

Package ‘bedbaser’

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Title A BEDbase client

Version 1.5.0

Description A client for BEDbase. bedbaser provides access to the API at api.bedbase.org. It also includes convenience functions to import BED files into GRanges objects and BEDsets into GRangesLists.

URL <https://github.com/waldronlab/bedbaser>

BugReports <https://github.com/waldronlab/bedbaser/issues>

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bedbaser-package *bedbaser: A BEDbase client*

Description

A client for BEDbase. bedbaser provides access to the API at api.bedbase.org. It also includes convenience functions to import BED files into GRanges objects and BEDsets into GRangesLists.

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See Also

Useful links:

- <https://github.com/waldronlab/bedbaser>
- Report bugs at <https://github.com/waldronlab/bedbaser/issues>

bb_beds_in_bedset	<i>Get BEDs associated with BEDset</i>
-------------------	--

Description

Return a tibble of BED files in BEDset given its id.

Usage

```
bb_beds_in_bedset(bedbase, bedset_id)
```

Arguments

bedbase	BEDbase() object
bedset_id	integer(1) BEDset record identifier

Value

[tibble](#) of BED files in BEDset

Examples

```
bedbase <- BEDbase()
ex_bedset <- bb_example(bedbase, "bedset")
bb_beds_in_bedset(bedbase, ex_bedset$id)
```

bb_bed_text_search	<i>Search BED files by text</i>
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Description

Return all available BED files ranked by relevance to the keywords. Uses the [bedhost API](#) default of 10 records and an initial offset of 0.

Usage

```
bb_bed_text_search(
  bedbase,
  query,
  genome = NULL,
  assay = NULL,
  limit = 10,
  offset = 0
)
```

Arguments

bedbase	BEDbase() object
query	character() keywords to search
genome	character() (default NULL) genome to search
assay	character() (default NULL) assay to search
limit	integer(1) (default 10) maximum number of results
offset	integer(1) (default 0) page offset of results

Value

[tibble](#) of results

Examples

```
bedbase <- BEDbase()
bb_bed_text_search(bedbase, "hg38")
```

bb_example

Get the example BED file or BEDset with metadata

Description

Get the example BED file or BEDset available through [bedhost](#). Useful for an initial exploration of bedbaser with an example BED file and BEDset in BEDbase.

Usage

```
bb_example(bedbase, rec_type = c("bed", "bedset"))
```

Arguments

bedbase	BEDbase() object
rec_type	character(1) bed or bedset

Value

list() bed files or bedsets

Examples

```
bedbase <- BEDbase()
ex_bed <- bb_example(bedbase, "bed")
str(ex_bed)
ex_bedset <- bb_example(bedbase, "bedset")
str(ex_bedset)
```

bb_list_beds	<i>List BEDs</i>
--------------	------------------

Description

List BED files available through **bedhost**. By default uses the bedhost default of 1000 records and an initial offset of 0.

Usage

```
bb_list_beds(  
  bedbase,  
  genome = NULL,  
  bed_compliance = NULL,  
  limit = 1000,  
  offset = 0  
)
```

Arguments

bedbase	BEDbase() object
genome	character(1) (default NULL) genome keyword
bed_compliance	character(1) (default NULL) bed compliance, e.g., 'bed6+4'
limit	integer(1) (default 1000) maximum records
offset	integer(1) (default 0) page token of records

Value

[tibble](#) of BED records

Examples

```
bedbase <- BEDbase()  
bb_list_beds(bedbase)
```

bb_list_bedsets	<i>List BEDsets</i>
-----------------	---------------------

Description

List BEDsets available through **bedhost**. By default uses the bedhost default of 1000 records and an initial offset of 0.

Usage

```
bb_list_bedsets(bedbase, query = "", limit = 1000, offset = 0)
```

Arguments

bedbase	BEDbase() object
query	character() (default "") keyword
limit	integer(1) (default 1000) maximum records
offset	integer(1) (default 0) page token of records

Value

[tibble](#) of BEDset records

Examples

```
bedbase <- BEDbase()
bb_list_bedsets(bedbase)
```

bb_metadata	<i>Get metadata for a BED file or BEDset</i>
-------------	--

Description

Get metadata for a BED file or BEDset given its id. Abort if not found or id is not not 32 characters.

Usage

```
bb_metadata(bedbase, id, full = FALSE)
```

Arguments

bedbase	BEDbase() object
id	integer(1) record or object identifier
full	logical(1) (default FALSE) include full record with stats, files, and metadata

Value

list() metadata

Examples

```
bedbase <- BEDbase()

ex_bed <- bb_example(bedbase, "bed")
bb_metadata(bedbase, ex_bed$id)

ex_bedset <- bb_example(bedbase, "bedset")
bb_metadata(bedbase, ex_bedset$id)
```

bb_save	<i>Save a BED file or BEDset to a path given an id</i>
---------	--

Description

Save a BED file or a BEDset to a local path. If the path does not exist, `bb_save()` will abort.

Usage

```
bb_save(bedbase, bed_or_bedset_id, path, quietly = TRUE)
```

Arguments

bedbase	BEDbase() object
bed_or_bedset_id	integer(1) BED or BEDset record identifier
path	character(1) directory to save file
quietly	logical(1) (default TRUE) display messages

Value

An invisible NULL

Examples

```
bedbase <- BEDbase()
ex_bed <- bb_example(bedbase, "bed")
bb_save(bedbase, ex_bed$id, tempdir())
```

bb_stats	<i>Get BEDbase statistics</i>
----------	-------------------------------

Description

Get statistics on available BED files, BEDsets, and genomes.

Usage

```
bb_stats(bedbase, detailed = FALSE)
```

Arguments

bedbase	BEDbase() object
detailed	logical(1) if TRUE display detailed information

Value

An invisible NULL

Examples

```
bedbase <- BEDbase()
bb_stats(bedbase)
```

bb_to_granges *Create a GRanges object given a BED id*

Description

Create a GRanges object given a BED id. Columns and types are generated for broad and narrow peak files. Known columns and types can be passed as a named vector through `extra_cols`. Otherwise, `bb_to_granges()` attempts to determine the column type and substitute dummy column names.

Usage

```
bb_to_granges(bedbase, bed_id, extra_cols = NULL, quietly = TRUE)
```

Arguments

bedbase	BEDbase() object
bed_id	integer(1) BED record identifier
extra_cols	character() (default NULL) extra column names to construct GRanges objects
quietly	logical(1) (default TRUE) display messages

Value

[GRanges](#)

Examples

```
bedbase <- BEDbase()
ex_bed <- bb_example(bedbase, "bed")
bb_to_granges(bedbase, ex_bed$id)
```

bb_to_grangeslist *Create a GRangesList object given a BEDset id*

Description

Create a GRangesList object given a BEDset id

Usage

```
bb_to_grangeslist(bedbase, bedset_id, quietly = TRUE)
```

Arguments

bedbase	BEDbase() object
bedset_id	integer(1) BEDset record identifier
quietly	logical(1) (default TRUE) display messages

Value

[GRangesList](#)

Examples

```
bedbase <- BEDbase()
bedset_id <- "lola_hg38_ucsc_features"
bb_to_grangeslist(bedbase, bedset_id)
```

BEDbase

An R client for BEDbase

Description

bedbaser exposes the [bedhost API](#) and includes convenience functions for common tasks, such as to import a BED file by id into a GRanges object and a BEDset by its id into a GRangesList.

Usage

```
BEDbase(cache_path, quietly = FALSE)

getCache(x, cache_type = c("bedfiles", "bedsets"))

setCache(x, cache_path, quietly = TRUE)
```

Arguments

cache_path	character(1)
quietly	logical(1) (default TRUE) display messages
x	BEDbase() object
cache_type	character(1) bedfiles or bedsets

Details

BEDbase() creates a cache similar to that of the [Geniml BBClient's cache](#).

The convenience functions are as follows

- `bedbaser::BEDbase()`: API service constructor
- `bedbaser::getCache()`: Retrieve cache
- `bedbaser::setCache()`: Set path to cache
- `bedbaser::bb_stats()`: Retrieve BEDbase statistics
- `bedbaser::bb_example()`: Retrieve an example BED file or BEDset

- `bedbaser::bb_metadata()`: Retrieve metadata for a BED file or BEDset
- `bedbaser::bb_list_beds()`: List all BED files
- `bedbaser::bb_list_bedsets()`: List all BEDsets
- `bedbaser::bb_beds_in_bedset()`: List BED files in BEDset
- `bedbaser::bb_bed_text_search()`: Search BED files by text
- `bedbaser::bb_to_granges()`: Create a GRanges object from a BED id
- `bedbaser::bb_to_grangeslist()`: Create a GRangesList from a BEDset id
- `bedbaser::bb_save()`: Save a BED file to a path.

Value

BEDbase object

Examples

```
bedbase <- BEDbase(cache_path = tempdir())
ex_bed <- bb_example(bedbase, "bed")
bb_metadata(bedbase, ex_bed$id)
```

BEDbase-class

BEDbase class

Description

BEDbase class

Value

BEDbase class instance

getCache,BEDbase-method

Return cache path

Description

Return cache path

Usage

```
## S4 method for signature 'BEDbase'
getCache(x, cache_type = c("bedfiles", "bedsets"))
```

Arguments

`x` BEDbase() object
`cache_type` character(1) bedfiles or bedsets

Value

BiocFileCache() object of BED files

Examples

```
bedbase <- BEDbase(tempdir())
getCache(bedbase, "bedfiles")
```

operations, BEDbase-method

Display API functions

Description

Display functions defined through the **bedhost API** and their corresponding parameters.

Usage

```
## S4 method for signature 'BEDbase'
operations(x, ..., .deprecated = FALSE)
```

Arguments

x	BEDbase() object
...	other options
.deprecated	(default FALSE) if deprecated

Value

list() API endpoints

Examples

```
bedbase <- BEDbase()
operations(bedbase)
```

schemas,BEDbase-method

Display bedhost API schemas

Description

Display bedhost API schemas

Usage

```
## S4 method for signature 'BEDbase'
schemas(x)
```

Arguments

x BEDbase() object

Value

list() API endpoints

Examples

```
bedbase <- BEDbase()
schemas(bedbase)
```

setCache,BEDbase-method

Set cache along path

Description

Create a cache for BED files and BEDsets like [Geniml BBClient's cache](#).

Usage

```
## S4 method for signature 'BEDbase'
setCache(x, cache_path, quietly = TRUE)
```

Arguments

x BEDbase() object
 cache_path character(1)
 quietly logical(1) (default TRUE) display messages

Value

[BiocFileCache\(\)](#) object of BED files

Examples

```
bedbase <- BEDbase(tempdir())
bedbase <- setCache(bedbase, "/tmp")
```

tags, BEDbase-method *Display functions for a tag*

Description

Display functions available through the API associated with a tag keyword in **bedhost**.

Usage

```
## S4 method for signature 'BEDbase'
tags(x, .tags, .deprecated = FALSE)
```

Arguments

x	BEDbase() object
.tags	character() tags for filtering operations
.deprecated	(default FALSE) if deprecated

Value

list() API endpoints

Examples

```
bedbase <- BEDbase()
unique(tags(bedbase)$tag)
tags(bedbase, "bedset")
```

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