

Package ‘pepXMLTab’

May 2, 2024

Type Package

Title Parsing pepXML files and filter based on peptide FDR.

Version 1.38.0

Date 2015-09-20

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Description Parsing pepXML files based one XML package.

The package tries to handle pepXML files generated from different softwares.

The output will be a peptide-spectrum-matching tabular file.

The package also provide function to filter the PSMs based on FDR.

License Artistic-2.0

Depends R (>= 3.0.1)

Imports XML(>= 3.98-1.1)

Suggests RUnit, BiocGenerics

biocViews ImmunoOncology, Proteomics, MassSpectrometry

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

git_branch RELEASE_3_19

git_last_commit 421cd31

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-01

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pepXML2tab

Generate a data frame objects from a pepXML file.

Description

The pepXML2tab() function generates a data frame from a pepXML file.

Usage

```
pepXML2tab(pepxml, ...)
```

Arguments

| | |
|--------|---|
| pepxml | a character contains the path and name of a pepXML file |
| ... | additional arguments |

Details

Read peptide identification from pepXML file into an data frame object.

Value

a data frame object, each row represent a PSM (peptide spectrum match) from the pepXML file

Author(s)

Xiaojing Wang

Examples

```
## MyriMatch example
pepxml <- system.file("extdata/pepxml", "Myrimatch.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)

## Mascot example
pepxml <- system.file("extdata/pepxml", "Mascot.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)

## SEQUEST example
pepxml <- system.file("extdata/pepxml", "SEQUEST.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)

## XTandem example
pepxml <- system.file("extdata/pepxml", "XTandem.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)
```

| | |
|-----------|---|
| PSMfilter | <i>Filter the peptide identification.</i> |
|-----------|---|

Description

The PSMfilter() function filter the peptide identification based on user chosen paramter.

Usage

```
PSMfilter(PSMtab, pepFDR = 0.01, scorecolumn = "mvh", hitrank = 1,  
          minpeplen = 6, decoyprefix = "rev_", ...)
```

Arguments

| | |
|-------------|---|
| PSMtab | a data frame contain peptide identification from a pepXML file |
| pepFDR | filter the peptides based on this chosen FDR, default is 0.01. |
| scorecolumn | which column is chosen to calculate FDR |
| hitrank | an integer indicates how many peptides to retain for a spectrum. A spectrum can match to multiple peptides. Default is 1. |
| minpeplen | an integer of minimum peptide length |
| decoyprefix | a character indicates decoy sequence in the 'protein' column. Usually is 'rev_' or 'DECOY_'. |
| ... | additional arguments |

Details

Filter the peptide identification based on FDR, hit rank, or peptide length.

Value

a data frame object, contain PSMs (peptide spectrum match) passed the filters.

Author(s)

Xiaoqing Wang

Examples

```
##MyriMatch example  
pepxml <- system.file("extdata/pepxml", "Myrimatch.pepXML",  
                     package="pepXMLTab")  
tttt <- pepXML2tab(pepxml)  
passed <- PSMfilter(tttt, pepFDR=0.01, scorecolumn='mvh', hitrank=1,  
                   minpeplen=6, decoyprefix='rev_')
```

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