

# 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 resulted in large number of chromosome ranges

**Version** 3.14.1

**Encoding** UTF-8

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**Depends** R (>= 3.2), methods, grid, IRanges (>= 2.13.12), Biostrings (>= 2.47.6), GenomicRanges (>= 1.31.8), S4Vectors (>= 0.17.25), VennDiagram

**Imports** BiocGenerics (>= 0.1.0), GO.db, biomaRt, BSgenome, GenomicFeatures, GenomeInfoDb, matrixStats, AnnotationDbi, limma, multtest, RBGL, graph, BiocInstaller, stats, regioneR, DBI, ensemblDb, Biobase, seqinr, idr, GenomicAlignments, DelayedArray, SummarizedExperiment, Rsamtools

**Suggests** reactome.db, BSgenome.Ecoli.NCBI.20080805, BSgenome.Hsapiens.UCSC.hg19, org.Ce.eg.db, org.Hs.eg.db, BSgenome.Celegans.UCSC.ce10, BSgenome.Drerio.UCSC.danRer7, EnsDb.Hsapiens.v75, EnsDb.Hsapiens.v79, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, gplots, BiocStyle, rtracklayer, knitr, rmarkdown, testthat, trackViewer, motifStack, OrganismDbi

**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 supplied by users. Starting 2.0.5, new functions have been added for finding the peaks with bi-directional promoters with summary statistics (peaksNearBDP), for summarizing the occurrence of motifs in peaks (summarizePatternInPeaks) and for adding other IDs to annotated peaks or enrichedGO (addGeneIDs). This package leverages the biomaRt, IRanges, Biostrings, BSgenome, GO.db, multtest and stat packages.

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## R topics documented:

ChIPpeakAnno-package	3
addAncestors	5
addGeneIDs	5
addMetadata	7
annoGR-class	8
annoPeaks	9
annotatedPeak	11
annotatePeakInBatch	12
assignChromosomeRegion	15
bdp	18
BED2RangedData	19
bindist-class	20
binOverFeature	20
binOverGene	21
binOverRegions	22
ChIPpeakAnno-deprecated	23
condenseMatrixByColnames	25
convert2EntrezID	25
countPatternInSeqs	26
cumulativePercentage	27
egOrgMap	28
enrichedGO	29
estFragmentLength	30
estLibSize	31
ExonPlusUtr.human.GRCh37	31
featureAlignedDistribution	32
featureAlignedExtendSignal	33
featureAlignedHeatmap	34
featureAlignedSignal	36
findEnhancers	37
findOverlappingPeaks	38
findOverlapsOfPeaks	40
findVennCounts	42
getAllPeakSequence	43
getAnnotation	44
getEnrichedGO	45

getEnrichedPATH . . . . .	47
getVennCounts . . . . .	48
GFF2RangedData . . . . .	49
HOT.spots . . . . .	50
IDRfilter . . . . .	52
makeVennDiagram . . . . .	53
mergePlusMinusPeaks . . . . .	54
myPeakList . . . . .	56
oligoFrequency . . . . .	56
oligoSummary . . . . .	57
peakPermTest . . . . .	58
Peaks.Ste12.Replicate1 . . . . .	60
Peaks.Ste12.Replicate2 . . . . .	60
Peaks.Ste12.Replicate3 . . . . .	61
peaksNearBDP . . . . .	62
permPool-class . . . . .	63
pie1 . . . . .	64
plotBinOverRegions . . . . .	65
preparePool . . . . .	66
reCenterPeaks . . . . .	67
summarizeOverlapsByBins . . . . .	68
summarizePatternInPeaks . . . . .	69
tileCount . . . . .	70
tileGRanges . . . . .	71
toGRanges . . . . .	72
translatePattern . . . . .	74
TSS.human.GRCh37 . . . . .	74
TSS.human.GRCh38 . . . . .	75
TSS.human.NCBI36 . . . . .	76
TSS.mouse.GRCm38 . . . . .	76
TSS.mouse.NCBIM37 . . . . .	77
TSS.rat.RGSC3.4 . . . . .	78
TSS.rat.Rnor_5.0 . . . . .	78
TSS.zebrafish.Zv8 . . . . .	79
TSS.zebrafish.Zv9 . . . . .	80
wgEncodeTfbsV3 . . . . .	80
write2FASTA . . . . .	81
xget . . . . .	82

**Index****84**


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ChIPpeakAnno-package    *Batch annotation of the peaks identified from either ChIP-seq or ChIP-chip experiments.*

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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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LazyLoad: yes

## Author(s)

Lihua Julie Zhu, Jianhong Ou, Hervé Pagès, Claude Gazin, Nathan Lawson, Simon Lin, David Lapointe and Michael Green

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## References

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## Examples

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

---

addAncestors	<i>Add GO IDs of the ancestors for a given vector of GO ids</i>
--------------	---

---

**Description**

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

**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"))
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
  - mgi: 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 dataframe 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**

<code>ol</code>	An object of <code>overlappingPeaks</code> , which is output of <a href="#">findOverlapsOfPeaks</a> .
<code>colNames</code>	Names of metadata column to be added. If it is <code>NULL</code> , <code>addMetadata</code> will guess what to add.
<code>FUN</code>	A function to be called
<code>...</code>	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])
o1 <- findOverlapsOfPeaks(peaks1, peaks2)
addMetadata(o1)
```

---

annoGR-class

*Class* annoGR

---

**Description**

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

**Usage**

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

**Arguments**

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 <a href="#">OrganismDb</a> . It is used for extracting gene symbol for <a href="#">geneModel</a> group for <a href="#">TxDb</a>



## Objects from the Class

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

## 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

## Coercion

`as(from, "annoGR")`: Creates a annoGR object from a GRanges object.

`as(from, "GRanges")`: Create a GRanges object from a annoGR object.

## Methods

**info** Print basic info for annoGR object

**annoGR("TxDb"), annoGR("EnsDb")** Create a annoGR object from [TxDb](#) or [EnsDb](#) object

## Author(s)

Jianhong Ou

## Examples

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

---

annoPeaks

*Annotate peaks*

---

## 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	<p>Specifying the criteria to associate peaks with annotation. Here is how to use it together with the parameter bindingRegion</p> <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> <p><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.</p>
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(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**

```
data(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.

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

start\_position start position of the feature such as gene

end\_position end position of the feature such as the 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 (Sys.getenv("USER")=="jianhongou") {
  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     *Obtain the distance to the nearest TSS, miRNA, and/or exon for a list of peaks*

---

## 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"),
  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 bioMaRt package for details
featureType	A character vector used with mart argument if AnnotationData is not supplied; it's value is "TSS", "miRNA" or "Exon"
AnnotationData	A <a href="#">GRanges</a> or <a href="#">annoGR</a> object. It can be obtained from function getAnnotation or customized annotation of class GRanges containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). Pre-compiled annotations, such as TSS.human.NCBI36, TSS.mouse.NCBIM37, TSS.rat.RGSC3.4 and TSS.zebrafish.Zv8, are provided by this package (attach them with data() function). Another method to provide annotation data is to obtain through biomaRt real time by using the parameters of mart and featureType
output	<p><b>nearestLocation (default)</b> will output the nearest features calculated as Peak-Loc - FeatureLocForDistance</p> <p><b>overlapping</b> will output overlapping features with maximum gap specified as maxgap between peak range and feature range</p> <p><b>shortestDistance</b> will output nearest features</p> <p><b>both</b> will output all the nearest features, in addition, will output any features that overlap the peak that is not the nearest features</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>

	<b>upstream</b> will output all upstream features with maximum gap.
	<b>downstream</b> will output all downstream features with maximum gap.
	<b>upstreamORdownstream</b> will output all upstream features with maximum gap or downstream with maximum gap
	<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 bindingRegion). Otherwise, it will report the closest promoter in one direction.
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 select.
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. 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.
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 be 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> </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.

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
start_position	start position of the feature such as gene
end_position	end position of the feature such as the gene
strand	1 or + for positive strand and -1 or - for negative strand where the feature is located
shortestDistance	The shortest distance from either end of peak to either end the feature.
fromOverlappingOrNearest	nearest: indicates this feature's start (feature's end for features at minus strand) is closest to the peak start; Overlapping: indicates this feature overlaps with this peak although it is not the nearest feature start

**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**

```
#if (interactive()){
  ## example 1: annotate myPeakList by TxDb or EnsDb.
  data(myPeakList)
  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 binding 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 RangedData
## 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)
#}

```

---

### 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=1000L, immediate.downstream.cutoff=1000L,
    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="#">TxDb</a> 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="#">TxDb</a> 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 1000 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 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>

**Value**

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



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

annotatePeakInBatch, findOverlapsOfPeaks, getEnriched, makeVennDiagram, addGeneIDs, peaksNearBDP, summarizePeaks

### Examples

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

```

    TxDb=TxDb)
  }
}

```

---

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(Sys.getenv("USER")=="jianhongou"){
  library(EnsDb.Hsapiens.v75)
  data("myPeakList")
  annoGR <- annoGR(EnsDb.Hsapiens.v75)
  seqlevelsStyle(myPeakList) <- seqlevelsStyle(annoGR)
  ChIPpeakAnno:::bdp(myPeakList, annoGR)
}

```

---

BED2RangedData      *Convert BED format to RangedData*

---

### Description

Convert BED format to RangedData. This function will be depreciated.

### Usage

```
BED2RangedData(data.BED, header=FALSE, ...)
```

### Arguments

data.BED	BED format data frame or BED filename, please refer to <a href="http://genome.ucsc.edu/FAQ/FAQformat#format">http://genome.ucsc.edu/FAQ/FAQformat#format</a> for details
header	TRUE or FALSE, default to FALSE, indicates whether data.BED file has BED header
...	any parameter need to be passed into read.delim function

### Value

RangedData 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.

strand	1 for positive strand and -1 for negative strand where the feature is located. Default to 1 if not present in the BED formatted data frame
--------	--

### Note

For converting the peakList in BED format to RangedData before calling annotatePeakInBatch function

### Author(s)

Lihua Julie Zhu

### See Also

See also as [toGRanges](#).

### Examples

```
test.bed = data.frame(cbind(chrom = c("1", "2"),
                           chromStart=c("100", "1000"),
                           chromEnd=c("200", "1100"),
                           name=c("peak1", "peak2")))
test.rangedData = BED2RangedData(test.bed)
```

---

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="in`

### Slots

`counts` vector of "integer" The count number in each binding range

`mids` vector of "integer" The center of each range relevant to feature

`halfBinSize` "integer", length must be 1. the fixed half-width of each binding range

`bindingType` a "character". could be "TSS", "geneEnd"

`featureType` a "character". could be "transcript", "exon"

### Methods

`$, $<-` Get or set the slot of `bindist`

### 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 [SimpleRleList](#) or [RleList](#). It represents the coverage for samples.  
**TxDb**                An object of [TxDb](#). 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")== "jianhongou"){
  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)
  }
}

```

---

binOverRegions            *coverage of chromosome regions*

---

**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**

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.
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")=="jianhongou"){
  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)
  }
}
```

---

ChIPpeakAnno-deprecated

*Deprecated Functions in Package ChIPpeakAnno*

---

**Description**

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

**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"), ...)
BED2RangedData(data.BED, header=FALSE, ...)
GFF2RangedData(data.GFF, header=FALSE, ...)

```

**Arguments**

Peaks1	RangedData: See example below.
Peaks2	RangedData: 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> or <a href="#">RangedData</a> : See also <a href="#">findOverlapsOfPeaks</a> . Or any parameter need to be passed into read.delim function for 2RangedData function.
header	TRUE or FALSE, default to FALSE, indicates whether data file has header
data.BED	BED format data frame or BED filename, please refer to <a href="http://genome.ucsc.edu/FAQ/FAQformat#format">http://genome.ucsc.edu/FAQ/FAQformat#format</a> for details
data.GFF	GFF format data frame or GFF file name, please refer to <a href="http://genome.ucsc.edu/FAQ/FAQformat#format">http://genome.ucsc.edu/FAQ/FAQformat#format</a> for details

**Details**

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

**See Also**

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



---

 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

```
filepath =
  system.file("extdata", "examplePattern.fa", package="ChIPpeakAnno")
dict = readDNASTringSet(filepath = filepath, format="fasta", use.names=TRUE)
sequences = c("ACTGGGGGGGCTGGGCCCCCAAAT",
              "AAAAAACCCCTTTGGCCATCCCGGGACGGGCCCAT",
              "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 PMID: 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)
```

---

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**

```
data(enrichedGO)
```

### **Format**

A list of 3 dataframes.

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

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

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)
```

---

```
estFragmentLength      estimate the fragment length
```

---

**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(Sys.getenv("USER")=="jianhongou"){
  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(Sys.getenv("USER")=="jianhongou"){
  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**

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

**Format**

RangedData 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.

```
strand 1 for positive strand and -1 for negative strand
description description of the transcript
ensembl_gene_id gene id
utr5start 5' UTR start
utr5end 5' UTR end
utr3start 3' UTR start
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.
zeroAt	zero point position of feature.gr
n.tile	The number of tiles to generate for each element of feature.gr, default is 100
...	any paramters could be used by <a href="#">matplot</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="1")
```

---

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 ddownstream 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(Sys.getenv("USER")=="jianhongou"){
  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)<7500000]
    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**

cvglists	List of <a href="#">SimpleRleList</a> or <a href="#">RleList</a>
feature.gr	An object of <a href="#">GRanges</a> with identical width.
upstream, downstream	Set the feature.gr to upstream and dwonstream from the center of the feature.gr if they are set.
n.tile	The number of tiles to generate for each element of feature.gr, default is 100
...	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)

```

---

findEnhancers	<i>Find possible enhancers depend on DNA interaction data</i>
---------------	---

---

### 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.
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 = "nearest-BiDirectionalPromoters" and bindingRegion = c(-5000, 3000)</li> </ul> <p><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.</p>
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)
```

---

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

---

**Description**

Find the overlapping peaks for two input peak ranges.

This function is to keep the backward compatibility with previous versions for RangedData object.

The new function findOverlapsOfPeaks is recommended.

Convert RangedData to GRanges with toGRanges function.

**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            RangedData: See example below.

Peaks2            RangedData: 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.

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 GRanges or RangedData: See also <a href="#">findOverlapsOfPeaks</a> .

### Details

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	RangedData 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 =
  RangedData(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),space=c(6,6,6,6,5))
peaks2 =
  RangedData(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),space=c(6,6,6,6,5))
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("min", "merge", "keepAll"))

```

**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.

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 1, while set it to "min" will count it as the minimal involved peaks in any group of connected/overlapped peaks.

**Details**

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



**Value**

return value is An object of overlappingPeaks.

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

---

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

---

### Description

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

### Usage

```
findVennCounts(Peaks, NameOfPeaks, maxgap = -1L, minoverlap = 0L,
               totalTest, useFeature=FALSE)
```

### Arguments

Peaks	RangedDataList: 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 findOverlaps() to detect overlaps. See <a href="#">?findOverlaps</a> in the <b>IRanges</b> package for a description of these arguments.
totalTest	Numeric value to specify the total number of tests performed to obtain the list of peaks.
useFeature	TRUE or FALSE, default FALSE, true means using feature field in the Ranged-Data for calculating overlap, false means using chromosome range for calculating overlap.

### Value

p.value	hypergeometric testing result
vennCounts	vennCounts objects containing counts for Venn Diagram generation, see details in limma package vennCounts

### Author(s)

Lihua Julie Zhu

### See Also

makeVennDiagram

---

getAllPeakSequence      *Obtain genomic sequences around the peaks*

---

### 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	RangedData used if mart object is parsed in which can be obtained from getAnnotation with featureType="TSS". For example, data(TSS.human.NCBI36), data(TSS.mouse.NCBI36), data(GO.rat.RGSC3.4) and data(TSS.zebrafish.Zv8). If not supplied, then annotation will be obtained from biomaRt automatically using the mart object

### 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](#) or [RangedData](#) 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.

strand	1 for positive strand and -1 for negative strand where the feature is located
description	description of the feeature 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

### 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

```
if (interactive())
{
  mart <- useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")
  Annotation <- getAnnotation(mart, featureType="TSS")
}
```

---

getEnrichedGO	<i>Obtain enriched gene ontology (GO) terms that near the peaks</i>
---------------	---

---

### 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)
```

### 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.

### Value

A list with 3 elements

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

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

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

**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)
  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      *Obtain enriched PATH that near the peaks*

---

### 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)

```

### 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, reactome.db
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

### Value

A dataframe of enriched path with the following variables.

path.id	KEGG PATH ID
EntrezID	Entrez ID
count.InDataset	count of this PATH in this dataset
count.InGenome	count of this PATH in the genome
pvalue	pvalue from the hypergeometric test
totaltermInDataset	count of all PATH in this dataset

totaltermInGenome  
                                   count of all PATH in the genome  
 PATH                              PATH name

**Author(s)**

Jianhong Ou

**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()) {
  data(annotatedPeak)
  library(org.Hs.eg.db)
  library(reactome.db)
  enriched.PATH = getEnrichedPATH(annotatedPeak, orgAnn="org.Hs.eg.db",
                                   pathAnn="reactome.db", maxP=0.01,
                                   minPATHterm=10, multiAdjMethod=NULL)
  head(enriched.PATH)
}
```

---

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 [GRanges](#) or [RangedData](#): 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.



- by region, feature or base, default region. feature means using feature field in the RangedData or GRanges 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 vennCounts

### Author(s)

Jianhong Ou

### See Also

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

### Examples

```
if(Sys.getenv("USER")== "jianhongou"){
  peaks1 = RangedData(IRanges(start = c(967654, 2010897, 2496704),
                                end = c(967754, 2010997, 2496804),
                                names = c("Site1", "Site2", "Site3")),
                    space = c("1", "2", "3"),
                    strand=as.integer(1),
                    feature=c("a", "b", "c"))
  peaks2 =
    RangedData(IRanges(start=c(967659, 2010898, 2496700, 3075866, 3123260),
                        end=c(967869, 2011108, 2496920, 3076166, 3123470),
                        names = c("t1", "t2", "t3", "t4", "t5")),
              space = c("1", "2", "3", "1", "2"),
              strand = c(1, 1, -1,-1,1),
              feature=c("a","c","d","e", "a"))
  getVennCounts(peaks1,peaks2)
  getVennCounts(peaks1,peaks2, by="feature")
  getVennCounts(peaks1, peaks2, by="base")
}
```

---

GFF2RangedData

*Convert GFF format to RangedData*

---

### Description

Convert GFF format to RangedData. This function will be depreciated. Use function toGRanges instead.

**Usage**

```
GFF2RangedData(data.GFF,header=FALSE, ...)
```

**Arguments**

data.GFF	GFF format data frame or GFF file name, please refer to <a href="http://genome.ucsc.edu/FAQ/FAQformat#format">http://genome.ucsc.edu/FAQ/FAQformat#format</a> for details
header	TRUE or FALSE, default to FALSE, indicates whether data.GFF file has GFF header
...	any parameter need to be passed into read.delim function

**Value**

RangedData 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.

strand            1 for positive strand and -1 for negative strand where the feature is located.

**Note**

For converting the peakList in GFF format to RangedData before calling annotatePeakInBatch function

**Author(s)**

Lihua Julie Zhu

**Examples**

```
test.GFF = data.frame(cbind(seqname = c("chr1", "chr2"),
source=rep("Macs", 2),
feature=rep("peak", 2),
start=c("100", "1000"),
end=c("200", "1100"),
score=c(60, 26),
strand=c(1, -1),
frame=c(".", 2),
group=c("peak1", "peak2")))
test.rangedData = GFF2RangedData(test.GFF)
```

---

HOT.spots

*High Occupancy of Transcription Related Factors regions*


---

**Description**

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

**Usage**

```
data("HOT.spots")
```

**Format**

An object of GRangesList

**Details**

How to generated the data:

```
temp <- tempfile()
url <- "http://metatracks.encodegenetics.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.encodegenetics.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)
```

IDRfilter

*Filter peaks by IDR (irreproducible discovery rate)***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, [GRanges](#) object.  
bamfileA, bamfileB  
                  file path of bam files.  
maxgap, minoverlap  
                  Used in the internal call to `findOverlaps()` to detect overlaps. See `?findOverlaps` in the **IRanges** 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**

```
if(interactive()){
  path <- system.file("extdata", "reads", package="MMDiffBamSubset")
  if(file.exists(path)){
    bamfileA <- file.path(path, "reads", "WT_2.bam")
    bamfileB <- file.path(path, "reads", "Resc_2.bam")
    WT.AB2.Peaks <- file.path(path, "peaks", "WT_2_Macs_peaks.xls")
    Resc.AB2.Peaks <- file.path(path, "peaks", "Resc_2_Macs_peaks.xls")
    peaksA=toGRanges(WT.AB2.Peaks, format="MACS")
    peaksB=toGRanges(Resc.AB2.Peaks, format="MACS")
    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"), method = c("hyperG",
                "permutation"), TxDb, ...)

```

### 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 <a href="#">findOverlaps()</a> to detect overlaps. See <a href="#">?findOverlaps</a> in the <b>IRanges</b> 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 <a href="#">GRanges</a> 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.
method	method used for p value calculation. hyperG means hypergeometric test and permutation means <a href="#">peakPermTest</a>
TxDb	An object of <a href="#">TxDb</a>
...	Additional arguments to be passed to <a href="#">venn.diagram</a>

### Details

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

**Value**

In addition to a Venn Diagram produced, a p.value is calculated by hypergeometric test to determine whether the peaks or features are overlapped significantly.

**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)

  makeVennDiagram(list(peaks1, peaks2), NameOfPeaks=c("TF1", "TF2"),
                  totalTest=100)

  ##### 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")
    }

```

---

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

```
data(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, last = 1e+06)
```

### Arguments

sequence	The sequences packaged in DNASTringSet, DNASTring object or output of function <a href="#">getAllPeakSequence</a> .
MarkovOrder	Markov order.
last	The sequence size to be analyzed.



**Value**

A numeric vector.

**Author(s)**

Jianhong Ou

**See Also**

See Also as [oligoSummary](#)

**Examples**

```
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 Markove chain.

**Usage**

```
oligoSummary(sequence, oligoLength = 6L, freqs = NULL,
             MarkovOrder = 3L, quickMotif = FALSE, revcomp=FALSE,
             maxsize=100000)
```

**Arguments**

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

**Value**

A list is returned.

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

---

peakPermTest

*Permutation Test for two given peak lists*

---

**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 [GRanges](#)  
ntimes number of permutations  
seed random seed  
mc.cores The number of cores to use. see [mclapply](#).  
maxgap See [findOverlaps](#) in the [IRanges](#) 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

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

### Format

RangedData 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 space containing the chromosome where the peak is located.

### References

Philippe Lefrançois, 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

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

### Format

RangedData 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 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**

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

**Format**

RangedData 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 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
```

---

peaksNearBDP                      *obtain the peaks near bi-directional promoters*

---

### 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`            [GRanges](#) or [RangedData](#): See example below

`AnnotationData`      annotation 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)`.

`MaxDistance`         Specify the maximum gap allowed between the peak and nearest gene

`...`                    Not used

### Value

A list of 4

`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

`percentPeaksWithBDP`      The percent of input peaks containing bi-directional promoters

`n.peaks`                The total number of input peaks

`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 (Sys.getenv("USER")=="jianhongou")
{
  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	<i>Class "permPool"</i>
----------------	-------------------------

---

**Description**

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

**Objects from the Class**

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

**Slots**

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

**Methods**

`$`, `$<-` Get or set the slot of `permPool`

**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**

x	a vector of non-negative numerical quantities. The values in x are displayed as the areas of pie slices.
labels	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 <code>par("fg")</code> is used.
border, lty	(possibly vectors) arguments passed to <code>polygon</code> 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="#">matplot</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)
  }
}

```

preparePool

*prepare data for permutation test***Description**

prepare data for permutation test [peakPermTest](#)

**Usage**

```

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

```

**Arguments**

TxDb	an object of <a href="#">TxDb</a>
template	an object of <a href="#">GRanges</a>
bindingDistribution	an object of <a href="#">bindist</a>
bindingType	the relevant position to features
featureType	feature type, transcript or exon.
seqn	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(Sys.getenv("USER")=="jianhongou"){
  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	<i>re-center the peaks</i>
---------------	----------------------------

---

## 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,
                        windowSize=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

```
f1s <- list.files(system.file("extdata", package="GenomicAlignments"),
                 recursive=TRUE, pattern="*bam$", full=TRUE)
names(f1s) <- basename(f1s)
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, f1s, windowSize=50, step=10)
```

---

```
summarizePatternInPeaks
```

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

---

### Description

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

### Usage

```
summarizePatternInPeaks(patternFilePath, format = "fasta", skip=0L,
                        BSgenomeName, peaks, outfile, append = FALSE)
```

### Arguments

patternFilePath	A character vector containing the path to the file to read the patterns from.
format	Either "fasta" (the default) or "fastq"
skip	Single non-negative integer. The number of records of the pattern file to skip before beginning to read in records.
BSgenomeName	BSgenome object. Please refer to available.genomes in BSgenome package for details
peaks	<a href="#">GRanges</a> or <a href="#">RangedData</a> containing the peaks
outfile	A character vector containing the path to the file to write the summary output.
append	TRUE or FALSE, default FALSE

### Value

A data frame with 3 columns as n.peaksWithPattern (number of peaks with the pattern), n.totalPeaks (total number of peaks in the input) and Pattern (the corresponding pattern). The summary will consider both strand (including reverse complement).

### Author(s)

Lihua Julie Zhu

### Examples

```
peaks = RangedData(IRanges(start=c(100, 500), end=c(300, 600),
                          names=c("peak1", "peak2")),
                  space=c("NC_008253", "NC_010468"))
filepath =system.file("extdata", "examplePattern.fa",
                     package="ChIPpeakAnno")
library(BSgenome.Ecoli.NCBI.20080805)
summarizePatternInPeaks(patternFilePath=filepath, format="fasta",
                       skip=0L, BSgenomeName=Ecoli, peaks=peaks)
```

---

tileCount	<i>Perform overlap queries between reads and genome by windows</i>
-----------	--

---

### 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=1e6, step=1e6,
          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

```
f1s <- list.files(system.file("extdata", package="GenomicAlignments"),
                 recursive=TRUE, pattern="*bam$", full=TRUE)
names(f1s) <- basename(f1s)
genes <- GRanges(seqlengths = c(chr2L=7000, chr2R=10000))
se <- tileCount(f1s, 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 <a href="#">GRanges</a> 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 RangedData or MACS output file to GRanges

**Usage**

```
## S4 method for signature 'character'
toGRanges(data, format=c("BED", "GFF",
                        "MACS", "MACS2", "MACS2.broad",
                        "narrowPeak", "broadPeak",
                        "others"),
          header=FALSE, comment.char="#", colNames=NULL, ...)
## S4 method for signature 'connection'
toGRanges(data, format=c("BED", "GFF",
                        "MACS", "MACS2", "MACS2.broad",
                        "narrowPeak", "broadPeak",
                        "others"),
          header=FALSE, comment.char="#", colNames=NULL, ...)
## S4 method for signature 'data.frame'
toGRanges(data, colNames=NULL, ...)
## S4 method for signature 'TxDb'
toGRanges(data, feature=c("gene", "transcript", "exon",
                        "CDS", "fiveUTR", "threeUTR",
                        "microRNA", "tRNAs", "geneModel"),
          OrganismDb, ...)
## S4 method for signature 'EnsDb'
toGRanges(data,
          feature=c("gene", "transcript", "exon", "disjointExons"),
          ...)
```

**Arguments**

data	an object of data.frame, TxDb or EnsDb, or the file name of data to be imported. Alternatively, data can be a readable txt-mode connection (See ?read.table).
format	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.
feature	annotation type
header	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: header is set to TRUE if and only if the first row contains one fewer field than the number of columns.
comment.char	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.
...	parameters passed to <a href="#">read.table</a>
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(Sys.getenv("USER")=="jianhongou"){
  ## MACS connection
  macs <- readLines(macs)
  macs <- textConnection(macs)
  macsOutput <- toGRanges(macs, format="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")
  ## 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	<i>TSS annotation for human sapiens (GRCh37) obtained from biomaRt</i>
------------------	--

---

**Description**

TSS annotation for human sapiens (GRCh37) obtained from biomaRt

**Usage**

```
data(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.

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**

```
data(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**

```
data(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.

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 biomaRt*

---

**Description**

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

**Usage**

```
data(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.

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	<i>TSS annotation data for mouse (NCBIM37) obtained from biomaRt</i>
-------------------	--

---

**Description**

TSS annotation data for mouse (NCBIM37) obtained from biomaRt

**Usage**

```
data(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.

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**

```
data(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.

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 biomaRt*


---

**Description**

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

**Usage**

```
data(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.

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 biomaRt*

---

**Description**

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

**Usage**

```
data(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 strand information. In addition, the following variables are included.

```
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**

```
data(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 strand information. In addition, the following variables are included.

```
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)
```

---

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**

```
data("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.bed.gz>

**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("CCCCCCCCGGGGG", "TTTTTTTAAAAAA"))

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

---

xget

*Return the value from a Bimap objects*

---

**Description**

Search by name for an Bimap object.

**Usage**

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

**Arguments**

x, envir, mode, ifnotfound, inherits  
 see [mget](#)

output            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)
```

# Index

## \*Topic **classes**

- annoGR-class, 8
- bindist-class, 20
- permPool-class, 63

## \*Topic **datasets**

- annotatedPeak, 11
- enrichedGO, 29
- ExonPlusUtr.human.GRCh37, 31
- HOT.spots, 50
- myPeakList, 56
- Peaks.Ste12.Replicate1, 60
- Peaks.Ste12.Replicate2, 60
- Peaks.Ste12.Replicate3, 61
- TSS.human.GRCh37, 74
- TSS.human.GRCh38, 75
- TSS.human.NCBI36, 76
- TSS.mouse.GRCm38, 76
- TSS.mouse.NCBIM37, 77
- TSS.rat.RGSC3.4, 78
- TSS.rat.Rnor\_5.0, 78
- TSS.zebrafish.Zv8, 79
- TSS.zebrafish.Zv9, 80
- wgEncodeTfbsV3, 80

## \*Topic **graph**

- makeVennDiagram, 53

## \*Topic **misc**

- addAncestors, 5
- addGeneIDs, 5
- addMetadata, 7
- annoPeaks, 9
- annotatePeakInBatch, 12
- assignChromosomeRegion, 15
- bdp, 18
- BED2RangedData, 19
- binOverFeature, 20
- condenseMatrixByColnames, 25
- convert2EntrezID, 25
- countPatternInSeqs, 26
- egOrgMap, 28
- estFragmentLength, 30
- estLibSize, 31
- featureAlignedDistribution, 32
- featureAlignedExtendSignal, 33

- featureAlignedHeatmap, 34
- featureAlignedSignal, 36
- findEnhancers, 37
- findOverlappingPeaks, 38
- findOverlapsOfPeaks, 40
- findVennCounts, 42
- getAllPeakSequence, 43
- getAnnotation, 44
- getEnrichedGO, 45
- getEnrichedPATH, 47
- getVennCounts, 48
- GFF2RangedData, 49
- IDRfilter, 52
- mergePlusMinusPeaks, 54
- oligoFrequency, 56
- oligoSummary, 57
- peakPermTest, 58
- peaksNearBDP, 62
- pie1, 64
- preparePool, 66
- reCenterPeaks, 67
- summarizeOverlapsByBins, 68
- summarizePatternInPeaks, 69
- tileCount, 70
- tileGRanges, 71
- toGRanges, 72
- translatePattern, 74
- write2FASTA, 81
- xget, 82

## \*Topic **package**

- ChIPpeakAnno-package, 3
- \$,bindist-method (bindist-class), 20
- \$,permPool-method (permPool-class), 63
- \$<-,bindist-method (bindist-class), 20
- \$<-,permPool-method (permPool-class), 63

- acf, 30
- addAncestors, 5
- addGeneIDs, 5, 14
- addMetadata, 7
- annoGR, 12, 14, 18, 21, 67
- annoGR (annoGR-class), 8
- annoGR, EnsDb-method (annoGR-class), 8
- annoGR, GRanges-method (annoGR-class), 8

- annoGR, TxDb-method (annoGR-class), 8
- annoGR-class, 8
- annoPeaks, 9, 13, 14, 18
- annotatedPeak, 11
- annotatePeakInBatch, 10, 12, 38, 41
- assignChromosomeRegion, 15
  
- BamFileList, 68, 70
- bdp, 18
- BED2RangedData, 19
- BED2RangedData-deprecated  
(BED2RangedData), 19
- bindist, 20, 59, 66
- bindist (bindist-class), 20
- bindist-class, 20
- bindist-method (bindist-class), 20
- binOverFeature, 20
- binOverGene, 21, 23, 65
- binOverRegions, 22, 22, 65
  
- ChIPpeakAnno (ChIPpeakAnno-package), 3
- ChIPpeakAnno-deprecated, 23
- ChIPpeakAnno-package, 3
- coerce, annoGR, GRanges-method  
(annoGR-class), 8
- coerce, GRanges, annoGR-method  
(annoGR-class), 8
- condenseMatrixByColNames, 25
- convert2EntrezID, 25
- countPatternInSeqs, 26
- cumulativePercentage, 27
  
- Date, 8, 9
- Deprecated, 24
  
- egOrgMap, 28
- enrichedGO, 29
- EnsDb, 8, 9, 72
- estFragmentLength, 30, 34
- estLibSize, 31, 34
- ExonPlusUtr.human.GRCh37, 31
  
- featureAlignedDistribution, 32, 35, 36
- featureAlignedExtendSignal, 33
- featureAlignedHeatmap, 33, 34, 36
- featureAlignedSignal, 32–35, 36
- findEnhancers, 37
- findOverlappingPeaks, 14, 38, 41, 49
- findOverlappingPeaks-deprecated  
(findOverlappingPeaks), 38
- findOverlaps, 24, 38, 40, 42, 48, 52, 53, 58
- findOverlapsOfPeaks, 7, 8, 24, 39, 40, 54
- findVennCounts, 42
  
- format, 65
- frequency, 57, 58
  
- GAlignmentPairs, 68, 70
- GAlignments, 68, 70
- GAlignmentsList, 68, 70
- getAllPeakSequence, 43, 56, 57
- getAnnotation, 14, 44
- getBM, 6, 7
- getEnrichedGO, 45
- getEnrichedPATH, 47
- getVennCounts, 41, 48
- GFF2RangedData, 49
- GFF2RangedData-deprecated  
(GFF2RangedData), 49
- GRanges, 8–10, 12, 14, 18, 21, 24, 27, 32, 33,  
35–37, 39–41, 43, 44, 48, 52, 53, 58,  
62, 66–71, 73
- GRangesList, 68, 70
  
- HOT.spots, 50
  
- IDRfilter, 52
- info (annoGR-class), 8
- info, annoGR-method (annoGR-class), 8
  
- legend, 65
- listAttributes(mart), 6
- listFilters(mart), 6
  
- makeVennDiagram, 14, 41, 49, 53
- matplot, 32, 65
- mergePlusMinusPeaks, 54
- mget, 82, 83
- myPeakList, 56
  
- numOverlaps, 59
  
- oligoFrequency, 56
- oligoSummary, 57, 57
- OrganismDb, 73
- overlappingPeaks, 7
- overlappingPeaks (findOverlapsOfPeaks),  
40
- overlappingPeaks-class  
(findOverlapsOfPeaks), 40
  
- peakPermTest, 20, 53, 54, 58, 63, 66
- Peaks.Ste12.Replicate1, 60
- Peaks.Ste12.Replicate2, 60
- Peaks.Ste12.Replicate3, 61
- peaksNearBDP, 14, 62
- permPool, 59, 63
- permPool (permPool-class), 63

permPool-class, [63](#)  
permPool-method (permPool-class), [63](#)  
permTest, [59](#)  
pie, [65](#)  
pie1, [64](#)  
plotBinOverRegions, [22](#), [23](#), [65](#)  
preparePool, [20](#), [59](#), [63](#), [66](#)

RangedData, [24](#), [39](#), [44](#), [48](#), [62](#), [69](#)  
RangedSummarizedExperiment, [68](#), [70](#)  
read.table, [73](#)  
reCenterPeaks, [67](#)  
RleList, [22](#), [23](#), [32](#), [35](#), [36](#)

SimpleRleList, [22](#), [23](#), [32](#), [35](#), [36](#)  
summarizeOverlaps, [27](#), [68](#), [70](#)  
summarizeOverlapsByBins, [68](#)  
summarizePatternInPeaks, [14](#), [69](#)

tileCount, [70](#)  
tileGRanges, [71](#)  
toGRanges, [19](#), [24](#), [72](#)  
toGRanges, character-method (toGRanges),  
[72](#)  
toGRanges, connection-method  
(toGRanges), [72](#)  
toGRanges, data.frame-method  
(toGRanges), [72](#)  
toGRanges, EnsDb-method (toGRanges), [72](#)  
toGRanges, RangedData-method  
(toGRanges), [72](#)  
toGRanges, TxDb-method (toGRanges), [72](#)  
translatePattern, [74](#)  
TSS.human.GRCh37, [74](#)  
TSS.human.GRCh38, [75](#)  
TSS.human.NCBI36, [76](#)  
TSS.mouse.GRCm38, [76](#)  
TSS.mouse.NCBIM37, [77](#)  
TSS.rat.RGSC3.4, [78](#)  
TSS.rat.Rnor\_5.0, [78](#)  
TSS.zebrafish.Zv8, [79](#)  
TSS.zebrafish.Zv9, [80](#)  
TxDb, [8](#), [9](#), [16](#), [22](#), [23](#), [53](#), [59](#), [66](#), [72](#), [73](#)

useMart, [6](#)

venn.diagram, [53](#), [54](#)

wgEncodeTfbsV3, [80](#)  
write2FASTA, [81](#)

xget, [82](#)