

# Package ‘mfdb’

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**Description** Creates and manages a PostgreSQL database suitable for storing fisheries data and aggregating ready for use within a Gadget <<https://gadget-framework.github.io/gadget2/>> model. See <<https://mareframe.github.io/mfdb/>> for more information.

**License** GPL-3

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mfdb-package	<i>MareFrame DB querying library</i>
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## Description

Tools to query a MareFrame DB and reformat results in forms useful for GADGET and EwE models.

## Introduction & Schema description

Before doing anything with **mfdb**, it is worth knowing a bit about how data is stored. Broadly, there are 2 basic types of table in **mfdb**, *taxonomy* and *measurement* tables.

The measurement tables store all forms of sample data supported, at the finest available detail. These are then aggregated when using any of the mfdb query functions. All measurement data is separated by case study, so multiple case studies can be loaded into a database without conflicts.

Taxonomy tables store all possible values for terms and their meaning, to ensure consistency in the data. For example, 'species' stores short-names and full latin names of all known species to MFDB, to ensure consistency in naming.

Most Taxonomies have defaults which are populated when the database is created, and their definitions are stored as data attached to this package. See [mfdb-data](#) for more information on these. Others, such as 'areacell' and 'sampling\_type' are case study specific, and you will need to define your terms before you can import data.

## Importing data

Unless you are working with a remote database, you will need to populate the database at least once before you are able to do any querying. The steps your script needs to do are:

**Connect to database:** Use the `mfdb()` function. This will create tables / populate taxonomies if necessary.

**Define areas & divisions:** `mfdb` models space in the following way:

**areacell** The finest level of detail stored in the database. Every measurement (e.g. temperature, length sample) is assigned to an areacell. This will generally correspond to ICES gridcells, however there is no requirement to do so. You might augment gridcell information with depth, or include divisions when the measurement doesn't correlate to a specific areacell.

**division** Collections of areacells, e.g. ICES subdivisions, or whatever is appropriate.

Finally, when querying, divisions are grouped together into named collections, for instance `mfdb_group(north = 1:3, south = 4:6)` will put anything in divisions 1–3 under an area named "north", 4–5 under an area named "south".

Before you can upload any measurements, you have to define the areacells that they will use. You do this using the `mfdb_import_area()` function. This allows you to import tables of area/division information, such as:

```
mfdb_import_area(mdb, data.frame( area = c('101', '102', '103', '401', '402', '403'),
  division = c('1', '1', '1', '4', '4', '4'), ))
```

If you want areas to be part of multiple divisions, then you can use `mfdb_import_division()` to import extra revisions.

**Define sampling types:** Any survey data can have a sampling type defined, which then can be used when querying data. If you want to use a sampling type, then define it using `mfdb_import_sampling_type()`.

**Import temperature data:** At this point, you can start uploading actual measurements. The easiest of which is temperature. Upload a table of areacell/month/temperature data using `mfdb_import_temperature()`.

**Import survey data:** Finally, import any survey data using `mfdb_import_survey()`. Ideally upload your data in separate chunks. For example, if you have length and age-length data, don't combine them in R, upload them separately and both will be used when querying for length data. This keeps the process simple, and allows you to swap out data as necessary.

**Import stomach survey:** Stomach surveys are imported in much the same way, however there are 2 data.frames, one representing predators, one preys. The column 'stomach\_name' links the two, which can contain any numeric / character value, as long as it is unique for predators and prey measurements are assigned to the correct stomach.

See `mfdb_import_survey` for more information or [the demo directory](#) for concrete examples.

**Dumping / Restoring a DB:** You can also dump/import a dump from another host using the postgres `pg_dump` and `pg_restore` commands. You can dump/restore individual schemas (i.e. the case study you give to the `mfdb()` command), to list all the schemas installed run `SELECT DISTINCT(table_schema) FROM information_schema.tables from psql`. Note that if you use `mfdb('Baltic')`, the Postgres schema name will be lower-cased.

Create a dump of your chosen schema with the following command:

```
pg_dump --schema=baltic -Fc mf > baltic.dump
```

This will make a dump of the "baltic" case study into "baltic.tar". It can then be restored onto another computer with the following:

```
pg_restore --clean -d mf baltic.dump
```

If you already have a baltic schema you wish to preserve, you can rename it first by issuing ALTER SCHEMA baltic RENAME TO baltic\_o in psql. Once the restore is done you can rename the new schema and put the name of the old schema back.

## Querying data

There are a selection of querying functions available, all of which work same way. You give a set of parameters, each of which can be a vector of data you wish returned, for instance year = 1998:2000 or species = c('COD').

If also grouping by this column (i.e. 'year', 'timestep', 'area' and any other columns given, e.g. 'age'), then the parameter will control how this grouping works, e.g. maturity\_stage = mfdb\_group(imm = 1, mat = 2:5) will result in the maturity\_stage column having either 'imm' or 'mat'. These will also be used to generate GADGET aggregation files later.

For example, the following queries the temperature table:

```
defaults <- list(
  area = mfdb_group("101" = ),
  timestep = mfdb_timestep_quarterly, # Group months to create 2 timesteps for each year
  year = 1996:2005)
agg_data <- mfdb_temperature(mdb, defaults)
```

All functions will result in a list of data.frame result tables (generally only one, unless you requested bootstrapping). Each are suitable for feeding into a gadget function to output into model files.

See [mfdb\\_sample\\_count](#) for more information or [the demo directory](#) for concrete examples.

## Creating GADGET files

Finally, there are a set of functions that turn the output of queries into GADGET model files. These work on a [gadget\\_directory](#) object, which can either be an existing GADGET model to alter, or an empty / nonexistant directory.

Generally, the result of an mfdb query will be enough to create a corresponding GADGET file, for instance, the following will create a GADGET area file in your gadget directory:

```
gadget_dir_write(gd,gadget_areafile(
  size = mfdb_area_size(mdb, defaults)[[1]],
  temperature = mfdb_temperature(mdb, defaults)[[1]]))
```

See [gadget\\_areafile](#) or [gadget\\_likelihood\\_component](#) for more information or [the demo directory](#) for concrete examples.

**Stock and fleet files:** Stocks and fleets aren't explicitly defined in the database. Instead, they are defined by querying on a column that differentiates them. For example, if your "immature cod" stock is defined as cod that is between maturity stages 1 and 2, then if querying for a stockdistribution component, one could do:

```
mfdb_sample_count(mdb, c('maturity_stage', 'age', 'length'), list(
  species = 'COD',
  maturity_stage = c(imm = 1:2, mat = 3:5),
  . . .
))
```

...and the maturity\_stage column will be treated as the stock.

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### See Also

[rgadget](#), [Gadget user guide](#)

---

ewe\_model

*MareFrame DB Rpath interface*

---

### Description

Transform the results of MFDB queries for use in an Rpath model

### Usage

```
mfdb_rpath_params(area_data,
  survey_data,
  catch_data,
  consumption_data,
  create_rpath_params = stop("Set create_rpath_params = Rpath::create.rpath.params"),
  living_groups = character(0),
  detritus_groups = c("Detritus"))
```

**Arguments**

area_data	Results of an <code>mfdb_area_size</code> query, aggregating the whole area
survey_data	Results of an <code>mfdb_sample_totalweight</code> query, normally for one year, aggregated by the model's functional groups
catch_data	Results of an <code>mfdb_sample_totalweight</code> query, normally for one year, aggregated by the model's functional groups and 'vessel'
consumption_data	Results of an <code>mfdb_stomach_preypeighratio</code> query, aggregated by functional groups
living_groups	Additional Rpath groups of "Living" type
detritus_groups	Additional Rpath groups of "Detritus" type
create_rpath_params	RPath isn't currently in a public repository, so to avoid depending on it you need to give <code>mfdb_rpath_params</code> the Rpath function, i.e. <code>Rpath::create.rpath.params</code> .

**Details**

EwE requires stanzas and groups of stanzas, these are made up using the first and any other groupings in MFDB. For example, if `survey_data` was made with a query like `mfdb_sample_totalweight(mdb, c('species', 'age'), ...)`, then the species will make up the generated `stanza_groups`, and age will make up the stanzas within those groups.

`catch_data` requires data that is also aggregated by vessel, this will be ignored for the purposes of deciding the stanza/stanza\_group.

`consumption_data` treats prey groupings separate to predator groupings, and all will be added to the diet matrix.

See [mfdb\\_sample\\_totalweight](#) for more information on how groupings can be used in queries.

**Value**

Returns an `Rpath.params` object populated with the provided data.

**Examples**

```
# See demo/example-ewe.R for a full-length example
```

---

`gadget_areafile`

*Gadget area files*

---

**Description**

Structures representing a GADGET area file

**Usage**

```
gadget_areafile(size, temperature, area = attr(size, 'area'))
```

**Arguments**

size	data.frame as produced by <code>mfdb_area_size</code>
temperature	data.frame as produced by <code>mfdb_temperature</code>
area	Optional. <code>mfdb_group</code> that you used to specify area. By default pulls it from annotations on the size object.

**Details**

Once formed, you can then use `gadget_dir_write` to write this out to a GADGET areafile.

**Value**

List of class 'gadget\_areafile' that represents the area file contents.

**Examples**

```
# Open a temporary database connection
mdb <- mfdb(tempfile(fileext = '.duckdb'))

# Define 2 areacells of equal size
mfdb_import_area(mdb, data.frame(name=c("divA", "divB"), size=1))

# We want to have 3 area groups, 2 for original cells, one aggregating across the lot
area_group <- mfdb_group(
  divA = c("divA"),
  divB = c("divB"),
  divAB = c("divA", "divB"))

# Make up temperature data
temps <- expand.grid(year=c(1998,2000), month=c(1:12), areacell=c("divA", "divB"))
temps$temperature <- runif(nrow(temps), 5, 10)
mfdb_import_temperature(mdb, temps)

# Create an areafile from 2 mfdb queries
areafile <- gadget_areafile(
  mfdb_area_size(mdb, list(
    area = area_group))[[1]],
  mfdb_temperature(mdb, list(
    year = 1998:2000,
    timestep = mfdb_timestep_quarterly,
    area = area_group))[[1]])
areafile

# Write this to a gadget_directory
gadget_dir_write(gadget_directory(tempfile()), areafile)
```

```

# Check data in file matches input data
stopifnot(identical(
  areafile$size,
  c(divA=1, divB=1, divAB=2)))
stopifnot(all.equal(
  mean(areafile$temperature[areafile$temperature$area == 1, 'mean']),
  mean(temps[temps$areacell == 'divA', 'temperature']),
  tolerance = 1e-2))
stopifnot(all.equal(
  mean(areafile$temperature[areafile$temperature$area == 2, 'mean']),
  mean(temps[temps$areacell == 'divB', 'temperature']),
  tolerance = 1e-2))
stopifnot(all.equal(
  mean(areafile$temperature[areafile$temperature$area == 3, 'mean']),
  mean(temps[, 'temperature']),
  tolerance = 1e-2))

mfdb_disconnect(mdb)

```

---

gadget\_directory

*Gadget directory objects*


---

## Description

Structures representing a directory of data files

## Usage

```

gadget_directory(dir, mainfile = "main")
gadget_dir_write(gd, obj)
gadget_dir_read(gd, file_name, missing_okay = TRUE, file_type = c())

```

## Arguments

dir	Name of directory, will be created if it doesn't exist.
mainfile	Name of the GADGET mainfile to use.
gd	A gadget_directory object.
obj	The gadget_file, or gadget_likelihood_component to write.
file_name	File to read out of the directory and turn into a gadget_file.
missing_okay	If true, return an empty file instead of complaining that the given file does not exist.
file_type	A character vector that alters how the file is parsed. Currently either NULL or "bare_component", which implies we write "something" instead of "[something]".



**Details**

These functions handle reading and writing of files to a directory containing GADGET model files.

First a `gadget_directory` object needs to be created with `gadget_directory`, this ensures the directory exists and stores the name of the mainfile to use.

Any portion of a gadget model can then be written out with `gadget_dir_write`. You do not need to tell it which files in the model to update, since this is worked out based on what you are writing out.

**Value**

`gadget_directory` returns a list of class 'gadget\_directory', containing the location of the mainfile that the gadget configuration will use.

`gadget_dir_write` returns NULL

`gadget_dir_read` returns a `gadget_file` object from `read.gadget_file`

**Examples**

```
# Create a gadget directory
gd <- gadget_directory(tempfile())

# Read in the likelihood file
likelihood <- gadget_dir_read(gd, 'likelihood')

# Write out an area file to "(tempfile)/areas", replacing any existing file
gadget_dir_write(gd, gadget_file("areas", components = list(list(north = 1:3, south = 4:7))))

# Replace a likelihood component if one already exists with
# the same name/type or append it to the bottom
gadget_dir_write(gd, gadget_likelihood_component("understocking", name = "frank"))
```

---

gadget\_file

*Gadget file objects*


---

**Description**

Structures representing an individual GADGET data file.

**Usage**

```
gadget_file(file_name, components = list(), data = NULL, file_type = c())
## S3 method for class 'gadget_file'
print(x, ...)
## S3 method for class 'gadget_file'
as.character(x, ...)
read.gadget_file(file_name, file_type = c(), fileEncoding = "UTF-8")
```

**Arguments**

file_name	Filename the output should be written to / read from
components	A list of lists, representing each component. See details.
data	A data.frame representing the tabular data at the end of a file.
file_type	A character vector that alters how the file is parsed. Currently either NULL or "bare_component", which implies we write "something" instead of "[something]".
x	gadget_file object
fileEncoding	File's character set. Defaults to UTF-8
...	Unused

**Details**

For our purposes, a gadget file is broken down into components, where the first component is any key/value data at the top of the file. Each section separated by "[something]" is considered a new component. Each component is a list of key/values, where values can be vectors of multiple values. Also components can have comments prepended by adding a "preamble" attribute.

In slight deviation to GADGET spec, we insist that tabular data begins with "; - data -", to avoid any ambiguity on when it starts.

**Value**

gadget\_file Returns a gadget\_file object, a list of components.

print.gadget\_file Prints the gadget file as it would be written to the filesystem.

as.character.gadget\_file Returns a character string of the gadget file as it would be written to the filesystem.

read.gadget\_file Returns a gadget\_file object, a list of components.

**Examples**

```
# Simple key/values
gadget_file("age", components = list(
  list(length = 5, age = 1:5)))

# Multiple components
gadget_file("likelihood", components = list(
  list(),
  component = structure(list(type = "penalty"), preamble = list("comment")),
  component = structure(list(type = "penalty"), preamble = list("", "another comment"))))

# Data
gadget_file("agelen", components = list(
  list(stocknames = "cod")), data = data.frame(
  area = c(102, 103),
  number = c(2345, 5023)))
```

---

gadget\_fleetfile      *Gadget fleet files*

---

## Description

Structures representing fleet file components

## Usage

```
gadget_fleet_component(type,
  name = type,
  livesonareas = unique(data$area),
  multiplicative = 1,
  suitability = NULL,
  fleetfile = 'fleet',
  data = stop("data not provided"),
  ...)
```

## Arguments

type	Required. Type of fleet component to create, e.g. 'totalfleet'
name	Optional. A descriptive name for the fleet component, defaults to the type.
livesonareas	Optional. Vector of area names, defaults to all unique areas in data.
multiplicative	Optional. Defaults to 1
suitability	Optional. Defaults to empty string
fleetfile	Optional. The fleet file to put the component in. Defaults to 'fleet'.
data	Required. The data.frame to use for 'amountfile'. Areas are translated into integers before adding to amountfile.
...	Extra parameters for the component, see details

## Details

effortfleet requires the following extra parameters:

**catchability** A list of stock names to catchability constants

quotafleet requires the following extra parameters:

**quotafunction** Function name, e.g. 'simple'

**biomasslevel** Vector of biomass levels

**quotalevel** Vector of fishing levels

## Value

A gadget\_fleet\_component object that can then be added to a fleetfile with gadget\_dir\_write

**Examples**

```

mdb <- mfdb(tempfile(fileext = '.duckdb'))
gd <- gadget_directory(tempfile())

# Define 2 areacells of equal size
mfdb_import_area(mdb, data.frame(name=c("divA", "divB"), size=1))

# Define 2 vessels
mfdb_import_vessel_taxonomy(mdb, data.frame(
  name = c('1.RSH', '2.COM'),
  full_name = c('Research', 'Commercial'),
  stringsAsFactors = FALSE))

# Make up some samples
samples <- expand.grid(
  year = 1998,
  month = 5,
  areacell = c("divA", "divB"),
  species = 'COD',
  vessel = c('1.RSH', '2.COM'),
  length = c(0,40,80))
samples$count <- runif(nrow(samples), 20, 90)
mfdb_import_survey(mdb, data_source = "x", samples)

# Make a 'totalfleet' component
fc <- gadget_fleet_component(
  'totalfleet',
  name = 'research',
  data = mfdb_sample_count(mdb, c(), list(
    vessel = '1.RSH',
    area = mfdb_group(x = 'divA', y = 'divB'),
    year = 1998,
    step = mfdb_timestep_yearly))[[1]])
fc

# Write out to a directory
gadget_dir_write(gd, fc)

gadget_fleet_component(
  'effortfleet',
  name = 'commercial',
  suitability = "function constant 4;",
  catchability = list(stockA=4, stockB=5),
  quotafunction = 'simple',
  biomasslevel = c(1000, 2000),
  quotalevel = c(0.1, 0.4, 0.9),
  data = mfdb_sample_count(mdb, c(), list(
    vessel = '2.COM',
    area = mfdb_group(x = 'divA', y = 'divB'),
    year = 1998,
    step = mfdb_timestep_yearly))[[1]])

```

```

gadget_fleet_component(
  'quotafleet',
  name = 'commercial',
  suitability = "function constant 4;",
  catchability = list(stockA=4, stockB=5),
  quotafunction = 'simple',
  biomasslevel = c(1000, 2000),
  quotalevel = c(0.1, 0.4, 0.9),
  data = mfdb_sample_count(mdb, c(), list(
    vessel = '2.COM',
    area = mfdb_group(x = 'divA', y = 'divB'),
    year = 1998,
    step = mfdb_timestep_yearly))[[1]])

mfdb_disconnect(mdb)

```

---

gadget\_likelihood\_component

*Gadget likelihood components*


---

## Description

Structures representing a component of a GADGET likelihood file.

## Usage

```

gadget_likelihood_component(type, weight = 0, name = type,
  likelihoodfile = 'likelihood', ...)

```

## Arguments

type	Type of group to create. One of penalty, understocking, catchstatistics, catchdistribution, stockdistribution.
name	A descriptive name for the component
weight	A numeric weighting
likelihoodfile	The likelihood file this component should end up in
...	Extra parameters for the group. See details.

## Details

In addition, penalty understands:

**data** A data.frame with 2 columns, "switch" and "power"

catchstatistics understands:

**data\_function** The function Gadget should use, by default guesses based on the function that generated data

**data** A data.frame probably generated by `mfdb_sample_meanlength_stddev`

**area** An list of areas, taken from `attr(data, "area")` if not supplied

**age** An list of ages, taken from `attr(data, "age")` if not supplied

**fleetnames** List of fleet names

**stocknames** List of stock names

`catchdistribution` understands:

**data\_function** The function Gadget should use, by default uses `sumofsquares`

**data\_function\_params** Extra parameters to supply to gadget, based on the function

**aggregationlevel** TRUE or FALSE, defaults to FALSE

**overconsumption** TRUE or FALSE, defaults to FALSE

**epsilon** Numeric, defaults to 10

**data** A data.frame probably generated by `mfdb_sample_meanlength_stddev`

**area** An list of areas, taken from `attr(data, "area")` if not supplied

**age** An list of ages, taken from `attr(data, "age")` if not supplied

**length** An list of lengths, taken from `attr(data, "length")` if not supplied

**fleetnames** List of fleet names

**stocknames** List of stock names

`stockdistribution` understands:

**data\_function** The function Gadget should use, by default uses `sumofsquares`

**overconsumption** TRUE or FALSE, defaults to FALSE

**epsilon** Numeric, defaults to 10

**data** A data.frame probably generated by `mfdb_sample_meanlength_stddev`

**area** An list of areas, taken from `attr(data, "area")` if not supplied

**age** An list of ages, taken from `attr(data, "age")` if not supplied

**length** An list of lengths, taken from `attr(data, "length")` if not supplied

**fleetnames** List of fleet names

**stocknames** List of stock names

`surveydistribution` understands:

**data** A data.frame probably generated by `mfdb_sample_meanlength_stddev`

**area** An list of areas, taken from `attr(data, "area")` if not supplied

**length** An list of lengths, taken from `attr(data, "length")` if not supplied

**age** An list of ages, taken from `attr(data, "age")` if not supplied

**stocknames** List of stock names

**fittype, slope, intercept** Fit options, see GADGET manual

**parameters** A vector of length 2

**suitability** A single suitability function

**epsilon** Numeric, defaults to 10

**likelihoodtype** String, see GADGET manual

surveyindices understands:

**sitype** What data the component is based on, see GADGET manual

**biomass** 0 or 1, defaults to 0

**data** A data.frame probably generated by `mfdb_sample_meanlength_stddev`

**area** An list of areas, taken from `attr(data, "area")` if not supplied

**age** An list of ages, taken from `attr(data, "age")` if not supplied

**length** An list of lengths, taken from `attr(data, "length")` if not supplied

**fleetnames** List of fleet names

**stocknames** List of stock names

**surveynames** List of acoustic survey names

**fittype, slope, intercept** Fit options, see GADGET manual

stomachcontent understands:

**data\_function** Function GADGET will use

**epsilon** To be used when calculated probability is low

**prey\_labels** Either a vector of stock names to be used for all preys, or a list to match preys, see below

**prey\_digestion\_coefficients** Optional. Either a vector of coefficients fo be used for all preys, or a list to match preys, see below

**predator\_names** Vector of predator stock names

**data** A data.frame probably generated by `mfdb_sample_meanlength_stddev`

Both `prey_labels` and `prey_digestion_coefficients` allow you to match parts of prey labels and use repetition. For instance, `list("cod.mat" = "mature_cod", "cod" = "cod", "other")` will give "cod.mat" the label "mature\_cod", "cod.imm" the label "cod", and anything else will get "other". You can also use regular expression syntax, for example "cod[0-9]".

migrationpenalty understands:

**stockname** Stock name

**powercoeffs** 2 power coefficients

## Value

A `gadget_likelihood_component` object that can then be written to a likelihood file with `gadget_dir_write`

**Examples**

```
# Create a penalty component
component <- gadget_likelihood_component("penalty",
  name = "bounds",
  weight = "0.5",
  data = data.frame(
    switch = c("default"),
    power = c(2),
    stringsAsFactors = FALSE))
component

# Create an understocking component
component <- gadget_likelihood_component("understocking", name ="understock")
component

# Any example could be added to a file with the following:-
gd <- gadget_directory(tempfile())
gadget_dir_write(gd, component)
```

---

gadget\_stockfile      *Gadget stock files*

---

**Description**

Structures representing a GADGET stock file

**Usage**

```
gadget_stockfile_extremes(stock_name, data)
gadget_stockfile_refweight(stock_name, data)
gadget_stockfile_initialconditions(stock_name, data)
gadget_stockfile_recruitment(stock_name, data)
```

**Arguments**

stock_name	A name, e.g. cod. imm, used as the name for the stockfile
data	A data.frame used to generate the data. See details.

**Details**

The columns required in the data varies depends on which function you are using.

`gadget_stockfile_extremes` requires age and length columns and populates `minlength`, `minage`, `maxlength`, `maxage`. The values are obtained by the grouping used, rather than the maximum values in the data. If you want the minimum and maximum from the data, query with `length = NULL`, `age = NULL`, so the table contains "all" and the grouping contains the actual minimum and maximum.

`gadget_stockfile_refweight` requires a length column and a mean column representing mean weight for that length group. It populates the `refweightfile` and `dl`.



`gadget_stockfile_initialconditions` requires area, age, length, number and mean (weight) columns. Populates initialconditions minlength, minage, maxlength, maxage, dl and the numberfile. As before, the min/max values are populated using the groupings you specify, not the min/max available data.

`gadget_stockfile_recruitment` requires year, step, area, age, length, number and mean (weight) columns. Populates doesrenew, minlength, maxlength, dl, numberfile.

## Value

The return value is a `gadget_stockfile` object that can be written to the filesystem with `gadget_dir_write`.

## Examples

```

mdb <- mfdb(tempfile(fileext = '.duckdb'))

# Define 2 areacells of equal size
mfdb_import_area(mdb, data.frame(name=c("divA", "divB"), size=1))

# Make up some samples
samples <- expand.grid(
  year = 1998,
  month = c(1:12),
  areacell = c("divA", "divB"),
  species = 'COD',
  age = c(1:5),
  length = c(0,40,80))
samples$count <- runif(nrow(samples), 20, 90)
mfdb_import_survey(mdb, data_source = "x", samples)

imm_data <- mfdb_sample_meanweight(mdb, c('age', 'length'), list(
  age = NULL, # The age column will say 'all', but will know the min/max
  length = mfdb_step_interval('', 10, to = 100),
  species = 'COD'))

# Write both min/max and refweighfile into our gadget directory
component <- gadget_stockfile_extremes('cod.imm', imm_data[[1]])
component

component <- gadget_stockfile_refweight('cod.imm', imm_data[[1]])
component

gadget_dir_write(gadget_directory(tempfile()), component)

mfdb_disconnect(mdb)

```

**Description**

Create a class representing a connection to a MareFrame DB

**Usage**

```
mfdb(schema_name,
      db_params = list(),
      destroy_schema = FALSE,
      save_temp_tables = FALSE)

mfdb_disconnect(mdb)
```

**Arguments**

schema_name	<p>This can be one of:</p> <ol style="list-style-type: none"> <li>1. Postgresql schema name</li> <li>2. A file path ending with ".sqlite" to connect to a SQLite file database</li> <li>3. A file path ending with ".duckdb" to connect to a DuckDB file database</li> </ol> <p>If connecting to a SQLite/DuckDB database, <i>db_params</i> should remain empty (<i>schema_name</i> will be used as a dbname).</p> <p>If connecting to a Postgres database, it can be used to store any number of case studies, by storing them in separate <i>schemas</i>. This parameter defines the schema to connect to, and can contain any lower case characters or underscore.</p>
db_params	<p>Extra parameters to supply to <code>DBI::dbConnect</code>. By default it will search for a "mf" database locally, but you can override any of the parameters, in particular host, dbname, user, password. See <code>?RPostgres::Postgres</code> for more information.</p> <p>If dbname looks like a SQLite database filename, then MFDB will use the <code>RSQLite</code> driver. If <code>dbdir</code> is set, then MFDB will use the <code>duckdb</code> driver. Otherwise, <code>RPostgres</code> will be used.</p> <p><i>db_params</i> can also be supplied by environment variable, for example if a <code>MFDB_DBNAME</code> environment variable is set then it will be used instead of any dbname supplied here.</p>
destroy_schema	<p>Optional boolean. If true, all mfdb tables will be destroyed when connecting. This allows you to start populating your case study from scratch if required. The function will return <code>NULL</code>, you need to call <code>mfdb</code> again to connect, at which point the mfdb tables will be recreated and you can populate with data again.</p>
save_temp_tables	<p>Optional boolean. If true, any temporary tables will be made permanent for later inspection.</p>
mdb	<p>Database connection created by <code>mfdb()</code>.</p>

**Value**

A 'mfdb' object representing the DB connection

## Examples

```
# Connect to a SQLite database file
mdb <- mfdb(tempfile(fileext = '.sqlite'))
mfdb_disconnect(mdb)

## Not run: # NB: Requires a PostgreSQL installation, see README

# Connect to local DB, as the "examples" case study
mdb <- mfdb('examples')
mfdb_disconnect(mdb)

# Connect to remote server, will prompt for username/password
if (interactive()) {
  mdb <- mfdb('examples', db_params = list(host = "mfdb.rhi.hi.is"))
}

## End(Not run)
```

---

mfdb-data

*MareFrame DB Datasets*


---

## Description

Data sets representing the content of taxonomies used in the database.

## Usage

```
case_study
gear
institute
market_category
maturity_stage
sex
species
vessel_type
```

## Details

All of these tables represent acceptable values for use when importing data. You can see the content of an individual taxonomy at the R command line, e.g. `mfdb: :gear`

Each of the datasets will have the following columns.

**id** A numeric ID to be used internally

**name** An alphanumeric ID to be used when importing and reporting data.

**description** Some text describing the option.

**t\_group** Groups together several items to query all in one go. e.g. for institutes you can query 'NOR' to get all institutes in Norway.

The taxonomies are used in the following locations:

**case\_study** Possible case studies, use when connecting with `mfdb()`

**gear, institute, vessel\_type** Used to describe the dataset being imported with `mfdb_import_survey()`

**sex, maturity\_stage, species** Used for individual sample points when using `mfdb_import_survey()`

---

mfdb\_aggregate\_group *MareFrame DB groups*

---

## Description

Represent a grouping of data to be applied when summarising area, timestep, age or length.

## Usage

```
# Named grouping of discrete items
mfdb_group(...)

# Pre-baked mfdb_groups for timesteps
mfdb_timestep_yearly
mfdb_timestep_biannually
mfdb_timestep_quarterly

# Grouping of discrete items, names generated by prefix
mfdb_group_numbered(prefix, ...)

# make (count) mfdb_groups, by sampling (count) times from (group)
mfdb_bootstrap_group(count, group, seed = NULL)
```

## Arguments

...	For <code>mfdb_group</code> , all named arguments are expected to be a named list of members for that group. For <code>mfdb_group_numbered</code> , the members do not have to be named, a name will be generated based on the prefix.
prefix	When generating numeric group names, the character prefix to append to the beginning.
group	For <code>mfdb_bootstrap_group</code> , the <code>mfdb_group</code> to do sampling with replacement from.
count	For <code>mfdb_bootstrap_group</code> , how many times to sample each member of the given group.
seed	For <code>mfdb_bootstrap_group</code> , if you want your groups to remain consistent across sessions, then specify a random integer as per RNG.

## Value

An `mfdb_aggregate` object that can then be used in querying functions such as `mfdb_sample_count`

**Examples**

```
## Aggregate age into 2 groups. "young" (for ages 1--3) and
## "old" (for ages 4--6)
g1 <- mfdb_group(young = c(1,2,3), old = c(4,5,6))

## Aggregate areas into "area1" and "area2".
g2 <- mfdb_group_numbered("area", c(1011,1012,1013), c(1021,1022))

## Take 3 samples with replacement from each group in area
g3 <- mfdb_bootstrap_group(3, g2)
```

---

mfdb\_aggregate\_interval

*MareFrame DB intervals*


---

**Description**

Represent a uniform or non-uniform interval.

**Usage**

```
mfdb_interval(prefix, vect, open_ended = FALSE)
```

**Arguments**

prefix	(required) A character prefix to prepend to minimum to create list names
vect	(required) A vector representing the minimum for each group, and the maximum
open_ended	If TRUE / c('upper'), the last group will ignore it's upper bound and include any value. If c('lower'), the first group will ignore it's lower bound include everything < the first value in vect. If c('upper', 'lower'), both the above occur. This is useful when creating plus groups for GADGET, as GADGET will still be presented a bounded group, but will contain all remaining data.

**Value**

An mfdb\_aggregate object that can then be used in querying functions such as mfdb\_sample\_count

**Examples**

```
## Make groups of len40 (40--60), len60 (60--80)
g1 <- mfdb_interval("len", c(40, 60, 80))

## Use seq to make life easier
g2 <- mfdb_interval("len", seq(40, 80, by = 20))

## Create groups len40: [40, 60), len60: [60, inf) (but [60, 80) in the GADGET model)
g1 <- mfdb_interval("len", c(40, 60, 80), open_ended = c("upper"))
```

---

 mfdb\_aggregate\_na\_group

*MareFrame DB aggregate NAs*


---

### Description

A decorator for other MFDB attributes to file NAs into another group, either one created by the main function or not.

### Usage

```
mfdb_na_group(sub_aggregate, na_group)
```

### Arguments

sub\_aggregate    An mfdb\_aggregate produced by another function, e.g. mfdb\_step\_interval  
 na\_group        The group to assign NAs to, e.g. "len\_unknown"

### Details

The NA group won't be added to any aggregate files generated by MFDB, since the output would be invalid.

### Value

An mfdb\_aggregate object that can then be used in querying functions such as mfdb\_sample\_count

### Examples

```
length <- mfdb_na_group(mfdb_step_interval("len", 10), 'len_unknown')
```

---

 mfdb\_aggregate\_step\_interval

*MareFrame DB intervals*


---

### Description

Groups data into uniform intervals

### Usage

```
mfdb_step_interval(prefix, by, from = 0, to = NULL, open_ended = FALSE)
```

**Arguments**

prefix	(required) A character prefix to prepend to minimum to create list names
by	(required) Increment of the sequence. NB: Must be an integer
from, to	Start / end of the sequence. Defaults to 0 / infinity respectively.
open_ended	If TRUE / c('upper'), the last group will ignore it's upper bound and include any value. If c('lower'), the first group will ignore it's lower bound include everything < the first value in vect. If c('upper', 'lower'), both the above occur. This is useful when creating plus groups for GADGET, as GADGET will still be presented a bounded group, but will contain all remaining data.

**Value**

An mfdb\_aggregate object that can then be used in querying functions such as mfdb\_sample\_count

**Examples**

```
## Make groups of len0 (0--5), len5 (5--10), ... len45(45--50)
g1 <- mfdb_step_interval("len", 5, to = 50)

## Make groups of len0 (0--5), len5 (5--10), ... len45(45--50), len50(50--inf)
g2 <- mfdb_step_interval("len", 5, to = 50, open_ended = TRUE)
```

---

```
mfdb_aggregate_unaggregated
  MareFrame DB unaggregated data
```

---

**Description**

Tell mfdb functions not to aggregate this column, just return all values.

**Usage**

```
mfdb_unaggregated(omitNA = FALSE, like = c(), not_like = c())
```

**Arguments**

omitNA	Skip over rows where column is NA
like	Vector of SQL like expressions to check column against
not_like	Vector of SQL like expressions to check column against

**Details**

SQL like expressions can use the wildcards "\_" to match any character and "

**Value**

An mfdb\_aggregate object that can then be used in querying functions such as mfdb\_sample\_count

**Examples**

```
# All vessels with a name ending with 'e' or 'd'
mfdb_unaggregated(like = c("%e", "%d"))
```

---

mfdb\_bulk

*MareFrame DB Dump / Restore*


---

**Description**

Dump / Restore entire case studies.

**Usage**

```
mfdb_cs_dump(mdb, out_location)
mfdb_cs_restore(mdb, in_location)
```

**Arguments**

`mdb` (required) A database connection created by `mfdb()`

`in_location, out_location` (required) A filesystem directory or `'tar.gz'` file to dump / restore database contents.

**Details**

Deprecated: These commands aren't strictly necessary any more. In most situations it will be easier to use Postgres' `pg_dump` and `pg_restore`. See [mfdb-package](#) for some examples of how to do it. These functions don't offer much more functionality and much slower.

`mfdb_cs_dump` copies all data from the database/case-study that `mdb` is connected to, and writes it out to files in `out_location`. If this ends with `'tar.gz'`, then all files will be put into a tarball with the name

`mfdb_cs_restore` will remove any case-study data, and replaces it with the content of `in_location`, a directory or tarball.

**Value**

NULL

**Examples**

```
# Copy data from one database to another, note they don't have to be the same type
mdb_out <- mfdb(tempfile(fileext = '.sqlite'))
mdb_in <- mfdb(tempfile(fileext = '.duckdb'))

dump_path <- tempfile(fileext='.tar.gz')
mfdb_cs_dump(mdb_out, dump_path)
mfdb_cs_restore(mdb_in, dump_path)
```



```
mfdb_disconnect(mdb_in)
mfdb_disconnect(mdb_out)
```

---

mfdb\_dplyr

*MareFrame DB dplyr interface*

---

## Description

Use mfdb tables with dplyr

## Usage

```
mfdb_dplyr_table(mdb, table_name, include_cols = all_cols)
mfdb_dplyr_survey_index(mdb, include_cols = all_cols)
mfdb_dplyr_division(mdb, include_cols = all_cols)
mfdb_dplyr_sample(mdb, include_cols = all_cols)
mfdb_dplyr_predator(mdb, include_cols = all_cols)
mfdb_dplyr_preym(mdb, include_cols = all_cols)
```

## Arguments

mdb	An object created by mfdb()
table_name	A table name to query in
include_cols	Any additional columns to include in output, see details.

## Details

Warning: Whilst these might be handy for exploration, there is no guarantee that code using these will continue to work from one version of MFDB to the next.

There is one function for each measurement table. By default every possible taxonomy column is included. However this is somewhat inefficient if you do not require the data, in which case specify the columns required with `include_cols`. See `mfdb::mfdb_taxonomy_tables` for possible values.

To query taxonomy tables, use `mfdb_dplyr_table`, which works for any supplied table name. See `mfdb::mfdb_taxonomy_tables` for possible values for `table_name`.

## Value

A dplyr table object, for you to do as you please.

**Examples**

```

mdb <- mfdb(tempfile(fileext = '.duckdb'))

# Include as many columns as possible
mfdb_dplyr_sample(mdb)

# Only include 'data_source' and 'species' columns, as well as measurements
mfdb_dplyr_sample(mdb, c('data_source', 'species'))

# Query the sampling_type table
mfdb_dplyr_table(mdb, 'sampling_type')

mfdb_disconnect(mdb)

```

mfdb\_helpers

*MareFrame tools & helpers***Description**

Misc. functions to aid working with an MFDB database.

**Usage**

```

# Find species from abbreviated names
mfdb_find_species(partial_name, single_matches_only = FALSE)

```

**Arguments**

**partial\_name** Vector of partial species names, e.g. "Gad Mor", "gad. Mor.", "Gadus Mor", will all match "Cod (Gadus Morhua)".

**single\_matches\_only** Logical, default FALSE. If true, return NA for partial\_names with multiple or zero matches.

**Value**

A matrix of all potential id, name & descriptions for each item in partial\_name.

**Examples**

```

mfdb_find_species(c("gad mor", "tube worms"))
#           gad mor           tube worms
# id      8791030402           1e+10
# name    "COD"              "TBX"
# description "Cod (Gadus Morhua)" "Tube Worms (Tubeworms)"

# Can also generate a map to help insert a data.frame of foreign data
stomachs <- read.csv(text = '
stomach_name,species,digestion_stage,length,weight,count

```

```

A,Palaemon Elegans,1,1,10,5
A,Palaemon Elegans,1,4,40,1
B,Palaemon Elegans,1,1,10,5
B,Palaemon Elegans,4,1,10,5
B,Palaemon Elegans,5,1,10,NA
B,Palaemon Elegans,5,1,10,NA
C,Crango Crango,2,3.5,9.5,3
D,Palaemon Elegans,1,1.4,10,1
D,Crango Crango,5,4,40,1
E,Worms,1,1.4,10,1
', stringsAsFactors = TRUE)

# Work out a map from all Prey_Species_Name values to MFDB species codes
species_map <- mfdb_find_species(levels(stomachs$species), single_matches_only = TRUE)['name',]

# Put the new levels back onto the species column
levels(stomachs$species) <- unlist(species_map)

stomachs

```

---

```
mfdb_helpers_mfdb_concatenate_results
```

*MareFrame Query Utilities*

---

## Description

Aggregate data from the database in a variety of ways

## Usage

```
mfdb_concatenate_results(...)
```

## Arguments

... Any number of data.frames produced by mfdb query functions with identical columns, e.g. mfdb\_sample\_count

## Value

Given any number of data.frames from mfdb query functions with identical columns, produces a combined data.frame, similar to `rbind` but preserving the attributes required to produce aggregation files.

---

mfdb\_import\_data      *MareFrame Data Import functions*


---

## Description

Functions to import data into MareFrame DB

## Usage

```
mfdb_import_temperature(mdb, data_in)
mfdb_import_survey(mdb, data_in, data_source = 'default_sample')
mfdb_import_survey_index(mdb, data_in, data_source = 'default_index')
mfdb_import_stomach(mdb, predator_data, prey_data, data_source = "default_stomach")
```

## Arguments

**mdb**                    Database connection created by mfdb().

**data\_in, predator\_data, prey\_data**  
                           A data.frame of survey data to import, see details.

**data\_source**        A name for this data, e.g. the filename it came from. Used so you can replace it later without disturbing other data.

## Details

All functions will replace existing data in the case study with new data, unless you specify a `data_source`, in which case then only existing data with the same `data_source` will be replaced.

If you want to remove the data, import empty `data.frames` with the same `data_source`.

`mfdb_import_temperature` imports temperature time-series data for areacells. The `data_in` should be a `data.frame` with the following columns:

**id** A numeric ID for this areacell (will be combined with the case study number internally)

**year** Required. Year each sample was taken, e.g. `c(2000, 2001)`

**month** Required. Month (1–12) each sample was taken, e.g. `c(1, 12)`

**areacell** Required. Areacell sample was taken within

**temperature** The temperature at given location/time

`mfdb_import_survey` imports institution surveys and commercial sampling for your case study. The `data_in` should be a `data.frame` with the following columns:

**institute** Optional. An institute name, see `mfdb::institute` for possible values

**gear** Optional. Gear name, see `mfdb::gear` for possible values

**vessel** Optional. Vessel defined previously with `mfdb_import_vessel_taxonomy(...)`

**tow** Optional. Tow defined previously with `mfdb_import_tow_taxonomy(...)`

**sampling\_type** Optional. A `sampling_type`, see `mfdb::sampling_type` for possible values

**year** Required. Year each sample was taken, e.g. c(2000, 2001)

**month** Required. Month (1–12) each sample was taken, e.g. c(1, 12)

**areacell** Required. Areacell sample was taken within

**species** Optional, default c(NA). Species of sample, see mfdb::species for possible values

**age** Optional, default c(NA). Age of sample, or mean age

**sex** Optional, default c(NA). Sex of sample, see mfdb::sex for possible values

**length** Optional, default c(NA). Length of sample / mean length of all samples

**length\_var** Optional, default c(NA). Sample variance, if data is already aggregated

**length\_min** Optional, default c(NA). Minimum theoretical length, if data is already aggregated

**weight** Optional, default c(NA). Weight of sample / mean weight of all samples

**weight\_var** Optional, default c(NA). Sample variance, if data is already aggregated

**weight\_total** Optional, default c(NA). Total weight of all samples, can be used with count = NA to represent an unknown number of samples

**liver\_weight** Optional, default c(NA). Weight of sample / mean liver weight of all samples

**liver\_weight\_var** Optional, default c(NA). Sample variance, if data is already aggregated

**gonad\_weight** Optional, default c(NA). Weight of sample / mean gonad weight of all samples

**gonad\_weight\_var** Optional, default c(NA). Sample variance, if data is already aggregated

**stomach\_weight** Optional, default c(NA). Weight of sample / mean stomach weight of all samples

**stomach\_weight\_var** Optional, default c(NA). Sample variance, if data is already aggregated

**count** Optional, default c(1). Number of samples this row represents (i.e. if the data is aggregated)

mfdb\_import\_survey\_index adds indices that can be used as abundance information, for example. Before using mfdb\_import\_survey\_index, make sure that the index\_type you intend to use exists by using mfdb\_import\_cs\_taxonomy. The data\_in should be a data.frame with the following columns:

**index\_type** Required. the name of the index data you are storing, e.g. 'acoustic'

**year** Required. Year each sample was taken, e.g. c(2000, 2001)

**month** Required. Month (1–12) each sample was taken, e.g. c(1, 12)

**areacell** Required. Areacell sample was taken within

**value** Value of the index at this point in space/time

mfdb\_import\_stomach imports data on predators and prey. The predator and prey data are stored separately, however they should be linked by the stomach\_name column. If a prey has a stomach name that doesn't match a predator, then an error will be returned.

The predator\_data should be a data.frame with the following columns:

**stomach\_name** Required. An arbitrary name that provides a link between the predator and prey tables

**institute** Optional. An institute name, see mfdb::institute for possible values

**gear** Optional. Gear name, see mfdb::gear for possible values

**vessel** Optional. Vessel defined previously with `mfdb_import_vessel_taxonomy(mdb, ...)`

**tow** Optional. Tow defined previously with `mfdb_import_tow_taxonomy(...)`

**sampling\_type** Optional. A `sampling_type`, see `mfdb::sampling_type` for possible values

**year** Required. Year each sample was taken, e.g. `c(2000, 2001)`

**month** Required. Month (1–12) each sample was taken, e.g. `c(1, 12)`

**areacell** Required. Areacell sample was taken within

**species** Optional, default `c(NA)`. Species of sample, see `mfdb::species` for possible values

**age** Optional, default `c(NA)`. Age of sample, or mean age

**sex** Optional, default `c(NA)`. Sex of sample, see `mfdb::sex` for possible values

**maturity\_stage** Optional, default `c(NA)`. Maturity stage of sample, see `mfdb::maturity_stage` for possible values

**stomach\_state** Optional, default `c(NA)`. Stomach state of sample, see `mfdb::stomach_state` for possible values

**length** Optional, default `c(NA)`. Length of sample

**weight** Optional, default `c(NA)`. Weight of sample

The `prey_data` should be a `data.frame` with the following columns:

**stomach\_name** Required. The stomach name of the predator this was found in

**species** Optional, default `c(NA)`. Species of sample, see `mfdb::species` for possible values

**digestion\_stage** Optional, default `c(NA)`. Stage of digestion of the sample, see `mfdb::digestion_stage` for possible values

**length** Optional, default `c(NA)`. Length of sample / mean length of all samples

**weight** Optional, default `c(NA)`. Weight of sample / mean weight of all samples

**weight\_total** Optional, default `c(NA)`. Total weight of all samples

**count** Optional, default `c(NA)`. Number of samples this row represents (i.e. if the data is aggregated), `count = NA` represents an unknown number of samples

## Value

NULL

## Examples

```

mdb <- mfdb(tempfile(fileext = '.duckdb'))

# We need to set-up vocabularies first
mfdb_import_area(mdb, data.frame(
  id = c(1,2,3),
  name = c('35F1', '35F2', '35F3'),
  size = c(5)))
mfdb_import_vessel_taxonomy(mdb, data.frame(
  name = c('1.RSH', '2.COM'),
  stringsAsFactors = FALSE))
mfdb_import_sampling_type(mdb, data.frame(

```

```

name = c("RES", "LND"),
description = c("Research", "Landings"),
stringsAsFactors = FALSE))

data_in <- read.csv(text = '
year,month,areacell,species,age,sex,length
1998,1,35F1,COD,3,M,140
1998,1,35F1,COD,3,M,150
1998,1,35F1,COD,3,F,150
')

data_in$institute <- 'MRI'
data_in$gear <- 'GIL'
data_in$vessel <- '1.RSH'
data_in$sampling_type <- 'RES'
mfdb_import_survey(mdb, data_in, data_source = 'cod-1998')

mfdb_disconnect(mdb)

```

---

mfdb\_import\_taxonomy *MareFrame Taxonomy import functions*

---

## Description

Functions to import taxonomy data into MareFrame DB

## Usage

```

mfdb_import_area(mdb, data_in)
mfdb_import_division(mdb, data_in)
mfdb_import_sampling_type(mdb, data_in)
mfdb_import_bait_type_taxonomy(mdb, data_in)
mfdb_import_population_taxonomy(mdb, data_in)
mfdb_import_port_taxonomy(mdb, data_in)
mfdb_import_tow_taxonomy(mdb, data_in)
mfdb_import_net_type_taxonomy(mdb, data_in)
mfdb_import_trip_taxonomy(mdb, data_in)
mfdb_import_vessel_taxonomy(mdb, data_in)
mfdb_import_vessel_owner_taxonomy(mdb, data_in)

mfdb_empty_taxonomy(mdb, taxonomy_name)

mfdb_import_cs_taxonomy(mdb, taxonomy_name, data_in)

```

## Arguments

mdb	Database connection created by <code>mfdb()</code> .
taxonomy_name	The name of the taxonomy to import, if there isn't a special function for it. See <code>mfdb::mfdb_taxonomy_tables</code> for possible values.
data_in	A <code>data.frame</code> of data to import, see details.

## Details

MFDB taxonomies define the values you can use when importing / querying for data. They need to be populated with the values you need before data is imported. Most taxonomies are pre-populated by the MFDB package, so you should use the predefined values. Others however this does not make sense, so should be done separately. This is what these functions do.

`mfdb_import_division` is a special case, which imports groupings of areacells into divisions, if you haven't already done this with `mfdb_import_area` or your divisions are too complicated to represent this way. The `data_in` should be a list of areacell vectors, with division names. For example, `list(divA = c('45G01', '45G02', '45G03'))`

Beyond this, all functions accept the following columns:

**id** Optional. A numeric ID to use internally, defaults to 1..n

**name** Required. A vector of short names to use in data, e.g. "SEA"

**t\_group** Optional. A vector of the that groups together a set of values

Note that the database doesn't use your short names internally. This means you can rename items by changing what name is set to. `t_group` allows taxonomy values to be grouped together. For example, giving all vessels in a fleet the same `t_group` you can then query the entire fleet as well as individually.

`mfdb_import_area` imports areacell information for your case study. Beyond the above, you can also provide the following:

**size** The size of the areacell

**depth** The depth of the areacell

**division** The name of the division this areacell is part of

`mfdb_import_vessel_taxonomy` imports names of vessels into the taxonomy table, so they can be used when importing samples. As well as the above, you can also specify:

**full\_name** Optional. The full name of this vessel

**length** Optional. The length of the vessel in meters

**power** Optional. The vessel's engine power in KW

**tonnage** Optional. The vessel's gross tonnage

**vessel\_owner** Optional. The short name of the vessel owner (see `mfdb_import_vessel_owner_taxonomy`)

`mfdb_import_vessel_owner_taxonomy` imports names of vessels owners into a taxonomy table, to be used when importing vessels. As well as `name/t_group`, you can also specify:

**full\_name** Optional. The full name of the owning organisation

`mfdb_import_tow_taxonomy` imports names of vessels into the taxonomy table, so they can be used when importing samples. As well as the above, you can also specify:

**latitude** Optional.

**longitude** Optional.

**depth** Optional. Depth in meters



**length** Optional. Length in meters

mfdb\_import\_port\_taxonomy imports names of ports that trips can start/finish at. As well as id/name, you can provide:

**latitude** Optional. Latitude as real number

**longitude** Optional. Longitude as real number

**institute** Optional. Institute (from institute taxonomy, could be country) responsible for port

mfdb\_import\_trip\_taxonomy imports names of trips that samples can be labelled part of. As well as id/name, you can provide:

**latitude** Optional. Latitude as real number

**longitude** Optional. Longitude as real number

**start\_date** Optional. Start date-time, as YYYY-MM-DD or YYYY-MM-DD HH:MM:SS

**end\_date** Optional. End date-time, as YYYY-MM-DD or YYYY-MM-DD HH:MM:SS

**crew** Optional. Number of crew on-board

**oil\_consumption** Optional. Total oil consumption for trip

**start\_port** Optional. Name of port (from port taxonomy) trip started

**end\_port** Optional. Name of port (from port taxonomy) trip finished

mfdb\_import\_sampling\_type imports sampling types so that you can then use these against records in the sample table. You can also provide:

**description** Optional. A vector of descriptive names, e.g. "sea sampling"

mfdb\_empty\_taxonomy allows you to empty out a taxonomy of previous data. The import functions insert or update values that already exist, based on the numeric ID for these values. They do not delete anything, as it may be impossible to remove rows without destroying existing data.

However, if e.g. you want to replace the species taxonomy with an entirely different one you will need to flush it first, before you import any data. Use this function, then `mfdb_import_species_taxonomy` to import the new taxonomy.

NB: This won't be possible if there is some data already using any of the terms. It is best used before your database is populated.

## Value

NULL

**Description**

Aggregate data from the database in a variety of ways

**Usage**

```
mfdb_area_size(mdb, params)
mfdb_area_size_depth(mdb, params)
mfdb_temperature(mdb, params)
mfdb_survey_index_mean(mdb, cols, params, scale_index = NULL)
mfdb_survey_index_total(mdb, cols, params, scale_index = NULL)
mfdb_sample_count(mdb, cols, params, scale_index = NULL)
mfdb_sample_meanlength(mdb, cols, params, scale_index = NULL)
mfdb_sample_meanlength_stddev(mdb, cols, params, scale_index = NULL)
mfdb_sample_totalweight(mdb, cols, params, measurements = c('overall'))
mfdb_sample_meanweight(mdb, cols, params, scale_index = NULL,
                        measurements = c('overall'))
mfdb_sample_meanweight_stddev(mdb, cols, params, scale_index = NULL,
                              measurements = c('overall'))
mfdb_sample_rawdata(mdb, cols, params, scale_index = NULL)
mfdb_sample_scaled(mdb, cols, params, abundance_scale = NULL, scale = 'tow_length')
mfdb_stomach_preycount(mdb, cols, params)
mfdb_stomach_preymeanlength(mdb, cols, params)
mfdb_stomach_preymeanweight(mdb, cols, params)
mfdb_stomach_preypeighratio(mdb, cols, params)
mfdb_stomach_presenceratio(mdb, cols, params)
```

**Arguments**

<code>mdb</code>	An object created by <code>mfdb()</code>
<code>cols</code>	Any additional columns to group by, see details.
<code>params</code>	A list of parameters, see details.
<code>scale_index</code>	Optional. <code>survey_index</code> used to scale results before aggregation, either "tow_length", "area_size" or from <a href="#">mfdb_import_survey_index</a>
<code>abundance_scale</code>	Optional. Same as <code>scale_index</code>
<code>scale</code>	Optional. A scale to apply to the resulting values, e.g. 'tow_length'
<code>measurements</code>	Optional, default 'overall'. A vector of measurement names to use, one of overall, liver, gonad, stomach

## Details

The items in the params list either restrict data that is returned, or groups data if they are also in the cols vector, or are 'year', 'timestep', or 'area'.

If you are grouping by the column, params should contain one of the following:

**NULL** Don't do any grouping, instead put 'all' in the resulting column. For example, age = NULL results in "all".

**character / numeric vector** Aggregate all samples together where they match. For example, year = 1990:2000 results in 1990, ... , 2000.

**mfd\_b\_unaggregated()** Don't do any aggregation for this column, return all possible values.

**mfd\_b\_group()** Group several discrete items together. For example, age = mfd\_b\_group(young = 1:3, old = 4:5) results in "young" and "old".

**mfd\_b\_interval()** Group irregular ranges together. For example, length = mfd\_b\_interval('len', c(0, 10, 100, 1000)) results in "len0", "len10", "len100" (1000 is the upper bound to len100).

**mfd\_b\_step\_interval()** Group regular ranges together. For example, length = mfd\_b\_step\_interval('len', to = 100, by = 10) results in "len0", "len10", ... , "len90".

In addition, params can contain other arguments to purely restrict the data that is returned.

**institute** A vector of institute names / countries, see mfd\_b::institute for possible values

**gear** A vector of gear names, see mfd\_b::gear for possible values

**vessel** A vector of vessel names, see mfd\_b::vessel for possible values

**sampling\_type** A vector of sampling\_type names, see mfd\_b::sampling\_type for possible values

**species** A vector of species names, see mfd\_b::species for possible values

**sex** A vector of sex names, see mfd\_b::sex for possible values

To save specifying the same items repeatedly, you can use list concatenation to keep some defaults, for example:

```
defaults <- list(year = 1998:2000)
mfd_b_sample_meanlength(mdb, c('age'), c(list(), defaults))
```

scale\_index allows you to scale samples before aggregation. If it contains the name of a survey index (see [mfd\\_b\\_import\\_survey\\_index](#)), then any counts will be scaled by the value for that areacell before and used in aggregation / weighted averages. As a special case, you can use "tow\_length" to scale counts by the tow length.

## Value

All will return a list of data.frame objects. If there was no bootstrapping requested, there will be only one. Otherwise, there will be one for each sample.

The columns of these data frames depends on the function called.

**mfd\_b\_area\_size** Returns area, (total area) size

**mfd\_b\_area\_size\_depth** Returns area, (total area) size, mean depth, weighted by area size

**mfdb\_temperature** Returns year, step, area, (mean) temperature

**mfdb\_survey\_index\_mean** Returns year, step, area, (group cols), (mean) survey index

**mfdb\_survey\_index\_total** Returns year, step, area, (group cols), (sum) survey index

**mfdb\_sample\_count** Returns year, step, area, (group cols), number (i.e sum of count)

**mfdb\_sample\_meanlength** Return year, step, area, (group cols), number (i.e sum of count), mean (length)

**mfdb\_sample\_meanlength\_stddev** As mfdb\_sample\_meanlength, but also returns std. deviation.

**mfdb\_sample\_totalweight** Returns year,step,area,(group cols),total (weight of group)

**mfdb\_sample\_meanweight** Returns year, step, area, (group cols), number (i.e sum of count), mean (weight)

**mfdb\_sample\_meanweight\_stddev** As mfdb\_sample\_meanweight, but also returns std. deviation.

**mfdb\_sample\_rawdata** Returns year,step,area,(group cols),number of samples, raw\_weight and raw\_length.  
NB: No grouping of results is performed, instead all matching table entries are returned

**mfdb\_sample\_scaled** Returns year, step, area, (group cols), number (i.e. sum of count, scaled by tow\_length), mean\_weight (scaled by tow\_length)

**mfdb\_stomach\_preycount** Returns year, step, area, (group cols), number (of prey found in stomach)

**mfdb\_stomach\_preymeanlength** Returns year, step, area, (group cols), number (of prey found in stomach), mean\_length (of prey found in stomach). NB: Entries where count is NA (i.e. totals) are ignored with this function.

**mfdb\_stomach\_preymeanweight** Returns year, step, area, (group cols), number (of unique stomachs in group), mean\_weight (per unique stomach).

**mfdb\_stomach\_preypeighratio** Returns year, step, area, (group cols), ratio (of selected prey in stomach to all prey by weight)

**mfdb\_stomach\_presenceratio** Returns year, step, area, (group cols), ratio (of selected prey in stomach to all prey by count)

### Examples

```

mdb <- mfdb(tempfile(fileext = '.duckdb'))

# Define 2 areacells of equal size
mfdb_import_area(mdb, data.frame(name=c("divA", "divB"), size=1))

# Make up some samples
samples <- expand.grid(
  year = 1998,
  month = c(1:12),
  areacell = c("divA", "divB"),
  species = 'COD',
  age = c(1:5),
  length = c(0,40,80))
samples$count <- runif(nrow(samples), 20, 90)

```

```

mfdb_import_survey(mdb, data_source = "x", samples)

# Query numbers by age and length
agg_data <- mfdb_sample_count(mdb, c('age', 'length'), list(
  length = mfdb_interval("len", seq(0, 500, by = 30)),
  age = mfdb_group('young' = c(1,2), old = 3),
  year = c(1998)))
agg_data

# Use in a catchdistribution likelihood component
gadget_dir_write(gadget_directory(tempfile()), gadget_likelihoood_component("catchdistribution",
  name = "cdist",
  weight = 0.9,
  data = agg_data[[1]],
  area = attr(agg_data[[1]], "area"),
  age = attr(agg_data[[1]], "age")))

mfdb_disconnect(mdb)

```

mfdb\_sharing

*MareFrame DB sharing options***Description**

Alter database privileges

**Usage**

```
mfdb_share_with(mdb, user_or_role, query = TRUE, import = FALSE)
```

**Arguments**

<code>mdb</code>	(required) A database connection created by <code>mfdb()</code>
<code>user_or_role</code>	(required) Another database user, or a role, or 'public' to share with all users
<code>query</code>	Should the user be able to query the current case study?
<code>import</code>	Should the user be able to import more data current case study?

**Details**

This allows you to share case study data between users. This is most useful when using a shared database. Only the owner of the schema (i.e. the user that created it) will be able to change table structure (i.e. upgrade MFDB versions).

By default nothing is shared between users.

**Value**

NULL

**Examples**

```
## Not run: # NB: Requires a PostgreSQL installation, and creation of extra users  
  
mdb <- mfdb('examples')  
  
mfdb_share_with(mdb, 'gelda') # Allow DB user gelda to query the 'examples' case study data  
  
## End(Not run)
```

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