Package: pepXMLTab (via r-universe)

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Type Package

Title Parsing pepXML files and filter based on peptide FDR.

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Author Xiaojing Wang

Maintainer Xiaojing Wang <xiaojing.wang@vanderbilt.edu>

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

Config/pak/sysreqs libxml2-dev

Repository https://bioc.r-universe.dev

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Contents

pepXML2tab 2
PSMfilter 3

Index **4**

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 *Filter the peptide indentification.*

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)

Xiaojing 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_')
```

Index

pepXML2tab, 2
PSMfilter, 3