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,
  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 *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 *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 *Save a BED file or BEDset to a path given an id*

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 *Get BEDbase statistics*

Description

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

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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