

Package ‘RforProteomics’

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Type Package

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

Version 1.2.1

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Imports R.utils, Biobase, rpx, biocViews, interactiveDisplay, BiocInstaller

Suggests mzR, MSnbase, xcms, msdata, isobar, MALDIquant, MALDIquantForeign, readBrukerFlexData, rTAN-DEM, synapter, synapterdata, IPPD, Rdisop, OrgMassSpecR, BRAIN, rols, hpar, GO.db, org.Hs.eg.db, biomaRt, RColorBrewer, ggplot2, reshape2, knitr, xtable

Enhances cleaver

Description This package contains code to illustrate the 'Using R and Bioconductor for proteomics data analysis' manuscript. The vignette describes the code and data needed to reproduce the examples and figures described in the paper as well as functions to download the PXD000001 data files.

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

biocViews ExperimentData, MassSpectrometry, Proteomics, MassSpectrometryData

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VignetteBuilder knitr

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R topics documented:

downloadData	2
getPackagesInBiocView	2
getPXD000001mzData	3
getPXD000001mzTab	4

getPXD000001mzXML	4
getThermoHelaPRTC	5
packageDF	6
proteomicsPackages	6
RforProteomics	7

Index	8
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downloadData	<i>Download a file</i>
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Description

Unless already present, downloads src in the destdir directory.

Usage

```
downloadData(src, destdir = ".", unpack = TRUE, ...)
```

Arguments

src	The url of the file to download.
destdir	The destination directory. Default is ".".
unpack	Should src be uncompressed? Default is TRUE.
...	Additional paramters passed to download.file .

Value

Invisible returns the full path of the downloaded file.

Author(s)

Laurent Gatto

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

getPXD000001mzData *Download the PXD000001 mzTab file*

Description

Unless already present, downloads the PXD000001 mzData file in the destdir directory. The resulting file is named PRIDE_Exp_Complete_Ac_22134.xml

Usage

```
getPXD000001mzData(destdir = ".")
```

Arguments

destdir	A character with the destination folder.
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Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

getPXD000001mzTab *Download the PXD000001 mzTab file*

Description

Unless already present, downloads the PXD000001 mzTab file in the destdir directory. The resulting file is named F063721.dat-mztab.txt.

Usage

```
getPXD000001mzTab(destdir = ".")
```

Arguments

destdir A character with the destination folder.

Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

getPXD000001mzXML *Download the PXD000001 mzXML file*

Description

Unless already present, downloads the PXD000001 mzXML file in the destdir directory. The resulting file is named TMT_Erwinia_1uLSike_Top10HCD_iso12_45stepped_60min_01.mzXML.

Usage

```
getPXD000001mzXML(destdir = ".")
```

Arguments

destdir A character with the destination folder.

Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

getThermoHelaPRTC *Download Thermo Hela PRTC data*

Description

Downloads on of multiple Thermo Hela/PRTC data files.

Usage

```
getThermoHelaPRTC(src, destdir = ".")
```

Arguments

src	The name of the file to be downloaded. If missing, a vector of possible filenames is returned. If "all", all files are downloaded. Alternatively, a pattern can be used to grep the files from the output getThermoHelaPRTC() the files to be downloaded.
destdir	Destination directory. Default is ".".

Value

Invisibly return the path of the downloaded files.

Author(s)

Laurent Gatto

See Also

downloadData

Examples

```
getThermoHelaPRTC()  
getThermoHelaPRTC("design")  
## Not run:  
getThermoHelaPRTC("all")  
  
## End(Not run)
```

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 "MassSepctrometryData" (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)
massSpectrometryPackages(biocv)
massSpectrometryDataPackages(biocv)
```

Arguments

biocv	A character with the Bioconductor version to search for relevant packages. If missing, the running version is used.
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Value

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

Author(s)

Laurent Gatto

RforProteomics *Opens RforProteomics vignettes*

Description

Opens the package vignettes.

Usage

```
RforProteomics()
```

Value

An instance of class vignette, as returned by [vignette](#)

Author(s)

Laurent Gatto

Index

`download.file`, [2](#)

`downloadData`, [2](#)

`getPackagesInBiocView`, [2](#)

`getPXD000001mzData`, [3](#)

`getPXD000001mzTab`, [4](#)

`getPXD000001mzXML`, [4](#)

`getThermoHeLaPRTC`, [5](#)

`massSpectrometryDataPackages`
(`proteomicsPackages`), [6](#)

`massSpectrometryPackages`
(`proteomicsPackages`), [6](#)

`packageDF`, [6](#)

`proteomicsPackages`, [6](#)

`RforProteomics`, [7](#)

`vignette`, [7](#)