

Package ‘rquery’

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Type Package

Title Relational Query Generator for Data Manipulation at Scale

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<https://winvector.github.io/rquery/>

BugReports <https://github.com/WinVector/rquery/issues>

Description A piped query generator based on Edgar F. Codd's relational algebra, and on production experience using 'SQL' and 'dplyr' at big data scale. The design represents an attempt to make 'SQL' more teachable by denoting composition by a sequential pipeline notation instead of nested queries or functions. The implementation delivers reliable high performance data processing on large data systems such as 'Spark', databases, and 'data.table'. Package features include: data processing trees or pipelines as observable objects (able to report both columns produced and columns used), optimized 'SQL' generation as an explicit user visible table modeling step, plus explicit query reasoning and checking.

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Encoding UTF-8

Depends R (>= 3.4.0), wrapr (>= 1.9.6)

Imports utils, stats, methods

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| | |
|---------------------|---------------------------------------------------|
| actualize_join_plan | <i>Execute an ordered sequence of left joins.</i> |
|---------------------|---------------------------------------------------|

Description

Please see `vignette('DependencySorting', package = 'rquery')` and `vignette('joinController', package = 'rquery')` for more details.

Usage

```
actualize_join_plan(
  columnJoinPlan,
  ...,
  jointype = "LEFT",
  add_ind_cols = FALSE,
  checkColClasses = FALSE
)
```

Arguments

| | |
|------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>columnJoinPlan</code> | columns to join, from <code>build_join_plan</code> (and likely altered by user). Note: no column names must intersect with names of the form <code>table_CLEANEDTABNAME_present</code> . |
| <code>...</code> | force later arguments to bind by name. |
| <code>jointype</code> | character, type of join to perform ("LEFT", "INNER", "RIGHT", ...). |
| <code>add_ind_cols</code> | logical, if TRUE add indicators showing which tables supplied rows. |
| <code>checkColClasses</code> | logical if true check for exact class name matches |

Value

join optree

See Also

[describe_tables](#), [build_join_plan](#), [inspect_join_plan](#), [graph_join_plan](#)

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  # example data
  DBI::dbWriteTable(my_db,
                    "meas1",
                    data.frame(id= c(1,2),
                               weight= c(200, 120),
                               height= c(60, 14)))
  DBI::dbWriteTable(my_db,
                    "meas2",
                    data.frame(pid= c(2,3),
                               weight= c(105, 110),
                               width= 1))
  # get the initial description of table defs
  tDesc <- describe_tables(my_db, qc(meas1, meas2))
  # declare keys (and give them consistent names)
  tDesc$keys[[1]] <- list(PatientID= 'id')
  tDesc$keys[[2]] <- list(PatientID= 'pid')
  # build the column join plan
  columnJoinPlan <- build_join_plan(tDesc)
  # decide we don't want the width column
  columnJoinPlan$want[columnJoinPlan$resultColumn=='width'] <- FALSE
  # double check our plan
  if(!is.null(inspect_join_plan(tDesc, columnJoinPlan,
                               checkColClasses= TRUE))) {
    stop("bad join plan")
  }
  # actualize as left join op_tree
  optree <- actualize_join_plan(columnJoinPlan,
                               checkColClasses= TRUE)
  cat(format(optree))
  print(execute(my_db, optree))
  if(requireNamespace("DiagrammeR", quietly = TRUE)) {
    DiagrammeR::grViz(op_diagram(optree))
  }
  DBI::dbDisconnect(my_db)
}

```

 affine_transform

Implement an affine transformaton

Description

Implement an affine transformaton

Usage

```
affine_transform(source, linear_transform, offset, ..., env = parent.frame())
```

Arguments

| | |
|------------------|----------------------------------------------------------------------------------------------|
| source | relop source (or data.frame source) |
| linear_transform | matrix with row names taken from source column names (inputs), and column names are outputs. |
| offset | vector of offsets with names same as column names of linear_transform. |
| ... | force later arguments to bind by name |
| env | environment to look for values in. |

Value

relop node

Examples

```

if (requireNamespace("DBI", quietly = TRUE) &&
    requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- data.frame(AUC = 0.6, R2 = 0.2)
  source <- rq_copy_to(my_db, 'd',
                      d,
                      overwrite = TRUE,
                      temporary = TRUE)
  linear_transform <- matrix(c(1, 1, 2, -1, 1, 0, 0, 0), nrow = 2)
  rownames(linear_transform) <- c("AUC", "R2")
  colnames(linear_transform) <- c("res1", "res2", "res3", "res4")
  offset <- c(5, 7, 1, 0)
  names(offset) <- colnames(linear_transform)

  optree <- affine_transform(source, linear_transform, offset)
  cat(format(optree))

  sql <- to_sql(optree, my_db)
  cat(sql)

  print(DBI::dbGetQuery(my_db, sql))
  print(as.matrix(d) %*% linear_transform + offset)

  DBI::dbDisconnect(my_db)
}

```

apply_right.relop

Execute pipeline treating pipe_left_arg as local data to be copied into database.

Description

Execute pipeline treating pipe_left_arg as local data to be copied into database.

Usage

```
## S3 method for class 'relop'
apply_right(
  pipe_left_arg,
  pipe_right_arg,
  pipe_environment,
  left_arg_name,
  pipe_string,
  right_arg_name
)
```

Arguments

pipe_left_arg left argument.

pipe_right_arg pipe_right_arg argument.

pipe_environment
environment to evaluate in.

left_arg_name name, if not NULL name of left argument.

pipe_string character, name of pipe operator.

right_arg_name name, if not NULL name of right argument.

Value

data.frame

See Also

[rquery_apply_to_data_frame](#)

Examples

```
# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  # set up example database and
  # db execution helper
  db <- DBI::dbConnect(RSQLite::SQLite(),
    "memory:")
  RSQLite::initExtension(db)
  old_o <- options(list("rquery.rquery_db_executor" = list(db = db)))

  # operations pipeline/tree
  optree <- mk_td("d", "x") %.>%
    extend(., y = x*x)
```

```

# wrapr dot pipe apply_right dispatch
# causes this statment to apply optree
# to d.
data.frame(x = 1:3) %>% optree %>% print(.)

# remote example
rq_copy_to(db, "d",
            data.frame(x = 7:8),
            overwrite = TRUE,
            temporary = TRUE)

# wrapr dot pipe apply_right dispatch
# causes this statment to apply optree
# to db.
db %>% optree %>% print(.)

# clean up
options(old_o)
DBI::dbDisconnect(db)
}

```

apply_right_S4,ANY,rquery_db_info-method
Apply pipeline to a database.

Description

Apply pipeline to a database with relop

Usage

```

## S4 method for signature 'ANY,rquery_db_info'
apply_right_S4(
  pipe_left_arg,
  pipe_right_arg,
  pipe_environment,
  left_arg_name,
  pipe_string,
  right_arg_name
)

```

Arguments

pipe_left_arg relop operation tree
 pipe_right_arg rquery_db_info
 pipe_environment
 environment to evaluate in.

left_arg_name name, if not NULL name of left argument.
pipe_string character, name of pipe operator.
right_arg_name name, if not NULL name of right argument.

Value

result

apply_right_S4,data.frame,relap_arrow-method
S4 dispatch method for apply_right.

Description

compose a data.frame and a relap_arrow class

Usage

```
## S4 method for signature 'data.frame,relap_arrow'  
apply_right_S4(  
  pipe_left_arg,  
  pipe_right_arg,  
  pipe_environment,  
  left_arg_name,  
  pipe_string,  
  right_arg_name  
)
```

Arguments

pipe_left_arg left argument
pipe_right_arg pipe_right_arg argument
pipe_environment environment to evaluate in
left_arg_name name, if not NULL name of left argument.
pipe_string character, name of pipe operator.
right_arg_name name, if not NULL name of right argument.

Value

result

```
apply_right_S4, relop_arrow, relop_arrow-method
S4 dispatch method for apply_right.
```

Description

compose two `relop_arrow` classes

Usage

```
## S4 method for signature 'relop_arrow,relop_arrow'
apply_right_S4(
  pipe_left_arg,
  pipe_right_arg,
  pipe_environment,
  left_arg_name,
  pipe_string,
  right_arg_name
)
```

Arguments

`pipe_left_arg` left argument
`pipe_right_arg` `pipe_right_arg` argument
`pipe_environment`
 environment to evaluate in
`left_arg_name` name, if not NULL name of left argument.
`pipe_string` character, name of pipe operator.
`right_arg_name` name, if not NULL name of right argument.

Value

result

```
arrow Data arrow
```

Description

A categorical arrow mapping a table to a table.

Usage

```
arrow(pipeline, ..., free_table_key = NULL, strict = FALSE)
```

Arguments

| | |
|----------------|-----------------------------------------------------------|
| pipeline | pipeline with one source table |
| ... | not used, force later argument to be referred to by name. |
| free_table_key | name of table to consider free (input) to the pipeline |
| strict | logical, if TRUE excess columns are considered an error |

Value

relop_arrow wrapping of pipeline

| | |
|--------------|-----------------------------------------------------------------------------------------------------------|
| assign_slice | <i>Assign a value to a slice of data (set of rows meeting a condition, and specified set of columns).</i> |
|--------------|-----------------------------------------------------------------------------------------------------------|

Description

Uses if_else_block.

Usage

```
assign_slice(source, testexpr, columns, value, env = parent.frame())
```

Arguments

| | |
|----------|-----------------------------------------------------|
| source | optree relop node or data.frame. |
| testexpr | character containing the test expression. |
| columns | character vector of column names to alter. |
| value | value to set in matching rows and columns (scalar). |
| env | environment to look to. |

Details

Note: ifbtest_* is a reserved column name for this procedure.

Value

optree or data.frame.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(
    my_db,
    'd',
    data.frame(i = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),
              a = c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1),
              b = c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1),
              r = runif(10)),
    temporary=TRUE, overwrite=TRUE)

  optree <- d %>%
    assign_slice(.,
                 testexpr = qe(r<0.5),
                 columns = qc(a, b),
                 value = 2)
  cat(format(optree))

  sql <- to_sql(optree, my_db)
  cat(sql)

  print(DBI::dbGetQuery(my_db, sql))

  DBI::dbDisconnect(my_db)
}

```

 build_join_plan

Build a join plan.

Description

Please see `vignette('DependencySorting', package = 'rquery')` and `vignette('joinController', package = 'rquery')` for more details.

Usage

```
build_join_plan(tDesc, ..., check = TRUE)
```

Arguments

| | |
|-------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| tDesc | description of tables from describe_tables (and likely altered by user). Note: no column names must intersect with names of the form table_CLEANTABNAME_present. |
| ... | force later arguments to bind by name. |
| check | logical, if TRUE check the join plan for consistency. |

Value

detailed column join plan (appropriate for editing)

See Also

[describe_tables](#), [inspect_join_plan](#), [graph_join_plan](#), [actualize_join_plan](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- data.frame(id=1:3, weight= c(200, 140, 98))
  DBI::dbWriteTable(my_db,"d1", d)
  DBI::dbWriteTable(my_db,"d2", d)
  tDesc <- describe_tables(my_db, c("d1", "d2"))
  tDesc$keys[[1]] <- list(PrimaryKey= 'id')
  tDesc$keys[[2]] <- list(PrimaryKey= 'id')
  print(build_join_plan(tDesc))
  DBI::dbDisconnect(my_db)
}
```

columns_used

Return columns used

Description

Return columns used

Usage

```
columns_used(x, ..., using = NULL)
```

Arguments

x rquery operation tree.
 ... generic additional arguments (not used)
 using character, if not NULL set of columns used from above.

Value

vector of table qualified column names.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d1 <- rq_copy_to(my_db, 'd1',
                  data.frame(AUC = 0.6, R2 = 0.2))
  d2 <- rq_copy_to(my_db, 'd2',
                  data.frame(AUC = 0.6, D = 0.3))
  optree <- natural_join(d1, d2, by = "AUC")
  cat(format(optree))
  print(columns_used(optree))
  DBI::dbDisconnect(my_db)
}

```

column_names

Return column names

Description

Return column names

Usage

```
column_names(x, ...)
```

Arguments

x rquery operation tree.
... generic additional arguments

Value

vector of column names

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d1 <- rq_copy_to(my_db, 'd1',
                  data.frame(AUC = 0.6, R2 = 0.2))
  d2 <- rq_copy_to(my_db, 'd2',
                  data.frame(AUC = 0.6, D = 0.3))
  optree <- natural_join(d1, d2, by = "AUC")
  cat(format(optree))
  print(column_names(optree))
  DBI::dbDisconnect(my_db)
}

```

commencify

Hyderdrive (science fiction show) synonym for [execute](#)

Description

Run the data query.

Usage

```
commencify(
  source,
  optree,
  ...,
  limit = NULL,
  source_limit = NULL,
  overwrite = TRUE,
  temporary = TRUE,
  allow_executor = TRUE,
  temp_source = mk_tmp_name_source("rquery_ex"),
  env = parent.frame()
)
```

Arguments

| | |
|----------------|-------------------------------------------------------------------------------------------------|
| source | data.frame or database connecton (rquery_db_info class or DBI connections preferred). |
| optree | relop operation tree. |
| ... | force later arguments to bind by name. |
| limit | numeric, if set limit to this many rows during data bring back (not used when landing a table). |
| source_limit | numeric if not NULL limit sources to this many rows. |
| overwrite | logical if TRUE drop an previous table. |
| temporary | logical if TRUE try to create a temporary table. |
| allow_executor | logical if TRUE allow any executor set as rquery.rquery_executor to be used. |
| temp_source | temporary name generator. |
| env | environment to work in. |

Value

data.frame

See Also

[execute](#)

Examples

```

# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  old_o <- options(list("rquery.rquery_db_executor" = list(db = my_db)))
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- extend_se(d, c("v" %:=% "AUC + R2", "x" %:=% "pmax(AUC,v)"))

  print(optree)

  cat(format(optree))

  v <- execute(my_db, optree)
  print(v)

  v2 <- execute(data.frame(AUC = 1, R2 = 2), optree)
  print(v2)

  options(old_o)
  DBI::dbDisconnect(my_db)
}

```

complete_design

Complete an experimental design.

Description

Complete an experimental design.

Usage

```
complete_design(design_table, data_table)
```

Arguments

design_table optree or for experimental design.
data_table optree for data.

Value

joined and annotated table optree.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) &&
    requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")

  # example experimental design
  values <- list(nums = 1:3, lets = c("a", "b"))
  design <- expand_grid(my_db, values)

  # not quite matching data
  data <- build_frame(
    "nums", "lets" |
      1L , "a" |
      1L , "b" |
      77L , "a" | # out of place ID
      2L , "b" |
      3L , "a" |
      3L , "a" | # duplicated
      3L , "b" )
  data$row_number <- seq_len(nrow(data))
  data <- rq_copy_to(my_db, "data", data)

  # compare/augment
  res <- complete_design(design, data)
  cat(format(res))
  res <- materialize(my_db, res)

  print("completed data design")
  print(execute(my_db, res))

  # look for dups (can use extend_se(partation) on
  # databases with window fns.
  print("duplicate key rows:")
  res %>%
    project_se(.,
      groupby = column_names(design),
      "count" %:=% "SUM(1)") %>%
    select_rows_se(., "count>1") %>%
    execute(my_db, .) %>%
    print(.)

  # look for data that was not in design
  print("data rows not in design:")
  data %>%
    natural_join(., res,
      jointype = "LEFT",
      by = column_names(design)) %>%
    select_rows_se(., "is.na(row_in_design_table)") %>%
    execute(my_db, .) %>%
    print(.)

```

```

    DBI::dbDisconnect(my_db)
  }

```

convert_yaml_to_pipeline

Convert a series of simple objects (from YAML deserializaton) to an rquery pipeline.

Description

Convert a series of simple objects (from YAML deserializaton) to an rquery pipeline.

Usage

```
convert_yaml_to_pipeline(rep, ..., source = NULL, env = parent.frame())
```

Arguments

| | |
|--------|-------------------------------------------------|
| rep | input objects |
| ... | not used, force later arguments to bind by name |
| source | input rquery node |
| env | environment to evaluate in |

Value

rquery operator tree

count_null_cols

Count NULLs per row for given column set.

Description

Build a query that counts the number of nulls in each row.

Usage

```
count_null_cols(source, cols, count)
```

Arguments

| | |
|--------|--------------------------------------|
| source | incoming rel_op tree or data.frame. |
| cols | character, columns to track |
| count | character, column to write count in. |

Value

rel_op node or data.frame (depending on input).

See Also

[null_replace](#), [mark_null_cols](#)

Examples

```
# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(my_db)
  old_o <- options(list("rquery.rquery_db_executor" = list(db = my_db)))

  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = c(0.6, 0.5, NA),
                             R2 = c(1.0, 0.9, NA)))
  op_tree <- d %>% count_null_cols(., c("AUC", "R2"), "nnull")
  cat(format(op_tree))
  sql <- to_sql(op_tree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))

  # ad-hoc mode
  data.frame(AUC=c(1,NA,0.5), R2=c(NA,1,0)) %>%
    op_tree %>%
    print(.)

  # cleanup
  options(old_o)
  DBI::dbDisconnect(my_db)
}
```

 db_td

Construct a table description from a database source.

Description

Build structures (table name, column names, and quoting strategy) needed to represent data from a remote table.

Usage

```
db_td(db, table_name, ..., qualifiers = NULL)
```

```
dbi_table(db, table_name, ..., qualifiers = NULL)
```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| db | database connection |
| table_name | name of table |
| ... | not used, force later argument to bind by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Details

Note: in examples we use `rq_copy_to()` to create data. This is only for the purpose of having easy portable examples. With big data the data is usually already in the remote database or Spark system. The task is almost always to connect and work with this pre-existing remote data and the method to do this is `db_td` which builds a reference to a remote table given the table name.

Value

a relop representation of the data

Functions

- `dbi_table`: old name for `db_td`

See Also

[mk_td](#), [local_td](#), [rq_copy_to](#), [materialize](#), [execute](#), [to_sql](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  rq_copy_to(my_db,
             'd',
             data.frame(AUC = 0.6, R2 = 0.2),
             overwrite = TRUE,
             temporary = TRUE)
  d <- db_td(my_db, 'd')
  print(d)
  sql <- to_sql(d, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  cols <- columns_used(d)
  print(cols)

  sql2 <- to_sql(d, my_db, using = "AUC")
  cat(sql2)
  print(DBI::dbGetQuery(my_db, sql2))
  DBI::dbDisconnect(my_db)
}
```

| | |
|-----------------|---------------------------------------------|
| describe_tables | <i>Build a nice description of a table.</i> |
|-----------------|---------------------------------------------|

Description

Please see <http://www.win-vector.com/blog/2017/05/managing-spark-data-handles-in-r/> for details. Note: one usually needs to alter the keys column which is just populated with all columns.

Usage

```
describe_tables(db, tablenames, ..., keyInspector = key_inspector_all_cols)
```

Arguments

| | |
|--------------|----------------------------------------------------------------|
| db | database handle |
| tablenames | character, names of tables to describe. |
| ... | force later arguments to bind by name. |
| keyInspector | function that determines preferred primary key set for tables. |

Details

Please see `vignette('DependencySorting', package = 'rquery')` and `vignette('joinController', package = 'rquery')` for more details.

Value

table describing the data.

See Also

[build_join_plan](#), [graph_join_plan](#), [actualize_join_plan](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {  
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")  
  ex <- example_employee_date(my_db)  
  print(describe_tables(my_db, ex$tableName,  
                        keyInspector = key_inspector_sqlite))  
  DBI::dbDisconnect(my_db)  
}
```

| | |
|--------------|---------------------------------------------------------------|
| drop_columns | <i>Make a drop columns node (not a relational operation).</i> |
|--------------|---------------------------------------------------------------|

Description

Note: must keep at least one column.

Usage

```
drop_columns(source, drops, ..., strict = FALSE, env = parent.frame())
```

Arguments

| | |
|--------|-----------------------------------------------------------------------|
| source | source to drop columns from. |
| drops | list of distinct column names. |
| ... | force later arguments to bind by name |
| strict | logical, if TRUE do check columns to be dropped are actually present. |
| env | environment to look to. |

Value

drop columns node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {  
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")  
  d <- rq_copy_to(my_db, 'd',  
                 data.frame(AUC = 0.6, R2 = 0.2))  
  optree <- drop_columns(d, 'AUC')  
  cat(format(optree))  
  sql <- to_sql(optree, my_db)  
  cat(sql)  
  print(DBI::dbGetQuery(my_db, sql))  
  DBI::dbDisconnect(my_db)  
}
```

| | |
|----|----------------------------------------------|
| ex | <i>Execute a wrapped execution pipeline.</i> |
|----|----------------------------------------------|

Description

Execute a ops-dag using 'codewrap()' data as values.

Usage

```
ex(ops, ..., env = parent.frame())
```

Arguments

| | |
|-----|-------------------------------------------------------|
| ops | rquery pipeline with tables formed by 'wrap()'. |
| ... | not used, force later argument to be referred by name |
| env | environment to work in. |

Value

data.frame result

Examples

```
if(requireNamespace('rqdatatable')) {  
  d <- data.frame(x = 1:3, y = 4:6)  
  d %>%  
    wrap(.) %>%  
    extend(., z := x + y) %>%  
    ex(.)  
}
```

| | |
|---------|----------------------------------------------------------------------|
| execute | <i>Execute an operator tree, bringing back the result to memory.</i> |
|---------|----------------------------------------------------------------------|

Description

Run the data query.

Usage

```
execute(
  source,
  optree,
  ...,
  limit = NULL,
  source_limit = NULL,
  overwrite = TRUE,
  temporary = TRUE,
  allow_executor = TRUE,
  temp_source = mk_tmp_name_source("rquery_ex"),
  env = parent.frame()
)
```

Arguments

| | |
|----------------|-------------------------------------------------------------------------------------------------|
| source | data.frame or database connecton (rquery_db_info class or DBI connections preferred). |
| optree | relop operation tree. |
| ... | force later arguments to bind by name. |
| limit | numeric, if set limit to this many rows during data bring back (not used when landing a table). |
| source_limit | numeric if not NULL limit sources to this many rows. |
| overwrite | logical if TRUE drop an previous table. |
| temporary | logical if TRUE try to create a temporary table. |
| allow_executor | logical if TRUE allow any executor set as rquery.rquery_executor to be used. |
| temp_source | temporary name generator. |
| env | environment to work in. |

Value

data.frame

See Also

[materialize](#), [db_td](#), [to_sql](#), [rq_copy_to](#), [mk_td](#)

Examples

```
# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  old_o <- options(list("rquery.rquery_db_executor" = list(db = my_db)))
  d <- rq_copy_to(my_db, 'd',
    data.frame(AUC = 0.6, R2 = 0.2))
  optree <- extend_se(d, c("v" :=% "AUC + R2", "x" :=% "pmax(AUC,v)"))
}
```



```

print(optree)

cat(format(optree))

v <- execute(my_db, optree)
print(v)

v2 <- execute(data.frame(AUC = 1, R2 = 2), optree)
print(v2)

options(old_o)
DBI::dbDisconnect(my_db)
}

```

expand_grid

Cross product vectors in database.

Description

Cross product vectors in database.

Usage

```

expand_grid(
  db,
  values,
  ...,
  temporary = TRUE,
  table_name = (wrapr::mk_tmp_name_source("eg"))(),
  qualifiers = NULL
)

```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| db | database handle |
| values | named list of value vectors. |
| ... | force later arguments to bind by name. |
| temporary | logical if TRUE try to make temporary table. |
| table_name | name to land result as. |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

table handle.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) &&
    requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  values <- list(nums = 1:3, lets = c("a", "b"))
  res <- expand_grid(my_db, values)
  print(res)
  execute(my_db, res)
  DBI::dbDisconnect(my_db)
}

```

 extend

Extend data by adding more columns.

Description

Create a node similar to a Codd extend relational operator (add derived columns).

Usage

```

extend(
  source,
  ...,
  partitionby = NULL,
  orderby = NULL,
  reverse = NULL,
  display_form = NULL,
  env = parent.frame()
)

```

```

extend_nse(
  source,
  ...,
  partitionby = NULL,
  orderby = NULL,
  reverse = NULL,
  display_form = NULL,
  env = parent.frame()
)

```

Arguments

| | |
|-------------|---------------------------------------|
| source | source to select from. |
| ... | new column assignment expressions. |
| partitionby | partitioning (window function) terms. |

| | |
|--------------|----------------------------------------------|
| orderby | ordering (in window function) terms. |
| reverse | reverse ordering (in window function) terms. |
| display_form | character presentation form |
| env | environment to look for values in. |

Details

Partitionby and orderby can only be used with a database that supports window-functions (such as PostgreSQL, Spark, and so on).

Supports bquote() .()-style name abstraction with the extension that – promotes strings to names (please see here: <https://github.com/WinVector/rquery/blob/master/Examples/Substitution/Substitution.md>).

Note: if any window/aggregation functions are present then at least one of partitionby or orderby must be non empty. For this purpose partitionby=1 is allowed and means "single partition on the constant 1."

Value

extend node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  NEWCOL <- as.name("v")
  NEWVALUE = "zz"
  optree <- extend(d, .(NEWCOL) %:=% ifelse(AUC>0.5, R2, 1.0), .(NEWVALUE) %:=% 6)
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}
```

extend_se

Extend data by adding more columns.

Description

Create a node similar to a Codd extend relational operator (add derived columns).

Usage

```
extend_se(
  source,
  assignments,
  ...,
  partitionby = NULL,
  orderby = NULL,
  reverse = NULL,
  display_form = NULL,
  env = parent.frame()
)
```

Arguments

| | |
|--------------|----------------------------------------------|
| source | source to select from. |
| assignments | new column assignment expressions. |
| ... | force later arguments to bind by name |
| partitionby | partitioning (window function) terms. |
| orderby | ordering (in window function) terms. |
| reverse | reverse ordering (in window function) terms. |
| display_form | character presentation form |
| env | environment to look for values in. |

Details

Partitionby and orderby can only be used with a database that supports window-functions (such as PostgreSQL, Spark and so on).

Note: if any window/aggregation functions are present then at least one of partitionby or orderby must be non empty. For this purpose partitionby=1 is allowed and means "single partition on the constant 1."

Value

extend node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- extend_se(d, c("v" %:= "AUC + R2", "x" %:= "pmax(AUC,v)"))
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
}
```

```

# SQLite can not run the following query
optree2 <- extend_se(d, "v" %:=% "rank()",
                    partitionby = "AUC", orderby = "R2")
sql2 <- to_sql(optree2, my_db)
cat(sql2)

DBI::dbDisconnect(my_db)
}

```

| | |
|-------------|-------------------------------------------|
| format_node | <i>Format a single node for printing.</i> |
|-------------|-------------------------------------------|

Description

Format a single node for printing.

Usage

```
format_node(node)
```

Arguments

| | |
|------|---------------------------------------|
| node | node of operator tree to be formatted |
|------|---------------------------------------|

Value

character display form of the node

| | |
|-------------|------------------------------------------|
| getDBOption | <i>Get a database connection option.</i> |
|-------------|------------------------------------------|

Description

Note: we are moving away from global options to options in the DB handle.

Usage

```
getDBOption(db, optname, default, connection_options = list())
```

Arguments

| | |
|--------------------|--------------------------------------|
| db | database connection handle. |
| optname | character, single option name. |
| default | what to return if not set. |
| connection_options | name list of per connection options. |

Value

option value

Examples

```
if(requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  print(getDBOption(my_db, "use_DBI_dbExecute"))
  DBI::dbDisconnect(my_db)
}
```

graph_join_plan

Build a draw-able specification of the join diagram

Description

Please see `vignette('DependencySorting', package = 'rquery')` and `vignette('joinController', package = 'rquery')` for more details.

Usage

```
graph_join_plan(columnJoinPlan, ..., groupByKeys = TRUE, graphOpts = NULL)
```

Arguments

| | |
|----------------|-------------------------------------------------|
| columnJoinPlan | join plan |
| ... | force later arguments to bind by name |
| groupByKeys | logical if true build key-equivalent sub-graphs |
| graphOpts | options for graphViz |

Value

grViz diagram spec

See Also

[describe_tables](#), [build_join_plan](#), [actualize_join_plan](#)

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  # note: employeanddate is likely built as a cross-product
  #   join of an employee table and set of dates of interest
  #   before getting to the join controller step. We call
  #   such a table "row control" or "experimental design."
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(my_db)
  tDesc <- example_employee_date(my_db)
  # fix order by hand, please see rquery::topo_sort_tables for
  # how to automate this.
  ord <- match(c('employeanddate', 'orgtable', 'activity', 'revenue'),
              tDesc$tableName)
  tDesc <- tDesc[ord, , drop=FALSE]
  columnJoinPlan <- build_join_plan(tDesc, check= FALSE)
  # unify keys
  columnJoinPlan$resultColumn[columnJoinPlan$resultColumn=='id'] <- 'eid'
  # look at plan defects
  print(paste('problems:',
             inspect_join_plan(tDesc, columnJoinPlan)))
  diagramSpec <- graph_join_plan(columnJoinPlan)
  # to render as JavaScript:
  if(requireNamespace("DiagrammeR", quietly = TRUE)) {
    print(DiagrammeR::grViz(diagramSpec))
  }
  DBI::dbDisconnect(my_db)
  my_db <- NULL
}

```

if_else_block

*Build a sequence of statements simulating an if/else block-
if(){}else{}*.

Description

This device uses expression-`ifelse(, ,)` to simulate the more powerful per-row block-`if(){}else{}`. The difference is expression-`ifelse(, ,)` can choose per-row what value to express, whereas block-`if(){}else{}` can choose per-row where to assign multiple values. By simulation we mean: a sequence of quoted mutate expressions are emitted that implement the transform. These expressions can then be optimized into a minimal number of no-dependency blocks by `extend_se` for efficient execution. The idea is the user can write legible code in this notation, and the translation turns it into safe and efficient code suitable for execution either on `data.frames` or at a big data scale using RPostgreSQL or sparklyr.

Usage

```
if_else_block(testexpr, ..., thenexprs = NULL, elseexprs = NULL)
```

Arguments

testexpr character containing the test expression.
 ... force later arguments to bind by name.
 thenexprs named character then assignments (altering columns, not creating).
 elseexprs named character else assignments (altering columns, not creating).

Details

Note: ifebtest_* is a reserved column name for this procedure.

Value

sequence of statements for extend_se().

See Also

[if_else_op](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  # Example: clear one of a or b in any row where both are set.
  # Land random selections early to avoid SQLite bug.
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(
    my_db,
    'd',
    data.frame(i = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),
               a = c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1),
               b = c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1),
               r = runif(10),
               edited = 0),
    temporary=TRUE, overwrite=TRUE)

  program <- if_else_block(
    testexpr = qe((a+b)>1),
    thenexprs = c(
      if_else_block(
        testexpr = qe(r >= 0.5),
        thenexprs = qae(a :=% 0),
        elseexprs = qae(b :=% 0)),
      qae(edited :=% 1)))
  print(program)

  optree <- extend_se(d, program)
  cat(format(optree))

  sql <- to_sql(optree, my_db)
  cat(sql)
```



```

print(DBI::dbGetQuery(my_db, sql))

# Why we need to land the random selection early
# for SQLite:
q <- "SELECT r AS r1, r AS r2 FROM (
      SELECT random() AS r FROM (
        SELECT * from ( VALUES(1),(2) )
      ) a
    ) b"
print(DBI::dbGetQuery(my_db, q))

DBI::dbDisconnect(my_db)
}

```

if_else_op

*Build a relop node simulating a per-row block-if(){}else{}.***Description**

This device uses expression-`ifelse(, ,)` to simulate the more powerful per-row `block-if(){}else{}.` The difference is `expression-ifelse(, ,)` can choose per-row what value to express, whereas `block-if(){}else{}.` can choose per-row where to assign multiple values. By simulation we mean: a sequence of quoted mutate expressions are emitted that implement the transform. These expressions can then be optimized into a minimal number of no-dependency blocks by `extend_se` for efficient execution. The idea is the user can write legible code in this notation, and the translation turns it into safe and efficient code suitable for execution either on `data.frames` or at a big data scale using `RPostgreSQL` or `sparklyr`.

Usage

```

if_else_op(
  source,
  testexpr,
  ...,
  thenexprs = NULL,
  elseexprs = NULL,
  env = parent.frame()
)

```

Arguments

| | |
|------------------------|--------------------------------------------------------------------|
| <code>source</code> | optree relop node or <code>data.frame</code> . |
| <code>testexpr</code> | character containing the test expression. |
| <code>...</code> | force later arguments to bind by name. |
| <code>thenexprs</code> | named character then assignments (altering columns, not creating). |
| <code>elseexprs</code> | named character else assignments (altering columns, not creating). |
| <code>env</code> | environment to look to. |

Details

Note: ifebtest_* is a reserved column name for this procedure.

Value

operator tree or data.frame.

See Also

[if_else_block](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  # Example: clear one of a or b in any row where both are set.
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(
    my_db,
    'd',
    data.frame(i = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),
              a = c(0, 0, 1, 1, 1, 1, 1, 1, 1, 1),
              b = c(0, 1, 0, 1, 1, 1, 1, 1, 1, 1),
              edited = NA),
    temporary=TRUE, overwrite=TRUE)

  optree <- d %>%
    if_else_op(.,
              testexpr = qe((a+b)>1),
              thenexprs = qae(a :=% 0,
                              b :=% 0,
                              edited :=% 1),
              elseexprs = qae(edited :=% 0))
  cat(format(optree))

  sql <- to_sql(optree, my_db)
  cat(sql)

  print(DBI::dbGetQuery(my_db, sql))

  DBI::dbDisconnect(my_db)
}
```

Description

Please see `vignette('DependencySorting', package = 'rquery')` and `vignette('joinController', package = 'rquery')` for more details.

Usage

```
inspect_join_plan(tDesc, columnJoinPlan, ..., checkColClasses = FALSE)
```

Arguments

| | |
|------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>tDesc</code> | description of tables, from describe_tables (and likely altered by user). |
| <code>columnJoinPlan</code> | columns to join, from build_join_plan (and likely altered by user). Note: no column names must intersect with names of the form <code>table_CLEANEDTABNAME_present</code> . |
| <code>...</code> | force later arguments to bind by name. |
| <code>checkColClasses</code> | logical if true check for exact class name matches |

Value

NULL if okay, else a string

See Also

[describe_tables](#), [build_join_plan](#), [graph_join_plan](#), [actualize_join_plan](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  # example data
  DBI::dbWriteTable(my_db,
                    "d1",
                    data.frame(id= 1:3,
                               weight= c(200, 140, 98),
                               height= c(60, 24, 12)))
  DBI::dbWriteTable(my_db,
                    "d2",
                    data.frame(pid= 2:3,
                               weight= c(130, 110),
                               width= 1))
  # get the initial description of table defs
  tDesc <- describe_tables(my_db, qc(d1, d2))
  # declare keys (and give them consistent names)
  tDesc$keys[[1]] <- list(PrimaryKey= 'id')
  tDesc$keys[[2]] <- list(PrimaryKey= 'pid')
  # build the join plan
  columnJoinPlan <- build_join_plan(tDesc)
  # confirm the plan
  print(inspect_join_plan(tDesc, columnJoinPlan,
```

```

                                checkColClasses= TRUE))
# damage the plan
columnJoinPlan$sourceColumn[columnJoinPlan$sourceColumn=='width'] <- 'wd'
# find a problem
print(inspect_join_plan(tDesc, columnJoinPlan,
                        checkColClasses= TRUE))
DBI::dbDisconnect(my_db)
}

```

key_inspector_all_cols

Return all columns as guess of preferred primary keys.

Description

Return all columns as guess of preferred primary keys.

Usage

```
key_inspector_all_cols(db, tablename)
```

Arguments

| | |
|-----------|--------------------------|
| db | database handle |
| tablename | character, name of table |

Value

map of keys to keys

See Also

describe_tables

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  DBI::dbWriteTable(my_db,
                    "d",
                    data.frame(x=1:3, y=NA))
  print(key_inspector_all_cols(my_db, "d"))
  DBI::dbDisconnect(my_db)
}

```

`key_inspector_postgresql`

Return all primary key columns as guess at preferred primary keys for a PostgreSQL handle.

Description

Return all primary key columns as guess at preferred primary keys for a PostgreSQL handle.

Usage

```
key_inspector_postgresql(db, tablename)
```

Arguments

| | |
|------------------------|--------------------------|
| <code>db</code> | database handle |
| <code>tablename</code> | character, name of table |

Value

map of keys to keys

See Also

`describe_tables`

`key_inspector_sqlite` *Return all primary key columns as guess at preferred primary keys for a SQLite handle.*

Description

Return all primary key columns as guess at preferred primary keys for a SQLite handle.

Usage

```
key_inspector_sqlite(db, tablename)
```

Arguments

| | |
|------------------------|--------------------------|
| <code>db</code> | database handle |
| <code>tablename</code> | character, name of table |

Value

map of keys to keys

See Also

describe_tables

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  DBI::dbExecute(my_db, "
    CREATE TABLE orgtable (
      eid TEXT,
      date INTEGER,
      dept TEXT,
      location TEXT,
      PRIMARY KEY (eid, date)
    )
  ")
  print(key_inspector_sqlite(my_db, "orgtable"))
  DBI::dbDisconnect(my_db)
}

```

local_td

Construct a table description of a local data.frame.

Description

Construct a table description of a local data.frame.

Usage

```

local_td(
  d,
  ...,
  name = NULL,
  name_source = wrapr::mk_tmp_name_source("rqltd"),
  env = parent.frame()
)

```

Arguments

| | |
|-------------|-----------------------------------------------------------|
| d | data.frame or name of data.frame to use as a data source. |
| ... | not used, force later arguments to be optional. |
| name | if not null name to user for table. |
| name_source | temporary name source. |
| env | environment to work in. |

Value

a relop representation of the data

See Also

[db_td](#), [mk_td](#)

Examples

```
d <- data.frame(x = 1)
local_td(d)
local_td("d")
local_td(as.name("d"))
local_td(data.frame(x = 1))
d %>% local_td # needs wrapr 1.5.0 or newer to capture name
```

| | |
|------------------|----------------------------------------------------------|
| lookup_by_column | <i>Use one column to pick values from other columns.</i> |
|------------------|----------------------------------------------------------|

Description

The pick column selects values from the columns it names (per-row).

Usage

```
lookup_by_column(
  source,
  pick,
  result,
  ...,
  tmp_name_source = wrapr::mk_tmp_name_source("qn"),
  temporary = TRUE,
  qualifiers = NULL,
  f_dt_factory = NULL
)
```

Arguments

| | |
|-----------------|------------------------------------------------------------|
| source | source to select from (relop or data.frame). |
| pick | character scalar, name of column to control value choices. |
| result | character scalar, name of column to place values in. |
| ... | force later arguments to be bound by name |
| tmp_name_source | wrapr::mk_tmp_name_source(), temporary name generator. |

| | |
|--------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| temporary | logical, if TRUE use temporary tables. |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |
| f_dt_factory | optional signature f_dt_factory(pick, result) returns function with signature f_dt(d, nd) where d is a data.table. The point is the function must come from a data.table enabled package. Please see rqdatatable::make_dt_lookup_by_column for an example. |

Examples

```
df = data.frame(x = c(1, 2, 3, 4),
               y = c(5, 6, 7, 8),
               choice = c("x", "y", "x", "z"),
               stringsAsFactors = FALSE)

# library("rqdatatable")
# df %>%
#   lookup_by_column(., "choice", "derived")

if (requireNamespace("DBI", quietly = TRUE) &&
    requireNamespace("RSQLite", quietly = TRUE)) {
  db <- DBI::dbConnect(RSQLite::SQLite(),
                      ":memory:")
  RSQLite::initExtension(db)
  dr <- rq_copy_to(db, "dRemote", df,
                  overwrite = TRUE,
                  temporary = TRUE)

  ops <- dr %>%
    lookup_by_column(., "choice", "derived")
  cat(format(ops))

  execute(db, ops) %>%
    print(.)

  DBI::dbDisconnect(db)
}
```

make_assignments

Make a list of assignments, applying many functions to many columns.

Description

Make a list of assignments, applying each function to each column named. Intended to be used as an argument in extend_se() or project_se().

Usage

```
make_assignments(columns, funs, ..., sep = "_", prefix = TRUE)
```

Arguments

| | |
|---------|---------------------------------------------------------------------|
| columns | character, vector of column names to take values from. |
| funs | character, names of functions to apply. |
| ... | not used, forced later parameters to bind by name |
| sep | character, naming separator |
| prefix | logical, if TRUE place function names prior, else after in results. |

Examples

```
assignments <- make_assignments(c('x', 'y'), c('mean', med = 'median'))
print(assignments)
ops <- mk_td('d', c('x', 'y')) %.>% project_se(., assignments)
cat(format(ops))
```

| | |
|-------------------|------------------------------------------|
| map_column_values | <i>Remap values in a set of columns.</i> |
|-------------------|------------------------------------------|

Description

Remap values in a set of columns.

Usage

```
map_column_values(source, colmap, ..., null_default = FALSE)
```

Arguments

| | |
|--------------|---------------------------------------------------------------------------|
| source | optree relop node or data.frame. |
| colmap | data.frame with columns column_name, old_value, new_value. |
| ... | force later arguments to bind by name. |
| null_default | logical, if TRUE map non-matching values to NULL (else they map to self). |

Value

implementing optree or altered data.frame

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(),
                        ":memory:")

  d <- rq_copy_to(my_db, 'd',
                 data.frame(a = c("1", "2", "1", "3"),
                           b = c("1", "1", "3", "2"),
                           c = c("1", "2", "3", "4"),
                           stringsAsFactors = FALSE),
                 temporary = TRUE,
                 overwrite = TRUE)

  mp <- build_frame(
    "column_name", "old_value", "new_value" |
    "a"           , "1"         , "10"        |
    "a"           , "2"         , "20"        |
    "b"           , "1"         , "100"       |
    "b"           , "3"         , "300"       )

  # example
  op_tree <- d %.>%
    map_column_values(., mp)
  cat(format(op_tree))
  sql <- to_sql(op_tree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))

  # cleanup
  DBI::dbDisconnect(my_db)
}

```

mark_null_cols

Indicate NULLs per row for given column set.

Description

Build a query that creates NULL indicators for nulls in selected columns.

Usage

```
mark_null_cols(source, cols)
```

Arguments

| | |
|--------|-----------------------------------------------------------------------------------|
| source | incoming rel_op tree or data.frame. |
| cols | named character, values are columns to track, names are where to land indicators. |

Value

rel_op node or data.frame (depending on input).

See Also

[null_replace](#), [count_null_cols](#)

Examples

```
# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(my_db)
  old_o <- options(list("rquery.rquery_db_executor" = list(db = my_db)))

  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = c(0.6, 0.5, NA),
                             R2 = c(1.0, 0.9, NA)))
  op_tree <- d %>% mark_null_cols(., qc(AUC_NULL, R2_NULL) %:=%
                                qc(AUC, R2))

  cat(format(op_tree))
  sql <- to_sql(op_tree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))

  # ad-hoc mode
  data.frame(AUC=c(1,NA,0.5), R2=c(NA,1,0)) %>%
    op_tree %>%
    print(.)

  # cleanup
  options(old_o)
  DBI::dbDisconnect(my_db)
}
```

materialize

Materialize an optree as a table.

Description

Run the data query as a CREATE TABLE AS . Think of as a function that can be applied to relop trees, not as a component to place in pipelines.

Usage

```
materialize(
  db,
  optree,
  table_name = mk_tmp_name_source("rquery_mat")(),
  ...,
  limit = NULL,
  source_limit = NULL,
  overwrite = TRUE,
  temporary = FALSE,
  qualifiers = NULL
)
```

Arguments

| | |
|--------------|--------------------------------------------------------------------------------------------------|
| db | database connecton (rquery_db_info class or DBI connections preferred). |
| optree | relop operation tree. |
| table_name | character, name of table to create. |
| ... | force later arguments to bind by name. |
| limit | numeric if not NULL result limit (to use this, last statement must not have a limit). |
| source_limit | numeric if not NULL limit sources to this many rows. |
| overwrite | logical if TRUE drop an previous table. |
| temporary | logical if TRUE try to create a temporary table. |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

table description

See Also

[db_td](#), [execute](#), [to_sql](#), [rq_copy_to](#), [mk_td](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")

  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2),
                 temporary = TRUE, overwrite = TRUE)
  optree <- extend_se(d, c("v" %:=% "AUC + R2", "x" %:=% "pmax(AUC,v)"))
  cat(format(optree))
  res <- materialize(my_db, optree, "example")
}
```

```

    cat(format(res))
    sql <- to_sql(res, my_db)
    cat(sql)
    print(DBI::dbGetQuery(my_db, sql))

    DBI::dbDisconnect(my_db)
  }

```

materialize_node *Create a materialize node.*

Description

Write results into a specified table. Result is transient, lives only for the duration of the pipeline calculation. This node is only used to break up or un-nest calculations, not for value sharing or re-use.

Usage

```

materialize_node(
  source,
  table_name = (wrapr::mk_tmp_name_source("rquerymn"))(),
  ...,
  qualifiers = NULL
)

```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| source | source to work from (relop node) |
| table_name | character, name of caching table |
| ... | not used, force later argument to bind by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Details

Note this node can not be used in multiple paths in the same rel_op tree as it re-uses table names and re-computes each time called.

Value

relop materialize_node

See Also

[rsummary_node](#), [non_sql_node](#)

`mk_td`*Make a table description directly.*

Description

Build minimal structures (table name and column names) needed to represent data from a remote table.

Usage

```
mk_td(table_name, columns, ..., qualifiers = NULL, q_table_name = NULL)
```

```
table_source(table_name, columns, ..., qualifiers = NULL, q_table_name = NULL)
```

Arguments

| | |
|---------------------------|------------------------------------------------------------------------------------------------------|
| <code>table_name</code> | character, name of table |
| <code>columns</code> | character, column names of table (non-empty and unique values). |
| <code>...</code> | not used, force later argument to bind by name |
| <code>qualifiers</code> | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |
| <code>q_table_name</code> | optional character, qualified table name, note: has to be re-generated for different DB connections. |

Details

Generate a query that returns contents of a table, we could try to eliminate this (replace the query with the table name), but there are features one can work with with the query in place and SQL optimizers likely make this zero-cost anyway.

Value

a relop representation of the data

Functions

- `table_source`: old name for `mk_td`

See Also

[db_td](#), [local_td](#)

[db_td](#), [local_td](#), [rq_copy_to](#), [materialize](#), [execute](#), [to_sql](#)

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  rq_copy_to(my_db,
             'd',
             data.frame(AUC = 0.6, R2 = 0.2),
             overwrite = TRUE,
             temporary = TRUE)
  d <- mk_td('d',
            columns = c("AUC", "R2"))
  print(d)
  sql <- to_sql(d, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}

```

natural_join

Make a natural_join node.

Description

Natural join is a join by identity on all common columns specified in the `by` argument. Any common columns not specified in the `by` argument are coalesced into a single column preferring the first or "a" table.

Usage

```
natural_join(a, b, ..., by, jointype = "INNER", env = parent.frame())
```

Arguments

| | |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------|
| <code>a</code> | source to select from. |
| <code>b</code> | source to select from. |
| <code>...</code> | force later arguments to bind by name |
| <code>by</code> | character, set of columns to match. If <code>by</code> is a named character vector the right table will have columns renamed. |
| <code>jointype</code> | type of join ('INNER', 'LEFT', 'RIGHT', 'FULL'). |
| <code>env</code> | environment to look to. |

Value

natural_join node.

Examples

```

if(requireNamespace("DBI", quietly = TRUE) &&
  requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(),
                        ":memory:")

  d1 <- rq_copy_to(
    my_db, 'd1',
    build_frame(
      "key", "val", "val1" |
      "a" , 1 , 10 |
      "b" , 2 , 11 |
      "c" , 3 , 12 ))
  d2 <- rq_copy_to(
    my_db, 'd2',
    build_frame(
      "key", "val", "val2" |
      "a" , 5 , 13 |
      "b" , 6 , 14 |
      "d" , 7 , 15 ))

  # key matching join
  optree <- natural_join(d1, d2,
                        jointype = "LEFT", by = 'key')
  execute(my_db, optree) %>%
    print(.)

  DBI::dbDisconnect(my_db)
}

```

non_sql_node

Wrap a non-SQL node.

Description

Note: non-SQL nodes are allowed to delete/overwrite both both the incoming and outgoing tables, so do not point them to non-temporary structures. Also they tend to land all columns (losing narrowing optimization), so can be expensive and should be used sparingly. Finally their result can only be used once in a pipeline (else they will try to clobber their own result).

Usage

```

non_sql_node(
  source,
  ...,
  f_db = NULL,
  f_df = NULL,

```



```

    f_dt = NULL,
    incoming_table_name,
    incoming_qualifiers = NULL,
    outgoing_table_name,
    outgoing_qualifiers = NULL,
    columns_produced,
    display_form = "non_sql_node",
    orig_columns = TRUE,
    temporary = TRUE,
    check_result_details = TRUE,
    env = parent.frame()
)

```

Arguments

| | |
|----------------------|-----------------------------------------------------------------------------------------------------------------------------|
| source | source to work from (data.frame or relop node) |
| ... | force later arguments to bind by name |
| f_db | database implementation signature: f_db(db, incoming_table_name, outgoing_table_name, nd, ...) (db being a database handle) |
| f_df | data.frame implementation signature: f_df(data.frame, nd) (NULL defaults to taking from database). |
| f_dt | data.table implementation signature: f_dt(data.table, nd) (NULL defaults f_df). |
| incoming_table_name | character, name of incoming table |
| incoming_qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |
| outgoing_table_name | character, name of produced table |
| outgoing_qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |
| columns_produced | character, names of additional columns produced |
| display_form | character, how to print node |
| orig_columns | logical if TRUE select all original columns. |
| temporary | logical, if TRUE mark tables temporary. |
| check_result_details | logical, if TRUE enforce result type and columns. |
| env | environment to look to. |

Value

non-sql node.

See Also

[rsummary_node](#), [quantile_node](#)

| | |
|----------------|----------------------------------------------------------------------------------------------------------------|
| normalize_cols | <i>Build an optree pipeline that normalizes a set of columns so each column sums to one in each partition.</i> |
|----------------|----------------------------------------------------------------------------------------------------------------|

Description

This is an example of building up a desired pre-prepared pipeline fragment from relop nodes.

Usage

```
normalize_cols(source, columns, ..., partitionby = NULL, env = parent.frame())
```

Arguments

| | |
|-------------|-------------------------------------------------------------------|
| source | relop tree or data.frame source. |
| columns | character, columns to normalize. |
| ... | force later arguments to bind by name. |
| partitionby | partitioning (window function) column names to define partitions. |
| env | environment to look for values in. |

Examples

```
# by hand logistic regression example
scale <- 0.237
d <- mk_td("survey_table",
           c("subjectID", "surveyCategory", "assessmentTotal"))
optree <- d %>%
  extend(.,
         probability :=%
           exp(assessmentTotal * scale)) %>%
  normalize_cols(.,
                "probability",
                partitionby = 'subjectID') %>%
  pick_top_k(.,
             partitionby = 'subjectID',
             orderby = c('probability', 'surveyCategory'),
             reverse = c('probability')) %>%
  rename_columns(., 'diagnosis' :=% 'surveyCategory') %>%
  select_columns(., c('subjectID',
                    'diagnosis',
                    'probability')) %>%
  orderby(., 'subjectID')
cat(format(optree))
```

| | |
|--------------|------------------------------------|
| null_replace | <i>Create a null_replace node.</i> |
|--------------|------------------------------------|

Description

Replace NA/NULL is specified columns with the given replacement value.

Usage

```
null_replace(src, cols, value, ..., note_col = NULL, env = parent.frame())
```

Arguments

| | |
|----------|---------------------------------------------------------------------------------|
| src | relop or data.frame data source. |
| cols | character, columns to work on. |
| value | scalar, value to write. |
| ... | force later arguments to bind by name. |
| note_col | character, if not NULL record number of columns altered per-row in this column. |
| env | environment to look to. |

Value

null_replace node or data.frame.

See Also

[count_null_cols](#), [mark_null_cols](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d1 <- rq_copy_to(my_db, 'd1',
                  data.frame(A = c(NA, 2, 3, NA), B = c(3, NA, 4, NA)))
  optree <- null_replace(d1, qc(A, B),
                        0.0, note_col = "alterations")
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}
```

| | |
|------------|----------------------------------------------|
| op_diagram | <i>Build a diagram of a optree pipeline.</i> |
|------------|----------------------------------------------|

Description

Build a diagram of a optree pipeline.

Usage

```
op_diagram(optree, ..., merge_tables = FALSE, show_table_columns = TRUE)
```

Arguments

| | |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| optree | operation tree pipeline (or list of such). |
| ... | force other argument to be by name. |
| merge_tables | logical, if TRUE merge all same table references into one node. rel_op nodes that declare a materialize_as name will be cross-linked. |
| show_table_columns | logical, if TRUE show table columns. |

Value

character DiagrammeR::grViz() ready text.

Examples

```
d <- mk_td('d',
           columns = qc(AUC, R2))
optree <- d %>%
  extend(., v :=% ifelse(AUC>0.5, R2, 1.0)) %>%
  quantile_node(.) %>%
  natural_join(., d, jointype = "LEFT", by = "AUC") %>%
  orderby(., "AUC")

cat(format(optree))

cat(op_diagram(optree))

if(requireNamespace("DiagrammeR", quietly = TRUE)) {
  optree %>%
    op_diagram(., merge_tables = TRUE) %>%
    DiagrammeR::grViz(.) %>%
    print(.)
  ## or to render to png
  # optree %>%
  #   op_diagram(., merge_tables = TRUE) %>%
  #   DiagrammeR::DiagrammeR(diagram = ., type = "grViz") %>%
```

```
# DiagrammeRsvg::export_svg(.) %>%
# charToRaw(.) %>%
# rsvg::rsvg_png(., file = "diagram1.png")
}
```

orderby

Make an orderby node (not a relational operation).

Description

Order a table by a set of columns (not general expressions) and limit number of rows in that order.

Usage

```
orderby(
  source,
  cols = NULL,
  ...,
  reverse = NULL,
  limit = NULL,
  env = parent.frame()
)
```

Arguments

| | |
|---------|-----------------------------------------------------------------|
| source | source to select from. |
| cols | order by named columns ascending. |
| ... | force later arguments to be bound by name |
| reverse | character, which columns to reverse ordering of top descending. |
| limit | number limit row count. |
| env | environment to look to. |

Details

Note: this is a relational operator in that it takes a table that is a relation (has unique rows) to a table that is still a relation. However, most relational systems do not preserve row order in storage or between operations. So without the limit set this is not a useful operator except as a last step prior to pulling data to an in-memory data.frame (which does preserve row order).

Value

orderby node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- orderby(d, cols = "AUC", reverse = "AUC", limit=4)
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}

```

order_expr

Make a order_expr node.

Description

order_expr() uses bquote() .()-style escaping.

Usage

```
order_expr(source, expr, env = parent.frame())
```

```
order_expr_nse(source, expr, env = parent.frame())
```

Arguments

| | |
|--------|---------------------------|
| source | source to select from. |
| expr | expression to order_expr. |
| env | environment to look to. |

Value

select columns node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2, z = 3))
  TARGETCOL = as.name("AUC")
  optree <- order_expr(d, .(TARGETCOL)/R2) %>%
  select_columns(., "R2")
}

```

```

    cat(format(optree))
    sql <- to_sql(optree, my_db)
    cat(sql)
    print(DBI::dbGetQuery(my_db, sql))
    DBI::dbDisconnect(my_db)
  }

```

| | |
|---------------|--------------------------------|
| order_expr_se | <i>Make a order_expr node.</i> |
|---------------|--------------------------------|

Description

Make a order_expr node.

Usage

```
order_expr_se(source, expr, env = parent.frame())
```

Arguments

| | |
|--------|----------------------------------------------|
| source | source to select from. |
| expr | expression to order_expr in ascending order. |
| env | environment to look for values in. |

Value

select columns node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- order_expr_se(d, "AUC/R2")
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}

```

| | |
|------------|-----------------------------------------------------------|
| order_rows | <i>Make an orderby node (not a relational operation).</i> |
|------------|-----------------------------------------------------------|

Description

Order a table by a set of columns (not general expressions) and limit number of rows in that order.

Usage

```
order_rows(
  source,
  cols = NULL,
  ...,
  reverse = NULL,
  limit = NULL,
  env = parent.frame()
)
```

Arguments

| | |
|---------|----------------------------------------------------------------|
| source | source to select from. |
| cols | order by columns ascending. |
| ... | force later arguments to be bound by name |
| reverse | character, which columns to reverse ordering of to descending. |
| limit | number limit row count. |
| env | environment to look to. |

Details

Note: this is a relational operator in that it takes a table that is a relation (has unique rows) to a table that is still a relation. However, most relational systems do not preserve row order in storage or between operations. So without the limit set this is not a useful operator except as a last step prior to pulling data to an in-memory data.frame (which does preserve row order).

Value

order_by node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- order_rows(d, cols = "AUC", reverse = "AUC", limit=4)
  cat(format(optree))
}
```



```

    sql <- to_sql(optree, my_db)
    cat(sql)
    print(DBI::dbGetQuery(my_db, sql))
    DBI::dbDisconnect(my_db)
  }

```

| | |
|------------|-------------------------------------------------------------------------------------------------------|
| pick_top_k | <i>Build an optree pipeline that selects up to the top k rows from each group in the given order.</i> |
|------------|-------------------------------------------------------------------------------------------------------|

Description

This is an example of building up a desired pre-prepared pipeline fragment from relop nodes.

Usage

```

pick_top_k(
  source,
  ...,
  partitionby = NULL,
  orderby = NULL,
  reverse = NULL,
  k = 1L,
  order_expression = "row_number()",
  order_column = "row_number",
  keep_order_column = TRUE,
  env = parent.frame()
)

```

Arguments

| | |
|-------------------|-------------------------------------------------------------------------|
| source | relop tree or data.frame source. |
| ... | force later arguments to bind by name. |
| partitionby | partitioning (window function) column names. |
| orderby | character, ordering (in window function) column names. |
| reverse | character, reverse ordering (in window function) of these column names. |
| k | integer, number of rows to limit to in each group. |
| order_expression | character, command to compute row-order/rank. |
| order_column | character, column name to write per-group rank in (no ties). |
| keep_order_column | logical, if TRUE retain the order column in the result. |
| env | environment to look for values in. |

Examples

```
# by hand logistic regression example
scale <- 0.237
d <- mk_td("survey_table",
           c("subjectID", "surveyCategory", "assessmentTotal"))
optree <- d %>%
  extend(.,
         probability :=%
           exp(assessmentTotal * scale)) %>%
  normalize_cols(.,
                 "probability",
                 partitionby = 'subjectID') %>%
  pick_top_k(.,
             partitionby = 'subjectID',
             orderby = c('probability', 'surveyCategory'),
             reverse = c('probability', 'surveyCategory')) %>%
  rename_columns(., 'diagnosis' :=% 'surveyCategory') %>%
  select_columns(., c('subjectID',
                     'diagnosis',
                     'probability')) %>%
  orderby(., 'subjectID')
cat(format(optree))
```

```
pre_sql_sub_expr      pre_sql_sub_expr
```

Description

represents an expression. Unnamed list of pre_sql_terms and character.

Usage

```
pre_sql_sub_expr(terms, info = NULL)
```

Arguments

| | |
|-------|--------------------------------------------------------------------------------------|
| terms | list of pre_sql tokens |
| info | named list of extra info with a name slot containing a single string without spaces. |

Value

```
pre_sql_sub_expr
```

| | |
|---------|----------------------------------------------------------------|
| project | <i>project data by grouping, and adding aggregate columns.</i> |
|---------|----------------------------------------------------------------|

Description

Supports bquote() .()-style name abstraction including .(-) notation to promote strings to names (please see here: <https://github.com/WinVector/rquery/blob/master/Examples/Substitution/Substitution.md>).

Usage

```
project(source, ..., groupby = c(), env = parent.frame())
```

```
project_nse(source, ..., groupby = c(), env = parent.frame())
```

```
aggregate_nse(source, ..., groupby = c(), env = parent.frame())
```

Arguments

| | |
|---------|------------------------------------|
| source | source to select from. |
| ... | new column assignment expressions. |
| groupby | grouping columns. |
| env | environment to look for values in. |

Value

project node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(),
                        "memory:")
  d <- rq_copy_to(
    my_db, 'd',
    data.frame(group = c('a', 'a', 'b', 'b'),
              val = 1:4,
              stringsAsFactors = FALSE))

  op_tree <- d %.>%
    project(., groupby = "group", vmax %:= max(val))
  cat(format(op_tree))
  sql <- to_sql(op_tree, my_db)
  cat(sql)
  execute(my_db, op_tree) %.>%
    print(.)
}
```

```

op_tree <- d %.>%
  project(., groupby = NULL, vmax :=% max(val))
cat(format(op_tree))
sql <- to_sql(op_tree, my_db)
cat(sql)
execute(my_db, op_tree) %.>%
  print(.)

DBI::dbDisconnect(my_db)
}

```

project_se

project data by grouping, and adding aggregate columns.

Description

project data by grouping, and adding aggregate columns.

Usage

```

project_se(source, assignments, ..., groupby = c(), env = parent.frame())
aggregate_se(source, assignments, ..., groupby = c(), env = parent.frame())

```

Arguments

| | |
|-------------|-----------------------------------------------|
| source | source to select from. |
| assignments | new column assignment expressions. |
| ... | not used, force later arguments to be by name |
| groupby | grouping columns. |
| env | environment to look for values in. |

Value

project node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(),
                        "memory:")
  d <- rq_copy_to(
    my_db, 'd',
    data.frame(group = c('a', 'a', 'b', 'b'),
              val = 1:4,
              stringsAsFactors = FALSE))
}

```

```

op_tree <- d %.>%
  project_se(., groupby = "group", "vmax" :=% "max(val)")
cat(format(op_tree))
sql <- to_sql(op_tree, my_db)
cat(sql)
execute(my_db, op_tree) %.>%
  print(.)

op_tree <- d %.>%
  project_se(., groupby = NULL, "vmax" :=% "max(val)")
cat(format(op_tree))
sql <- to_sql(op_tree, my_db)
cat(sql)
execute(my_db, op_tree) %.>%
  print(.)

DBI::dbDisconnect(my_db)
}

```

| | |
|---------------|----------------------------------------------------------------------------------------------------------------|
| quantile_cols | <i>Compute quantiles of specified columns (without interpolation, needs a database with window functions).</i> |
|---------------|----------------------------------------------------------------------------------------------------------------|

Description

Compute quantiles of specified columns (without interpolation, needs a database with window functions).

Usage

```

quantile_cols(
  db,
  incoming_table_name,
  ...,
  probs = seq(0, 1, 0.25),
  probs_name = "quantile_probability",
  cols = rq_colnames(db, incoming_table_name),
  qualifiers = NULL
)

```

Arguments

| | |
|---------------------|---------------------------------------|
| db | database connection |
| incoming_table_name | name of table to compute quantiles of |
| ... | force later arguments to bind by name |

| | |
|------------|--------------------------------------------------------------------------------------------------|
| probs | numeric, probabilities to compute quantiles of |
| probs_name | character name for probability column |
| cols | character, columns to compute quantiles of |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

data.frame of quantiles

See Also

[quantile_node](#), [rsummary](#)

| | |
|---------------|----------------------------------------------------------------------------------------------------------------|
| quantile_node | <i>Compute quantiles over non-NULL values (without interpolation, needs a database with window functions).</i> |
|---------------|----------------------------------------------------------------------------------------------------------------|

Description

Please see https://github.com/WinVector/rquery/blob/master/extras/Summary_Example.md for an example.

Usage

```
quantile_node(
  source,
  cols = NULL,
  ...,
  probs_name = "quantile_probability",
  probs = seq(0, 1, 0.25),
  tmp_name_source = wrapr::mk_tmp_name_source("qn"),
  temporary = TRUE,
  qualifiers = NULL
)
```

Arguments

| | |
|-----------------|--------------------------------------------------------------------------------------------------|
| source | source to select from (relop or data.frame). |
| cols | character, compute quantiles for these columns (NULL indicates all columns). |
| ... | force later arguments to be bound by name |
| probs_name | character, column name to write probs in. |
| probs | numeric quantiles to compute |
| tmp_name_source | wrapr::mk_tmp_name_source(), temporary name generator. |
| temporary | logical, if TRUE use temporary tables |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Details

This is a `non_sql_node`, so please see [non_sql_node](#) for some of the issues for this node type.

Value

table of quantiles

See Also

[quantile_cols](#), [rsummary](#), [non_sql_node](#)

| | |
|------------------|-----------------------------|
| quote_identifier | <i>Quote an identifier.</i> |
|------------------|-----------------------------|

Description

Quote an identifier.

Usage

```
quote_identifier(x, id)
```

Arguments

| | |
|----|--------------------------------------------------------|
| x | database handle or <code>rquery_db_info</code> object. |
| id | character to quote |

Value

quoted identifier

| | |
|---------------|----------------------|
| quote_literal | <i>Quote a value</i> |
|---------------|----------------------|

Description

Quote a value

Usage

```
quote_literal(x, o)
```

Arguments

| | |
|---|--------------------------------------------------------|
| x | database handle or <code>rquery_db_info</code> object. |
| o | value to quote |

Value

quoted string

| | |
|--------------|-----------------------|
| quote_string | <i>Quote a string</i> |
|--------------|-----------------------|

Description

Quote a string

Usage

quote_string(x, s)

Arguments

| | |
|---|-------------------------------------------|
| x | database handle or rquery_db_info object. |
| s | character to quote |

Value

quoted string

| | |
|------------------|----------------------------|
| quote_table_name | <i>Quote a table name.</i> |
|------------------|----------------------------|

Description

Quote a table name.

Usage

quote_table_name(x, id, ..., qualifiers = character(0))

Arguments

| | |
|------------|-----------------------------------------------------------------------------------------|
| x | database handle or rquery_db_info object. |
| id | character to quote |
| ... | not used, force later arguments to bind by name. |
| qualifiers | named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

quoted identifier

| | |
|----------------|-----------------------------------------------------------------|
| rename_columns | <i>Make a rename columns node (copies columns not renamed).</i> |
|----------------|-----------------------------------------------------------------|

Description

Make a rename columns node (copies columns not renamed).

Usage

```
rename_columns(source, cmap, env = parent.frame())
```

Arguments

| | |
|--------|-------------------------------------------------------------------------|
| source | source to rename from. |
| cmap | map written as new column names as keys and old column names as values. |
| env | environment to look to. |

Value

rename columns node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2, z = 3))
  op_tree <- rename_columns(d, c('R2' :=% 'AUC', 'AUC' :=% 'R2'))
  cat(format(op_tree))
  sql <- to_sql(op_tree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}
```

| | |
|------------|----------------------------------------------|
| row_counts | <i>Build an optree pipeline counts rows.</i> |
|------------|----------------------------------------------|

Description

This is an example of building up a desired pre-prepared pipeline fragment from relop nodes.

Usage

```
row_counts(source, ..., groupby = character(0), env = parent.frame())
```

Arguments

| | |
|---------|----------------------------------------------|
| source | relop tree or data.frame source. |
| ... | force later arguments to bind by name. |
| groupby | partitioning (window function) column names. |
| env | environment to look for values in. |

Examples

```
# by hand logistic regression example
d <- mk_td("survey_table",
          c("subjectID", "surveyCategory", "assessmentTotal"))
optree <- d %>%
  row_counts(., groupby = "subjectID")
cat(format(optree))
```

rquery

rquery: Relational Query Generator for Data Manipulation

Description

rquery supplies a piped query generator based on Edgar F. Codd's relational algebra and operator names (plus experience using SQL and dplyr at big data scale). The design represents an attempt to make SQL more teachable by denoting composition a sequential pipeline notation instead of nested queries or functions. Package features include: data processing trees or pipelines as observable objects (able to report both columns produced and columns used), optimized SQL generation as an explicit user visible modeling step, and convenience methods for applying query trees to in-memory data.frames.

Details

Note: rquery is a "database first" design. This means choices are made that favor database implementation. These include: capturing the entire calculation prior to doing any work (and using recursive methods to inspect this object, which can limit the calculation depth to under 1000 steps at a time), preferring "tame column names" (which isn't a bad idea in 'R' anyway as columns and variables are often seen as cousins), and not preserving row or column order (or supporting numeric column indexing). Also, rquery does have a fast in-memory implementation: rqdatatable (thanks to the data.table, so one can in fact use 'rquery' without a database).

```
rquery_apply_to_data_frame
```

Execute optree in an environment where d is the only data.

Description

Default DB uses RSQLite (so some functions are not supported).

Usage

```
rquery_apply_to_data_frame(
  d,
  optree,
  ...,
  limit = NULL,
  source_limit = NULL,
  allow_executor = TRUE,
  env = parent.frame()
)
```

Arguments

| | |
|----------------|------------------------------------------------------------------------------|
| d | data.frame or named list of data.frames. |
| optree | rquery rel_op operation tree. |
| ... | force later arguments to bind by name. |
| limit | integer, if not NULL limit result to no more than this many rows. |
| source_limit | numeric if not NULL limit sources to this many rows. |
| allow_executor | logical if TRUE allow any executor set as rquery.rquery_executor to be used. |
| env | environment to look to. |

Value

data.frame result

Examples

```
# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(db)
  old_o <- options(list("rquery.rquery_db_executor" = list(db = db)))

  optree <- mk_td("d", c("AUC", "R2", "D")) %.>%
  extend(., c %:=% sqrt(R2)) %.>%
  orderby(., cols = "R2", reverse = "R2")
}
```

```

d <- data.frame(AUC = 0.6, R2 = c(0.1, 0.2), D = NA, z = 2)
v <- rquery_apply_to_data_frame(d, optree)
print(v)

# now load up a table without an R2 column,
# want to show this is caught
d <- data.frame(z = 1)
tryCatch(
  rquery_apply_to_data_frame(d, optree),
  error = function(e) { as.character(e) }
) %>%
  print(.)

options(old_o)
DBI::dbDisconnect(db)
}

```

rquery_db_info

Build a db information stand-in

Description

Build a db information stand-in

Usage

```

rquery_db_info(
  ...,
  connection = NULL,
  is_dbi = FALSE,
  identifier_quote_char = "\"",
  string_quote_char = "'",
  overrides = NULL,
  note = "",
  connection_options = rq_connection_advice(connection),
  db_methods = rquery_default_methods()
)

```

Arguments

... force all arguments to be by name.

connection connection handle to database or Spark.

is_dbi if TRUE the database connection can be used with DBI.

identifier_quote_char character, quote to put around identifiers.

| | |
|--------------------|-------------------------------------------|
| string_quote_char | character, quote to put around strings. |
| overrides | named list of functions to place in info. |
| note | character note to add to display form. |
| connection_options | named list of per-connection options. |
| db_methods | named list of to_sql methods. |

Value

rquery_db_info object

rquery_default_db_info

An example rquery_db_info object useful for formatting SQL without a database connection.

Description

An example rquery_db_info object useful for formatting SQL without a database connection.

Usage

rquery_default_db_info()

Value

a rquery_db_info without a connection and vanilla settings.

rq_colnames

List table column names.

Description

List table column names.

Usage

rq_colnames(db, table_name, ..., qualifiers = NULL)

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| db | Connection handle |
| table_name | character table name |
| ... | not used, force later argument to bind by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

character list of column names

| | |
|-------------|------------------------------------------------------------|
| rq_coltypes | <i>Get column types by example values as a data.frame.</i> |
|-------------|------------------------------------------------------------|

Description

Example values not necessarily all from same row. Taking values from different rows is to try to work around NA not carrying type/class info in many cases.

Usage

```
rq_coltypes(
  db,
  table_name,
  ...,
  qualifiers = NULL,
  prefer_not_NA = FALSE,
  force_check = FALSE
)
```

Arguments

| | |
|---------------|--------------------------------------------------------------------------------------------------|
| db | Connection handle. |
| table_name | character table name referring to a non-empty table. |
| ... | force later arguments to bind by name. |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |
| prefer_not_NA | logical, if TRUE try to find a non-NA example for all columns (FALSE just for logical columns). |
| force_check | logical, if TRUE perform checks regardless of check_logical_column_types option setting. |

Value

single row data.frame with example values, not all values necessarily from same database row.

Examples

```
if(requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")

  # getDBOption(db, "check_logical_column_types", FALSE)
  # options(rq_connection_tests(db))
}
```

```

# getDBOption(db, "check_logical_column_types", FALSE)

d <- data.frame(w= c(NA, 1L),
               x= c(NA, 2.0),
               y= factor(c(NA, "x")),
               z= c(NA, "y"),
               want = c(1, 0),
               stringsAsFactors=FALSE)
d <- rq_copy_to(db, "d", d,
               overwrite = TRUE,
               temporary = TRUE)
res <- d %>%
  extend(.,
        wc :=% ifelse(w>1, "x", "y"),
        wn :=% ifelse(w>1, 1, 2),
        xc :=% ifelse(x>1, "x", "y"),
        xn :=% ifelse(x>1, 1, 2),
        yc :=% ifelse(y=="a", "x", "y"),
        yn :=% ifelse(y=="a", "x", "y")) %>%
  materialize(db, .)
resn <- DBI::dbQuoteIdentifier(db, res$table_name)
print("full table types")
print(str(DBI::dbGetQuery(db, paste("SELECT * FROM", resn))))
print("single row mis-reported types")
print(str(DBI::dbGetQuery(db, paste("SELECT * FROM", resn, "WHERE want=1"))))
print("rq_coltypes correct synthetic example row types")
print(str(rq_coltypes(db, res$table_name, force_check = TRUE)))
DBI::dbDisconnect(db)
}

```

`rq_connection_advice` *Get advice for a DB connection (beyond tests).*

Description

These settings are set by the package maintainers based on experience with specific databases.

Usage

```
rq_connection_advice(db)
```

Arguments

`db` database connection handle

Value

named list of options

See Also

[rq_connection_tests](#)

Examples

```
if(requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {  
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")  
  print(rq_connection_name(my_db))  
  print(rq_connection_advice(my_db))  
  DBI::dbDisconnect(my_db)  
}
```

| | |
|--------------------|----------------------------------------------------------|
| rq_connection_name | <i>Build a canonical name for a db connection class.</i> |
|--------------------|----------------------------------------------------------|

Description

Build a canonical name for a db connection class.

Usage

```
rq_connection_name(db)
```

Arguments

db Database connection handle.

Value

character, key version of handle for option lookups.

Examples

```
if(requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {  
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")  
  print(rq_connection_name(my_db))  
  DBI::dbDisconnect(my_db)  
}
```

rq_connection_tests *Try and test database for some option settings.*

Description

These settings are estimated by experiments. This is not the full set of options- but just the ones tested here.

Usage

```
rq_connection_tests(db, ..., overrides = NULL, use_advice = TRUE)
```

Arguments

| | |
|------------|------------------------------------------------------------------------------------|
| db | database connection handle. |
| ... | force later arguments to bind by name. |
| overrides | named character vector or list, options (just name, not DB qualification) to force |
| use_advice | logical if TRUE incorporate hard-coded advice. |

Details

Note: tests are currently run in the default schema. Also it is normal to see some warning/error messages as different database capabilities are tested.

Value

named list of options

See Also

[rq_connection_advice](#)

Examples

```
if(requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  print(rq_connection_name(my_db))
  print(rq_connection_tests(my_db,
    overrides = c("use_DBI_dbExistsTable" = FALSE)))
  # the following would set options
  # print(options(rq_connection_tests(my_db)))
  DBI::dbDisconnect(my_db)
}
```

| | |
|------------|--------------------------------------------------|
| rq_copy_to | <i>Copy local R table to remote data handle.</i> |
|------------|--------------------------------------------------|

Description

Copy local R table to remote data handle.

Usage

```
rq_copy_to(  
  db,  
  table_name,  
  d,  
  ...,  
  qualifiers = NULL,  
  overwrite = FALSE,  
  temporary = TRUE,  
  rowidcolumn = NULL  
)
```

Arguments

| | |
|-------------|--------------------------------------------------------------------------------------------------|
| db | database connection handle. |
| table_name | name of table to create. |
| d | data.frame to copy to database. |
| ... | force later argument to be by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |
| overwrite | logical, if TRUE try to overwrite existing table. |
| temporary | logical, if TRUE try to mark table as temporary. |
| rowidcolumn | character, name to land row-ids. |

Value

a relap representation of the data

See Also

[db_td](#), [mk_td](#), [materialize](#), [execute](#), [to_sql](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))

  sql <- to_sql(d, db)
  cat(sql)
  print(DBI::dbGetQuery(db, "SELECT * FROM d"))
  DBI::dbDisconnect(db)
}
```

| | |
|------------|-------------------------------------------------------------------------------------|
| rq_execute | <i>Execute a query, typically an update that is not supposed to return results.</i> |
|------------|-------------------------------------------------------------------------------------|

Description

Execute a query, typically an update that is not supposed to return results.

Usage

```
rq_execute(db, q)
```

Arguments

| | |
|----|----------------------------|
| db | database connection handle |
| q | character query |

Value

nothing

See Also

[db_td](#)

| | |
|--------------|----------------------------------------------------------------------------------------|
| rq_get_query | <i>Execute a get query, typically a non-update that is supposed to return results.</i> |
|--------------|----------------------------------------------------------------------------------------|

Description

Execute a get query, typically a non-update that is supposed to return results.

Usage

```
rq_get_query(db, q)
```

Arguments

| | |
|----|----------------------------|
| db | database connection handle |
| q | character query |

Value

nothing

See Also

[db_td](#)

| | |
|---------|-----------------------------------------|
| rq_nrow | <i>Count rows and return as numeric</i> |
|---------|-----------------------------------------|

Description

Count rows and return as numeric

Usage

```
rq_nrow(db, table_name, ..., qualifiers = NULL)
```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| db | database connection |
| table_name | character, name of table |
| ... | not used, force later argument to bind by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

numeric row count

See Also

[db_td](#)

| | |
|-----------------|---------------------|
| rq_remove_table | <i>Remove table</i> |
|-----------------|---------------------|

Description

Remove table

Usage

```
rq_remove_table(db, table_name, ..., qualifiers = NULL)
```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| db | database connection. |
| table_name | character, name of table to create. |
| ... | not used, force later argument to bind by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

logical TRUE if table existed, else FALSE

See Also

[db_td](#)

| | |
|-----------------|---------------------------------|
| rq_table_exists | <i>Check if a table exists.</i> |
|-----------------|---------------------------------|

Description

Check if a table exists.

Usage

```
rq_table_exists(db, table_name, ..., qualifiers = NULL)
```

Arguments

| | |
|------------|--------------------------------------------------------------------------------------------------|
| db | Connection handle |
| table_name | character table name |
| ... | not used, force later argument to bind by name |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

logical TRUE if table exists.

See Also

[db_td](#)

| | |
|------|----------------------------------|
| rstr | <i>Quick look at remote data</i> |
|------|----------------------------------|

Description

Quick look at remote data

Usage

```
rstr(  
  my_db,  
  tableName,  
  ...,  
  displayRows = 10,  
  countRows = TRUE,  
  qualifiers = NULL  
)
```

```
rlook(
  my_db,
  tableName,
  ...,
  displayRows = 10,
  countRows = TRUE,
  qualifiers = NULL
)
```

Arguments

| | |
|-------------|--------------------------------------------------------------------------------------------------|
| my_db | database handle |
| tableName | name of table to look at |
| ... | not used, force later arguments to bind by name |
| displayRows | number of rows to sample |
| countRows | logical, if TRUE return row count. |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Value

str view of data

Examples

```
if ( requireNamespace("DBI", quietly = TRUE) &&
    requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  DBI::dbWriteTable(my_db,
                    'd',
                    data.frame(AUC = 0.6, R2 = 0.2),
                    overwrite = TRUE,
                    temporary = TRUE)
  rlook(my_db, 'd')
  DBI::dbDisconnect(my_db)
}
```

rsummary

Compute usable summary of columns of remote table.

Description

Compute per-column summaries and return as a `data.frame`. Warning: can be an expensive operation.

Usage

```
rsummary(
  db,
  tableName,
  ...,
  countUniqueNum = FALSE,
  quartiles = FALSE,
  cols = NULL,
  qualifiers = NULL
)
```

Arguments

| | |
|----------------|--------------------------------------------------------------------------------------------------|
| db | database connection. |
| tableName | name of table. |
| ... | force additional arguments to be bound by name. |
| countUniqueNum | logical, if TRUE include unique non-NA counts for numeric cols. |
| quartiles | logical, if TRUE add Q1 (25%), median (50%), Q3 (75%) quartiles. |
| cols | if not NULL set of columns to restrict to. |
| qualifiers | optional named ordered vector of strings carrying additional db hierarchy terms, such as schema. |

Details

For numeric columns includes NaN in nna count (as is typical for R, e.g., `is.na(NaN)`).

Value

data.frame summary of columns.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) &&
    requireNamespace("RSQLite", quietly = TRUE)) {
  d <- data.frame(p= c(TRUE, FALSE, NA),
                 s= NA,
                 w= 1:3,
                 x= c(NA,2,3),
                 y= factor(c(3,5,NA)),
                 z= c('a',NA,'a'),
                 stringsAsFactors=FALSE)
  db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(db)
  rq_copy_to(db, "dRemote", d,
             overwrite = TRUE, temporary = TRUE)
  print(rsummary(db, "dRemote"))
  DBI::dbDisconnect(db)
}
```



```
}

```

| | |
|---------------|------------------------------------------------|
| rsummary_node | <i>Create an rsummary relop operator node.</i> |
|---------------|------------------------------------------------|

Description

This is a non_sql_node, so please see [non_sql_node](#) for some of the issues for this node type.

Usage

```
rsummary_node(
  source,
  ...,
  quartiles = FALSE,
  tmp_name_source = wrapr::mk_tmp_name_source("sn"),
  temporary = TRUE
)
```

Arguments

| | |
|-----------------|------------------------------------------------------------------|
| source | incoming source (relop node or data.frame). |
| ... | force later arguments to be by name |
| quartiles | logical, if TRUE add Q1 (25%), median (50%), Q3 (75%) quartiles. |
| tmp_name_source | wrapr::mk_tmp_name_source(), temporary name generator. |
| temporary | logical, if TRUE use temporary tables |

Value

rsummary node

See Also

[quantile_node](#), [non_sql_node](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  d <- data.frame(p= c(TRUE, FALSE, NA),
                 s= NA,
                 w= 1:3,
                 x= c(NA,2,3),
                 y= factor(c(3,5,NA)),
                 z= c('a',NA,'a'),
                 stringsAsFactors=FALSE)
```

```

db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
RSQLite::initExtension(db)
rq_copy_to(db, "dRemote", d,
           overwrite = TRUE,
           temporary = TRUE)

ops <- db_td(db, "dRemote") %>%
  extend(., v %:=% ifelse(x>2, "x", "y")) %>%
  rsummary_node(.)
cat(format(ops))

print(to_sql(ops, db))

reshdl <- materialize(db, ops)
print(DBI::dbGetQuery(db, to_sql(reshdl, db)))

DBI::dbDisconnect(db)
}

```

| | |
|------------------|----------------------------------|
| run_rquery_tests | <i>Run rquery package tests.</i> |
|------------------|----------------------------------|

Description

For all files with names of the form "`^test_+\.R$`" in the package directory `unit_tests` run all functions with names of the form "`^test_+.$`" as RUnit tests. Attaches RUnit and `pkg`, requires RUnit. Stops on error.

Usage

```

run_rquery_tests(
  ...,
  verbose = TRUE,
  package_test_dirs = "unit_tests",
  test_dirs = character(0),
  stop_on_issue = TRUE,
  stop_if_no_tests = TRUE,
  require_RUnit_attached = FALSE,
  require_pkg_attached = TRUE,
  rngKind = "Mersenne-Twister",
  rngNormalKind = "Inversion"
)

```

Arguments

| | |
|----------------------|--------------------------------------------------|
| <code>...</code> | not used, force later arguments to bind by name. |
| <code>verbose</code> | logical, if TRUE print more. |

package_test_dirs directory names to look for in the installed package.
 test_dirs paths to look for tests in.
 stop_on_issue logical, if TRUE stop after errors or failures.
 stop_if_no_tests logical, if TRUE stop if no tests were found.
 require_RUnit_attached logical, if TRUE require RUnit be attached before testing.
 require_pkg_attached logical, if TRUE require pkg be attached before testing.
 rngKind pseudo-random number generator method name.
 rngNormalKind pseudo-random normal generator method name.

Details

Based on Rcpp doRUnit.R. This version is GPL-3, works derived from it must be distributed GPL-3.

Value

RUnit test results (invisible).

select_columns *Make a select columns node (not a relational operation).*

Description

Make a select columns node (not a relational operation).

Usage

```
select_columns(source, columns, env = parent.frame())
```

Arguments

source source to select from.
 columns list of distinct column names.
 env environment to look to.

Value

select columns node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- select_columns(d, 'AUC')
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}

```

select_rows

Make a select rows node.

Description

Supports `bquote()` `()`-style name abstraction including `.` (`-`) notation to promote strings to names (please see here: <https://github.com/WinVector/rquery/blob/master/Examples/Substitution/Substitution.md>).

Usage

```
select_rows(source, expr, env = parent.frame())
```

```
select_rows_nse(source, expr, env = parent.frame())
```

Arguments

| | |
|--------|----------------------------|
| source | source to select from. |
| expr | expression to select rows. |
| env | environment to look to. |

Value

select rows node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2, z = 3))
  TARGETCOL = as.name("AUC")
}

```

```

optree <- select_rows(d, .(TARGETCOL) >= 0.5) %>%
  select_columns(., "R2")
cat(format(optree))
sql <- to_sql(optree, my_db)
cat(sql)
print(DBI::dbGetQuery(my_db, sql))
DBI::dbDisconnect(my_db)
}

```

| | |
|----------------|---------------------------------|
| select_rows_se | <i>Make a select rows node.</i> |
|----------------|---------------------------------|

Description

Make a select rows node.

Usage

```
select_rows_se(source, expr, env = parent.frame())
```

Arguments

| | |
|--------|------------------------------------|
| source | source to select from. |
| expr | expression to select rows. |
| env | environment to look for values in. |

Value

select rows node.

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- select_rows_se(d, "AUC >= 0.5")
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}

```

| | |
|----------|------------------------------------------|
| setDBOpt | <i>Set a database connection option.</i> |
|----------|------------------------------------------|

Description

If db is of class rquery_db_info it sets the appropriate connection option, not the global state.

Usage

```
setDBOpt(db, optname, val)
```

Arguments

| | |
|---------|--------------------------------|
| db | rquery_db_info instance |
| optname | character, single option name. |
| val | value to set |

Value

db

| | |
|-------------|------------------------------------------|
| setDBOption | <i>Set a database connection option.</i> |
|-------------|------------------------------------------|

Description

Note: we are moving away from global options to options in the DB handle. Prefer [setDBOpt](#).

Usage

```
setDBOption(db, optname, val)
```

Arguments

| | |
|---------|--------------------------------|
| db | database connection handle. |
| optname | character, single option name. |
| val | value to set |

Value

original options value

| | |
|---------------|-----------------------------------|
| set_indicator | <i>Make a set indicator node.</i> |
|---------------|-----------------------------------|

Description

Create a new column indicating the membership of another column in a given set.

Usage

```
set_indicator(
  source,
  rescol,
  testcol,
  testvalues,
  ...,
  translate_quotes = FALSE,
  env = parent.frame()
)
```

Arguments

| | |
|------------------|-----------------------------------------------------------------------------------|
| source | source to select from. |
| rescol | name of column to land indicator in. |
| testcol | name of column to check. |
| testvalues | values to check for. |
| ... | force later arguments to bind by name |
| translate_quotes | logical if TRUE translate quotes to SQL choice (simple replacement, no escaping). |
| env | environment to look to. |

Value

set_indicator node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(),
                        ":memory:")

  d <- rq_copy_to(my_db, 'd',
                 data.frame(a = c("1", "2", "1", "3"),
                           b = c("1", "1", "3", "2"),
                           q = 1,
```

```

                                stringsAsFactors = FALSE),
                                temporary = TRUE,
                                overwrite = TRUE)

# example
set <- c("1", "2")
op_tree <- d %.>%
  set_indicator(., "one_two", "a", set) %.>%
  set_indicator(., "z", "a", c())
print(column_names(op_tree))
print(columns_used(op_tree))
cat(format(op_tree))
sql <- to_sql(op_tree, my_db)
cat(sql)
print(DBI::dbGetQuery(my_db, sql))

op_tree2 <- d %.>%
  set_indicator(., "one_two", "a", set) %.>%
  set_indicator(., "z", "b", c()) %.>%
  select_columns(., c("z", "one_two"))
print(column_names(op_tree2))
print(columns_used(op_tree2))

# cleanup
DBI::dbDisconnect(my_db)
}

```

sql_expr_set

Build a query that applies a SQL expression to a set of columns.

Description

Build a query that applies a SQL expression to a set of columns.

Usage

```
sql_expr_set(source, cols, expr)
```

Arguments

| | |
|--------|-----------------------------------------------------------------------------------------------------------------------|
| source | incoming rel_op tree or data.frame. |
| cols | character, columns to operate in. If a named array names are where results are landed, values names of value columns. |
| expr | character or list of character and names, expression to apply to columns "." stands for column value to use. |

Value

rel_op node or data.frame (depending on input).

See Also

[null_replace](#), [count_null_cols](#), [mark_null_cols](#)

Examples

```
# WARNING: example tries to change rquery.rquery_db_executor option to RSQLite and back.
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(my_db)
  old_o <- options(list("rquery.rquery_db_executor" = list(db = my_db)))

  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = c(NA, 0.5, NA),
                           R2 = c(1.0, 0.9, NA),
                           delta = 3,
                           cat = c("a", NA, "c"),
                           stringsAsFactors = FALSE))

  # example
  op_tree <- d %>% sql_expr_set(., qc(AUC, R2), ". + 1")
  cat(format(op_tree))
  sql <- to_sql(op_tree, my_db)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))

  # ex2 names (but not marked as names)
  op_tree2 <- d %>% sql_expr_set(., qc(AUC, R2),
                               ". + 1 + delta")
  cat(to_sql(op_tree2, my_db))

  # ex3 names (also so marked)
  op_tree3 <- d %>% sql_expr_set(., qc(AUC, R2),
                               list(". + 1 +", as.name("delta")))
  cat(to_sql(op_tree3, my_db))

  # cleanup
  options(old_o)
  DBI::dbDisconnect(my_db)
}
```

sql_node

Make a general SQL node.

Description

Make a general SQL node.

Usage

```
sql_node(
  source,
  exprs,
  ...,
  mods = NULL,
  orig_columns = TRUE,
  expand_braces = TRUE,
  translate_quotes = TRUE,
  env = parent.frame()
)
```

Arguments

| | |
|------------------|-----------------------------------------------------------------------------------|
| source | source to work from. |
| exprs | SQL expressions |
| ... | force later arguments to bind by name |
| mods | SQL modifiers (GROUP BY, ORDER BY, and so on) |
| orig_columns | logical if TRUE select all original columns. |
| expand_braces | logical if TRUE use col notation to ensure col is a column name. |
| translate_quotes | logical if TRUE translate quotes to SQL choice (simple replacement, no escaping). |
| env | environment to look to. |

Value

sql node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  # example database connection
  my_db <- DBI::dbConnect(RSQLite::SQLite(),
                        ":memory:")
  # load up example data
  d <- rq_copy_to(
    my_db, 'd',
    data.frame(v1 = c(1, 2, NA, 3),
              v2 = c(NA, "b", NA, "c"),
              v3 = c(NA, NA, 7, 8),
              stringsAsFactors = FALSE))

  # look at table
  execute(my_db, d)

  # get list of columns
```

```

vars <- column_names(d)
print(vars)

# build a NA/NULLs per-row counting expression.
# names are "quoted" by wrapping them with as.name().
# constants can be quoted by an additional list wrapping.
expr <- lapply(vars,
  function(vi) {
    list("+ (CASE WHEN (",
      as.name(vi),
      "IS NULL ) THEN 1.0 ELSE 0.0 END)")
  })
expr <- unlist(expr, recursive = FALSE)
expr <- c(list(0.0), expr)
cat(paste(unlist(expr), collapse = " "))

# instantiate the operator node
op_tree <- d %.>%
  sql_node(., "num_missing" %:=% list(expr))
cat(format(op_tree))

# examine produced SQL
sql <- to_sql(op_tree, my_db)
cat(sql)

# execute
execute(my_db, op_tree) %.>%
  print(.)

# whole process wrapped in convenience node
op_tree2 <- d %.>%
  count_null_cols(., vars, "nnull")
execute(my_db, op_tree2) %.>%
  print(.)

# sql_node also allows marking variable in quoted expressions
ops <- d %.>%
  sql_node(., qae(sqrt_v1 = sqrt(.[v1])))
execute(my_db, ops) %.>%
  print(.)

# marking variables allows for error-checking of column names
tryCatch({
  ops <- d %.>%
    sql_node(., qae(sqrt_v1 = sqrt(.[v1_misspelled])))
},
  error = function(e) {print(e)})

DBI::dbDisconnect(my_db)
}

```

| | |
|-------------|-------------------------------------------|
| tables_used | <i>Return vector of table names used.</i> |
|-------------|-------------------------------------------|

Description

Return vector of table names used.

Usage

```
tables_used(node, ...)
```

Arguments

| | |
|------|-------------------------|
| node | rquery tree to examine. |
| ... | (not used) |

Value

names of tables used.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d1 <- rq_copy_to(my_db, 'd1',
                  data.frame(AUC = 0.6, R2 = 0.2))
  d2 <- rq_copy_to(my_db, 'd2',
                  data.frame(AUC = 0.6, D = 0.3))
  optree <- natural_join(d1, d2, by = "AUC")
  cat(format(optree))
  print(tables_used(optree))
  DBI::dbDisconnect(my_db)
}
```

| | |
|------------|--------------------------------|
| theta_join | <i>Make a theta_join node.</i> |
|------------|--------------------------------|

Description

Theta join is a join on an arbitrary predicate.

Usage

```
theta_join(
  a,
  b,
  expr,
  ...,
  jointype = "INNER",
  suffix = c("_a", "_b"),
  env = parent.frame()
)
```

```
theta_join_nse(
  a,
  b,
  expr,
  ...,
  jointype = "INNER",
  suffix = c("_a", "_b"),
  env = parent.frame()
)
```

Arguments

| | |
|----------|-------------------------------------------------------|
| a | source to select from. |
| b | source to select from. |
| expr | unquoted join condition |
| ... | force later arguments to be by name |
| jointype | type of join ('INNER', 'LEFT', 'RIGHT', 'FULL'). |
| suffix | character length 2, suffices to disambiguate columns. |
| env | environment to look for values in. |

Value

theta_join node.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d1 <- rq_copy_to(my_db, 'd1',
                  data.frame(AUC = 0.6, R2 = 0.2))
  d2 <- rq_copy_to(my_db, 'd2',
                  data.frame(AUC2 = 0.4, R2 = 0.3))
  optree <- theta_join(d1, d2, AUC >= AUC2)
  cat(format(optree))
  sql <- to_sql(optree, my_db)
  cat(sql)
}
```



```

optree <- theta_join_se(d1, d2, "AUC >= AUC2")
cat(format(optree))
sql <- to_sql(optree, my_db)
cat(sql)
print(DBI::dbGetQuery(my_db, sql))
DBI::dbDisconnect(my_db)
}

```

topo_sort_tables *Topologically sort join plan so values are available before uses.*

Description

Depends on igraph package. Please see vignette('DependencySorting', package = 'rquery') and vignette('joinController', package = 'rquery') for more details.

Usage

```
topo_sort_tables(columnJoinPlan, leftTableName, ...)
```

Arguments

```

columnJoinPlan  join plan
leftTableName   which table is left
...             force later arguments to bind by name

```

Value

list with dependencyGraph and sorted columnJoinPlan

Examples

```

if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE) &&
    requireNamespace('igraph', quietly = TRUE)) {
  # note: employeanddate is likely built as a cross-product
  #       join of an employee table and set of dates of interest
  #       before getting to the join controller step. We call
  #       such a table "row control" or "experimental design."
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  RSQLite::initExtension(my_db)
  tDesc <- example_employee_date(my_db)
  columnJoinPlan <- build_join_plan(tDesc, check= FALSE)
  # unify keys
  columnJoinPlan$resultColumn[columnJoinPlan$resultColumn=='id'] <- 'eid'
  # look at plan defects
  print(paste('problems:',
              inspect_join_plan(tDesc, columnJoinPlan)))
}

```

```

# fix plan
sorted <- topo_sort_tables(columnJoinPlan, 'employeeanddate')
print(paste('problems: ',
           inspect_join_plan(tDesc, sorted$columnJoinPlan)))
print(plot(sorted$dependencyGraph))
DBI::dbDisconnect(my_db)
my_db <- NULL
}

```

to_sql

Return SQL implementation of operation tree.

Description

Add to last argument and pass all others through.

Usage

```

to_sql(
  x,
  db,
  ...,
  limit = NULL,
  source_limit = NULL,
  indent_level = 0,
  tnum = mk_tmp_name_source("tsql"),
  append_cr = TRUE,
  using = NULL
)

```

Arguments

| | |
|--------------|--------------------------------------------------------|
| x | rquery operation tree. |
| db | DBI database handle or rquery_db_info object. |
| ... | generic additional arguments (not used). |
| limit | numeric if not NULL limit result to this many rows. |
| source_limit | numeric if not NULL limit sources to this many rows. |
| indent_level | level to indent. |
| tnum | temp sub-query name generator. |
| append_cr | logical if TRUE end with CR. |
| using | character, if not NULL set of columns used from above. |

Value

SQL command

See Also

[db_td](#), [materialize](#), [execute](#), [rq_copy_to](#), [mk_td](#)

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d1 <- rq_copy_to(my_db, 'd1',
                  data.frame(AUC = 0.6, R2 = 0.2))
  d2 <- rq_copy_to(my_db, 'd2',
                  data.frame(AUC = 0.6, D = 0.3))
  optree <- natural_join(d1, d2, by = "AUC")
  cat(format(optree))
  print(to_sql(optree, my_db))
  DBI::dbDisconnect(my_db)
}
```

to_transport_representation

Convert an rquery op diagram to a simple representation, appropriate for conversion to YAML.

Description

Convert an rquery op diagram to a simple representation, appropriate for conversion to YAML.

Usage

```
to_transport_representation(ops, ..., convert_named_vectors_to_lists = TRUE)
```

Arguments

| | |
|--------------------------------|-------------------------------------------------|
| ops | rquery operator dag |
| ... | not used, force later arguments to be by name |
| convert_named_vectors_to_lists | logical, if TRUE convert named vectors to lists |

Value

representation structure

| | |
|----------|------------------------------------------------------------|
| unionall | <i>Make an unionall node (not a relational operation).</i> |
|----------|------------------------------------------------------------|

Description

Concatenate tables by rows.

Usage

```
unionall(sources, env = parent.frame())
```

Arguments

| | |
|---------|--------------------------------------------|
| sources | list of relop trees or list of data.frames |
| env | environment to look to. |

Value

order_by node or altered data.frame.

Examples

```
if (requireNamespace("DBI", quietly = TRUE) && requireNamespace("RSQLite", quietly = TRUE)) {
  my_db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  d <- rq_copy_to(my_db, 'd',
                 data.frame(AUC = 0.6, R2 = 0.2))
  optree <- unionall(list(d, d, d))
  cat(format(optree))
  sql <- to_sql(optree, my_db, limit = 2)
  cat(sql)
  print(DBI::dbGetQuery(my_db, sql))
  DBI::dbDisconnect(my_db)
}
```

| | |
|------|-----------------------------------------------|
| wrap | <i>Wrap a data frame for later execution.</i> |
|------|-----------------------------------------------|

Description

Create a table description that includes the actual data. Prevents wasteful table copies in immediate pipelines. Used with `ex()`.

Usage

```
wrap(d, ..., table_name = NULL, env = parent.frame())
```

Arguments

| | |
|------------|-------------------------------------------------------|
| d | data.frame |
| ... | not used, force later argument to be referred by name |
| table_name | character, name of table |
| env | environment to work in. |

Value

a table description, with data attached

Examples

```
if(requireNamespace('rqdatatable')) {  
  d <- data.frame(x = 1:3, y = 4:6)  
  d %>%  
    wrap(.) %>%  
    extend(., z := x + y) %>%  
    ex(.)  
}
```

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