

Package: RforProteomics (via r-universe)

October 10, 2026

Type Package

Title Companion package to the 'Using R and Bioconductor for proteomics data analysis' publication

Version 1.51.1

Depends R (>= 3.5)

Imports biocViews, BiocManager

Suggests MSnbase (>= 2.35.2), QFeatures, AnnotationDbi, rpx (>= 2.0.3), DT, knitr, rmarkdown, BiocStyle, mzR, xcms, msdata, MALDIquant (>= 1.12), MALDIquantForeign, readBrukerFlexData, Rdisop, OrgMassSpecR, SummarizedExperiment, BRAIN, hpar, GO.db, org.Hs.eg.db, e1071, biomaRt, RColorBrewer, ggplot2, reshape2, xtable, lattice, mzID, pRoloc, pRolocdata, MSnID, msmsTests, msmsEDA, corrplot, beanplot, Heatplus, gplots, VennDiagram, protViz, genefilter, plotly, gridExtra, dplyr, lubridate, magick, cleaver

Description This package contains code to illustrate the 'Using R and Bioconductor for proteomics data analysis' and 'Visualisation of proteomics data using R and Bioconductor' manuscripts. The vignettes describe the code and data needed to reproduce the examples and figures described in the paper and functionality for proteomics visualisation. It also contain various function to discover R software for mass spectrometry and proteomics.

URL <http://lgatto.github.com/RforProteomics/>

biocViews ExperimentData, MassSpectrometryData, ReproducibleResearch

License Artistic-2.0

VignetteBuilder knitr

Encoding UTF-8

Config/roxygen2/version 8.0.0

Config/pak/sysreqs make libxml2-dev

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

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getPackagesInBiocView	<i>Packages in a biocView</i>
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Description

Finds the package names that have a specific biocView.

Usage

```
getPackagesInBiocView(  
  view,  
  rep = c("BioCsoft", "BioCann", "BioCexp", "BioCextra"),  
  biocVersion  
)
```

Arguments

- view The biocView of interest. For example "Proteomics".
- rep Repository of interest. One of "BioCsoft", "BioCann", "BioCexp" or "BioCextra".
- biocVersion A character with the Bioconductor version of interest. For example "2.14".

Value

An instance of class BiocView. NULL if the the biocView was not found.

Author(s)

Laurent Gatto

new_ions

Create, analyse and detect ions

Description

This is the constructor function to generate a set of ions that can later be analysed with ‘analyse()’ and detected with ‘detect()’.

Usage

```
new_ions(npeaks = 10, mzrange = c(100, 1000), nimg = 100)

analyse(x, sleep = 0.1)

analyze(x, sleep = 0.1)

detect(x, new = FALSE)

spectrum(x, ...)
```

Arguments

npeaks	A ‘numeric’ scalar defining the number of unique peaks (M/Z values). Default is 10.
mzrange	A ‘numeric’ of length 2 defining the range of possible M/Z values. Default is ‘c(100, 1000)’.
nimg	A ‘numeric’ scalar. When analysing the ions, their separation along their M/Z values will be split along a sequence of length ‘nimg’. Default is 100.
x	An object of class ‘ions’.
sleep	How much time to wait before producing the next plot.
new	A ‘logical’ scalar, indicating if the separated ions (last frame of calling ‘analyse’) should be plotting, or whether the detection should be overlaid. Default is ‘FALSE’, to add the plot on top of the opened device.
...	Additional arguments passed to [graphics::plot()].

Value

An object of class ‘ions’.

‘analyse’, ‘detect’ and ‘spectrum’ are used for their side effect or producing plots. They all invisibly return ‘NULL’.

Author(s)

Laurent Gatto

Examples

```

set.seed(1L)
x <- new_ions(nimg = 5)
x
analyse(x)
detect(x)
spectrum(x)

```

packageDF	<i>Package descriptions</i>
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Description

Format a BiocView as a data.frame.

Usage

```
packageDF(x, nsub = TRUE, version = TRUE)
```

Arguments

x	An instance of class BiocView, as produced by getPackagesInBiocView.
nsub	A logical indicating "\n" are to be replaced by a space.
version	A logical specifying if the package version should be added.

Value

A data.frame with package information.

Author(s)

Laurent Gatto

proteomicsPackages	<i>Proteomics and MS biocView packages</i>
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Description

Searches for all the packages with the "Proteomics" (software), "MassSpectrometry" (software) and "MassSpectrometryData" (data) packages and return their names, titles and versions as a data.frame. The (unexported but documented) underlying functions are RforProteomics::getPackagesInBiocView (to find relevant package) and RforProteomics::packageDF (data.frame formatting).

Usage

```
proteomicsPackages(biocv, cache = FALSE)

massSpectrometryPackages(biocv, cache = FALSE)

massSpectrometryDataPackages(biocv, cache = FALSE)
```

Arguments

biocv	A character with the Bioconductor version to search for relevant packages. If missing, the running version is used.
cache	A logical indicating whether cached package information should be used. Default is FALSE. All except development versions are up-to-date.

Value

A data.frame with the respective package names, titles and versions.

Author(s)

Laurent Gatto

Examples

```
head(pp <- proteomicsPackages("3.0"))
ppc <- proteomicsPackages("3.0", cache = TRUE)
all.equal(pp, ppc)
```

RforProteomics	<i>Opens the package vignettes</i>
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Description

Opens the package and visualisation vignettes.

Usage

```
RforProteomics()

RProtVis()

RProtViz()
```

Value

An instance of class vignette. Used for its side effect, opening a vignette.

Author(s)

Laurent Gatto

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