5)`

---

plotBinOverRegions     *plot the coverage of regions*

---

## Description

plot the output of [binOverRegions](#) or [binOverGene](#)

## Usage

```
plotBinOverRegions(dat, ...)
```

## Arguments

dat	A list of matrix which indicate the coverage of regions per bin
...	Parameters could be used by <a href="#">matplotlib</a>

## Author(s)

Jianhong Ou

## See Also

[binOverRegions](#), [binOverGene](#)

## Examples

```
if(interactive()){  
  path <- system.file("extdata", package="ChIPpeakAnno")  
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)  
  library(rtracklayer)  
  files <- dir(path, "bigWig")  
  if(.Platform$OS.type != "windows"){  
    cvglists <- lapply(file.path(path, files), import,  
                      format="BigWig", as="RleList")  
    names(cvglists) <- sub(".bigWig", "", files)  
    d <- binOverGene(cvglists, TxDb.Hsapiens.UCSC.hg19.knownGene)  
    plotBinOverRegions(d)  
  }  
}
```

---

<b>preparePool</b>	<i>prepare data for permutation test</i>
--------------------	--

---

## Description

prepare data for permutation test [peakPermTest](#)

## Usage

```
preparePool(
  TxDb,
  template,
  bindingDistribution,
  bindingType = c("TSS", "geneEnd"),
  featureType = c("transcript", "exon"),
  seqn = NA
)
```

## Arguments

<b>TxDb</b>	an object of <a href="#">TxDb</a>
<b>template</b>	an object of <a href="#">GRanges</a>
<b>bindingDistribution</b>	an object of <a href="#">bindist</a>
<b>bindingType</b>	the relevant position to features
<b>featureType</b>	feature type, transcript or exon.
<b>seqn</b>	seqnames. If given, the pool for permutation will be restrict in the given chromosomes.

## Value

a list with two elements, grs, a list of [GRanges](#). N, the numbers of elements should be drawn from in each [GRanges](#).

## Author(s)

Jianhong Ou

## See Also

[peakPermTest](#), [bindist](#)

## Examples

```
if(interactive() || Sys.getenv("USER")=="jou"){
  path <- system.file("extdata", package="ChIPpeakAnno")
  peaksA <- toGRanges(file.path(path, "peaks.narrowPeak"),
                        format="narrowPeak")
  peaksB <- toGRanges(file.path(path, "MACS2_peaks.xls"), format="MACS2")
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  ppp <- preparePool(TxDb.Hsapiens.UCSC.hg19.knownGene,
                      peaksA, bindingType="TSS",
                      featureType="transcript")
}
```

---

reCenterPeaks

*re-center the peaks*

---

## Description

Create a new list of peaks based on the peak centers of given list.

## Usage

```
reCenterPeaks(peaks, width = 2000L, ...)
```

## Arguments

peaks	An object of <a href="#">GRanges</a> or <a href="#">annoGR</a> .
width	The width of new peaks
...	Not used.

## Value

An object of [GRanges](#).

## Author(s)

Jianhong Ou

## Examples

```
reCenterPeaks(GRanges("chr1", IRanges(1, 10)), width=2)
```

---

summarizeOverlapsByBins

*Perform overlap queries between reads and genomic features by bins*

---

## Description

summarizeOverlapsByBins extends [summarizeOverlaps](#) by providing fixed window size and step to split each feature into bins and then do queries. It will return counts by signalSummaryFUN, which applied to bins in one feature, for each feature.

## Usage

```
summarizeOverlapsByBins(  
  targetRegions,  
  reads,  
  windowHeight = 50,  
  step = 10,  
  signalSummaryFUN = max,  
  mode = countByOverlaps,  
  ...  
)
```

## Arguments

targetRegions	A <a href="#">GRanges</a> object of genomic regions of interest.
reads	A <a href="#">GRanges</a> , <a href="#">GRangesList</a> <a href="#">GAlignments</a> , <a href="#">GAlignmentsList</a> , <a href="#">GAlignmentPairs</a> or <a href="#">BamFileList</a> object that represents the data to be counted by <a href="#">summarizeOverlaps</a> .
windowSize	Size of windows
step	Step of windows
signalSummaryFUN	function, which will be applied to the bins in each feature.
mode	mode can be one of the pre-defined count methods. see <a href="#">summarizeOverlaps</a> . default is countByOverlaps, alia of countOverlaps(features, reads, ignore.strand=ignore.strand)
...	Additional arguments passed to <a href="#">summarizeOverlaps</a> .

## Value

A [RangedSummarizedExperiment](#) object. The assays slot holds the counts, rowRanges holds the annotation from features.

## Author(s)

Jianhong Ou

## Examples

```
fls <- list.files(system.file("extdata", package="GenomicAlignments"),
                   recursive=TRUE, pattern="*bam$", full=TRUE)
names(fls) <- basename(fls)
genes <- GRanges(
  seqnames = c(rep("chr2L", 4), rep("chr2R", 5), rep("chr3L", 2)),
  ranges = IRanges(c(1000, 3000, 4000, 7000, 2000, 3000, 3600,
                    4000, 7500, 5000, 5400),
                   width=c(rep(500, 3), 600, 900, 500, 300, 900,
                           300, 500, 500),
                   names=letters[1:11]))
se <- summarizeOverlapsByBins(genes, fls, windowHeight=50, step=10)
```

## summarizePatternInPeaks

*Output a summary of the occurrence and enrichment of each pattern in the sequences.*

## Description

Output a summary of the occurrence and enrichment of each pattern in the sequences.

## Usage

```
summarizePatternInPeaks(
  patternFilePath,
  format = "fasta",
  BSgenomeName,
  peaks,
  revcomp = TRUE,
  method = c("binom.test", "permutation.test"),
  expectFrequencyMethod = c("Markov", "Naive"),
  MarkovOrder = 3L,
  bgdForPerm = c("shuffle", "chromosome"),
  chromosome = c("asPeak", "random"),
  nperm = 1000,
  alpha = 0.05,
  ...
)
```

## Arguments

**patternFilePath**

Character value. The path to the file that contains the pattern.

**format**

Character value. The format of file containing the oligonucleotide pattern, either "fasta" (default) or "fastq".

BSgenomeName	Character value. BSgenome object. Please refer to available.genomes in BSgenome package for details.
peaks	Character value. <a href="#">GRanges</a> containing the peaks.
revcomp	Boolean value, if TRUE, also search the reverse compliment of pattern. Default is TRUE.
method	Character value. Method for pattern enrichment test, 'binom.test' (default) or 'permutation.test'.
expectFrequencyMethod	Character value. Method for calculating the expected probability of pattern occurrence, 'Markov' (default) or 'Naive'.
MarkovOrder	Integer value. The order of Markov chain. Default is 3.
bgdForPerm	Character value. The method for obtaining the background sequence. 'chromosome' (default) selects background chromosome from chromosomes, refer to 'chromosome' parameter; 'shuffle' will obtain the background sequence by shuffling any k-mers in peak sequences, refer to '...'.
chromosome	Character value. Relevant if "bgdForPerm='chromosome'". 'asPeak' means to use the same chromosomes in peaks; 'random' means to use all chromosomes randomly. Default is 'asPeak'.
nperm	Integer value. The number of permutation test, default is 1000.
alpha	Numeric value. The significant level for permutation test, default is 0.05.
...	Additional parameter passed to function <a href="#">shuffle_sequences</a>

## Details

Please see [shuffle\\_sequences](#) for the more information about 'shuffle' method.

## Value

A list including two data frames named 'motif\_enrichment' and 'motif\_occurrence'. The 'motif\_enrichment' has four columns:

- "patternNum": number of matched pattern
- "totalNumPatternWithSameLen": total number of pattern with the same length
- "expectedRate": expected rate of pattern for 'binom.test' method
- "patternRate": real rate of pattern for 'permutation.test' method
- "pValueBinomTest": p value of binom test for 'binom.test' method
- "cutOffPermutationTest": cut off of permutation test for 'permutation.test' method

The 'motif\_occurrence' has 14 columns:

- "motifChr": Chromosome of motif
- "motifStartInChr": motif start position in chromosome
- "motifEndInChr": motif end position in chromosome
- "motifName": motif name

- "motifPattern": motif pattern
- "motifStartInPeak": motif start position in peak
- "motifEndInPeak": motif end position in peak
- "motifFound": specific motif Found in peak
- "motifFoundStrand": strand of specific motif Found in peak, "-" means reverse complement of motif found in peaks
- "peakChr": Chromosome of peak
- "peakStart": peak start position
- "peakEnd": peak end position
- "peakWidth": peak width
- "peakStrand": peak strand

### Author(s)

Lihua Julie Zhu, Junhui Li, Kai Hu

### Examples

```
library(BSgenome.Hsapiens.UCSC.hg19)
filepath <- system.file("extdata", "examplePattern.fa",
                       package = "ChIPpeakAnno")
peaks <- GRanges(seqnames = c("chr17", "chr3", "chr12", "chr8"),
                  IRanges(start = c(41275784, 10076141, 4654135, 31024288),
                          end = c(41276382, 10076732, 4654728, 31024996),
                          names = paste0("peak", 1:4)))
result <- summarizePatternInPeaks(patternFilePath = filepath, peaks = peaks,
                                    BSgenomeName = Hsapiens)
```

---

tileCount

*Perform overlap queries between reads and genome by windows*

---

### Description

tileCount extends [summarizeOverlaps](#) by providing fixed window size and step to split whole genome into windows and then do queries. It will return counts in each windows.

### Usage

```
tileCount(
  reads,
  genome,
  windowSize = 1e+06,
  step = 1e+06,
  keepPartialWindow = FALSE,
  mode = countByOverlaps,
  ...
)
```

**Arguments**

reads	A <a href="#">GRanges</a> , <a href="#">GRangesList</a> <a href="#">GAlignments</a> , <a href="#">GAlignmentsList</a> , <a href="#">GAlignmentPairs</a> or <a href="#">BamFileList</a> object that represents the data to be counted by <a href="#">summarizeOverlaps</a> .
genome	The object from/on which to get/set the sequence information.
windowSize	Size of windows
step	Step of windows
keepPartialWindow	Keep last partial window or not.
mode	mode can be one of the pre-defined count methods. see <a href="#">summarizeOverlaps</a> . default is countByOverlaps, alia of countOverlaps(features, reads, ignore.strand=ignore.strand)
...	Additional arguments passed to <a href="#">summarizeOverlaps</a> .

**Value**

A [RangedSummarizedExperiment](#) object. The assays slot holds the counts, rowRanges holds the annotation from genome.

**Author(s)**

Jianhong Ou

**Examples**

```
fls <- list.files(system.file("extdata", package="GenomicAlignments"),
                   recursive=TRUE, pattern="*bam$", full=TRUE)
names(fls) <- basename(fls)
genes <- GRanges(seqlengths = c(chr2L=7000, chr2R=10000))
se <- tileCount(fls, genes, windowSize=1000, step=500)
```

---

tileGRanges	<i>Slide windows on a given <a href="#">GRanges</a> object</i>
-------------	--

---

**Description**

tileGRanges returns a set of genomic regions by sliding the windows in a given step. Each window is called a "tile".

**Usage**

```
tileGRanges(targetRegions, windowSize, step, keepPartialWindow = FALSE, ...)
```

**Arguments**

targetRegions A [GRanges](#) object of genomic regions of interest.  
windowSize Size of windows  
step Step of windows  
keepPartialWindow Keep last partial window or not.  
... Not used.

**Value**

A [GRanges](#) object.

**Author(s)**

Jianhong Ou

**Examples**

```
genes <- GRanges(  
  seqnames = c(rep("chr2L", 4), rep("chr2R", 5), rep("chr3L", 2)),  
  ranges = IRanges(c(1000, 3000, 4000, 7000, 2000, 3000, 3600,  
    4000, 7500, 5000, 5400),  
    width=c(rep(500, 3), 600, 900, 500, 300, 900,  
    300, 500, 500),  
    names=letters[1:11]))  
se <- tileGRanges(genes, windowSize=50, step=10)
```

---

toGRanges

*Convert dataset to GRanges*

---

**Description**

Convert UCSC BED format and its variants, such as GFF, or any user defined dataset such as MACS output file to [GRanges](#)

**Usage**

```
toGRanges(data, ...)  
  
## S4 method for signature 'connection'  
toGRanges(  
  data,  
  format = c("BED", "GFF", "GTF", "MACS", "MACS2", "MACS2.broad", "narrowPeak",  
    "broadPeak", "CSV", "others"),  
  header = FALSE,  
  comment.char = "#",
```

```

colNames = NULL,
...
)

## S4 method for signature 'TxDb'
toGRanges(
  data,
  feature = c("gene", "transcript", "exon", "CDS", "fiveUTR", "threeUTR", "tRNAs",
  "geneModel"),
  OrganismDb,
  ...
)

## S4 method for signature 'EnsDb'
toGRanges(
  data,
  feature = c("gene", "transcript", "exon", "disjointExons"),
  ...
)

## S4 method for signature 'character'
toGRanges(
  data,
  format = c("BED", "GFF", "GTF", "MACS", "MACS2", "MACS2.broad", "narrowPeak",
  "broadPeak", "CSV", "others"),
  header = FALSE,
  comment.char = "#",
  colNames = NULL,
  ...
)

```

## Arguments

<code>data</code>	an object of <code>data.frame</code> , <a href="#">TxDb</a> or <a href="#">EnsDb</a> , or the file name of data to be imported. Alternatively, <code>data</code> can be a readable txt-mode connection (See <code>?read.table</code> ).
<code>...</code>	parameters passed to <code>read.table</code>
<code>format</code>	data format. If the data format is set to BED, GFF, narrowPeak or broadPeak, please refer to <a href="http://genome.ucsc.edu/FAQ/FAQformat#format1">http://genome.ucsc.edu/FAQ/FAQformat#format1</a> for column order. "MACS" is for converting the excel output file from MACS1. "MACS2" is for converting the output file from MACS2. If set to CSV, must have columns: seqnames, start, end, strand.
<code>header</code>	A logical value indicating whether the file contains the names of the variables as its first line. If missing, the value is determined from the file format: <code>header</code> is set to TRUE if the first row contains one fewer field than the number of columns or the format is set to 'CSV'.
<code>comment.char</code>	character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.

colNames	If the data format is set to "others", colname must be defined. And the colname must contain space, start and end. The column name for the chromosome # should be named as space.
feature	annotation type
OrganismDb	an object of <a href="#">OrganismDb</a> . It is used for extracting gene symbol for geneModel group for <a href="#">TxDb</a>

### Value

An object of [GRanges](#)

### Author(s)

Jianhong Ou

### Examples

```
macs <- system.file("extdata", "MACS_peaks.xls", package="ChIPpeakAnno")
macsOutput <- toGRanges(macs, format="MACS")
if(interactive() || Sys.getenv("USER")=="jou"){
  ## MACS connection
  macs <- readLines(macs)
  macs <- textConnection(macs)
  macsOutput <- toGRanges(macs, format="MACS")
  close(macs)
  ## bed
  toGRanges(system.file("extdata", "MACS_output.bed", package="ChIPpeakAnno"),
            format="BED")
  ## narrowPeak
  toGRanges(system.file("extdata", "peaks.narrowPeak", package="ChIPpeakAnno"),
            format="narrowPeak")
  ## broadPeak
  toGRanges(system.file("extdata", "TAF.broadPeak", package="ChIPpeakAnno"),
            format="broadPeak")
  ## CSV
  toGRanges(system.file("extdata", "peaks.csv", package="ChIPpeakAnno"),
            format="CSV")
  ## MACS2
  toGRanges(system.file("extdata", "MACS2_peaks.xls", package="ChIPpeakAnno"),
            format="MACS2")
  ## GFF
  toGRanges(system.file("extdata", "GFF_peaks.gff", package="ChIPpeakAnno"),
            format="GFF")
  ## EnsDb
  library(EnsDb.Hsapiens.v75)
  toGRanges(EnsDb.Hsapiens.v75, feature="gene")
  ## TxDb
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  toGRanges(TxDb.Hsapiens.UCSC.hg19.knownGene, feature="gene")
  ## data.frame
  macs <- system.file("extdata", "MACS_peaks.xls", package="ChIPpeakAnno")
```

```

macs <- read.delim(macs, comment.char="#")
toGRanges(macs)
}

```

---

translatePattern	<i>translate pattern from IUPAC Extended Genetic Alphabet to regular expression</i>
------------------	---

---

## Description

translate pattern containing the IUPAC nucleotide ambiguity codes to regular expression. For example, Y->[C|T], R-> [A|G], S-> [G|C], W-> [A|T], K-> [T|U|G], M-> [A|C], B-> [C|G|T], D-> [A|G|T], H-> [A|C|T], V-> [A|C|G] and N-> [A|C|T|G].

## Usage

```
translatePattern(pattern)
```

## Arguments

pattern	a character vector with the IUPAC nucleotide ambiguity codes
---------	--

## Value

a character vector with the pattern represented as regular expression

## Author(s)

Lihua Julie Zhu

## See Also

countPatternInSeqs, summarizePatternInPeaks

## Examples

```

pattern1 = "AACCNWMK"
translatePattern(pattern1)

```

---

TSS.human.GRCh37

*TSS annotation for human sapiens (GRCh37) obtained from biomart*

---

### Description

TSS annotation for human sapiens (GRCh37) obtained from biomart

### Usage

```
TSS.human.GRCh37
```

### Format

A GRanges object with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strand information. In addition, the following variables are included.

```
list("description") description of the gene
```

### Details

The dataset TSS.human.GRCh37 was obtained by:

```
mart = useMart(biomart = "ENSEMBL_MART_ENSEMBL", host = "grch37.ensembl.org", path = "/biomart/martservice",
dataset = "hsapiens_gene_ensembl")
getAnnotation(mart, featureType = "TSS")
```

### Examples

```
data(TSS.human.GRCh37)
slotNames(TSS.human.GRCh37)
```

---

TSS.human.GRCh38

*TSS annotation for human sapiens (GRCh38) obtained from biomart*

---

### Description

TSS annotation for human sapiens (GRCh38) obtained from biomart

### Usage

```
TSS.human.GRCh38
```

### Format

A 'GRanges' [package "GenomicRanges"] object with ensembl id as names.

## Details

used in the examples Annotation data obtained by:

```
mart = useMart(biomart = "ensembl", dataset = "hsapiens_gene_ensembl")
getAnnotation(mart, featureType = "TSS")
```

## Examples

```
data(TSS.human.GRCh38)
slotNames(TSS.human.GRCh38)
```

---

TSS.human.NCBI36

*TSS annotation for human sapiens (NCBI36) obtained from biomaRt*

---

## Description

TSS annotation for human sapiens (NCBI36) obtained from biomaRt

## Usage

```
TSS.human.NCBI36
```

## Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strand information. In addition, the following variables are included.

```
list("description") description of the gene
```

## Details

used in the examples Annotation data obtained by:

```
mart = useMart(biomart = "ensembl_mart_47", dataset = "hsapiens_gene_ensembl", archive=TRUE)
getAnnotation(mart, featureType = "TSS")
```

## Examples

```
data(TSS.human.NCBI36)
slotNames(TSS.human.NCBI36)
```

---

**TSS.mouse.GRCm38***TSS annotation data for *Mus musculus* (GRCm38.p1) obtained from biomarRt*

---

### Description

TSS annotation data for *Mus musculus* (GRCm38.p1) obtained from biomarRt

### Usage

```
TSS.mouse.GRCm38
```

### Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strand information. In addition, the following variables are included.

```
list("description") description of the gene
```

### Details

Annotation data obtained by:

```
mart = useMart(biomart = "ensembl", dataset = "mmusculus_gene_ensembl")
getAnnotation(mart, featureType = "TSS")
```

### Examples

```
data(TSS.mouse.GRCm38)
slotNames(TSS.mouse.GRCm38)
```

---

**TSS.mouse.NCBIM37***TSS annotation data for mouse (NCBIM37) obtained from biomarRt*

---

### Description

TSS annotation data for mouse (NCBIM37) obtained from biomarRt

### Usage

```
TSS.mouse.NCBIM37
```

## Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strand information. In addition, the following variables are included.

**list("description")** description of the gene

## Details

Annotation data obtained by:

```
mart = useMart(biomart = "ensembl", dataset = "mmusculus_gene_ensembl")
getAnnotation(mart, featureType = "TSS")
```

## Examples

```
data(TSS.mouse.NCBIM37)
slotNames(TSS.mouse.NCBIM37)
```

---

TSS.rat.RGSC3.4

*TSS annotation data for rat (RGSC3.4) obtained from biomaRt*

---

## Description

TSS annotation data for rat (RGSC3.4) obtained from biomaRt

## Usage

```
TSS.rat.RGSC3.4
```

## Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strand information. In addition, the following variables are included.

**list("description")** description of the gene

## Details

Annotation data obtained by:

```
mart = useMart(biomart = "ensembl", dataset = "rnorvegicus_gene_ensembl")
getAnnotation(mart, featureType = "TSS")
```

## Examples

```
data(TSS.rat.RGSC3.4)
slotNames(TSS.rat.RGSC3.4)
```

---

**TSS.rat.Rnor\_5.0***TSS annotation data for Rattus norvegicus (Rnor\_5.0) obtained from biomarRt*

---

### Description

TSS annotation data for Rattus norvegicus (Rnor\_5.0) obtained from biomarRt

### Usage

```
TSS.rat.Rnor_5.0
```

### Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strand information. In addition, the following variables are included.

```
list("description") description of the gene
```

### Details

Annotation data obtained by:

```
mart = useMart(biomart = "ensembl", dataset = "rnorvegicus_gene_ensembl")
getAnnotation(mart, featureType = "TSS")
```

### Examples

```
data(TSS.rat.Rnor_5.0)
slotNames(TSS.rat.Rnor_5.0)
```

---

**TSS.zebrafish.Zv8***TSS annotation data for zebrafish (Zv8) obtained from biomarRt*

---

### Description

A GRanges object to annotate TSS for zebrafish (Zv8) obtained from biomarRt

### Usage

```
TSS.zebrafish.Zv8
```

## Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strinad information. In addition, the following variables are included.

**list("description")** description of the gene

## Details

Annotation data obtained by: 

```
mart <- useMart(biomart="ENSEMBL_MART_ENSEMBL", host="may2009.archive.ensembl.org", path="/biomart/martservice", dataset="drerio_gene_ensembl")  
getAnnotation(mart, featureType = "TSS")
```

## Examples

```
data(TSS.zebrafish.Zv8)  
slotNames(TSS.zebrafish.Zv8)
```

---

TSS.zebrafish.Zv9

*TSS annotation for Danio rerio (Zv9) obtained from biomaRt*

---

## Description

TSS annotation for Danio rerio (Zv9) obtained from biomaRt

## Usage

```
TSS.zebrafish.Zv9
```

## Format

GRanges with slot start holding the start position of the gene, slot end holding the end position of the gene, slot names holding ensembl gene id, slot seqnames holding the chromosome location where the gene is located and slot strand holding the strinad information. In addition, the following variables are included.

**list("description")** description of the gene

## Details

Annotation data obtained by:

```
mart <- useMart(biomart="ENSEMBL_MART_ENSEMBL", host="mar2015.archive.ensembl.org", path="/biomart/martservice", dataset="drerio_gene_ensembl")  
getAnnotation(mart, featureType = "TSS")
```

**Examples**

```
data(TSS.zebrafish.Zv9)
slotNames(TSS.zebrafish.Zv9)
```

---

**TxDb2GR***TxDb object to GRanges*

---

**Description**

convert TxDb object to GRanges

**Usage**

```
TxDb2GR(ranges, feature, OrganismDb)
```

**Arguments**

ranges	an Txdb object
feature	feature type, could be geneModel, gene, exon, transcript, CDS, fiveUTR, three-UTR, microRNA, and tRNA
OrganismDb	org db object

---

**wgEncodeTfbsV3***transcription factor binding site clusters (V3) from ENCODE*

---

**Description**

possible binding pool for human (hg19) from transcription factor binding site clusters (V3) from ENCODE data and removed the HOT spots

**Usage**

```
wgEncodeTfbsV3
```

**Format**

An object of GRanges.

## Details

How to generate the data:

```
temp <- tempfile()
download.file(file.path("http://hgdownload.cse.ucsc.edu", "goldenPath",
"hg19", "encodeDCC",
"wgEncodeRegTfbsClustered",
"wgEncodeRegTfbsClusteredV3.bed.gz"), temp)
data <- read.delim(gzfile(temp, "r"), header=FALSE)
unlink(temp)
colnames(data)[1:4] <- c("seqnames", "start", "end", "TF")
wgEncodeRegTfbsClusteredV3 <- GRanges(as.character(data$seqnames),
IRanges(data$start, data$end),
TF=data$TF)
data(HOT.spots)
hot <- reduce(unlist(HOT.spots))
ol <- findOverlaps(wgEncodeRegTfbsClusteredV3, hot)
wgEncodeTfbsV3 <- wgEncodeRegTfbsClusteredV3[-unique(queryHits(ol))]
wgEncodeTfbsV3 <- reduce(wgEncodeTfbsV3)
save(list="wgEncodeTfbsV3",
file="data/wgEncodeTfbsV3.rda",
compress="xz", compression_level=9)
```

## Source

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeRegTfbsClustered/wgEncodeRegTfbsClusteredV3>

## Examples

```
data(wgEncodeTfbsV3)
head(wgEncodeTfbsV3)
```

---

**write2FASTA***Write sequences to a file in fasta format*

---

**Description**

Write the sequences obtained from getAllPeakSequence to a file in fasta format leveraging writeFASTA in Biostrings package. FASTA is a simple file format for biological sequence data. A FASTA format file contains one or more sequences and there is a header line which begins with a > proceeding each sequence.

**Usage**

```
write2FASTA(mySeq, file = "", width = 80)
```

**Arguments**

mySeq	GRanges with variables name and sequence, e.g., results obtained from getAllPeakSequence
file	Either a character string naming a file or a connection open for reading or writing. If "" (the default for write2FASTA), then the function writes to the standard output connection (the console) unless redirected by sink
width	The maximum number of letters per line of sequence

**Value**

Output as FASTA file format to the naming file or the console.

**Author(s)**

Lihua Julie Zhu

**Examples**

```
peaksWithSequences = GRanges(seqnames=c("1", "2"),
  IRanges(start=c(1000, 2000),
  end=c(1010, 2010),
  names=c("id1", "id2")),
  sequence= c("CCCCCCCCGGGG", "TTTTTTAAAAAA"))

write2FASTA(peaksWithSequences, file="testseq.fasta", width=50)
```

---

<code>xget</code>	<i>Return the value from a Bimap objects</i>
-------------------	--

---

## Description

Search by name for an Bimap object.

## Usage

```
xget(
  x,
  envir,
  mode,
  ifnotfound = NA,
  inherits,
  output = c("all", "first", "last")
)
```

## Arguments

<code>x, envir, mode, ifnotfound, inherits</code>	
	see <a href="#">mget</a>
<code>output</code>	return the all or first item for each query

## Value

a character vector

## Author(s)

Jianhong Ou

## See Also

See Also as [mget](#), [mget](#)

## Examples

```
library(org.Hs.eg.db)
xget(as.character(1:10), org.Hs.egSYMBOL)
```

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