

Package ‘proBAMr’

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Type Package

Title Generating SAM file for PSMs in shotgun proteomics data

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Description Mapping PSMs back to genome. The package builds SAM file from shotgun proteomics data The package also provides function to prepare annotation from GTF file.

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Depends R (>= 3.0.1), IRanges, AnnotationDbi

Imports GenomicRanges, Biostrings, GenomicFeatures, txdbmaker, rtracklayer

Suggests GenomeInfoDbData, RUnit, BiocGenerics

biocViews ImmunoOncology, Proteomics, MassSpectrometry, Software, Visualization

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```
PrepareAnnotationGENCODE
```

prepare annotation from GENCODE

Description

prepare the annotation from GENCODE. Download GTF and FASTA files from GENCODE ftp first. Read introduction for more information.

Usage

```
PrepareAnnotationGENCODE(gtfFile, CDSfasta, pepfasta, annotation_path,
  dbsnp = NULL, splice_matrix = FALSE, COSMIC = FALSE, ...)
```

Arguments

<code>gtfFile</code>	specify GTF file location.
<code>CDSfasta</code>	path to the fasta file of coding sequence.
<code>pepfasta</code>	path to the fasta file of protein sequence.
<code>annotation_path</code>	specify a folder to store all the annotations.
<code>dbsnp</code>	specify a snp dataset to be used for the SNP annotation, default is NULL. (e.g. "snp135")
<code>splice_matrix</code>	whether generate a known exon splice matrix from the annotation. this is not necessary if you don't want to analyse junction results, default is FALSE.
<code>COSMIC</code>	whether to download COSMIC data, default is FALSE.
<code>...</code>	additional arguments

Value

several .RData files containing annotations needed for further analysis.

Author(s)

Xiaojing Wang

Examples

```
gtfFile <- system.file("extdata", "test.gtf", package="proBAMr")
CDSfasta <- system.file("extdata", "coding_seq.fasta", package="proBAMr")
pepfasta <- system.file("extdata", "pro_seq.fasta", package="proBAMr")
annotation_path <- tempdir()
PrepareAnnotationGENCODE(gtfFile, CDSfasta, pepfasta,
  annotation_path, dbsnp=NULL,
  splice_matrix=FALSE, COSMIC=FALSE)
```

PSMtab2SAM

*Generate SAM files from PSMs.***Description**

Generate SAM files from confident peptide-spectrum-matches (PSMs).

Usage

```
PSMtab2SAM(passedPSM, XScolumn = "mvh", exon_anno, proteinseq, procodingseq,
...)
```

Arguments

passedPSM	a data frame of PSMs passed FDR.
XScolumn	specify the column which represents the matching score.
exon_anno	a dataframe of exon annotations.
proteinseq	a dataframe containing protein ids and protein sequences.
procodingseq	a data frame cotaining coding sequence for each protein.
...	additional arguments

Value

a dataframe containing

Author(s)

Xiaojing Wang

Examples

```
load(system.file("extdata/GENCODE", "exon_anno.RData", package="proBAMr"))
load(system.file("extdata/GENCODE", "proseq.RData", package="proBAMr"))
load(system.file("extdata/GENCODE", "procodingseq.RData",
  package="proBAMr"))
options(stringsAsFactors=FALSE)
passedPSM <- read.table(system.file("extdata", "passedPSM.tab",
  package="proBAMr"), sep='\t', header=TRUE)
SAM <- PSMtab2SAM(passedPSM, XScolumn='mvh', exon, proteinseq,
  procodingseq)
write.table(SAM, file=paste(tempdir(), '/test.sam', sep=''),
  sep='\t', quote=FALSE, row.names=FALSE, col.names=FALSE)
```

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