FishErIes Size and functional TYpe model (FEISTY) in R

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Introduction

The R package **FEISTY** is to document the FEITY model and for further model development and research. This document describes how to run the FEISTY model in R.

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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 possiblity 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 prameters, 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 reulst 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 $gWW/m2$.

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:

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

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

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 ν 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:

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

The maximal consumption rate (c_{max_i}), clearance rate (or encounter rate, ν_i) and metabolism rate (μ_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:

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

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

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

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