Package ‘rbhl’

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Title Interface to the ‘Biodiversity’ ‘Heritage’ Library

Description Interface to ‘Biodiversity’ ‘Heritage’ Library (‘BHL’)
   (<http://www.biodiversitylibrary.org/> 'API'
   (<http://www.biodiversitylibrary.org/api2/docs/docs.html>). 'BHL' is a repository of 'digitized' literature on 'biodiversity' studies, including 'floras', research papers, and more.

Type Package

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**rbhl-package**

*R interface to the Biodiversity Heritage Library API.*

**Description**

R interface to the Biodiversity Heritage Library API.
bhl_authorsearch

Details

You need an API key to use the Biodiversity Heritage Library API. Get your BHL API key at http://www.biodiversitylibrary.org/getapikey.aspx. Put your API key in your .Rprofile file using e.g., options(BioHerLibKey = "YOURBHLAPIKEY"), and the functions within this package will be able to use your API key without you having to enter it every time you run a search.

See rbhl-defunct for defunct functions.

Author(s)

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bhl_authorsearch

Return a list of authors that match (fully or partially) the specified search string.

Description

The names searched are those contained in MARC 100a, 110a, 111a, 700a, 710a, and 711a library records.

Usage

bhl_authorsearch(name = NULL, as = "table", key = NULL, ...)

Arguments

name

full or partial name of the author for which to search (last name listed first, i.e. 'Darwin, Charles') (character)

as

(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key

Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...  

Curl options passed on to curl::HttpClient()

Examples

## Not run:
bhl_authorsearch(name='dimmock')
bhl_authorsearch(name='Jones')

## End(Not run)
Search BHL across many API methods.

Usage

```r
bhl_bioherlib(method = "GetPageMetadata", pageid = NULL, ocr = FALSE,
               names = FALSE, as = "table", key = NULL, ...)
```

Arguments

- `method`: The API method to use.
- `pageid`: The identifier of an individual page in a scanned book.
- `ocr`: return ocr text of the page (logical). Default: FALSE
- `names`: return the names that appear on the page (logical). Default: FALSE
- `as`: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key`: Your BHL API key, either enter, or loads from your `.Renviron` as BHL_KEY or from `.Rprofile` as bhl_key.
- `...`: Curl options passed on to `curl::HttpClient()`

Examples

```r
## Not run:
bhl_bioherlib(method='GetPageMetadata', pageid=1328690, ocr=TRUE,
               names=TRUE)
bhl_bioherlib(method='GetPageMetadata', pageid=1328690, ocr=TRUE,
               names=TRUE, as="xml")
bhl_bioherlib(method='GetPageMetadata', pageid=1328690, ocr=TRUE,
               names=TRUE, as="list")

## End(Not run)
```
bhl_booksearch

Search for titles and items in BHL.

Description

Search criteria includes title, author last name, volume, edition, year of publication, subject, language code, and collection identifier. Valid language codes and collection identifiers can be obtained from the getlanguages and getcollections functions. If year of publication is specified, it should be a 4-digit year. To execute a search, you must supply at least a title, author last name, or collection identifier.

Usage

bhl_booksearch(title = NULL, lname = NULL, volume = NULL,
    edition = NULL, year = NULL, collectionid = NULL, language = NULL,
    as = "table", key = NULL, ...)

Arguments

title string to search for in the title (character)
lname last name to search for (character)
volume volume to search for (numeric)
edition edition to search for (character)
year year to search for, four characters, e.g. 1970 (numeric)
collectionid collection identifier to search for (numeric)
language language to search for (character)

as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

... Curl options passed on to curl::HttpClient()

Note

Use bhl_getcollections() or bhl_getlanguages() to get acceptable terms

Examples

## Not run:
bhl_booksearch(title='Selborne', lname='White', volume=2, edition='new',
    year=1825, collectionid=4, language='eng')
bhl_booksearch(title='evolution', year=2000, as='json')
bhl_booksearch('evolution', year=2000, as='xml')
bhl_getauthorparts  

Return a list of parts (articles, chapters, etc) associated with a given BHL author identifier. Unless the identifier for a particular BHL author record is known in advance, this method should be used in combination with the AuthorSearch method.

Description

Note: haven’t seen examples for this function that work yet...

Usage

bhl_getauthorparts(creatorid, as = "table", key = NULL, ...)

Arguments

creatorid  
BHL identifier for a particular author (numeric)

as  
(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key  
Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...  
Curl options passed on to `crul::HttpClient()`

Examples

## Not run:
# bhl_getauthorparts(147)
# bhl_getauthorparts(39120, as='json')
# bhl_getauthorparts(39120, as='xml')
# bhl_getauthorparts(39120, as='list')

## End(Not run)
**bhl_getauthortitles**  
*Return a list of titles associated with a given BHL author identifier.*

**Description**

Unless the identifier for a particular BHL author record is known in advance, this method should be used in combination with the AuthorSearch method.

**Usage**

```r
bhl_getauthortitles(creatorid, as = "table", key = NULL, ...)
```

**Arguments**

- **creatorid**: BHL identifier for a particular author (numeric)
- **as**: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- **key**: Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- **...**: Curl options passed on to `curl::HttpClient()`

**Examples**

```r
## Not run:
bhl_getauthortitles(1970)
bhl_getauthortitles(1970, as='json')
bhl_getauthortitles(1970, as='xml')
bhl_getauthortitles(1970, as='list')

## End(Not run)
```

**bhl_getcollections**  
*Get a list of collections which are used to group titles and items. A single collection may contain either titles or items, but not both.*

**Description**

Get a list of collections which are used to group titles and items. A single collection may contain either titles or items, but not both.

**Usage**

```r
bhl_getcollections(as = "table", key = NULL, ...)
```
bhl_getinstitutions

Arguments

- **as** (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- **key** Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

Examples

```r
## Not run:
bhl_getcollections()
bhl_getcollections(as = 'list')
bhl_getcollections(as = 'json')
bhl_getcollections(as = 'xml')
```

Details

Get a list of institutions which have contributed to BHL in some way. These institutions may fill roles such as contributors, rights holders, and scanning institutions.
**bhl_getitembyidentifier**

Find and return metadata about an item or items that match a specific identifier.

**Description**

If you know the Internet Archive identifier for an item, use this method to look up the equivalent item in BHL.

**Usage**

```
bhl_getitembyidentifier(type = NULL, value = NULL, as = "table", key = NULL, ...)```

**Arguments**

- **type** the type of identifier (barcode or ia) (character)
- **value** the identifier value (character)
- **as** (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- **key** Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- **...** Curl options passed on to `curl::HttpClient()`

**Examples**

```
## Not run:
bhl_getinstitutions()

## End(Not run)
```

```
bhl_getitembyidentifier(type = 'ia', value = 'animalkingdomarr03cuvi')
bhl_getitembyidentifier(type = 'ia', value = 'animalkingdomarr03cuvi', as = 'json')
bhl_getitembyidentifier(type = 'ia', value = 'animalkingdomarr03cuvi', as = 'xml')

## End(Not run)
```
bhl_getitemmetadata  
*Return metadata about an item.*

**Description**

You may choose to include a list of the item’s pages.

**Usage**

```r
bhl_getitemmetadata(itemid = NULL, pages = TRUE, ocr = FALSE,
    parts = FALSE, as = "table", key = NULL, ...)
```

**Arguments**

- **itemid**  
  item id (character)

- **pages**  
  return the items pages (TRUE/FALSE)

- **ocr**  
  (logical) TRUE to return the ocr for the item’s pages. Setting this to TRUE apparently doesn’t return any actual ocr text, but leaving parameter here for now.

- **parts**  
  (logical) TRUE to return the item’s parts. Setting this to TRUE apparently doesn’t return any parts text, but leaving parameter here for now.

- **as**  
  (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

- **key**  
  Your BHL API key, either enter, or loads from your `.Renviron` as BHL_KEY or from `.Rprofile` as bhl_key.

- **...**  
  Curl options passed on to `crul::HttpClient()`

**Examples**

```r
## Not run:
bhl_getitemmetadata('16800', TRUE)
bhl_getitemmetadata('16800', TRUE, as='xml')
bhl_getitemmetadata('16800', TRUE, as='json')
bhl_getitemmetadata('16800', TRUE, as='list')

# bhl_getitemmetadata(20419, pages=FALSE, parts=TRUE)

## End(Not run)
```
bhl_getitempages

Return a list of an item’s pages.

Description

Return a list of an item’s pages.

Usage

bhl_getitempages(itemid, ocr = FALSE, as = "table", key = NULL, ...)

Arguments

itemid the item id (character)
ocr return ocr text of the page (TRUE/FALSE)
as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
... Curl options passed on to crul::HttpClient()

Examples

## Not run:
bhl_getitempages('16800')
bhl_getitempages('16800', as='json')
bhl_getitempages('16800', as='xml')

# Return ocr text
bhl_getitempages('16800', TRUE)

## End(Not run)

bhl_getitemparts

Return a list of an item’s parts.

Description

Return a list of an item’s parts.

Usage

bhl_getitemparts(itemid, as = "table", key = NULL, ...)
bhl_getlanguages

Arguments

itemid  the item id (character)

as        (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key       Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...      Curl options passed on to crul::HttpClient()

Examples

## Not run:
bhl_getitemparts(35600)
bhl_getitemparts(35600, 'json')
bhl_getitemparts(35600, 'xml')

## End(Not run)

bhl_getlanguages  Get a list of languages in which materials in BHL have been written.

Description

Get a list of languages in which materials in BHL have been written.

Usage

bhl_getlanguages(as = "table", key = NULL, ...)

Arguments

as        (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key       Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...      Curl options passed on to crul::HttpClient()
bhl_getpagemetadata

Examples

```r
## Not run:
bhl_getlanguages()
bhl_getlanguages('json')
bhl_getlanguages('xml')
bhl_getlanguages('list')

## End(Not run)
```

---

bhl_getpagemetadata  Return metadata about a page.

Description

You may choose to include the OCR text and a list of names found on the page.

Usage

```r
bhl_getpagemetadata(page = NULL, ocr = FALSE, names = FALSE,
                     as = "table", key = NULL, ...)
```

Arguments

- **page**: page number to get
- **ocr**: return ocr text of the page (TRUE/FALSE)
- **names**: return the names that appear on the page (TRUE/FALSE)
- **as**: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- **key**: Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- **...**: Curl options passed on to `curl::HttpClient()`

Examples

```r
## Not run:
bhl_getpagemetadata(page=1328690, ocr=TRUE)
bhl_getpagemetadata(page=1328690, ocr=TRUE, as='json')
bhl_getpagemetadata(page=1328690, ocr=TRUE, as='xml')
bhl_getpagemetadata(page=1328690, ocr=TRUE, as='list')

## End(Not run)
```
bhl_getpagenames  

Return a list of names that appear on a page.

Description

Return a list of names that appear on a page.

Usage

bhl_getpagenames(page = NULL, as = "table", key = NULL, ...)

Arguments

page  
page number to get

as  
(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key  
Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...  
Curl options passed on to curl::HttpClient()

Examples

## Not run:
bhl_getpagenames('1328690')
bhl_getpagenames('1328690', 'json')
bhl_getpagenames('1328690', 'list')

## End(Not run)

bhl_getpageocrtext  

Return the OCR-generated text of a page.

Description

Return the OCR-generated text of a page.

Usage

bhl_getpageocrtext(page = NULL, as = "table", key = NULL, ...)
bhl_getpartbibtex

Return a citation for a part, using the BibTeX format.

Arguments

- **partid**: The identifier of an individual part (article, chapter, etc) (numeric)
- **as**: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- **key**: Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- **...**: Curl options passed on to `crul::HttpClient()`

Examples

```
# Not run:
bhl_getpartbibtex(1000)
bhl_getpartbibtex(1000, "json")
```

## End(Not run)
bhl_getpartbyidentifier

*Return a list of the identifiers of all unpublished items.*

**Description**

Return a list of the identifiers of all unpublished items.

**Usage**

```r
bhl_getpartbyidentifier(type = NULL, value = NULL, as = "table",
key = NULL, ...)
```

**Arguments**

- `type` The type of identifier (doi, oclc, issn, isbn, lccn, ddc, nal, nlm, coden)
- `value` The identifier value
- `as` (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key` Your BHL API key, either enter, or loads from your `.Renviron` as `BHL_KEY` or from `.Rprofile` as `bhl_key`.
- `...` Curl options passed on to `crul::HttpClient()`

**Examples**

```r
## Not run:
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12')
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12', as='json')
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12', as='xml')
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12', as='list')

## End(Not run)
```

bhl_getpartmetadata

*Return a list of an item’s pages.*

**Description**

Return a list of an item’s pages.

**Usage**

```r
bhl_getpartmetadata(partid, key = NULL, ...)
```
bhl_getpartnames

Arguments

partid The identifier of an individual part (article, chapter, etc) (numeric)
key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or
from .Rprofile as bhl_key.
... Curl options passed on to curl::HttpClient()

Examples

## Not run:
bhl_getpartmetadata(10409)

## End(Not run)

bhl_getpartnames Return a list of scientific names associated with a part.

Description

Return a list of scientific names associated with a part.

Usage

bhl_getpartnames(partid, as = "table", key = NULL, ...)

Arguments

partid The identifier of an individual part (article, chapter, etc) (character)
as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or
from .Rprofile as bhl_key.
... Curl options passed on to curl::HttpClient()

Examples

## Not run:
bhl_getpartnames(7443)
bhl_getpartnames(7443, "xml")
bhl_getpartnames(7443, "json")
bhl_getpartnames(7443, "list")

## End(Not run)
bhl_getsubjectparts  
*Return a list of parts (articles, chapters, etc) associated with a subject.*

### Description

Note: haven’t seen examples for this function that work yet...

### Usage

```r
bhl_getsubjectparts(subject = NULL, as = "table", key = NULL, ...)
```

### Arguments

- `subject`  
  the full or partial subject for which to search (character)

- `as`  
  (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that `as="table"` can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

- `key`  
  Your BHL API key, either enter, or loads from your `.Renviron` as `BHL_KEY` or from `.Rprofile` as `bhl_key.

- `...`  
  Curl options passed on to `curl::HttpClient()`

### Examples

```r
## Not run:
bhl_getsubjectparts('frogs')
bhl_getsubjectparts('diptera', 'xml')
bhl_getsubjectparts('diptera', 'json')

## End(Not run)
```

---

bhl_getsubjecttitles  
*Return a list of titles associated with a subject.*

### Description

Return a list of titles associated with a subject.

### Usage

```r
bhl_getsubjecttitles(subject = NULL, as = "table", key = NULL, ...)
```
### bhl_gettitlebibTex

**Arguments**

- `subject`: the full or partial subject for which to search (character)
- `as`: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that `as="table"` can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key`: Your BHL API key, either enter, or loads from your `.Renviron` as `BHL_KEY` or from `.Rprofile` as `bhl_key`.
- `...`: Curl options passed on to `cru::HttpClient()`

### Examples

```r
## Not run:
bhl_getsubjecttitles('diptera')
bhl_getsubjecttitles('diptera', 'xml')
bhl_getsubjecttitles('diptera', 'json')
```

### bhl_gettitlebibTex

Return a citation for a title, using the BibTeX format.

**Description**

Return a citation for a title, using the BibTeX format.

**Usage**

```r
bhl_gettitlebibTex(titleid = NULL, as = "list", key = NULL, ...)
```

**Arguments**

- `titleid`: the identifier of an individual title (numeric)
- `as`: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that `as="table"` can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key`: Your BHL API key, either enter, or loads from your `.Renviron` as `BHL_KEY` or from `.Rprofile` as `bhl_key`.
- `...`: Curl options passed on to `cru::HttpClient()`

### Examples

```r
## Not run:
bhl_gettitlebibTex(1726)
bhl_gettitlebibTex(1726, 'json')
```

## End(Not run)
**bhl_gettitlebyidentifier**

*Find and return metadata about a title or titles that match a specific identifier.*

**Description**

Find and return metadata about a title or titles that match a specific identifier.

**Usage**

```r
bhl_gettitlebyidentifier(type = NULL, value = NULL, as = "table",
key = NULL, ...)
```

**Arguments**

- `type` the type of identifier (oclc, issn, isbn, lccn, ddc, nal, nlm, coden) character
- `value` the identifier value (numeric)
- `as` (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key` Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- `...` Curl options passed on to `curl::HttpClient()`

**Examples**

```r
## Not run:
bhl_gettitlebyidentifier('oclc', 2992225)
bhl_gettitlebyidentifier('oclc', 2992225, 'json')
bhl_gettitlebyidentifier('oclc', 2992225, 'xml')
## End(Not run)
```

---

**bhl_gettitleitems**

*Return a list of a title’s items (books).*

**Description**

Return a list of a title’s items (books).

**Usage**

```r
bhl_gettitleitems(titleid, as = "table", key = NULL, ...)
```
bhl_gettitlemetadata

Get title metadata

Arguments

titleid the identifier of an individual title (numeric)

as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

... Curl options passed on to crul::HttpClient()

Examples

## Not run:
bhl_gettitleitems(1726)
bhl_gettitleitems(1726, as='xml')
bhl_gettitleitems(1726, as='list')

## End(Not run)

Description

Return metadata about a title. You may choose to include a list of the items (books) associated with the title.

Usage

bhl_gettitlemetadata(titleid = NA, items = FALSE, as = "list",
key = NULL, ...)

Arguments

titleid the identifier of an individual title (numeric)

items (logical) TRUE of FALSE (default) to include items

as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

... Curl options passed on to crul::HttpClient()
bhl_getunpublisheditems

Return a list of the identifiers of all unpublished items.

Usage

bhl_getunpublisheditems(as = "table", key = NULL, ...)

Arguments

as
(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key
Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...Curl options passed on to crul::HttpClient()

Examples

## Not run:
bhl_getunpublisheditems()
bhl_getunpublisheditems("xml")
bhl_getunpublisheditems("json")

## End(Not run)
bhl_getunpublishedparts

    Return a list of the identifiers of all unpublished parts (articles, chapters, etc).

Description

Return a list of the identifiers of all unpublished parts (articles, chapters, etc).

Usage

    bhl_getunpublishedparts(as = "table", key = NULL, ...)

Arguments

as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
... Curl options passed on to curl::HttpClient()

Examples

## Not run:
    bhl_getunpublishedparts()
    bhl_getunpublishedparts("json")
    bhl_getunpublishedparts("xml")

## End(Not run)

bhl_getunpublishedtitles

    Return a list of the identifiers of all unpublished titles.

Description

Return a list of the identifiers of all unpublished titles.

Usage

    bhl_getunpublishedtitles(as = "table", key = NULL, ...)
Arguments

as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

date Start date of range between which to count names (optional)

date End date of range between which to count names (optional)
as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

... Curl options passed on to curl::HttpClient()

Examples

## Not run:
bhl_getunpublishedtitles()
bhl_getunpublishedtitles('json')
bhl_getunpublishedtitles('xml')

## End(Not run)

bhl_namecount Return the number of unique names found on pages in BHL.

Description

Names both with and without NameBank identifiers are counted.

Usage

bhl_namecount(startdate = NULL, enddate = NULL, as = "table", key = NULL, ...)

Arguments

startdate start date of range between which to count names (optional)

date End date of range between which to count names (optional)
as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

... Curl options passed on to curl::HttpClient()

Details

BEWARE: this API call can take a long time. They are likely working on speeding up the service, but slow for now.
bhl_namegetdetail

**Examples**

```r
## Not run:
bhl_namecount(startdate = '10/15/2009', enddate = '10/17/2009', as='json')

## End(Not run)
```

bhl_namegetdetail

Get basic title, item, and page metadata for each page on which the specified name appears.

**Description**

Get basic title, item, and page metadata for each page on which the specified name appears.

**Usage**

```r
bhl_namegetdetail(namebankid = NULL, name = NULL, as = "table",
    key = NULL, ...)
```

**Arguments**

- `namebankid` (not used if 'name' specified) NameBank identifier for a name (numeric)
- `name` (not used if 'namebankid' specified) a complete name string (character)
- `as` (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key` Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- `...` Curl options passed on to `curl::HttpClient()`

**Examples**

```r
## Not run:
# bhl_namegetdetail(namebankid = 3501464)
# bhl_namegetdetail(name = 'poa annua')

## End(Not run)
```
bhl_namelist

List the unique names.

Description

By using the startrow and batchsize parameters appropriately, you can pull the list all at once, or in batches (i.e. 1000 names at a time). Names both with and without NameBank identifiers are returned.

Usage

bhl_namelist(startrow = NULL, batchsize = NULL, startdate = NULL, enddate = NULL, as = "table", key = NULL, ...)

Arguments

startrow       first name to return (if using as an offset)
batchsize     number of names to return (numeric)
startdate     (optional) start date of range between which to count names (date)
enddate       (optional) end date of range between which to count names (date)
as            (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key            Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...            Curl options passed on to `curl::HttpClient()`

Examples

## Not run:
```
bhl_namelist(startrow=1, batchsize=99, startdate='10/15/2009',
             enddate='10/16/2009')
bhl_namelist(startrow=1, batchsize=5, startdate='10/15/2009',
             enddate='10/31/2009', as='json')
```
## End(Not run)
bhl_namesearch  

Search for a particular name.

**Description**

Names both with and without NameBank identifiers are returned.

**Usage**

```r
bhl_namesearch(name = NULL, as = "table", key = NULL, ...)
```

**Arguments**

- **name**: species name (character)
- **as**: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- **key**: Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- **...**: Curl options passed on to `crl::HttpClient()`

**Examples**

```r
# Not run:
bhl_namesearch('poa annua')
bhl_namesearch(name='helianthus annuus')
bhl_namesearch(name='helianthus annuus', as='xml')
bhl_namesearch(name='helianthus annuus', as='json')
```

# End(Not run)

bhl_openurl  

Not sure how this differs from their other API...

**Description**

Not sure how this differs from their other API...

**Usage**

```r
bhl_openurl(genre = NULL, title = NULL, aufirst = NULL, aulast = NULL, date = NULL, spage = NULL, issue = NULL, version = 0.1, as = "list", key = NULL, ...)
```
Arguments

**genre**
Book genre

**title**
Book title

**aufirst**
First author

**aulast**
Last author

**date**
Date of publication

**spage**
Start page

**issue**
Issue number

**version**
One of 0.1 or 1.0

**as**
(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.

**key**
Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

...Curl options passed on to **curl::HttpClient()**

Examples

```r
## Not run:
bhl_openurl(
  genre="book",
  title="Manual of North American Diptera",
  aufirst="Samuel Wendell",
  aulast="Williston",
  date=1908,
  spage=16)

  aufirst="Samuel Wendell", aulast="Williston", date=1908, spage=16)

  aufirst="Samuel Wendell", aulast="Williston", date=1908, spage=16,
  as='xml')

## End(Not run)
```

---

**bhl_partsearch**

Search for parts of books in BHL, such as articles, chapters, or treatments. Search criteria includes title, container (journal or book title), author, date of publication, volume, series, and issue.

---

**Description**

To execute a search, you must supply at least a title or author.
**bhl_partsearch**

**Usage**

```r
bhl_partsearch(title = NULL, containerTitle = NULL, author = NULL,
    date = NULL, volume = NULL, series = NULL, issue = NULL,
    as = "table", key = NULL, ...)
```

**Arguments**

- `title`: Title of the work
- `containerTitle`: Container title of the work
- `author`: Author of the work
- `date`: Date of the work
- `volume`: Volume of the work
- `series`: Series of the work
- `issue`: Issue of the work
- `as`: (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
- `key`: Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
- `...`: Curl options passed on to `crul::HttpClient()`

**Details**

The metadata returned by this method includes Part Identifier, Part URL, Item ID, Page ID for the start page, Genre, Title, Container Title, Publication Details, Volume, Series, Issue, Date, Page Range, Language, rights information, authors, keywords, identifiers, pages, and related parts. For more information, see the "Data Elements" section of this documentation.

**Examples**

```r
## Not run:
bhl_partsearch(title='Critical approach to the definition of Darwinian units')
bhl_partsearch(author='Charles Darwin')

## End(Not run)
```
bhl_subjectsearch
Return a list of subjects that match (fully or partially) the specified search string.

Description
Return a list of subjects that match (fully or partially) the specified search string.

Usage
bhl_subjectsearch(subject, as = "table", key = NULL, ...)

Arguments

subject (character) the full or partial subject for which to search (character)
as (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...
Curl options passed on to curl::HttpClient()

Examples
## Not run:
bhl_subjectsearch('diptera')
bhl_subjectsearch('diptera', "json")
## End(Not run)

bhl_titlesearchsimple
Perform a simple title search.

Description
The full title (as specified in MARC 245a and MARC 245b library records) is searched for the specified string. Basic metadata for all full and partial matches is returned.

Usage
bhl_titlesearchsimple(title = NA, as = "table", key = NULL, ...)
Arguments

title  full or partial title for which to search (character)
as   (character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key   Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.

Examples

```r
## Not run:
bhl_titlesearchsimple('nematocerous')
bhl_titlesearchsimple('husbandry')
## End(Not run)
```

getpages

Get many OCR-generated pages given a single item id

Description

Get many OCR-generated pages given a single item id

Usage

```r
getpages(itemid, key = NULL, ...)
```

Arguments

itemid  the item id (character). Required
key   Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key

Examples

```r
## Not run:
books <- bhl_booksearch(title='Selborne', lname='White', volume=2,
                         edition='new', year=1825, collectionid=4, language='eng')
getpages(itemid = 168800)
## End(Not run)
```
rbhl-defunct  
*Defunct functions in rbhl*

**Description**

These functions are gone, no longer available.

**Details**

- `bhl_getpartendnote()`: BHL removed this API method.
- `bhl_gettitleendnote()`: BHL removed this API method.

---

rbhlmethods  
*Data.frame of all the BHL API methods from the BHL website.*

**Description**

Data.frame of all the BHL API methods from the BHL website.
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