

Package ‘ProteomicsAnnotationHubData’

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Title Transform public proteomics data resources into Bioconductor
Data Structures

Version 1.24.0

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Description These recipes convert a variety and a growing number of
public proteomics data sets into easily-used standard
Bioconductor data structures.

Depends AnnotationHub (>= 2.1.45), AnnotationHubData,

Imports mzR (>= 2.3.2), MSnbase, Biostrings, GenomeInfoDb, utils,
Biobase, BiocManager, RCurl

Suggests knitr, BiocStyle, rmarkdown, testthat

biocViews DataImport, Proteomics

VignetteBuilder knitr

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URL <https://github.com/lgatto/ProteomicsAnnotationHubData>

BugReports <https://github.com/lgatto/ProteomicsAnnotationHubData/issues>

Collate ProteomicsAnnotationHubData.R utils.R PAHD.R zzz.R

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identicalRemLoc	<i>Are the remote and local instances identical</i>
-----------------	---

Description

This function compares the metadata of a remote object `rem` available on AnnotationHub and a local PAHD object. If these are identical, TRUE is returned, FALSE otherwise.

Usage

```
identicalRemLoc(rem, loc)
```

Arguments

- `rem` An instance of class AnnotationHub
- `loc` An instance of class AnnotationHubMetadata

Value

A logical

makeAnnotationHubMetadata	<i>Make an AnnotationHubMeta resource</i>
---------------------------	---

Description

Takes a list of PAHD instances and returns a subset matching the requested resource.

Usage

```
makeAnnotationHubMetadata(x, resource = proteomicsAnnotationHubDataResources)
```

Arguments

x	A list of PAHD instances.
resource	A character of length 1 with the desired resource. See <code>proteomicsAnnotationHubDataResources</code> for a list of available resources.

Value

A list of PAHD instances, matching resource.

PAHD	<i>Prepare data for inclusion into AnnotationHub</i>
------	--

Description

Reads `ProteomicsAnnotationHubData` dcf files and prepares them for inclusion into AnnotationHub. See `ProteomicsAnnotationDataHub{}` for details and an example.

Usage

```
PAHD(x, resourceDir)
```

Arguments

x	One of multiple <code>ProteomicsAnnotationHubData</code> dcf files.
resourceDir	A character containing the directory holding the files (for instance PRIDE). If missing, will be inferred from the first <code>RDataPath</code> field of x.

Details

Note: Current limitation is that all the files are expected to reside in a single resource directory.

Value

A list of PAHD objects that can be used to prepare and submit data to AnnotationHub. See `ProteomicsAnnotationHub()` for details.

Author(s)

```
Laurent Gatto ## example file for the PXD000001 data f <- list.files(system.file("extdata", package = "ProteomicsAnnotationHubData"), full.names = TRUE) PXD000001 <- PAHD(f) length(PXD000001)
PXD000001[[1]]
```

PAHD-class

An S4 class for ProteomicsAnnotationHubData objects

Description

This class is a simple temporary container that extends the AnnotationHubMetadata. Please read that documentation for details. This class is likely to evolve in the future. See [PAHD](#) for to construct these objects from dcf files.

ProteomicsAnnotationHubData

Get started with ProteomicsAnnotationHubData

Description

Read the ProteomicsAnnotationHubData vignette to get started with using Proteomics data from AnnotationHub and writing new recipes. Use `availableProteomicsAnnotationHubData()` to get a vector of available experiments. Use `proteomicsAnnotationHubDataResources()` to get a vector of available resources.

Usage

```
ProteomicsAnnotationHubData()
```

```
availableProteomicsAnnotationHubData
```

```
proteomicsAnnotationHubDataResources
```

Format

An object of class character of length 1.

Value

Used for its side-effect of opening the package vignette. A vector of experiment identifiers.

Author(s)

Laurent Gatto

Examples

```
availableProteomicsAnnotationHubData
```

readPahdFiles	<i>Reads one or multiple PAHD template files</i>
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Description

Reads one or multiple ProteomicsAnnotationHubData dcf files into a matrix that can be processed with [PAHD](#). Comment lines starting with # will be removed. See `ProteomicsAnnotationDataHub()` for details.

Usage

```
readPahdFiles(file)
```

Arguments

file A character with one of multiple file names.

Value

A matrix containing

Author(s)

Laurent Gatto

Examples

```
## example file for the PXD000001 data
f <- list.files(system.file("extdata", package = "ProteomicsAnnotationHubData"),
                full.names = TRUE, pattern = "PXD000001.dcf")
readPahdFiles(f)
```

writePahdTemplate	<i>Write a ProteomicsAnnotationHubData template</i>
-------------------	---

Description

Writes a simple template in dcf format (like an R package DESCRIPTION file) that, once completed (see `ProteomicsAnnotationHub()` for details), can be imported with [readPahdFiles](#) or directly processed with [PAHD](#). Note that these dcf files support comments (as opposed to DESCRIPTION files). Lines starting with # will be removed when parsed by [readPahdFiles](#).

Usage

```
writePahdTemplate(filename = "")
```

Arguments

filename	The name of the file to write the template in. Default is "", i.e. write output to the console.
----------	---

Value

Use for its side effect of preparing a annotation template.

Author(s)

Laurent Gatto <lg390@cam.ac.uk>

Examples

```
writePahdTemplate()
```

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