

# Package ‘rbace’

October 14, 2022

**Type** Package

**Title** 'Bielefeld' Academic Search Engine ('BASE') Client

**Description** Interface to the API for the 'Bielefeld' Academic Search Engine ('BASE') (<<https://www.base-search.net/>>). 'BASE' is a search engine for more than 150 million scholarly documents from more than 7000 sources. Methods are provided for searching for documents, as well as getting information on higher level groupings of documents: collections and repositories within collections. Search includes faceting, so you can get a high level overview of number of documents across a given variable (e.g., year). 'BASE' asks users to respect a rate limit, but does not enforce it themselves; we enforce that rate limit.

**Version** 0.2.2

**License** MIT + file LICENSE

**URL** <https://docs.ropensci.org/rbace/>,  
<https://github.com/ropensci/rbace>

**BugReports** <https://github.com/ropensci/rbace/issues>

**Encoding** UTF-8

**Language** en-US

**LazyLoad** yes

**Imports** crul, xml2, data.table, tibble

**Suggests** testthat, vcr, webmockr

**RoxygenNote** 7.1.1

**X-schema.org-applicationCategory** Literature

**X-schema.org-keywords** text-ming, literature, scholarly, citations,  
search

**X-schema.org-isPartOf** <https://ropensci.org>

**NeedsCompilation** no

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rbace-package	<i>rbace</i>
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### Description

Bielefeld Academic Search Engine Client

### Author(s)

Scott Chamberlain

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bs_profile	<i>Get the profile for a repository</i>
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### Description

Get the profile for a repository

### Usage

```
bs_profile(target, ...)
```

### Arguments

target	(character) Internal name of a single repository as delivered in <a href="#">bs_repositories()</a>
...	curl options passed on to <a href="#">crul::verb-GET</a>

### Value

a data.frame, of two columns: "name", "value". "name" holds the "value" description. you can pivot the data.frame to wide by e.g., `tidyr::pivot_wider(x)`

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bs_repositories	<i>List repositories for a collection</i>
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**Description**

List repositories for a collection

**Usage**

```
bs_repositories(coll, ...)
```

**Arguments**

coll	(character) collection code. For existing, pre-defined collections see Appendix, section "Collection-related queries" in the Appendix of <a href="https://www.base-search.net/about/download/base">https://www.base-search.net/about/download/base</a>
...	curl options passed on to <a href="#">crul::verb-GET</a>

**Value**

a data.frame of two columns: "name", "internal\_name"

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bs_retry_options	<i>bs_search retry options</i>
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**Description**

bs\_search retry options

**Usage**

```
bs_retry_options(  
  pause_base = 1,  
  pause_cap = 60,  
  pause_min = 1,  
  times = 3,  
  terminate_on = NULL,  
  retry_only_on = NULL,  
  onwait = NULL  
)
```



**Arguments**

query	(character) query string. For syntax details see Appendix, section "Query syntax"
target	(character) Internal name of a single repository as delivered in <a href="#">bs_repositories()</a>
coll	(character) collection code. For existing, pre-defined collections see Appendix, section "Collection-related queries"
boost_oa	(logical) Push open access documents upwards in the result list. Default: FALSE
hits	(integer) number of results to return. Default: 10. Max: 100
offset	(integer) record to start at. Default: 0. Max: 1000
fields	(character) Fields to return. This doesn't appear to be working though. The result records only contain fields listed in the comma-separated field list. For existing, pre-defined fields see Appendix, section "Fields"
sortby	(character) field to sort by. A sort ordering must include a single field name (see Appendix, section "Fields", table column "Sorting"), followed by a whitespace (escaped as + or %20 in URL strings), followed by sort direction (asc or desc). Default: sorts by relevance
facets	(character) The response contains an extra section "facet_counts/facet_fields" with fields from the comma-separated facets list. This section provides a breakdown or summary of the results. From the user's perspective, faceted search breaks up search results into multiple categories, typically showing counts for each, and allows the user to "drill down" or further restrict their search results based on those facets. Use of faceting does not affect the results section of a search response. For existing, pre-defined facet fields see Appendix, section "Fields", table column "Facet".
facet_limit	(numeric) Maximum number of constraint counts that should be returned for the facet fields. Default: 100; min:1; max: 500
facet_sort	(character) Ordering of the facet field constraints: count - sort by count (highest count first); index - alphabetical sorting. Default: count
filter	(character) a string with the value to be used. html escaping will be automatically done; embed string in I() to avoid html escaping. This parameter gets used by fq solr parameter on the server
raw	(logical) If TRUE returns raw XML, default: FALSE
parse	(character) One of 'list' or 'df'
retry	(list) use <a href="#">bs_retry_options()</a> to make a named list of retry options to pass on to the HTTP request. default values are passed for you, but you can change them by setting an option in <a href="#">bs_retry_options()</a>
...	Facet field based query options (See Facet below) or curl options passed on to <a href="#">crul::verb-GET</a>
x	input to <a href="#">bs_meta</a>

**Details**

BASE asks that requests are not more frequent than 1 per second, so we enforce the rate limit internally. if you do a single request not in a for loop/lapply type situation, this won't be inoked, but will if doing a for loop/lapply call, and there's no sleep invoked

**Value**

XML as character string if `parse = FALSE` or `data.frame`

**Facet**

You can optionally pass in search term for specific facet fields. See example. For existing, pre-defined facet fields see Appendix at [https://www.base-search.net/about/download/base\\_interface.pdf](https://www.base-search.net/about/download/base_interface.pdf), section "Fields", table column "Facet"

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