

# FishErles Size and functional TYpe model in R (FEISTY)

Ken H Andersen and Karline Soetaert Yixin Zhao

2024

## Aim.

This document describes how to run the Feisty model in R.

DESCRIBE IT BETTER

## existing parameter data sets

Several functions to create suitable parameter inputs are included:

- `setupBasic` creates a basic three-species setup as described in Petrik et al (2019)
- `setupBasic2` creates a basic three-species setup as `setupBasic()`, but generalised to: more realistic sizes, Generalized size-based feeding, the possibility of more then 3 size groups in each group
- `setupVertical` makes a basic four-species setup that distinguishes between visual and twilight predators and that includes vertical distribution of zooplankton
- `setupPelagicSpecies` makes a basic setup with just pelagic fish, and with feeding preferences according to the size ratios of predators and prey.

blabla

## Example

The model is first run with the default 3-functional group parameters, created with `setupBasic()`. Then two similar parameter datasets are created, with rates doubled or halved.

```
p <- setupBasic()
knitr::kable(p$resources, digits=2)
```

	K	r	mc	mLower	mUpper	u0
smallZoo	100	1	0.00	NA	NA	NA
largeZoo	100	1	0.02	NA	NA	NA
benthos	5	1	0.25	NA	NA	NA
Spare_position	0	1	5.59	NA	NA	NA

```
knitr::kable(p$fishes, digits=2)
```

	mc	mLower	mUpper	z	psiMature	mortF	mort0	Cmax	metabolism	V
smallPel_1	0.02	0.0	0.5	500	0.0	0.00	0.1	51.72	7.81	149.69
smallPel_2	11.18	0.5	250.0	500	0.5	0.30	0.1	10.94	2.63	43.19
largePel_1	0.02	0.0	0.5	500	0.0	0.00	0.1	51.72	7.81	149.69
largePel_2	11.18	0.5	250.0	500	0.0	0.03	0.1	10.94	2.63	43.19
largePel_3	5590.17	250.0	125000.0	500	0.5	0.30	0.1	2.31	0.89	12.46
demersals_1	0.02	0.0	0.5	500	0.0	0.00	0.1	51.72	7.81	149.69
demersals_2	11.18	0.5	250.0	500	0.0	0.03	0.1	10.94	2.63	43.19
demersals_3	5590.17	250.0	125000.0	500	0.5	0.30	0.1	2.31	0.89	12.46

```
knitr::kable(p$groups, digits=2)
```

	epsRepro	epsAssim
smallPel	0.01	0.7
largePel	0.01	0.7
demersals	0.01	0.7

Function *paramAddPhysiology* is used to change the allometric rates:

```
p2 <- paramAddPhysiology(p, ac = 40, am = 8, ae=140)
p3 <- paramAddPhysiology(p, ac = 10, am = 2, ae=35)
```

The model can now be run for all parameter sets; the result for the last 20 years are shown.

```
out1 <- simulateFEISTY(p=p, times=seq(0, 200, length.out=1000), bCust=T)
out2 <- simulateFEISTY(p=p2, times=seq(0, 200, length.out=1000), bCust=T)
out3 <- simulateFEISTY(p=p3, times=seq(0, 200, length.out=1000), bCust=T)
# plot(out1, out2, out3, which=5:12, lty=1, lwd=2, subset=time>180)
# plot(out1, out2, out3, which=c("smallZoo", "largeZoo", "smallBenthos",
# "totBiomass.smallPel", "totBiomass.largePel", "totBiomass.Demersals"),
# lty=1, lwd=2, subset=time>180)
```

## Appendix 1. The size-based model

### Fish dynamics

For each fish stage, the dynamics of its biomass reads (see de Roos et al., 2008):

$$\frac{dC_i}{dt} = G_i - F_i + (e_{a_i} - m_i) \cdot C_i - r_{p_i} \cdot C_i$$

where  $C_i$  is expressed e.g. in  $gWW/m^2$ .

The losses due to growth are:

$$F_i = \frac{g_i - m_i}{1 - \frac{1}{z_i}^{1-m_i/g_i}} \cdot C_i$$

and the growth in each stage is:

$$G_1 = \sum_{i=1}^N \{\psi_{repro} \cdot r_{p_i} \cdot C_i\}$$

$$G_i = F_{i-1} \quad \text{for } i > 1$$

Here  $g = (1 - \psi_{mat}) \cdot e^+$  is the energy available for growth,  $e_a^+ = \max(0, e_a)$ , and  $z_i = \frac{s_{i+1}}{s_i}$  is the size ratio of the stages.

Available energy for growth or reproduction comes from assimilated food (left term) minus basal respiration (right term):

$$e_a = \psi_{Ass} \cdot \frac{E}{c_{max} + E} \cdot c_{max} - \mu$$

$c_{max}$  is the maximum consumption rate, and the encounter rates,  $E$ , are calculated as:

$$E = \nu \cdot (\theta \times C)$$

with  $\nu$  the clearance rate, and  $\theta_{i,j}$  the feeding preference matrix for consumer  $i$  feeding on prey  $j$ .

Reproduction ( $r_p$ ) only occurs when there is an energy surplus:

$$r_p = \psi_{mat} \cdot e^+$$

Total mortality is the sum of predation mortality, basal mortality and fishing-induced mortality:

$$m = \theta^t \times \left\{ \frac{c_{max} \cdot \nu}{c_{max} + E} \cdot C \right\} + m_0 + m_F$$

The maximal consumption rate ( $c_{max_i}$ ), clearance rate (or encounter rate,  $\nu_i$ ) and metabolism rate ( $\mu_i$ ) is, for each fish stage estimated as a function of its mean size ( $m_i$ ):

$$c_{max_i} = a_c \cdot m_i^{b_c}; \quad \nu_i = a_e \cdot m_i^{b_e}; \quad \mu_i = a_\mu \cdot m_i^{b_\mu}$$

### Resource dynamics

Logistic growth or chemostat-like dilution describes how the resource density evolves over time:

$$\frac{dR}{dt} = r \cdot R \cdot \left(1 - \frac{R}{K}\right) - m_R \cdot R,$$

$$\frac{dR}{dt} = r \cdot (K - R) - m_R \cdot R,$$

where the second term in each equation is the resource mortality due to feeding by fishes.

## References

- R Core Team (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.
- Van Denderen et al. 2020. Emergent global biogeography of marine fish food webs. *Global Ecology and Biogeography*, DOI: 10.1111/geb.13348
- Petrik, CM, Stock, CA, Andersen, KH, van Denderen, PD, Watson, JR 2019. Bottom-up drivers of global patterns of demersal, forage, and pelagic fishes. *Progress in Oceanography*, 176, 102124. DOI: 10.1016/j.pocean.2019.102124
- De Roos, A.M., Schellekens, T., Van Kooten, T., Van De Wolfshaar, K., Claessen, D., Persson, L., 2008. Simplifying a physiologically structured population model to a stage-structured biomass model. *Theor. Popul Biol.* 73, 47–62.