

# Package ‘AnnotationHubData’

October 18, 2022

**Type** Package

**Title** Transform public data resources into Bioconductor Data Structures

**Version** 1.26.1

**Encoding** UTF-8

**Depends** R (>= 3.2.2), methods, utils, S4Vectors (>= 0.7.21), IRanges (>= 2.3.23), GenomicRanges, AnnotationHub (>= 2.15.15)

**Suggests** RUnit, knitr, BiocStyle, grasp2db, GenomeInfoDbData, rmarkdown, HubPub

**Imports** GenomicFeatures, Rsamtools, rtracklayer, BiocGenerics, jsonlite, BiocManager, biocViews, BiocCheck, graph, AnnotationDbi, Biobase, Biostrings, DBI, GenomeInfoDb (>= 1.15.4), OrganismDbi, RSQLite, AnnotationForge, futile.logger (>= 1.3.0), XML, RCurl

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

**License** Artistic-2.0

**LazyLoad** yes

**biocViews** DataImport

**VignetteBuilder** knitr

**Collate** Message-class.R ImportPreparer-class.R  
makeAnnotationHubResource.R HubMetadata-class.R  
AnnotationHubMetadata-class.R utils.R updateResources.R  
ahmToJson.R webAccessFunctions.R makeChEA.R makedbSNPVCF.R  
makeEncodeDCC.R makeEnsemblGtfToGRanges.R makeEnsemblFasta.R  
makeEpigenomeRoadmap.R makeGencodeFasta.R makeGencodeGFF.R  
makeGrasp2Db.R makeHaemCode.R makeInparanoid8ToDbs.R  
makeNCBIToOrgDbs.R makeStandardOrgDbsToSqlite.R  
makeStandardTxDbsToSqlite.R makeRefNet.R makeUCSCChain.R  
makeUCSC2Bit.R makeUCSCTracks.R  
trackWithAuxiliaryTableToGRangesRecipe.R

UCSCTrackUpdateChecker.R makeEnsemblTwoBit.R  
validationFunctions.R

**git\_url** <https://git.bioconductor.org/packages/AnnotationHubData>

**git\_branch** RELEASE\_3\_15

**git\_last\_commit** a04119c

**git\_last\_commit\_date** 2022-04-28

**Date/Publication** 2022-10-18

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AnnotationHubData-package

*Transform public data resources into Bioconductor Data Structures*

---

## Description

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

**Details**

This package provides a set of methods which convert bioinformatic data resources into standard Bioconductor data types. For example, a UCSC genome browser track, expressed as a BED file, is converted into a GRanges object. Not every valuable data resource can be transformed quite so easily; some require more elaborate transformation, and hence a more specialized recipe. Every effort is made to limit the number of recipes required. One strategy that helps with the principle of "zero curation": unless absolutely required, the "cooked" version of the data resource produced by a recipe is a simple and unembellished reflection of the original data in its downloaded form.

**Author(s)**

Dan Tenenbaum, Paul Shannon

**See Also**

AnnotationHubMetadata-class, makeAnnotationHubMetadata

---

AnnotationHubMetadata-class

*Class "AnnotationHubMetadata" and methods*

---

**Description**

AnnotationHubMetadata is used to represent record(s) in the server data base.

**Usage**

```
AnnotationHubMetadata(AnnotationHubRoot, SourceUrl, SourceType,
  SourceVersion, SourceLastModifiedDate, SourceMd5 =
  NA_character_, SourceSize, DataProvider, Title,
  Description, Species, TaxonomyId, Genome, Tags,
  Recipe, RDataClass, RDataDateAdded, RDataPath,
  Maintainer, ..., BiocVersion = BiocManager::version(),
  Coordinate_1_based = TRUE, Notes = NA_character_,
  DispatchClass, Location_Prefix =
  "https://bioconductorhubs.blob.core.windows.net/annotationhub/")
```

```
toJson(x)
constructSeqInfo(species, genome)
```

```
metadata(x, ...)
hubError(x)
inputFiles(object, ...)
outputFile(object)
ahmToJson(ahm)
deleteResources(id)
getImportPreparerClasses()
```

```
makeAnnotationHubResource(objName, makeAnnotationHubMetadataFunction,
  ..., where)
```

### Arguments

AnnotationHubRoot	character(1) Absolute path to directory structure containing resources to be added to AnnotationHub. Internal use only.
SourceUrl	character() URL of original resource(s).
SourceType	character() Form of original data, e.g., BED, FASTA, etc. <code>getValidSourceTypes()</code> list currently acceptable values. If nothing seems appropriate for your data reach out to <code>maintainer@bioconductor.org</code> .
SourceVersion	character(1) Version of original file.
SourceLastModifiedDate	POSIXct() The date when the source was last modified.
SourceMd5	character() md5 hash of original file.
SourceSize	numeric(1) Size of original file in bytes.
DataProvider	character(1) Provider of original data, e.g., NCBI, UniProt etc.
Title	character(1) Title for the resource with version or genome build as appropriate.
Description	character(1) Description of the resource. May include details such as data type, format, study origin, sequencing technology, treated vs control, number of samples etc.
Species	character(1) Species name. For help on valid species see <code>getSpeciesList</code> , <code>validSpecies</code> , or <code>suggestSpecies</code> .
TaxonomyId	character(1) NCBI code. There are checks for valid taxonomyId given the Species which produce warnings. See <code>GenomeInfoDb::loadTaxonomyDb()</code> for full validation table.
Genome	character(1) Name of genome build.
Tags	character() Free-form tags that serve as search terms.
Recipe	character(1) Name of recipe function. Only applicable to recipes created by the Bioconductor core team and included in AnnotationHubData base code.
RDataClass	character() Class of derived R object, e.g., GRanges. Length must match the length of RDataPath.
RDataDateAdded	POSIXct() Date resource was added to AnnotationHub. The default is today's date and is auto-generated when metadata are constructed. Resources will appear in snapshots with a date greater than or equal to the RDataDateAdded.
RDataPath	character() File path to where object is stored in AWS S3 bucket or on the web. This field should be the remainder of the path to the resource. The <code>Location_Prefix</code> will be prepended to RDataPath for the full path to the resource. If the resource is stored in Bioconductor's AWS S3 buckets, it should start with the name of the package associated with the metadata and should not start with a leading slash. It should include the resource file name. For strongly associated files, like a bam file and its index file, the two files should be separated with a colon <code>:</code> . This will link a single hub id with the multiple files.

Maintainer	character(1) Maintainer name and email address, 'A Maintainer <a href="mailto:a.maintainer@email.com">a.maintainer@email.com</a> '
BiocVersion	character(1). The first Bioconductor version the resource was made available for. Unless removed from the hub, the resource will be available for all versions greater than or equal to this field.
Coordinate_1_based	logical(1) Do coordinates start with 1 or 0?
DispatchClass	character(1). Determines how data are loaded into R. The value for this field should be 'Rda' if the data were serialized with <code>save()</code> and 'Rds' if serialized with <code>saveRDS</code> . The filename should have the appropriate 'rda' or 'rds' extension. A number of dispatch classes are pre-defined in <code>AnnotationHub/R/AnnotationHubResource-class.R</code> with the suffix 'Resource'. For example, if you have sqlite files, the <code>AnnotationHubResource-class.R</code> defines <code>SQLiteFileResource</code> so the <code>DispatchClass</code> would be <code>SQLiteFile</code> . Contact <code>maintainer@bioconductor.org</code> if you are not sure which class to use. The function <code>AnnotationHub::DispatchClassList()</code> will output a matrix of currently implemented <code>DispatchClass</code> and brief description of utility. If a predefine class does not seem appropriate contact <code>maintainer@bioconductor.org</code> .
Location_Prefix	character(1) URL location of AWS S3 bucket or web site where resource is located.
Notes	character() Notes about the resource.
ahm	An instance of class <code>AnnotationHubMetadata</code> .
x	An instance of class <code>AnnotationHubMetadata</code> .
object	An <code>AnnotationHubRecipe</code> instance.
species	character(1) The organism, e.g., "Homo sapiens".
genome	character(1) The genome build, e.g., "hg19".
id	An id whose DB record is to be fully deleted.
objName	character(1) The name of the <code>PreparerClass</code> used for dispatch.
makeAnnotationHubMetadataFunction	function Function (name) that makes <code>AnnotationHubMetadata</code> objects from the resource(s).
where	Environment where function definition is defined. Default value is sufficient.
...	Additional arguments passed to methods.

### Value

`AnnotationHubMetadata` returns an instance of the class.

`jsonPath` returns a `character(1)` representation of the full path to the location of the json file associated with this record.

`toJson` returns the JSON representation of the record.

`fromJson` returns an instance of the class, as parsed from the JSON file.

**Objects from the Class**

Objects can be created by calls to the constructor, `AnnotationHubMetadata()`.

**Author(s)**

Dan Tenenbaum and Marc Carlson

**Examples**

```
getClass("AnnotationHubMetadata")
```

---

flog

*flog*

---

**Description**

Write logging message to console and a file.

**Usage**

```
flog(level, ...)
```

**Arguments**

level	A character(1) string object.
...	Further arguments.

**Details**

Writes the message to the console and to a file.

**Value**

None.

**Author(s)**

Dan Tenenbaum

**See Also**

`futile.logger`

---

ImportPreparer-class    *Class* ImportPreparer *and generic* newResources

---

### Description

The ImportPreparer and derived classes are used for dispatch during data discovery (see [newResources](#)). There is one ImportPreparer class for each data source for [AnnotationHubMetadata](#).

newResources is a generic function; with methods implemented for each ImportPreparer.

### Author(s)

Martin Morgan

### See Also

[AnnotationHubMetadata](#).

### Examples

```
getImportPreparerClasses()
```

---

makeAnnotationHubMetadata

*Make AnnotationHubMetadata objects from csv file of metadata*

---

### Description

Make AnnotationHubMetadata objects from .csv files located in the "inst/extdata/" package directory of an AnnotationHub package.

### Usage

```
makeAnnotationHubMetadata(pathToPackage, fileName=character())
```

### Arguments

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

fileName        Name of metadata file(s) with csv extension. If none are provided, all files with .csv extension in "inst/extdata" will be processed.

## Details

- `makeAnnotationHubMetadata`: Reads the resource metadata from .csv files into a [AnnotationHubMetadata](#) object. The `AnnotationHubMetadata` is inserted in the AnnotationHub database. Intended for internal use or package authors checking the validity of package metadata.
- Formatting metadata files:
 

`makeAnnotationHubMetadata` reads .csv files of metadata located in "inst/extdata". Internal functions perform checks for required columns and data types and can be used by package authors to validate their metadata before submitting the package for review.

The rows of the .csv file(s) represent individual Hub resources (i.e., data objects) and the columns are the metadata fields. All fields should be a single character string of length 1.

Required Fields in metadata file:

  - Title: character(1). Name of the resource. This can be the exact file name (if self-describing) or a more complete description.
  - Description: character(1). Brief description of the resource, similar to the 'Description' field in a package DESCRIPTION file.
  - BiocVersion: character(1). The first Bioconductor version the resource was made available for. Unless removed from the hub, the resource will be available for all versions greater than or equal to this field. Generally the current devel version of Bioconductor.
  - Genome: character(1). Genome. Can be NA.
  - SourceType: character(1). Format of original data, e.g., FASTA, BAM, BigWig, etc. `getValidSourceTypes()` list currently acceptable values. If nothing seems appropriate for your data reach out to `maintainer@bioconductor.org`.
  - SourceUrl: character(1). Optional location of original data files. Multiple urls should be provided as a comma separated string.
  - SourceVersion: character(1). Version of original data.
  - Species: character(1). Species. For help on valid species see `getSpeciesList`, `validSpecies`, or `suggestSpecies`. Can be NA.
  - TaxonomyId: character(1). Taxonomy ID. There are checks for valid taxonomyId given the Species which produce warnings. See `GenomeInfoDb::loadTaxonomyDb()` for full validation table. Can be NA.
  - Coordinate\_1\_based: logical. TRUE if data are 1-based. Can be NA
  - DataProvider: character(1). Name of company or institution that supplied the original (raw) data.
  - Maintainer: character(1). Maintainer name and email in the following format: Maintainer Name <username@address>.
  - RDataClass: character(1). R / Bioconductor class the data are stored in, e.g., `GRanges`, `SummarizedExperiment`, `ExpressionSet` etc. If the file is loaded or read into R what is the class of the object.
  - DispatchClass: character(1). Determines how data are loaded into R. The value for this field should be 'Rda' if the data were serialized with `save()` and 'Rds' if serialized with `saveRDS`. The filename should have the appropriate 'rda' or 'rds' extension. There are other available DispatchClass types and the function `AnnotationHub::DispatchClassList()` A number of dispatch classes are pre-defined in `AnnotationHub/R/AnnotationHubResource-class.R` with the suffix 'Resource'. For example, if you have sqlite files, the `AnnotationHubResource-class.R` defines `SQLiteFileResource` so the DispatchClass would be `SQLiteFile`. Contact `maintainer@bioconductor.org` if you are not sure which class to use. The function



AnnotationHub::DispatchClassList() will output a matrix of currently implemented DispatchClass and brief description of utility. If a predefine class does not seem appropriate contact maintainer@bioconductor.org. An all purpose DispathClass is FilePath that instead of trying to load the file into R, will only return the path to the locally downloaded file.

- Location\_Prefix: character(1). Do not include this field if data are stored in the Bioconductor AWS S3; it will be generated automatically.  
If data will be accessed from a location other than AWS S3 this field should be the base url.
- RDataPath: character(). This field should be the remainder of the path to the resource. The Location\_Prefix will be prepended to RDataPath for the full path to the resource. If the resource is stored in Bioconductor's AWS S3 buckets, it should start with the name of the package associated with the metadata and should not start with a leading slash. It should include the resource file name. For strongly associated files, like a bam file and its index file, the two files should be separates with a colon :. This will link a single hub id with the multiple files.
- Tags: character() vector. 'Tags' are search terms used to define a subset of resources in a Hub object, e.g, in a call to query.  
'Tags' are automatically generated from the 'biocViews' in the DESCRIPTION and applied to all resources of the metadata file. Optionally, maintainers can define 'Tags' column of the metadata to define tags for each resource individually. Multiple 'Tags' are specified as a colon separated string, e.g., tags for two resources would look like this:

```
Tags=c("tag1:tag2:tag3", "tag1:tag3")
```

NOTE: The metadata file can have additional columns beyond the 'Required Fields' listed above. These values are not added to the Hub database but they can be used in package functions to provide an additional level of metadata on the resources.

More on Location\_Prefix and RDataPath. These two fields make up the complete file path url for downloading the data file. If using the Bioconductor AWS S3 bucket the Location\_Prefix should not be included in the metadata file[s] as this field will be populated automatically. The RDataPath will be the directory structure you uploaded to S3. If you uploaded a directory 'MyAnnotation/', and that directory had a subdirectory 'v1/' that contained two files 'counts.rds' and 'coldata.rds', your metadata file will contain two rows and the RDataPaths would be 'MyAnnotation/v1/counts.rds' and 'MyAnnotation/v1/coldata.rds'. If you host your data on a publicly accessible site you must include a base url as the Location\_Prefix. If your data file was at 'ftp://myinstituteserver/biostats/project2/counts.rds', your metadata file will have one row and the Location\_Prefix would be 'ftp://myinstituteserver/' and the RDataPath would be 'biostats/project2/counts.rds'.

### Value

A named list the length of fileName. Each element is a list of of AnnotationHubMetadata objects created from the .csv file.

### See Also

- [updateResources](#)
- [AnnotationHubMetadata](#) class

## Examples

```
## Each row of the metadata file represents a resource added to one of
## the 'Hubs'. This example creates a metadata.csv file for a single resource.
## In the case of multiple resources, the arguments below would be character
## vectors that produced multiple rows in the data.frame.

meta <- data.frame(
  Title = "RNA-Sequencing dataset from study XYZ",
  Description = paste0("RNA-seq data from study XYZ containing 10 normal ",
    "and 10 tumor samples represented as a",
    "SummarizedExperiment"),
  BiocVersion = "3.4",
  Genome = "GRCh38",
  SourceType = "BAM",
  SourceUrl = "http://www.path/to/original/data/file",
  SourceVersion = "Jan 01 2016",
  Species = "Homo sapiens",
  TaxonomyId = 9606,
  Coordinate_1_based = TRUE,
  DataProvider = "GEO",
  Maintainer = "Your Name <youremail@provider.com>",
  RDataClass = "SummarizedExperiment",
  DispatchClass = "Rda",
  ResourceName = "FileName.rda"
)

## Not run:
## Write the data out and put in the inst/extdata directory.
write.csv(meta, file="metadata.csv", row.names=FALSE)

## Test the validity of metadata.csv
makeAnnotationHubMetadata("path/to/mypackage")

## End(Not run)
```

---

makeEnsemblFasta	<i>Functions to convert Ensembl FASTA files to FaFile and TwoBitFile for inclusion in AnnotationHub.</i>
------------------	--

---

## Description

Transform an Ensembl FASTA file to a Bioconductor FaFile or ToBitFile.

## Usage

```
makeEnsemblFastaToAHM(currentMetadata, baseUrl = "ftp://ftp.ensembl.org/pub/",
  baseDir = "fasta/", release,
  justRunUnitTest = FALSE,
  BiocVersion = BiocManager::version())
```

```
makeEnsemblTwoBitToAHM(currentMetadata, baseUrl = "ftp://ftp.ensembl.org/pub/",
                        baseDir = "fasta/", release,
                        justRunUnitTest = FALSE,
                        BiocVersion = BiocManager::version())

ensemblFastaToFaFile(ahm)

ensemblFastaToTwoBitFile(ahm)
```

## Arguments

currentMetadata	Currently not used. Intended to be a list of metadata to filter, i.e., records that do not need to be processed again. Need to remove or fix.
baseUrl	ftp file location.
baseDir	ftp file directory.
release	Integer version number, e.g., "84".
justRunUnitTest	A logical. When TRUE, a small number of records (usually 5) are processed instead of all.
BiocVersion	A character(1) Bioconductor version. The resource will be available in Bioconductor $\geq$ to this version. Default value is the current version, specified with <code>BiocManager::version()</code> .
ahm	List of AnnotationHubMetadata instances.

## Details

`makeEnsemblFastaToAHM` and `makeEnsemblTwoBitToAHM` process metadata into a list of `AnnotationHubMetadata` objects.

`ensemblFastaToFaFile` unzips a .gz files, creates an index and writes out .rz and .rz.fai files to disk. `ensemblFastaToTwoBit` converts a fasta file to twobit format and writes the .2bit file out to disk.

## Value

`makeEnsemblFastaToAHM` and `makeEnsemblTwoBitToAHM` return a list of `AnnotationHubMetadata` objects.

`ensemblFastaToFaFile` write out .rz and .rz.fai files to disk. `ensemblFastaToTwoBit` writes out a .2bit file to disk.

## Author(s)

Bioconductor Core Team

**See Also**

- [updateResources](#)
- [AnnotationHubMetadata](#)

**Examples**

```
## updateResources() generates metadata, process records and
## pushes files to AWS S3 buckets. See ?updateResources for details.

## 'release' is passed to makeEnsemblFastaToFaFile.
## Not run:
meta <- updateResources("/local/path",
                        BiocVersion = c("3.2", "3.3"),
                        preparerClasses = "EnsemblFastaImportPreparer",
                        metadataOnly = TRUE, insert = FALSE,
                        justRunUnitTest = FALSE, release = "83")

## End(Not run)
```

---

makeGencodeFasta

*Recipe to add Gencode FASTA resources to AnnotationHub*


---

**Description**

Create metadata and process raw Gencode FASTA files for inclusion in AnnotationHub

**Usage**

```
makeGencodeFastaToAHM(currentMetadata,
                      baseUrl="ftp://ftp.ebi.ac.uk/pub/databases/gencode/",
                      species=c("Human", "Mouse"), release,
                      justRunUnitTest=FALSE,
                      BiocVersion=BiocManager::version())

gencodeFastaToFaFile(ahm)
```

**Arguments**

currentMetadata	Currently not used. Intended to be a list of metadata to filter, i.e., records that do not need to be processed again. Need to remove or fix.
baseUrl	ftp file location.
species	A character(1) of the species. Currently "Human" and "Mouse" are supported.
release	A character string of the release number.

justRunUnitTest	A logical. When TRUE, a small number of records (usually 5) are processed instead of all.
BiocVersion	A character vector of Bioconductor versions the resources should be available for.
ahm	List of AnnotationHubMetadata instances.

### Details

- Documentation: <http://www.gencodegenes.org/releases/>
- File download location: <ftp://ftp.ebi.ac.uk/pub/databases/gencode/>. Gencode\_human and Gencode\_mouse are used.
- Files downloaded: Code is currently specific for human and mouse. Files chosen for download are described in `AnnotationHubData:::gencodeDescription()`.

### Value

makeGencodeFastaAHM returns a list of AnnotationHubMetadata instances. gencodeFastaToFastaFile returns nothing.

### Author(s)

Bioconductor Core Team.

### See Also

- [updateResources](#)
- [AnnotationHubMetadata](#)

### Examples

```
## updateResources() generates metadata, process records and
## pushes files to AWS S3 buckets.

## To run the GencodeFasta recipe specify
## 'preparerClasses = GencodeFastaImportPreparer'. The 'species' and 'release'
## arguments are passed to makeGencodeFastaAHM().
## Not run:
meta <- updateResources("/local/path",
                        BiocVersion = c("3.2", "3.3"),
                        preparerClasses = "GencodeFastaImportPreparer",
                        metadataOnly = TRUE, insert = FALSE,
                        justRunUnitTest = FALSE)

## End(Not run)
```

---

makeStandardOrgDbs      *Functions to add OrgDb and TxDb sqlite files to AnnotationHub*

---

### Description

Add OrgDb and TxDb sqlite files to AnnotationHub

### Usage

```
makeStandardOrgDbsToAHM(currentMetadata, justRunUnitTest = FALSE,
                          BiocVersion = BiocManager::version(),
                          downloadOrgDbs = TRUE)
```

```
makeStandardTxDbToAHM(currentMetadata, justRunUnitTest = FALSE,
                       BiocVersion = BiocManager::version(), TxDb)
```

```
makeNCBIToOrgDbsToAHM(currentMetadata, justRunUnitTest = FALSE,
                       BiocVersion = BiocManager::version(),
                       baseUrl = "ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/")
```

### Arguments

currentMetadata	Historically was intended to be a list of metadata to filter, i.e., records that do not need to be processed again. In some recipes this is used as a way to pass additional arguments. Need to remove or make consistent.
baseUrl	A character(). The file location.
justRunUnitTest	A logical. When TRUE, a small number of records (usually $\leq 5$ ) are processed instead of all.
BiocVersion	A character(1). The resource will be available for Bioconductor versions greater than and equal to this version. Default is BiocManager::version().
TxDbs	Character vector of the TxDb names; generally includes TxDb's that were new or updated for the current release.
downloadOrgDbs	A logical. Indicates if all OrgDb packages in the Bioconductor repo should be downloaded and installed. This should be TRUE the first time the recipe is run and can be FALSE for subsequent runs when testing.

### Details

makeStandardOrgDbsToAHM and makeStandardTxDbToAHM extracts the sqlite files from the existing OrgDb and TxDb packages in the Bioconductor repositories and generate associated metadata.

makeNCBIToOrgDbsToAHM creates sqlite files and metadata for 1000 organisms with the makeOrgPackageFromNCBI function. These organisms are less 'main stream' than those hosted in the Bioconductor repository (makeStandardOrgDbsToAHM) and the databases are less comprehensive because data only come from one source, NCBI.

**Value**

List of AnnotationHubMetadata objects.

**Author(s)**

Bioconductor Core Team

**See Also**

- [updateResources](#)
- [AnnotationHubMetadata](#)

**Examples**

```
## Not run:
## In Bioconductor 3.5, one new TxDb was added and 4 active
## tracks were updated. This piece of code shows how to add these 5
## packages to AnnotationHub.

## Step I: generate metadata
##
## Generate the metadata with the low-level helper for inspection.
TxDbms <- c("TxDb.Ggallus.UCSC.galGal5.refGene",
            "TxDb.Celegans.UCSC.ce11.refGene",
            "TxDb.Rnorvegicus.UCSC.rn5.refGene",
            "TxDb.Dmelanogaster.UCSC.dm6.ensGene",
            "TxDb.Rnorvegicus.UCSC.rn6.refGene")
meta <- makeStandardTxDbmsToAHM(currentMetadata=list(AnnotationHubRoot="TxDbms"),
                               justRunUnitTest=FALSE,
                               TxDbms = TxDbms)

## Once the low-level helper runs with no errors, try generating the
## metadata with the high-level wrapper updateResources(). Setting
## metadataOnly=TRUE will generate metadata only and not push resources
## to data bucket. insert=FALSE prevents the metadata from being inserted in the
## database.
##
## The metadata generated by updateResources() will be the same as that
## generated by makeStandardTxDbmsToAHM(). Both should be a list the same
## length as the number of TxDbms specified.
meta <- updateResources("TxDbms",
                       preparerClasses="TxDbFromPkgsImportPreparer",
                       metadataOnly=TRUE, insert = FALSE,
                       justRunUnitTest=FALSE, TxDbms = TxDbms)

INFO [2017-04-11 09:12:09] Preparer Class: TxDbFromPkgsImportPreparer
complete!
> length(meta)
[1] 5

## Step II: push resources to Azure
```

```

##
## If the metadata looks correct we are ready to push resources to Azure.
## Set metadataOnly=FALSE but keep insert=FALSE.

## export an environment variable with a core generated SAS URL for
## upload example:
## export AZURE_SAS_URL='https://bioconductorhubs.blob.core.windows.net/staginghub?sp=racwl&st=2022-02-08T15:5

meta <- updateResources("TxDb",
                        BiocVersion="3.5",
                        preparerClasses="TxDbFromPkgsImportPreparer",
                        metadataOnly=FALSE, insert = FALSE,
                        justRunUnitTest=FALSE, TxDb = TxDb)

## Step III: insert metadata in AnnotationHub production database
##
## Inserting the metadata in the database is usually done as a separate step
## and with the help of the AnnotationHub docker.
## Set metadataOnly=TRUE and insert=TRUE.
meta <- updateResources("TxDb",
                        BiocVersion="3.5",
                        preparerClasses="TxDbFromPkgsImportPreparer",
                        metadataOnly=FALSE, insert = FALSE,
                        justRunUnitTest=FALSE, TxDb = TxDb)

## End(Not run)

```

---

updateResources

*updateResources*

---

## Description

Add new resources to AnnotationHub

## Usage

```

updateResources(AnnotationHubRoot, BiocVersion = BiocManager::version(),
                preparerClasses = getImportPreparerClasses(),
                metadataOnly = TRUE, insert = FALSE,
                justRunUnitTest = FALSE, ...)

```

```

pushResources(allAhms, uploadToRemote = TRUE, download = TRUE)

```

```

pushMetadata(allAhms, url)

```

## Arguments

AnnotationHubRoot

Local path where files will be downloaded.



BiocVersion	A character(1) Bioconductor version. The resource will be available in Bioconductor $\geq$ to this version. Default value is the current version, specified with <code>BiocManager::version()</code> .
preparerClasses	One of the <code>ImportPreparer</code> subclasses defined in <code>getImportPreparer()</code> . This class is used for dispatch during data discovery.
metadataOnly	A logical to specify the processing of metadata only or both metadata and data files. When FALSE, metadata are generated and data files are downloaded, processed and pushed to their final location in S3 buckets. <code>metadata = TRUE</code> produces only metadata and is useful for testing.
insert	NOTE: This option is for inserting metadata records in the production data base (done by Bioconductor core team member) and is for internal use only. A logical to control if metadata are inserted in the AnnotationHub 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 <code>insert = TRUE</code> , the "AH_SERVER_POST_URL" global option must be set to the http location of the AnnotationHubServer in the global environment or .Rprofile. Additionally, <code>azcopy</code> command line tools must be installed on the local machine to push files to Azure buckets. See <a href="#">upload_to_azure</a> .
justRunUnitTest	A logical. When TRUE, a small number of records (usually 5) are processed instead of all.
allAhms	List of <code>AnnotationHubMetadata</code> objects.
url	URL of AnnotationHub database where metadata will be inserted.
uploadToRemote	A logical indicating whether resources should be uploaded to remote bioconductor default location. Currently Azure Data Lakes.
download	A logical indicating whether resources should be downloaded from resource url.
...	Arguments passed to other methods such as <code>regex</code> , <code>baseUrl</code> , <code>baseDir</code> .

## Details

- `updateResources`:  
`updateResources` is responsible for creating metadata records and downloading, processing and pushing data files to their final resting place. The
- `preparerClasses` argument is used in method dispatch to determine which recipe is used.  
By manipulating the `metadataOnly`, `insert` and `justRunUnitTest` arguments one can flexibly test the metadata for a small number of records with or without downloading and processing the data files.
- global options:  
When `insert = TRUE` the "AH\_SERVER\_POST\_URL" option must be set to the https location of the AnnotationHub db.

**Value**

A list of AnnotationHubMetadata objects.

**Author(s)**

Martin Morgan, Marc Carlson

**See Also**

- [AnnotationHubMetadata](#)
- [upload\\_to\\_azure](#)

**Examples**

```
## Not run:

## -----
## Inspect metadata:
## -----
## A useful first step in testing a new recipe is to generate and
## inspect a small number of metadata records. The combination of
## 'metadataOnly=TRUE', 'insert=FALSE' and 'justRunUnitTest=TRUE'
## generates metadata for the first 5 records and does not download or
## process any data.

meta <- updateResources("/local/path",
                        BiocVersion = "3.3",
                        preparerClasses = "EnsemblFastaImportPreparer",
                        metadataOnly = TRUE, insert = FALSE,
                        justRunUnitTest = TRUE,
                        release = "84")

INFO [2015-11-12 07:58:05] Preparer Class: EnsemblFastaImportPreparer
Ailuropoda_melanoleuca.ailMel1.cdna.all.fa.gz
Ailuropoda_melanoleuca.ailMel1.dna_rm.toplevel.fa.gz
Ailuropoda_melanoleuca.ailMel1.dna_sm.toplevel.fa.gz
Ailuropoda_melanoleuca.ailMel1.dna.toplevel.fa.gz
Ailuropoda_melanoleuca.ailMel1.ncrna.fa.gz

## The return value is a list of metadata for the first 5 records:

> names(meta)
[1] "FASTA cDNA sequence for Ailuropoda melanoleuca"
[2] "FASTA DNA sequence for Ailuropoda melanoleuca"
[3] "FASTA DNA sequence for Ailuropoda melanoleuca"
[4] "FASTA DNA sequence for Ailuropoda melanoleuca"
[5] "FASTA ncRNA sequence for Ailuropoda melanoleuca"

## Each record is of class AnnotationHubMetadata:
```

```

> class(meta[[1]])
[1] "AnnotationHubMetadata"
attr(,"package")
[1] "AnnotationHubData"

## -----
## Insert metadata in the db and process/push data files:
## -----
## This next code chunk creates the metadata and downloads and processes
## the data (metadataOnly=FALSE). If all files are successfully pushed to
## to their final resting place, metadata records are inserted in the
## AnnotationHub db (insert=TRUE). Metadata insertion is done by a
## Bioconductor team member; contact maintainer@bioconductor.org for help.

meta <- updateResources("local/path",
                        BiocVersion = "3.5",
                        preparerClasses = "EnsemblFastaImportPreparer",
                        metadataOnly = FALSE, insert = TRUE,
                        justRunUnitTest = FALSE,
                        regex = ".*release-81")

## -----
## Recovery helpers:
## -----

## pushResources() and pushMetadata() are both called from updateResources()
## but can be used solo for testing or completing a run that
## terminated unexpectedly.

## Download, process and push to azure the last 2 files in 'meta':
sub <- meta[length(meta) - 1:length(meta)]
pushResources(sub)

## Insert metadata in the AnotationHub db for the last 2 files in 'meta':

pushMetadata(sub, url = getOption("AH_SERVER_POST_URL"))

## End(Not run)

```

---

upload\_to\_azure

*Upload a file to Microsoft Azure Data Lake*


---

## Description

This function is for uploading a file resource to the Microsoft Azure Data Lake.

## Usage

```
upload_to_azure(file, sas)
```

**Arguments**

file	The file or directory to upload.
sas	A SAS url for the designated destination on Microsoft Azure Data Lake.

**Details**

Uses the [azcopy Command Line Interface](#) to copy a file to Microsoft Azure Data Lake. Assumes azcopy is properly installed and that the azcopy program is in your PATH. The function performs a recursive automatically so it can take a file or directory for upload. The SAS URL is generated on Azure by someone who has permission to the desired destination. Please be sure to use the SAS url and not the SAS token. The sas url can be provided as an argument; if the argument is not provided it will search for a system environment variable 'AZURE\_SAS\_URL'.

**Value**

TRUE on success. If the command fails, the function will exit with an error.

**Author(s)**

Lori Shepherd

**Examples**

```
## Not run:
upload_to_azure("myfile.txt", "https://sasurl")

## End(Not run)
```

---

upload_to_S3	<i>Upload a file to Amazon S3</i>
--------------	-----------------------------------

---

**Description**

This function is for uploading a file resource to the S3 cloud.

**Usage**

```
upload_to_S3(file, remotename, bucket, profile, acl="public-read")
```

**Arguments**

file	The file to upload.
remotename	The name this file should have in S3, including any "keys" that are part of the name. This should not start with a slash (if it does, the leading slash will be removed), but can contain forward slashes.
bucket	Name of the S3 bucket to copy to.
profile	Corresponds to a profile set in the config file for the AWS CLI (see <a href="#">the documentation</a> ). If this argument is omitted, the default profile is used.
acl	Should be one of private, public-read, or public-read-write.

## Details

Uses the [AWS Command Line Interface](#) to copy a file to Amazon S3. Assumes the CLI is properly configured and that the aws program is in your PATH. The CLI should be configured with the credentials of a user who has permission to upload to the appropriate bucket. It's recommended to use [IAM](#) to set up users with limited permissions.

There is an RAmazonS3 package but it seems to have issues uploading files to S3.

## Value

TRUE on success. If the command fails, the function will exit with an error.

## Author(s)

Dan Tenenbaum

## Examples

```
## Not run:
upload_to_S3("myfile.txt", "foo/bar/baz/yourfile.txt")
# If this is successful, the file should be accessible at
# http://s3.amazonaws.com/annotationhub/foo/bar/baz/yourfile.txt

## End(Not run)
```

---

validationFunctions    *ValidationFunctions*

---

## Description

Functions to assist in the validation process of creating the metadata.csv file for Hub Resources

## Usage

```
getSpeciesList(verbose=FALSE)

validSpecies(species, verbose=TRUE)

suggestSpecies(query, verbose=FALSE, op=c("|", "&"))

getValidSourceTypes()

checkSpeciesTaxId(txid, species, verbose=TRUE)

validDispatchClass(dc, verbose=TRUE)
```

**Arguments**

species	species to validate (may be single value or list)
query	terms to query. Whether AND or OR is determined by argument op.
verbose	should additional information and useful tips be displayed
op	Should searching of multiple terms be conditional OR (" ") or AND ("&")
txid	taxonomy id (single value or list)
dc	Dispatch class to validate (may be single value or list)

**Details**

- `getSpeciesList`: Provides a list of valid species as determined by the `GenomeInfoDbData` package `specData.rda` file.
- `validSpecies`: True/False if argument is considered a valid species based on the list generated by `getSpeciesList`. A species may be deemed invalid if the capitalization mismatches or punctuation mismatches. Use `suggestSpecies` to find similar terms.
- `suggestSpecies`: Based on a term or multiple terms suggest possible valid species.
- `getValidSourceTypes`: returns list of acceptable values for `SourceType` in `metadata.csv`. If you think a valid source type should be added to the list please reach out to `maintainer@bioconductor.org`
- `checkSpeciesTaxId`: cross validates a list of species and taxonomy ids for expected values based on `GenomeInfoDb::loadTaxonomyDb()`. Warning when there is a mismatch.
- `validDispatchClass`: TRUE/FALSE if argument is considered a valid `DispatchClass` based on the currently available methods in `AnnotationHub`. Use `AnnotationHub::DispatchClassList()` to see the table of currently available methods. If a currently available method is not appropriate for your resource, please reach out to Lori Shepherd <`Lori.Shepherd@roswellpark.org`> to request a new method be added.

**Value**

- For `getSpeciesList`: character vector of valid species
- For `validSpecies`: True/False if all species given as argument are valid
- For `suggestSpecies`: `data.frame` of taxonomy id and species name of possible valid species based on given query key words.
- For `getValidSourceTypes`: character vector of valid source types.
- For `checkSpeciesTaxId`: NULL if check is verified, If `verbose` is true a table of suggested values along with the warning.
- For `validDispatchClass`: True/False if all dispatch class given as argument are valid

**Author(s)**

Lori Shepherd

**See Also**

- [AnnotationHubMetadata](#)
- [makeAnnotationHubMetadata](#)

**Examples**

```
species = getSpeciesList()

# following is TRUE

validSpecies("Homo sapiens")
# followin is FALSE because of starting "h"
validSpecies("homo sapiens")

# can provide multiple, if any are not valid FALSE
# TRUE
validSpecies(c("Homo sapiens", "Canis domesticus"))

suggestSpecies("Canis")

getValidSourceTypes()

checkSpeciesTaxId(1003232, "Edhazardia aedis")
checkSpeciesTaxId(9606, "Homo sapiens")

validDispatchClass("GRanges")
```

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