

# Package ‘HCABrowser’

October 16, 2019

**Type** Package

**Title** Browse the Human Cell Atlas data portal

**Version** 1.0.1

**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, googleAuthR, httr, jsonlite, methods, plyr, readr, rlang, stringr, tibble, tidygraph, tidyr, utils

**Suggests** BiocStyle, knitr, rmarkdown, testthat

**Collate** AllClasses.R AllGenerics.R authorization.R filter-utilities.R hca-api.R iteration-utilities.R data.R

**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\_9

**git\_last\_commit** a6684b6

**git\_last\_commit\_date** 2019-08-23

**Date/Publication** 2019-10-15

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

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

**R topics documented:**

activate	2
fields	3
filter.HCABrowser	3
hca-api-methods	4
HCABrowser	8
HCABrowser-class	9
nextResults	9
per_page	10
ProjectBrowser	10
ProjectBrowser-class	11
pullBundles	11
pullFiles	12
resetEsQuery	12
results	13
results,SearchResult-method	13
select.HCABrowser	14
show,HCABrowser-method	14
show,SearchResult-method	15
showBundles	15
undoEsQuery	16
values,HCABrowser-method	16
<b>Index</b>	<b>18</b>

---

activate	<i>Activate files or bundles of HCABrowser Object</i>
----------	---

---

**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". Determines whether bundles or files should be shown.

**Value**

An HCABrowser with the selected activation

---

fields	<i>List supported fields of an HCABrowser object</i>
--------	--

---

**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()
hca %>% fields
```

---

filter.HCABrowser	<i>Filter HCABrowser objects</i>
-------------------	----------------------------------

---

**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 translated 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 separated 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

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

search_after	character(1). <b>**Search-After-Context**</b> . 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_json.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 attempts 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 <a href="https://tools.ietf.org/html/draft-cavage-http-signatures">https://tools.ietf.org/html/draft-cavage-http-signatures</a> 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 property 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	<i>The HCABrowser Class</i>
------------------	-----------------------------

---

**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	<i>Next Results</i>
-------------	---------------------

---

**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	<i>Set per_page argument of HCABrowser object</i>
----------	---

---

**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
```

---

ProjectBrowser	<i>The Project Browser Class</i>
----------------	----------------------------------

---

**Description**

A still tentative class that displays Human Cell Atlas information by projects.

**Usage**

```
ProjectBrowser(url = "https://dss.data.humancellatlas.org/v1")
```

**Arguments**

url	character(1) The url of the Human Cell Atlas.
-----	---

**Value**

a ProjectBrowser object

**Author(s)**

Daniel Van Twisk

**Examples**

```
pb <- ProjectBrowser()
pb
```

---

ProjectBrowser-class    *The Project Browser Class*

---

**Description**

A still tentative class that displays Human Cell Atlas information by projects.

**Arguments**

url                    character(1) The url of the Human Cell Atlas.

**Author(s)**

Daniel Van Twisk

---

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	<i>Obtain file uuids from a HCABrowser object</i>
-----------	---

---

**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	<i>Reset the query of a HCABrowser object to the default query</i>
--------------	--

---

**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 translated 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 separated 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 representation 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 representation 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 available 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

- [.HCABrowser \(HCABrowser-class\), 9](#)
- [.ProjectBrowser \(ProjectBrowser-class\), 11](#)
- [activate, 2](#)
- [activate, HCABrowser-method \(activate\), 2](#)
  
- [deleteBundle \(hca-api-methods\), 4](#)
- [deleteBundle, HCABrowser-method \(hca-api-methods\), 4](#)
- [deleteCollection \(hca-api-methods\), 4](#)
- [deleteCollection, HCABrowser-method \(hca-api-methods\), 4](#)
- [deleteSubscription \(hca-api-methods\), 4](#)
- [deleteSubscription, HCABrowser-method \(hca-api-methods\), 4](#)
  
- [fields, 3](#)
- [fields, HCABrowser-method \(fields\), 3](#)
- [filter.HCABrowser, 3](#)
  
- [getBundle \(hca-api-methods\), 4](#)
- [getBundle, HCABrowser-method \(hca-api-methods\), 4](#)
- [getBundlesCheckout \(hca-api-methods\), 4](#)
- [getBundlesCheckout, HCABrowser-method \(hca-api-methods\), 4](#)
- [getCollection \(hca-api-methods\), 4](#)
- [getCollection, HCABrowser-method \(hca-api-methods\), 4](#)
- [getFile \(hca-api-methods\), 4](#)
- [getFile, HCABrowser-method \(hca-api-methods\), 4](#)
- [getSubscription \(hca-api-methods\), 4](#)
- [getSubscription, HCABrowser-method \(hca-api-methods\), 4](#)
- [getSubscriptions \(hca-api-methods\), 4](#)
- [getSubscriptions, HCABrowser-method \(hca-api-methods\), 4](#)
  
- [hca-api-methods, 4](#)
- [HCABrowser, 8](#)
- [HCABrowser-class, 9](#)
- [headFile \(hca-api-methods\), 4](#)
  
- [headFile, HCABrowser-method \(hca-api-methods\), 4](#)
  
- [nextResults, 9](#)
- [nextResults, HCABrowser-method \(nextResults\), 9](#)
  
- [patchCollection \(hca-api-methods\), 4](#)
- [patchCollection, HCABrowser-method \(hca-api-methods\), 4](#)
- [per\\_page, 10](#)
- [per\\_page, HCABrowser-method \(per\\_page\), 10](#)
- [postBundlesCheckout \(hca-api-methods\), 4](#)
- [postBundlesCheckout, HCABrowser-method \(hca-api-methods\), 4](#)
- [postSearch \(hca-api-methods\), 4](#)
- [postSearch, HCABrowser-method \(hca-api-methods\), 4](#)
- [ProjectBrowser, 10](#)
- [ProjectBrowser-class, 11](#)
- [pullBundles, 11](#)
- [pullBundles, HCABrowser-method \(pullBundles\), 11](#)
- [pullFiles, 12](#)
- [pullFiles, HCABrowser-method \(pullFiles\), 12](#)
- [putBundle \(hca-api-methods\), 4](#)
- [putBundle, HCABrowser-method \(hca-api-methods\), 4](#)
- [putCollection \(hca-api-methods\), 4](#)
- [putCollection, HCABrowser-method \(hca-api-methods\), 4](#)
- [putFile \(hca-api-methods\), 4](#)
- [putFile, HCABrowser-method \(hca-api-methods\), 4](#)
- [putSubscription \(hca-api-methods\), 4](#)
- [putSubscription, HCABrowser-method \(hca-api-methods\), 4](#)
  
- [resetEsQuery, 12](#)
- [resetEsQuery, HCABrowser-method \(resetEsQuery\), 12](#)
- [results, 13](#)

results,HCABrowser-method (results), [13](#)  
results,SearchResult-method, [13](#)

select.HCABrowser, [14](#)

show,HCABrowser-method, [14](#)

show,SearchResult-method, [15](#)

showBundles, [15](#)

showBundles,HCABrowser-method  
(showBundles), [15](#)

undoEsQuery, [16](#)

undoEsQuery,HCABrowser-method  
(undoEsQuery), [16](#)

values,HCABrowser-method, [16](#)