

# Package ‘DuckDBDataFrame’

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**Title** DuckDB-Backed DataFrame and Table Structures

**Description** Provides DuckDB-backed implementations of core tabular data structures including DuckDBTable, DuckDBDataFrame, and DuckDBColumn. These classes extend Bioconductor's S4Vectors framework to enable efficient, out-of-memory operations on large tabular datasets using DuckDB's analytical database engine. The package includes SQL function discovery, connection management, and support for list columns and embeddings stored in ARRAY[] columns.

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**URL** <https://github.com/Genentech/DuckDBDataFrame>

**BugReports** <https://github.com/Genentech/DuckDBDataFrame/issues>

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'DuckDBEmbeddings-class.R' 'DuckDBDataFrame-class.R'  
'DuckDBDataFrame-internals.R' 'DuckDBDataFrame-package.R'  
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|                         |                                                                      |
|-------------------------|----------------------------------------------------------------------|
| DuckDBDataFrame-package |                                                                      |
|                         | <i>DuckDBDataFrame: DuckDB-Backed DataFrame and Table Structures</i> |

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Description

Provides DuckDB-backed implementations of core tabular data structures including DuckDBTable, DuckDBDataFrame, and DuckDBColumn. These classes extend Bioconductor’s S4Vectors framework to enable efficient, out-of-memory operations on large tabular datasets using DuckDB’s analytical database engine. The package includes SQL function discovery, connection management, and support for list columns and embeddings stored in ARRAY[] columns.

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## See Also

Useful links:

- <https://github.com/Genentech/DuckDBDataFrame>
- Report bugs at <https://github.com/Genentech/DuckDBDataFrame/issues>

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arrow-types

*Arrow type helpers for the DuckDB package suite*

---

## Description

Utilities for narrowing integer types and converting between [DataType](#) objects and Arrow type names. Used by **BiocDuckDB** and **DuckDBArray** for Parquet schema selection and parallel-safe type passing.

## Usage

```
arrowIntType(range)
```

```
arrowType(x)
```

```
arrowTypeToName(type)
```

```
arrowTypeFromName(name)
```

## Arguments

|       |                                                                                                  |
|-------|--------------------------------------------------------------------------------------------------|
| range | Length-two numeric vector c(min, max) for <a href="#">arrowIntType</a> .                         |
| x     | An R vector for <a href="#">arrowType</a> .                                                      |
| type  | An <a href="#">DataType</a> or Arrow type name (character) for <a href="#">arrowTypeToName</a> . |
| name  | Length-one character Arrow type name (e.g. "uint16") for <a href="#">arrowTypeFromName</a> .     |

## Details

`arrowIntType` selects the narrowest unsigned or signed Arrow integer type that can represent range. `arrowType` infers an Arrow type from an R vector, narrowing integers when possible.

`arrowTypeFromName` and `arrowTypeToName` implement a small registry of scalar Arrow types used when passing type information to BiocParallel workers (where `DataType` external pointers do not serialize reliably).

## Value

`arrowIntType`, `arrowType` An [DataType](#).

`arrowTypeToName` A length-one character Arrow type name.

`arrowTypeFromName` An [DataType](#).

## Author(s)

Patrick Aboyoun

**See Also**

[parquet-io](#), [writeParquet](#), [writeCoordArray](#)

**Examples**

```
arrowIntType(c(0L, 10L))
arrowType(1:10L)
arrowTypeToName(arrow::uint16())
arrowTypeFromName("uint16")
```

---

DuckDBAtomicList-class

*DuckDBAtomicList objects*

---

**Description**

The DuckDBAtomicList class extends [AtomicList](#) and [DuckDBColumn](#) to represent list columns extracted from a [DuckDBDataFrame](#) object.

**Value**

Objects of class DuckDBAtomicList extend [AtomicList](#).

**Accessors**

In the code snippets below, `x` is a DuckDBAtomicList object:

`length(x)`: Get the number of list elements in `x`.

`names(x)`: Get the names of the list elements of `x`.

`elementNROWS(x)`: Get the length of each list element in `x`.

`elementType(x)`: Get the type of the list elements; one of "logical", "integer", "integer64", "numeric", "character", or "factor".

`dimtbls(x, drop = TRUE)`, `dimtbls(x) <- value`: Get or set the list of dimension tables used to define partitions for efficient queries. If `drop = TRUE`, then it returns a named `DataFrameList` object, else it returns an environment containing a `dimtbls` named `DataFrameList` element.

**Coercion**

`as.list(x)`: Coerces `x` to a list.

`realize(x, BACKEND = getAutoRealizationBackend())`: Realize an object into memory or on disk using the equivalent of `realize(as.list(x), BACKEND)`.

**Subsetting**

In the code snippets below, `x` is a DuckDBAtomicList object:

`x[i]`: Returns a DuckDBAtomicList object containing the selected list elements.

`x[[i]]`: Extracts the list element at position `i` as an atomic vector.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` list elements of `x`. If `n` is negative, returns all but the last `abs(n)` list elements of `x`.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` list elements of `x`. If `n` is negative, returns all but the first `abs(n)` list elements of `x`.

**Author(s)**

Patrick Aboyoun

**See Also**

- [DuckDBColumn-class](#) for atomic columns
- [AtomicList](#) for the base class
- [List](#) for the List class hierarchy

**Examples**

```
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
df <- data.frame(
  id = sprintf("gene%02d", 1:5),
  int_list = I(lapply(1:5, function(i) seq_len(i)))
)
arrow::write_parquet(df, tf)
ddf <- DuckDBDataFrame(tf, keycol = "id")
lst <- ddf[["int_list"]]
lst
elementNROWS(lst)
```

---

DuckDBColumn-class      *DuckDBColumn objects*


---

**Description**

The DuckDBColumn class extends [Vector](#) to represent a column extracted from a [DuckDBDataFrame](#) object.

**Value**

Objects of class DuckDBColumn extend [Vector](#).

**Accessors**

In the code snippets below, *x* is a DuckDBColumn object:

`length(x)`: Get the number of elements in *x*.

`names(x)`: Get the names of the elements of *x*.

`dimtbls(x, drop = TRUE)`, `dimtbls(x) <- value`: Get or set the list of dimension tables used to define partitions for efficient queries. If `drop = TRUE`, then it returns a named `DataFrameList` object, else it returns an environment containing a `dimtbls` named `DataFrameList` element.

`type(x)`, `type(x) <- value`: Get or set the data type of the elements; one of "logical", "integer", "integer64", "double", "character", or "factor" (a "character" column with a recorded `collevels` entry).

`levels(x)`, `nlevels(x)`: Get the recorded factor levels (or their count), or NULL (`0` for `nlevels`) if *x* is not a "factor"-typed column. Does not materialize *x*. There is no `levels<-` replacement method; relabeling levels would need to remap the underlying stored values, not just the recorded level set.

**Coercion**

`as.vector(x)`: Coerces `x` to a vector.

`realize(x, BACKEND = getAutoRealizationBackend())`: Realize an object into memory or on disk using the equivalent of `realize(as.vector(x), BACKEND)`.

**Subsetting**

In the code snippets below, `x` is a `DuckDBColumn` object:

`x[i]`: Returns a `DuckDBColumn` object containing the selected elements.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` elements of `x`. If `n` is negative, returns all but the last `abs(n)` elements of `x`.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` elements of `x`. If `n` is negative, returns all but the first `abs(n)` elements of `x`.

**Author(s)**

Patrick Aboyoun

**See Also**

- [DuckDBColumn-utils](#) for the utilities
- [Vector](#) for the base class

**Examples**

```
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(cbind(model = rownames(mtcars), mtcars), tf)
df <- DuckDBDataFrame(tf, datacols = colnames(mtcars), keycol = "model")
cyl <- df[["cyl"]]
cyl
length(cyl)
mean(cyl)
head(cyl, 3)
```

**Description**

Common operations on [DuckDBColumn](#) objects.

**Value**

Method return types are documented in the sections above.

## SQL Methods

In the code snippets below, `x` is a `DuckDBColumn` object:

`sql_call(x, fun, ...)`: Applies the specified SQL function to all data columns of `x`.

`sql_fun(x, function_type = NULL, return_type = NULL, description = FALSE)`: Finds DuckDB SQL functions compatible with the data type of `x`. Returns a `data.frame` of matching functions with optional filtering by function type and return type.

## Group Generics

`DuckDBColumn` objects have support for S4 group generic functionality:

Arith `"+", "-", "*", "^", "%", "/", "/"`

Compare `"==", ">", "<", "!="`, `"<=", ">="`

Logic `"&", "|", "!"`

Ops `"Arith", "Compare", "Logic"`

Math `"abs", "sign", "sqrt", "ceiling", "floor", "trunc", "log", "log10", "log2", "acos", "acosh", "asin", "asinh", "atan", "atanh", "exp", "expm1", "cos", "cosh", "sin", "sinh", "tan", "tanh", "gamma", "lgamma"`

Summary `"max", "min", "range", "prod", "sum", "any", "all"`

See [S4groupGeneric](#) for more details.

## Numerical Data Methods

In the code snippets below, `x` is a `DuckDBColumn` object:

`anyNA(x)`: Returns a single logical: TRUE if any value in `x` is missing.

`is.finite(x)`: Returns a `DuckDBColumn` containing logicals that indicate which values are finite.

`is.infinite(x)`: Returns a `DuckDBColumn` containing logicals that indicate which values are infinite.

`is.na(x)`: Returns a `DuckDBColumn` containing logicals that indicate which values are missing (SQL NULL).

`is.nan(x)`: Returns a `DuckDBColumn` containing logicals that indicate which values are Not a Number.

`mean(x)`: Calculates the mean of `x`.

`var(x)`: Calculates the variance of `x`.

`sd(x)`: Calculates the standard deviation of `x`.

`median(x)`: Calculates the median of `x`.

`quantile(x, probs = seq(0, 1, 0.25), names = TRUE, type = 7)`: Calculates the specified quantiles of `x`.

`probs` A numeric vector of probabilities with values in `[0,1]`.

`names` If TRUE, the result has names describing the quantiles.

`type` Either 1 or 7 that specifies the quantile algorithm detailed in [quantile](#).

`mad(x, constant = 1.4826)`: Calculates the median absolute deviation of `x`.

`constant` The scale factor.

`IQR(x, type = 7)`: Calculates the interquartile range of `x`.

type Either 1 or 7 that specifies the quantile algorithm detailed in [quantile](#).

pmax(..., na.rm = FALSE): Returns the parallel maxima of multiple DuckDBColumn objects. All arguments must be DuckDBColumn objects with compatible dimensions.

pmin(..., na.rm = FALSE): Returns the parallel minima of multiple DuckDBColumn objects. All arguments must be DuckDBColumn objects with compatible dimensions.

## Character Methods

In the code snippets below, x is a DuckDBColumn object:

nchar(x): Returns a DuckDBColumn containing the number of characters in each string.

tolower(x): Returns a DuckDBColumn with all strings converted to lowercase.

toupper(x): Returns a DuckDBColumn with all strings converted to uppercase.

chartr(old, new, x): Returns a DuckDBColumn with characters translated.

old Characters to be translated.

new Characters to translate to.

substr(x, start, stop): Returns a DuckDBColumn containing substrings extracted by position.

start Integer starting position (1-indexed).

stop Integer ending position (inclusive).

substring(x, first, last = 1000000L): Returns a DuckDBColumn containing substrings extracted by position.

first Integer starting position (1-indexed).

last Integer ending position (inclusive).

grepl(pattern, x, ignore.case = FALSE, fixed = FALSE): Returns a DuckDBColumn containing logicals indicating pattern matches.

pattern Character string containing a regular expression.

ignore.case If TRUE, case-insensitive matching.

fixed If TRUE, pattern is a fixed string not regex.

sub(pattern, replacement, x, ignore.case = FALSE, fixed = FALSE): Returns a DuckDBColumn with first match of pattern replaced.

pattern Character string containing a regular expression.

replacement Replacement string.

ignore.case If TRUE, case-insensitive matching.

fixed If TRUE, pattern is a fixed string not regex.

gsub(pattern, replacement, x, ignore.case = FALSE, fixed = FALSE): Returns a DuckDBColumn with all matches of pattern replaced.

pattern Character string containing a regular expression.

replacement Replacement string.

ignore.case If TRUE, case-insensitive matching.

fixed If TRUE, pattern is a fixed string not regex.

startsWith(x, prefix): Returns a DuckDBColumn containing logicals indicating if strings start with the specified prefix.

endsWith(x, suffix): Returns a DuckDBColumn containing logicals indicating if strings end with the specified suffix.

paste(..., sep = " ", collapse = NULL): Concatenates multiple DuckDBColumn objects using the specified separator. The collapse argument is not supported. All arguments must be DuckDBColumn objects with compatible dimensions.

## General Methods

In the code snippets below, `x` is a `DuckDBColumn` object:

`unique(x)`: Returns a `DuckDBColumn` containing the distinct rows.

`x %in% table`: Returns a `DuckDBColumn` containing logicals that indicate the elements of `x` in `table`.

`table(...)`: Returns a table containing the counts across the distinct values.

## Sparsity Methods

In the code snippets below, `x` is a `DuckDBColumn` object:

`is_nonzero(x)`: Returns a `DuckDBColumn` containing logicals that indicate if the elements of `x` are non-zero.

`nzcount(x)`: Returns the total number of non-zero values.

## Author(s)

Patrick Aboyoun

## See Also

- [DuckDBColumn-class](#) for the main class
- [Vector](#) for the base class

## Examples

```
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(cbind(model = rownames(mtcars), mtcars), tf)
df <- DuckDBDataFrame(tf, datacols = colnames(mtcars), keycol = "model")
mpg <- df[["mpg"]]
mean(mpg)
sd(mpg)
unique(mpg)[1:5]
```

---

DuckDBConnection

*Acquire and Release the DuckDB Connection*

---

## Description

Acquire and Release the DuckDB connection used by the **BiocDuckDB** package.

## Usage

```
loadExtension(conn, extension, optional = FALSE)

configureOutOfCore(conn)

configureCloud(conn)

acquireDuckDBConn(
  conn = dbConnect(duckdb(), bigint = "integer64", array = "matrix")
)

releaseDuckDBConn()
```

## Arguments

|                        |                                                                                                                                                                             |
|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>conn</code>      | A <code>duckdb_connection</code> object.                                                                                                                                    |
| <code>extension</code> | A character string naming a DuckDB extension (e.g. "spatial").                                                                                                              |
| <code>optional</code>  | If TRUE, an extension that is unknown to the build or cannot be installed (permission / network) produces a warning and is skipped rather than an error. Defaults to FALSE. |

## Details

`acquireDuckDBConn` will add a `duckdb_connection` object to the **BiocDuckDB** package cache. `releaseDuckDBConn` will remove the `duckdb_connection` object from that cache. `loadExtension` installs and loads a DuckDB extension on the shared connection; it is used by companion packages (e.g. **DuckDBSpatial**) to ensure their required extension ("spatial") is available.

`configureOutOfCore` is called automatically by `acquireDuckDBConn` when the shared connection is first created; call it again (on `acquireDuckDBConn()`) after changing an option to re-apply. Each setting is read from an R option first, then an environment variable, and left at the DuckDB default when neither is set:

| Setting                  | Option                                                 | Environment variable                             |
|--------------------------|--------------------------------------------------------|--------------------------------------------------|
| memory limit             | <code>DuckDBDataFrame.memory_limit</code>              | <code>BIOCDUCKDB_MEMORY_LIMIT</code>             |
| threads                  | <code>DuckDBDataFrame.threads</code>                   | <code>BIOCDUCKDB_THREADS</code>                  |
| spill directory          | <code>DuckDBDataFrame.temp_directory</code>            | <code>BIOCDUCKDB_TEMP_DIRECTORY</code>           |
| preserve insertion order | <code>\DuckDBDataFrame.preserve_insertion_order</code> | <code>BIOCDUCKDB_PRESERVE_INSERTION_ORDER</code> |

Setting `memory_limit` (e.g. "16GB" or "80%") and `temp_directory` guards against the OS killing the process before DuckDB can spill a large aggregation/sort/join; `preserve_insertion_order = FALSE` avoids buffering a whole result to preserve row order on a Tahoe-scale export where order is not significant.

The spill `temp_directory` is always set and created (recursively): when neither the option nor the environment variable is given it defaults to a temp subdirectory of `R_user_dir("DuckDBDataFrame", "cache")` rather than DuckDB's default under the R session tempdir, which on batch schedulers (e.g. SLURM's per-job /tmp) can be small or cleaned mid-session and make a spill fail to create its directory. Point `BIOCDUCKDB_TEMP_DIRECTORY` at roomy scratch for large out-of-core sorts.

The `memory_limit` likewise gets a package default when unset: 80% of the most-restrictive detected ceiling – an explicit SLURM allocation (`SLURM_MEM_PER_NODE`, or `SLURM_MEM_PER_CPU` times `SLURM_CPUS_ON_NODE`), the cgroup limit (`v2 memory.max` then `v1 memory.limit_in_bytes`,

read from the job's own cgroup resolved via `/proc/self/cgroup` before the mount root), then physical RAM. DuckDB's own default is 80% of `*physical*` RAM, which ignores a SLURM / cgroup cap and can over-commit (near-OOM on the first large scan); the detected default keeps a big aggregation spilling within the job's allocation. When nothing can be detected (e.g. macOS) DuckDB's default is left in place.

threads is likewise defaulted when unset: the most-restrictive detected CPU allocation – a SLURM allocation (SLURM\_CPUS\_PER\_TASK, or SLURM\_CPUS\_ON\_NODE) then the cgroup CFS quota (v2 `cpu.max`, v1 `cpu.cfs_quota_us/cpu.cfs_period_us`, read from the job's own cgroup subpath before the mount root). DuckDB otherwise defaults to hardware concurrency, which ignores a SLURM/cgroup cpuset and over-subscribes on a shared node (each extra thread also carries working memory against the memory cap). When no allocation is detected, DuckDB's default is left in place.

### Value

`acquireDuckDBConn` returns a cached `duckdb_connection` object. `releaseDuckDBConn` returns NULL, invisibly. `loadExtension` installs (if needed) and loads extension on `conn`, returning the load status invisibly. `configureOutOfCore` applies out-of-core engine settings (buffer-pool memory limit, worker threads, spill directory, insertion-order preservation) to `conn` from R options or environment variables, returning NULL invisibly.

### Author(s)

Patrick Aboyoun

### Examples

```
releaseDuckDBConn()
conn <- acquireDuckDBConn()
identical(conn, acquireDuckDBConn())
releaseDuckDBConn()
releaseDuckDBConn()
```

---

DuckDBDataFrame-class    *DuckDBDataFrame* objects

---

### Description

The `DuckDBDataFrame` class extends both [DuckDBTable](#) and [DataFrame](#) to represent a DuckDB table as a [DataFrame](#) object.

### Details

`DuckDBDataFrame` adds [DataFrame](#) semantics to a DuckDB table. It achieves a balance between the flexibility of a `tbl_duckdb_connection` object and the familiarity of a [DataFrame](#) object.

### Value

Objects of class `DuckDBDataFrame` extend [DataFrame](#).

## Constructor

`DuckDBDataFrame(conn, datacols = colnames(conn), keycol = NULL, dimtbl = NULL, type = NULL, collevels = NULL)`  
 Creates a `DuckDBDataFrame` object.

`conn` Either a character vector containing the paths to parquet, csv, or gzipped csv data files; a string that defines a duckdb read\_\* data source; a `DuckDBDataFrame` object; or a `tbl_duckdb_connection` object.

`datacols` Either a character vector of column names from `conn` or a named expression that will be evaluated in the context of `conn` that defines the data.

`keycol` An optional string specifying the column name from `conn` that will define the foreign key in the underlying table, or a named list containing a character vector where the name of the list element defines the foreign key and the character vector set the distinct values for that key. If missing, a `row_number` column is created as an identifier.

`dimtbl` A optional named `DataFrameList` that specifies the dimension table associated with the `keycol`. The name of the list element must match the name of the `keycol` list. Additionally, the `DataFrame` object must have row names that match the distinct values of the `keycol` list element and columns that define partitions in the data table for efficient querying.

`type` An optional named character vector where the names specify the column names and the values specify the column type; one of "logical", "integer", "integer64", "double", or "character".

`collevels` An optional named list, keyed by data column name, that restores factor columns on materialization (each element a list with a character levels vector and a TRUE/FALSE ordered flag). Primarily used by `readParquet()`.

## Accessors

In the code snippets below, `x` is a `DuckDBDataFrame` object:

`dim(x)`: Length two integer vector defined as `c(nrow(x), ncol(x))`.

`nrow(x), ncol(x)`: Get the number of rows and columns, respectively.

`NROW(x), NCOL(x)`: Same as `nrow(x)` and `ncol(x)`, respectively.

`dimnames(x)`: Length two list of character vectors defined as `list(rownames(x), colnames(x))`.

`rownames(x), colnames(x)`: Get the names of the rows and columns, respectively.

`coltypes(x), coltypes(x) <- value`: Get or set the data type of the columns; one of "logical", "integer", "integer64", "double", "character", or "factor" (a "character" column with a recorded `collevels` entry).

`dimtbls(x, drop = TRUE), dimtbls(x) <- value`: Get or set the list of dimension tables used to define partitions for efficient queries. If `drop = TRUE`, then it returns a named `DataFrameList` object, else it returns an environment containing a `dimtbls` named `DataFrameList` element.

## Coercion

`as.data.frame(x)`: Coerces `x` to a `data.frame`.

`as.matrix(x)`: Coerces `x` to a matrix.

`as(from, "DFrame")`: Converts a `DuckDBDataFrame` object to a `DFrame` object. This process involves first loading the data into memory using `as.data.frame`. The resulting `data.frame` is then coerced into a `DFrame`. Additionally, any associated metadata and `mcols` (metadata columns) are preserved and added to the `DFrame`, if they exist.

`realize(x, BACKEND = getAutoRealizationBackend())`: Realize an object into memory or on disk using the equivalent of `realize(as(x, "DFrame"), BACKEND)`.

## Subsetting

In the code snippets below, `x` is a `DuckDBDataFrame` object:

`x[i, j, drop = TRUE]`: Returns either a new `DuckDBDataFrame` object or a `DuckDBColumn` if selecting a single column and `drop = TRUE`.

`x[[i]]`: Extracts a `DuckDBColumn` object from `x`.

`x[[i]] <- value`: Replaces column `i` in `x` with `value`.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` rows of `x`. If `n` is negative, returns all but the last `abs(n)` rows of `x`.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` rows of `x`. If `n` is negative, returns all but the first `abs(n)` rows of `x`.

`subset(x, subset, select, drop = FALSE)`: Return a new `DuckDBDataFrame` using:

**subset** logical expression indicating rows to keep, where missing values are taken as `FALSE`.

**select** expression indicating columns to keep.

**drop** passed on to `[]` indexing operator.

## Combining

`cbind(...)`: Creates a new `DuckDBDataFrame` object by concatenating the columns of the input objects. The returned `DuckDBDataFrame` object concatenates the metadata across the input objects. The metadata columns of the returned `DuckDBDataFrame` object are obtained by combining the metadata columns of the input object with `combineRows()`.

## Displaying

The `show()` method for `DuckDBDataFrame` objects obeys global options `showHeadLines` and `showTailLines` for controlling the number of head and tail rows and columns to display.

## Author(s)

Patrick Aboyoun, Aaron Lun

## See Also

- [DuckDBTable-class](#) for the table base class
- [DuckDBTable-utils](#) for the table base class utilities
- [DuckDBColumn-class](#) for the extracted column class
- [DuckDBColumn-utils](#) for the extracted column utilities
- [DuckDBTransposedDataFrame-class](#) for the transposed `DataFrame` class
- [DuckDBDataFrameList-class](#) for the split `DataFrame` class
- [DataFrame](#) for the base class

## Examples

```
# Mocking up a file:
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(cbind(model = rownames(mtcars), mtcars), tf)

# Creating our DuckDB-backed data frame:
```

```
df <- DuckDBDataFrame(tf, datacols = colnames(mtcars), keycol = "model")
df

# Extraction yields a DuckDBColumn:
df$carb

# Slicing DuckDBDataFrame objects:
df[,1:5]
df[1:5,]

# Combining by DuckDBDataFrame and DuckDBColumn objects:
combined <- cbind(df, df)
class(combined)
combined2 <- cbind(df, some_new_name=df[,1])
class(combined2)
```

---

DuckDBDataFrameList-class

*DuckDBDataFrameList objects*


---

## Description

The DuckDBDataFrame class extends [SplitDataFrameList](#).

## Value

Objects of class DuckDBDataFrameList extend [List](#).

## Constructor

`split(x, f)`: Creates a DuckDBDataFrameList object.

`x` A DuckDBDataFrame object to split.

`f` A DuckDBColumn object to split `x` by.

## Accessors

In the code snippets below, `x` is a DuckDBDataFrameList object:

`length(x)`: Get the number of elements in `x`.

`names(x)`, `names(x) <- value`: Get or set the names of the elements of `x`.

`mcols(x)`, `mcols(x) <- value`: Get or set the metadata columns.

`elementNROWS(x)`: Get the length (or nb of row for a matrix-like object) of each of the elements.

`dimtbls(x, drop = TRUE)`, `dimtbls(x) <- value`: Get or set the list of dimension tables used to define partitions for efficient queries. If `drop = TRUE`, then it returns a named `DataFrameList` object, else it returns an environment containing a `dimtbls` named `DataFrameList` element.

`dims(x)`: Get the two-column matrix indicating the number of rows and columns for each of the list elements.

`nrows(x)`, `ncols(x)`: Get the number of rows and columns, respectively, for each of the list elements.

`dimnames(x)`: Get the list of two [CharacterLists](#), the first holding the rownames and the second the column names.

`rownames(x), colnames(x)`: Get the [CharacterList](#) of row and column names, respectively.

`commonColnames(x), commonColnames(x) <- value`: Get or set the character vector of column names present in the individual DataFrames in `x`.

`columnMetadata(x), columnMetadata(x) <- value`: Get the [DataFrame](#) of metadata along the columns, i.e., where each column in `x` is represented by a row in the metadata. The metadata is common across all elements of `x`. Note that calling `mcols(x)` returns the metadata on the [DataFrame](#) elements of `x`.

### Coercion

In the code snippets below, `x` is a `DuckDBDataFrameList` object:

`unlist(x)`: Returns the underlying `DuckDBDataFrame` object.

`as(from, "DFrameList")`: Converts a `DuckDBDataFrameList` object to a `DFrameList` object. This process involves first loading the data into memory using `as(from, "DFrame")`. The resulting `DFrame` is then split into a `DFrameList`. Additionally, any associated metadata and `mcols` (metadata columns) are preserved and added to the `DFrameList`, if they exist.

`realize(x, BACKEND = getAutoRealizationBackend())`: Realize an object into memory or on disk using the equivalent of `realize(as(x, "DFrameList"), BACKEND)`.

### Subsetting

In the code snippets below, `x` is a `DuckDBDataFrameList` object:

`x[i]`: Returns a `DuckDBDataFrameList` object containing the selected elements.

`x[[i]]`: Return the selected `DuckDBDataFrame` by `i`, where `i` is an numeric or character vector of length 1.

`x$name`: Similar to `x[[name]]`, but `name` is taken literally as an element name.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` elements of `x`. If `n` is negative, returns all but the last `abs(n)` elements of `x`.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` elements of `x`. If `n` is negative, returns all but the first `abs(n)` elements of `x`.

### Author(s)

Patrick Aboyoun

### See Also

- [DuckDBDataFrame-class](#) for the unsplit class
- [SplitDataFrameList](#) for the base class

### Examples

```
# Mocking up a file:
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(cbind(model = rownames(mtcars), mtcars), tf)

# Creating our DuckDB-backed data frame:
```

```
df <- DuckDBDataFrame(tf, datacols = colnames(mtcars), keycol = "model")
dflist <- split(df, df$cyl)
dflist
```

---

DuckDBEmbeddings-class

*DuckDBEmbeddings objects*


---

## Description

The DuckDBEmbeddings class extends [RectangularData](#) and [DuckDBColumn](#) to represent a single dimensionality reduction embedding (e.g., PCA, UMAP, tSNE) stored in DuckDB using an ARRAY[] column.

## Details

DuckDBEmbeddings provides a DuckDB-backed container for storing a single embedding as a 2D rectangular object where rows represent cells and columns represent dimensions within that embedding. The embedding is stored as a single ARRAY[] column in the underlying DuckDB table, enabling efficient storage and lazy evaluation.

## Value

Objects of class DuckDBEmbeddings extend [RectangularData](#).

## Accessors

In the code snippets below, x is a DuckDBEmbeddings object:

**dim(x):** Returns integer vector of length 2: c(nrow(x), ncol(x)) where nrow is the number of cells and ncol is the ARRAY size (number of dimensions in the embedding).

**nrow(x), ncol(x):** Get the number of rows (cells) and columns (dimensions), respectively.

**NROW(x), NCOL(x):** Same as nrow(x) and ncol(x), respectively.

**dimnames(x):** Returns list of length 2: list(rownames(x), colnames(x)).

**rownames(x), colnames(x):** Get the names of the rows (cell IDs) and columns (dimension names), respectively.

**length(x):** Get the number of cells (same as nrow(x)).

**names(x):** Get the cell IDs (same as rownames(x)).

**type(x):** Get the ARRAY data type. Returns enhanced format "array<double,50>" or raw DuckDB format "DOUBLE[50]" depending on schema detection.

**coltypes(x):** Get the R element type (e.g., "numeric" for DOUBLE arrays, "integer" for INTEGER arrays). Handles both type formats.

**dimtbls(x, drop = TRUE), dimtbls(x) <- value:** Get or set the list of dimension tables used to define partitions for efficient queries. If drop = TRUE, then it returns a named DataFrameList object, else it returns an environment containing a dimtbls named DataFrameList element.

## Subsetting

In the code snippets below, `x` is a `DuckDBEmbeddings` object:

`x[i, j, drop=TRUE]`: Subset cells (rows) and/or dimensions (columns). When both `i` and `j` are missing, returns `x`. When `drop=TRUE` and the result is a single cell or single dimension, returns a vector. Otherwise returns a matrix or `DuckDBEmbeddings` object.

`x[i]`: Subset cells (rows), returns a `DuckDBEmbeddings` object with the selected cells.

`head(x, n = 6L)`: Returns the first `n` cells of the embedding.

`tail(x, n = 6L)`: Returns the last `n` cells of the embedding.

## Coercion

`as.matrix(x)`: Coerces the embedding to a matrix with cells as rows and dimensions as columns.

`realize(x, BACKEND = getAutoRealizationBackend())`: Realize an object into memory or on disk using the equivalent of `realize(as.matrix(x), BACKEND)`.

## Author(s)

Patrick Aboyoun

## See Also

- [DuckDBNumericList-class](#) for the base class
- [DuckDBTable-class](#) for the underlying table representation

## Examples

```
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
n <- 10L
mat <- matrix(rnorm(n * 5), nrow = n)
df <- data.frame(
  cell_id = sprintf("cell_%02d", seq_len(n)),
  pca = I(asplit(mat, 1L)),
  stringsAsFactors = FALSE
)
arrow::write_parquet(df, tf)
emb <- DuckDBDataFrame(tf, keycol = "cell_id")[[ "pca" ]]
emb
dim(emb)
head(emb, 3)
```

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DuckDBSelfHits-class    *DuckDBSelfHits objects*

---

## Description

The `DuckDBSelfHits` class extends the [SelfHits-class](#) class from `S4Vectors` for DuckDB tables.

## Details

DuckDBSelfHits provides lazy evaluation for large graph structures (e.g., = KNN graphs, similarity matrices) by storing edge lists in DuckDB-backed tables. This enables efficient storage and querying of pairwise relationships without materializing all edges in memory.

The class stores the parallel slots ('from', 'to', and any metadata columns) in a [DuckDBDataFrame](#), while keeping the scalar 'nLnode' and 'nRnode' slots materialized for fast validation.

## Value

Objects of class DuckDBSelfHits extend [SelfHits-class](#).

## Constructor

**DuckDBSelfHits(conn, from, to, nnode, mcols = NULL, keycol = NULL, dimtbl = NULL, nodes = NULL):**  
Creates a DuckDBSelfHits object.

**conn** Either a character vector containing the paths to parquet, csv, or gzipped csv data files; a string that defines a duckdb read\_\* data source; a DuckDBDataFrame object; or a tbl\_duckdb\_connection object.

**from** Either NULL or a string specifying the column from conn that defines the query/left nodes (1-indexed).

**to** Either NULL or a string specifying the column from conn that defines the subject/right nodes (1-indexed).

**nnode** Single integer specifying the number of nodes in the graph. Must be positive. This is the only slot that remains materialized.

**mcols** Optional character vector specifying additional columns that define edge metadata (e.g., "weight", "distance", "x").

**keycol** An optional string specifying the column name from conn that will define the foreign key in the underlying table, or a named list containing a character vector where the name of the list element defines the foreign key and the character vector sets the distinct values for that key. If missing, a row\_number column is created as an identifier for each edge.

**dimtbl** An optional named DataFrameList that specifies the dimension table associated with the keycol. The name of the list element must match the name of the keycol list. Additionally, the DataFrame object must have row names that match the distinct values of the keycol list element.

**nodes** An optional integer vector specifying the node ids. If NULL (default), uses implicit encoding c(NA\_integer\_, -nnode) representing 1:nnode. Can be an explicit integer vector for non-contiguous node subsets, optionally named for node aliases.

## Accessors

In the code snippets below, x is a DuckDBSelfHits object:

**length(x):** Get the number of edges (hits).

**from(x), queryHits(x):** Get the query/left node indices as a [DuckDBColumn](#).

**to(x), subjectHits(x):** Get the subject/right node indices as a [DuckDBColumn](#).

**nnode(x), nLnode(x), nRnode(x):** Get the number of nodes. All three return the same value for SelfHits.

**queryLength(x), subjectLength(x):** Get the number of left/right nodes. For SelfHits, both return nnode(x).

`countLnodeHits(x)`, `countQueryHits(x)`: Count the number of hits for each left/query node. Returns an integer vector of length `nLnode(x)`. When nodes are implicit (1:nnode), returns an unnamed vector with positional indexing. When nodes are explicit, returns a named vector where names are the node IDs as characters. This operation materializes the from column.

`countRnodeHits(x)`, `countSubjectHits(x)`: Count the number of hits for each right/subject node. Returns an integer vector of length `nRnode(x)`. When nodes are implicit (1:nnode), returns an unnamed vector with positional indexing. When nodes are explicit, returns a named vector where names are the node IDs as characters. This operation materializes the to column.

`mcols(x)`, `mcols(x) <- value`: Get or set the edge metadata columns.

### Coercion

`as(from, "DuckDBDataFrame")`: Creates a [DuckDBDataFrame](#) object with from, to, and mcols.

`as.data.frame(x)`: Coerces x to a data.frame.

`as(from, "SelfHits")`: Converts a DuckDBSelfHits object to a materialized SelfHits object. This will load all edges into memory.

`as(from, "dgCMatrix")`: Converts to a sparse matrix. Equivalent to `as(as(from, "SelfHits"), "dgCMatrix")`.

`realize(x, BACKEND = getAutoRealizationBackend())`: Realize an object into memory or on disk using the equivalent of `realize(as(x, "SelfHits"), BACKEND)`.

### Subsetting

In the code snippets below, x is a DuckDBSelfHits object:

`x[i]` **or** `extractROWS(x, i)`: Returns a DuckDBSelfHits object with edge-based subsetting (subsets edges directly by index, does NOT filter by nodes).

`extractNODES(x, i)`: Returns a DuckDBSelfHits object with node-based subsetting. Updates the nodes slot to track the subset, and filters edges lazily via SQL to include only edges where BOTH from and to are in the node subset. Filtering is applied when data is materialized via `tblconn()`, `as.data.frame()`, or coercion methods.

`head(x, n = 6L)`: If n is non-negative, returns the first n edges. If n is negative, returns all but the last `abs(n)` edges.

`tail(x, n = 6L)`: If n is non-negative, returns the last n edges. If n is negative, returns all but the first `abs(n)` edges.

### Operations

`sort(x, decreasing = FALSE)`: Returns a DuckDBSelfHits with edges sorted by from node, then by to node. The sorting is performed lazily using SQL ORDER BY.

`t(x)`: Transpose the graph by swapping from and to columns.

`c(x, ...)`: Concatenate multiple DuckDBSelfHits objects.

### Displaying

The `show()` method for DuckDBSelfHits objects obeys global options `showHeadLines` and `showTailLines` for controlling the number of edges to display.

### Author(s)

Patrick Aboyoun

**See Also**

- [SelfHits-class](#) for the base class
- [colPairs](#) for usage in SingleCellExperiment
- [DuckDBDataFrame](#) for the underlying storage

**Examples**

```
# Create an example edge list:
edges <- data.frame(
  from = c(1, 1, 2, 3, 4, 4, 5),
  to = c(2, 5, 3, 4, 2, 5, 1),
  weight = c(0.8, 0.6, 0.9, 0.7, 0.85, 0.75, 0.65),
  distance = c(1.2, 2.3, 1.5, 1.8, 1.4, 2.1, 2.5)
)
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(edges, tf)

# Create the DuckDBSelfHits object
hits <- DuckDBSelfHits(tf, from = "from", to = "to", nnode = 5,
  mcols = c("weight", "distance"))

hits

# Access edge data
from(hits)
to(hits)
mcols(hits)

# Convert to sparse matrix (materializes)
mat <- as(hits, "dgCMatrix")
```

DuckDBTable-class

*DuckDBTable objects***Description**

The DuckDBTable class extends the [RectangularData](#) virtual class for DuckDB tables by wrapping a `tbl_duckdb_connection` object.

**Details**

The DuckDBTable class provides a way to define a DuckDB table as a [RectangularData](#) object. It supports *standard 2D API* such as `dim()`, `nrow()`, `ncol()`, `dimnames()`, `x[i, j]` and `cbind()`, but does not support `rbind()`.

**Value**

Objects of class DuckDBTable extend [RectangularData](#).

## Constructor

`DuckDBTable(conn, datacols = colnames(conn), keycols = NULL, dimtbls = NULL, type = NULL, collevels = NULL)`  
Creates a `DuckDBTable` object.

`conn` Either a character vector containing the paths to parquet, csv, or gzipped csv data files; a string that defines a duckdb `read_*` data source; a `DuckDBDataFrame` object; or a `tbl_duckdb_connection` object.

`datacols` Either a character vector of column names from `conn` or a named expression that will be evaluated in the context of `conn` that defines the data.

`keycols` An optional character vector of column names from `conn` that will define the set of foreign keys in the underlying table, or a named list of character vectors where the names of the list define the foreign keys and the character vectors set the distinct values for those keys. If missing, a `row_number` column is created as an identifier.

`dimtbls` Either `NULL`, a named `DataFrameList` object, or an environment containing a named `DataFrameList` "dimtbls" element that specifies the dimension tables associated with the `keycols`. The name of the list elements match the names of the `keycols` list. Additionally, the `DataFrame` objects have row names that match the distinct values of the corresponding `keycols` list element and columns that define partitions in the data table for efficient querying.

`type` An optional named character vector where the names specify the column names and the values specify the column type; one of "logical", "integer", "integer64", "double", or "character".

`collevels` An optional named list, keyed by data column name, that restores factor columns on materialization. Each element is a list with a character `levels` vector and a `TRUE/FALSE` ordered flag; columns not named are left unchanged. Primarily used by `readParquet()` to recover factors recorded in a product's schema.

## Accessors

In the code snippets below, `x` is a `DuckDBTable` object:

`dim(x)`: Length two integer vector defined as `c(nrow(x), ncol(x))`.

`nrow(x), ncol(x)`: Get the number of rows and columns, respectively.

`NROW(x), NCOL(x)`: Same as `nrow(x)` and `ncol(x)`, respectively.

`dimnames(x)`: Length two list of character vectors defined as `list(rownames(x), colnames(x))`.

`rownames(x), colnames(x)`: Get the names of the rows and columns, respectively.

`coltypes(x), coltypes(x) <- value`: Get or set the data type of the columns. Getter returns one of "logical", "integer", "integer64", "double", "character", "factor" (a "character" column with a recorded `collevels` entry; see [DuckDBTable](#)), or complex type strings like "list<integer>", "array<numeric,128>", "struct", "map", "blob", or "geometry". Setter accepts atomic types only (not "factor"; recasting a factor column's underlying type drops its `collevels` entry, per `coltypes<-`'s documented behavior).

`dimtbls(x, drop = TRUE), dimtbls(x) <- value`: Get or set the list of dimension tables used to define partitions for efficient queries. If `drop = TRUE`, then it returns a named `DataFrameList` object, else it returns an environment containing a `dimtbls` named `DataFrameList` element.

## Coercion

`as.data.frame(x)`: Coerces `x` to a `data.frame`.

## Subsetting

In the code snippets below, `x` is a `DuckDBTable` object:

`x[i, j]`: Return a new `DuckDBTable` of the same class as `x` made of the selected rows and columns.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` rows of `x`. If `n` is negative, returns all but the last `abs(n)` rows of `x`.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` rows of `x`. If `n` is negative, returns all but the first `abs(n)` rows of `x`.

## Author(s)

Patrick Aboyoun

## See Also

- [DuckDBTable-utils](#) for the utilities
- [RectangularData](#) for the base class

## Examples

```
# Create a data.frame from the Titanic data
df <- do.call(expand.grid, c(dimnames(Titanic), stringsAsFactors = FALSE))
df$fate <- as.integer(Titanic[as.matrix(df)])

# Write data to a parquet file
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(df, tf)

tbl <- DuckDBTable(tf, datacols = "fate", keycols = c("Class", "Sex", "Age", "Survived"))
```

---

DuckDBTable-utils

*Common operations on DuckDBTable objects*

---

## Description

Common operations on [DuckDBTable](#) objects.

## Value

Method return types are documented in the sections above.

## SQL Methods

In the code snippets below, `x` is a `DuckDBTable` object:

`sql_call(x, fun, ...)`: Applies the specified SQL function to all data columns of `x`.

`sql_fun(x, function_type = NULL, return_type = NULL, description = FALSE)`: Finds DuckDB SQL functions compatible with the data type of `x`. Returns a `data.frame` of matching functions with optional filtering by function type and return type.

## Group Generics

DuckDBTable objects have support for S4 group generic functionality:

```
Arith "+", "-", "*", "^", "%", "%/%", "/"
Compare "==", ">", "<", "!=", "<=", ">="
Logic "&", "|", "!"
Ops "Arith", "Compare", "Logic"
Math "abs", "sign", "sqrt", "ceiling", "floor", "trunc", "log", "log10", "log2", "acos",
    "acosh", "asin", "asinh", "atan", "atanh", "exp", "expm1", "cos", "cosh", "sin",
    "sinh", "tan", "tanh", "gamma", "lgamma"
Summary "max", "min", "range", "prod", "sum", "any", "all"
```

See [S4groupGeneric](#) for more details.

## Numerical Data Methods

In the code snippets below, `x` is a DuckDBTable object:

`anyNA(x)`: Returns a single logical: TRUE if any value in `x` is missing.

`is.finite(x)`: Returns a DuckDBTable containing logicals that indicate which values are finite.

`is.infinite(x)`: Returns a DuckDBTable containing logicals that indicate which values are infinite.

`is.na(x)`: Returns a DuckDBTable containing logicals that indicate which values are missing (SQL NULL).

`is.nan(x)`: Returns a DuckDBTable containing logicals that indicate which values are Not a Number.

`mean(x)`: Calculates the mean of `x`.

`var(x)`: Calculates the variance of `x`.

`sd(x)`: Calculates the standard deviation of `x`.

`median(x)`: Calculates the median of `x`.

`quantile(x, probs = seq(0, 1, 0.25), names = TRUE, type = 7)`: Calculates the specified quantiles of `x`.

`probs` A numeric vector of probabilities with values in [0,1].

`names` If TRUE, the result has names describing the quantiles.

`type` Either 1 or 7 that specifies the quantile algorithm detailed in [quantile](#).

`mad(x, constant = 1.4826)`: Calculates the median absolute deviation of `x`.

`constant` The scale factor.

`IQR(x, type = 7)`: Calculates the interquartile range of `x`.

`type` Either 1 or 7 that specifies the quantile algorithm detailed in [quantile](#).

`pmax(..., na.rm = FALSE)`: Returns the parallel maxima of multiple DuckDBTable objects. All arguments must be DuckDBTable objects with compatible dimensions.

`pmin(..., na.rm = FALSE)`: Returns the parallel minima of multiple DuckDBTable objects. All arguments must be DuckDBTable objects with compatible dimensions.

## Character Methods

In the code snippets below, `x` is a DuckDBTable object:

- `nchar(x)`: Returns a DuckDBTable containing the number of characters in each string.
- `tolower(x)`: Returns a DuckDBTable with all strings converted to lowercase.
- `toupper(x)`: Returns a DuckDBTable with all strings converted to uppercase.
- `chartr(old, new, x)`: Returns a DuckDBTable with characters translated.
  - `old` Characters to be translated.
  - `new` Characters to translate to.
- `substr(x, start, stop)`: Returns a DuckDBTable containing substrings extracted by position.
  - `start` Integer starting position (1-indexed).
  - `stop` Integer ending position (inclusive).
- `substring(x, first, last = 1000000L)`: Returns a DuckDBTable containing substrings extracted by position.
  - `first` Integer starting position (1-indexed).
  - `last` Integer ending position (inclusive).
- `grepl(pattern, x, ignore.case = FALSE, fixed = FALSE)`: Returns a DuckDBTable containing logicals indicating pattern matches.
  - `pattern` Character string containing a regular expression.
  - `ignore.case` If TRUE, case-insensitive matching.
  - `fixed` If TRUE, pattern is a fixed string not regex.
- `sub(pattern, replacement, x, ignore.case = FALSE, fixed = FALSE)`: Returns a DuckDBTable with first match of pattern replaced.
  - `pattern` Character string containing a regular expression.
  - `replacement` Replacement string.
  - `ignore.case` If TRUE, case-insensitive matching.
  - `fixed` If TRUE, pattern is a fixed string not regex.
- `gsub(pattern, replacement, x, ignore.case = FALSE, fixed = FALSE)`: Returns a DuckDBTable with all matches of pattern replaced.
  - `pattern` Character string containing a regular expression.
  - `replacement` Replacement string.
  - `ignore.case` If TRUE, case-insensitive matching.
  - `fixed` If TRUE, pattern is a fixed string not regex.
- `startsWith(x, prefix)`: Returns a DuckDBTable containing logicals indicating if strings start with the specified prefix.
- `endsWith(x, suffix)`: Returns a DuckDBTable containing logicals indicating if strings end with the specified suffix.
- `paste(..., sep = " ", collapse = NULL)`: Concatenates multiple DuckDBTable objects column-wise using the specified separator. The collapse argument is not supported. All arguments must be DuckDBTable objects with compatible dimensions.

## General Methods

In the code snippets below, `x` is a DuckDBTable object:

- `unique(x)`: Returns a DuckDBTable containing the distinct rows.
- `x %in% table`: Returns a DuckDBTable containing logicals that indicate if the values in each of the columns of `x` are in `table`.
- `table(...)`: Returns a table containing the counts across the distinct values.

**List Methods**

In the code snippets below, `x` is a `DuckDBTable` object:

`elementNROWS(x)`: Returns a `DuckDBTable` containing the number of elements in each list column of `x`.

**Sparsity Methods**

In the code snippets below, `x` is a `DuckDBTable` object:

`is_nonzero(x)`: Returns a `DuckDBTable` containing logicals that indicate if the values in each of the columns of `x` are non-zero.

`nzcount(x)`: Returns the total number of non-zero values.

`is_sparse(x)`: Returns `TRUE` since data are stored in a sparse array representation.

**Author(s)**

Patrick Aboyoun

**See Also**

- [DuckDBTable-class](#) for the main class
- [RectangularData](#) for the base class

**Examples**

```
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(cbind(model = rownames(mtcars), mtcars), tf)
tbl <- DuckDBTable(tf, datacols = colnames(mtcars), keycol = "model")
mean(tbl[, "mpg"])
head(tbl, 3)
```

---

DuckDBTransposedDataFrame-class

*DuckDBTransposedDataFrame objects*

---

**Description**

The `DuckDBTransposedDataFrame` class extends [TransposedDataFrame](#) to represent a DuckDB table as a [TransposedDataFrame](#) object.

**Details**

`DuckDBTransposedDataFrame` objects are constructed by calling `t()` on a [DuckDBDataFrame](#) object.

**Value**

Objects of class `DuckDBTransposedDataFrame` extend [RectangularData](#).

**Constructor**

`t(x)`: Creates a DuckDBTransposedDataFrame object from a DuckDBDataFrame object.

**Accessors**

In the code snippets below, `x` is a DuckDBTransposedDataFrame object:

`dim(x)`: Length two integer vector defined as `c(nrow(x), ncol(x))`.

`nrow(x)`, `ncol(x)`: Get the number of rows and columns, respectively.

`NROW(x)`, `NCOL(x)`: Same as `nrow(x)` and `ncol(x)`, respectively.

`dimnames(x)`: Length two list of character vectors defined as `list(rownames(x), colnames(x))`.

`rownames(x)`, `colnames(x)`: Get the names of the rows and columns, respectively.

**Subsetting**

In the code snippets below, `x` is a DuckDBTransposedDataFrame object:

`x[i, j, drop = TRUE]`: Returns either a new DuckDBTransposedDataFrame object or a DuckDB-Column if selecting a single row and `drop = TRUE`.

**Displaying**

The `show()` method for DuckDBTransposedDataFrame objects obeys global options `showHeadLines` and `showTailLines` for controlling the number of head and tail rows to display.

**Author(s)**

Patrick Aboyoun

**See Also**

- [DuckDBDataFrame-class](#) for the DataFrame class
- [TransposedDataFrame](#) for the base class

**Examples**

```
# Mocking up a file:
tf <- tempfile(fileext = ".parquet")
on.exit(unlink(tf))
arrow::write_parquet(cbind(model = rownames(mtcars), mtcars), tf)

# Creating our DuckDB-backed data frame:
tdf <- t(DuckDBDataFrame(tf, datacols = colnames(mtcars), keycol = "model"))
tdf

# Slicing DuckDBTransposedDataFrame objects:
tdf[,1:5]
tdf[1:5,]
```

---

`keynames`*Key Names and Key Count*

---

**Description**

Get the keycols names, keycols dimension names, or keycols count of an object.

**Usage**

```
keynames(x)

keydimnames(x, value)

keydimnames(x) <- value

nkey(x)

nkeydim(x)
```

**Arguments**

|                    |                                                   |
|--------------------|---------------------------------------------------|
| <code>x</code>     | An object to get the keycols related information. |
| <code>value</code> | A character vector of keycols dimension names.    |

**Value**

`keynames` and `keydimnames` return character vectors. `nkey` and `nkeydim` return a single integer.

**Author(s)**

Patrick Aboyoun

**Examples**

```
keynames
showMethods("keynames")

keydimnames
showMethods("keydimnames")

nkey
showMethods("nkey")
```

parquet-io

*Parquet I/O utilities for the DuckDB package suite***Description**

Shared append validation, SQL COPY TO helpers, and lazy [DuckDBTable](#) export used by **Bioc-DuckDB** and **DuckDBArray**. End users should call [writeParquet](#) or [writeCoordArray](#) rather than these functions directly.

**Usage**

```

validateAppendOffset(offset)

readParquetSchema(path, columns = NULL)

reconcileParquetSchema(path, columns, arrowtypes)

checkHiveAppendPartitions(
  path,
  indexcols,
  grid_suffix,
  grid,
  along,
  group_offset
)

checkAppendPart(path, part, part_digits = 0L)

parquetPartPath(path, part, part_digits = 0L)

validateWriteParquetPart(part)

setupFlatParquetWrite(
  path,
  append = FALSE,
  offset = 0L,
  part = NULL,
  part_digits = 0L,
  indexcol = NULL,
  reconcile_columns = NULL,
  create = TRUE
)

escapeSQLPath(path)

quoteSQLColumns(conn, cols)

buildParquetCopySQL(
  query_sql,
  target_path,
  order_cols = NULL,

```

```

    partition_by = NULL,
    row_group_size = NULL,
    append = FALSE
)

writeDuckDBTableParquet(
  x,
  path,
  indexcol = "__index__",
  keycol = "__name__",
  dimtbl = NULL,
  append = FALSE,
  offset = 0L,
  part = NULL,
  part_digits = 0L,
  cluster_by = NULL,
  index_max = NULL,
  row_group_size = 491520L,
  ...
)

splitParquetPart(
  path,
  n_parts,
  part_digits = 0L,
  conn = acquireDuckDBConn(),
  row_group_size = 491520L
)

```

### Arguments

|                   |                                                                                                                                                                                                                                                              |
|-------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| offset            | Non-negative integer scalar; global index shift for flat table append ( <a href="#">validateAppendOffset</a> ).                                                                                                                                              |
| path              | Directory containing Parquet files or hive partitions.                                                                                                                                                                                                       |
| columns           | Character vector of column names required in an existing dataset schema.                                                                                                                                                                                     |
| arrowtypes        | Named list of <a href="#">DataType</a> objects or length-one character Arrow type names (names must match columns). NULL elements adopt the on-disk type; non-NULL elements must match the existing type exactly ( <a href="#">reconcileParquetSchema</a> ). |
| indexcols         | Character vector of index column names for hive layout.                                                                                                                                                                                                      |
| grid_suffix       | Partition directory suffix (e.g. "group__").                                                                                                                                                                                                                 |
| grid              | <a href="#">ArrayGrid</a> for the current write slab.                                                                                                                                                                                                        |
| along             | Integer index of the append dimension along which group_offset applies.                                                                                                                                                                                      |
| group_offset      | Partition-group offset along along for hive append.                                                                                                                                                                                                          |
| part              | Non-negative integer; flat part-<n>.parquet index.                                                                                                                                                                                                           |
| part_digits       | Zero-padding width for part in the filename.                                                                                                                                                                                                                 |
| append            | Logical; enable flat multi-part append ( <a href="#">setupFlatParquetWrite</a> ).                                                                                                                                                                            |
| indexcol          | Optional index column name for lazy table export.                                                                                                                                                                                                            |
| reconcile_columns | Character vector of columns to pin on append via <a href="#">reconcileParquetSchema</a> .                                                                                                                                                                    |
| create            | Logical; create path when missing ( <a href="#">setupFlatParquetWrite</a> ).                                                                                                                                                                                 |

|                |                                                                                                                                                                                                                                                                                                                                                |
|----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| conn           | DBI connection for <a href="#">quoteSQLColumns</a> and <a href="#">splitParquetPart</a> .                                                                                                                                                                                                                                                      |
| cols           | Character vector of column names to quote.                                                                                                                                                                                                                                                                                                     |
| query_sql      | Inner SELECT (or SELECT ... WHERE ...) for <a href="#">buildParquetCopySQL</a> .                                                                                                                                                                                                                                                               |
| target_path    | Destination file or directory path for <a href="#">buildParquetCopySQL</a> .                                                                                                                                                                                                                                                                   |
| order_cols     | Optional character vector of ORDER BY expressions (pre-quoted identifiers or SQL expressions).                                                                                                                                                                                                                                                 |
| partition_by   | Optional character vector of hive partition column names (pre-quoted identifiers) for PARTITION_BY.                                                                                                                                                                                                                                            |
| row_group_size | Optional integer ROW_GROUP_SIZE. Used by <a href="#">buildParquetCopySQL</a> and by <a href="#">writeDuckDBTableParquet</a> which defaults it to 491520L (240 x the 2048 DuckDB STANDARD_VECTOR_SIZE) to match the convention used by the coord-array and flat arrow writers; previously the lazy export fell back to DuckDB's 122880 default. |
| x              | A <a href="#">DuckDBTable</a> object ( <a href="#">writeDuckDBTableParquet</a> ).                                                                                                                                                                                                                                                              |
| keycol         | Optional primary-key column name for lazy table export.                                                                                                                                                                                                                                                                                        |
| dimtbl         | Optional single-row <a href="#">DataFrame</a> of partition columns.                                                                                                                                                                                                                                                                            |
| n_parts        | Number of files to split into ( <a href="#">splitParquetPart</a> ).                                                                                                                                                                                                                                                                            |

## Details

These functions implement the shared append contract (fail before write, no silent overwrite):

- Flat sample/feature tables use part-\*.parquet files; checkAppendPart and reconcileParquetSchema apply.
- Hive-partitioned coord arrays use <index><suffix>=<n>/ directories; checkHiveAppendPartitions guards partition collisions.
- readParquetSchema reads the first \*.parquet file found under path (recursive search).

## Value

validateAppendOffset Integer scalar.

readParquetSchema [Schema](#) object.

reconcileParquetSchema Named list of resolved DataType objects.

checkHiveAppendPartitions, checkAppendPart NULL, invisibly.

parquetPartPath Character path to a part-\*.parquet file.

validateWriteParquetPart Integer scalar or NULL.

setupFlatParquetWrite Named list with validated flat-write parameters (path, part, offset, pq\_path, flat\_part, subsequent\_part).

escapeSQLPath Escaped path string.

quoteSQLColumns Character vector of quoted identifiers.

buildParquetCopySQL Complete COPY TO SQL string.

writeDuckDBTableParquet List with path, dir, nrow, sample\_df, colnames, part, append, and subsequent\_part.

splitParquetPart Character vector of the resulting part-\*.parquet paths, invisibly.

**Functions**

- `writeDuckDBTableParquet()`: Lazy DuckDBTable SQL Parquet export.
- `splitParquetPart()`: Split a directory's single flat part-\*.parquet file into `n_parts` smaller ones, in place, preserving row order and factor columns.

**Author(s)**

Patrick Aboyoun

**See Also**

[writeParquet](#), [writeCoordArray](#)

**Examples**

```
path <- tempfile()
dir.create(path)
on.exit(unlink(path, recursive = TRUE), add = TRUE)
pq <- file.path(path, "part-0.parquet")
arrow::write_parquet(data.frame(x = 1:3L, y = letters[1:3]), pq)
validateAppendOffset(0L)
readParquetSchema(path, columns = c("x", "y"))
tbl <- DuckDBTable(pq)
quoteSQLColumns(dbconn(tbl), c("x", "y"))

path2 <- tempfile()
dir.create(path2)
on.exit(unlink(path2, recursive = TRUE), add = TRUE)
arrow::write_parquet(data.frame(x = 1:100L), file.path(path2, "part-0.parquet"))
splitParquetPart(path2, n_parts = 4L)
list.files(path2)
```

---

parquet-io-cluster      *Cluster-on-write keys and helpers*

---

**Description**

Clustering keys for [writeParquet](#)'s `cluster_by` argument, plus the in-memory reorder they imply. Writing with a clustering key physically orders rows so each Parquet row group covers a tight region, letting DuckDB's row-group zonemaps prune groups outside a range query.

**Usage**

```
zorder(cols, bits = 16L, by = NULL)

hilbert(cols, bits = 16L, by = NULL)

clusterSort(df, cluster_by)

clusterOrderSQL(conn, subquery_sql, cluster_by, available = NULL)

columnExtents(conn, subquery_sql, cols)
```

## Arguments

|                           |                                                                                                                                                                    |
|---------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cols</code>         | Character vector of numeric column names to cluster by. <code>hilbert()</code> requires exactly two.                                                               |
| <code>bits</code>         | Grid resolution per axis (default 16; a $2^{16}$ grid). Higher = finer; keep <code>length(cols) * bits &lt;= 62</code> so the Morton code fits a 64-bit integer.   |
| <code>by</code>           | Optional character vector of columns ordered lexicographically before the curve (a composite categorical-prefix key); NULL for a pure space-filling key.           |
| <code>df</code>           | A <code>data.frame</code> or <a href="#">DataFrame</a> ( <code>clusterSort</code> ).                                                                               |
| <code>cluster_by</code>   | A <code>zorder()/hilbert()</code> spec or a character vector of columns ( <code>clusterSort</code> ).                                                              |
| <code>conn</code>         | A DuckDB <code>DBIConnection</code> ( <code>clusterOrderSQL</code> , <code>columnExtents</code> ).                                                                 |
| <code>subquery_sql</code> | A SQL SELECT string whose output rows are to be ordered ( <code>clusterOrderSQL</code> ) or measured ( <code>columnExtents</code> ).                               |
| <code>available</code>    | Optional character vector of the subquery's output column names, used to validate that the <code>cluster_by</code> columns exist ( <code>clusterOrderSQL</code> ). |

## Details

`zorder()` orders by a Morton (Z-order) code over `cols` (any number of numeric columns), lowered SQL-side to a generated bit-interleave ORDER BY (no extension needed). `hilbert()` orders by the native DuckDB spatial ST\_Hilbert curve (exactly two numeric columns, better locality, requires the spatial extension). A plain character vector is a lexicographic ordering (best for the leading column). `clusterSort()` is the in-memory counterpart used by the materializing `data.frame` / `DataFrame` write path (Hilbert falls back to Morton there). Its double-precision Morton code is exact only for `length(cols) * bits <= 52`; the lazy SQL path (unsigned 64-bit) is exact to 62, so for a total above 52 bits the two write paths may order rows differently. Keep `length(cols) * bits` at or below 52 when both paths must agree byte-for-byte.

`by` adds a *composite* key: the named (typically low-cardinality categorical) columns are ordered lexicographically *before* the space-filling curve, i.e. ORDER BY `by...`, `curve(cols)`. This keeps each by-group's rows contiguous so the group's own zonemaps / run-length encoding stay tight (e.g. `zorder(c("x", "y"), by = "gene")` for a viewport+gene workload, or `zorder(c("x", "y"), by = "__sample__")` to keep a COO assay's sample-slice pruning). The prefix columns are **not** interleaved into the Morton code, so they cost none of the bits budget.

`clusterOrderSQL()` is the SQL-side counterpart of `clusterSort()`: it lowers a `cluster_by` spec (from `zorder()` / `hilbert()` or a plain character vector) plus an inner `subquery_sql` into a character vector of ORDER BY expressions suitable for [buildParquetCopySQL](#)'s `order_cols`. It is the primitive a lazy or coordinate-array writer (e.g. **DuckDBArray**) calls to cluster a COPY TO without re-deriving the Morton/Hilbert generator, so the whole suite keeps one curve implementation. Returns NULL for a NULL spec. `columnExtents()` returns each column's finite `[min, max]` over the subquery (one cheap scalar pass), useful for building bounding-box windows or grid resolutions downstream.

## Value

`zorder, hilbert` A `DuckDBClusterSpec` for `writeParquet(cluster_by=)`.

`clusterSort` `df` reordered by the clustering key (same class, same columns); a no-op when `cluster_by` is NULL, `df` is empty, or a key column is absent.

`clusterOrderSQL` Character vector of ORDER BY expressions for `buildParquetCopySQL(order_cols=)`, or NULL when `cluster_by` is NULL.

`columnExtents` List (one element per column) of numeric `c(min, max)` finite extents.

**Examples**

```
zorder(c("x", "y"))
hilbert(c("x", "y"), bits = 12L)
clusterSort(data.frame(x = c(9, 1, 5), y = c(9, 1, 5)), zorder(c("x", "y")))
```

set\_row\_number

*Internal generics and helpers for the BiocDuckDB suite***Description**

These generics and helper functions are the low-level extension points shared across the BiocDuckDB packages (for example **DuckDBArray** and **DuckDBGRanges** define methods on the generics). They are exported so companion packages can dispatch methods on them across package boundaries, but they are not part of the public user-facing API and are not intended for direct use by end users.

**Usage**

```
set_row_number(conn)

keycols(x)

has_row_number(x)

makePrettyCharacterMatrixForDisplay(x)
```

**Arguments**

conn            A `tbl_duckdb_connection`.

x               A [DuckDBTable](#)-derived object.

**Value**

`keycols()` returns the named list of key-dimension index vectors. `has_row_number()` returns a logical scalar indicating whether the object is addressed by a generated row number (rather than named keys). `set_row_number()` returns the integer64 row-number encoding for a connection. `makePrettyCharacterMatrixForDisplay()` returns a character matrix used by the `show()` method.

sql\_call

*Call DuckDB SQL Functions on BiocDuckDB Objects***Description**

Apply any DuckDB SQL function to a BiocDuckDB object. This is a low-level interface that provides direct access to DuckDB's extensive SQL function library. The function is applied lazily and only executed when the result is materialized.

**Usage**

```
sql_call(x, fun, ...)
```

**Arguments**

|                  |                                                                                                                             |
|------------------|-----------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>   | A BiocDuckDB object (DuckDBTable, DuckDBColumn, DuckDBDataFrame, or DuckDBAtomicList).                                      |
| <code>fun</code> | A character string naming the SQL function to call.                                                                         |
| <code>...</code> | Additional arguments passed to the SQL function. Arguments are coerced to SQL literals or column references as appropriate. |

**Details**

This function applies the specified SQL function to all data columns in the object. For common operations, consider using dedicated methods or convenience wrappers (e.g., `sort`, `unique`, `%in%`). Available SQL functions are documented in DuckDB's function reference: <https://duckdb.org/docs/sql/functions/overview>

**Value**

An object of the same class as `x` with the SQL function applied to all data columns. The operation is lazy and only executed when the result is materialized via `as.vector()`, `as.list()`, or similar.

**Argument Handling**

Arguments in `...` are converted to SQL expressions as follows:

- **Character:** SQL string literal (automatically quoted)
- **Numeric:** SQL numeric literal
- **Logical:** SQL boolean literal (TRUE/FALSE)
- **NULL:** SQL NULL
- **name/symbol:** SQL column reference (unquoted, from `as.name()`)
- **sql():** Raw SQL expression (from `dplyr::sql()`, not quoted)

**Author(s)**

Patrick Aboyoun

**Examples**

```
# sql_call() applies any DuckDB SQL function to a column
df <- data.frame(x = c(1.4, 2.6, 3.5), y = c(-1, 2, -3))
path <- tempfile(fileext = ".parquet")
arrow::write_parquet(df, path)
ddf <- DuckDBDataFrame(path, datacols = c("x", "y"))

sql_call(ddf$x, "round", 0) # ROUND(x, 0)
sql_call(ddf$y, "abs")      # ABS(y)

showMethods("sql_call")
unlink(path)
```

sql\_fun

*Find Compatible DuckDB SQL Functions for BiocDuckDB Objects***Description**

Query DuckDB's function catalog to find SQL functions that are compatible with a BiocDuckDB object's data type. This is useful for discovering what operations can be performed on a particular column type.

**Usage**

```
sql_fun(x, function_type = NULL, return_type = NULL, description = FALSE)
```

**Arguments**

|               |                                                                                                                                                                                                                         |
|---------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x             | A BiocDuckDB object (DuckDBTable, DuckDBColumn, DuckDBDataFrame, or DuckDBAtomicList).                                                                                                                                  |
| function_type | Optional character vector of function types to filter for. If NULL (default), returns all function types. Options: "scalar", "aggregate", "macro", "table", "pragma", "table_macro"                                     |
| return_type   | Optional character vector of return types to filter for. If NULL (default), returns all functions. Common values: "BOOLEAN", "INTEGER", "DOUBLE", "VARCHAR", "ANY", "INTEGER[]", "DOUBLE[]", "VARCHAR[]", "ANY[]", etc. |
| description   | Logical; if TRUE, include function descriptions in output. Default is FALSE.                                                                                                                                            |

**Details**

This function queries DuckDB directly via DESCRIBE to get the column's exact type (e.g., INTEGER[], DOUBLE[], VARCHAR[]), then searches duckdb\_functions() for functions that accept that type as the first parameter. It matches both the exact type and generic types (T[], ANY[], ANY[]) that work with any type.

The results are grouped by function name with distinct return types collected into a list for functions that have multiple overloads.

**Value**

A data.frame with the following columns:

- **function\_name**: Name of the function
- **alias\_of**: If this is an alias, the canonical function name
- **function\_type**: Type of function (scalar, aggregate, etc.)
- **return\_type**: List of distinct return types for this function
- **description**: (if description = TRUE) Function description

**Author(s)**

Patrick Aboyoun

**Examples**

```
# sql_fun() lists the DuckDB SQL functions applicable to a column
df <- data.frame(x = c(1.4, 2.6, 3.5), y = c(-1, 2, -3))
path <- tempfile(fileext = ".parquet")
arrow::write_parquet(df, path)
ddf <- DuckDBDataFrame(path, datacols = c("x", "y"))

head(sql_fun(ddf$x)) # all applicable functions
head(sql_fun(ddf$x, function_type = "scalar")) # filter by function type

showMethods("sql_fun")
unlink(path)
```

tblconn

*Accessing DB Table Information***Description**

Get a database table connection object

**Usage**

```
tblconn(x, select = TRUE, filter = TRUE)
```

**Arguments**

|        |                                                                                                    |
|--------|----------------------------------------------------------------------------------------------------|
| x      | An object with a database table connection.                                                        |
| select | A logical value indicating whether to apply column selections to the database table connection.    |
| filter | A logical value indicating whether to apply key column filtering to the database table connection. |

**Value**

returns a database table connection object.

**Author(s)**

Patrick Aboyoun

**Examples**

```
tblconn
showMethods("tableconn")
```

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