Package ‘bedbaser’

April 5, 2026

Title A BEDbase client

Version 1.2.6

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

biocViews Software, DataImport, ThirdPartyClient

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Depends R (>= 4.5.0)

Imports AnVIL (>= 1.16.0), BiocFileCache, curl, dplyr, GenomeInfoDb, GenomicRanges, httr, methods, purrr, rtracklayer, rlang, R.utils, stats, stringr, tibble, tidyr, tools, utils

Suggests BiocStyle, knitr, liftOver, testthat (>= 3.0.0), withr

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

VignetteBuilder knitr

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/bedbaser

git_branch RELEASE_3_22

git_last_commit fbd1715

git_last_commit_date 2026-02-27

Repository Bioconductor 3.22

Date/Publication 2026-04-05

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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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