

# Package ‘ChIPpeakAnno’

October 9, 2013

**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** 2.8.0

**Date** 2013-03-20

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**Depends** R (>= 2.10), grid,VennDiagram, BiocGenerics (>= 0.1.0),biomaRt, multtest, IRanges, Biostrings, BSgenome,BSgenome.Ecoli.NCBI.20080805, GO.db, org.Hs.eg.db, I

**Imports** gplots, BiocGenerics, biomaRt, multtest, IRanges, Biostrings,BSgenome, GO.db, limma, AnnotationDbi, GenomicFeatures

**biocViews** Annotation, ChIPseq, ChIPchip

**Suggests** reactome.db, RUnit, BiocGenerics

**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

**License** GPL (>= 2)

**LazyLoad** yes

**R topics documented:**

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

---

**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**

Package: ChIPpeakAnno  
Type: Package  
Version: 2.0.6  
Date: 2011-10-31  
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LazyLoad: yes

**Author(s)**

Lihua Julie Zhu, Herve Pages, Claude Gazin, Nathan Lawson, Simon Lin, David Lapointe and Michael Green

Maintainer: Lihua Julie Zhu <julie.zhu@umassmed.edu>

**References**

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8. N. L. Johnson, S. Kotz and A. W. Kemp (1992) *Univariate Discrete Distributions*, Second Edition. New York: Wiley
9. 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**

getAnnotation, annotatePeakInBatch, getAllPeakSequence, write2FASTA, convert2EntrezID, addAncestors, getEnrichedGO, BED2RangedData, GFF2RangedData, makeVennDiagram, findOverlappingPeaks, addGeneIDs, peaksNearBDP, summarizePatternInPeaks)

**Examples**

```

if (interactive())
{
data(myPeakList)
  data(TSS.human.NCBI36)

myPeakList1 = myPeakList[1:6,]

annotatedPeak = annotatePeakInBatch(myPeakList1, AnnotationData=TSS.human.NCBI36)

peaks = RangedData(IRanges(start=c(100, 500), end=c(300, 600),
names=c("peak1", "peak2")), space=c("NC_008253", "NC_010468"))
library(BSgenome.Ecoli.NCBI.20080805)

peaksWithSequences = getAllPeakSequence(peaks, upstream = 20,
downstream = 20, genome = Ecoli)
write2FASTA(peaksWithSequences, file="testseq.fasta", width=50)

filepath =system.file("extdata", "examplePattern.fa", package="ChIPpeakAnno")
summarizePatternInPeaks(patternFilePath=filepath, format="fasta", skip=0L, BSgenomeName=Ecoli, peaks=peaks)

library(org.Hs.eg.db)
annotatedPeak.withSymbol =addGeneIDs(annotatedPeak,"org.Hs.eg.db",c("symbol"))
enrichedGO = getEnrichedGO(annotatedPeak, orgAnn ="org.Hs.eg.db", maxP=0.01,
multiAdj=FALSE, minGOterm=10, multiAdjMethod="")

enriched.biologicalprocess = enrichedGO$bp
enriched.molecularfunction = enrichedGO$mf
enriched.cellularcomponent = enrichedGO$cc

data(annotatedPeak)
y = annotatedPeak$distancetoFeature[!is.na(annotatedPeak$distancetoFeature)]
hist(y, xlab="Distance To Nearest TSS", main="", breaks=1000,
xlim=c(min(y)-100, max(y)+100))

annotatedBDP = peaksNearBDP(myPeakList1, AnnotationData=TSS.human.NCBI36,
MaxDistance=5000,PeakLocForDistance = "middle", FeatureLocForDistance = "TSS")
c(annotatedBDP$percentPeaksWithBDP, annotatedBDP$n.peaks, annotatedBDP$n.peaksWithBDP)
}

```

---

addAncestors

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


---

**Description**

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

**Usage**

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

**Arguments**

go.ids            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)
```

**Arguments**

annotatedPeak    RangedData such as data(annotatedPeak) 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  
silence          TRUE or FALSE. If TRUE, will not show unmapped entrez id for feature ids.  
mart              mart object, see [useMart](#) of biomaRt package for details

## Details

One of orgAnn and mart should be assigned.

- When 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", "genename", "pfam", "pmid", "prosite", "refseq", "symbol", "unigene" and "uniprot". Some IDs are unique to a 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
- When 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\(mart\)](#) and valid attributes name listed by [listAttributes\(mart\)](#) 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, wiki-gene\_name, mirbase\_transcript\_name.

## Value

RangedData if the input is a RangedData or dataframe with added IDs if input is a character vector.

## Author(s)

Jianhong Ou, Lihua Julie Zhu

## References

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

**See Also**

[getBM](#), [AnnotationDbi](#)

**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"))
mart=useMart(biomart="ensembl",dataset="hsapiens_gene_ensembl")
addGeneIDs(annotatedPeak[1:6,],mart=mart,IDs2Add=c("external_gene_id","entrezgene"))
```

---

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**

RangedData 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 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

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

**Details**

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

## Examples

```

data(annotatedPeak)
str(annotatedPeak)
if (interactive()) {
y = annotatedPeak$distancetoFeature[!is.na(annotatedPeak$distancetoFeature)]
hist(as.numeric(as.character(y)), xlab="Distance To Nearest TSS", main="", breaks=1000,
ylim=c(0, 50), xlim=c(min(as.numeric(as.character(y)))-100,
max(as.numeric(as.character(y)))+100))
}

```

---

annotatePeakInBatch	<i>obtain the distance to the nearest TSS, miRNA, exon et al for a list of peak intervals</i>
---------------------	-----------------------------------------------------------------------------------------------

---

## Description

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

## Usage

```

annotatePeakInBatch(myPeakList, mart, featureType = c("TSS", "miRNA", "Exon"),
AnnotationData, output=c("nearestStart", "overlapping", "both"), multiple=c(TRUE, FALSE),
maxgap=0, PeakLocForDistance = c("start", "middle", "end"),
FeatureLocForDistance = c("TSS", "middle", "start", "end", "geneEnd"), select=c("all", "first", "last",

```

## Arguments

myPeakList	RangedData: See example below
mart	used if AnnotationData not supplied, a mart object, see useMart of bioMaRt package for details
featureType	used if AnnotationData not supplied, TSS, miRNA or exon
AnnotationData	annotation data obtained from getAnnotation or customized annotation of class RangedData 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) . If not supplied, then annotation will be obtained from biomaRt automatically using the parameters of mart and featureType
output	nearestStart (default): will output the nearest features calculated as peak start - feature start (feature end if feature resides at minus strand); overlapping: will output overlapping features with maximum gap specified as maxgap between peak range and feature range; both: will output all the nearest features, in addition, will output any features that overlap the peak that is not the nearest features.
multiple	not applicable when output is nearestStart. 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	Non-negative integer. Intervals with a separation of maxgap or less are considered to be overlapping
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.

**Value**

RangedData 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	NearestStart: 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

**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**

findOverlappingPeaks, makeVennDiagram, addGeneIDs, peaksNearBDP, summarizePatternInPeaks

**Examples**

```

if (interactive())
{
  ## example 1: annotate myPeakList (RangedData) with TSS.human.NCBI36 (RangedData)
  data(myPeakList)
  data(TSS.human.NCBI36)
  annotatedPeak = annotatePeakInBatch(myPeakList[1:6,], AnnotationData=TSS.human.NCBI36)
  as.data.frame(annotatedPeak)
  ## example 2: 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 = RangedData(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=as.integer(1), space=c(6,6,6,6,5,4,4))
  literature = RangedData(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=c(1,1,1,1,1,-1,-1), space=c(6,6,6,6,5,4,4))
  annotatedPeak1= annotatePeakInBatch(myexp, AnnotationData = literature)
  pie(table(as.data.frame(annotatedPeak1)$insideFeature))
  as.data.frame(annotatedPeak1)
  #### use BED2RangedData or GFF2RangedData to convert BED format or GFF format
  #### to RangedData before calling annotatePeakInBatch
  test.bed = data.frame(cbind(chrom = c("4", "6"), chromStart=c("100", "1000"),
  chromEnd=c("200", "1100"), name=c("peak1", "peak2")))
  test.rangedData = BED2RangedData(test.bed)
  annotatePeakInBatch(test.rangedData, AnnotationData = literature)
  test.GFF = data.frame(cbind(seqname = c("chr4", "chr4"), 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)
  as.data.frame(annotatePeakInBatch(test.rangedData, AnnotationData = literature))
}

```

---

 assignChromosomeRegion

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

---

### Description

Summarizing 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.dow
```

### Arguments

peaks.RD	peaks in RangedData or GRanges: See example below
exon	exon data obtained from getAnnotation or customized annotation of class RangedData containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). Will not use anymore! use <a href="#">TranscriptDb</a> instead.
TSS	TSS data obtained from getAnnotation or customized annotation of class RangedData 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). Will not use anymore! use <a href="#">TranscriptDb</a> instead.
utr5	5 prime UTR data obtained from getAnnotation or customized annotation of class RangedData containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). Will not use anymore! use <a href="#">TranscriptDb</a> instead.
utr3	3 prime UTR data obtained from getAnnotation or customized annotation of class RangedData containing additional variable: strand (1 or + for plus strand and -1 or - for minus strand). Will not use anymore! use <a href="#">TranscriptDb</a> instead.
proximal.promoter.cutoff	Specify the cutoff in bases to be classified as proximal promoter region. Peaks that reside within proximal.promoter.cutoff upstream from or overlap with transcription start site are classified as proximal promoters. Peaks that reside upstream over proximal.promoter.cutoff from gene start are classified as enhancers. The default is 1000 bases.
immediate.downstream.cutoff	Specify the cutoff in bases to be classified as immediate downstream. 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	NucleotideLevel (TRUE or FALSE) to allow both 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, then 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. Default=NULL
TranscriptDb	an object of <a href="#">TranscriptDb</a>

**Value**

jaccard	Jaccard Index
Exons	Percent of peaks reside in exon regions.
Introns	Percent of peaks reside in intron regions.
fiveUTRs	Percent of peaks reside in 5 prime UTR regions.
threeUTRs	Percent of peaks reside in 3 prime UTR regions.
Promoter	Percent of peaks reside in proximal promoter regions.
ImmediateDownstream	Percent of peaks reside in immediate downstream regions.
Enhancer.Silencer	Percent of peaks reside in enhancer/silencer regions.

**Author(s)**

Jianhong Ou, 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, getEnrichedGO, getEnrichedPATH, makeVennDiagram, addGeneIDs, peaksNearBDP, summarizePatternInPeaks

**Examples**

```
if (interactive())
{
library(ChIPpeakAnno)
##Display the list of genomes available at UCSC:
#library(rtracklayer)
#ucscGenomes()[, "db"]
## Display the list of Tracks supported by makeTranscriptDbFromUCSC()
#supportedUCSCtables()
##Retrieving a full transcript dataset for Human from UCSC
TranscriptDb <- makeTranscriptDbFromUCSC(genome="hg19", tablename="ensGene")
exons <- exons(TranscriptDb, columns=NULL)
fiveUTRs <- unique(unlist(fiveUTRsByTranscript(TranscriptDb)))
```

```

Feature.distribution <- assignChromosomeRegion(exons, nucleotideLevel=TRUE, TranscriptDb=TranscriptDb)
barplot(Feature.distribution$percentage)
assignChromosomeRegion(fiveUTRs, nucleotideLevel=FALSE, TranscriptDb=TranscriptDb)
data(myPeakList)
assignChromosomeRegion(myPeakList, nucleotideLevel=TRUE, precedence=c("Exons", "Introns", "fiveUTRs", "threeUTRs"))
}

```

---

BED2RangedData	<i>convert BED format to RangedData</i>
----------------	-----------------------------------------

---

## Description

convert BED format to RangedData

## 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

## 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)

```

---

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 such as ensemble gene id, gene symbol, refseq id 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	<i>Output total number of patterns found in the input sequences</i>
--------------------	---------------------------------------------------------------------

---

**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("ACTGGGGGGGCCTGGGCCCAAT", "AAAAAACCCCTTTGGCCATCCCGGGACGGGCCAT", "ATCGAAATTCC")
countPatternInSeqs(pattern=dict[1], sequences=sequences)
countPatternInSeqs(pattern=dict[2], sequences=sequences)
pattern = DNASTringSet("ATNGMAA")
countPatternInSeqs(pattern=pattern, sequences=sequences)
```

---

enrichedGO

*Enriched Gene Ontology terms used as example*

---

**Description**

Enriched Gene Ontology terms used as example

**Usage**

```
data(enrichedGO)
```

**Format**

A list of 3 variables.

bp enriched biological process with 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

**Examples**

```

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

```

---

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, feature=Type="ExonPlusUtr")`

### Examples

```

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

```

---

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

---

### Description

Find the overlapping peaks for two input peak ranges.

### Usage

```

findOverlappingPeaks(Peaks1, Peaks2, maxgap = 0L, minoverlap=1L, multiple = c(TRUE, FALSE),
NameOfPeaks1 = "TF1", NameOfPeaks2 = "TF2",
select=c("all", "first", "last", "arbitrary"), annotate = 0)

```

### Arguments

Peaks1	RangedData: See example below.
Peaks2	RangedData: See example below.
maxgap	Non-negative integer. Intervals with a separation of maxgap or less are considered to be overlapping.
minoverlap	Non-negative integer. Intervals with an overlapping of minoverlap or more are considered to be overlapping.
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.

### 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

- 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
- 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, 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)
}

```

---

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 = 0L, minoverlap = 1L, 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	Non-negative integer. Intervals with a separation of maxgap or less are considered to be overlapping.
minoverlap	Non-negative integer. Intervals with an overlapping of minoverlap or more are considered to be overlapping.
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

### Note

```

if (interactive())
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"))
findVennCounts(RangedDataList(peaks1,peaks2), NameOfPeaks=c("TF1", "TF2"), maxgap=0,totalTest=100,
useFeature=FALSE) findVennCounts(RangedDataList(peaks1,peaks2), NameOfPeaks=c("TF1", "TF2"),
maxgap=0,totalTest=100, useFeature=TRUE)
```

**Author(s)**

Lihua Julie Zhu

**See Also**

makeVennDiagram

getAllPeakSequence      *Obtain genomic sequences around the peaks*

**Description**

Obtain genomic sequences around the peaks leveraging BSgenome and biomaRt package

**Usage**

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

**Arguments**

myPeakList	RangedData: 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 getAn-notation with featureType="TSS". For example, data(TSS.human.NCBI36), data(TSS.mouse.NCBIM37) data(GO.rat.RGSC3.4) and data(TSS.zebrafish.Zv8). If not supplied, then anno-tation will be obtained from biomaRt automatically using the mart object

**Value**

RangedData 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 space holding the chromosome location 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

**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 = RangedData(IRanges(start=c(100, 500), end=c(300, 600), names=c("peak1", "peak2")), space=c("NC_008253", "
library(BSgenome.Ecoli.NCBI.20080805)
seq = getAllPeakSequence(peaks, upstream = 20, downstream = 20, genome = Ecoli)
write2FASTA(seq, file="test.fa")
```

---

getAnnotation

---

*Obtain the TSS, exon or miRNA annotation for the specified species*


---

**Description**

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

**Usage**

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

**Arguments**

mart	mart object, see useMart of bioMaRt package for details
featureType	TSS, miRNA, Exon, 5'UTR, 3'UTR, transcript or Exon plus UTR

**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
description	description of the feature such as gene

**Note**

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

**Author(s)**

Lihua Julie Zhu

**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

---

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


---

**Description**

Obtain enriched gene ontology (GO) terms that are near the 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, multiAdj=FALSE, minGOterm=10, multiAdjMethod="")
```

**Arguments**

annotatedPeak	RangedData 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
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
multiAdj	Whether apply multiple hypothesis testing adjustment, TRUE or FALSE
minGOterm	minimum count in a genome for a GO term to be included
multiAdjMethod	multiple testing procedures, for details, see mt.rawp2adjp in multtest package

**Value**

A list of 3

- 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$cc
if (interactive()) {
  data(annotatedPeak)
  library(org.Hs.eg.db)
  enriched.GO = getEnrichedGO(annotatedPeak[1:6,], orgAnn="org.Hs.eg.db", maxP=0.01,
    multiAdj=FALSE, minGOterm=10, multiAdjMethod="")
  dim(enriched.GO$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	RangedData 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)  
}
```

---

GFF2RangedData	<i>convert GFF format to RangedData</i>
----------------	-----------------------------------------

---

**Description**

convert GFF format to RangedData

**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#format3">http://genome.ucsc.edu/FAQ/FAQformat#format3</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)
```

---

makeVennDiagram	<i>Make Venn Diagram from two peak ranges</i>
-----------------	-----------------------------------------------

---

### Description

Make Venn Diagram from two peak ranges and also calculate p-value for determining whether two peak ranges overlap significantly.

### Usage

```
makeVennDiagram(Peaks, NameOfPeaks, maxgap=0L, minoverlap=1L, 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	Non-negative integer. Intervals with a separation of maxgap or less are considered to be overlapping.
minoverlap	Non-negative integer. Intervals with an overlapping of minoverlap or more are considered to be overlapping.
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.
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.
...	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, p.value is obtained from hypergeometric test for determining whether the two peak ranges or features overlap significantly.

### Author(s)

Lihua Julie Zhu, Jianhong Ou

### See Also

[findOverlappingPeaks](#), [venn.diagram](#)

**Examples**

```

if (interactive())
{
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","f"))
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","b","c","d","a"))
makeVennDiagram(RangedDataList(peaks1,peaks2), NameOfPeaks=c("TF1", "TF2"),
  totalTest=100,scaled=F, euler.d=F)

makeVennDiagram(RangedDataList(peaks1,peaks2), NameOfPeaks=c("TF1", "TF2"),
  totalTest=100,useFeature=FALSE)

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

makeVennDiagram(RangedDataList(peaks1,peaks2, peaks1, peaks2), NameOfPeaks=c("TF1", "TF2","TF3", "TF4"), totalTe
main = "Venn Diagram for 4 peak lists",fill=c(1,2,3,4))
}

```

myPeakList

*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**

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**

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)
```

---

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)
str(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 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 10:37doi:10.1186/1471-2164-10-37

**Examples**

```
data(Peaks.Ste12.Replicate2)
str(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 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 10:37doi:10.1186/1471-2164-10-37

**Examples**

```
data(Peaks.Ste12.Replicate3)
str(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, mart, AnnotationData, MaxDistance=5000, PeakLocForDistance = c("start", "middle", "end", "geneEnd"), FeatureLocForDistance = c("TSS", "middle", "start", "end", "geneEnd"))
```

### Arguments

myPeakList	RangedData: See example below
mart	used if AnnotationData not supplied, a mart object, see useMart of bioMaRt package for details
AnnotationData	annotation data obtained from getAnnotation or customized annotation of class RangedData 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) . If not supplied, then annotation will be obtained from biomaRt automatically using the parameters of mart and featureType TSS
MaxDistance	Specify the maximum gap allowed between the peak and nearest gene
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

### Value

A list of 4

peaksWithBDP	annotated Peaks containing bi-directional promoters. RangedData 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: NearestStart: indicates this PeakLocForDistance is closest to the FeatureLocForDistance

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

## 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)
annotatedBDP = peaksNearBDP(myPeakList[1:6,], AnnotationData=TSS.human.NCBI36,
MaxDistance=5000,PeakLocForDistance = "middle",
```

```

FeatureLocForDistance = "TSS")
c(annotatedBDP$percentPeaksWithBDP, annotatedBDP$n.peaks, annotatedBDP$n.peaksWithBDP)
}

```

---

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)
```

## 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	RangedData 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).

## 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", "
filepath =system.file("extdata", "examplePattern.fa", package="ChIPpeakAnno")
library(BSgenome.Ecoli.NCBI.20080805)
summarizePatternInPeaks(patternFilePath=filepath, format="fasta", skip=0L, BSgenomeName=Ecoli, peaks=peaks)

```

---

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**

RangedData with slot start holding the start position of the gene, slot end holding the end position of the gene, slot rownames holding ensembl gene 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 gene

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

---

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**

RangedData with slot start holding the start position of the gene, slot end holding the end position of the gene, slot rownames holding ensembl gene 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 gene

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

---

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

---

**Description**

TSS annotation data for mouse (NCBIM37) obtained from biomaRt

**Usage**

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

**Format**

RangedData with slot start holding the start position of the gene, slot end holding the end position of the gene, slot rownames holding ensembl gene 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 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**

RangedData with slot start holding the start position of the gene, slot end holding the end position of the gene, slot rownames holding ensembl gene 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 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.zebrafish.Zv8      *TSS annotation data for zebrafish (Zv8) obtained from biomaRt*

---

**Description**

TSS annotation data for zebrafish (Zv8) obtained from biomaRt

**Usage**

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

**Format**

RangedData with slot start holding the start position of the gene, slot end holding the end position of the gene, slot rownames holding ensembl gene 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 gene

**Details**

Annotation data obtained by:

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

**Examples**

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

---

write2FASTA	<i>write sequences to a file in fasta format</i>
-------------	--------------------------------------------------

---

### 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 `>` preceding each sequence.

### Usage

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

### Arguments

<code>mySeq</code>	RangedData with variables name and sequence ,e.g., results obtained from <code>getAllPeakSequence</code>
<code>file</code>	Either a character string naming a file or a connection open for reading or writing. If "" (the default for <code>write2FASTA</code> ), then the function writes to the standard output connection (the console) unless redirected by <code>sink</code>
<code>width</code>	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 = RangedData(IRanges(start=c(1000, 2000), end=c(1010, 2010)),
names=c("id1", "id2"), sequence= c("CCCCCCCCGGGG", "TTTTTTTAAAAA"))
write2FASTA(peaksWithSequences, file="testseq.fasta", width=50)
```

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