Package ‘bedrockbio’

May 7, 2026

Title Open-Access Computational Biology Datasets

Version 1.3.0

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 (>= 4.1)

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

Suggests testthat (>= 3.0.0)

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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`describe_table` *Describe a table's metadata, citation, and columns*

Description

Describe a table's metadata, citation, and columns

Usage

```
describe_table(name)
```

Arguments

`name`	Table identifier (e.g., "ukb_ppp.pqtls")

Value

A named list with name, description, citation, source_url, license, and columns.

Examples

```
## Not run:
library(bedrockbio)
info <- describe_table("ukb_ppp.pqtls")
info$name

## End(Not run)
```

`list_tables` *List available tables in the Bedrock Bio library*

Description

List available tables in the Bedrock Bio library

Usage

```
list_tables()
```

Value

A character vector of table identifiers

Examples

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

## End(Not run)
```

`load_table` *Lazily query a table*

Description

Lazily query a table

Usage

```
load_table(name, ...)
```

Arguments

`name`	Table identifier (e.g., "ukb_ppp.pqtls")
`...`	Required partition filters (e.g., ancestry = "EUR", protein_id = "A0FGR8")

Value

A lazy `tbl` backed by DuckDB, compatible with dplyr verbs.

Examples

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

df <- load_table(
  "dbsnp.vcf",
  assembly = "GRCh38",
  chromosome = "22"
) |>
  select(rsid, position, ref_allele, alt_allele) |>
  head(5) |>
  collect()

## End(Not run)
```

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