Package ‘sbtools’

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<https://www.sciencebase.gov> interfaces. ScienceBase is a data cataloging and
 collaborative data management platform. Functions included for querying
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Description

This package provides a rich interface to USGS’s ScienceBase [https://www.sciencebase.gov/](https://www.sciencebase.gov/) - a data cataloging and collaborative data management platform. For further information, see the sbtools manuscript [here](#).

Functions are included for searching for data, retrieving, creating, and updating datasets.

Details

Functionality in this package allows all users to query ScienceBase for data using a variety of metadata types (query_sb_text, query_sb_doi, query_sb_spatial). Items and associated information can be requested by item_get including item parents item_get_parent and children item_list_children. Data and attached files can be accessed for all available items through provided functionality (e.g., item_get_wfs and item_file_download).

Authentication

See the function authenticate_sb to authenticate. You’ll be required to pass in your ScienceBase username and password.

Authenticated users can create, update, and remove items (item_list_children, item_list_children, item_create, item_update, item_rm).

Feedback

Report any feedback or bugs at [https://github.com/USGS-R/sbtools/issues](https://github.com/USGS-R/sbtools/issues)

```r
authenticate_sb
```

Authenticate to SB for subsequent calls

Description

This connects to SB, authenticates and gets a session token for communicating with SB. If you do not supply a username or password, you will be prompted to enter them.

Usage

authenticate_sb(username, password)

Arguments

- `username` Sciencebase username
- `password` Sciencebase password, prompts user if not supplied
current_session  Return current cached session

Description
Returns the currently cached SB session. If there is no authenticated session, returns NULL. Emits a warning if the session has expired.

Usage
current_session()

Examples
```
session = current_session()
#null unless currently authenticated
session
```

folder_create  Create a folder

Description
Create a special kind of item on ScienceBase that is intended to be a "folder" that contains one or more child items. This is similar to a standard item (item_create) but defaults to showing child-items on the ScienceBase web interface.

Usage
folder_create(parent_id = user_id(), name, ..., session = current_session())

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>parent_id</td>
<td>An sbitem object or character ScienceBase ID corresponding to the parent item (folder)</td>
</tr>
<tr>
<td>name</td>
<td>(character) the folder name</td>
</tr>
<tr>
<td>...</td>
<td>Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE</td>
</tr>
<tr>
<td>session</td>
<td>Session object from authenticate_sb. Defaults to anonymous or last authenticated session</td>
</tr>
</tbody>
</table>

Value
A response object
**identifier_exists**

### Examples

```r
## Not run:
folder_create(name="foobar345")
## End(Not run)
```

---

**identifier_exists**  
*Check if identifier exists*

### Description

This function quickly checks to see if an identifier exists. It does a quick head request to skip the overhead of item metadata retrieval. This will also return FALSE if the identifier exists but is associated with an item that is unavailable due to permission restrictions.

### Usage

```r
identifier_exists(sb_id, ..., session = current_session())
```

### Arguments

- `sb_id`  
  An `sbitem` object or a character ScienceBase ID corresponding to the item
- `...`  
  Additional parameters are passed on to **GET**, **POST**, **HEAD**, **PUT**, or **DELETE**
- `session`  
  Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

### Value

Logical, TRUE or FALSE

### Examples

```r
# identifier exists  
identifier_exists(sb_id = "4f4e4b24e4b07f02db6aea14")

# identifier does not exist  
identifier_exists(sb_id = "aaaaaakkkkkbbbbb")
```
is_logged_in  
Check whether you’re logged into a ScienceBase session

Description

Check whether you’re logged into a ScienceBase session

Usage

is_logged_in(..., session = current_session())

Arguments

... Additional parameters are passed on to GET
session SB session object from authenticate_sb

Value

Logical, TRUE or FALSE

Examples

## Not run:
is_logged_in()

## End(Not run)

items_create  
Create many new SB items

Description

A method to create multiple ScienceBase items with a single call and a single HTTP service request. Can be useful for improving performance of creating a large number of items at once.

Usage

items_create(  
  parent_id = user_id(),
  title,
  ...,
  info = NULL,
  session = current_session()
)
items_create

Arguments

- **parent_id**: An `sbitem` object or character ScienceBase ID corresponding to the parent item (folder). This must be of length 1 or more. If length 1, then we recycle it for every item.
- **title**: Two or more titles for the new SB items
- **info** *(optional)*: list of metadata info for the new items. for each item include a named list of variables

Details

The length of the `title` and `info` values must be the same length - however, the `parent_id` can be of length 1 or equal to the length of each of `title` and `info` parameters

Value

One or more objects of class `sbitem` in a list

Examples

```r
## Not run:
# helper function to make a random name
aname <- function() paste0(sample(letters, size = 5, replace = TRUE), collapse = "")

# Create some items - by default we use your user ID
items_create(title = c(aname(), aname()))

# add additional items in the info parameter - by default we use your user ID
items_create(title = c(aname(), aname()),
info = list(
  list(contacts = list(list(name = "Suzy"))),
  list(contacts = list(list(name = "Brandy")))
))

# another example with more information - by default we use your user ID
items_create(title = c(aname(), aname()),
info = list(
  list(contacts = list(list(name = "Suzy"))),
  list(contacts = list(list(name = "Brandy")))
))

# Pass an object of class sbitem
(x <- folder_create(user_id(), aname()))
items_create(x, title = c(aname(), aname()))

## End(Not run)
```
items_update

Update many SB items with new metadata

Description

A method to update multiple ScienceBase items with a single call and a single HTTP service request. Can be useful for improving performance of updating a large number of items at once.

Usage

\[
\text{items_update}(\text{sb\_id}, \text{info}, ..., \text{session} = \text{current\_session()} )
\]

Arguments

- `sb\_id`: An `sbitem` object or a character ScienceBase ID corresponding to the item
- `info`: list of metadata info (key-value pairs) to change on the item
- `...`: Additional parameters are passed on to `PUT`
- `session`: Session object from `authenticate\_sb`. Defaults to anonymous or last authenticated session

Details

If length of `sb\_id` > 1, then length of `info` input must be the same

Value

One or more objects of class `sbitem` in a list

Examples

```r
# Not run:
# helper function to make a random name
aname <- function() paste0(sample(letters, size = 5, replace = TRUE), collapse = "")

res <- items_create(user\_id(), title = c(aname(), aname()))
out <- items_update(res, info = list( list(title = aname()), list(title = aname()) ) )
vapply(out, "[[", "", "title")

# End(Not run)
```
items_upsert

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Either creates or updates (if items already exist)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Usage</th>
</tr>
</thead>
<tbody>
<tr>
<td>items_upsert(</td>
</tr>
<tr>
<td>parent_id = user_id(),</td>
</tr>
<tr>
<td>title = NULL,</td>
</tr>
<tr>
<td>...,</td>
</tr>
<tr>
<td>info = NULL,</td>
</tr>
<tr>
<td>session = current_session()</td>
</tr>
<tr>
<td>)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Arguments</th>
</tr>
</thead>
<tbody>
<tr>
<td>parent_id</td>
</tr>
<tr>
<td>title</td>
</tr>
<tr>
<td>...</td>
</tr>
<tr>
<td>info</td>
</tr>
<tr>
<td>session</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>An object of class sbitem</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Examples</th>
</tr>
</thead>
<tbody>
<tr>
<td>## Not run:</td>
</tr>
<tr>
<td># helper function to make a random name</td>
</tr>
<tr>
<td>aname &lt;- function() paste0(sample(letters, size = 5, replace = TRUE), collapse = &quot;&quot;)</td>
</tr>
<tr>
<td># Create some item - by default we use your user ID</td>
</tr>
<tr>
<td>z1 &lt;- item_create(title = aname())</td>
</tr>
<tr>
<td>z2 &lt;- item_create(title = aname())</td>
</tr>
<tr>
<td># Upsert items</td>
</tr>
<tr>
<td>(x &lt;- items_upsert(list(z1, z2), title = c(aname(), aname())))</td>
</tr>
<tr>
<td># Call item_upsert again, updates this time</td>
</tr>
<tr>
<td>items_upsert(x, info = list(</td>
</tr>
<tr>
<td>contacts = list(list(name = &quot;Suzy&quot;))</td>
</tr>
<tr>
<td>)</td>
</tr>
</tbody>
</table>
## item_append_files

### Description

Adds a file to an item

### Usage

```
item_append_files(sb_id, files, ..., session = current_session())
```

### Arguments

- `sb_id` An `sbitem` object or a character ScienceBase ID corresponding to the item
- `files` A file path to upload.
- `...` Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- `session` Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

### Value

An object of class `sbitem`

### Examples

```r
## Not run:
res <- item_create(user_id(), "testing 123")
cat("foo bar", file = "foobar.txt")
item_append_files(res$id, "foobar.txt")
## End(Not run)
```
item_create

Create a new SB item

Description

Create a new item on ScienceBase with the requested parent and item title. Info can be provided to populate metadata at the time of creation.

Usage

```r
item_create(
  parent_id = user_id(),
  title,
  ..., info,
  session = current_session()
)
```

Arguments

- `parent_id` An sbitem object or character ScienceBase ID corresponding to the parent item (folder)
- `title` The title of the new SB item
- `...` Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE
- `info` (optional) list of metadata info for the new item
- `session` Session object from authenticate_sb. Defaults to anonymous or last authenticated session

Value

An object of class sbitem

Examples

```r
## Not run:
# Create an item - by default we use your user ID
item_create(title = "testing 123")

# Pass an object of class sbitem
x <- folder_create(user_id(), "foobar456")
item_create(x, "foobar456-item")

## End(Not run)
```
item_exists

**Description**
returns TRUE if touple already belongs to a sciencebase item, FALSE if not

**Usage**

```r
item_exists(scheme, type, key, ..., session = current_session())
```

**Arguments**

- `scheme`: the identifier scheme
- `type`: the identifier type
- `key`: the identifier key
- `...`: Additional parameters are passed on to `GET`
- `session`: an SB session

**Value**

boolean for whether item exists

**Examples**

```r
## Not run:
item_exists('mda_streams','ts_doobs','nwis_01018035')
item_exists('mda_streams','site_root','nwis_01018035')
## End(Not run)

item_file_download

**Description**
Function to download files attached to an item on SB. Either files can be specified directly using the `names` and `destinations` parameters, or a `dest_dir` can be supplied where all attached files will be written with the names as stored on SB.
item_file_download

Usage

```r
item_file_download(
  sb_id,
  ..., 
  names, 
  destinations, 
  dest_dir, 
  session = current_session(), 
  overwrite_file = FALSE
)
```

Arguments

- **sb_id**: An `sbitem` object or a character ScienceBase ID corresponding to the item
- **...**: Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- **names**: String vector list of file names attached to item that you wish to download.
- **destinations**: String vector list of destinations for requested files. Must be same length as names
- **dest_dir**: A directory path for saving files when names parameter is omitted
- **session**: Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session
- **overwrite_file**: Boolean indicating if file should be overwritten if it already exists locally

Value

Character vector of full paths to local files

Author(s)

Luke Winslow

Examples

```r
## Not run:
#downloads two files attached to this item
item_file_download('548b2b31e4b03f6463662a4', dest_dir=tempdir())

#downloads a specific file attached to this item
item_file_download('548b2b31e4b03f6463662a4', names='gdp.txt',
  destinations=file.path(tempdir(), 'fname.txt'))

## End(Not run)
```
**item_get**

*Retrieve SB item*

**Description**

Retrieves an item and its metadata from ScienceBase based on its unique ID. Errors if the requested item ID does not exist or access is restricted due to permissions.

**Usage**

```r
item_get(sb_id, ..., session = current_session())
```

**Arguments**

- `sb_id` 
  An `sbitem` object or a character ScienceBase ID corresponding to the item
- `...` 
  Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- `session` 
  Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

**Value**

An object of class `sbitem`

**Examples**

```r
# Get an item
item_get("4f4e4b24e4b07f02db6aea14")

# Search for item IDs, then pass to item_get
library("httr")
res <- query_items(list(s = "Search", q = "water", format = "json"))
if(res$status != 404) {
  ids <- vapply(httr::content(res)$items, "{[", ", ", "id"")
  lapply(ids[1:3], item_get)
}
```
**item_get_fields**

*Retrieve specific fields from an SB item*

**Description**

Retrieve specific fields from an SB item

**Usage**

```r
item_get_fields(sb_id, fields, ..., drop = TRUE, session = current_session())
```

**Arguments**

- `sb_id` An `sbitem` object or a character ScienceBase ID corresponding to the item
- `fields` a vector of fields
- `...` Additional parameters are passed on to `GET, POST, HEAD, PUT, or DELETE`
- `drop` logical. If only one field is selected, should the list format be dropped?
- `session` Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

**Value**

List serialization of chosen metadata for an SB item

**Examples**

```r
# Get certain fields from an item
item_get_fields("4f4e4b24e4b07f02db6aea14", c('title', 'citation', 'contacts'))

# If only 1 field selection, do or don't drop list format
item_get_fields("4f4e4b24e4b07f02db6aea14", 'title')
item_get_fields("4f4e4b24e4b07f02db6aea14", 'title', drop = FALSE)
```

**item_get_parent**

*Get an item’s parent ID*

**Description**

Retrieves the parent of a supplied item based on the ScienceBase item tree hierarchy.

**Usage**

```r
item_get_parent(sb_id, ..., session = current_session())
```
item_get_wfs

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sb_id</td>
<td>An <code>sbitem</code> object or a character ScienceBase ID corresponding to the item</td>
</tr>
<tr>
<td>as_sf</td>
<td>boolean, return data in sf format</td>
</tr>
<tr>
<td>...</td>
<td>Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE</td>
</tr>
<tr>
<td>session</td>
<td>Session object from <code>authenticate_sb</code>. Defaults to anonymous or last authenticated session</td>
</tr>
</tbody>
</table>

Value

An item object representing the parent of the supplied item.

Examples

```
item_get_parent("4f4e4b24e4b07f02db6aea14")
item_get_parent(item_get("4f4e4b24e4b07f02db6aea14"))
```

Description

This function attempts to download the spatial layer data attached to the requested SB item. SB exposes discrete spatial objects (points, polygons) as web services based on the Open Geospatial Consortium, Web Feature Service (WFS) standardized interface. This requires the following libraries not by default installed with sbtools: sf, httr, and xml2. You can install them simply by running `install.packages(c("xml2","httr","sf"))`.

Usage

```
item_get_wfs(sb_id, as_sf = FALSE, ..., session)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sb_id</td>
<td>An <code>sbitem</code> object or a character ScienceBase ID corresponding to the item</td>
</tr>
<tr>
<td>as_sf</td>
<td>boolean, return data in sf format</td>
</tr>
<tr>
<td>...</td>
<td>Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE</td>
</tr>
<tr>
<td>session</td>
<td>Session object from <code>authenticate_sb</code>. Defaults to anonymous or last authenticated session</td>
</tr>
</tbody>
</table>
item_list_children

Return IDs for all child items

Description

Returns a list of child IDs for a ScienceBase item

Usage

item_list_children(
  sb_id,
  fields = c("id", "title"),
  ..., 
  session = current_session(),
  limit = 20
)

Arguments

sb_id An sbitem object or a character ScienceBase ID corresponding to the item
fields A character vector of requested data fields. Defaults to ‘id’ and ‘title’. Full list of possible fields is available online in SB documentation.
... Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE
session Session object from authenticate_sb. Defaults to anonymous or last authenticated session
limit Max children returned.

Value

List of sbitem for each child item.

Examples

## Not run:
item_list_children(user_id())

## End(Not run)

item_list_children(as.sbitem('5060b03ae4b00fc20c4f3c8b'))
item_list_children(item_get('5060b03ae4b00fc20c4f3c8b'))
item_list_files

Get list of files attached to SB item

Description

Lists all files attached to a SB item. Files can be downloaded from ScienceBase using item_file_download. (advanced) Recursive options lists all files attached to an item and all children items.

Usage

item_list_files(sb_id, recursive = FALSE, ..., session = current_session())

Arguments

- sb_id: An sbitem object or a character ScienceBase ID corresponding to the item
- recursive: (logical) List files recursively. Default: FALSE
- ...: Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE
- session: Session object from authenticate_sb. Defaults to anonymous or last authenticated session

Value

A data.frame with columns fname, size, and url. If item has no attached files, returns a zero row data.frame.

Examples

code

item_list_files("4f4e4b24e4b07f02db6aea14")

# Not run:
# list files recursively
# create item
id <- item_create(user_id(), title="some title")
# 1. create nested item w/ file
file <- system.file("examples", "books.json", package = "sbtools")
id2 <- item_create(id, title = "newest-thing")
item_upload_create(id2, file)
# 2. create nested item w/ file
file <- system.file("examples", "species.json", package = "sbtools")
id3 <- item_create(id, title = "a-new-thing")
item_upload_create(id3, file)
# 3. create nested item w/ file
file <- system.file("examples", "data.csv", package = "sbtools")
id4 <- item_create(id, title = "another-thing")
item_upload_create(id4, file)
item_list_files(id = '56562348e4b07e7ea53e09d', recursive = FALSE) # default
item_list_files(id = '56562348e4b07e7ea53e09d', recursive = TRUE)
## End(Not run)

---

**item_move**

*Move item from one folder to another*

### Description

Move item from one folder to another

### Usage

```r
item_move(sb_id, id_new, ..., session = current_session())
```

### Arguments

- **sb_id**: An `sbitem` object or a character ScienceBase ID corresponding to the item
- **id_new**: Folder/item to move id to. A ScienceBase ID or something that can be coerced to a SB item ID by `as.sbitem`
- **...**: Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- **session**: Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

### Value

An object of class `sbitem`. Same as `id`, but with new parent ID

### Examples

```r
## Not run:
# create 1st folder
(fold1 <- folder_create(user_id(), "bear123"))
(res <- item_create(fold1, "item-to-move"))

# create 2nd folder
(fold2 <- folder_create(user_id(), "bear456"))

# move item in 1st folder to 2nd folder
(res2 <- item_move(res, fold2))

# test identical
identical(res2$parentId, fold2$id)
## End(Not run)
```
### item_rename_files  
**Rename item attached files**

**Description**

Renames files attached to an SB item.

**Usage**

```r
item_rename_files(sb_id, names, new_names, ..., session = current_session())
```

**Arguments**

- **sb_id**: An `sbitem` object or a character ScienceBase ID corresponding to the item
- **names**: List of names of files to rename
- **new_names**: List of new file names to use
- **...**: Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- **session**: Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

**Examples**

```r
## Not run:

names = c("file1.txt", "file2.txt")
new_names = c("newname1.txt", "newname2.txt")

item_rename_files('sbid', names, new_names)

## End(Not run)
```

### item_replace_files  
**Replace files associated with an item**

**Description**

replaces existing files associated with an item with a new one. (Currently does not support multi-file uploads.) This function will not append an existing collection of files. If that is desired, use `item_append_files`.

**Usage**

```r
item_replace_files(sb_id, files, ..., all = FALSE, session = current_session())
```
 Remove item from SB

Description

Remove an item from ScienceBase. This is not reversible and will delete an item and its attached files. (advanced) Recursive is to be used with care and could result in unexpected file deletion.

Usage

```r
item_rm(
  sb_id,
  ...,  
  limit = 1000,  
  recursive = FALSE,  
  session = current_session()
)
```

Arguments

- **sb_id**: An `sbitem` object or a character ScienceBase ID corresponding to the item
- **files**: A character vector of file paths
- **...**: Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- **all**: A boolean indicating if all attached files should be removed before uploading new files. `FALSE` if only files with matching names should be replaced. If you wish to upload files with duplicate names, see `item_append_files`. Defaults to `FALSE`.
- **session**: Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

Value

- `httr` response object
item_rm_files

Remove files associated with an item

Description

Removes existing files associated with an item.

This function is the key way to remove files attached to SB items.

Usage

```r
item_rm_files(sb_id, files, ..., session = current_session())
```

Arguments

- `sb_id`: An `sbitem` object or a character ScienceBase ID corresponding to the item
- `files`: A character vector of file names to remove. If not supplied, defaults to removing all attached files.
- `...`: Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- `session`: Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

Value

An updated object of class `sbitem`

Examples

```r
## Not run:
res <- item_create(user_id(), "item456")
cat("foo bar", file = "foobar.txt")
item_append_files(res, "foobar.txt")
res <- item_get(res)
res$files[[1]]$name
res2 <- item_rm_files(res)
res2$files

## End(Not run)
```
item_update

Update a SB item with new metadata

Description

Updates metadata associated with a ScienceBase item based on supplied list of new or updated metadata elements.

Usage

item_update(sb_id, info, ..., session = current_session())

Arguments

- **sb_id**: An sbitem object or a character ScienceBase ID corresponding to the item
- **info**: list of metadata info (key-value pairs) to change on the item
- **...**: Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE
- **session**: Session object from authenticate_ssb. Defaults to anonymous or last authenticated session

Value

An object of class sbitem

Examples

```r
## Not run:
res <- item_create(user_id(), "item-to-update")
out <- item_update(res, list(title = "item-updated"))
out$title

## End(Not run)
```

item_update_identifier

Add custom identifier to an existing item

Description

Adds or updates an item’s alternative identifier. This can add additional identifiers or update those already in place. See query_item_identifier for finding items based on alternative identifier.
Usage

```r
item_update_identifier(
  sb_id,
  scheme,
  type,
  key,
  ..., 
  session = current_session()
)
```

Arguments

- `sb_id`: An `sbitem` object or a character ScienceBase ID corresponding to the item
- `scheme`: The identifier scheme
- `type`: The identifier type
- `key`: The identifier key
- `...`: Additional parameters are passed on to `GET`, `POST`, `HEAD`, `PUT`, or `DELETE`
- `session`: Session object from `authenticate_sb`. Defaults to anonymous or last authenticated session

Examples

```r
## Not run:
session = authenticate_sb("user@usgs.gov")
item_update_identifier("5485fd99e4b02acb4f0c7e81", "scheme", "type", "key", session=session)

## End(Not run)
```

---

**item_upload_create**

Upload file(s) and create a new item

Description

Create a new item with files attached, all in one call to SB

Usage

```r
item_upload_create(parent_id, files, ..., session = current_session())
```
item_upsert

Arguments

parent_id  An sbitem object or character ScienceBase ID corresponding to the parent item (folder)
files  A string vector of paths to files to be uploaded
...  Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE
session  Session object from authenticate_sb. Defaults to anonymous or last authenticated session

Value

An object of class sbitem

Examples

```r
## Not run:
# You'll need a parent id for a folder/item
## here, using your highest level parent folder
file <- system.file("examples", "books.json", package = "sbtools")
item_upload_create(user_id(), file)
## End(Not run)
```

Description

Either creates or updates (if item already exists)

Usage

```r
item_upsert(
  parent_id = user_id(),
  title = NULL,
  ...,
  info = NULL,
  session = current_session()
)
```

Arguments

parent_id  An sbitem object or character ScienceBase ID corresponding to the parent item (folder)
title  The title of the new SB item
...  Additional parameters are passed on to GET, POST, HEAD, PUT, or DELETE
info  (optional) list of metadata info for the new item
session  Session object from authenticate_sb. Defaults to anonymous or last authenticated session
Value

An object of class sbitem

Examples

```r
## Not run:
# helper function to make a random name
aname <- function() paste0(sample(letters, size = 5, replace = TRUE), collapse = "")

# Create an item - by default we use your user ID
(x <- item_upsert(title = aname()))

# Call item_upsert again, updates this time
item_upsert(x, info = list(
  contacts = list(list(name = "Suzy")))
)

## End(Not run)
```

query_items

Query SB for items using generic query parameters

Description

Query SB for items using generic query parameters

Usage

`query_items(query_list, ..., session = current_session())`

Arguments

- `query_list`: List of item query selectors. See Details.
- `...`: Additional parameters are passed on to `GET`
- `session`: Session object from `authenticate_sb`

Details

The following is a list of query parameters you can use in the `query_list` parameter.

- `s` (character): Only option: "Search"
- `format` (character): One of "json", "xml", "csv", or "atom"
- `q` (character): Query string
- `q` (character): Lucene query string
- `max` (integer): Number of records to return. Default: 20
query_items

- offset (integer): Record to start at. Default: 1
- fields (character): Character vector of fields to return
- folderId (character): Alphanumeric string representing folder ID
- parentId (character): Alphanumeric string representing folder ID. This can be used to return all children items within the folder, but not within sub-folders.
- sort (character): One of "firstContact", "dateCreated", "lastUpdated", or "title". By default sorted by search score
- order (character): One of "asc" or "desc"
- ids Vector of item ids.
- ancestors (character): Alphanumeric string representing folder ID. This can be used to return all children items within the folder, even within sub-folders. Used as a filter
- tags Filter by tags, e.g, "distribution". Used as a filter
- browseCategory One of .... Used as a filter
- browseType One of .... Used as a filter
- dateRange A json string with keys dateType and choice. Where dateType is one of Acquisition, Award, Collected, dateCreated, Received, Reported, Transmitted, Due, End, Info, lastUpdated, Publication, Release, or Start. And where choice is one of day, week, month, year, or range (if range selected, also supply start and end keys with dates of the form YYYY-MM-DD). Used as a filter
- projectStatus One of Active, Approved, Completed, In Progress, Proposed. Used as a filter
- spatialQuery A WKT string. Used as a filter
- extentQuery Use existing extents (footprints) to search against item bounding boxes and representational points. This is an alphanumeric string.

Value

An object of class response

See Also

query_item_identifier, query_item_in_folder

Examples

## Not run:
# Basic query
library("httr")
res <- query_items(list(s = "Search", q = "water", format = "json"))
httr::content(res)

# Paging
## max - number of results
res <- query_items(list(s = "Search", q = "water", format = "json", max = 2))
length(httr::content(res)$items)
res <- query_items(list(s = "Search", q = "water", format = "json", max = 30))
length(httr::content(res)$items)
## offset - start at certain record

```r
res <- query_items(list(s = "Search", q = "water", format = "json", max = 30, offset = 10))
httr::content(res)
```

## links - use links given in output for subsequent queries

```r
httr::content(httr::GET(content(res)$nextlink$url))
```

## Return only certain fields

```r
res <- query_items(list(s = "Search", q = "water", format = "json", fields = 'title'))
httr::content(res)$items[[1]]
```

## Search a folder ID

```r
res <- query_items(list(s = "Search", q = "water", format = "json", folderId = '504216b9e4b04b508bfd337d'))
httr::content(res)$items
```

## Filter by ancestor

```r
query_items(list(s = "Search", ancestors = "4f831626e4b0e84f6086809b", format = "json"))
```

## Filter by tags

```r
content(query_items(list(s = "Search", tags = "distribution", format = "json")))
```

## Filter by browse category

```r
content(query_items(list(s = "Search", browseCategory = "Image", format = "json")))
```

## Filter by browse type

```r
content(query_items(list(s = "Search", browseType = "Collection", format = "json")))
```

## Filter by WKT geometry string

```r
wkt1 <- "POLYGON((-104.4 41.0,-95.1 41.0,-95.1 37.5,-104.4 37.5,-104.4 41.0))"
wkt2 <- "POLYGON((-104.4 38.3,-95.2 38.3,-95.2 33.7,-104.4 34.0,-104.4 38.3))"
content(query_items(list(s = "Search", spatialQuery = wkt1, format = "json")))
content(query_items(list(s = "Search", spatialQuery = wkt1, spatialQuery = wkt2, format = "json")))
```

## Project status

```r
content(query_items(list(s = "Search", projectStatus = "Active", format = "json")))
```

## Date range

```r
query_items(list(s = "Search", dateRange = '{"dateType":"Collected","choice":"year"}', format = "json"))
query_items(list(s = "Search", dateRange = '{"dateType":"lastUpdated","choice":"month"}', format = "json"))
query_items(list(s = "Search", dateRange = '{"dateType":"Release","choice":"range","start":"2014-09-01","end":"2015-09-01"}', format = "json"))
```

## Extent query

```r
## just a alphanumeric code
content(query_items(list(s = "Search", extentQuery = '2873462', format = "json")))
```
query_item_identifier

Description
Find all items under a scheme or also query by for a specific type and key

Usage

query_item_identifier(
    scheme,
    type = NULL,
    key = NULL,
    ...
)

Arguments

scheme (required) The identifier scheme

Arguments

type (optional) The identifier type

Arguments

key (optional) The identifier key

Arguments

... Additional parameters are passed on to GET

Arguments

session (optional) SB Session to use, not provided queries public items only

Arguments

limit (optional) Max number of matching items to return

Value
The SB item id for the matching item. NULL if no matching item found.
Examples

```r
## Not run:
authenticate_sb()

ex_item = item_create(title='identifier example')
item_update_identifier(ex_item, 'project1', 'dataset1', 'key1')
ex2_item = item_create(title='identifier example 2')
item_update_identifier(ex2_item, 'project1', 'dataset1', 'key2')

#query the specific item
query_item_identifier('project1', 'dataset1', 'key1')

#or get the collection of items based on the ID hierarchy
query_item_identifier('project1')

item_rm(ex_item)
item_rm(ex2_item)

## End(Not run)
```

---

**query_item_in_folder**  
*Search within an SB folder*

**Description**

Search for text in the title, abstract, etc. within an SB folder and any subfolders.

**Usage**

```r
query_item_in_folder(
  text, 
  folder, 
  ..., 
  session = current_session(), 
  limit = 20 
)
```

**Arguments**

- **text**: text in the title, abstract, etc. of the desired item
- **folder**: an SB item ID for the folder to search in
- **session**: (optional) SB Session to use, not provided queries public items only
- **limit**: Max number of matching items to return
- Additional parameters are passed on to `GET`
query_sb

Value

A list of matching items as sbitem objects.

query_sb

Query SB for items using generic query parameters

Description

Generic SB query function to construct advanced queries.

The following is a list of query parameters you can use in the query_list parameter.

• q (character): Query string
• q (character): Lucene query string
• fields (character): Character vector of fields to return
• folderId (character): Alphanumeric string representing folder ID
• parentId (character): Alphanumeric string representing folder ID. This can be used to return all children items within the folder, but not within sub-folders.
• sort (character) One of "firstContact", "dateCreated", "lastUpdated", or "title". By default sorted by search score
• order (character) One of "asc" or "desc"
• ids Vector of item ids.
• ancestors (character): Alphanumeric string representing folder ID. This can be used to return all children items within the folder, even within sub-folders. Used as a filter
• tags Filter by tags, e.g, "distribution". Used as a filter
• browseCategory One of .... Used as a filter
• browseType One of .... Used as a filter
• dateRange A json string with keys dateType and choice. Where dateType is one of Acquisition, Award, Collected, dateCreated, Received, Reported, Transmitted, Due, End, Info, lastUpdated, Publication, Release, or Start. And where choice is one of day, week, month, year, or range (if range selected, also supply start and end keys with dates of the form YYYY-MM-DD). Used as a filter
• projectStatus One of Active, Approved, Completed, In Progress, Proposed. Used as a filter
• spatialQuery A WKT string. Used as a filter
• extentQuery Use existing extents (footprints) to search against item bounding boxes and representational points. This is an alphanumeric string.

Usage

query_sb(query_list, ..., limit = 20, session = current_session())
Arguments

query_list  List of item query selectors. See Details.

...  Additional parameters are passed on to GET

limit  Maximum number of returned items. Will do paging to retrieve results when limit is over 1000. Use with caution, queries 10k results are slow.

session  Session object from authenticate_sb

Value

A list of sbitem objects

See Also

query_items

Examples

## Not run:
query_sb(list(q = "water"))

# Search by project status
query_sb(list(projectStatus = "Active"))

# Search a folder ID
query_sb(list(q = "water", folderId = '504216b9e4b04b508bfd337d'))

# Filter by ancestor
query_sb(list(ancestors = "4f831626e4b0e84f6086809b"))

# Filter by tags
query_sb(list(tags = "distribution"))

# Filter by browse category
query_sb(list(browseCategory = "Image"))

# Filter by browse type
query_sb(list(browseType = "Map Service"))

# Filter by WKT geometry string
wkt1 <- "POLYGON((-104.4 41.0,-95.1 41.0,-95.1 37.5,-104.4 37.5,-104.4 41.0))"
wkt2 <- "POLYGON((-104.4 38.3,-95.2 38.3,-95.2 33.7,-104.4 34.0,-104.4 38.3))"
query_sb(list(spatialQuery = wkt1))
query_sb(list(spatialQuery = wkt2))

# Date range
query_sb(list(dateRange = 'dateType:"Collected","choice":"year"'))
query_sb(list(dateRange = 'dateType:"lastUpdated","choice":"month"'))
query_sb(list(dateRange = 'dateType:"Release","choice":"range","start":"2014-09-01","end":"2015-09-01"'))
query_sb_datatype

## End(Not run)

query_sb_datatype  Query SB for specific data type

Description

Queries ScienceBase for items with matching datatype.

Usage

query_sb_datatype(datatype, ..., limit = 20, session = current_session())

Arguments

datatype  Character string indicating datatype. See sb_datatypes for full list of available datatypes.
...
limit  Maximum number of returned items. Will do paging to retrieve results when limit is over 1000. Use with caution, queries 10k results are slow.
session  Session object from authenticate_sb

Value

A list of sbitem objects. List of length 0 means no matches were found.

Examples

#query for items with WFS Layer data
query_sb_datatype('Static Map Image')

#query for US Topo maps
query_sb_datatype('Map Service')
query_sb_date

Query SB for items within a date range

Description

Queries ScienceBase for items with timestamps within a certain date/time range.

Usage

```r
query_sb_date(
  start = as.POSIXct("1970-01-01"),
  end = Sys.time(),
  date_type = "lastUpdated",
  ...
  limit = 20,
  session = current_session()
)
```

Arguments

- `start`: Start date as `POSIXct` object. Defaults to 1970-01-01
- `end`: End date as `POSIXct` object. Defaults to today.
- `date_type`: Which object timestamp to query against. Options are (case sensitive): 'Acquisition', 'Award', 'Collected', 'dateCreated', 'Received', 'Reported', 'Transmitted', 'Due', 'End', 'Info', 'lastUpdated', 'Publication', 'Release', 'Repository Created', 'Repository Updated', 'Start'.
- `...`: Additional parameters are passed on to `GET`
- `limit`: Maximum number of returned items. Will do paging to retrieve results when limit is over 1000. Use with caution, queries 10k results are slow.
- `session`: Session object from `authenticate_sb`

Examples

```r
## Not run:
# find items updated today
query_sb_date(Sys.time(), Sys.time())

# find items with publications from the 1970's
query_sb_date(as.POSIXct('1970-01-01'), as.POSIXct('1980-01-01'),
  date_type='Publication', limit=1000)
```

## End(Not run)
query_sb_doi | Query SB for specific DOI (Digital Object Identifier)

Description

Queries for ScienceBase items with a specific DOI identifier. In ScienceBase, these are stored as additional unique identifiers.

Usage

```r
query_sb_doi(doi, ..., limit = 20, session = current_session())
```

Arguments

- **doi**
  DOI to search for as character
- **...**
  Additional parameters are passed on to `GET`
- **limit**
  Maximum number of returned items. Will do paging to retrieve results when limit is over 1000. Use with caution, queries 10k results are slow.
- **session**
  Session object from `authenticate_sb`

Value

A list of `sbitem` objects. List of length 0 means no matches were found.

Examples

```
# Two example DOI-specific queries
query_sb_doi("10.5066/F7M043G7")
query_sb_doi("10.5066/F7Z60M35")
```

query_sb.spatial | Query SB based on spatial extent

Description

Queries ScienceBase based on a spatial bounding box. Accepts either an `sp` spatial data object (uses the spatial object’s bounding box) or long/lat coordinates defining the bounding box limits.
Usage

```r
query_sb_spatial(
  bbox,
  long,
  lat,
  bb_wkt,
  ...,
  limit = 20,
  session = current_session()
)
```

Arguments

- **bbox**: An sp spatial data object. The bounding box of the object is used for the query.
- **long**: A vector of longitude values that will define the boundaries of a bounding box. Min and Max of supplied longitudes are used. (alternate option to bbox).
- **lat**: A vector of latitude values that will define the boundaries of a bounding box. Min and Max of supplied latitude are used. (alternate option to bbox).
- **bb_wkt**: A character string using the Well Known Text (WKT) standard for defining spatial data. Must be a POLYGON WKT object.
- **...**: Additional parameters are passed on to `GET`
- **limit**: Maximum number of returned items. Will do paging to retrieve results when limit is over 1000. Use with caution, queries 10k results are slow.
- **session**: Session object from `authenticate_s`b

Examples

```r
# specify the latitude and longitude points to define the bounding box range.
# This is simply bottom left and top right points
query_sb_spatial(long=c(-104.4, -95.1), lat=c(37.5, 41.0), limit=3)

# use a pre-formatted WKT polygon to grab data
query_sb_spatial(bb_wkt="POLYGON((-104.4 41.0,-95.1 41.0,-95.1 37.5,-104.4 37.5,-104.4 41.0))", limit=3)
```

---

```r
query_sb_text
```

*Query SB for items containing specific text*

Description

Queries for ScienceBase items that have matching text in the title or description

Usage

```r
query_sb_text(text, ..., limit = 20, session = current_session())
```
Arguments

- `text`: Text string for search
- `...`: Additional parameters are passed on to `GET`
- `limit`: Maximum number of returned items. Will do paging to retrieve results when limit is over 1000. Use with caution, queries 10k results are slow.
- `session`: Session object from `authenticate_sb`

Value

A list of `sbitem` objects. List of length 0 means no matches were found.

Examples

```r
#query for the package maintainer's name
query_sb_text('Luke Winslow')

#query for one of the old river gaging stations
query_sb_text('Lees Ferry')
```

---

### sbitem

*ScienceBase item class*

Description

ScienceBase item class

Usage

```r
as.sbitem(x, ...)
```

## Default S3 method:
```r
as.sbitem(x, ...)
```

```r
is.sbitem(x)
```

Arguments

- `x`: Input, variety of things, character, list, or sbitem class object
- `...`: Further args passed on to `item_get`, only in the method for character class inputs
Examples

# Single item from item_get()
item_get("4f4e4b24e4b07f02db6aea14")

# Get many w/ e.g., an lapply() call
library("httr")
res <- query_items(list(s = "Search", q = "water", format = "json"))
if(res$status != 404) {
  ids <- vapply(httr::content(res)$items, "[[", ",", "id")
  (out <- lapply(ids[1:3], item_get))
}

# create item class from only an item ID
as.sbitem("4f4e4b24e4b07f02db6aea14")

# sbitem gives back itself
(x <- as.sbitem("4f4e4b24e4b07f02db6aea14"))
as.sbitem(x)

---

**sb_datatypes**

*Query SB for all available datatypes*

**Description**

Queries ScienceBase for the list of all available datatypes. This can be coupled with `query_sb_datatype` to query based on the type of data.

**Usage**

```r
sb_datatypes(limit = 50, session = current_session())
```

**Arguments**

- `limit`  
  Maximum number of returned items. Will do paging to retrieve results when `limit` is over 1000. Use with caution, queries 10k results are slow.
- `session`  
  Session object from `authenticate_sb`

**Examples**

```r
#return all datatypes (limit 50 by default)
sb_datatypes()
```
**sb_ping**  
*Ping ScienceBase to see if it’s available*

**Description**
Ping ScienceBase to see if it’s available

**Usage**
sb_ping(...)

**Arguments**
... Additional parameters are passed on to GET

**Value**
Boolean (TRUE) indicating if a connection to ScienceBase can be established and if it is responding as expected. FALSE otherwise.

**Examples**
#TRUE if all is well and SB can be contacted
sb_ping()

---

**session_details**  
*Get session info*

**Description**
Get the details associated with current ScienceBase user session.

**Usage**

```r
session_details(..., session = current_session())
```

**Arguments**
... Additional parameters are passed on to GET

```r
cURRENT_SESSION
```

**Value**
list, if not logged in states that, but if logged in, user details
Examples

## Not run:
session_info()

## End(Not run)

---

session_logout  *Logout of a ScienceBase session*

Description

Logout of a ScienceBase session

Usage

```
session_logout(..., session = current_session())
```

Arguments

- `...`: Additional parameters are passed on to `GET` session
- `session`: SB session object from `authenticate_sb`

Value

invisible, returns nothing if logged out, or errors with message

Examples

## Not run:
session_logout()

## End(Not run)

---

session_renew  *Checks current session and re-authenticates if necessary*

Description

Checks the state of your Sciencebase session, re-authenticates if the session is expired, and simply renews if the session is active.

Usage

```
session_renew(password, ..., username, session = current_session())
```
Arguments

- **password**: The password to use, if needed, to renew the session.
- **...**: Any additional parameters are currently ignored.
- **username**: Optional. Used only to confirm that the current username is what you expect; if you want to switch usernames, use `authenticate_sb()` instead of this function.
- **session**: SB session object from `authenticate_sb`. Default is the current session.

Value

Returns the session object.

Examples

```r
## Not run:
# an empty call is sufficient if the session is current,
# but will break if haven't been logged in before
session_renew()

# include a password if session may be expired
session_renew('newpass')

# optionally confirm the value of the current username
session_renew(username='olduser@usgs.gov', 'newpass')

## End(Not run)
```

---

**session_validate**  
*Validate sbtools session state*

**Description**

A session is considered valid if it is NULL or a true, non-expired SB session

**Usage**

```
session_validate(session = current_session())
```

**Arguments**

- **session**: sbtools session object (from `authenticate_sb`)

**Details**

This validates the underlying RCurl session. The session object becomes invalid if the R session has been saved to disk or persisted through an R restart. This verifies that the session object is either valid, or is a NULL object, which means no session state is being persisted. Note, this does not verify the credentials are valid or that you have permission to access the SB item, so it does not guarantee a successful request.
Value

TRUE/FALSE indicating if session is valid and can be used. Returns TRUE if session is NULL as well.

Examples

```r
## Not run:
session = authenticate_sb('user@usgs.gov')
#return true as underlying RCurl session is valid
session_validate(session)
## End(Not run)
```

---

### set_endpoint

**Set SB endpoint**

**Description**

Sets the internal URLs used to either the production or development (beta) SB server. URLs are stored internally to the package.

**Usage**

```r
set_endpoint(endpoint = c("production", "development"))
```

**Arguments**

- `endpoint` Indicate which SB endpoint you want to use options: `c('production', 'development')`

**Author(s)**

Luke Winslow

**Examples**

```r
set_endpoint('prod')
# getting item from production SB servers
item_get('5060b03ae4b00fc20c4f3c8b')

set_endpoint('dev')
# getting item from beta SB servers
item_get('521e4686e4b051c878dc35d0')
```
user_id

Get your parent ID

Description
Required for creating items

Usage
user_id(..., session = current_session())

Arguments
... Additional parameters are passed on to POST
session Session object from authenticate_sb

Value
A single character string, your user id

Examples
## Not run:
user_id()

## End(Not run)
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