

Package ‘proBAMr’

April 15, 2020

Type Package

Title Generating SAM file for PSMs in shotgun proteomics data

Version 1.20.0

Date 2016-03-31

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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, rtracklayer

Suggests RUnit, BiocGenerics

biocViews ImmunoOncology, Proteomics, MassSpectrometry, Software, Visualization

NeedsCompilation no

git_url <https://git.bioconductor.org/packages/proBAMr>

git_branch RELEASE_3_10

git_last_commit 4566fc2

git_last_commit_date 2019-10-29

Date/Publication 2020-04-14

R topics documented:

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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

| | |
|-----------------|---|
| gtffile | specify GTF file location. |
| CDSfasta | path to the fasta file of coding sequence. |
| pepfasta | path to the fasta file of protein sequence. |
| annotation_path | specify a folder to store all the annotations. |
| dbsnp | specify a snp dataset to be used for the SNP annotation, default is NULL. (e.g. "snp135") |
| splice_matrix | 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. |
| COSMIC | whether to download COSMIC data, default is FALSE. |
| ... | additional arguments |

Value

several .RData files containing annotations needed for further analysis.

Author(s)

Xiaoqing 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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