

Supporting information for: *fluxweb: an R package to easily estimate energy fluxes in food webs*

Benoit Gauzens^{1,2}, Andrew Barnes^{1,3,4}, Darren Gilling^{1,5}, Jes Hines^{1,5}, Malte Jochum⁶, Jonathan S. Lefcheck⁷, Benjamin Rosenbaum^{1,2}, Shaopeng Wang^{1,2,8}, and Ulrich Brose^{1,2}

¹EcoNetLab, German Centre for Integrative Biodiversity Research (iDiv)
Halle-Jena-Leipzig, Deutscher Platz 5e, 04103 Leipzig, Germany

²Institute of Biodiversity, University of Jena, Dornburger Str. 159, 07743 Jena, Germany

³School of Science, University of Waikato, Private Bag 3105, Hamilton 3204, New Zealand

⁴Institute of Landscape Ecology, University of Münster, Heisenbergstrasse 2, 48149 Münster, Germany

⁵Institute of Biology, Leipzig University, Johannisallee 21, 04103 Leipzig, Germany

⁶Institute of Plant Sciences, University of Bern, Altenbergrain 21, 3013 Bern, Switzerland

⁷Tennenbaum Marine Observatories Network, MarineGEO, Smithsonian Institution, Edgewater, Maryland

⁸Institute of Ecology, College of Urban and Environmental Science, Peking University, Beijing 100871, China

1 Supplementary information I - mathematical resolution

1.1 Efficiencies depending on predator identity

We will consider in the following that feeding efficiencies depend on predator identity. We define e as the vector of efficiencies and W as the matrix such that W_{ij} is the proportion of energy entering j that is obtained from i ($\sum_j W_{ij} = 1$). F_{ij} is the flux from species i to j . L_i , the energy loss of species i is defined by:

$$L_i = X_i + \sum_{j=1}^n F_{ij}, \quad (1)$$

where n is the number of species and X_i are the physiological losses of species i . Thus, for satisfying the equilibrium criteria, F_i , the sum of fluxes entering i is:

$$F_i = \frac{1}{e_i} \left(X_i + \sum_{j=1}^n F_{ij} \right). \quad (2)$$

As W_{ij} sets the proportion of energy entering j obtained from species i , using $F_{ij} = W_{ij}F_j$, we can write

$$F_i = \frac{1}{e_i} \left(X_i + \sum_{j=1}^n W_{ij}F_j \right), \quad (3)$$

where values W_{ij} are estimated accordingly to species preferences (w_{ij}) and prey abundances:

$$W_{ij} = \frac{w_{ij}B_i}{\sum_{k=1}^n w_{kj}B_k}. \quad (4)$$

We then have:

$$e_i F_i = X_i + \sum_{j=1}^n W_{ij}F_j, \quad (5)$$

which can be rewritten as:

$$\text{diag}(E)F = X + WF, \quad (6)$$

where $\text{diag}(e)$ is the diagonal matrix such that $\text{diag}(e)_{ii} = e_i$. Provided that $(\text{diag}(e) - W)$ is invertible, the system solves as:

$$F = (\text{diag}(e) - W)^{-1} X. \quad (7)$$

Then, all fluxes $F_{ij} = W_{ij}F_j$ are derived from F_j using W .

1.2 Efficiencies depending on prey identity

Another common method is to define feeding efficiencies according to prey identity. This section proposes a method to adapt the previous framework to this case.

As preferences are defined at the prey level, we need to adapt the previous framework by adding a nutrient node on which all basal species feed with an

efficiency of one. Then, eq.3 becomes:

$$F_i \left(\sum_{j=1}^n W_{ji} e_j + b_i \right) = X_i + \sum_{j=1}^n W_{ij} F_j \quad (8)$$

$$\Leftrightarrow F_i \left(\sum_{j=1}^n W_{ij}^T e_j + b_i \right) = X_i + \sum_{j=1}^n W_{ij} F_j \quad (9)$$

where b_i is 1 if i is a basal species, 0 otherwise. This can be rewritten as:

$$\text{diag}(W^T e + \vec{b}) F = X + W F, \quad (10)$$

and, provided that $(\text{diag}(W^T e + \vec{b}) - W)$ is invertible, solved by:

$$F = (\text{diag}(W^T e + \vec{b}) - W)^{-1} X \quad (11)$$

1.3 Efficiencies depending on the link identity

It is possible to generalise this approach to efficiencies defined for each prey-predator couple. The solution needs the definition of matrix U such as $U_{ij} = W_{ij} e_{ij}$. Then, eq. 3 becomes:

$$F_i \sum_{j=1}^n U_{ij}^T = X_i + \sum_{j=1}^n W_{ij} F_j \quad (12)$$

and the system then reads:

$$\text{diag}(U^T \vec{1}) F = X + W F \quad (13)$$

where $\vec{1}$ is the vector of ones. System is solved as:

$$F = (\text{diag}(U^T \vec{1}) - W)^{-1} X \quad (14)$$

2 Supplementary information II - Stability

This document presents how the fluxes calculated under the steady state hypothesis can easily be used to assess system stability, following the framework of Moore and De Ruiter [1]. Here we use resilience as a definition of stability. Resilience is determined from the Jacobian matrix. The system is in a stable equilibrium only if the real parts of eigenvalues from the Jacobian are all negative. In this case, resilience is the absolute value of the real part of the largest eigenvalue, which is the value returned by the *stability* function

from the *fluxweb* package.

Another measure of stability, provided by the function *make.stability*, is to find the minimal value of a scalar s defining the proportion of physiological losses related to species density. In this case, physiological loss terms in the diagonal of the Jacobian matrix are now defined as sX_i and directly affect the resilience value, s being the measure of stability. We will show in the following section how fluxes at equilibrium can relate to a Lotka-Volterra system in an equilibrium state, and how to compute the Jacobian matrix, first assuming that feeding efficiencies relate to predator identity and then assuming that they depend on prey identity.

2.1 Derivation of the Jacobian matrix

2.1.1 Preferences defined at predator level

We can consider the following system of equations, describing the dynamics of population biomasses in a community:

$$\frac{dB_i}{dt} = r_i B_i - \sum_j a_{ij} B_i B_j \quad (\text{for producers}) \quad (15a)$$

$$\frac{dB_i}{dt} = -X_i B_i + \sum_j e_i a_{ji} B_i B_j - \sum_j a_{ij} B_i B_j \quad (\text{for consumers}) \quad (15b)$$

a_{ij} is the coefficient of interaction between prey i and predator j and r_i is the relative growth rate of producer i . P_i and p_i respectively define the sets of predators and prey of species i . This model assumes a type I functional response f_{ij} defined as:

$$f_{ij} = a_{ij} B_i. \quad (16)$$

As the whole method assumes that fluxes and biomasses are at an equilibrium state, we have:

$$F_{ij} = a_{ij} B_i^* B_j^*, \quad (17)$$

B_i^* denoting biomass of species i at equilibrium. Then, off-diagonal elements α_{ij} from the Jacobian matrix correspond to the per capita effects (effect of one unit of species biomass). Considering the possible presence of cycles of length 1 (species i is at the same time a prey and a predator of species j), off diagonal elements are

$$\alpha_{ij} = \frac{\delta \frac{dB_i}{dt}}{\delta B_j} = e_i a_{ji} B_i - a_{ij} B_i \quad i \neq j \quad (18)$$

and at equilibrium, from eq. 17 we have $B_i^* = \frac{F_{ij}}{a_{ij}B_j^*}$ and $B_i^* = \frac{F_{ji}}{a_{ji}B_j^*}$. We can use it to replace elements from eq. 18 and obtain:

$$\alpha_{ij} = e_i \frac{F_{ji}}{B_j^*} - \frac{F_{ij}}{B_j^*} \quad i \neq j \quad (19)$$

Diagonal elements, considering possible cannibalistic loops, for producers (p) and consumers (c) are:

$$\alpha_{pp} = r_p - \sum_j c_{pj} B_j \quad (20a)$$

$$\alpha_{cc} = -X_c + 2e_c a_{cc} B_c + \sum_{j \neq c} e_c a_{jc} B_j - 2a_{cc} B_c - \sum_{j \neq c} a_{cj} B_j \quad (20b)$$

$$= -X_c + e_c a_{cc} B_c + \sum_j e_c a_{jc} B_j - a_{cc} B_c - \sum_j a_{cj} B_j \quad (20c)$$

with $a_{ii} \neq 0$ only if species i is cannibalistic. Again, using $B_i^* = \frac{F_{ij}}{a_{ij}B_j^*}$ and $B_i^* = \frac{F_{ji}}{a_{ji}B_j^*}$ we obtain at equilibrium:

$$\alpha_{pp} = r_p - \frac{1}{B_p^*} \sum_j F_{pj} \quad (21a)$$

$$\alpha_{cc} = -X_c + \frac{F_{cc}}{B_c^*} (e_c - 1) + e_c \sum_j \frac{F_{jc}}{B_c^*} - \sum_j \frac{F_{cj}}{B_c^*} \quad (21b)$$

We can observe here that α_{cc} can be rewritten as

$$\alpha_{cc} = -X_c + \frac{F_{cc}}{B_c^*} (e_c - 1) + \frac{1}{B_c^*} (e_c F_c - L_c) \quad (22)$$

where F_i sets the sum of fluxing ingoing to species i and L_i its losses due to consumption. As we assume a steady state, ingoing fluxes compensate outgoing fluxes plus physiological losses: $e_c F_i = L_i + X_i$. From that, we obtain:

$$\alpha_{cc} = -X_c + \frac{F_{cc}}{B_c^*} (e_c - 1) - \frac{X_c}{B_c^*} \quad (23)$$

2.1.2 Efficiencies defined at prey level

The Lotka Voltera system is now written as:

$$\frac{dB_i}{dt} = r_i B_i - \sum_j a_{ij} B_i B_j \quad (\text{for producers}) \quad (24a)$$

$$\frac{dB_i}{dt} = -X_i B_i + \sum_j e_j a_{ji} B_i B_j - \sum_j a_{ij} B_i B_j \quad (\text{for consumers}) \quad (24b)$$

Here e_j defines efficiency of prey species j . At equilibrium, off-diagonal elements of the Jacobian are as above:

$$\alpha_{ij} = e_j \frac{F_{ji}}{B_j^*} - \frac{F_{ij}}{B_j^*} \quad i \neq j \quad (25)$$

Diagonal elements, considering possible cannibalistic loops, for producers (p) and consumers (c) are:

$$\alpha_{pp} = r_p - \sum_j a_{pj} B_j \quad (26a)$$

$$\alpha_{cc} = -X_c + 2e_c a_{cc} B_c + \sum_{j \neq c} e_j a_{jc} B_j - 2a_{cc} B_c - \sum_{j \neq c} a_{cj} B_j \quad (26b)$$

$$= -X_c + e_c a_{cc} B_c + \sum_j e_j a_{jc} B_j - a_{cc} B_c - \sum_j a_{cj} B_j \quad (26c)$$

which, at equilibrium leads, like above, to:

$$\alpha_{pp} = r_p - \frac{1}{B_p^*} \sum_j F_{pj} \quad (27a)$$

$$\alpha_{cc} = -X_c + \frac{F_{cc}}{B_c^*} (e_c - 1) + \sum_j e_j \frac{F_{jc}}{B_c^*} - \sum_j \frac{F_{cj}}{B_c^*} \quad (27b)$$

2.1.3 Preferences defined at link level

Following the same mathematical derivation as before, we obtain:

$$\alpha_{ij} = e_{ij} \frac{F_{ji}}{B_j^*} - \frac{F_{ij}}{B_j^*} \quad i \neq j \quad (28a)$$

$$\alpha_{pp} = r_p - \frac{1}{B_p^*} \sum_j F_{pj} \quad (28b)$$

$$\alpha_{cc} = -X_c + \frac{F_{cc}}{B_c^*} (e_{cc} - 1) + \sum_j e_{jc} \frac{F_{jc}}{B_c^*} - \sum_j \frac{F_{cj}}{B_c^*} \quad (28c)$$

3 Supplementary information III - sensitivity to input parameters

We estimated here if the uncertainty or the lack of precision of the estimation of parameters tended to lead to large errors in the estimation of fluxes. To do so, we used the *sensitivity* function to estimate the sensitivity of the *fluxing*

function to input parameters. The *sensitivity* function applies a random variation to a selected input parameter of the *fluxing* function. As a result, it returns a matrix containing, for each for each flux, its average coefficient of variation, estimated as:

$$cv = \frac{F''[i, j] - F[i, j]}{F[i, j]}$$

where $F[i, j]$ is the flux from species i to species j when no variation is applied to parameters and $F''[i, j]$ is its equivalent when a random variation is applied.

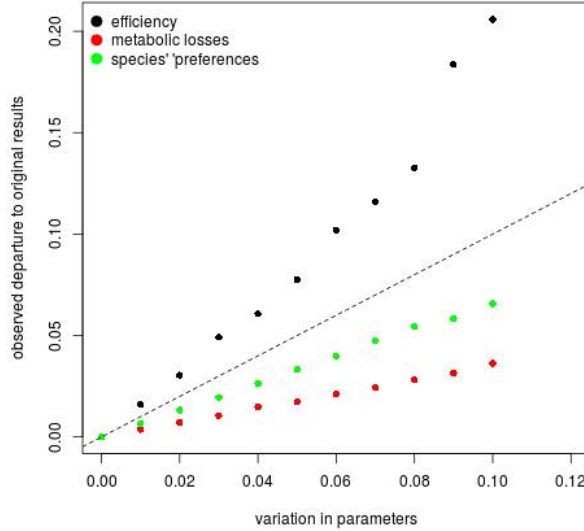


Figure 1: Representation of output uncertainties of the *fluxing* function (y axis) when a random variation is applied to an input parameter. The x axis represent the uncertainty applied to parameters (*var* argument of the *sensitivity* function). The dashed line represents the identity.

Here, we considered the sensitivity of the *fluxing* function to the *losses*, *efficiencies* and *preferences* parameters using the *species.level* example. For each of these parameters, we simulated an uncertainty on the precision of the estimation method by increasing the value of the *var* parameter of *sensitivity* from 0 to 0.12 (by steps of 0.01) using 50 replicates each. Thus, for each flux and each parameter variation, we obtained the standard deviation of its departure (*cv*) to the original value. To summarise these results,

we calculated the mean of these standard deviations over all fluxes for each parameter variation. We then obtained a scalar value representative of the uncertainty of the result of the *fluxing* function depending on the lack of precision of parameter estimation. The fig. 1 was generated using the following code:

```
attach(species.level)
set.seed(12)
losses = 0.71*bodymasses^-0.25

# creation of vectors to store the standard deviation of c.v.
# for each uncertainty level
sd.cvs.eff = c()
sd.cvs.los = c()
sd.cvs.mat = c()

for (var in seq(0, 0.12, 0.01)){
  cat("var: ", var, "\n")
  # for efficiencies
  res = sensitivity(fluxing, "efficiencies", var, 50,
                    mat = mat,
                    biomasses = biomasses,
                    losses = losses,
                    efficiencies = efficiencies)
  sd.cvs.eff = c(sd.cvs.eff, mean(res[[2]], na.rm = T))

  # for losses
  res = sensitivity(fluxing, "losses", var, 50,
                    mat = mat,
                    biomasses = biomasses,
                    losses = losses,
                    efficiencies = efficiencies)
  sd.cvs.los = c(sd.cvs.los, mean(res[[2]], na.rm = T))

  # for preferences
  res = sensitivity(fluxing, "mat", var, 50,
                    mat = mat,
                    biomasses = biomasses,
                    losses = losses,
                    efficiencies = efficiencies)
```



```

sd.cvs.mat = c(sd.cvs.mat, mean(res[[2]], na.rm = T))
}

plot(sd.cvs.eff ~ seq, xlim = c(0,0.12),
      xlab = "variation in parameters",
      ylab = "observed departure to original results",
      pch = 16)
points(sd.cvs.los ~ seq, col = "red", pch = 16)
points(sd.cvs.mat ~ seq, col = "green", pch = 16)
abline(a = 0, b= 1, lty = 2)
legend("topleft",
       legend = c("efficiency", "metabolic losses",
                  "species" "preferences"),
       col = c("black", "red", "green"),
       pt.cex = 1.5, bty = "n",
       pt.bg = c("black", "red", "green"), pch = 21)

```

References

- [1] John C Moore and Peter C de Ruiter. *Energetic Food Webs:An analysis of real and model ecosystems*. Oxford University Press, 2012.