Package ‘rfishbase’

May 9, 2026

Title R Interface to 'FishBase'

Description A programmatic interface to 'FishBase', re-written based on an accompanying 'RESTful' API. Access tables describing over 30,000 species of fish, their biology, ecology, morphology, and more. This package also supports experimental access to 'SeaLifeBase' data, which contains nearly 200,000 species records for all types of aquatic life not covered by 'FishBase.'

Version 5.0.3

Encoding UTF-8

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URL `https://docs.ropensci.org/rfishbase/`, `https://github.com/ropensci/rfishbase`

BugReports `https://github.com/ropensci/rfishbase/issues`

Depends R (>= 4.1.0)

Imports glue, stringr, purrr, dplyr, duckdbfs (>= 0.0.9), rlang, magrittr, memoise, xml2

Suggests testthat, rmarkdown, knitr, covr, spelling, curl

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Language en-US

NeedsCompilation no

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Repository CRAN

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Contents

`available_releases` *List available releases*

Description

List available releases

Usage

```
available_releases(server = c("fishbase", "sealifebase"))
```

Arguments

`server`	fishbase or sealifebase

Examples

```
available_releases()
```

`brains` *brains*

Description

brains

Usage

```
brains(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species brains

Examples

```
 ## Not run:
brains("Oreochromis niloticus")

## End(Not run)
```

`common_names` *common names*

Description

Return a table of common names

Usage

```
common_names(
  species_list = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  Language = "English",
  fields = NULL
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`Language`	a string specifying the language for the common name, e.g. "English"
`fields`	subset to these columns. (recommend to omit this and handle manually)

Details

Note that there are many common names for a given sci name

Value

a data.frame of common names by species queried. If multiple species are queried, The resulting data.frames are concatenated.

Examples

```
common_names("Bolbometopon muricatum")
```

`common_to_sci` *common_to_sci*

Description

Return a list of scientific names corresponding to given the common name(s).

Usage

```
common_to_sci(
  x,
  Language = "English",
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL
)
```

Arguments

`x`	a common name or list of common names
`Language`	a string specifying the language for the common name, e.g. "English"
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.

Details

If more than one scientific name matches the common name (e.g. "trout"), the function will simply return a list of all matching scientific names. If given more than one common name, the resulting strings of matching scientific names are simply concatenated.

Value

a character vector of scientific names

See Also

synonyms

Examples

```
common_to_sci(c("Bicolor cleaner wrasse", "humphead parrotfish"), Language="English")
common_to_sci(c("Coho Salmon", "trout"))
```

---

country *country*

Description

return a table of country for the requested species, as reported in FishBASE.org

Usage

```
country(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Examples

```
## Not run:
country("Bolbometopon muricatum")

## End(Not run)
```

`countrysub` *countrysub*

Description

return a table of countrysub for the requested species

Usage

```
countrysub(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Examples

```
## Not run:
countrysub(species_list(Genus='Labroides'))

## End(Not run)
```

`countrysubref` *countrysubref*

Description

return a table of countrysubref

Usage

```
countrysubref(
  server = getOption("FISHBASE_API", "fishbase"),
  version = get_latest_release(),
  db = default_db(),
  ...
)
```

Arguments

`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Examples

```
## Not run:
countrysubref()

## End(Not run)
```

`c_code` *c_code*

Description

return a table of country information for the requested c_code, as reported in FishBASE.org

Usage

```
c_code(
  c_code = NULL,
  server = getOption("FISHBASE_API", "fishbase"),
  version = get_latest_release(),
  db = default_db(),
  ...
)
```

Arguments

`c_code`	a C_Code or list of C_Codes (FishBase country code)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Examples

```
c_code(440)
```

`diet` *diet*

Description

diet

Usage

```
diet(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species diet

References

http://www.fishbase.org/manual/english/fishbasethe_diet_table.htm

Examples

```
## Not run:
diet()

## End(Not run)
```

`diet_items` *diet_items*

Description

diet_items

Usage

```
diet_items(...)
```

Arguments

`...`	additional arguments (not used)

Value

a table of diet_items

Examples

```
## Not run:
diet_items()

## End(Not run)
```

`ecology` *ecology*

Description

ecology

Usage

```
ecology(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Details

By default, will only return one entry (row) per species. Increase limit to get multiple returns for different stocks of the same species, though often data is either identical to the first or simply missing in the additional stocks.

Value

a table of species ecology data

References

http://www.fishbase.org/manual/english/fishbasethe_ecology_table.htm

Examples

```
## Not run:
ecology("Oreochromis niloticus")

## trophic levels and standard errors for a list of species
ecology(c("Oreochromis niloticus", "Salmo trutta"),
        fields=c("SpecCode", "FoodTroph", "FoodSeTroph", "DietTroph", "DietSeTroph"))

## End(Not run)
```

`ecosystem` *ecosystem*

Description

ecosystem

Usage

```
ecosystem(
  species_list = NULL,
  fields = NULL,
  server = getOption("FISHBASE_API", "fishbase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species ecosystems data

Examples

```
## Not run:
ecosystem("Oreochromis niloticus")

## End(Not run)
```

`estimate` *estimate*

Description

estimate

Usage

```
estimate(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
```

```
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of estimates from some models on trophic levels

References

http://www.fishbase.us/manual/English/FishbaseThe_FOOD_ITEMS_table.htm

Examples

```
## Not run:
estimate("Oreochromis niloticus")

## End(Not run)
```

`faoareas` *faoareas*

Description

return a table of species locations as reported in FishBASE.org FAO location data

Usage

```
faoareas(
  species_list = NULL,
  fields = NULL,
  server = getOption("FISHBASE_API", "fishbase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a tibble, empty tibble if no results found

Examples

```
faoareas()
```

`fb_tables` *List the tables available on fishbase/sealifebase*

Description

These table names can be used to access each of the corresponding tables using `[fb_tbl()]`. Please note that following RDB design, it is often necessary to join multiple tables. Other data cleaning steps are sometimes necessary as well.

Usage

```
fb_tables(server = c("fishbase", "sealifebase"), version = "latest")
```

Arguments

`server`	Access data from fishbase or sealifebase?
`version`	Version, see `available_releases()`

Examples

```
fb_tables()
```

`fb_tbl` *Access a fishbase or sealifebase table*

Description

Please note that rfishbase accesses static snapshots of the raw database tables used by FishBase and Sealifebase websites. Because these are static snapshots, they may lag behind the latest available information on the web interface, but should provide stable results.

Usage

```
fb_tbl(
  tbl,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  collect = TRUE
)
```

Arguments

`tbl`	table name, as it appears in the database. See `fb_tables()` for a list.
`server`	Access data from fishbase or sealifebase?
`version`	Version, see `available_releases()`
`db`	database connection, deprecated
`collect`	should we return an in-memory table? Generally best to leave as TRUE unless RAM is too limited. A remote table can be used with most dplyr functions (filter, select, joins, etc) to further refine.

Details

Please also note that the website pages are not organized precisely along the lines of these tables. A given page for a species may draw on data from multiple tables, and sometimes presents the data in a processed or summarized form. Following RDB design, it is often necessary to join multiple tables. Other data cleaning steps are sometimes necessary as well.

Examples

```
fb_tbl("species")
```

`fecundity` *fecundity*

Description

fecundity

Usage

```
fecundity(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species fecundity

Examples

```
## Not run:
fecundity("Oreochromis niloticus")

## End(Not run)
```

`fishbase`	*A table of all the the species found in FishBase, including taxonomic classification and the Species Code (SpecCode) by which the species is identified in FishBase.*

Description

A table of all the the species found in FishBase, including taxonomic classification and the Species Code (SpecCode) by which the species is identified in FishBase.

Author(s)

Carl Boettiger `<carl@ropensci.org>`

`fooditems`	*fooditems*

Description

fooditems

Usage

```
fooditems(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species fooditems

References

http://www.fishbase.org/manual/english/fishbasethe_food_items_table.htm

Examples

```
## Not run:
fooditems("Oreochromis niloticus")

## End(Not run)
```

---

genetics *genetics*

Description

genetics

Usage

```
genetics(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species genetics data

Examples

```
## Not run:
genetics("Oreochromis niloticus")
genetics("Labroides dimidiatus")

## End(Not run)
```

`introductions` *introductions*

Description

introductions

Usage

```
introductions(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species introductions data

Examples

```
## Not run:
introductions("Oreochromis niloticus")

## End(Not run)
```

`larvae` *larvae*

Description

larvae

Usage

```
larvae(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of larval data

Examples

```
## Not run:
larvae("Oreochromis niloticus")

## End(Not run)
```

`length_freq` *length_freq*

Description

return a table of species fooditems

Usage

```
length_freq(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of length_freq information by species; see details

References

http://www.fishbase.org/manual/english/lengthfrequency.htm

Examples

```
## Not run:
length_freq("Oreochromis niloticus")

## End(Not run)
```

`length_length` *length_length*

Description

return a table of lengths

Usage

```
length_length(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Details

This table contains relationships for the conversion of one length type to another for over 8,000 species of fish, derived from different publications, e.g. Moutopoulos and Stergiou (2002) and Gaygusuz et al (2006), or from fish pictures, e.g. Collette and Nauen (1983), Compagno (1984) and Randall (1997). The relationships, which always refer to centimeters, may consist either of a regression linking two length types, of the form: Length type (2) = a + b x Length type (1) Length type (2) = b' x Length type (1) The available length types are, as elsewhere in FishBase, TL = total length; FL = fork length; SL = standard length; WD = width (in rays); OT = other type (to be specified in the Comment field). When a version of equation (1) is presented, the length range, the number of fish used in the regression, the sex and the correlation coefficient are presented, if available. When a version of equation (2) is presented, the range and the correlation coefficient are omitted, as the ratio in (2) will usually be estimated from a single specimen, or a few fish covering a narrow range of lengths.

Note on column naming: The columns `Length1` and `Length2` follow FishBase's internal database convention, which may appear counterintuitive. `Length1` is the *unknown* length being predicted, and `Length2` is the *known* length used as the predictor. The formula is therefore: `Length1 = a + b * Length2`. This matches the FishBase website, which labels the columns "Unknown length" and "Known length" respectively.

Value

a table of lengths

References

http://www.fishbase.org/manual/english/PDF/FB_Book_CBinohlan_Length-Length_RF_JG.pdf

Examples

```
## Not run:
length_length("Oreochromis niloticus")

## End(Not run)
```

`length_weight` *length_weight*

Description

The LENGTH-WEIGHT table presents the a and b values of over 5,000 length-weight relationships of the form W = a x Lb, pertaining to about over 2,000 fish species.

Usage

```
length_weight(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Details

See references for official documentation. From FishBase.org: Length-weight relationships are important in fisheries science, notably to raise length-frequency samples to total catch, or to estimate biomass from underwater length observations. The units of length and weight in FishBase are centimeter and gram, respectively. Thus when length-weight relationships are not in cm-g, the intercept 'a' is transformed as follows:

a'(cm, g) = a (mm, g)*10^b a'(cm, g) = a (cm, kg)*1000 a'(cm, g) = a (mm, mg)*10^b/1000 a'(cm, g) = a (mm, kg)*10^b*1000

However, published length-weight relationships are sometimes difficult to use, as they may be based on a length measurement type (e.g., fork length) different from ones length measurements (expressed e.g., as total length). Therefore, to facilitate conversion between length types, an additional LENGTH-LENGTH table, #' presented below, was devised which presents linear regressions or ratios linking length types (e.g., FL vs. TL). We included a calculated field with the weight of a 10 cm fish (which should be in the order of 10 g for normal, fusiform shaped fish), to allow identification of gross errors, given knowledge of the body form of a species.

Value

a table of length_weight information by species; see details

References

http://www.fishbase.org/manual/english/fishbasethe_length_weight_table.htm

Examples

```
## Not run:
length_weight("Oreochromis niloticus")

## End(Not run)
```

`load_taxa` *load_taxa*

Description

Show scientific classification of taxa Note: species_names() is an alias for load taxa.

Usage

```
load_taxa(server = c("fishbase", "sealifebase"), version = "latest", ...)
```

Arguments

`server`	Either "fishbase" (the default) or "sealifebase"
`version`	the version of the database you want. Will default to the latest available; see `available_releases()`.
`...`	for compatibility with previous versions

Value

the taxa list

`maturity` *maturity*

Description

maturity

Usage

```
maturity(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species maturity

Examples

```
## Not run:
maturity("Oreochromis niloticus")

## End(Not run)
```

`morphology` *morphology*

Description

morphology

Usage

```
morphology(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species morphology data

Examples

```
 ## Not run:
morphology("Oreochromis niloticus")

## End(Not run)
```

`morphometrics` *morphometrics*

Description

morphometrics

Usage

```
morphometrics(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species morphometrics data

Examples

```
## Not run:
morphometrics("Oreochromis niloticus")

## End(Not run)
```

oxygen *oxygen*

Description

oxygen

Usage

```
oxygen(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species oxygen data

Examples

```
 ## Not run:
oxygen("Oreochromis niloticus")

## End(Not run)
```

`popchar` *popchar*

Description

Table of maximum length (Lmax), weight (Wmax) and age (tmax)

Usage

```
popchar(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Details

See references for official documentation. From FishBase.org: This table presents information on maximum length (Lmax), weight (Wmax) and age (tmax) from various localities where a species occurs. The largest values from this table are also entered in the SPECIES table. The POPCHAR table also indicates whether the Lmax, Wmax and tmax values or various combinations thereof refer to the same individual fish.

References

http://www.fishbase.org/manual/english/fishbasethe_popchar_table.htm

Examples

```
## Not run:
popchar("Oreochromis niloticus")

## End(Not run)
```

`popgrowth` *popgrowth*

Description

This table contains information on growth, natural mortality and length at first maturity, which serve as inputs to many fish stock assessment models. The data can also be used to generate empirical relationships between growth parameters or natural mortality estimates, and their correlates (e.g., body shape, temperature, etc.), a line of research that is useful both for stock assessment and for increasing understanding of the evolution of life-history strategies

Usage

```
popgrowth(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of population growth information by species; see details

References

http://www.fishbase.org/manual/english/fishbasethe_popgrowth_table.htm

Examples

```
## Not run:
popgrowth("Oreochromis niloticus")

## End(Not run)
```

---

popqb *popqb*

Description

popqb

Usage

```
popqb(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species popqb

References

http://www.fishbase.org/manual/english/fishbasethe_popqb_table.htm

Examples

```
## Not run:
popqb("Oreochromis niloticus")

## End(Not run)
```

`predators` *predators*

Description

predators

Usage

```
predators(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of predators

References

http://www.fishbase.org/manual/english/fishbasethe_predators_table.htm

Examples

```
## Not run:
predators("Oreochromis niloticus")

## End(Not run)
```

`ration` *ration*

Description

ration

Usage

```
ration(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species ration

References

http://www.fishbase.org/manual/english/fishbasethe_ration_table.htm

Examples

```
## Not run:
ration("Oreochromis niloticus")

## End(Not run)
```

`references` *references*

Description

references

Usage

```
references(
  codes = NULL,
  fields = NULL,
  server = getOption("FISHBASE_API", "fishbase"),
  version = get_latest_release(),
  db = default_db(),
  ...
)
```

Arguments

`codes`	One or more Fishbase reference numbers, matching the RefNo field
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a tibble (data.frame) of reference data

Examples

```
## Not run:
references(codes = 1)
references(codes = 1:6)
references(codes = 1:6, fields = c('Author', 'Year', 'Title'))
references() # all references

## End(Not run)
```

`reproduction` *reproduction*

Description

reproduction

Usage

```
reproduction(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species reproduction

Examples

```
## Not run:
reproduction("Oreochromis niloticus")

## End(Not run)
```

`sealifebase` *A table of all the the species found in SeaLifeBase, including taxonomic classification and the Species Code (SpecCode) by which the species is identified in SeaLifeBase*

Description

A table of all the the species found in SeaLifeBase, including taxonomic classification and the Species Code (SpecCode) by which the species is identified in SeaLifeBase

Author(s)

Carl Boettiger <`carl@ropensci.org`>

`spawning` *spawning*

Description

spawning

Usage

```
spawning(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species spawning

Examples

```
## Not run:
spawning("Oreochromis niloticus")

## End(Not run)
```

`species` *species*

Description

Provide wrapper to work with species lists.

Usage

```
species(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Details

The Species table is the heart of FishBase. This function provides a convenient way to query, tidy, and assemble data from that table given an entire list of species. For details, see: http://www.fishbase.org/manual/english/fishb

Species scientific names are defined according to fishbase taxonomy and nomenclature.

Value

a data.frame with rows for species and columns for the fields returned by the query (FishBase 'species' table)

Examples

```
## Not run:

species(c("Labroides bicolor", "Bolbometopon muricatum"))


## End(Not run)
```

`species_by_ecosystem` *Species list by ecosystem*

Description

Species list by ecosystem

Usage

```
species_by_ecosystem(
  ecosystem,
  species_list = NULL,
  server = getOption("FISHBASE_API", "fishbase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`ecosystem`	(character) an ecosystem name
`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species ecosystems data

Examples

```
## Not run:
species_by_ecosystem(ecosystem = "Arctic", server = "sealifebase")

## End(Not run)
```

`species_names` *species_names*

Description

Show scientific classification of taxa Note: species_names() is an alias for load_taxa().

Usage

```
species_names(server = c("fishbase", "sealifebase"), version = "latest", ...)
```

Arguments

`server`	Either "fishbase" (the default) or "sealifebase"
`version`	the version of the database you want. Will default to the latest available; see `available_releases()`.
`...`	for compatibility with previous versions

Value

the taxa list

`speed` *speed*

Description

speed

Usage

```
speed(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species speed data

Examples

```
## Not run:
speed("Oreochromis niloticus")

## End(Not run)
```

`stocks` *stocks*

Description

stocks

Usage

```
stocks(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".

`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species stocks data

Examples

```
## Not run:
stocks("Oreochromis niloticus")

## End(Not run)
```

`swimming` *swimming*

Description

swimming

Usage

```
swimming(
  species_list = NULL,
  fields = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`fields`	subset to these columns. (recommend to omit this and handle manually)
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a table of species swimming data

Examples

```
## Not run:
swimming("Oreochromis niloticus")

## End(Not run)
```

`synonyms` *synonyms*

Description

Check for alternate versions of a scientific name

Usage

```
synonyms(
  species_list = NULL,
  server = c("fishbase", "sealifebase"),
  version = "latest",
  db = NULL,
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Details

For further information on fields returned, see: http://www.fishbase.org/manual/english/fishbasethe_synonyms_table.htm

Value

A table with information about the synonym. Will generally be only a single row if a species name is given. If a FishBase SpecCode is given, all synonyms matching that SpecCode are shown, and the table indicates which one is Valid for FishBase. This may or may not match the valid name for Catalog of Life (Col), also shown in the table. See examples for details.

`validate_names` *validate_names*

Description

Check for alternate versions of a scientific name and return the scientific names FishBase recognizes as valid

Usage

```
validate_names(
  species_list,
  server = getOption("FISHBASE_API", "fishbase"),
  version = get_latest_release(),
  db = default_db(),
  ...
)
```

Arguments

`species_list`	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
`server`	Either "fishbase" or "sealifebase".
`version`	a version string for the database. See `available_releases()` for details.
`db`	database connection, now deprecated.
`...`	additional arguments, currently ignored

Value

a string of the validated names

Examples

```
validate_names("Abramites ternetzi")
```

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