Package 'AnnotationHub'

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Type Package

Title Client to access AnnotationHub resources

Version 2.12.1

biocViews Infrastructure, DataImport, GUI, ThirdPartyClient

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Description This package provides a client for the Bioconductor
AnnotationHub web resource. The AnnotationHub web resource
provides a central location where genomic files (e.g., VCF, bed,
wig) and other resources from standard locations (e.g., UCSC,
Ensembl) can be discovered. The resource includes metadata about
each resource, e.g., a textual description, tags, and date of
modification. The client creates and manages a local cache of
files retrieved by the user, helping with quick and reproducible
access.

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Depends BiocGenerics (>= 0.15.10)

Imports utils, methods, grDevices, RSQLite, BiocInstaller, curl,
AnnotationDbi (>= 1.31.19), S4Vectors, interactiveDisplayBase,
httr, yaml

Suggests IRanges, GenomicRanges, GenomeInfoDb, VariantAnnotation,
Rsamtools, rtracklayer, BiocStyle, knitr, AnnotationForge,
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Enhances AnnotationHubData

Collate AnnotationHubOption.R AllGenerics.R Hub-class.R db-utils.R
AnnotationHub-class.R AnnotationHubResource-class.R
BEDResource-class.R ProteomicsResource-class.R
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VignetteBuilder knitr

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R topics documented:

AnnotationHub-package   *Light-weight AnnotationHub 3.0 Client*

Description

Client for discovery and retrieval of Bioconductor annotation resources.

Author(s)

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See Also

AnnotationHub-class

Examples

```
## Not run:
library(AnnotationHub)
hub = AnnotationHub()
hub

## End(Not run)
```

AnnotationHub-objects   *AnnotationHub objects and their related methods and functions*

Description

Use `AnnotationHub` to interact with Bioconductor's AnnotationHub service. Query the instance to discover and use resources that are of interest, and then easily download and import the resource into R for immediate use.

Use `AnnotationHub()` to retrieve information about all records in the hub. If working offline, add argument `localHub=TRUE` to work with a local, non-updated hub; It will only have resources available that have previously been downloaded.

Discover records in a hub using `mcols()`, `query()`, `subset()`, `[`, and `display()`.

Retrieve individual records using `[[`. On first use of a resource, the corresponding files or other hub resources are downloaded from the internet to a local cache. On this and all subsequent uses the files are quickly input from the cache into the R session.

AnnotationHub records can be added (and sometimes removed) at any time. `snapshotDate()` restricts hub records to those available at the time of the snapshot. `possibleDates()` lists snapshot dates valid for the current version of Bioconductor.

The location of the local cache can be found (and updated) with `getAnnotationHubCache` and `setAnnotationHubCache`; `removeCache` removes all cache resources.

Constructors

`AnnotationHub(..., hub=getAnnotationHubOption("URL"),`   `cache=getAnnotationHubOption("CACHE'`
     Create an `AnnotationHub` instance, possibly updating the current database of records.

Accessors

In the code snippets below, `x` and `object` are AnnotationHub objects.

`hubCache(x)`: Gets the file system location of the local AnnotationHub cache.

`hubUrl(x)`: Gets the URL for the online hub.

`length(x)`: Get the number of hub records.

`names(x)`: Get the names (AnnotationHub unique identifiers, of the form AH12345) of the hub records.

`fileName(x)`: Get the file path of the hub records as stored in the local cache (AnnotationHub files are stored as unique numbers, of the form 12345). NA is returned for those records which have not been cached.

`mcols(x)`: Get the metadata columns describing each record. Columns include:

     title Record title, frequently the file name of the object.

     dataprovider Original provider of the resource, e.g., Ensembl, UCSC.

     species The species for which the record is most relevant, e.g., 'Homo sapiens'.

     taxonomyid NCBI taxonomy identifier of the species.

     genome Genome build relevant to the record, e.g., hg19.

     description Textual description of the resource, frequently automatically generated from file path and other information available when the record was created.

tags Single words added to the record to facilitate identification, e.g,. TCGA, Roadmap.

rdataclass The class of the R object used to represent the object when imported into R, e.g., GRanges, VCFFile.

sourceurl Original URL of the resource.

sourectype Format of the original resource, e.g., BED file.

dbconn(x): Return an open connection to the underyling SQLite database.

dbfile(x): Return the full path the underyling SQLite database.

.db_close(conn): Close the SQLite connection conn returned by dbconn(x).

Subsetting and related operations

In the code snippets below, x is an AnnotationHub object.

x$name: Convenient reference to individual metadata columns, e.g., x$species.

x[i]: Numerical, logical, or character vector (of AnnotationHub names) to subset the hub, e.g., x[x$species == "Homo sapiens"].

x[[i]]: Numerical or character scalar to retrieve (if necessary) and import the resource into R.

query(x, pattern, ignore.case=TRUE, pattern.op= `&`): Return an AnnotationHub subset containing only those elements whose metadata matches pattern. Matching uses pattern as in [grepl](#) to search the as.character representation of each column, performing a logical `&` across columns. e.g., query(x, c("Homo sapiens", "hg19", "GTF")).

pattern A character vector of patterns to search (via grepl) for in any of the mcols() columns.

ignore.case A logical(1) vector indicating whether the search should ignore case (TRUE) or not (FALSE).

pattern.op Any function of two arguments, describing how matches across pattern elements are to be combined. The default `&` requires that only records with *all* elements of pattern in their metadata columns are returned. `&`, `|` and `!` are most notably available. See "?&" or ?base::Ops for more information.

subset(x, subset): Return the subset of records containing only those elements whose metadata satisfies the *expression* in subset. The expression can reference columns of mcols(x), and should return a logical vector of length length(x). e.g., subset(x, species == "Homo sapiens" & genome=="GRCh38").

display(object): Open a web browser allowing for easy selection of hub records via interactive tabular display. Return value is the subset of hub records identified while navigating the display.

recordStatus(hub, record): Returns a data.frame of the record id and status. hub must be a Hub object and record must be a character(1). Can be used to discover why a resource was removed from the hub.

Cache and hub management

In the code snippets below, x is an AnnotationHub object.

snapshotDate(x) and snapshotDate(x) <- value: Gets or sets the date for the snapshot in use. value should be one of possibleDates().

possibleDates(x): Lists the valid snapshot dates for the version of Bioconductor that is being run (e.g., BiocInstaller::biocVersion()).

cache(x) and cache(x) <- NULL: Adds (downloads) all resources in x, or removes all local resources corresponding to the records in x from the cache. In this case, x would typically be a small subset of AnnotationHub resources.

hubUrl(x): Gets the URL for the online AnnotationHub.

hubCache(x): Gets the file system location of the local AnnotationHub cache.

removeCache(x): Removes local AnnotationHub database and all related resources. After calling this function, the user will have to download any AnnotationHub resources again.

Coercion

In the code snippets below, x is an AnnotationHub object.

as.list(x): Coerce x to a list of hub instances, one entry per element. Primarily for internal use.

c(x, ...): Concatenate one or more sub-hub. Sub-hubs must reference the same AnnotationHub instance. Duplicate entries are removed.

Author(s)

Martin Morgan, Marc Carlson, Sonali Arora, and Dan Tenenbaum

Examples

```
## create an AnnotationHub object
library(AnnotationHub)
ah = AnnotationHub()

## Summary of available records
ah

## Detail for a single record
ah[1]

## and what is the date we are using?
snapshotDate(ah)

## how many resources?
length(ah)

## from which resources, is data available?
head(sort(table(ah$dataprovider), decreasing=TRUE))

## from which species, is data available ?
head(sort(table(ah$species),decreasing=TRUE))

## what web service and local cache does this AnnotationHub point to?
hubUrl(ah)
hubCache(ah)

### Examples ###

## One can  search the hub for multiple strings
ahs2 <- query(ah, c("GTF", "77","Ensembl", "Homo sapiens"))

## information about the file can be retrieved using
ahs2[1]
```

```
## one can further extract information from this show method
## like the sourceurl using:
ahs2$sourceurl
ahs2$description
ahs2$title

## We can download a file by name like this (using a list semantic):
gr <- ahs2[[1]]
## And we can also extract it by the names like this:
res <- ah[["AH28812"]]

## the gtf file is returned as a GenomicRanges object and contains
## data about which organism it belongs to, its seqlevels and seqlengths
seqinfo(gr)

## each GenomicRanges contains a metadata slot which can be used to get
## the name of the hub object and other associated metadata.
metadata(gr)
ah[metadata(gr)$AnnotationHubName]

## And we can also use "[" to restrict the things that are in the
## AnnotationHub object (by position, character, or logical vector).
## Here is a demo of position:
subHub <- ah[1:3]

if(interactive()) {
  ## Display method involves user interaction through web interface
  ah2 <- display(ah)
}

## recordStatus
recordStatus(ah, "TEST")
recordStatus(ah, "AH7220")
```

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getAnnotationHubOption

Get and set options for default AnnotationHub behavior.

Description

These functions get or set options for creation of new 'AnnotationHub' instances.

Usage

```
getAnnotationHubOption(arg)
setAnnotationHubOption(arg, value)
```

Arguments

arg	The character(1) hub options to set. see 'Details' for current options.
value	The value to be assigned to the hub option.

Details

Supported options include:

"URL": character(1). The base URL of the annotation hub. Default: `https://annotationhub.bioconductor.org`

"CACHE": character(1). The location of the hub cache. Default: ".AnnotationHub" in the user home directory.

"MAX_DOWNLOADS": numeric(1). The integer number of downloads allowed before triggering an error. This is to help avoid accidental download of a large number of AnnotationHub members.

"PROXY": `request` object returned by `httr::use_proxy()`. The `request` object describes a proxy connection allowing Internet access, usually through a restrictive firewall. Setting this option sends all AnnotationHub requests through the proxy. Default: NULL.

In `setHubOption("PROXY", value)`, `value` can be one of NULL, a `request` object returned by `httr::use_proxy()`, or a well-formed URL as character(1). The URL can be completely specified by `http://username:password@proxy.dom.com:8080`; `username:password` and port (e.g. `:8080`) are optional.

Default values may also be determined by system and global R environment variables visible *before* the package is loaded. Use options or variables preceeded by "ANNOTATION_HUB_", e.g., `options(ANNOTATION_HUB_MAX_DOWNLOADS=10)` prior to package load sets the default number of downloads to 10.

Value

The requested or successfully set option.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
getAnnotationHubOption("URL")
## Not run:
setAnnotationHubOption("CACHE", "~/.myHub")

## End(Not run)
```

---

utilities   *Utility functions for discovering package-specific Hub resources.*

Description

List and load resources from ExperimentHub filtered by package name and optional search terms. Not Implemented for AnnotationHub.

Details

Currently `listResources` and `loadResources` are only meaningful for `ExperimentHub` objects.

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