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, readBrukerFlex-
   Data, rTAN-
   DEM, synapter,synapterdata, IPPD, Rdisop, OrgMassSpecR, BRAIN, rols, hpar,GO.db, org.Hs.eg.db, biomaRt, RCol-
   orBrewer, 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 descibed
   in the paper as well as functions to download the PXD000001 data files.

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

biocViews ExperimentData, MassSpectrometry, Proteomics,MassSpectrometryData

License Artistic-2.0

VignetteBuilder knitr

Author Laurent Gatto [aut, cre],Sebastian Gibb [ctb]

R topics documented:

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downloadData   *Download a file*

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

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getPackagesInBiocView *Packages in a biocView*

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

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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.

Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

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getPXD000001mzTab   *Download the PXD000001 mzTab file*

Description

Unless already present, downloads the PXD000001 mzTab file n 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

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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_isol2_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

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getThermoHelaPRTC   *Dowload 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)
```

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packageDF   *Package descriptions*

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

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proteomicsPackages   *Proteomics and MS biocView packages*

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.

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

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