

Package ‘AnnotationHub’

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Type Package

Title A client for retrieving Bioconductor objects from AnnotationHub

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Suggests RUnit, RCurl, Rsamtools

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Description A client for retrieving data from the Bioconductor AnnotationHub online services.

Collate AllGenerics.R hubUtils.R hubCache.R filter.R completion.R
getResource.R AnnotationHub-class.R test_AnnotationHub_package.R zzz.R

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biocViews Annotation, Infrastructure

LazyLoad yes

R topics documented:

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Description

AnnotationHub is the base class for interacting with the AnnotationHub services using Bioconductor. When using the AnnotationHub package, users will create an instance of this class and then apply filters on it in order to narrow down their annotation options to an amount that a human can reasonably look at.

Once an AnnotationHub is created, the user can see what resources are available by tab completion using the \$ argument. But before doing that, it is usually a good idea to use the filters method to set some restrictions.

What kind of restrictions? Well those can be listed by using the cols and keys methods to list them. Possible values for those can be found by using keys.

Once this is determined, a list object can be assigned using filters<-. The list needs to be named after values returned by the cols and keys methods, and to contain character vectors that contain results from the matching keys method.

All AnnotationHub have a snapshot date that by default is set to the most recent one. The snapshotDate method indicates which one is in use, but this value can also be set to previous dates.

Whenever you download a file from AnnotationHub it will automatically put the data in a local cache for future reference. The location of this cache can be found and even changed with the hubCache setters and getters. This cache provides a performance boost for users but it does not mean that you can use this on a plane without needing wireless access.

Usage

```
filters(x, ...)  
filters(x, ...) <- value  
hubUrl(x, ...)  
hubCache(x, ...)  
hubCache(x, ...) <- value  
hubResource(x, path = character(), ...)  
possibleDates(x, ...)  
snapshotDate(x, ...)  
snapshotDate(x, ...) <- value  
snapshotUrl(x, ...)  
snapshotUrls(x, ...)  
snapshotVersion(x, ...)  
keys(x, keytype)  
cols(x)  
keytypes(x)
```

Arguments

x the AnnotationHub object.

value	the value to be assigned. For filters method, this is a named list where the names are the kind of filters, and the values are character vectors of acceptable values
path	the (optional) path string.
keytype	the type of key you want to look up possible values for.
...	other arguments

Author(s)

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Examples

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

## what is the version of this snapshot?
snapshotVersion(ah)

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

## how many resources?
length(ah)

## list currently active filters
filters(ah)

## list values that can be used to filter on:
cols(ah)
keytypes(ah)

## list possible values for one of these filter types
head(keys(ah, keytype="Species"))

## OR retrieve metadata values about several keys at once
## (This approach may not always scale the way you want it to)
metadata(ah, cols = c("Species", "RDataPath"))

## create and apply a new filter to only include people
filters(ah) <- list(Species="Homo sapiens")

## now how many resources are there?
length(ah)

## what are the names for these resources?
head(names(ah))

## What are the URLs for these resources?
head(snapshotUrls(ah))
```

```
## what web service is this AnnotationHub pointing to?
hubUrl()
## and more explicitly
snapshotUrl()

## Where are the files that get downloaded being cached?
## (there is also a setter if you wish to assign this to another location)
hubCache(ah)

## Download a resource (using tab completion) and put it into "res"
res <- ah$goldenpath.hg19.encodeDCC.wgEncodeUwTfbs.wgEncodeUwTfbsMcf7CtcfStdPkRep1.narrowPeak_0.0.1.RData
```

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