

# Package ‘fishflux’

October 14, 2020

**Title** Model Elemental Fluxes in Fishes

**Version** 0.0.1.3

**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>

**License** MIT + file LICENSE

**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, httr, curl

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

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**Biarch** true

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fishflux-package	<i>The 'fishflux' package.</i>
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### 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

Stan Development Team (2020). RStan: the R interface to Stan. R package version 2.19.3. <https://mc-stan.org>

---

aspect_ratio	<i>A function to find aspect ratio</i>
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### 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	<i>Returns error if name is incorrect</i>
---------------------	---

---

### 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**

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

---

cnp\_mcmc

*cnp\_mcmc*


---

**Description**

cnp\_mcmc

**Usage**

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

**Arguments**

TL	Total length(s) in cm
param	<p>List of all parameter means (add "_m") and standard deviations (add "_sd") Default parameters are set with very low sd's. parameters:</p> <ul style="list-style-type: none"> <li>• Qc_m, Qc_sd: percentage C of dry mass fish</li> <li>• Qn_m, Qn_sd: percentage N of dry mass fish</li> <li>• Qp_m, Qp_sd: percentage P of dry mass fish</li> <li>• Dc_m, Dc_sd: percentage C of dry mass food</li> <li>• Dn_m, Dn_sd: percentage N of dry mass food</li> <li>• Dp_m, Dp_sd: percentage P of dry mass food</li> <li>• ac_m, ac_sd: C-specific assimilation efficiency</li> <li>• an_m, an_sd: N-specific assimilation efficiency</li> <li>• ap_m, ap_sd: P-specific assimilation efficiency</li> <li>• linf_m, linf_sd: Von Bertalanffy Growth parameter, theoretical maximum size in TL (cm)</li> <li>• k_m, k_sd: Von Bertalanffy Growth parameter, growth rate (yr<sup>-1</sup>)</li> <li>• t0_m, t0_sd: Von Bertalanffy Growth parameter (yr)</li> <li>• lwa_m, lwa_sd: Parameter length-weight relationship (g cm<sup>-1</sup>)</li> <li>• lwb_m, lwb_sd: Parameter length-weight relationship</li> <li>• mdw_m, wprop_sd: Ratio between dry weight and wet weight of fish</li> <li>• F0nz_m, F0nz_sd: N-specific turnover rate</li> <li>• F0pz_m, F0pz_sd: P-specific turnover rate</li> <li>• f0_m, f0_sd: Metabolic normalisation constant independent of body mass (g C g<sup>-alpha</sup> d<sup>-1</sup>)</li> <li>• alpha_m, alpha_sd: Metabolic rate mass-scaling exponent</li> </ul>

	<ul style="list-style-type: none"> <li>• theta_m, theta_sd: Activity scope</li> <li>• r_m, r_sd: Aspect ratio of caudal fin</li> <li>• h_m, h_sd: Trophic level</li> <li>• v_m, v_sd: Environmental temperature (degrees celcius)</li> </ul>
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

---

cnp_model_mcmc	<i>A function to predict N and P excretion, CNP egestion, CNP ingestion rate, using MCMC and stan</i>
----------------	---

---

### 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

```
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: <ul style="list-style-type: none"> <li>• Qc_m, Qc_sd: percentage C of dry mass fish</li> <li>• Qn_m, Qn_sd: percentage N of dry mass fish</li> <li>• Qp_m, Qp_sd: percentage P of dry mass fish</li> <li>• Dc_m, Dc_sd: percentage C of dry mass food</li> <li>• Dn_m, Dn_sd: percentage N of dry mass food</li> <li>• Dp_m, Dp_sd: percentage P of dry mass food</li> <li>• ac_m, ac_sd: C-specific assimilation efficiency</li> <li>• an_m, an_sd: N-specific assimilation efficiency</li> </ul>

- 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<sup>-1</sup>)
- t0\_m, t0\_sd: Von Bertalanffy Growth parameter (yr)
- lwa\_m, lwa\_sd: Parameter length-weight relationship (g cm<sup>-1</sup>)
- 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<sup>-alpha</sup> d<sup>-1</sup>)
- 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)
```

**Arguments**

mod	Output from <code>cnp_mod_mcmc()</code>
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))
extract(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

```
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

```
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

*get\_iter*


---

### Description

get\_iter

### Usage

```
get_iter(x)
```

### Arguments

x                    something



---

growth_params	<i>A function to find growth parameters on fishbase</i>
---------------	---

---

### 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	<i>A function to evaluate element limitation of the model</i>
------------	---

---

### 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 <code>cnp_model_mcmc()</code> .
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**

```
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**

```
data(metabolic_parameters)
```

**Format**

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

**Examples**

```
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

```
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	<i>A function to estimate <math>f_0</math> and <math>\alpha</math></i>
------------	--

---

**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**

```
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**

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

---

model_parameters	<i>A function to find a set of parameters</i>
------------------	---

---

**Description**

A function to find a set of parameters

**Usage**

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

**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 <a href="#">find_lw</a> .

**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	<i>A function to find errors in fish species names</i>
-------------	--

---

**Description**

This function allows you to check if there are errors in your fish species list and returns inaccurate scientific names

**Usage**

```
name_errors(sp)
```

**Arguments**

sp	A vector containing all your scientific species names.
----	--

**Examples**

```
library(fishflux)
name_errors(c("Chlorurus spilurus", "Zebrasoma scopas"))
name_errors(c("Chlorurus spilurus", "Zebrasoma copas"))
```

---

param_zebsco	<i>List of all parameters needed to run cnp_model for *Zebrasoma scopas*</i>
--------------	--

---

**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	<i>A function to plot results model</i>
----------	---

---

**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 <code>cnp_model_mcmc()</code>
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

**Examples**

```
library(fishflux)
mod <- cnp_model_mcmc(TL = 5:15, param = list(
  Qc_m = 40, Qn_m = 10, Qp_m = 4, Dn_sd = 0.05))
plot_cnp(mod = mod, y = c("Fp", "Gp", "Wp", "Ip"),
  x = "t1", probs = c(0.5, 0.8))
plot_cnp(mod = mod, y = "Fp", x = "t1",
  probs = c(0.5, 0.8, 0.95))
```

---

sensitivity	<i>A function to check the sensitivity of cnp_model predictions based on the variation of input parameters</i>
-------------	--

---

**Description**

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

**Usage**

```
sensitivity(
  TL,
  param,
  iter = 1000,
  par,
  out = c("Ic", "In", "Ip", "Gc", "Gn", "Gp", "Fc", "Fn", "Fp", "Wc", "Wn", "Wp"),
  ...
)
```

**Arguments**

TL	total length of a fish in cm
param	list of all parameter means (" <code>_m</code> ") and standard deviations (" <code>_sd</code> ") Default parameters are set with very low sd's. See <a href="#">cnp_model_mcmc</a> 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 <a href="#">cnp_model_mcmc</a>

**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"))
```

---

trophic_level	<i>A function to find trophic level</i>
---------------	---

---

**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	<i>Data frame with dry weight/ wet weight proportions for multiple reef fish families.</i>
-------------	--

---

**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.



**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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