Package ‘fishflux’

July 9, 2020

**Title**  Model Elemental Fluxes in Fishes

**Version**  0.0.1.1

**Description**  Model fluxes of carbon, nitrogen, and phosphorus with the use of a coupled bioenergetics and stoichiometric model that incorporates flexible elemental limitation. Additional functions to help the user to find parameters are included. Finally, functions to extract and visualize results are available as well. For an introduction, see vignette. For more information on the theoretical background of this model, see Schiettekatte et al. (2020) <doi:10.1111/1365-2435.13618>.

**URL**  https://nschiett.github.io/fishflux/

**BugReports**  https://github.com/nschiett/fishflux/issues

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**Encoding**  UTF-8

**Imports**  methods, Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), rstantools (>= 2.0.0), parallel, dplyr, fishualize, ggplot2, plyr, rfishbase, tidybayes, tidyr

**Depends**  R (>= 3.6.0)

**Suggests**  knitr, rmarkdown, testthat, covr

**LinkingTo**  BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.4.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

**SystemRequirements**  GNU make

**LazyData**  true

**RoxygenNote**  7.1.0

**VignetteBuilder**  knitr

**Biarch**  true

**NeedsCompilation**  yes

**Author**  Nina M. D. Schiettekatte [aut, cre], Diego Barneche [aut]

**Maintainer**  Nina M. D. Schiettekatte <nina.schiettekatte@gmail.com>

**Repository**  CRAN

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fishflux-package The ‘fishflux’ package.

Description

The ‘r fishflux’ package provides a tool to model fluxes of C (carbon), N (nitrogen) and P (phosphorus) in fish. It combines basic principles from elemental stoichiometry and metabolic theory. The package offers a userfriendly interface to make nutrient dynamic modelling available for anyone. ‘r fishflux’ is mostly targeted towards fish ecologists, wishing to predict nutrient ingestion, egestion and excretion to study fluxes of nutrients and energy. Main assets:

- Provides functions to model fluxes of Carbon, Nitrogen and Phosphorus for fish with or without the MCMC sampler provided by stan.
- Provides some tools to find the right parameters as inputs into the model
- Provides a plotting function to illustrate results

References

aspect_ratio

A function to find aspect ratio

Description

A function to find aspect ratio of a species on either species or genus level using rfishbase. It returns a data frame containing the aspect ratio and the level at which the aspect ratio was found (species or genus).

Usage

aspect_ratio(sp)

Arguments

sp A character value containing the species name

Examples

library(fishflux)
library(plyr)
aspect_ratio("Lutjanus griseus")
ldply(lapply(c("Chlorurus spilurus","Zebrasoma scopas"), aspect_ratio))

check_name_fishbase

Returns error if name is incorrect

Description

This is a wrapper function to which will return an error (via name_errors) if the provided species name is wrong.

Usage

check_name_fishbase(sp)

Arguments

sp A character value containing the species name
Examples

```r
library(fishflux)
check_name_fishbase("Lutjanus griseus")
```

Description

cnp_mcmc

Usage

cnp_mcmc(TL, param, iter, params_st, cor, ...)

Arguments

<table>
<thead>
<tr>
<th>TL</th>
<th>Total length(s) in cm</th>
</tr>
</thead>
<tbody>
<tr>
<td>param</td>
<td>List of all parameter means (add &quot;.m&quot;) and standard deviations (add &quot;.sd&quot;) Default parameters are set with very low sd.'s. parameters:</td>
</tr>
<tr>
<td></td>
<td>- Qc_m, Qc.sd: percentage C of dry mass fish</td>
</tr>
<tr>
<td></td>
<td>- Qn_m, Qn.sd: percentage N of dry mass fish</td>
</tr>
<tr>
<td></td>
<td>- Qp_m, Qp.sd: percentage P of dry mass fish</td>
</tr>
<tr>
<td></td>
<td>- Dc_m, Dc.sd: percentage C of dry mass food</td>
</tr>
<tr>
<td></td>
<td>- Dn_m, Dn.sd: percentage N of dry mass food</td>
</tr>
<tr>
<td></td>
<td>- Dp_m, Dp.sd: percentage P of dry mass food</td>
</tr>
<tr>
<td></td>
<td>- ac_m, ac.sd: C-specific assimilation efficiency</td>
</tr>
<tr>
<td></td>
<td>- an_m, an.sd: N-specific assimilation efficiency</td>
</tr>
<tr>
<td></td>
<td>- ap_m, ap.sd: P-specific assimilation efficiency</td>
</tr>
<tr>
<td></td>
<td>- linf_m, linf.sd: Von Bertalanffy Growth parameter, theoretical maximum size in TL (cm)</td>
</tr>
<tr>
<td></td>
<td>- k_m, k_sd: Von Bertalanffy Growth parameter, growth rate (yr^-1)</td>
</tr>
<tr>
<td></td>
<td>- t0_m, t0.sd: Von Bertalanffy Growth parameter (yr)</td>
</tr>
<tr>
<td></td>
<td>- lwa_m, lwa.sd: Parameter length-weight relationship (g cm^-1)</td>
</tr>
<tr>
<td></td>
<td>- lwb_m, lwb.sd: Parameter length-weight relationship</td>
</tr>
<tr>
<td></td>
<td>- mdw_m, wprop.sd: Ratio between dry weight and wet weight of fish</td>
</tr>
<tr>
<td></td>
<td>- F0nz_m, F0nz.sd: N-specific turnover rate</td>
</tr>
<tr>
<td></td>
<td>- F0pz_m, F0pz.sd: P-specific turnover rate</td>
</tr>
<tr>
<td></td>
<td>- f0_m, f0.sd: Metabolic normalisation constant independent of body mass (g C g^-alpha d^-1)</td>
</tr>
<tr>
<td></td>
<td>- alpha_m, alpha.sd: Metabolic rate mass-scaling exponent</td>
</tr>
</tbody>
</table>
cnp_model_mcmc

- theta_m, theta_sd: Activity scope
- r_m, r_sd: Aspect ratio of caudal fin
- h_m, h_sd: Trophic level
- v_m, v_sd: Environmental temperature (degrees celcius)

iter
A positive integer specifying the number of iterations. The default is 2000.

params_st
Standard parameters.

cor
A list of correlations between certain parameters: ro_Qc_Qn, ro_Qc_Qp, ro_Qn_Qp, ro_Dc_Dn, ro_Dc_Dp, ro_Dn_Dp, ro_lwa_lwb, ro_alpha_f0

... Additional arguments rstan::sampling, see ?rstan::sampling

---

**Description**

This function combines MTE and stoichiometric theory in order to predict necessary ingestion and excretion processes. A probability distribution is obtained by including uncertainty of parameters and using MCMC sampling with stan.

**Usage**

```r
cnp_model_mcmc(
  TL, 
  param, 
  iter = 1000, 
  cor = list(ro_Qc_Qn = 0.5, ro_Qc_Qp = -0.3, ro_Qn_Qp = -0.2, ro_Dc_Dn = 0.2, ro_Dc_Dp = -0.1, ro_Dn_Dp = -0.1, ro_lwa_lwb = 0.9, ro_alpha_f0 = 0.9), 
  ...
)
```

**Arguments**

- **TL**
  Total length(s) in cm
- **param**
  List of all parameter means (add "_m") and standard deviations (add "_sd") Default parameters are set with very low sd’s. parameters:
  - Qc_m, Qc_sd: percentage C of dry mass fish
  - Qn_m, Qn_sd: percentage N of dry mass fish
  - Qp_m, Qp_sd: percentage P of dry mass fish
  - Dc_m, Dc_sd: percentage C of dry mass food
  - Dn_m, Dn_sd: percentage N of dry mass food
  - Dp_m, Dp_sd: percentage P of dry mass food
  - ac_m, ac_sd: C-specific assimilation efficiency
  - an_m, an_sd: N-specific assimilation efficiency
• ap_m, ap_sd: P-specific assimilation efficiency  
• linf_m, linf_sd: Von Bertalanffy Growth parameter, theoretical maximum size in TL (cm)  
• k_m, k_sd: Von Bertalanffy Growth parameter, growth rate (yr^-1)  
• t0_m, t0_sd: Von Bertalanffy Growth parameter (yr)  
• lwa_m, lwa_sd: Parameter length-weight relationship (g cm^-1)  
• lwb_m, lwb_sd: Parameter length-weight relationship  
• mdw_m, wprop_sd: Ratio between dry weight and wet weight of fish  
• F0nz_m, F0nz_sd: N-specific turnover rate  
• F0pz_m, F0pz_sd: P-specific turnover rate  
• f0_m, f0_sd: Metabolic normalisation constant independent of body mass (g C g^-alpha d^-1)  
• alpha_m, alpha_sd: Metabolic rate mass-scaling exponent  
• theta_m, theta_sd: Activity scope  
• r_m, r_sd: Aspect ratio of caudal fin  
• h_m, h_sd: Trophic level  
• v_m, v_sd: Environmental temperature (degrees celcius)

iter  
A positive integer specifying the number of iterations. The default is 2000.

cor  
A list of correlations between certain parameters: ro_Qc_Qn, ro_Qc_Qp, ro_Qn_Qp, ro_Dc_Dn, ro_Dc_Dp, ro_Dn_Dp, ro_lwa_lwb, ro_alpha_f0

...  
Additional arguments rstan::sampling, see ?rstan:sampling

Details  
Returns a list with two objects: A stanfit object and a data.frame with a summary of all model components. See extract to extract a summary of predicted variables and limitation to get information on the limiting element.

Examples  
library(fishflux)
model <- cnp_model_mcmc(TL = 10, param = list(Qc_m = 40, Qn_m = 10, Qp_m = 4, theta_m = 3))

extract  
A function to extract specific model output parameters from result

Description  
A function to extract specific model output parameters from result

Usage  
extract(mod, par)
extract

Arguments
mod
Output from cnp_mod_mcmc()
par
Character vector specifying which output parameter that should be returned.

Details
Returns a data.frame with a summary of the selected output parameters

Value
Main model output parameters:

• F0c: C-specific minimal inorganic flux (g/day)
• F0n: N-specific minimal inorganic flux (g/day)
• F0p: P-specific minimal inorganic flux (g/day)
• Gc: Carbon-specific growth rate (g/day)
• Gn: Nitrogen-specific growth rate (g/day)
• Gp: Phosphorus-specific growth rate (g/day)
• Sc: C-specific minimal supply rate (g/day)
• Sn: N-specific minimal supply rate (g/day)
• Sp: P-specific minimal supply rate (g/day)
• Ic: Ingestion rate of C (g/day)
• In: Ingestion rate of N (g/day)
• Ip: Ingestion rate of P (g/day)
• Wc: Egestion rate of C (g/day)
• Wn: Egestion rate of N (g/day)
• Wp: Egestion rate of P (g/day)
• Fc: Total inorganic flux of C (respiration) (g/day)
• Fn: Total inorganic flux of N (excretion) (g/day)
• Fp: Total inorganic flux of P (excretion) (g/day)

Examples
model <- cnp_model_mcmc(TL = 5:10, param = list(Qc_m = 40, Qn_m = 10, Qp_m = 4))
extact(model, c("Fn","Fp"))
**find_lw**

*A function to find length-weight relationship parameters a and b*

**Description**

A function to find estimates length-weight relationship parameters available on fishbase. It returns a list of means and standard deviations of a and b obtained from: *Froese, R., J. Thorson and R.B. Reyes Jr., 2013. A Bayesian approach for estimating length-weight relationships in fishes. J. Appl. Ichthyol. (2013):1-7.* Please cite Froese et al. (2013), when using these values. The default mirror for fishbase is set to "de", please change this if needed for your location.

**Usage**

```r
find_lw(sp, mirror = "us")
```

**Arguments**

- **sp** A character value containing the species name
- **mirror** Mirror for fishbase (eg. "de", "org", "us", etc.) Default is "us".

**Examples**

```r
library(fishflux)
library(plyr)

# find length-weight relationship parameters for one species
find_lw("Lutjanus griseus")

# find length-weight relationship parameters for multiple species and return in dataframe
ldply(lapply(c("Chlorurus spilurus","Zebrasoma scopas"), find_lw))
```

---

**get_iter**

**Description**

**Usage**

```r
get_iter(x)
```

**Arguments**

- **x** something
growth_params

A function to find growth parameters on fishbase

Description

A function to find growth parameters of a species using rfishbase. It returns a data frame containing K, t0 and Linf, the source. This function is useful to see what is available on fishbase. Nevertheless, we strongly recommend to check the source and only use otolith based studies.

Usage

growth_params(sp, otolith = TRUE)

Arguments

sp A character value containing the species name
otolith A logical value. If TRUE, only results from otolith analysis are returned. If false, all growth studies will be returned.

Examples

library(fishflux)
growth_params("Lutjanus griseus")

limitation

A function to evaluate element limitation of the model

Description

This function allows you extract the proportions of the iterations for which c, n and p are the limiting element in the model.

Usage

limitation(mod, plot = TRUE)

Arguments

mod Model output from cnp_model_mcmc().
plot Argument to specify if results should be shown in a plot.
Details

Returns a data frame with:

- **tl** Total length, in cm
- **nutrient** c, n or p
- **prop_lim** the proportion of iterations for which there is limitation by the element

Examples

```r
library(fishflux)
mod <- cnp_model_mcmc(TL = 5, param = list(Qc_m = 40, Qn_m = 10, Qp_m = 4,
                                            Dc_sd = 0.1, Dn_sd = 0.05, Dp_sd = 0.05))
limitation(mod)
```

---

**metabolic_parameters** Data with metabolic parameters on family level

Description

Data frame containing means and sd for b0 and a for several fish families, extracted from Barneche & Allen (2018) These parameters can be used in calculations of metabolic rate in case respirometry data is not available.

Usage

```r
data(metabolic_parameters)
```

Format

An object of class `data.frame` with 20 rows and 5 columns.

Examples

```r
data(metabolic_parameters)
```
metabolic_rate

A function to calculate metabolic rates

Description

All model parameters below were estimated by Barneche & Allen 2018 Ecology Letters doi: 10.1111/ele.12947. These parameters are for the best model (Model 2 in the paper online supplementary material) of fish resting metabolic rates reported in the paper, which also includes trophic level as a covariate.

Usage

metabolic_rate(temp, troph, asp, B0, m_max, m, a, growth_g_day, f)

Arguments

- **temp**: Temperature in degrees Celsius
- **troph**: Trophic level (from 1 to 5)
- **asp**: The caudal fin aspect ratio, a proxy for activity level
- **B0**: Constant for resting metabolic rate. If NA, function will calculate an average.
- **m_max**: Maximum biomass fish (in g)
- **m**: Wet weight fish (in g)
- **a**: Resting metabolic rate mass-scaling exponent
- **growth_g_day**: Daily growth in grams of wet weight
- **f**: Activity scope (from 1 to 4)

Details

All model parameters below were estimated by Barneche & Allen 2018 Ecology Letters doi: 10.1111/ele.12947. These parameters are for the best model (Model 2 in the paper online supplementary material) of fish resting metabolic rates reported in the paper, which also includes trophic level as a covariate.

Examples

```r
library(fishflux)
fishflux::metabolic_rate(temp = 27, m_max = 600, m = 300, asp = 3,
troph = 2, f = 2, growth_g_day = 0.05, B0 = 0.2, a = 0.6 )
```
metabolism  

*A function to estimate f0 and alpha*

**Description**

All model parameters below were estimated by Barneche & Allen 2018 Ecology Letters doi: 10.1111/ele.12947. These parameters are for the best model (Model 2 in the paper online supplementary material) of fish resting metabolic rates reported in the paper, which also includes trophic level as a covariate.

**Usage**

```r
metabolism(family, temp, troph_m, troph_sd = 1e-10)
```

**Arguments**

- **family**: family fish
- **temp**: Temperature in degrees Celsius
- **troph_m**: Trophic level mean (from 1 to 5)
- **troph_sd**: Trophic level sd (optional)

**Details**

All model parameters below were estimated by Barneche & Allen 2018 Ecology Letters doi: 10.1111/ele.12947. These parameters are for the best model (Model 2 in the paper online supplementary material) of fish resting metabolic rates reported in the paper, which also includes trophic level as a covariate.

**Examples**

```r
library(fishflux)
metabolism(family = "Pomacentridae", temp = 27, troph_m = 2)
```

---

model_parameters  

*A function to find a set of parameters*

**Description**

A function to find a set of parameters

**Usage**

```r
model_parameters(sp, family, otolith = TRUE, temp, ...)
```
name_errors

Arguments

sp          Species name
family      family
otolith     TRUE or FALSE, if TRUE, function will only search fishbase for growth parameters that are based upon otolith analysis
temp        temperature
...         Additional arguments to find_lw.

Details

Returns a dataframe with all parameters that can be estimated

Examples

library(fishflux)
model_parameters(sp = "Scarus psittacus", family = "Scaridae", temp = 27)

name_errors(c("Chlorurus spilurus", "Zebrasoma scopas"))
name_errors(c("Chlorurus spilurus", "Zebrasoma copas"))
param_zebsco  
*List of all parameters needed to run cnp_model for *Zebrasoma scopas*

**Description**
List of all parameters needed to run cnp_model for *Zebrasoma scopas*

**Usage**

data(param_zebsco)

**Format**
An object of class list of length 37.

**Examples**

data(param_zebsco)

---

plot_cnp  
*A function to plot results model*

**Description**
This function allows you to plot an overview of the model results in function of the total length of fish

**Usage**

plot_cnp(mod, y, x = "tl", probs = c(0.8, 0.95))

**Arguments**

- **mod**: Model output from cnp_model_mcmc()
- **y**: Output variable(s) to be plotted. Can be a character or a character vector.
- **x**: Variable to be put on x-axis, "biomass" or "tl"
- **probs**: Width of the confidence
sensitivity

A function to check the sensitivity of cnp_model predictions based on the variation of input parameters

Description

This function runs the cnp_model fixing all parameters SD's but one to test for sensitivity

Usage

```r
sensitivity(
  TL,
  param,
  iter = 1000,
  par,
  ...
)
```

Arguments

- `TL` total length of a fish in cm
- `param` list of all parameter means ("_m") and standard deviations ("_sd") Default parameters are set with very low sd's. See `cnp_model_mcmc` for a list of all requested parameters
- `iter` A positive integer specifying the number of iterations. The default is 1000
- `par` Character vector specifying which input parameter sd's should be used for sensitivity.
- `out` Character vector specifying which output parameter sd's should be returned.
- `...` Other arguments that can be used from `cnp_model_mcmc`

Details

Returns a dataframe with sd's of model predictions. Row names indicate the variable, who's sd was used for the model run. Plots a heatplot with width of the 95
Examples

    library(fishflux)
    sensitivity(TL = 10, param = list(k_sd = 0.2, Dn_sd = 0.2, Dc_sd = 0.1),
                  par = c("k_sd","Dn_sd","Dc_sd"), out = c("Ic", "In", "Ip", "Gc"))

---

weight_prop

A function to find trophic level

Description

A function to find trophic level of a species on either species or genus level using rfishbase. It returns a data frame containing the trophic level and the level at which the trophic level was found (species or genus).

Usage

    trophic_level(sp)

Arguments

    sp

A character value containing the species name

Examples

    library(fishflux)
    library(plyr)
    trophic_level("Lutjanus griseus")
    ldply(lapply(c("Chlorurus spilurus","Zebrasoma scopas"), trophic_level))

---

weight_prop

Data frame with dry weight/ wet weight proportions for multiple reef fish families.

Description

Data frame with dry weight/ wet weight proportions for multiple reef fish families.

Usage

    data(weight_prop)

Format

An object of class data.frame with 15 rows and 4 columns.
wprop

Examples

data(weight_prop)

---

wprop  A function to find the ratio of dry weight and wet weight of fish in local database

Description

This function searches the ratio of dry weight and wet weight of fish on the family level. If the family is not available, an average is returned.

Usage

wprop(family)

Arguments

family  family

Details

Returns a dataframe with the weight ratio (mdw) and it’s sd (mdw_sd).

Examples

library(fishflux)
wprop(family="Scaridae")
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