

# Package ‘dbi.table’

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**Type** Package

**Title** Database Queries Using 'data.table' Syntax

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**Description** Query database tables over a 'DBI' connection using 'data.table' syntax.

Attach database schemas to the search path. Automatically merge using foreign key constraints.

**License** MPL-2.0

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dbi.table-package	<i>DBI Table</i>
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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, check.names = FALSE, key = NULL, stringsAsFactors = FALSE)

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

## Arguments

conn	A <a href="#">DBIConnection</a> object, as returned by <a href="#">dbConnect</a> . Alternatively, a <a href="#">dbi.catalog</a> 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 <a href="#">Id</a> ), or a <a href="#">SQL</a> object (advanced) identifying a database object (e.g., table or view) on conn.
check.names	Just as check.names in <a href="#">data.table</a> and <a href="#">data.frame</a> .
key	A character vector of one or more column names to set as the resulting dbi.table's key.
stringsAsFactors	A logical value (default is FALSE). Convert all character columns to factors when executing the dbi.table's underlying SQL query and retrieving the result set.
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.frame`, it is coerced to a `dbi.table`.

When `i` is a `dbi.table`, the rows of `x` that match (according to the condition specified 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).

`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`.

`keyby` Same as `by`, but additionally sets the key of the resulting `dbi.table` to the columns provided in `by`. May also be `TRUE` or `FALSE` when `by` is provided as an alternative way to accomplish the same operation.

`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)]`.

## Value

A `dbi.table`.

## Keys

A key marks a `dbi.table` as sorted with an attribute "sorted". The sorted columns are the key. The key can be any number of columns. Unlike `data.table`, the underlying data are not physically sorted, so there is no performance improvement. However, there remain benefits to using keys:

1. The key provides a default order for window queries so that functions like `shift` and `cumsum` give reproducible output.

2. `dbi.table`'s `merge` method uses a `dbi.table`'s key to determin the default columns to merge on in the same way that `data.table`'s `merge` method does. Note: if a `dbi.table` has a foreign key relationship, that will be used to determin the default columns to merge on before the `dbi.table`'s key is considered.

A table's primary key is used as the default key when it can be determined.

### Differences vs. `data.table` Keys

There are a few key differences between `dbi.table` keys and `data.table` keys.

1. In `data.table`, NAs are always first. Some databases (e.g., PostgreSQL) sort NULLs last by default and some databases (e.g., SQLite) sort them first. `as.data.frame` does not change the order of the result set returned by the database. Note that `as.data.table` uses the `dbi.table`'s key so that the resulting `data.table` is sorted in the usual `data.table` way.
2. The sort is *not* stable: the order of ties may change on subsequent evaluations of the `dbi.table`'s underlying SQL query.

### Strict Processing of Keys

By default, when previewing data (`dbi.table`'s `print` method), the key is not included in the underlying SQL query's ORDER BY clause. However, the result set is sorted locally to resepct the key. This behavior is referred to as a *non-strict* evaluation of the key and the printed output labels the key (*non-strict*). To override the default behavior for a single preview, call `print` explicitly and provide the optional argument `strict = TRUE`. To change the default behavior, set the option `dbitable.print.strict` to `TRUE`.

Non-strict evaluation of keys reduces the time taken to retrieve the preview.

### 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 [...] method to subset the dbi.table
Album[AlbumId < 5, .(Title, nchar = paste(nchar(Title), "characters"))]

# use csql to see the underlying SQL query
```

```
csq1(Album[AlbumId < 5, #WHERE
           .(Title, #SELECT
             nchar = paste(nchar(Title), "characters"))])
```

---

**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

```
## S3 method for class 'dbi.table'
as.data.frame(
  x,
  row.names = NULL,
  optional = FALSE,
  ...,
  n = getOption("dbitable.max.fetch", 10000L)
)
```

## Arguments

<code>x</code>	a <a href="#">dbi.table</a> .
<code>row.names</code>	a logical value. This argument is not used.
<code>optional</code>	a logical value. This argument is not used.
<code>...</code>	additional arguments are ignored.
<code>n</code>	an integer value. When nonnegative, the underlying SQL query includes a 'LIMIT n' clause and <code>n</code> is also passed to <a href="#">dbFetch</a> . 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 `dbitable.max.fetch` to the desired default value of `n`.

## Value

a `data.frame`.

**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)[]
```

**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**

<code>x</code>	any R object.
<code>conn</code>	a connection handle returned by <code>dbConnect</code> . Alternatively, <code>conn</code> may be a <code>dbi.table</code> or a <code>dbi.catalog</code> ; in these cases, the connection handle is extracted from the provided object.
<code>type</code>	a character string. Possible choices are "auto", "query", and "temporary". See Details. The default "auto" uses <i>In Query</i> tables when <code>x</code> 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"))
```

---

**csql***See SQL***Description**

View a `dbi.table`'s underlying SQL query.

**Usage**

```
csql(x, n = getOption("dbitable.max.fetch", 10000L), strict = FALSE)
```

**Arguments**

<code>x</code>	a <code>dbi.table</code> .
<code>n</code>	a single integer value. When nonnegative, limits the number of rows returned by the query to <code>n</code> .
<code>strict</code>	a logical value. If <code>TRUE</code> and <code>x</code> has a key, the key is appended to the <code>ORDER BY</code> clause.

**Value**

none (invisible `NULL`).

---

**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 <a href="#">dbConnect</a> or a zero-argument function that returns a connection handle.
pos	an integer specifying position in <a href="#">search()</a> 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 <a href="#">conflicts</a> from attaching the database, unless that database contains an object <code>.conflicts.OK</code> . 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 <a href="#">menu</a> . 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**

[attach](#)

---

dbi.catalog	<i>Create a dbi.catalog</i>
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---

**Description**

A dbi.catalog represents a database catalog.

**Usage**

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

## Arguments

conn	a connection handle returned by <code>dbConnect</code> 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 <code>dbi.catalog</code> . By default (when <code>schemas</code> is missing), <code>dbi.catalog</code> loads all available schemas.

## 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)
```

---

dbi.table.DBI                    *DBI Methods for dbi.tables*

---

## Description

Call DBI methods using the underlying DBI connection.

## Usage

```
## S4 method for signature 'dbi.catalog'
dbAppendTable(conn, name, value, ..., row.names = NULL)

## S4 method for signature 'dbi.schema'
dbAppendTable(conn, name, value, ..., row.names = NULL)

## S4 method for signature 'dbi.table'
dbAppendTable(conn, name, value, ..., row.names = NULL)

## S4 method for signature 'dbi.catalog'
dbCreateTable(conn, name, fields, ..., row.names = NULL, temporary = FALSE)

## S4 method for signature 'dbi.schema'
dbCreateTable(conn, name, fields, ..., row.names = NULL, temporary = FALSE)
```

```
## S4 method for signature 'dbi.table'
dbCreateTable(conn, name, fields, ..., row.names = NULL, temporary = FALSE)

## S4 method for signature 'dbi.catalog,ANY'
dbExecute(conn, statement, ...)

## S4 method for signature 'dbi.schema,ANY'
dbExecute(conn, statement, ...)

## S4 method for signature 'dbi.table,ANY'
dbExecute(conn, statement, ...)

## S4 method for signature 'dbi.catalog'
dbGetInfo(dbObj, ...)

## S4 method for signature 'dbi.schema'
dbGetInfo(dbObj, ...)

## S4 method for signature 'dbi.table'
dbGetInfo(dbObj, ...)

## S4 method for signature 'dbi.table,missing'
dbGetQuery(conn, statement, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbGetQuery(conn, statement, ...)

## S4 method for signature 'dbi.schema,ANY'
dbGetQuery(conn, statement, ...)

## S4 method for signature 'dbi.table,ANY'
dbGetQuery(conn, statement, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbListFields(conn, name, ...)

## S4 method for signature 'dbi.schema,ANY'
dbListFields(conn, name, ...)

## S4 method for signature 'dbi.table,ANY'
dbListFields(conn, name, ...)

## S4 method for signature 'dbi.catalog'
dbListObjects(conn, prefix = NULL, ...)

## S4 method for signature 'dbi.schema'
dbListObjects(conn, prefix = NULL, ...)
```

```
## S4 method for signature 'dbi.table'
dbListObjects(conn, prefix = NULL, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbQuoteIdentifier(conn, x, ...)

## S4 method for signature 'dbi.schema,ANY'
dbQuoteIdentifier(conn, x, ...)

## S4 method for signature 'dbi.table,ANY'
dbQuoteIdentifier(conn, x, ...)

## S4 method for signature 'dbi.catalog'
dbQuoteLiteral(conn, x, ...)

## S4 method for signature 'dbi.schema'
dbQuoteLiteral(conn, x, ...)

## S4 method for signature 'dbi.table'
dbQuoteLiteral(conn, x, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbQuoteString(conn, x, ...)

## S4 method for signature 'dbi.schema,ANY'
dbQuoteString(conn, x, ...)

## S4 method for signature 'dbi.table,ANY'
dbQuoteString(conn, x, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbReadTable(conn, name, ...)

## S4 method for signature 'dbi.schema,ANY'
dbReadTable(conn, name, ...)

## S4 method for signature 'dbi.table,ANY'
dbReadTable(conn, name, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbRemoveTable(conn, name, ...)

## S4 method for signature 'dbi.schema,ANY'
dbRemoveTable(conn, name, ...)

## S4 method for signature 'dbi.table,ANY'
dbRemoveTable(conn, name, ...)
```

```

## S4 method for signature 'dbi.table,missing'
dbSendStatement(conn, statement, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbSendStatement(conn, statement, ...)

## S4 method for signature 'dbi.schema,ANY'
dbSendStatement(conn, statement, ...)

## S4 method for signature 'dbi.table,ANY'
dbSendStatement(conn, statement, ...)

## S4 method for signature 'dbi.catalog'
dbWithTransaction(conn, code, ...)

## S4 method for signature 'dbi.schema'
dbWithTransaction(conn, code, ...)

## S4 method for signature 'dbi.table'
dbWithTransaction(conn, code, ...)

## S4 method for signature 'dbi.catalog,ANY'
dbWriteTable(conn, name, value, ...)

## S4 method for signature 'dbi.schema,ANY'
dbWriteTable(conn, name, value, ...)

## S4 method for signature 'dbi.table,ANY'
dbWriteTable(conn, name, value, ...)

```

## Arguments

conn	A <a href="#">dbi.catalog</a> , <a href="#">dbi.schema</a> , or <a href="#">dbi.table</a> .
name	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
value	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
...	Additional parameters to pass to methods.
row.names	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
fields	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
temporary	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
statement	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).

db0bj	A <a href="#">dbi.catalog</a> , <a href="#">dbi.schema</a> , or <a href="#">dbi.table</a> .
prefix	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
x	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).
code	Please refer to the documentation for the generic function (links can be found in the 'See Also' section).

## See Also

[dbAppendTable](#), [dbCreateTable](#), [dbExecute](#), [dbGetInfo](#), [dbGetQuery](#), [dbListObjects](#), [dbReadTable](#), [dbQuoteIdentifier](#), [dbQuoteLiteral](#), [dbQuoteString](#), [dbRemoveTable](#), [dbSendStatement](#), [dbWithTransaction](#)

---

example_databases	<i>Example Databases</i>
-------------------	--------------------------

---

## Description

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

## Usage

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

## Value

a [DBIConnection](#) object, as returned by [dbConnect](#).

---

merge	<i>Merge two dbi.tables</i>
-------	-----------------------------

---

## Description

Merge two [dbi.tables](#). By default, the columns to merge on are determined by the first of the following cases to apply.

1. If x and y are each unmodified [dbi.tables](#) in the same [dbi.catalog](#) and if there is a single foreign key relating x and y (either x referencing y, or y referencing x), then it is used to set `by.x` and `by.y`.
2. If x and y have shared key columns, then they are used to set by (that is, `by = intersect(key(x), key(y))` when `intersect(key(x), key(y))` has length greater than zero).

3. If  $x$  has a key, then it is used to set by (that is,  $by = key(x)$  when  $key(x)$  has length greater than zero).
4. If  $x$  and  $y$  have columns in common, then they are used to set by (that is,  $by = intersect(names(x), names(y))$  when  $intersect(names(x), names(y))$  has length greater than zero).

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

## Usage

```
## S3 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 = TRUE,
  suffixes = c(".x", ".y"),
  no.dups = TRUE,
  recursive = FALSE,
  ...
)
```

## Arguments

<code>x, y</code>	<code>dbi.tables</code> sharing the same DBI connection. If $y$ is not a <code>dbi.table</code> but does inherit from <code>data.frame</code> , then it is coerced to a <code>dbi.table</code> using <code>as.dbi.table</code> . If $y$ is missing, a merge is performed for each of $x$ 's foreign keys.
<code>by</code>	a character vector of shared column names in $x$ and $y$ to merge on.
<code>by.x, by.y</code>	character vectors of column names in $x$ and $y$ to merge on.
<code>all</code>	a logical value. <code>all = TRUE</code> is shorthand to save setting both <code>all.x = TRUE</code> and <code>all.y = TRUE</code> .
<code>all.x</code>	a logical value. When <code>TRUE</code> , 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 <code>FALSE</code> so that only rows with data from both $x$ and $y$ are included in the output.
<code>all.y</code>	a logical value. Analogous to <code>all.x</code> above.
<code>sort</code>	a logical value. When <code>TRUE</code> (default), the key of the merged <code>dbi.table</code> is set to the <code>by / by.x</code> columns.
<code>suffixes</code>	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 <code>merge.data.frame</code> method.
<code>no.dups</code>	a logical value. When <code>TRUE</code> , suffixes are also appended to non-by.y column names in $y$ when they have the same column name as any <code>by.x</code> .

recursive	a logical value. Only used when y is missing. When TRUE, merge is called on each dbi.table prior to merging with x. See examples.
...	additional arguments are passed to <a href="#">as.dbi.table</a> .

## Details

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](#).

## See Also

[merge.data.table](#), [merge.data.frame](#)

## Examples

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

#The Album table has a foreign key constraint 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)

#Track has 3 foreign keys: merge with Album, Genre, and MediaType
merge(chinook$main$Track)

#Track references Album but not Artist, Album references Artist
#This dbi.table includes the artist name
merge(chinook$main$Track, recursive = TRUE)
```

## 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.

## Usage

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

## Arguments

expr	an expression involving at least one <code>dbi.table</code> and whose result can be coerced into a <code>data.table</code> .
envir	an environment. Where to evaluate <code>expr</code> .
ignore.row.order	a logical value. This argument is passed to <code>all.equal</code> .
verbose	a logical value. When <code>TRUE</code> , the output from <code>all.equal</code> is displayed in a message when <code>all.equal</code> returns anything other than <code>TRUE</code> .

## 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"))
```

---

sql.join	<i>Join dbi.tables</i>
----------	------------------------

---

## 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	<code>dbi.tables</code> to join. x and y must share the same <code>DBI connection</code> .
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., <code>common_name</code> ) then, when specifying the join predicate in on, use <code>prefixes[1]`common_name</code> to refer to the <code>common_name</code> column in x and <code>prefixes[2]`common_name</code> to refer to the <code>common_name</code> column in y. prefixes are also used to disambiguate the output column names.

## Value

a `dbi.table`.

## Examples

```
chinook <- dbi.catalog(chinook.duckdb)
Album <- chinook$main$Album
Artist <- chinook$main$Artist

sql.join(Album, Artist, type = "inner",
          on = Album.ArtistId == Artist.ArtistId,
          prefixes = c("Album.", "Artist."))

```

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