

Introduction to the use of fishflux

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Introduction

The **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. **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

Installing and loading fishflux

fishflux uses Markov Chain Monte Carlo simulations provided by stan. Therefore, the first step is to install stan.

GitHub

The best way to install the latest development version of **fishflux** is to instal it from GitHub.

```
install.packages("devtools")
devtools::install_github("nschiet/fishflux", dependencies=TRUE)
library(fishflux)
```

CRAN

fishflux will be available on CRAN in the future:

```
install.packages("fishflux")
library(fishflux)
```

Downloaded package file

Another option is to download the source file available on github here.

```
install.packages(path_to_fishflux_file, repos = NULL, type="source")
library(fishflux)
```

How to use fishflux?

fishflux is designed to follow three simple steps: 1. Find the right input parameters 2. Run the model simulation with those input parameters 3. Plot the model results

Find parameters

Below a table showing all parameters needed to run the mosel simulation. `fishflux` provides functions to find some of these parameters, but note that others have to be provided by the user at this stage.

Table 1: Species specific parameters. L_{inf} and k are parameters of the Von Beffalanty growth curve. F_p , F_n and F_c are the element contents of the fish's diet. k is a parameter defining the activity level of the fish

species	L_{inf}
a	expla
b	explb

A good place to start is to check if you are using the correct scientific name of your fish of interest. The function `name_errors` will tell you if the species name is correct. This function can be useful, especially when working with larger databases.

```
fishflux::name_errors("Zebrazoma scopas")
```

```
## Inaccurate species names found:
```

```
## [1] "Zebrazoma scopas"
```

When we have verified or corrected the species name we can start finding some parameters.

The `find_lw` function searches fishbase to find length-weight relationship parameters `lw_a` and `lw_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.*

```
fishflux::find_lw("Zebrasoma scopas")
```

```
##           species  lwa_m    lwa_sd lwb_m    lwb_sd
## 1 Zebrasoma scopas 0.02455 0.00272449 2.98 0.0255102
```

`growth_params()`, `trophic_level()` and “