

Package ‘rbhl’

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Title R interface to the Biodiversity Heritage Library.

Description Interface to Biodiversity Heritage Library (BHL) API methods. BHL is a repository of digitized literature on biodiversity studies, including floras, research papers, and more.

Type Package

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BugReports <https://github.com/ropensci/rbhl/issues>

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rbhl-package	<i>R interface to the Biodiversity Heritage Library API.</i>
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Description

R interface to the Biodiversity Heritage Library API.

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.

Author(s)

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bhl_authorsearch	<i>Return a list of authors that match (fully or partially) the specified search string.</i>
------------------	--

Description

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

Usage

```
bhl_authorsearch(name = NULL, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

name	full or partial name of the author for which to search (last name listed first, i.e. 'Darwin, Charles') (character)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'

Examples

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

## End(Not run)
```

bhl_bioherlib	<i>Search BHL across many API methods.</i>
---------------	--

Description

Search BHL across many API methods.

Usage

```
bhl_bioherlib(method = "GetPageMetadata", pageid = NULL, ocr = FALSE,
  names = FALSE, format = "json", key = NULL, output = "list",
  callopts = list())
```

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
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
key	your BHL API key, either enter, or loads from .Rprofile
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
callopts	Call options passed on to httr::GET.

Examples

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

## End(Not run)
```

bhl_booksearch	<i>Search for titles and items in BHL.</i>
----------------	--

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,
               format = "json", output = "list", key = NULL, callopts = list())
```

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)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

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, output='raw')
bhl_booksearch('evolution', year=2000, output='raw', format='xml')
bhl_booksearch('evolution', year=2000, output='parsed', format="xml")

## 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

```
bhl_getauthortitles(creatorid = NA, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

creatorid	BHL identifier for a particular author (numeric)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getauthortitles(1970)
bhl_getauthortitles(1970, output='raw')
bhl_getauthortitles(1970, output='raw', format='xml')

## End(Not run)
```

bhl_getcollections	<i>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.</i>
--------------------	--

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

```
bhl_getcollections(format = "json", output = "list", key = NULL,
  callopts = list())
```

Arguments

format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getcollections()
bhl_getcollections(out = 'raw')

## End(Not run)
```

 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, format = "json",
  output = "list", key = NULL, callopts = list())
```

Arguments

type	the type of identifier (barcode or ia) (character)
value	the identifier value (character)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi')
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi', format='xml')
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi', format='xml', output='raw')
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi', format='xml', output='parsed')

## End(Not run)
```

 bhl_getitemmetadata *Return metadata about an item.*

Description

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

Usage

```
bhl_getitemmetadata(itemid = NULL, pages = TRUE, format = "json",
  output = "list", key = NULL, callopts = list())
```

Arguments

itemid	item id (character)
pages	return the items pages (TRUE/FALSE)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getitemmetadata('16800', TRUE)
bhl_getitemmetadata('16800', TRUE, 'xml', 'parsed')
bhl_getitemmetadata('16800', TRUE, 'json', 'raw')
bhl_getitemmetadata('16800', TRUE, 'xml', 'raw')

## End(Not run)
```

bhl_getitempages	<i>Return a list of an item's pages.</i>
------------------	--

Description

Return a list of an item's pages.

Usage

```
bhl_getitempages(itemid = NA, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

itemid	the item id (character)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getitempages('16800')
bhl_getitempages('16800', 'xml', 'raw')
bhl_getitempages('16800', 'xml', 'parsed')

## End(Not run)
```

bhl_getlanguages	<i>Get a list of languages in which materials in BHL have been written.</i>
------------------	---

Description

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

Usage

```
bhl_getlanguages(format = "json", output = "list", key = NULL,
  callopts = list())
```

Arguments

format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getlanguages()
bhl_getlanguages(output='parsed')
bhl_getlanguages(output='raw')
bhl_getlanguages(output='raw', format='xml')

## End(Not run)
```

bhl_getpagemetadadata *Return metadata about a page.*

Description

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

Usage

```
bhl_getpagemetadadata(page = NULL, ocr = FALSE, names = FALSE,
  format = "json", output = "list", key = NULL, callopts = list())
```

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)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getpagemetadadata(page=1328690, ocr=TRUE, format='json')
bhl_getpagemetadadata(page=1328690, ocr=TRUE, format='xml')
bhl_getpagemetadadata(page=1328690, ocr=TRUE, format='xml', output='parsed')

## 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, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

page	page number to get
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getpagenames('1328690')
bhl_getpagenames('1328690', 'xml', 'raw')
bhl_getpagenames('1328690', 'xml', 'parsed')

## 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, ocr = FALSE, names = FALSE,
  format = "json", output = "list", key = NULL, callopts = list())
```

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)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getpageocrtext(1328690, FALSE, FALSE, 'json')
bhl_getpageocrtext(1328690, FALSE, FALSE, 'xml', 'raw')
bhl_getpageocrtext(1328690, FALSE, FALSE, 'xml', 'parsed')

## 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

```
bhl_getsubjecttitles(subject = NULL, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

subject	the full or partial subject for which to search (character)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getsubjecttitles('diptera')
bhl_getsubjecttitles('diptera', 'xml', 'raw')
bhl_getsubjecttitles('diptera', 'xml', 'parsed')

## End(Not run)
```

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

Description

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

Usage

```
bhl_gettitlebibTex(titleid = NULL, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

titleid	the identifier of an individual title (numeric)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_gettitlebibTex(1726)
bhl_gettitlebibTex(1726, output='raw')
bhl_gettitlebibTex(1726, format='xml', output='raw')
bhl_gettitlebibTex(1726, format='xml', output='parsed')

## 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

```
bhl_gettitlebyidentifier(type = NULL, value = NULL, format = "json",
  output = "list", key = NULL, callopts = list())
```

Arguments

type	the type of identifier (oclc, issn, isbn, lccn, ddc, nal, nlm, coden) character
value	the identifier value (numeric)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_gettitlebyidentifier('oclc', 2992225)
bhl_gettitlebyidentifier('oclc', 2992225, output='raw')
bhl_gettitlebyidentifier('oclc', 2992225, format='xml', output='raw')
bhl_gettitlebyidentifier('oclc', 2992225, format='xml', output='parsed')

## End(Not run)
```

bhl_gettitleendNote *Return a citation for a title, using the EndNote format.*

Description

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

Usage

```
bhl_gettitleendNote(titleid = NA, key = NULL, callopts = list())
```

Arguments

titleid	the identifier of an individual title (numeric)
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_gettitleendNote(1726)

## 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

```
bhl_gettitleitems(titleid = NULL, format = "json", output = "list",
  key = NULL, callopts = list())
```

Arguments

titleid	the identifier of an individual title (numeric)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_gettitleitems(1726)
bhl_gettitleitems(1726, output='raw')
bhl_gettitleitems(1726, format='xml', output='raw')
bhl_gettitleitems(1726, format='xml', output='parsed')

## End(Not run)
```

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

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, format = "json",
  output = "list", key = NULL, callopts = list())
```

Arguments

titleid	the identifier of an individual title (numeric)
items	(logical) TRUE of FALSE (default) to include items
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_gettitlemetadata(1726, TRUE)
bhl_gettitlemetadata(1726, output='raw')
bhl_gettitlemetadata(1726, format='xml', output='raw')
bhl_gettitlemetadata(1726, format='xml', output='parsed')

## End(Not run)
```

```
bhl_getunpublisheditems
```

Return a list of the identifiers of all unpublished items.

Description

Return a list of the identifiers of all unpublished items.

Usage

```
bhl_getunpublisheditems(format = "json", output = "list", key = NULL,
  callopts = list())
```

Arguments

format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getunpublisheditems()
bhl_getunpublisheditems(output='raw')
bhl_getunpublisheditems(format='xml', output='raw')
bhl_getunpublisheditems(format='xml', output='parsed')

## 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(format = "json", output = "list", key = NULL,
  callopts = list())
```

Arguments

format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
key	your BHL API key, either enter, or loads from .Rprofile
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_getunpublishedtitles()
bhl_getunpublishedtitles(output='raw')
bhl_getunpublishedtitles(format='xml', output='raw')
bhl_getunpublishedtitles(format='xml', output='parsed')

## 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

```
bhl_openurl(genre = NULL, title = NULL, afirst = NULL, aulast = NULL,
  date = NULL, spage = NULL, issue = NULL, version = 0.1,
  format = "json", key = NULL, output = "list", callopts = list())
```

Arguments

genre	Book genre
title	Book title
afirst	First author
aulast	Last author
date	Date of publication
spage	Start page
issue	Issue number
version	One of 0.1 or 1.0
format	either XML ("xml") or JSON ("json") format
key	your BHL API key, either enter, or loads from .Rprofile
output	Output format, one of list, raw, or parsed
callopts	Options to pass on to httr::GET

Examples

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

bhl_openurl(genre="book", title="Manual+of+North+American+Diptera",
  afirst="Samuel Wendell", aulast="Williston", date=1908, spage=16, output='raw')

bhl_openurl(genre="book", title="Manual+of+North+American+Diptera",
  afirst="Samuel Wendell", aulast="Williston", date=1908, spage=16, output='parsed')
```

```
bhl_openurl(genre="book", title="Manual+of+North+American+Diptera",
  aufirst="Samuel Wendell", aulast="Williston", date=1908, spage=16,
  format='xml', output='parsed')

## 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 = NA, format = "json", key = NULL,
  output = "list", callopts = list())
```

Arguments

subject	the full or partial subject for which to search (character)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
key	your BHL API key, either enter, or loads from .Rprofile
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_subjectsearch('diptera')

## 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, format = "json", key = NULL,
  output = "list", callopts = list())
```

Arguments

title	full or partial title for which to search (character)
format	either XML ('xml') or JSON ('json') format. If output='list', format is forced to equal 'json'
key	your BHL API key, either enter, or loads from .Rprofile
output	Return a list, raw json or xml, or parsed data (character). Default: 'list'
callopts	Call options passed on to httr::GET.

Examples

```
## Not run:
bhl_titlesearchsimple('nematoceros')
bhl_titlesearchsimple('husbandry')

## End(Not run)
```

query2message	<i>Internal function to convert API query to message printed in the console.</i>
---------------	--

Description

Internal function to convert API query to message printed in the console.

Usage

```
query2message(url, x)
```

Arguments

url	The base url for the API.
x	List of named parameters to be used in API call.

Examples

```
url <- "http://ropensci.org/"
args <- list(species='frog',author='joe')
message(query2message(url, args))
```

<code>rbhlmethods</code>	<i>Data.frame of all the BHL API methods.</i>
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Description

Data.frame of all the BHL API methods.

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