

Package: hypothesisr (via r-universe)

November 3, 2024

Type Package

Title Wrapper for the 'Hypothes.is' Web Annotation Service

Version 0.1.1.9000

Description Interact with the application programming interface for the web annotation service 'Hypothes.is' (See <http://hypothes.is> for more information.) Allows users to download data about public annotations, and create, retrieve, update, and delete their own annotations.

Imports dplyr, httr, jsonlite

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LazyData TRUE

RoxygenNote 5.0.1

Suggests testthat

URL <https://github.com/mdlincoln/hypothesisr>

BugReports <https://github.com/mdlincoln/hypothesisr/issues>

Repository <https://mdlincoln.r-universe.dev>

RemoteUrl <https://github.com/mdlincoln/hypothesisr>

RemoteRef HEAD

RemoteSha 7d7a22aeb9fee42fc0499f961638bcd9d554e838

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hs_create	<i>Create annotations</i>
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Description

Create annotations

Usage

```
hs_create(token, uri, user, permissions = list(read = "group:__world__",
  update = user, delete = user, admin = user), document = NULL,
  target = NULL, tags = NULL, text, custom = NULL)
```

Arguments

token	Character. Your account token, which you can generate at https://hypothes.is/register
uri	Character. The URI to be annotated.
user	Character. Your user account, normally in the format <code>acct:username@hypothes.is</code>
permissions	A named list with read, update, delete, and admin permissions. Defaults to setting global read permissions (<code>group:__world__</code>) and setting the user string for update, delete, and admin permissions.
document	A list describing the document. CURRENTLY IGNORED.
target	A list describing the highlight position of the annotation. CURRENTLY IGNORED
tags	Character. (optional) Tags to apply to the annotation.
text	Character. Text to put in the body of the annotation. This will be coerced into a character vector of length 1 using paste .
custom	Add arbitrary fields to the JSON object submitted to <code>hypothes.is</code> by means of a named list.

Value

Upon successful creation, returns a 22-character annotation ID. This ID may be retrieved using [hs_read](#).

Source

<https://h.readthedocs.io/en/latest/api/#create>

Examples

```
## Not run:
hs_create(token = user_token,
  uri = "https://github.com/mdlincoln/hypothesisr",
  user = "acct:mdlincoln@hypothes.is", tags = c("testing", "R"),
  text = "R made me!")

## End(Not run)
```

hs_delete	<i>Delete an annotation</i>
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Description

Delete an annotation

Usage

```
hs_delete(token, id)
```

Arguments

token	Character. Your account token, which you can generate at https://hypothes.is/register
id	Character. A hypothes.is annotation id.

Value

TRUE on successful deletion.

Source

<https://h.readthedocs.io/en/latest/api/#delete>

hs_read	<i>Retrieve a single annotation by ID</i>
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Description

Retrieve a single annotation by ID

Usage

```
hs_read(id)
```

Arguments

id Character. A hypotheses.is annotation id.

Value

A dataframe with the contents of that annotation.

Source

<https://h.readthedocs.io/en/latest/api/#read>

Examples

```
hs_read("WFMnSC3FEeaNvLeGkQeJbg")
```

<code>hs_reply</code>	<i>Create a reply to a comment</i>
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Description

This is a utility wrapper around [hs_create](#) that takes an original comment ID and creates a reply to it by adding the custom references field when constructing the annotation. Normal fields like

Usage

```
hs_reply(token, user, id, text, ...)
```

Arguments

token	Character. Your account token, which you can generate at https://hypothes.is/register
user	Character. Your user account, normally in the format <code>acct:username@hypothes.is</code>
id	Character. The annotation ID to reply to.
text	Character. Text to put in the body of the annotation. This will be coerced into a character vector of length 1 using paste .
...	Other arguments to pass to hs_create .

hs_search	<i>Search hypotheses annotations</i>
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Description

Search hypotheses annotations.

Usage

```
hs_search(limit = NULL, offset = NULL, sort = "updated", order = "asc",
          uri = NULL, user = NULL, text = NULL, any = NULL, custom = list())
```

Arguments

limit	Integer. The maximum number of annotations to return. (Default: 20)
offset	Integer. The minimum number of initial annotations to skip. This is used for pagination. For example if there are 65 annotations matching our search query and we're retrieving up to 30 annotations at a time, then to retrieve the last 5, set offset = 5. (Default = 0)
sort	Character. Specify which field the annotations should be sorted by: consumer, created, id, text, updated, uri, user.
order	Character. Specify which order annotations should be sorted by: asc or desc.
uri	Character. Search for annotations of a particular URI, for example <code>www.example.com</code> . URI searches will also find annotations of equivalent URIs. For example if the HTML document at <code>http://www.example.com/document.html?</code> includes a <code><link rel="canonical" href="http://www.example.com/canonical_document.html"></code> then annotations of <code>http://www.example.com/canonical_document.html</code> will also be included in the search results. Other forms of document equivalence that are supported include <code>rel="alternate"</code> links, DOIs, PDF file IDs, and more.
user	Character. Search for annotations by a particular user. For example, <code>tim</code> will find all annotations by users named <code>tim</code> at any provider, while <code>tim@hypothes.is</code> will only find annotations by <code>tim</code> on <code>hypothes.is</code>
text	Character. Search for annotations whose body text contains some text, for example: <code>foobar</code> .
any	Character. Search for annotations whose <code>quote</code> , <code>tags</code> , <code>text</code> , <code>uri.parts</code> or <code>user</code> fields match some query text.
custom	A named list of any field in the results returned by <code>hypothes.is</code> as a name, and the search text as values.

Value

A dataframe with annotation data.

Note

If any vectors are passed to these arguments, only the first values will be used.

Source

<https://h.readthedocs.io/en/latest/api/#search>

Examples

```
# Search for no more than 5 annotations containing the text "ulysses"
hs_search(text = "ulysses", limit = 5)
# Search with a custom field for tags
hs_search(custom = list(tags = "todo"))
# use the 'uri.parts' field to find annotations on a given domain (exclude
# the TLD, as this will result in all annotations on sites with, e.g., .org,
# as well.)
hs_search(custom = list(uri.parts = "programminghistorian"))
```

hs_search_all

Retrieve all annotation search results as a data frame

Description

Takes the same arguments as [hs_search](#) and pages through all available results, formatting the output as a data.frame.

Usage

```
hs_search_all(sort = "updated", order = "asc", uri = NULL, user = NULL,
              text = NULL, any = NULL, custom = list(), pagesize = 200,
              progress = interactive())
```

Arguments

sort	Character. Specify which field the annotations should be sorted by: consumer, created, id, text, updated, uri, user.
order	Character. Specify which order annotations should be sorted by: asc or desc.
uri	Character. Search for annotations of a particular URI, for example <code>www.example.com</code> . URI searches will also find annotations of equivalent URIs. For example if the HTML document at <code>http://www.example.com/document.html?</code> includes a <code><link rel="canonical" href="http://www.example.com/canonical_document.html"></code> then annotations of <code>http://www.example.com/canonical_document.html</code> will also be included in the search results. Other forms of document equivalence that are supported include <code>rel="alternate"</code> links, DOIs, PDF file IDs, and more.
user	Character. Search for annotations by a particular user. For example, <code>tim</code> will find all annotations by users named <code>tim</code> at any provider, while <code>tim@hypothes.is</code> will only find annotations by <code>tim</code> on <code>hypothes.is</code>
text	Character. Search for annotations whose body text contains some text, for example: <code>foobar</code> .

any	Character. Search for annotations whose quote, tags, text, uri.parts or user fields match some query text.
custom	A named list of any field in the results returned by hypothes.is as a name, and the search text as values.
pagesize	Integer. How many annotations to retrieve per query. Between 1 and 200. (Default: 200)
progress	Boolean. Should a progress bar be displayed during download?

Value

A dataframe with annotation data.

Examples

```
## Not run:
hs_search_all(text = "arxiv")

## End(Not run)
```

hs_update	<i>Update annotations</i>
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Description

Update annotations

Usage

```
hs_update(token, id, uri = NULL, user = NULL, permissions = NULL,
  document = NULL, target = NULL, tags = NULL, text = NULL,
  custom = NULL)
```

Arguments

token	Character. Your account token, which you can generate at https://hypothes.is/register .
id	Character. A hypothes.is annotation id.
uri	Character. The URI to be annotated.
user	Character. Your user account, normally in the format acct:username@hypothes.is
permissions	A named list with read, update, delete, and admin permissions. Defaults to setting global read permissions (group: __world__) and setting the user string for update, delete, and admin permissions.
document	A list describing the document. CURRENTLY IGNORED.
target	A list describing the highlight position of the annotation. CURRENTLY IGNORED

tags	Character. (optional) Tags to apply to the annotation.
text	Character. Text to put in the body of the annotation. This will be coerced into a character vector of length 1 using paste .
custom	Add arbitrary fields to the JSON object submitted to hypothes.is by means of a named list.

Value

TRUE on successful update.

Source

<https://h.readthedocs.io/en/latest/api/#update>

Examples

```
## Not run:
hs_update(user_token, "1Df9rC3EEea6ck-G5kLdXA", text = "Now even more annotate-y!")
## End(Not run)
```

hypothesisr *hypothesisr: Wrapper for the Hypothes.is API*

Description

Interact with the API for the web annotation service hypothes.is. Allows users to add, search for, and retrieve annotation data.

open_ *Functions for opening an annotation in the system browser*

Description

Functions for opening an annotation in the system browser

Usage

```
open_context(id)
```

```
open_annotation(id)
```

```
open_uri(id)
```


Arguments

id Annotation ID.

Functions

- `open_context`: Open an annotation in context, displaying the original webpage with an annotation overlay
- `open_annotation`: Open an annotation on the `hypothes.is` webpage
- `open_uri`: Open the original webpage to which the annotation links

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