

Package ‘rfishbase’

July 2, 2014

Description A programmatic interface to fishbase.org.

Title R Interface to FishBASE

Version 0.2-2

License CC0

Date 2012

URL <https://github.com/ropensci/rfishbase>

BugReports <https://github.com/ropensci/rfishbase/issues>

Depends R (>= 2.10)

Imports XML, RCurl (>= 1.6)

Suggests testthat

Author Carl Boettiger [aut, cre],Duncan Temple Lang [aut],Peter C. Wainwright [aut]

Maintainer Carl Boettiger <cboettig@gmail.com>

NeedsCompilation no

Repository CRAN

Date/Publication 2014-01-07 07:28:59

R topics documented:

familySearch	2
findSpecies	3
fish.data	3
fish_names	4
getDepth	4
getEnviroClimateRange	5
getIds	6
getLengthWeight	6

getMetabolism	7
getPictures	7
getQuantTraits	8
getRefs	9
getSize	9
getTrophicLevel	10
habitatSearch	11
labridtree	11
loadCache	12
updateCache	12
which_fish	13
Index	15

familySearch	<i>A function to find all fish that are members of a scientific Family</i>
--------------	--

Description

deprecated, see which_fish

Usage

```
familySearch(family, fish.data = NULL)
```

Arguments

family	The scientific family name. Can include grep matching, see examples
fish.data	the fishbase database or a subset

Details

The return value can be summed to give the number of matches, can be used as an index, e.g. fish.data[goby], to return the matches or to pass to another function. See examples.

Value

a logical vector of length(fish.data) indicating the matches.

findSpecies	Returns the matching indices in the data given a list of species names
-------------	--

Description

Returns the matching indices in the data given a list of species names

Usage

```
findSpecies(species, fish.data = NULL, path = NULL)
```

Arguments

species	a list of species names as "Genus_species" or "Genus species"
fish.data	the fishbase database or a subset
path	to cached copy of fishbase (optional, defaults to copy in package).

Details

underscores are removed automatically. Later versions may check names

Value

a logical vector of length(fish.data) indicating the matches, that can be used to subset the full database in calls to other functions.

Examples

```
## The distribution of maximum depth in Arctic fishes
data(fishbase)
data(labridtree)
myfish <- findSpecies(labridtree$tip.label, fish.data)
getDepth(fish.data[myfish])
```

fish.data	A cached copy of extracted FishBase data, 14 Febuary 2013.
-----------	--

Description

A cached copy of extracted FishBase data, 14 Febuary 2013.

Format

NULL

References

Froese, R. and D. Pauly. Editors. 2011. FishBase. World Wide Web electronic publication. www.fishbase.org, version (10/2011).

fish_names	<i>Return the scientific names, families, classes, or orders of the input data</i>
------------	--

Description

Return the scientific names, families, classes, or orders of the input data

Usage

```
fish_names(fish.data = NULL, name = c("ScientificName", "Family", "Class",
  "Order"), path = NULL)
```

Arguments

name	return the Scientific Name or Family, Class, or Order.
fish.data	the fishbase database fish.data or a subset. Defaults to cached copy
path	to updated copy of the cache; optional.

Value

the names of the matching fish.

Examples

```
data(fishbase)
sex_swap <- which_fish("change sex", using="lifecycle", fish.data)
africa <- which_fish("Africa", using="distribution", fish.data)
fish_names(fish.data[africa & sex_swap])
```

getDepth	<i>Returns available depth range data</i>
----------	---

Description

Returns available depth range data

Usage

```
getDepth(fish.data = NULL, path = NULL)
```

Arguments

fish.data the fishbase database or a subset
path to cached copy of fishbase (optional, defaults to copy in package).

Value

a matrix of traits by fish. Returns min-max depth, min-max usual depth

Examples

```
## The distribution of maximum depth in Arctic fishes  
data(fishbase)  
arctic <- which_fish(" Arctic ", "distribution", fish.data)  
traits <- getDepth(fish.data[arctic])  
hist(traits[, "deep"])
```

getEnviroClimateRange *get the Environment, Climate, and Range of a species.*

Description

get the Environment, Climate, and Range of a species.

Usage

```
getEnviroClimateRange(fish.data = NULL, path = NULL)
```

Arguments

fish.data the fishbase database fish.data or a subset,
path to cached copy of fishbase (optional, defaults to copy in package).

Value

a list of the values in the Enviroment / Climate / Range data. See <https://github.com/ropensci/rfishbase/issues/13>

Examples

```
## Not run:  
library(rfishbase)  
data(fishbase)  
out <- getEnviroClimateRange(fish.data[1:3])  
cat(out[[1]]) # cat for pretty printing  
  
## End(Not run)
```

getIds	<i>get fishbase id numbers</i>
--------	--------------------------------

Description

get fishbase id numbers

Usage

```
getIds(fish.data = NULL, path = NULL)
```

Arguments

fish.data	the fishbase database fish.data or a subset,
path	to cached copy of fishbase (optional, defaults to copy in package).

Value

the ids numbers corresponding to positions along fish.data object in use

getLengthWeight	<i>get the length weight table</i>
-----------------	------------------------------------

Description

Gets the length weight table into R. (e.g. this table: <http://www.fishbase.org/PopDyn/LWRRelationshipList.php?ID=2&Genus>)

Usage

```
getLengthWeight(fish.data = NULL, path = NULL)
```

Arguments

fish.data	the fishbase database fish.data or a subset,
path	to cached copy of fishbase (optional, defaults to copy in package).

Value

a list of tables for each species given.

getMetabolism	<i>get metabolism table (oxygen consumption).</i>
---------------	---

Description

See the "Metabolism" page on Fishbase for the speices for details.

Usage

```
getMetabolism(fish.data = NULL, path = NULL)
```

Arguments

fish.data	the fishbase database fish.data or a subset,
path	to cached copy of fishbase (optional, defaults to copy in package).

Details

See example online table for details: <http://www.fishbase.org/physiology/OxygenDataList.php?ID=2&GenusName=Oreochromis>

Value

A list of tables with an entry for each fish in fish.data.

Examples

```
## Not run:  
data(fishbase)  
getMetabolism(fish.data[1])  
  
## End(Not run)
```

getPictures	<i>getPictures from the fishbase database</i>
-------------	---

Description

get urls of fishbase images given a genus and species

Usage

```
getPictures(scientific_name, type = c("adult", "juvenile", "larvae",  
  "stamps"), what = c("actual", "thumbnail", "author"), download = FALSE,  
  ...)
```

Arguments

scientific_name	the space-separated genus and species names
type	the kind of photo requested: adult, juvenile, larvae, or stamps.
what	character specifying what to return: actual image, thumbnail, or author name?
download	logical, download to working directory?
...	additional options to download.file

Value

list of image urls. If download=TRUE, will also download images to working directory.

getQuantTraits	<i>Returns all quantitative trait values found in the morphology data</i>
----------------	---

Description

Returns all quantitative trait values found in the morphology data

Usage

```
getQuantTraits(fish.data = NULL, path = NULL)
```

Arguments

fish.data	the fishbase database or a subset
path	to cached copy of fishbase (optional, defaults to copy in package).

Value

a matrix of traits by fish. Returns min-max numbers recorded for vertebrae, spines (anal and dorsal), and rays (anal and dorsal).

Examples

```
data(fishbase)
## The distribution of anal ray fins in red-colored fish
redfish <- which_fish(" red ", "diagnostic", fish.data)
traits <- getQuantTraits(fish.data[redfish])
hist(traits[, "min.anal.rays"])
```

getRefs	<i>Returns the FishBase reference id numbers matching a query.</i>
---------	--

Description

Returns the FishBase reference id numbers matching a query.

Usage

```
getRefs(using = c("trophic", "habitat", "lifecycle", "morphology",  
  "diagnostic", "distribution", "ScientificName", "Genus", "Family", "Class",  
  "Order", "size"), fish.data = NULL, path = NULL)
```

Arguments

using	which entry type for the search
fish.data	the fishbase database or a subset
path	to cached copy of fishbase (optional, defaults to copy in package).

Examples

```
data(fishbase)  
a <- which_fish("invertebrates", "trophic")  
refs <- getRefs("trophic", fish.data[a])  
toprefs <- sort(table(unlist(refs)), decreasing=TRUE)
```

getSize	<i>Returns available size data of specified type (length, weight, or age)</i>
---------	---

Description

Returns available size data of specified type (length, weight, or age)

Usage

```
getSize(fish.data = NULL, value = c("length", "weight", "age"),  
  path = NULL)
```

Arguments

fish.data	the fishbase database or a subset
value	the measure to return: maximum recorded length (cm), maximum weight (g), or maximum age (years). Defaults to length; many entries lack weight and age.
path	to updated copy of the cache; optional.

Value

a numeric vector of length(fish.data) with the values requested

Examples

```
data(fishbase)
yr <- getSize(fish.data, "age")
hist(yr, breaks=40, main="Age Distribution", xlab="age (years)");
nfish <- length(fish.data)
```

getTrophicLevel	<i>get trophic level</i>
-----------------	--------------------------

Description

get a quantitative estimate of the trophic level for the species requested. See the "Ecology" page on Fishbase for the speices.

Usage

```
getTrophicLevel(fish.data = NULL, path = NULL, as_table = FALSE,
  from = c("diet composition", "individual food items"), unfished = FALSE,
  justSE = FALSE, justReference = FALSE)
```

Arguments

fish.data	the fishbase database fish.data or a subset,
path	to cached copy of fishbase (optional, defaults to copy in package).
as_table	logical. if True, returns the whole table. Otherwise (default), returns the element from the table that is specified by the other options.
from	use the diet composition or the individual food items? See fishbase.org for details on these differences. Both may or may not be available.
unfished	return the estimate for unfished population (default FALSE). See fishbase.org for details.
justSE	return the standard deviation to the estimated trophic level. If FALSE, returns the estimated value, so you must use two calls, or use as_table=TRUE, to get both values.
justReference	logical. return the reference used for estimation (without other data).

Value

depends on the arguments given above. Default is to return the (fished) diet composition estimate (often used as the default in fishbase.org).

habitatSearch	<i>A function to search for the occurrences of any keyword in habitat description</i>
---------------	---

Description

deprecated, see which_fish

Usage

```
habitatSearch(keyword, fish.data = NULL)
```

Arguments

keyword	pattern to be used by grep
fish.data	the fishbase database fish.data or a subset,

Details

Deprecated. This functionality is provided by which_fish.

Value

a logical vector of length(fish.data) indicating the matches, that can be used to subset the full database in calls to other functions.

labridtree	<i>An example phylogeny of labrid fish</i>
------------	--

Description

An example phylogeny of labrid fish

Format

NULL

References

Price, S. a, Wainwright, P. C., Bellwood, D. R., Kazancioglu, E., Collar, D. C., & Near, T. J. (2010). Functional innovations and morphological diversification in parrotfishes. *Evolution; international journal of organic evolution*, 3057-3068. doi:10.1111/j.1558-5646.2010.01036.x

loadCache	<i>Load an updated cache</i>
-----------	------------------------------

Description

Load an updated cache

Usage

```
loadCache(path = NULL)
```

Arguments

path location where cache is located

Value

loads the object fish.data into the working space.

See Also

[updateCache](#)

Examples

```
## Not run:  
updateCache()  
loadCache()  
  
## End(Not run)
```

updateCache	<i>Update the cached copy of fishbase data</i>
-------------	--

Description

Update the cached copy of fishbase data

Usage

```
updateCache(path = ".")
```

Arguments

path where cache should be stored. (default to working directory)

Details

the update is slow, avoiding straining the server or client. please allow this call to run overnight for a complete upgrade.

Value

a date-fishdata.Rdat file.

See Also

[loadCache](#)

Examples

```
## Not run:
  updateCache()
  loadCache()

## End(Not run)
```

which_fish	<i>which_fish is the the generic search function for fishbase a variety of description types</i>
------------	--

Description

which_fish is the the generic search function for fishbase a variety of description types

Usage

```
which_fish(keyword, using = c("trophic", "habitat", "lifecycle", "morphology",
  "diagnostic", "distribution", "ScientificName", "Genus", "Family", "Class",
  "Order", "size", "all"), fish.data = NULL, path = NULL)
```

Arguments

keyword	pattern to be used by grep
using	the type of search, one of: "trophic", "habitat", "lifecycle", "morphology", "diagnostic", "distribution", "ScientificName", "Genus", "Family", "Class", "Order", or "size" See examples.
fish.data	the fishbase database fish.data or a subset
path	to cached copy of fishbase (optional, defaults to copy in package).

Value

a logical vector of length(fish.data) indicating the matches.

See Also

fish_names

Examples

```
data(fishbase)
invert <- which_fish("invertebrate|mollusk", using="trophic", fish.data)
fish_names(fish.data[invert])
sex_swap <- which_fish("change sex", using="lifecycle", fish.data)
africa <- which_fish("Africa", using="distribution", fish.data)
## recall we can sub-set
fish_names(fish.data[africa & sex_swap])
reef <- which_fish("reef", "habitat", fish.data)
redfish <- which_fish(" red ", "diagnostic", fish.data)
bluefish <- which_fish(" blue ", "diagnostic", fish.data)
sum(redfish) > sum(bluefish)
```

Index

- *Topic **cache**
 - loadCache, [12](#)
 - updateCache, [12](#)
- *Topic **datasets**
 - fish.data, [3](#)
 - labridtree, [11](#)
- *Topic **data**
 - fish.data, [3](#)
 - labridtree, [11](#)
- *Topic **utilities**
 - familySearch, [2](#)
 - findSpecies, [3](#)
 - fish_names, [4](#)
 - getQuantTraits, [8](#)
 - getRefs, [9](#)
 - getSize, [9](#)
 - habitatSearch, [11](#)
 - which_fish, [13](#)

- familySearch, [2](#)
- findSpecies, [3](#)
- fish.data, [3](#)
- fish_names, [4](#)

- getDepth, [4](#)
- getEnviroClimateRange, [5](#)
- getIds, [6](#)
- getLengthWeight, [6](#)
- getMetabolism, [7](#)
- getPictures, [7](#)
- getQuantTraits, [8](#)
- getRefs, [9](#)
- getSize, [9](#)
- getTrophicLevel, [10](#)

- habitatSearch, [11](#)

- labridtree, [11](#)
- loadCache, [12](#), [13](#)

- updateCache, [12](#), [12](#)

- which_fish, [13](#)