Package ‘HCABrowser’

October 17, 2020

Type Package

Title Browse the Human Cell Atlas data portal

Version 1.4.0

Description Search, browse, reference, and download resources from
the Human Cell Atlas data portal. Development of this package is
supported through funds from the Chan / Zuckerberg initiative.

Depends R (>= 3.6.0), dplyr

Imports BiocFileCache, S4Vectors, curl, googleAuthR, httr, jsonlite,
methods, plyr, readr, rlang, stringr, tibble, tidygraph, tidyr,
utils

Suggests BiocStyle, knitr, rmarkdown, testthat

License Artistic-2.0

Encoding UTF-8

LazyData true

URL `https://github.com/Bioconductor/HCABrowser`

RoxygenNote 6.1.1

biocViews DataImport, Sequencing

BugReports `https://github.com/Bioconductor/HCABrowser/issues`

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/HCABrowser

git_branch RELEASE_3_11

git_last_commit 3d709b6

git_last_commit_date 2020-04-27

Date/Publication 2020-10-16

Author Daniel Van Twisk [aut],
Martin Morgan [aut],
Bioconductor Package Maintainer [cre]

Maintainer Bioconductor Package Maintainer <`maintainer@bioconductor.org`>

R topics documented:

`activate` *Activate files or bundles of HCABrowser Object*

Description

Activate files or bundles of HCABrowser Object

Usage

```
## S4 method for signature 'HCABrowser'
activate(hca, what = c("bundles", "files"))
```

Arguments

`hca`	An HCABrowser object
`what`	Either "bundles" or "files". Deterimines whether bundles or files should be shown.

Value

An HCABrowser with the selected activation

`fields` *List supported fields of an HCABrowser object*

Description

List supported fields of an HCABrowser object

Usage

```
## S4 method for signature 'HCABrowser'
fields(hca)
```

Arguments

`hca`	An HCABrowser object.

Value

A tibble indicating fields that can be queried upon.

Examples

```
hca <- HCABrowser()
fields(hca)
```

`filter.HCABrowser` *Filter HCABrowser objects*

Description

Filter HCABrowser objects

Usage

```
## S3 method for class 'HCABrowser'
filter(.data, ..., .preserve)
```

Arguments

`.data`	an HCABrowser object to perform a query on.
`...`	further argument to be tranlated into a query to select from. These arguments can be passed in two ways, either as a single expression or as a series of expressions that are to be seperated by commas.
`.preserve`	unused.

Value

a HCABrowser object containing the resulting query.

Examples

```
hca <- HCABrowser()
hca2 <- hca %>% filter(organ.text == "brain")
hca2
```

`hca-api-methods` *HCA API methods*

Description

Methods to access the Human Cell Atlas's Data Coordination Platform (HCA DCP) by means of the platform's REST API.

Check the status of a checkout request

Usage

```
getBundlesCheckout(hca, ...)
deleteBundle(hca, ...)
getBundle(hca, ...)
putBundle(hca, ...)
postBundlesCheckout(hca, ...)
putCollection(hca, ...)
deleteCollection(hca, ...)
getCollection(hca, ...)
patchCollection(hca, ...)
getFile(hca, ...)
headFile(hca, ...)
putFile(hca, ...)
postSearch(hca, ...)
getSubscriptions(hca, ...)
putSubscription(hca, ...)
deleteSubscription(hca, ...)
getSubscription(hca, ...)

## S4 method for signature 'HCABrowser'
getBundlesCheckout(hca, checkout_job_id,
  replica = c("aws", "gcp", "azure"))

## S4 method for signature 'HCABrowser'
deleteBundle(hca, uuid, replica = c("aws", "gcp",
  "azure"), version = NULL, reason = NULL)

## S4 method for signature 'HCABrowser'
getBundle(hca, uuid, replica = c("aws", "gcp",
  "azure"), version = NULL, directurls = NULL, presignedurls = FALSE,
  token = NULL)

## S4 method for signature 'HCABrowser'
putBundle(hca, uuid, replica = c("aws", "gcp",
```

```
  "azure"), version = NULL, creator_uid, files)

## S4 method for signature 'HCABrowser'
postBundlesCheckout(hca, uuid, replica = c("aws",
  "gcp", "azure"), destination = NULL, email = NULL)

## S4 method for signature 'HCABrowser'
putCollection(hca, uuid, replica = c("aws", "gcp",
  "azure"), version, contents, description, details, name)

## S4 method for signature 'HCABrowser'
deleteCollection(hca, uuid, replica = c("aws",
  "gcp", "azure"))

## S4 method for signature 'HCABrowser'
getCollection(hca, uuid, replica = c("aws", "gcp",
  "azure"), version = NULL)

## S4 method for signature 'HCABrowser'
patchCollection(hca, uuid, replica = c("aws",
  "gcp", "azure"), version, add_contents, description, details, name,
  remove_contents)

## S4 method for signature 'HCABrowser'
getFile(hca, uuid, replica = c("aws", "gcp",
  "azure"), token = NULL, version = NULL)

## S4 method for signature 'HCABrowser'
headFile(hca, uuid, replica = c("aws", "gcp",
  "azure"), version = NULL)

## S4 method for signature 'HCABrowser'
putFile(hca, uuid, creator_uid, source_url,
  version = NULL)

## S4 method for signature 'HCABrowser'
postSearch(hca, replica = c("aws", "gcp",
  "azure"), output_format = c("summary", "raw"), es_query = NULL,
  per_page = 100, search_after = NULL, json = NULL)

## S4 method for signature 'HCABrowser'
getSubscriptions(hca, replica = c("aws", "gcp",
  "azure"))

## S4 method for signature 'HCABrowser'
putSubscription(hca, replica = c("aws", "gcp",
  "azure"), attachments, callback_url, encoding, es_query, form_fields,
  hmac_key_id, hmac_secret_key, method, payload_form_field)

## S4 method for signature 'HCABrowser'
deleteSubscription(hca, uuid, replica = c("aws",
  "gcp", "azure"))
```

```
## S4 method for signature 'HCABrowser'
getSubscription(hca, uuid, replica = c("aws",
  "gcp", "azure"))
```

Arguments

`hca`	An HCABrowser object that is the subject of the request.
`checkout_job_id`	character(1). A RFC4122-complliant ID for the checkout job request.
`replica`	character(1). A replica to fetch form. Can either be set to "aws", "gcp", or "azure". DEFAULT is "aws".
`uuid`	character(1). A RFC4122-compliant ID for the bundle.
`version`	character(1). Timestamp of bundle creation in RFC3339.
`reason`	character(1). User-friendly reason for the bundle or timestamp- specific bundle deletion.
`directurls`	logical(1). Include direct-access URLs in the response. This is mutually exclusive with the `presignedurls` parameter. DEFAULT is `NULL`.
`presignedurls`	logical(1). Include presigned URLs in the response. This is mutually exclusive with the directurls parameter.
`token`	`Token`. Token to manage retries. End users constructing queries should not set this parameter. Use `get_token()` to generate.
`creator_uid`	character(1). User ID who is creating this bundle.
`files`	list. (ADD DESCRIPTION ON STRUCTURE OF THIS ARGUMENT)
`destination`	character(1). User-owned destination storage bucket.
`email`	character(1). An email address to send status updates to.
`contents`	list. A list of objects describing links to files, bundles, other collections, and metadata fragments that are part of the collection.
`description`	character(1). A long description of the collection, formatted in Markdown.
`details`	list. Supplementary JSON metadata for the collection. (ADD DESCRIPTION OF STRUCTURE)
`name`	character(1). A short name identifying the collection.
`add_contents`	list. List of items to remove from the collection. Items must match exactly to be removed. Items not found in the collection are ignored. (ADD DESCRIPTION OF LIST OBJECT)
`remove_contents`	list. List of items to remove from the collection. Items must match exactly to be removed. Items not found in the collection are ignored.
`source_url`	character(1). Cloud URL for source data.
`output_format`	character(1). Specifies the output format. Either "summary" or "raw". The default format, "summary", is a list of UUIDs for bundles that match the query. Set this parameter to "raw" to get the verbatim JSON metadata for bundles that match the query.
`es_query`	list. Elasticsearch query. (ADD DESCRIPTION OF STRUCTURE)
`per_page`	numeric(1). Max number of results to return per page.

`search_after`	character(1). **Search-After-Context**. An internal state pointer parameter for use with pagination. The API client should not need to set this parameter directly; it should instead directly fetch the URL given in the "Link" header.
`json`	character(1) of a json query to be executed.
`attachments`	list. The set of bundle metadata items to be included in the payload of a notification request to a subscriptionendpoint. Each property in this object represents an attachment to the notification payload. Each attachment will be a child property of the "attachments" property of the payload. The name of such a child property can be chosen freely provided it does not start with an underscore. For example, if the subscription is “‘ "attachments": "taxon": "type": "jmespath", "expression": "files.biomaterial_j son.biomaterials[].content.biomaterial_core.ncbi_taxon_id[]" “‘ the corresponding notification payload will contain the following entry “‘ "attachments": "taxon": [9606, 9606] “‘ If a general error occurs during the processing of attachments, the notification will be sent with ‘attachments‘ containing only the reserved ‘_errors‘ attachment containing a string describing the error. If an error occurs during the processing of a specific attachment, the notification will be sent with all successfully processed attachments and additionally the ‘_errors‘ attachment containing an object with one property for each failed attachment. For example, “‘ "attachments": "taxon": [9606, 9606] "_errors" "biomaterial": "Some error occurred" “‘ The value of the ‘attachments‘ property must be less than or equal to 128 KiB in size when serialized to JSON and encoded as UTF-8. If it is not, the notification will be sent with "attachments": "_errors": "Attachments too large (131073 bytes)"
`callback_url`	character(1). The subscriber’s URL. An HTTP request is made to the specified URL for every attempt to deliver a notification to the subscriber. If the HTTP response code is 2XX, the delivery attempt is considered successful and no more attemtpts will be made. Otherwise, more attempts will be made with an exponentially increasing delay between attempts, until an attempt is successful or the a maximum number of attempts is reached.
`encoding`	character(1). The MIME type describing the encoding of the request body. Either "application/json" or "multipart/form-data".
`form_fields`	list. A collection of static form fields to be supplied in the request body, alongside the actual notification payload.
`hmac_key_id`	character(1). An optional key ID to use with "hmac_secret_key".
`hmac_secret_key`	character(1). The key for signing requests to the subscriber’s URL. The signature will be constructed according to https://tools.ietf.org/html/draft-cavage-http-signatures and transmitted in the HTTP ‘Authorization‘ header.
`method`	The HTTP request method to use when delivering a notification to the subscriber.
`payload_form_field`	character(1). The name of the form field that will hold the notification payload when the request is made. If the default name of the payload field collides with that of a field in ‘form_fields‘, this porperty can be used to rename the payload and avoid the collision. This property is ignored unless ‘encoding‘ is ‘multipart/form-data‘.
`...`	Other arguments

Value

an HCABrowser object

Author(s)

Daniel Van Twisk

Examples

```
hca <- HCABrowser()
#addmore
```

`HCABrowser` *The HCABrowser Class*

Description

The HCABrowser Class

Usage

```
HCABrowser(url = "https://dss.data.humancellatlas.org/v1",
  fields_path = system.file("extdata", "fields_and_values.json", package
  = "HCABrowser"), per_page = 10)
```

Arguments

`url`	character(1) the url of the Human Cell Atlas resource.
`fields_path`	character(1) path to the fields json file.
`per_page`	numeric(1) numbers of pages to view at a time.

Value

an HCABrowser object

Author(s)

Daniel Van Twisk

Examples

```
hca <- HCABrowser()
hca
```

`HCABrowser-class` *The HCABrowser Class*

Description

The HCABrowser Class

Arguments

`url`	character(1) the url of the Human Cell Atlas resource.
`fields_path`	character(1) path to the fields json file.
`per_page`	numeric(1) numbers of pages to view at a time.

Author(s)

Daniel Van Twisk

`nextResults` *Next Results*

Description

Fetch the next set of bundles from a Human Cell Atlas Object

Usage

```
## S4 method for signature 'HCABrowser'
nextResults(result)
```

Arguments

`result`	A HCABrowser object that has further bundles to display.

Value

A Human Cell Atlas object that displays the next results

Author(s)

Daniel Van Twisk

Examples

```
hca <- HCABrowser()
hca <- nextResults(hca)
hca
```

`per_page` *Set per_page argument of an HCABrowser object*

Description

note that no more than 10 pages can be displayed at once

Usage

```
## S4 method for signature 'HCABrowser'
per_page(hca, n)
```

Arguments

`hca`	a HCABrowser object
`n`	the new per_page value

Value

a HCABrowser with updated per_page value

Examples

```
hca <- HCABrowser()
#hca <- per_page(hca, 5)
hca
```

`pullBundles` *Obtain bundle fqids from a HCABrowser object*

Description

Obtain bundle fqids from a HCABrowser object

Usage

```
## S4 method for signature 'HCABrowser'
pullBundles(hca, n = hca@per_page)
```

Arguments

`hca`	A HCABrowser object
`n`	integer(1) number of bundle fqids to pull

Value

character(1) of bundle fqids

Examples

```
hca <- HCABrowser()
hca <- hca %>% pullBundles
```

`pullFiles` *Obtain file uuids from a HCABrowser object*

Description

Obtain file uuids from a HCABrowser object

Usage

```
## S4 method for signature 'HCABrowser'
pullFiles(hca, n = 10)
```

Arguments

`hca`	A HCABrowser object
`n`	integer(1) number of files to pull

Value

character(1) of

Examples

```
hca <- HCABrowser()
#hca <- hca %>% pullFiles
hca
```

`resetEsQuery` *Reset the query of a HCABrowser object to the default query*

Description

Reset the query of a HCABrowser object to the default query

Usage

```
## S4 method for signature 'HCABrowser'
resetEsQuery(hca)
```

Arguments

`hca`	A HCABrowser object

Value

A HCABrowser object with the search reset

Examples

```
hca <- HCABrowser()
hca <- hca %>% filter(organ.text == brain)
hca <- hca %>% filter(organ.text != brain)
hca <- hca %>% resetEsQuery
hca
```

`results` *Obtain search results from a HCABrowser Object*

Description

Returns a tibble either showing bundles or files based on whichever is activated.

Usage

```
## S4 method for signature 'HCABrowser'
results(object, n = object@per_page,
  all = FALSE, .output_format = c("raw", "summary"))
```

Arguments

`object`	A Human Cell Atlas object.
`n`	numeric(1) number of elements to return.
`all`	logical(1) whether to return all elements.
`.output_format`	unused.

Value

a tibble

`results,SearchResult-method` *Get results of SearchResult object*

Description

Get results of SearchResult object

Usage

```
## S4 method for signature 'SearchResult'
results(object)
```

Arguments

`object`	A Searchresult to obtain the result slot value from

Value

tibble of the results of the HCABrowser query

`select.HCABrowser` *Select fields from a HCABrowser object*

Description

Select fields from a HCABrowser object

Usage

```
## S3 method for class 'HCABrowser'
select(.data, ..., .output_format = c("raw",
  "summary"))
```

Arguments

`.data`	an HCABrowser object to perform a selection on
`...`	further argument to be tranlated into an expression to select from. These arguments can be passed in two ways, either as a character vector or as a series of expressions that are the fields that are to be selected seperated by commas.
`.output_format`	unused.

Value

a HCABrowser object containing the results of the selection.

Examples

```
hca <- HCABrowser()
hca2 <- hca %>% select('paired_end')
hca2

hca3 <- hca %>% select(c('organ.text', 'paired_end'))
hca3
```

`show,HCABrowser-method` *Show HCABrowser object*

Description

Show HCABrowser object

Usage

```
## S4 method for signature 'HCABrowser'
show(object)
```

Arguments

`object`	An HCAbrowser object to show

Value

outputs a text represntation of the object

`show,SearchResult-method` *Show Search Result*

Description

Show Search Result

Usage

```
## S4 method for signature 'SearchResult'
show(object)
```

Arguments

`object`	a SearchResult object to show

Value

outputs a text represntation of the object

`showBundles` *Obtain all bundles from an hca object using there bundle fqids*

Description

Obtain all bundles from an hca object using there bundle fqids

Usage

```
## S4 method for signature 'HCABrowser'
showBundles(hca, bundle_fqids)
```

Arguments

`hca`	a HCABrowser object to search for bundles on.
`bundle_fqids`	a character()

Value

A HCABrowser object displaying the selected bundles

Examples

```
hca <- HCABrowser()
hca_bundles <- hca %>% pullBundles
hca2 <- hca %>% showBundles(hca_bundles)
hca2
```

`undoEsQuery` *Undo previous filter queries on a HCABrowser object*

Description

Undo previous filter queries on a HCABrowser object

Usage

```
## S4 method for signature 'HCABrowser'
undoEsQuery(hca, n = 1L)
```

Arguments

`hca`	A HCABrowser object
`n`	integer(1) the number of filter queries to undo

Value

A HCABrowser object with n fewer queries

Examples

```
hca <- HCABrowser()
hca <- hca %>% filter(organ.text == brain)
hca <- hca %>% filter(organ.text == heart)
hca <- hca %>% filter(organ.text != brain)
#hca <- hca %>% undoEsquery(n = 2)
hca
```

`values,HCABrowser-method` *List all values for certain fields*

Description

List all values for certain fields

Usage

```
## S4 method for signature 'HCABrowser'
values(x, fields = c(), ...)
```

Arguments

`x`	An HCABrowser Object.
`fields`	a character vector of fields to display avaiable values for.
`...`	Other arguments.

Value

a list of possible values for a filter

Examples

```
hca <- HCABrowser()
vals <- hca %>% values
vals
vals2 <- hca %>% values('organ.text')
vals2
```

Index