Mizer : : CHEAT SHEET

setting up the Multi-Species Model

mizer
Multi-Species Size Spectrum Modelling in R

Running Your First Model

Mizer is an ecosystem model to project fish communities under fishing pressure.

1. Choose a model type. Mizer offers three types of models as default. A community model, a trait-based model and a multi-species (MS) model.

   mizer::**newCommunityParams()**- Specifies the community model

   mizer::**newTraitParams()**- Specifies the trait-based model

   mizer::**newMultispeciesParams()**- Specifies the MS model

   To get started, let's choose the multi-species.

2. Set the model parameters.

   Params <- newMultispeciesParams(NS_species_params)

   Here we assign the North Sea dataset that comes with Mizer to the MS model. The only required argument is the dataframe of species specific parameter values.

3. Run a simulation.

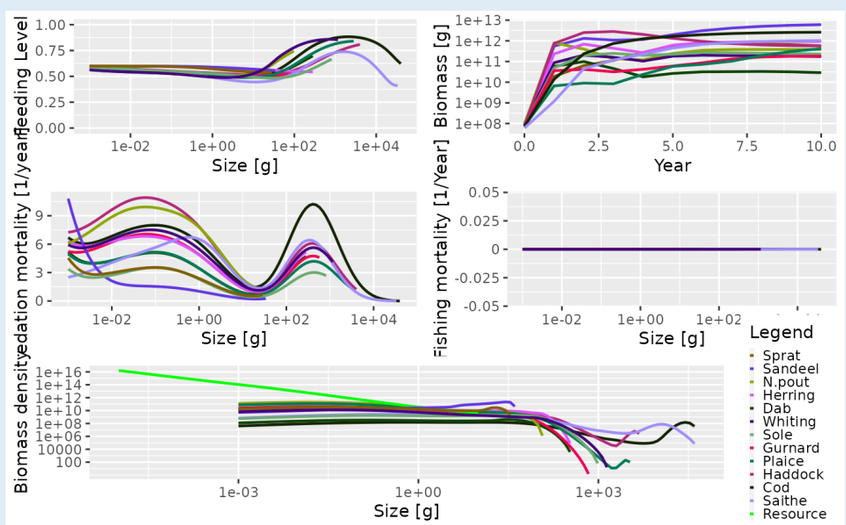
   sim <- project(Params)

   Project simulates the ecosystem using our parameters

4. Explore Results

   plot(sim)

   Plot makes 5 diagnostic plots to assess our model results (below)



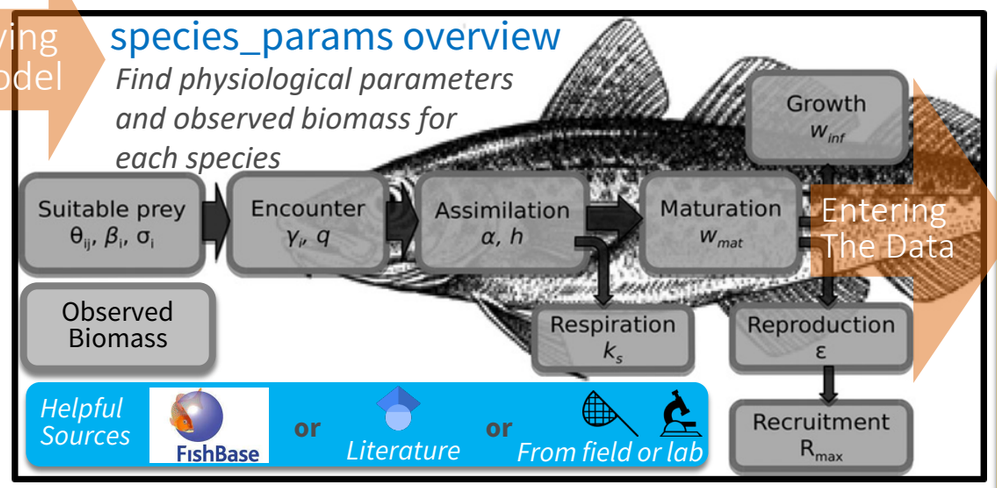
5. Experiment with different model variations and parameters

   See the other panels to customize and improve your own ecosystem model

Improving The Model

species_params overview

Find physiological parameters and observed biomass for each species



Entering The Data

newMultispeciesParams()

Data Frame · Array · Number · Vector · String

User Provided · Optional

Argument and Default Value	Data	Source	Purpose
species_params			*Species specific parameters*
interaction = NULL			*Predator-Prey Interactions*
no_w = 100			*Number of size bins*
min_w = 0.001			*Size of eggs*
max_w = NA			*Largest consumer size*
min_w_pp = NA			*Smallest resource size*
pred_kernel = NULL			*Species-size specific predation kernel*
search_vol = NULL			*Species-size specific search volume*
intake_max = NULL			*Species-size specific maximum intake rate*
metab = NULL			*Species-size specific metabolic rate*
p = 0.7			*Allometric metabolic exponent*
z0 = NULL			*Species-size external mortality rate*
z0pre = 0.6			*Coefficient of extenral mortality rate*
z0exp = n - 1			*Exponent of external mortality rate*
maturity = NULL			*Species-size specific maturity*
repro_prop = NULL			*Species-size specific reproduction*
RDD = "BevertonHoltRDD"			*Function for reproduction rate*
resource_rate = NULL			*Resource birth rates*
resource_capacity = NULL			*Resource carrying capacity*
gear_params = NULL			*Dataframe of fishing gears*
selectivity = NULL			*Species specific gear selectivity*
catchability = NULL			*Species specific gear catchability*
initial_effort = NULL			*Initial fishing effort*
n = 2/3			*Allometric growth exponent*
r_pp = 10			*Coefficient of resource birth rates*
kappa = 1e+11			*Coefficient of resource carrying capacity*
lambda = 2.05			*Exponent of resource carrying capacity*
w_pp_cutoff = 10			*Max size of resource*
resource_dynamics = "resource_semichemostat"			*Function for resources*

Key Model Requirements

The species_params Data Frame

Parameter	Source	Purpose
species		*Species name*
k		*Metabolic rate*
ks		*Standard metabolism*
p		*Metabolic exponent*
z0		*External mortality*
w_mat		*Maturity weight*
w_mat25		*25% maturity*
w_inf		*Asymptotic weight*
w_min		*Egg size*
beta		*Preferred predator/prey ratio*
sigma		*Predation kernel width*
k_vb		*Growth coefficient*
t0		*Theoretical age zero length*
f0		*Feeding value*
fc		*Critical feeding level*
alpha		*Assimilation efficiency*
interaction_resource		*Interaction strength*
erepro		*Reproductive effiency*
Rmax		*Max reproduction*
biomass_observed		*Observed biomass*

How to convert length (l_inf) of a species to w_inf?

$$W_\infty = a \cdot L_\infty^b$$

a = Length-Weight Coefficient
b = Length-Weight Exponent

No "a" or "b"? Try using of a = 0.001 $\frac{g}{cm^3}$ and b = 3*

Making Your Interactions Matrix

An interaction matrix is the spatial overlap between species with values ranging 0-1 for each species.

Mizer::inter *This shows an example matrix*

The gear_params Data Frame

This dataframe contains species, gear, selectivity functions & arguments, and catchability.

species	gear	sel_func	knife_edge_size	catchability
Sprat	knife_edge_gear	knife_edge	13	1
Sandeel	knife_edge_gear	knife_edge	4	1

Setting resource parameters

These parameters control the amount of "food" available for all fish species. By default these are provided but will likely need adjustment to match the size of your system.

* Froese (2006) J. Appl. Ichthyol. 22 (2006), 241–253