

Package ‘bedbaser’

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Title A BEDbase client

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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 *Get BEDs associated with BEDset*

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 *Search BED files by text*

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, limit = 10, offset = 0)
```

Arguments

bedbase	BEDbase() object
query	character() keywords 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_type = NULL, limit = 1000, offset = 0)
```

Arguments

bedbase	BEDbase() object
genome	character(1) (default NULL) genome keyword
bed_type	character(1) (default NULL) bed file type
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 = NULL, limit = 1000, offset = 0)
```

Arguments

bedbase	BEDbase() object
query	character() (default NULL) 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
Get metadata for a BED file or BEDset

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, file_type = "bed", quietly = TRUE)
```

Arguments

bedbase	BEDbase() object
bed_or_bedset_id	integer(1) BED or BEDset record identifier
path	character(1) directory to save file
file_type	character(1) (default "bed") bed, bigbed, etc.
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_to_granges	<i>Create a GRanges object given a BED id</i>
---------------	---

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,
  file_type = "bed",
  extra_cols = NULL,
  quietly = TRUE
)
```

Arguments

bedbase	BEDbase() object
bed_id	integer(1) BED record identifier
file_type	character(1) bed or bigbed
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	<i>Create a GRangesList object given a BEDset id</i>
-------------------	--

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()
bb_to_grangeslist(bedbase, "lola_hg38_ucsc_features")
```

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_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	<i>BEDbase class</i>
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Description

BEDbase class

Value

BEDbase class instance

<i>getCache, BEDbase-method</i>	<i>Return cache path</i>
---------------------------------	--------------------------

Description

Return cache path

Usage

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

Arguments

<code>x</code>	BEDbase() object
<code>cache_type</code>	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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