Package: rgbio (via r-universe)

May 27, 2026

Title High-Performance GenBank I/O using 'gb-io'

Version 0.4.0

Description Interfaces with the 'gb-io' Rust crate to provide fast reading and writing of GenBank files. Supports parsing of sequences, features, and metadata into R-friendly data structures.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Config/rextendr/version 0.4.2

SystemRequirements Cargo (Rust's package manager), rustc >= 1.65.0, xz

Depends R (>= 4.2)

Suggests Biostrings, GenomicRanges, IRanges, S4Vectors, tibble, knitr, rmarkdown, testthat

VignetteBuilder knitr

Config/pak/sysreqs xz-utils libclang-dev

Repository https://richardstoeckl.r-universe.dev

Date/Publication 2026-05-27 13:37:35 UTC

RemoteUrl https://github.com/richardstoeckl/rgbio

RemoteRef v0.4.0

RemoteSha b96a0a9f89d571692fe9e1388d2274c03f19b49d

Contents

`read_gbk` *Read a GenBank file*

Description

Reads one or more GenBank records and returns selected components in either Bioconductor, tidy, or base format.

Usage

```
read_gbk(
  file,
  format = "bioconductor",
  sequences = TRUE,
  features = TRUE,
  metadata = TRUE,
  records = NULL,
  validate = TRUE
)
```

Arguments

`file`	Character path to a GenBank file.
`format`	Output format. One of "bioconductor", "tidy", or "base".
`sequences`	Logical; include sequence data.
`features`	Logical; include feature annotations.
`metadata`	Logical; include record metadata.
`records`	Integer indices or character accession/name selectors.
`validate`	Logical; validate parsed records.

Value

A variable object based on selected components. Returns either a single object or a named list with `sequences`, `features`, and/or `metadata`.

`read_genbank` *Read a GenBank file*

Description

Deprecated compatibility wrapper for `read_gbk()`.

Usage

```
read_genbank(file)
```

Arguments

`file`	Path to a GenBank file.

Value

Parsed records in legacy list format.

`write_gbk` *Write GenBank records*

Description

Writes GenBank records from sequence, feature, and metadata components.

Usage

```
write_gbk(
  file,
  sequences,
  features = NULL,
  metadata = NULL,
  append = FALSE,
  validate = TRUE,
  line_width = 80
)
```

Arguments

`file`	Character path to output file.
`sequences`	DNAStringSet or named character vector.
`features`	GRanges with `type` and `qualifiers` in `mcols()`, or tidy feature table with columns `type`, `start`, `end`, `strand`, `qualifiers`.
`metadata`	DataFrame, data.frame, or list with record metadata.
`append`	Logical; append to file.
`validate`	Logical; validate inputs.
`line_width`	Integer sequence line width.

Value

Logical TRUE on success.

`write_genbank` *Write a GenBank file*

Description

Deprecated compatibility wrapper for `write_gbk()`.

Usage

```
write_genbank(file, sequence, features, metadata = list())
```

Arguments

`file`	Path to output file.
`sequence`	Sequence string.
`features`	Feature table with columns key, location, qualifiers.
`metadata`	Metadata list.

Value

Logical TRUE on success.

Index