

# Package ‘rfishbase’

April 7, 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

**License** CC0

**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

**RoxygenNote** 7.3.3

**Language** en-US

**NeedsCompilation** no

**Author** Carl Boettiger [cre, aut] (ORCID:  
<<https://orcid.org/0000-0002-1642-628X>>),  
Scott Chamberlain [aut] (ORCID:  
<<https://orcid.org/0000-0003-1444-9135>>),  
Duncan Temple Lang [aut],  
Peter Wainwright [aut],  
Kevin Cazelles [ctb] (ORCID: <<https://orcid.org/0000-0001-6619-9874>>),  
Guohuan Su [ctb] (ORCID: <<https://orcid.org/0000-0003-0091-9773>>)

**Maintainer** Carl Boettiger <cboettig@gmail.com>

**Repository** CRAN

**Date/Publication** 2026-04-07 05:10:16 UTC

## Contents

available_releases . . . . .	3
brains . . . . .	3
common_names . . . . .	4
common_to_sci . . . . .	5
country . . . . .	6
countrysub . . . . .	7
countrysubref . . . . .	7
c_code . . . . .	8
diet . . . . .	9
diet_items . . . . .	10
ecology . . . . .	10
ecosystem . . . . .	11
estimate . . . . .	12
faoareas . . . . .	13
fb_tables . . . . .	14
fb_tbl . . . . .	15
fecundity . . . . .	16
fishbase . . . . .	17
fooditems . . . . .	17
genetics . . . . .	18
introductions . . . . .	19
larvae . . . . .	20
length_freq . . . . .	21
length_length . . . . .	22
length_weight . . . . .	23
load_taxa . . . . .	24
maturity . . . . .	25
morphology . . . . .	26
morphometrics . . . . .	27
oxygen . . . . .	28
popchar . . . . .	29
popgrowth . . . . .	30
popqb . . . . .	31
predators . . . . .	32
ration . . . . .	33
references . . . . .	34
reproduction . . . . .	35
sealifebase . . . . .	36
spawning . . . . .	36
species . . . . .	37
species_by_ecosystem . . . . .	38
species_names . . . . .	39
speed . . . . .	39
stocks . . . . .	40
swimming . . . . .	41
synonyms . . . . .	42

<i>available_releases</i>	3
<i>validate_names</i> . . . . .	43
<b>Index</b>	<b>44</b>

---

<i>available_releases</i>	<i>List available releases</i>
---------------------------	--------------------------------

---

### **Description**

List available releases

### **Usage**

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

### **Arguments**

server            fishbase or sealifebase

### **Examples**

```
available_releases()
```

---

<i>brains</i>	<i>brains</i>
---------------	---------------

---

### **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 <a href="#">available_releases()</a> 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	<i>common names</i>
--------------	---------------------

---

**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 <a href="#">available_releases()</a> 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	<i>common_to_sci</i>
---------------	----------------------

---

**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 <a href="#">available_releases()</a> 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	<i>country</i>
---------	----------------

---

**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**

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

**Examples**

```

## Not run:
countrysubref()

## End(Not run)

```

---

c_code	<i>c_code</i>
--------	---------------

---

**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 <a href="#">available_releases()</a> for details.
db	database connection, now deprecated.
...	additional arguments, currently ignored

**Examples**

```
c_code(440)
```

---

diet	<i>diet</i>
------	-------------

---

**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 <a href="#">available_releases()</a> 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](http://www.fishbase.org/manual/english/fishbasethe_diet_table.htm)

**Examples**

```
## Not run:
diet()

## End(Not run)
```

---

diet_items	<i>diet_items</i>
------------	-------------------

---

**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	<i>ecology</i>
---------	----------------

---

**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 <a href="#">available_releases()</a> 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](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**

<code>species_list</code>	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
<code>fields</code>	subset to these columns. (recommend to omit this and handle manually)
<code>server</code>	Either "fishbase" or "sealifebase".
<code>version</code>	a version string for the database. See <a href="#">available_releases()</a> for details.
<code>db</code>	database connection, now deprecated.
<code>...</code>	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 <a href="#">available_releases()</a> 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](http://www.fishbase.us/manual/English/FishbaseThe_FOOD_ITEMS_table.htm)

### Examples

```

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

## End(Not run)

```

---

faoareas	<i>faoareas</i>
----------	-----------------

---

### 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 <a href="#">available_releases()</a> 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 <a href="#">available_releases()</a>

**Examples**

```
fb_tables()
```

---

fb_tbl	<i>Access a fishbase or sealifebase table</i>
--------	---

---

### 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 <a href="#">fb_tables()</a> for a list.
server	Access data from fishbase or sealifebase?
version	Version, see <a href="#">available_releases()</a>
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	<i>fecundity</i>
-----------	------------------

---

### 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 <a href="#">available_releases()</a> 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	<i>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.</i>
----------	---

---

**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	<i>fooditems</i>
-----------	------------------

---

**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 <a href="#">available_releases()</a> 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](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 <a href="#">available_releases()</a> 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	<i>introductions</i>
---------------	----------------------

---

## 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 <a href="#">available_releases()</a> 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	<i>larvae</i>
--------	---------------

---

## Description

larvae

## Usage

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

## Arguments

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

## Value

a table of larval data

## Examples

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

---

length_freq	<i>length_freq</i>
-------------	--------------------

---

**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 <a href="#">available_releases()</a> 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	<i>length_length</i>
---------------	----------------------

---

### 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 <a href="#">available_releases()</a> 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](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	<i>length_weight</i>
---------------	----------------------

---

**Description**

The LENGTH-WEIGHT table presents the a and b values of over 5,000 length-weight relationships of the form  $W = a \times L^b$ , 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 <a href="#">available_releases()</a> 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:

$$a'(cm, g) = a(mm, g) \cdot 10^b \quad a'(cm, g) = a(cm, kg) \cdot 1000 \quad a'(cm, g) = a(mm, mg) \cdot 10^b / 1000 \quad a'(cm, g) = a(mm, kg) \cdot 10^b / 1000$$

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](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 <a href="#">available_releases()</a> .
...	for compatibility with previous versions

**Value**

the taxa list

---

maturity	<i>maturity</i>
----------	-----------------

---

**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 <a href="#">available_releases()</a> 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 <a href="#">available_releases()</a> 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	<i>morphometrics</i>
---------------	----------------------

---

## 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 <a href="#">available_releases()</a> 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	<i>oxygen</i>
--------	---------------

---

## Description

oxygen

## Usage

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

## Arguments

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

## Value

a table of species oxygen data

## Examples

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

---

popchar	<i>popchar</i>
---------	----------------

---

## 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 <a href="#">available_releases()</a> 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](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

<code>species_list</code>	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
<code>fields</code>	subset to these columns. (recommend to omit this and handle manually)
<code>server</code>	Either "fishbase" or "sealifebase".
<code>version</code>	a version string for the database. See <a href="#">available_releases()</a> for details.
<code>db</code>	database connection, now deprecated.
<code>...</code>	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](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**

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

**Value**

a table of species popqb

**References**

[http://www.fishbase.org/manual/english/fishbasethe\\_popqb\\_table.htm](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**

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

**Value**

a table of predators

**References**

[http://www.fishbase.org/manual/english/fishbasethe\\_predators\\_table.htm](http://www.fishbase.org/manual/english/fishbasethe_predators_table.htm)

**Examples**

```

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

## End(Not run)

```

---

ration	<i>ration</i>
--------	---------------

---

## 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 <a href="#">available_releases()</a> 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](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 <a href="#">available_releases()</a> 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	<i>reproduction</i>
--------------	---------------------

---

## 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 <a href="#">available_releases()</a> 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	<i>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</i>
-------------	--

---

**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	<i>spawning</i>
----------	-----------------

---

**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 <a href="#">available_releases()</a> 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	<i>species</i>
---------	----------------

---

**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 <a href="#">available_releases()</a> 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 <a href="#">available_releases()</a> 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	<i>species_names</i>
---------------	----------------------

---

**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 <a href="#">available_releases()</a> .
...	for compatibility with previous versions

**Value**

the taxa list

---

speed	<i>speed</i>
-------	--------------

---

**Description**

speed

**Usage**

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

**Arguments**

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

<code>species_list</code>	A vector of scientific names (each element as "genus species"). If empty, a table for all fish will be returned.
<code>fields</code>	subset to these columns. (recommend to omit this and handle manually)
<code>server</code>	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	<i>swimming</i>
----------	-----------------

---

**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**

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

**Details**

For further information on fields returned, see: [http://www.fishbase.org/manual/english/fishbasethe\\_synonyms\\_table.htm](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	<i>validate_names</i>
----------------	-----------------------

---

**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 <a href="#">available_releases()</a> for details.
db	database connection, now deprecated.
...	additional arguments, currently ignored

**Value**

a string of the validated names

**Examples**

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

# Index

## \* data

- fishbase, 17
- sealifebase, 36
- available\_releases, 3
- available\_releases(), 4–9, 11–23, 25–43
- brains, 3
- c\_code, 8
- common\_names, 4
- common\_to\_sci, 5
- country, 6
- countrysub, 7
- countrysubref, 7
- diet, 9
- diet\_items, 10
- ecology, 10
- ecosystem, 11
- estimate, 12
- faoareas, 13
- fb\_tables, 14
- fb\_tables(), 15
- fb\_tbl, 15
- fecundity, 16
- fishbase, 17
- fooditems, 17
- genetics, 18
- introductions, 19
- larvae, 20
- length\_freq, 21
- length\_length, 22
- length\_weight, 23
- load\_taxa, 24
- maturity, 25
- morphology, 26
- morphometrics, 27
- oxygen, 28
- popchar, 29
- popgrowth, 30
- poplf (length\_freq), 21
- popll (length\_length), 22
- poplw (length\_weight), 23
- popqb, 31
- predators, 32
- ration, 33
- references, 34
- reproduction, 35
- sci\_to\_common (common\_names), 4
- sealifebase, 36
- spawning, 36
- species, 37
- species\_by\_ecosystem, 38
- species\_names, 39
- speed, 39
- stocks, 40
- swimming, 41
- synonyms, 6, 42
- validate\_names, 43