

Package ‘HCABrowser’

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Type Package

Title Browse the Human Cell Atlas data portal

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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.

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filter.HCABrowser *Filter HCABrowser objects*

Description

Filter HCABrowser objects

Usage

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

Arguments

<code>.data</code>	an HCABrowser object to perform a query on.
<code>...</code>	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.
<code>.preserve</code>	unused.

Value

a HCABrowser object containing the resulting query.

Examples

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

 getEsQuery,HCABrowser-method

Get Elastic Search query as JSON

Description

Get Elastic Search query as JSON

Usage

```
## S4 method for signature 'HCABrowser'
getEsQuery(x)
```

Arguments

x An HCABrowser object

Value

A json object of the elastic search query in the HCABrowser object

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.

Usage

```
listBundles(x, ...)
getBundleCheckout(x, ...)
getBundle(x, ...)
checkoutBundle(x, ...)
getFile(x, ...)
headFile(x, ...)
searchBundles(x, ...)
```

```
## S4 method for signature 'HCABrowser'
listBundles(x, replica = c("aws", "gcp"), token, per_page = 100, search_after)
```

```
## S4 method for signature 'HCABrowser'
getBundleCheckout(x, replica = c("aws", "gcp"), checkout_job_id)
```

```
## S4 method for signature 'HCABrowser'
getBundle(
  x,
  uuid,
```

```

    version,
    replica = c("aws", "gcp"),
    directurls,
    presignedurls,
    token,
    per_page = 500
)

## S4 method for signature 'HCABrowser'
checkoutBundle(x, uuid, version, replica = c("aws", "gcp"), json_request_body)

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

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

## S4 method for signature 'HCABrowser'
searchBundles(
  x,
  json_request_body = getEsQuery(x),
  output_format = c("summary", "raw"),
  replica = c("aws", "gcp"),
  per_page = 100,
  search_after
)

```

Arguments

<code>x</code>	An HCABrowser object that is the subject of the request.
<code>replica</code>	character(1). A replica to fetch from. Can either be set to "aws", "gcp", or "azure". DEFAULT is "aws".
<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>per_page</code>	numeric(1). Max number of results to return per page.
<code>search_after</code>	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.
<code>checkout_job_id</code>	character(1). A RFC4122-compliant ID for the checkout job request.
<code>uuid</code>	character(1). A RFC4122-compliant ID for the bundle.
<code>version</code>	character(1). Timestamp of bundle creation in RFC3339.
<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>json_request_body</code>	character(1) of a json query to be executed.
<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.

... Additional arguments.

Value

an HCABrowser object

Author(s)

Daniel Van Twisk

Examples

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

HCABrowser

The HCABrowser Class

Description

The HCABrowser Class

Usage

```
HCABrowser(
  host = "dss.data.humancellatlas.org",
  api_url = "https://dss.data.humancellatlas.org/v1/swagger.json",
  per_page = 10
)
```

Arguments

host	character(1) path to hca-dcp server
api_url	character(1) path to hca-dcp api 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

per_page numeric(1) numbers of pages to view at a time.
host character(1) path to hca-dcp server
api_url character(1) path to schema

Value

An HCABrowser object.

Author(s)

Daniel Van Twisk

Examples

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

parseToSearchResults *Parse results from a search query to a Search Results object*

Description

Parse results from a search query to a Search Results object

Usage

```
parseToSearchResults(res)
```

Arguments

res the results from an HCA query.

Value

a SearchResults object.

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

Description

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

Usage

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

Arguments

x	an HCABrowser object
n	the new per_page value

Value

a HCABrowser with updated per_page value

Examples

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

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(x)
```

Arguments

x	A HCABrowser object
---	---------------------

Value

A HCABrowser object with the search reset

Examples

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

 results

Get results of SearchResult object

Description

Get results of SearchResult object

Usage

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

Arguments

x A Searchresult to obtain the result slot value from

Value

list of the results of the HCABrowser query

Examples

```
sr <- new("SearchResult")
results(sr)
```

 SearchResult

The SearchResults Class

Description

A glass generated after parsing a search query with the method `parseToSearchResults`. Contains a list of all information gleaned from the search query.

Usage

```
SearchResult(es_query, results, first_hit, last_hit, total_hits)
```

Arguments

es_query A quosure of the current es_query.
 results A list of all result from the query.
 first_hit numeric(1) the first bundle currently shown.
 last_hit numeric(1) the last bundle currently shown.
 total_hits numeric(1) the number of bundles that can be shown.

Value

A Search Result object

Examples

```
sr <- new("SearchResult")
sr
```

select.HCABrowser	<i>Select fields from a HCABrowser object</i>
-------------------	---

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

Examples

```
sr <- new('SearchResult')  
sr
```

`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(x, n = 1L)
```

Arguments

<code>x</code>	A HCABrowser object
<code>n</code>	integer(1) the number of filter queries to undo

Value

A HCABrowser object with n fewer queries

Examples

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

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