

Package ‘dbSequence’

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Title DuckDB-Backed Interface for Large-Scale Genomic Data

Version 0.99.1

Description Provides a DuckDB-backed infrastructure for working with large-scale genomic data that exceeds available memory. Supports lazy evaluation of genomic ranges and efficient overlap queries. Integrates with Bioconductor classes (GRanges, BiocIO) and provides plyranges-compatible API.

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BugReports <https://github.com/dbverse-org/dbSequence/issues>

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dbSequence-package	<i>dbSequence: DuckDB-Backed Interface for Large-Scale Genomic Data</i>
--------------------	---

Description

dbSequence provides DuckDB-backed infrastructure for genomic interval and sequence-derived data that are too large to work with comfortably in memory. It imports common genomics file formats into DuckDB, keeps range operations lazy, and interoperates with Bioconductor classes such as [GenomicRanges::GRanges](#).

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See Also

Useful links:

- <https://github.com/dbverse-org/dbSequence>
- Report bugs at <https://github.com/dbverse-org/dbSequence/issues>

asRanges

Extract genomic ranges from dbSequence objects

Description

Extract genomic ranges from dbSequence objects

Usage

```
asRanges(x, ...)
```

Arguments

x	(required) A dbSequence object
...	(optional) Additional arguments

Value

A view of the dbSequence with only range columns (seqnames, start, end, strand)

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_path <- tempfile(fileext = ".duckdb")
db_seq <- read_bed(bed, dest = DuckDBFile(db_path), lazy = FALSE)
asRanges(db_seq)
```

as_granges

Convert objects to GRanges

Description

S3 generic for converting various objects to GRanges. This generic is provided for plyranges compatibility when plyranges is not loaded.

S3 method for plyranges compatibility. Converts a dbSequence object to a GRanges object by collecting data from DuckDB.

Usage

```
as_granges(.data, ..., keep_mcols = TRUE)

## Default S3 method:
as_granges(.data, ..., keep_mcols = TRUE)

## S3 method for class 'dbSequence'
as_granges(.data, ..., keep_mcols = TRUE)
```

Arguments

.data	A dbSequence object
...	Additional arguments (currently unused)
keep_mcols	logical: whether to keep metadata columns (default: TRUE)

Details

This method enables plyranges-style workflows: `db_seq %>% as_granges()`

Note that this collects all data from DuckDB into memory. For large datasets, consider filtering first using dplyr verbs.

Value

A GRanges object

A GRanges object

Examples

```
# Import BED file to dbSequence
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)

# Convert to GRanges (collects data)
gr <- as_granges(db_seq)
```

as_ranges-dbSequence-method

Extract range columns as a view

Description

Returns a view of the dbSequence with only the core range columns (seqnames, start, end, strand). This is useful for range operations that don't need metadata columns.

Usage

```
## S4 method for signature 'dbSequence'
asRanges(x, ...)
```

Arguments

x (required) A dbSequence object
 ... (optional) Additional arguments (currently unused)

Value

A dbSequence view with only range columns

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_path <- tempfile(fileext = ".duckdb")
db_seq <- read_bed(bed, dest = DuckDBFile(db_path), lazy = FALSE)
asRanges(db_seq)
```

coerce-methods

Coercion methods between dbSequence and GRanges

Description

Methods for converting between dbSequence and GRanges objects.

as(dbSequence, "GRanges") materializes a dbSequence object into an in-memory GRanges object, triggering data collection from the DuckDB database.

as(GRanges, "dbSequence") loads a GRanges object into a DuckDB table and wraps it as dbSequence, enabling lazy evaluation of operations.

Arguments

from Object to convert (dbSequence or GRanges)

Value

Converted object (GRanges or dbSequence respectively)

compute.dbSequence	<i>Materialize a dbSequence in DuckDB</i>
--------------------	---

Description

S3 method for `dplyr::compute()` that materializes the underlying lazy query into a DuckDB table, returning a new `dbSequence` pointing at the computed table.

Usage

```
compute.dbSequence(
  x,
  name = tableName(x),
  temporary = TRUE,
  overwrite = TRUE,
  ...
)
```

Arguments

<code>x</code>	A <code>dbSequence</code> object
<code>name</code>	Character table name to create. Defaults to <code>tableName(x)</code> .
<code>temporary</code>	Logical, create a temporary table (default: <code>TRUE</code>)
<code>overwrite</code>	Logical, overwrite existing table (default: <code>TRUE</code>)
<code>...</code>	Passed to <code>dplyr::compute()</code> .

Value

A `dbSequence` object backed by the materialized table.

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)
materialized <- compute.dbSequence(db_seq, name = "bed_materialized")
materialized
```

compute_coverage	<i>Compute coverage over a region</i>
------------------	---------------------------------------

Description

Compute coverage (count of overlapping fragments) in bins across a genomic region. This is useful for visualization and summarizing fragment density.

Usage

```
compute_coverage(x, region, window = 100, ...)
```

```
## S3 method for class 'dbSequence'
compute_coverage(x, region, window = 100, ...)
```

Arguments

x	A dbSequence object
region	A GRanges object or string like "chr1:1000-2000"
window	Bin size in base pairs (default: 100)
...	Additional arguments

Value

A data frame with columns: bin_start, bin_end, count

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
fragments <- read_bed(bed)
coverage <- compute_coverage(fragments, "chr1:100-500", window = 100)
coverage
```

dbSequence

Constructor for dbSequence objects

Description

Creates a dbSequence object by wrapping a table name. This is typically called internally by import methods.

Usage

```
dbSequence(table_name, file_source = NULL, .conn = NULL)
```

Arguments

table_name	(required) character: name of the table in the DuckDB database
file_source	(required) character or DuckDBFile: source file or database
.conn	(optional) DBIConnection: existing connection for in-memory databases (default: NULL)

Value

A dbSequence object

Examples

```
db_path <- tempfile(fileext = ".duckdb")
con <- DBI::dbConnect(duckdb::duckdb(), dbdir = db_path)
DBI::dbWriteTable(con, "ranges", data.frame(seqnames = "chr1", start = 1, end = 10))
DBI::dbDisconnect(con, shutdown = TRUE)

db_seq <- dbSequence("ranges", DuckDBFile(db_path))
db_seq
```

dbSequence-class	<i>dbSequence objects</i>
------------------	---------------------------

Description

S4 class for genomic sequences stored in DuckDB

Extends dbData to wrap genomic data stored in DuckDB tables.

Slots

value dplyr tbl representing the genomic data in the database (inherited from dbData)

name character table name in database (inherited from dbData)

file_source character source file path or identifier (immutable after creation)

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)
db_seq
```

DuckDBFile	<i>Constructor for DuckDBFile objects</i>
------------	---

Description

Creates a DuckDBFile object that wraps a file path for DuckDB databases. This is a simple path wrapper following the BiocFile pattern and supports both file paths and in-memory databases.

Usage

```
DuckDBFile(resource)
```

Arguments

resource (required) character: path to DuckDB file. Can be a file path or ":memory:" for in-memory databases

Value

DuckDBFile object containing the path information

Examples

```
# Create DuckDBFile for existing database
db_file <- DuckDBFile(tempfile(fileext = ".duckdb"))

# Create DuckDBFile for in-memory database
mem_db <- DuckDBFile(":memory:")
```

DuckDBFile-class	<i>DuckDBFile objects</i>
------------------	---------------------------

Description

File class for DuckDB database files, extending BiocFile

This mirrors the *File* classes in *rtracklayer*, giving us a concrete object to dispatch `import()` / `export()` methods **to**. Extends `BiocFile` to be compatible with `BiocIO` import/export framework.

Slots

`path` Character string specifying the path to the DuckDB database file. Can be a file path or `":memory:"` for in-memory databases.

Examples

```
db_file <- DuckDBFile(tempfile(fileext = ".duckdb"))
db_file
```

<code>fileSource</code>	<i>Accessor for file_source slot</i>
-------------------------	--------------------------------------

Description

This method prevents modification of the `file_source` slot after object creation. The `file_source` is set during import and should not be changed to maintain data integrity.

Usage

```
fileSource(object)

## S4 method for signature 'dbSequence'
fileSource(object)

fileSource(object) <- value

## S4 replacement method for signature 'dbSequence'
fileSource(object) <- value
```

Arguments

object	A dbSequence object
value	New value (will be rejected)

Value

The file_source value

Always errors because file sources are immutable after creation.

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)
fileSource(db_seq)
try(fileSource(db_seq) <- "other.bed")

bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)
try(fileSource(db_seq) <- "other.bed")
```

filter_by_overlaps	<i>Filter ranges by overlap</i>
--------------------	---------------------------------

Description

Filter a dbSequence object to only include ranges that overlap with a set of query ranges. This operation is performed in DuckDB using efficient SQL filtering.

Usage

```
filter_by_overlaps(x, y, ...)

## S3 method for class 'dbSequence'
filter_by_overlaps(x, y, ...)
```

Arguments

x	A dbSequence object
y	A GRanges object or dbSequence object representing query ranges
...	Additional arguments (currently unused)

Details

Two intervals overlap if: start1 <= end2 AND start2 <= end1 AND chr1 == chr2

The operation is pushed down to DuckDB, so only matching rows are retrieved.

Value

A dbSequence object filtered to overlapping ranges

Examples

```
# Filter fragments to a specific region
bed <- system.file("extdata", "example.bed", package = "dbSequence")
fragments <- read_bed(bed)
region <- GenomicRanges::GRanges("chr1:100-500")
filtered <- filter_by_overlaps(fragments, region)
filtered
```

```
import,BamFile,missing,ANY-method
Import BAM files into DuckDB
```

Description

Import BAM files into DuckDB

Usage

```
## S4 method for signature 'BamFile,missing,ANY'
import(con, format, text, dest, table_name = "bam_data", .conn = NULL, ...)
```

Arguments

con	A file connection object.
format	Import format; unused for these methods.
text	Text input; unused for these methods.
dest	A DuckDBFile destination.
table_name	Table name to create.
.conn	Optional existing DBI connection.
...	Additional arguments.

Value

A dbSequence object backed by a DuckDB table.

```
import,BEDFile,missing,ANY-method
Import BED files into DuckDB
```

Description

Import BED files into DuckDB

Usage

```
## S4 method for signature 'BEDFile,missing,ANY'
import(con, format, text, dest, table_name = "bed_data", ...)
```

Arguments

<code>con</code>	A file connection object.
<code>format</code>	Import format; unused for these methods.
<code>text</code>	Text input; unused for these methods.
<code>dest</code>	A DuckDBFile destination.
<code>table_name</code>	Table name to create.
<code>...</code>	Additional arguments.

Value

A `dbSequence` object backed by a DuckDB table.

`import,character,missing,ANY-method`

Import character file paths into DuckDB (auto-detect format)

Description

Import character file paths into DuckDB (auto-detect format)

Usage

```
## S4 method for signature 'character,missing,ANY'
import(con, format, text, dest, table_name = NULL, ...)
```

Arguments

<code>con</code>	A file path.
<code>format</code>	Import format; unused for these methods.
<code>text</code>	Text input; unused for these methods.
<code>dest</code>	A DuckDBFile destination.
<code>table_name</code>	Table name to create. If <code>NULL</code> , the file extension is used.
<code>...</code>	Additional arguments.

Value

A `dbSequence` object backed by a DuckDB table.

```
import,FastaFile,missing,ANY-method
  Import FASTA files into DuckDB
```

Description

Import FASTA files into DuckDB

Usage

```
## S4 method for signature 'FastaFile,missing,ANY'
import(con, format, text, dest, table_name = "fasta_data", ...)
```

Arguments

con	A file connection object.
format	Import format; unused for these methods.
text	Text input; unused for these methods.
dest	A DuckDBFile destination.
table_name	Table name to create.
...	Additional arguments.

Value

A dbSequence object backed by a DuckDB table.

```
import,GFFFile,missing,ANY-method
  Import GFF files into DuckDB
```

Description

Import GFF files into DuckDB

Usage

```
## S4 method for signature 'GFFFile,missing,ANY'
import(con, format, text, dest, table_name = "gff_data", ...)
```

Arguments

con	A file connection object.
format	Import format; unused for these methods.
text	Text input; unused for these methods.
dest	A DuckDBFile destination.
table_name	Table name to create.
...	Additional arguments.

Value

A dbSequence object backed by a DuckDB table.

```
import,GTFFile,missing,ANY-method
      Import GTF files into DuckDB
```

Description

Import GTF files into DuckDB

Usage

```
## S4 method for signature 'GTFFile,missing,ANY'
import(con, format, text, dest, table_name = "gtf_data", ...)
```

Arguments

con	A file connection object.
format	Import format; unused for these methods.
text	Text input; unused for these methods.
dest	A DuckDBFile destination.
table_name	Table name to create.
...	Additional arguments.

Value

A dbSequence object backed by a DuckDB table.

```
import,VcfFile,missing,ANY-method
      Import VCF files into DuckDB
```

Description

Import VCF files into DuckDB

Usage

```
## S4 method for signature 'VcfFile,missing,ANY'
import(con, format, text, dest, table_name = "vcf_data", ...)
```

Arguments

<code>con</code>	A file connection object.
<code>format</code>	Import format; unused for these methods.
<code>text</code>	Text input; unused for these methods.
<code>dest</code>	A DuckDBFile destination.
<code>table_name</code>	Table name to create.
<code>...</code>	Additional arguments.

Value

A `dbSequence` object backed by a DuckDB table.

<code>pool</code>	<i>Pool (aggregate) values by grouping columns</i>
-------------------	--

Description

Aggregates values in a lazy database table by grouping columns. This is the database-native equivalent of `dplyr::group_by() + summarise()` but with a simpler interface optimized for common pooling operations.

Usage

```
pool(
  x,
  group_by,
  value_col = NULL,
  fun = "sum",
  name = NULL,
  filter_zero = TRUE,
  temporary = TRUE,
  overwrite = TRUE,
  ...
)

## Default S3 method:
pool(
  x,
  group_by,
  value_col = NULL,
  fun = "sum",
  name = NULL,
  filter_zero = TRUE,
  temporary = TRUE,
  overwrite = TRUE,
  ...
)

## S3 method for class 'tbl_duckdb_connection'
```

```

pool(
  x,
  group_by,
  value_col = "x",
  fun = "sum",
  name = NULL,
  filter_zero = TRUE,
  temporary = TRUE,
  overwrite = TRUE,
  ...
)

## S3 method for class 'tbl_dbi'
pool(
  x,
  group_by,
  value_col = "x",
  fun = "sum",
  name = NULL,
  filter_zero = TRUE,
  temporary = TRUE,
  overwrite = TRUE,
  ...
)

## S3 method for class 'dbSequence'
pool(
  x,
  group_by,
  value_col = "score",
  fun = "sum",
  name = NULL,
  filter_zero = TRUE,
  temporary = TRUE,
  overwrite = TRUE,
  ...
)

```

Arguments

<code>x</code>	A <code>dbSequence</code> object, <code>tbl_duckdb_connection</code> , or other lazy table
<code>group_by</code>	Character vector of column names to group by
<code>value_col</code>	Character, the column to aggregate. Default is "score" for <code>dbSequence</code> , "x" for <code>tbl</code> objects.
<code>fun</code>	Character, aggregation function: "sum" (default), "mean", "count", "min", "max"
<code>name</code>	Character, optional name for the resulting computed table. If NULL, returns a lazy query without materializing.
<code>filter_zero</code>	Logical, if TRUE (default) filter out rows where aggregated value == 0
<code>temporary</code>	Logical, if TRUE (default) create a temporary table, otherwise create a permanent table
<code>overwrite</code>	Logical, if TRUE (default) overwrite existing table

... Additional arguments passed to `dplyr::compute()`

Value

Same type as input (lazy, still in database). For `dbSequence`, returns `dbSequence` if range columns are preserved, otherwise returns `tbl`.

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)

# Pool feature scores by feature name
pooled <- pool(db_seq, group_by = "name", value_col = "score")
pooled
```

read_bam	<i>Read a BAM file into DuckDB</i>
----------	------------------------------------

Description

plyranges-style function to read BAM files. Returns a `dbSequence` object backed by DuckDB.

Usage

```
read_bam(file, dest = DuckDBFile(":memory:"), table_name = "alignments", ...)
```

Arguments

<code>file</code>	Path to BAM file
<code>dest</code>	DuckDBFile or path: destination database (default: in-memory)
<code>table_name</code>	character: name for the table (default: "alignments")
...	Additional arguments passed to <code>import()</code>

Value

A `dbSequence` object

Note

Unlike `plyranges::read_bam` which returns a `DeferredGenomicRanges`, this function immediately imports the BAM data into DuckDB.

See Also

[import](#), [BamFile](#)

Examples

```
if (nzchar(system.file(package = "exonr"))) {
  bam <- system.file("extdata", "example.bam", package = "dbSequence")
  db_seq <- read_bam(bam, dest = DuckDBFile(tempfile(fileext = ".duckdb")))
  db_seq
}
```

read_bed

*Read a BED file into DuckDB***Description**

plyranges-style function to read BED files. Unlike the plyranges version which returns GRanges, this returns a dbSequence object backed by DuckDB for lazy evaluation.

Usage

```
read_bed(
  file,
  dest = DuckDBFile(":memory:"),
  table_name = "bed_data",
  lazy = TRUE,
  ...
)
```

Arguments

file	Path to BED file
dest	DuckDBFile or path: destination database (default: in-memory)
table_name	character: name for the table (default: "bed_data")
lazy	logical: if TRUE (default), do not import/copy the file into a DuckDB table. Instead, return a dbSequence backed by a DuckDB scan query (an inline SQL SELECT over the file). Call <code>dplyr::compute()</code> on the result to materialize when needed.
...	Additional arguments passed to <code>import()</code>

Value

A dbSequence object

See Also

[import](#), [BEDFile](#)

Examples

```
# Read BED file (lazy, stays in DuckDB)
bed <- system.file("extdata", "example.bed", package = "dbSequence")
db_seq <- read_bed(bed)

# Collect to GRanges when needed
gr <- as_granges(db_seq)
```

read_gff	<i>Read a GFF/GTF file into DuckDB</i>
----------	--

Description

plyranges-style function to read GFF files. Returns a dbSequence object backed by DuckDB.

Usage

```
read_gff(
  file,
  dest = DuckDBFile(":memory:"),
  table_name = "gff_data",
  lazy = TRUE,
  ...
)

read_gff3(
  file,
  dest = DuckDBFile(":memory:"),
  table_name = "gff_data",
  lazy = TRUE,
  ...
)
```

Arguments

file	Path to GFF file
dest	DuckDBFile or path: destination database (default: in-memory)
table_name	character: name for the table (default: "gff_data")
lazy	logical: if TRUE (default), do not import/copy the file into a DuckDB table. Instead, return a dbSequence backed by a DuckDB scan query (an inline SQL SELECT over the file). Call <code>dplyr::compute()</code> on the result to materialize when needed.
...	Additional arguments passed to <code>import()</code>

Value

A dbSequence object

See Also

[import](#), [GFFFile](#)

Examples

```
gff <- system.file("extdata", "example.gff3", package = "dbSequence")
db_seq <- read_gff(gff)
db_seq
```

read_vcf

Read a VCF file into DuckDB

Description

Read VCF variant files into DuckDB. Returns a dbSequence object.

Usage

```
read_vcf(
  file,
  dest = DuckDBFile(":memory:"),
  table_name = "variants",
  lazy = TRUE,
  ...
)
```

Arguments

file	Path to VCF file
dest	DuckDBFile or path: destination database (default: in-memory)
table_name	character: name for the table (default: "variants")
lazy	logical: if TRUE (default), do not import/copy the file into a DuckDB table. Instead, return a dbSequence backed by a DuckDB scan query (an inline SQL SELECT over the file). Call <code>dplyr::compute()</code> on the result to materialize when needed.
...	Additional arguments passed to <code>import()</code>

Value

A dbSequence object

See Also

[import](#), [VcfFile](#)

Examples

```
vcf <- system.file("extdata", "example.vcf", package = "dbSequence")
db_seq <- read_vcf(vcf)
db_seq
```

show,dbSequence-method

Show method for dbSequence objects

Description

Display a summary of the dbSequence object and preview the table data

Usage

```
## S4 method for signature 'dbSequence'  
show(object)
```

Arguments

object A dbSequence object

Value

Invisibly returns NULL.

show,DuckDBFile-method

Show method for DuckDBFile objects

Description

Display information about the DuckDBFile object.

Usage

```
## S4 method for signature 'DuckDBFile'  
show(object)
```

Arguments

object A DuckDBFile object

Value

Invisibly returns NULL.

`tableName`*Get table name from dbSequence*

Description

Extract the table name from a dbSequence object.

Usage

```
tableName(x)
```

```
## S4 method for signature 'dbSequence'  
tableName(x)
```

Arguments

`x` (required) A dbSequence object

Value

character: the table name

Examples

```
bed <- system.file("extdata", "example.bed", package = "dbSequence")  
db_seq <- read_bed(bed)  
tableName(db_seq)
```

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