# Package 'dbi.table'

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# Description

A dbi.table is a data structure that describes a SQL query (called the dbi.table's *underlying SQL query*). This query can be manipulated using data.table's [i, j, by] syntax.

# Usage

```
dbi.table(conn, id)
## S3 method for class 'dbi.table'
x[i, j, by, nomatch = NA, on = NULL]
```

# **Arguments**

conn	A DBIConnection object, as returned by dbConnect. Alternatively, a dbi.catalog or a dbi.table, in which case the new dbi.table will use the connection embedded in the provided object.
id	An Id, a character string (which will be converted to an Id by Id), or a SQL object (advanced) identifying a database object (e.g., table or view) on conn.
X	A dbi.table.
i	A logical expression of the columns of x, a dbi.table, or a data.frame. Use i to select a subset of the rows of x. Note: unlike data.table, i <i>cannot</i> be a vector.
	When i is a logical expression, the rows where the expression is TRUE are returned. If the expression contains a symbol foo that is not a column name of x but that is present in the calling scope, then the value of foo will be substituted into the expression if foo is a scalar, or if foo is a vector and is the right-hand-side argument to %in% or %chin% (substitution occurs when the extract ([) method is evaluated).
	When i inherits from data from a it is conred to a dhi tahla

When i inherits from data. frame, it is coerced to a dbi.table.

When i is a dbi.table, the rows of x that match (according to the condition specificed in on) the rows of i are returned. When nomatch == NA, all rows of i are returned (right outer join); when nomatch == NULL, only the rows of i that match a row of x are returned (inner join).

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j

A list of expressions, a literal character vector of column names of x, an expression of the form start\_name:end\_name, or a literal numeric vector of integer values indexing the columns of x. Use j to select (and optionally, transform) the columns of x.

by

A list of expressions, a literal character vector of column names of x, an expression of the form start\_name:end\_name, or a literal numeric vector of integer values indexing the columns of x. Use by to control grouping when evaluating j.

nomatch

Either NA or NULL.

on

- An unnamed character vector, e.g., x[i, on = c("a", "b")], used when columns a and b are common to both x and i.
- Foreign key joins: As a named character vector when the join columns have different names in x and i. For example, x[i, on = c(x1 = "i1", x2 = "i2")] joins x and i by matching columns x1 and x2 in x with columns i1 and i2 in i, respectively.
- Foreign key joins can also use the binary operator ==, e.g., x[i, on = c("x1 == i1", "x2 == i2")].
- It is also possible to use . () syntax as x[i, on = .(a, b)].
- Non-equi joins using binary operators >=, >, <=, < are also possible, e.g., x[i, on = c("x >= a", "y <= b")], or x[i, on = .(x >= a, y <= b)].</li>

#### Value

A dbi.table.

### See Also

- as.data.frame to retrieve the results set as a data.frame,
- csql to see the underlying SQL query.

# Examples

```
# open a connection to the Chinook example database using duckdb
duck <- chinook.duckdb()

# create a dbi.table corresponding to the Album table on duck
Album <- dbi.table(duck, DBI::Id(table_name = "Album"))

# the print method displays a 5 row preview
# print(Album)
Album

# 'id' can also be 'SQL'; use the same DBI connection as Album
Genre <- dbi.table(Album, DBI::SQL("chinook_duckdb.main.Genre"))

# use the extract (\code{[}) method to subset the dbi.table
Album[AlbumId < 5, .(Title, nchar = paste(nchar(Title), "characters"))]
# use csql to see the underlying SQL query</pre>
```

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as.data.frame

Coerce to a Data Frame

# Description

Execute a dbi.table's underlying SQL query and return the result set as a data.frame. By default, the result set is limited to 10,000 rows. See Details.

# Usage

```
## $3 method for class 'dbi.table'
as.data.frame(
    x,
    row.names = NULL,
    optional = FALSE,
    ...,
    n = getOption("dbi_table_max_fetch", 10000L)
)
```

#### **Arguments**

x a dbi.table.

row.names a logical value. This argument is not used.

optional a logical value. This argument is not used.

... additional arguments are ignored.

n an integer value. When nonnegative, the underlying SQL query includes a 'LIMIT n' clause and n is also passed to dbFetch. When negative, the underlying SQL query does not include a LIMIT clause and all rows in the result set are returned.

# Details

By default, as.data.frame returns up to 10,000 rows (see the n argument). To override this limit, either call as.data.frame and provide the n argument (e.g., n = -1 to return the entire result set), or set the option dbi\_table\_max\_fetch to the desired default value of n.

#### Value

```
a data.frame.
```

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#### See Also

```
as.data.frame (the generic method in the base package).
```

#### **Examples**

```
duck <- chinook.duckdb()
Artist <- dbi.table(duck, DBI::Id("Artist"))
as.data.frame(Artist, n = 7)[]</pre>
```

as.dbi.table

Coerce to DBI Table

# **Description**

Test whether an object is a dbi. table, or coerce it if possible.

#### Usage

```
is.dbi.table(x)
as.dbi.table(conn, x, type = c("auto", "query", "temporary"))
```

# **Arguments**

x any R object.

conn a connection handle returned by dbConnect. Alternatively, conn may be a

dbi.table or a dbi.catalog; in these cases, the connection handle is extracted

from the provided object.

type a character string. Possible choices are "auto", "query", and "temporary".

See Details. The default "auto" uses In Query tables when x has 500 or fewer

rows or when creating a temporary table on the database fails.

#### **Details**

Two types of tables are provided: *Temporary* (when type == "temporary") and *In Query* (when type == "query"). For *Temporary*, the data are written to a SQL temporary table and the associated dbi.table is returned. For *In Query*, the data are written into a CTE as part of the query itself useful when the connection does not permit creating temporary tables.

#### Value

```
a dbi.table.
```

# Note

The temporary tables created by this function are dropped (by calling dbRemoveTable) during garbage collection when they are no longer referenced.

# **Examples**

```
duck <- dbi.catalog(chinook.duckdb)
csql(as.dbi.table(duck, iris[1:4, 1:3], type = "query"))</pre>
```

csql

 $See\ SQL$ 

# Description

View a dbi.table's underlying SQL query.

# Usage

```
csql(x, n = getOption("dbi_table_max_fetch", 10000L))
```

# **Arguments**

x a dbi.table.

a single integer value. When nonnegative, limits the number of rows returned by the query to n.

# Value

```
none (invisible NULL).
```

```
\label{eq:continuous} DBI\ Methods\ for\ \texttt{dbi.table}s
```

# **Description**

Call DBI methods using the underlying DBI connection.

#### Usage

```
## S4 method for signature 'dbi.catalog, SQL'
dbExecute(conn, statement, ...)
## S4 method for signature 'dbi.schema, SQL'
dbExecute(conn, statement, ...)
## S4 method for signature 'dbi.table, SQL'
dbExecute(conn, statement, ...)
## S4 method for signature 'dbi.table,missing'
dbSendStatement(
  conn,
 statement,
 n = getOption("dbi_table_max_fetch", 10000L)
## S4 method for signature 'dbi.table, missing'
dbGetQuery(conn, statement, ..., n = getOption("dbi_table_max_fetch", 10000L))
## S4 method for signature 'dbi.catalog'
dbGetInfo(dbObj, ...)
## S4 method for signature 'dbi.schema'
dbGetInfo(dbObj, ...)
## S4 method for signature 'dbi.table'
dbGetInfo(dbObj, ...)
```

#### **Arguments**

```
conn a dbi.catalog, dbi.schema, or dbi.table.

statement a SQL object.

... other parameters passed on to methods.

n an integer value. A nonnegative value limits the number of records returned by the query. A negative value omits the LIMIT (or TOP) clause entirely.

db0bj a dbi.catalog, dbi.schema, or dbi.table.
```

#### See Also

dbExecute, dbGetInfo, dbSendStatement

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dbi.attach

Attach a Database Schema to the Search Path

# **Description**

The database schema is attached to the R search path. This means that the schema is searched by R when evaluating a variable, so that dbi.tables in the schema can be accessed by simply giving their names.

# Usage

```
dbi.attach(
  what,
  pos = 2L,
  name = NULL,
  warn.conflicts = FALSE,
  schema = NULL,
  graphics = TRUE
)
```

# **Arguments**

what a connection handle returned by dbConnect or a zero-argument function that

returns a connection handle.

pos an integer specifying position in search() where to attach.

name a character string specifying the name to use for the attached database.

warn.conflicts a logical value. If TRUE, warnings are printed about conflicts from attaching

the database, unless that database contains an object .conflicts.OK. A conflict

is a function masking a function, or a non-function masking a non-function.

schema a character string specifying the name of the schema to attach.

graphics a logical value; passed to menu. In interactive sessions, when schema is NULL

and multiple schemas are found on what, a menu is displayed to select a schema.

#### Value

an environment, the attached schema is invisibly returned.

#### See Also

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dbi.catalog

Create a dbi.catalog

#### **Description**

A dbi.catalog represents a database catalog.

# Usage

```
dbi.catalog(conn, schemas = NULL)
```

# **Arguments**

conn

a connection handle returned by  $\ensuremath{\mathsf{dbConnect}}$  or a zero-argument function that

returns a connection handle.

schemas

a character vector of distinct schema names. These schemas will be loaded into the dbi.catalog. The default schemas = NULL loads all schemas in the catalog.

#### Value

```
a dbi.catalog.
```

#### **Examples**

```
# chinook.duckdb is a zero-argument function that returns a DBI handle
(db <- dbi.catalog(chinook.duckdb))

# list schemas
ls(db)

# list the tables in the schema 'main'
ls(db$main)</pre>
```

example\_databases

Example Databases

# Description

These zero-argument functions return connections to the example databases included in the **dbi.table** package.

# Usage

```
chinook.sqlite()
chinook.duckdb()
```

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#### Value

a DBIConnection object, as returned by dbConnect.

merge

Merge two dbi.tables

#### **Description**

Merge two dbi.tables. The dbi.table method is similar to the data.table method except that the result set is only determined up to row order and is not sorted by default.

Default merge columns: if x has a foreign key constraint that references y then the columns comprising this key are used; see details. When a foreign key cannot be found, then the common columns between the two dbi.tabless are used.

Use the by, by . x, and by . y arguments explicitly to override this default.

#### Usage

```
## $3 method for class 'dbi.table'
merge(
    X,
    y,
    by = NULL,
    by.x = NULL,
    by.y = NULL,
    all = FALSE,
    all.x = all,
    all.y = all,
    sort = FALSE,
    suffixes = c(".x", ".y"),
    no.dups = TRUE,
    recursive = FALSE,
    ...
)
```

#### **Arguments**

```
    x, y
    dbi.tables sharing the same DBI connection.
    by A vector of shared column names in x and y to merge on.
    by.x, by.y
    character vectors of column names in x and y to merge on.
    all a logical value. all = TRUE is shorthand to save setting both all.x = TRUE and all.y = TRUE.
    all.x
    a logical value. When TRUE, rows from x that do not have a matching row in y are included. These rows will have NAs in the columns that are filled with values from y. The default is FALSE so that only rows with data from both x and y are included in the output.
```

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all.y	a logical value. Analogous to all.x above.
sort	a logical value. Currently ignored.
suffixes	a length-2 character vector. The suffixes to be used for making non-by column names unique. The suffix behavior works in a similar fashion to the $merge.data.frame$ method.
no.dups	a logical value. When TRUE, suffixes are also appended to non-by.y column names in y when they have the same column name as any by.x.
recursive	a logical value. Only used when y is missing. When TRUE, merge is called recursively on each of the just-merged dbi.tables. See examples.
	additional arguments are ignored.

#### **Details**

Foreign key constraints. Foreign keys can only be queried when (1) the dbi.table's schema is loaded, and (2) dbi.table understands the underlying database's information schema.

merge.dbi.table uses sql.join to join x and y then formats the result set to match the typical merge output.

#### Value

```
a dbi.table.
```

#### **Examples**

```
chinook <- dbi.catalog(chinook.duckdb)

#The Album table has a foreign key constriant that references Artist
merge(chinook$main$Album, chinook$main$Artist)

#When y is omitted, x's foreign key relationship is used to determine y
merge(chinook$main$Album)

#Multiple foreign keys are supported
csql(merge(chinook$main$Track))

#Track references Album but not Artist, Album references Artist
#This dbi.table includes Artist.Name as well
csql(merge(chinook$main$Track, recursive = TRUE))</pre>
```

reference.test

Test dbi.table vs. Reference Implementation

#### **Description**

Evaluate an expression including at least one dbi.table and compare the result with the *Reference Implementation*. This function is primarily for testing and is potentially very slow for large tables.

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#### Usage

```
reference.test(
  expr,
  envir = parent.frame(),
  ignore.row.order = TRUE,
  verbose = TRUE
```

#### **Arguments**

#### Value

a logical value.

# **Reference Implementation**

Suppose that id1 identifies a table in a SQL database and that [i, j, by] describes a subset/select/summarize operation using data.table syntax. The *Reference Implementation* for this operation is:

```
setDT(dbReadTable(conn, id1))[i, j, by]
```

More generally, for an expression involving multiple SQL database objects and using data.table syntax, the *Reference Implementation* would be to download each of these objects in their entirety, convert them to data.tables, then evaluate the expression.

The goal of the **dbi.table** is to generate an SQL query that produces the same results set as the Reference Implementation up to row ordering.

# Examples

```
library(data.table)
duck <- dbi.catalog(chinook.duckdb)
Album <- duck$main$Album
Artist <- duck$main$Artist
reference.test(merge(Album, Artist, by = "ArtistId"))</pre>
```

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sql.join	Join dbi.tables	

# **Description**

A SQL-like join of two dbi.tables that share the same DBI connection. All columns from both dbi.tables are returned.

# Usage

```
sql.join(x, y, type = "inner", on = NULL, prefixes = c("x.", "y."))
```

# **Arguments**

x, y	dbi.tables to join. x and y must share the same DBI connection.
type	a character string specifying the join type. Valid choices are "inner", "left", "right", "outer", and "cross".
on	a call specifying the join predicate. The symbols in on should be column names of x or column names of y, use prefixes as necessary.
prefixes	a 2-element character vector of distinct values. When x and y both have a column with the same name (e.g., common_name) then, when specifing the join predicate in on, use `prefixes[1]`common_name to refer to the common_name column in x and `prefixes[2]`common_name to refer to the common_name col-

umn in y. prefixes are also used to disambiguate the output column names.

# Value

```
a dbi.table.
```

# Examples

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