

# Package ‘dietr’

November 13, 2019

**Version** 1.0

**Date** 2019-10-17

**Title** Diet Estimated Trophic Levels

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**Depends** R (>= 3.5)

**Imports** rfishbase (>= 3.0)

**Description** Estimates fractional trophic level from quantitative and qualitative diet data and calculates electivity indices in R. Froese & Pauly (2000, ISBN: 9718709991).

**License** GPL (>= 2)

**LazyData** true

**RoxygenNote** 6.1.1

**Encoding** UTF-8

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**URL** <https://github.com/sborstein/dietr>

**BugReports** <https://github.com/sborstein/dietr/issues>

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2019-11-13 18:10:02 UTC

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|---------------------|--|
| ConvertFishbaseDiet | <i>Converts FishBase/SealifBase diet data obtained from rfishbase for use with dietr</i> |
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### Description

This converts diet data from rfishbase into a format usable with dietr.

### Usage

```
ConvertFishbaseDiet(ExcludeStage = NULL)
```

### Arguments

**ExcludeStage** a character vector, indicating which life stages to exclude. Must match stage names given by rfishbase (i.e. larvae, rec./juveniles, juv./adults, adults).

### Details

As of rfishbase 3.0, the package handles returning diet data differently than in previous versions. As currently implemented, rfishbase returns two different unjoined diet tables, one with the actual diet items and their percent contribution in the diet, and another that has the metadata for the diet record. This unfortunately is a difficult format to work with and easily extract out species of interest. Additionally, in previous versions you could specify species names or numbers and only return those of interest, the only function options in the current version are specifying a server. As such, if the function is run, it will return all diet data on the site, requiring users to subset out those of interest for them. We have implemented in this function a way to join the tables for use as well as filter based on life history stage (if necessary).

### Value

a list of length two, with two data frames. One containing the re-formatted diet items and their contributions and one containing the Taxonomy with species names.

### Author(s)

Samuel Borstein

**Examples**

```
#Convert Fishbase Diet Data
my.diets <- ConvertFishbaseDiet(ExcludeStage=NULL)
#Convert Fishbase Diet Data and exclude juvenile and larval records
my.diets <- ConvertFishbaseDiet(ExcludeStage=c("recruits/juv.", "larvae"))
```

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|                     |  |
|---------------------|--|
| ConvertFishbaseFood | <i>Converts FishBase/SealifBase food item diet data obtained from the diet function into a usable format for dietr</i> |
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**Description**

Converts FishBase/SealifBase food item diet data obtained from the diet function into a usable format for dietr

**Usage**

```
ConvertFishbaseFood(FishBaseFood, ExcludeStage = NULL)
```

**Arguments**

|              |   |
|--------------|---|
| FishBaseFood | a data frame produced by the rfishbase fooditem function  |
| ExcludeStage | a character, indicating which life stages to exclude. Must match stage names given by rfishbase (i.e. larvae, rec./juveniles, juv./adults, adults). |

**Details**

This converts the data frame produced by rfishbase fooditem function into a usable format for dietr.

**Value**

a list of length two, with two data frames. One containing the re-formatted food item data and one containing the Taxonomy with species names.

**Author(s)**

Samuel Borstein

**Examples**

```
#Get rfishbase food item data for a few species
my.food <- rfishbase::fooditems(c("Lutjanus apodus", "Epinephelus itajara"))
#use the ConvertFishbaseFood function to format it for dietr and exclude recruits/juveniles
cleaned.food <- ConvertFishbaseFood(FishBaseFood=my.food, ExcludeStage=c("larvae", "recruits/juv."))
```

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CortesPreyVals      *CortesPreyVals*

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**Description**

A data frame containing prey items and their respective trophic levels for Chondrichthyes prey from Cortes, 1999

**Usage**

CortesPreyVals

**Format**

A data frame of of 10 rows and 6 columns

- FoodI: Food category I.
- FoodII: Food category II.
- FoodIII: Food category III.
- Stage: Life history stage of the prey item.
- TL: Trophic level of the prey item.
- SE: Standard error around trophic level estimate of the prey item.

**References**

- Cortes E. 1999. Standardized diet compositions and trophic levels of sharks. ICES Journal of marine science 56:707-717.

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dietr      *Diet Estimated Trophic Levels in R*

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**Description**

Estimates fractional trophic level from quantitative and qualitative diet data and calculates electivity indices in R.

**Details**

Package: dietr

Type: Package

Title: An R package to estimate trophic level from diet and food item data

Version: 1.0

Date: 2019-10-17

License: GPL (>= 2)

This package allows users to calculate trophic levels from proportional diet data or from food items given trophic levels of the prey items. This package calculates trophic level following the procedures from TrophLab, which was a microsoft access program. This implementation is faster than the original microsoft access program and also allows for a hierarchical estimation of trophic level given a corresponding "taxonomy" data frame (i.e. estimate trophic level for a individual, population, species, etc.).

**Author(s)**

Samuel Borstein Maintainer: Samuel Borstein <sborstei@vols.utk.edu>

**See Also**

[Electivity](#), [ConvertFishbaseFood](#), [DietTroph](#), [FoodTroph](#)

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|-----------|--|
| DietTroph | <i>Calculates trophic level from percentage based quantitative diet data (volumetric, weight, etc.) for species, populations, and individuals.</i> |
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**Description**

Calculates trophic level from percentage based diet data following the routine described in TrophLab. While FishBase data obtained from rfishbase can be used, users can also upload their own data for use in with function (see vignette for a tutorial).

**Usage**

```
DietTroph(DietItems, PreyValues, Taxonomy, PreyClass = c("FoodI",
  "FoodII", "FoodIII", "Stage"), SumCheck = TRUE)
```

**Arguments**

|           |   |
|-----------|---|
| DietItems | A data frame with rows as individual entries and each row consisting of a prey classification and a corresponding diet percentages. The column names for prey classification of the diets should match those of PreyValues. The first column should contain the identifier of the individual and be named "Individual", The last column should contain the percent of the prey in the diet and be labelled "Percent". |
|-----------|---|

|            |   |
|------------|---|
| PreyValues | a data frame with rows as prey item names and columns containing the trophic level of the prey item and the standard error of that trophic item. The column names of PreyValues except for TL and SE should match those in DietItems. |
| Taxonomy   | a data frame starting with the least inclusive level progressing to more inclusive moving towards the right.  |
| PreyClass  | Column names of the PreyValues used for matching between DietItems and PreyValues, exclusive of TL and SE. Default is those of FishBase.  |
| SumCheck   | Logical. Should the sum of diet items be checked, and, if not equal to 100, recalculated?   |

**Value**

a list length of the columns in taxonomy, each containing trophic level estimation at the respective taxonomic level.

**Author(s)**

Samuel Borstein

**Examples**

```
#Get some food item data from rfishbase
library(rfishbase)
#convert FishBase data into data for trophic calculation using dietr
converted.diet <- ConvertFishbaseDiet(ExcludeStage=NULL)
#Subset three studies out, as this contains all studies from FishBase
my.diets <- converted.diet$DietItems[1:26,]
my.taxonomy <- converted.diet$Taxonomy[1:3,]
#Load Prey Values
data(FishBasePreyVals)
#Calculate Trophic Levels
my.TL <- DietTroph(DietItems = my.diets,PreyValues = FishBasePreyVals, Taxonomy =
my.taxonomy, PreyClass=c("FoodI","FoodII","FoodIII","Stage"))
```

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Electivity

*Calculates a variety of electivity indices and foraging ratios*

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**Description**

This function calculates the forage ratio and a variety of electivity indices. Included indices include Ivlev's (1961), Strauss' (1979), Jacob's Q and D (1974), Chesson's (1983)(Which is similar to Manly's Alpha (1974)), and Vanderploeg & Scavia (1979).

**Usage**

```
Electivity(Diet, Available, Indices = c("ForageRatio", "Ivlev",
  "Strauss", "JacobsQ", "JacobsD", "Chesson", "VanderploegScavia"),
  LogQ = TRUE, Depleting = FALSE)
```

**Arguments**

|           |   |
|-----------|---|
| Diet      | Data frame with data corresponding to consumed resources found in the diet. See details for formatting.                                 |
| Available | Data frame with data corresponding to the available resources. See details for formatting.  |
| Indices   | Character vector containing the names of the desired indices to calculate. See description for information on available indices.        |
| LogQ      | Logical. If true, should Jacob's Q be logged? This is the recommendation of Jacob, 1974. Default is TRUE, following the recommendation. |
| Depleting | Logical. If true, calculates Chesson's Case 2, where food depletion occurs and the available food is not constant. Default is False.    |

**Details**

This function calculates one or multiple electivity indices for one or more diet records for which one or more records of prey availability exists. For example, it is possible to calculate multiple indices for multiple diet records that may be from a number of sites with different prey availability all in one call of the function (see example which). Specifically, this function measures the following indices (and their input for the Indices argument) Ivlev's (1961) Forage Ratio ("ForageRatio") and electivity ("Ivlev"), Strauss' (1979) ("Strauss"), Jacobs (1974) Q ("JacobsQ") and D ("JacobsD"), Chesson (1983) (Which is similar to Manly's Alpha (1974)) ("Chesson"), and Vanderploeg & Scavia (1979) ("VanderploegScavia"). For those wishing to calculate Vanderploeg and Scavia's selectivity coefficient (W), please select "Chesson" as an argument for indices, which will calculate Chesson's alpha, which is identical to Vanderploeg and Scavia's selectivity coefficient (W).

The function takes two dataframes as input. The first argument, Diet, should be formatted as followed. Each row in the data frame should be a diet record. The first column should contain the name of the record to be calculated. The second column should contain the name linking the consumed prey in Diet to that in Available (example, name of the different habitats), which will be described below. All remaining columns should contain the abundance or relative abundance of the prey in the diet. These columns should also be named so they can be matched to Those in Available. The second data frame, Available should be formatted similar to Diet where each row describes a unique record for available prey. The remaining columns should contain the abundance or relative abundance of the prey that are available to be consumed. These columns should also be named so they can be matched to Those in Diet. # Users should define if their data is raw or relative abundance by using the Abundance argument. Note that these indices rely on relative abundance data for calculations. While it is recommended to have input data as relative abundances, the function automatically will calculate relative abundances (which has no effect on data that are already in units of relative abundance).

Indices are bounded by the following values. Ivlev's, Strauss', and Jacobs' D, and Vanderploeg & Scavia's indices are bounded between -1 and 1, with items closer to -1 representing avoided items, 0 randomly feeding, and 1 preferential items. Forage ratio values range between 1 and infinity

for preferred items while values between 0 and 1 represent avoided prey. Similar to forage ratio, Jacobs' Q ranges between 1 and infinity for preferred items and 0 and 1 for avoided prey, however  $\log_{10}(Q)$  is preferred as it provides the advantage of equal ranges and ranges from -infinity to +infinity for avoidance and preference respectively. This option can be selected in the function with the `logQ` argument, which by default is set to `TRUE`. Finally, Chesson's index ranges between 0 and 1 and preference is typically assessed using  $1/n$ , where  $n$  is the number of prey types. The value of  $1/n$  represents random feeding while values above and below  $1/n$  represent preference and avoidance respectively. For Chesson's index, users can also specify if the available resources are depleting, in which case the equation from case 2 of Chesson, 1983 is calculated. Note, this takes the log of  $(p-r)/p$  and values of 0 or negatives will return `NaN`.

### Value

List containing data frames for each electivity index selected.

### Author(s)

Samuel Borstein

### References

Chesson, J. 1983. The estimation and analysis of preference and its relationship to foraging models. *Ecology* 64:1297-1304. Ivlev, U. 1961. Experimental ecology of the feeding of fish. Yale University Press, New Haven. Jacobs, J. 1974. Quantitative measurement of food selection. *Oecologia* 14:413-417. Manly, B. 1974. A model for certain types of selection experiments. *Biometrics* 30:281-294. Strauss, R. E. 1979. Reliability Estimates for Ivlev's Electivity Index, the Forage Ratio, and a Proposed Linear Index of Food Selection. *Transactions of the American Fisheries Society* 108:344-352. Vanderploeg, H., and D. Scavia. 1979. Two electivity indices for feeding with special reference to zooplankton grazing. *Journal of the Fisheries Board of Canada* 36:362-365.

### Examples

```
#Load Electivity Data from Horn 1982
data(Horn1982)
#Run all electivity indices
my.indices <- Electivity(Diet = Horn1982$Consumed, Available = Horn1982$Available, Indices =
c("ForageRatio", "Ivlev", "Strauss", "JacobsQ", "JacobsD", "Chesson", "VanderploegScavia"), LogQ = TRUE,
Depleting = FALSE)
```

---

FishBasePreyVals

*FishBasePreyVals*

---

### Description

A data frame containing prey items and their respective trophic levels following FishBase and TrophLab.



**Usage**

```
FishBasePreyVals
```

**Format**

A data frame of of 384 rows and 6 columns

- FoodI: Food category I.
- FoodII: Food category II.
- FoodIII: Food category III.
- Stage: Life history stage of the prey item.
- TL: Trophic level of the prey item.
- SE: Standard error around trophic level estimate of the prey item.

**References**

- Froese R, and Pauly D. 2018. FishBase. <http://www.fishbase.org/2018>).
- Pauly D, Froese R, Sa-a P, Palomares M, Christensen V, and Rius J. 2000. TrophLab manual. ICLARM, Manila, Philippines.

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|           |   |
|-----------|---|
| FoodTroph | <i>Calculates trophic level from qualitative food item data for species, populations, and individuals using a random subsampling routine.</i> |
|-----------|---|

---

**Description**

Calculates trophic level from food items where quantitative contribution is unknown. Follows the routine described in TrophLab. While FishBase data obtained from rfishbase can be used, users can also upload their own data for use with the function.

**Usage**

```
FoodTroph(FoodItems, PreyValues, Taxonomy, PreyClass = c("FoodI",
  "FoodII", "FoodIII", "Stage"), Iter = 100, SE.Type = "TrophLab")
```

**Arguments**

|            |  |
|------------|--|
| FoodItems  | a data frame with rows as individuals and each row consisting of a prey item name.   |
| PreyValues | a data frame with rows as prey item names and columns containing the trophic level of the prey item and the standard error of that trophic item.   |
| Taxonomy   | a data frame with the least inclusive level in the leftmost column progressing to more inclusive with columns to the right.Can be a single column. |
| PreyClass  | Column names of the PreyValues used for matching between FoodItems and PreyValues, exclusive of TL and SE. Default is those of FishBase.           |

|         |  |
|---------|--|
| Iter    | Numeric representing how many iterations of the subsampling routine should be performed. Default is 100 (same as in TrophLab)                    |
| SE.Type | Type of SE to perform. Can be either TrophLab, Sims, or Both. Default is TrophLab. See details for a more in-depth description of these options. |

### Details

Users can set the number of iterations for the subsampling routine for the simulated ranking of trophic items used in calculating trophic levels. We have this set currently to match how it is implemented in TrophLab, at 100. We find this performs relatively well and is quite quick to do, but users could also increase this value with minimal impacts on runtime.

For calculating the SE (SE.Type parameter) around the estimated trophic level users have a few options. The current default follows TrophLab and uses the SE around the trophic levels of prey to estimate the SE which they also refer to as the omnivory index. Alternatively, users can select the Sims option, in which case the SE is estimated based on the estimated TL of the n number of subsampling routines. Users can also select "Both" if they would like to calculate both types of SE.

### Value

a list of data frames containing estimated trophic levels from food items at each taxonomic level provided by the user.

### Author(s)

Samuel Borstein

### Examples

```
#Get some food item data from rfishbase
library(rfishbase)
my.food <- rfishbase::fooditems(c("Lutjanus apodus", "Epinephelus itajara"))
#convert FishBase data into data for trophic calculation using TrophicLevelR
converted.foods <- ConvertFishbaseFood(my.food)
#Load Prey Values
data(FishBasePreyVals)
#Calculate Trophic Levels
my.TL <- FoodTroph(FoodItems = converted.foods$FoodItems, PreyValues = FishBasePreyVals, Taxonomy =
converted.foods$Taxonomy, PreyClass=c("FoodI", "FoodII", "FoodIII", "Stage"))
```

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Herichthys

*Herichthys*

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### Description

Raw supplementary data from Magalhaes et al., 2015 for the diets of *Herichthys minckleyi* used in a tutorial for the vignette.

**Usage**

Herichthys

**Format**

A data frame of of 519 rows and 40 columns

**References**

- Magalhaes IS, Ornelas-Garcia CP, Leal-Cardin M, Ramirez T, and Barluenga M. 2015. Untangling the evolutionary history of a highly polymorphic species: introgressive hybridization and high genetic structure in the desert cichlid fish *Herichthys minckleyi*. *Mol Ecol* 24:4505-4520. 10.1111/mec.13316

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Horn1982

*Horn1982*

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**Description**

Raw data from Horn, 1982. Prey consumption and availability are in percent weight. Not that as the values do not sum to 100, the relative abundance will be calculated.

**Usage**

Horn1982

**Format**

A list of length 2 containing two data frames.

- Available A data frame with 2 rows and 18 columns containing data on prey availability in two different years.
- Consumed A data frame with four rows and 19 columns containing data on prey consumption by two species in two different years..

**Details**

Data from Horn, 1982 for the diet of two species of Stichaeidae and prey availability over two years.

**References**

- Horn M, Murray S, and Edwards T. 1982. Dietary selectivity in the field and food preferences in the laboratory for two herbivorous fishes (*Cebidichthys violaceus* and *Xiphister mucosus*) from a temperate intertidal zone. *Marine Biology* 67:237-246.

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