

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/waldrnlab/bedbaser>

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

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Contents

bedbaser-package	2
bb_beds_in_bedset	3
bb_bed_text_search	3
bb_example	4
bb_list_beds	5
bb_list_bedsets	5
bb_metadata	6
bb_save	7
bb_stats	8
bb_to_granges	8
bb_to_grangeslist	9
BEDbase	10
BEDbase-class	11
getCache,BEDbase-method	11
operations,BEDbase-method	12
schemas,BEDbase-method	12
setCache,BEDbase-method	13
tags,BEDbase-method	14
Index	15

bedbaser-package	<i>bedbaser: A BEDbase client</i>
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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.

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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>
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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, 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	List BEDs
--------------	-----------

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	List BEDsets
-----------------	--------------

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	<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, 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 <i>GRangesList</i> object given a <i>BEDset</i> 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)
```

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	<i>BEDbase class</i>
---------------	----------------------

Description

BEDbase class

Value

BEDbase class instance

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

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	<i>Display functions for a tag</i>
---------------------	------------------------------------

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")
```

Index

* **internal**

- bedbaser-package, [2](#)
- .BEDbase (BEDbase-class), [11](#)
- bb_bed_text_search, [3](#)
- bb_beds_in_bedset, [3](#)
- bb_example, [4](#)
- bb_list_beds, [5](#)
- bb_list_bedsets, [5](#)
- bb_metadata, [6](#)
- bb_save, [7](#)
- bb_stats, [8](#)
- bb_to_granges, [8](#)
- bb_to_grangeslist, [9](#)
- BEDbase, [10](#)
- BEDbase-class, [11](#)
- bedbaser (bedbaser-package), [2](#)
- bedbaser-package, [2](#)
- BiocFileCache(), [13](#)
- getCache (BEDbase), [10](#)
- getCache, BEDbase-method, [11](#)
- GRanges, [9](#)
- GRangesList, [9](#)
- operations, BEDbase-method, [12](#)
- schemas, BEDbase-method, [12](#)
- setCache (BEDbase), [10](#)
- setCache, BEDbase-method, [13](#)
- tags, BEDbase-method, [14](#)
- tibble, [3–6](#)