

Package ‘bedrockbio’

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Title Open-Access Computational Biology Datasets

Version 2.0.0

Description Efficiently access the 'Bedrock Bio' library of open-access computational biology datasets. Lazily query datasets backed by 'DuckDB' and 'Apache Iceberg', with support for predicate pushdown and column projection to the cloud storage backend. This enables quick, iterative access to otherwise massive, unwieldy datasets without downloading them in full. See <<https://bedrock.bio>> for available datasets and documentation.

Language en-US

License GPL (>= 3)

URL <https://bedrock.bio>,
<https://github.com/bedrock-bio/bedrock-bio-client>

BugReports <https://github.com/bedrock-bio/bedrock-bio-client/issues>

Depends R (>= 4.2)

Imports curl, DBI, dbplyr, dplyr, duckdb, jsonlite

Suggests testthat (>= 3.0.0), withr

Config/testthat/edition 3

OS_type unix

Encoding UTF-8

RoxygenNote 7.3.3

NeedsCompilation no

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Repository CRAN

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Contents

describe_namespace	2
describe_table	3
list_namespaces	3
list_tables	4
load_table	4
Index	6

describe_namespace	<i>Describe a namespace: its name, citation, license, context, and tables</i>
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Description

Describe a namespace: its name, citation, license, context, and tables

Usage

```
describe_namespace(name)
```

Arguments

name	Namespace identifier.
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Value

A named list with name, citation, license, context, and tables (fully-qualified table identifiers). Use describe_table() for per-table details.

Examples

```
## Not run:
library(bedrockbio)
describe_namespace("ukb_ppp")$tables

## End(Not run)
```

describe_table	<i>Describe a table: its context, columns, and partitions</i>
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Description

Describe a table: its context, columns, and partitions

Usage

```
describe_table(name)
```

Arguments

name	Table identifier.
------	-------------------

Value

A named list with name, context, columns (each with name, type, description, nullable), and partitions (a named list of partition column to values and default). Filter on partition columns for fastest reads.

Examples

```
## Not run:  
library(bedrockbio)  
describe_table("ukb_ppp.pqt1s")$name  
  
## End(Not run)
```

list_namespaces	<i>List available namespaces (data sources)</i>
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Description

List available namespaces (data sources)

Usage

```
list_namespaces()
```

Value

A character vector of namespace identifiers.

Examples

```
## Not run:
library(bedrockbio)
list_namespaces()

## End(Not run)
```

list_tables	<i>List available tables, optionally filtered to one namespace</i>
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Description

List available tables, optionally filtered to one namespace

Usage

```
list_tables(namespace = NULL)
```

Arguments

namespace If given, return only that namespace's tables; otherwise all tables.

Value

A character vector of fully-qualified table identifiers.

Examples

```
## Not run:
library(bedrockbio)
list_tables("ukb_ppp")

## End(Not run)
```

load_table	<i>Lazily query a table</i>
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Description

Lazily query a table

Usage

```
load_table(name)
```

Arguments

name Table identifier.

Value

A lazy tbl backed by DuckDB, compatible with dplyr verbs. Filter on partition columns (see `describe_table()`) for fastest reads.

Examples

```
## Not run:  
library(bedrockbio)  
library(dplyr)  
  
load_table("dbsnp.vcf") |>  
  filter(assembly == "GRCh38", chromosome == "22") |>  
  select(rsid, position, ref_allele, alt_allele) |>  
  head(5) |>  
  collect()  
  
## End(Not run)
```

Index

`describe_namespace`, [2](#)

`describe_table`, [3](#)

`list_namespaces`, [3](#)

`list_tables`, [4](#)

`load_table`, [4](#)