

Package ‘ExperimentHubData’

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Type Package

Title Add resources to ExperimentHub

Version 1.0.0

biocViews Infrastructure, DataImport, GUI, ThirdPartyClient

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Description Functions to add metadata to ExperimentHub db and resource files to AWS S3 buckets.

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Depends utils, BiocGenerics (>= 0.15.10), S4Vectors, AnnotationHubData (>= 1.1.4)

Imports methods, ExperimentHub, BiocInstaller, DBI, BiocCheck, httr, curl

Suggests GenomeInfoDb, RUnit, knitr, BiocStyle

VignetteBuilder knitr

NeedsCompilation no

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| addResources | <i>addResources</i> |
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Description

Add resource metadata to a local ExperimentHub database

Usage

```
addResources(pathToPackage, insert = FALSE, ...)
```

Arguments

| | |
|---------------|--|
| pathToPackage | Full path to data package including package name; no trailing slash. |
| insert | A logical to control if metadata are inserted in the ExperimentHub db. By default this option is FALSE which is a useful state in which to test a new recipe and confirm the metadata fields are correct. When insert = TRUE, the "EXPERIMENT_HUB_SERVER_POST_URL" global option must be set to the http location of the ExperimentHubServer in the global environment or .Rprofile. This option controls Additionally, AWS command line tools must be installed on the local machine to push files to S3 buckets. See https://aws.amazon.com/cli/ for installation instructions. |
| ... | TDB. Currently not used. |

Details

When insert is TRUE, addResources attempts to add the metadata to the local database. A warning is thrown if duplicate files names are found in the local database or if any filenames in the new metadata match those in the existing database. Only metadata records with non-duplicated file names are added to the database. The file name is the name of the data file with the 'rda' extension.

Value

A list of [ExperimentHubMetadata](#) objects.

See Also

- [ExperimentHubMetadata](#)
- [AnnotationHubMetadata](#)

Examples

```
## Not run:
## Generate metadata for inspection
addResources("/home/vobencha/mypackage", insert=FALSE)
## Inset metadata into ExperimentHub database
addResources("/home/vobencha/mypackage", insert=TRUE)

## End(Not run)
```

ExperimentHubMetadata-class

Class [ExperimentHubMetadata](#) objects and methods

Description

[ExperimentHubMetadata](#) is used to represent record(s) in the server data base.

Usage

```

ExperimentHubMetadata(ExperimentHubRoot=NA_character_,
  BiocVersion=biocVersion(),
  SourceUrl=NA_character_,
  SourceType=NA_character_,
  SourceVersion=NA_character_,
  SourceLastModifiedDate=as.POSIXct(NA_character_),
  SourceMd5=NA_character_,
  SourceSize=NA_real_,
  DataProvider=NA_character_,
  Title=NA_character_,
  Description=NA_character_,
  Maintainer=NA_character_,
  Species=NA_character_,
  TaxonomyId=NA_integer_,
  Genome=NA_character_,
  Tags=NA_character_,
  RDataClass=NA_character_,
  RDataDateAdded=as.POSIXct(NA_character_),
  RDataPath=NA_character_,
  Coordinate_1_based=TRUE,
  Notes=NA_character_,
  DispatchClass=NA_character_,
  PreparerClass=NA_character_,
  Location_Prefix='http://s3.amazonaws.com/experimenthub/')

```

Arguments

| | |
|------------------------|--|
| ExperimentHubRoot | character(1) Prefix of the local path to resources to be added to ExperimentHub. Currently not used. |
| SourceUrl | character(1) TBD |
| SourceType | character(1) TBD |
| SourceVersion | character(1) TBD |
| SourceLastModifiedDate | POSIXct() Date when resource was last modified |
| SourceMd5 | character(1) md5 hash of original file |
| SourceSize | numeric(1) Number of bytes in original file |
| DataProvider | character(1) Original data provider |
| Title | character(1) Title for this resource |
| Description | character(1) Description of the resource |
| Species | character(1) Species name |
| TaxonomyId | character(1) NCBI code |
| Genome | character(1) Name of genome build |
| Tags | character() Free-form tags for search. biocViews from DESCRIPTION are added to the Tags. |
| RDataClass | character(1) Class of derived object (e.g. 'GRanges') |
| RDataDateAdded | POSIXct() Date added to ExperimentHub; used to determine snapshots. |

| | |
|--------------------|--|
| RDataPath | character(1) file path to serialized form |
| Maintainer | character(1) Maintainer name and email address, 'A Maintainer <code>a.maintainer@email.addr</code> ' |
| BiocVersion | character() Under which resource was built |
| Coordinate_1_based | logical(1) Do coordinates start with 1 or 0? |
| Location_Prefix | character(1) URL location of AWS S3 bucket. |
| Notes | character() Notes about the resource. |
| DispatchClass | character(1) Used internally. |
| PreparerClass | character(1) Used internally. |

Details

Instances of this class are generated by a call to `addResources`.

Value

A `ExperimentHubMetadata` object.

See Also

- [addResources](#)
- [ExperimentHub](#)

Examples

```
## TODO
```

```
makeExperimentHubMetadata
```

Make ExperimentHubMetadata objects from csv file of metadata

Description

Make `ExperimentHubMetadata` objects from `metadata.csv` file located in the `"inst/extdata/"` package directory of an `ExperimentHub` package.

Usage

```
makeExperimentHubMetadata(pathToPackage)
```

Arguments

`pathToPackage` Full path to data package including the package name; no trailing slash

Details

- `makeExperimentHubMetadata`: Reads the resource metadata in the `metadata.csv` file into a `ExperimentHubMetadata` object. The `ExperimentHubMetadata` is inserted in the `ExperimentHub` database. Intended for internal use or package authors checking the validity of package metadata.

Value

A list of ExperimentHubMetadata objects.

See Also

- [addResources](#)
- [readMetadataFromCsv](#)
- [ExperimentHubMetadata](#) class

Examples

```
## makeExperimentHubMetadata() reads data from inst/scripts/metadata.csv
## into ExperimentHubMetadata objects. These objects are used to insert
## metadata into the production database. This function is used internally
## by addResources() and is not intended to be called directly.

## For an example of how this works we can use the GSE62944 ExperimentHub
## package. Download the source tarball from:

# http://www.bioconductor.org/packages/devel/data/experiment/html/GSE62944.html

## and unpack it. Set 'pathToPackage' to point to the downloaded source.
## Then call the function:
## Not run:
makeExperimentHubMetadata("path/to/mypackage")

## End(Not run)
```

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