Package 'mizer'

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Title Multi-Species sIZE Spectrum Modelling in R

Type Package

Description A set of classes and methods to set up and run multi-species, trait based and community size spectrum ecological models, focused on the marine environment.

Maintainer Gustav Delius <gustav.delius@york.ac.uk>

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Imports assertthat, deSolve, dplyr, ggplot2, ggrepel, grid, lubridate, methods, plotly, plyr, progress, Rcpp, reshape2, rlang, lifecycle

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Author Gustav Delius [cre, aut, cph] (<https://orcid.org/0000-0003-4092-8228>),
Finlay Scott [aut, cph],
Julia Blanchard [aut, cph] (<https://orcid.org/0000-0003-0532-4824>),
Ken Andersen [aut, cph] (<https://orcid.org/0000-0002-8478-3430>),
Richard Southwell [ctb, cph]

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`mizer-package` *mizer: Multi-species size-based modelling in R*

Description

The mizer package implements multi-species size-based modelling in R. It has been designed for modelling marine ecosystems.

Details

Using **mizer** is relatively simple. There are three main stages:

1. *Setting the model parameters*. This is done by creating an object of class MizerParams. This includes model parameters such as the life history parameters of each species, and the range of the size spectrum. There are several setup functions that help to create a MizerParams objects for particular types of models:
   - `newCommunityParams()`
   - `newTraitParams()`
   - `newMultispeciesParams()`
2. *Running a simulation*. This is done by calling the `project()` function with the model parameters. This produces an object of MizerSim that contains the results of the simulation.
3. *Exploring results*. After a simulation has been run, the results can be explored using a range of plotting_functions, summary_functions and indicator_functions.

See the mizer website for full details of the principles behind mizer and how the package can be used to perform size-based modelling.

Author(s)

Maintainer: Gustav Delius <gustav.delius@york.ac.uk> (ORCID) [copyright holder]

Authors:

- Finlay Scott <drfinlayscott@gmail.com> [copyright holder]
- Julia Blanchard <julia.blanchard@utas.edu.au> (ORCID) [copyright holder]
- Ken Andersen <kha@aqua.dtu.dk> (ORCID) [copyright holder]

Other contributors:

- Richard Southwell <richard.southwell@york.ac.uk> [contributor, copyright holder]

See Also

Useful links:

- https://sizespectrum.org/mizer/
- https://github.com/sizespectrum/mizer
- Report bugs at https://github.com/sizespectrum/mizer/issues

addSpecies *Add new species*

Description

[Experimental]

Takes a MizerParams object and adds additional species with given parameters to the ecosystem. It sets the initial values for these new species to their steady-state solution in the given initial state of the existing ecosystem. This will be close to the true steady state if the abundances of the new species are sufficiently low. Hence the abundances of the new species are set so that they are at most 1/100th of the resource power law. Their reproductive efficiencies are set so as to keep them at that low level.

Usage

```
addSpecies(
  params,
  species_params,
  gear_params = data.frame(),
  initial_effort,
  interaction
)
```

Arguments

`params`	A mizer params object for the original system.
`species_params`	Data frame with the species parameters of the new species we want to add to the system.
`gear_params`	Data frame with the gear parameters for the new species. If not provided then the new species will not be fished.
`initial_effort`	A named vector with the effort for new fishing gear introduced in `gear_params`. New gear for which no effort is set via this vector will have an initial effort of 0. Should not include effort values for existing gear.
`interaction`	Interaction matrix. A square matrix giving either the interaction coefficients between all species or only those between the new species. In the latter case all interaction between an old and a new species are set to 1. If this argument is missing, all interactions involving a new species are set to 1.

Details

The resulting MizerParams object will use the same size grid where possible, but if one of the new species needs a larger range of w (either because a new species has an egg size smaller than those of existing species or a maximum size larger than those of existing species) then the grid will be expanded and all arrays will be enlarged accordingly.

If any of the rate arrays of the existing species had been set by the user to values other than those calculated as default from the species parameters, then these will be preserved. Only the rates for the new species will be calculated from their species parameters.

After adding the new species, the background species are not retuned and the system is not run to steady state. This could be done with `steady()`. The new species will have a reproduction level of 1/4, this can then be changed with `setBevertonHolt()`

Value

An object of type MizerParams

See Also

`removeSpecies()`

Examples

```
params <- newTraitParams()
species_params <- data.frame(
    species = "Mullet",
    w_inf = 173,
    w_mat = 15,
    beta = 283,
    sigma = 1.8,
    k_vb = 0.6,
    a = 0.0085,
    b = 3.11
)
params <- addSpecies(params, species_params)
plotSpectra(params)
```

`animateSpectra` *Animation of the abundance spectra*

Description

[Experimental]

Usage

```
animateSpectra(
  sim,
  species = NULL,
  time_range,
  wlim = c(NA, NA),
  ylim = c(NA, NA),
  power = 1,
  total = FALSE,
  resource = TRUE
)
```

Arguments

sim	A MizerSim object
species	Name or vector of names of the species to be plotted. By default all species are plotted.
time_range	The time range to animate over. Either a vector of values or a vector of min and max time. Default is the entire time range of the simulation.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA to refer to the existing minimum or maximum.
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to refer to the existing minimum or maximum. Any values below 1e-20 are always cut off.
power	The abundance is plotted as the number density times the weight raised to power. The default power = 1 gives the biomass density, whereas power = 2 gives the biomass density with respect to logarithmic size bins.
total	A boolean value that determines whether the total over all species in the system is plotted as well. Default is FALSE.
resource	A boolean value that determines whether resource is included. Default is TRUE.

Value

A plotly object

See Also

Other plotting functions: plot,MizerSim,missing-method, plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
animateSpectra(NS_sim, power = 2, wlim = c(0.1, NA), time_range = 1997:2007)
```

BevertonHoltRDD *Beverton Holt function to calculate density-dependent reproduction rate*

Description

Takes the density-independent rates R_{di} of egg production (as calculated by getRDI()) and returns reduced, density-dependent reproduction rates R_{dd} given as

$$R_{dd} = R_{di} \frac{R_{max}}{R_{di} + R_{max}}$$

where R_{max} are the maximum possible reproduction rates that must be specified in a column in the species parameter dataframe. (All quantities in the above equation are species-specific but we dropped the species index for simplicity.)

Usage

```
BevertonHoltRDD(rdi, species_params, ...)
```

Arguments

rdi	Vector of density-independent reproduction rates R_{di} for all species.
species_params	A species parameter dataframe. Must contain a column R_max holding the maximum reproduction rate R_{max} for each species.
...	Unused

Details

This is only one example of a density-dependence. You can write your own function based on this example, returning different density-dependent reproduction rates. Three other examples provided are RickerRDD(), SheperdRDD(), noRDD() and constantRDD(). For more explanation see setReproduction().

Value

Vector of density-dependent reproduction rates.

See Also

Other functions calculating density-dependent reproduction rate: RickerRDD(), SheperdRDD(), constantEggRDI(), constantRDD(), noRDD()

---

box_pred_kernel *Box predation kernel*

Description

A predation kernel where the predator/prey mass ratio is uniformly distributed on an interval.

Usage

```
box_pred_kernel(ppmr, ppmr_min, ppmr_max)
```

Arguments

ppmr	A vector of predator/prey size ratios
ppmr_min	Minimum predator/prey mass ratio
ppmr_max	Maximum predator/prey mass ratio

Details

Writing the predator mass as w and the prey mass as w_p, the feeding kernel is 1 if w/w_p is between ppmr_min and ppmr_max and zero otherwise. The parameters need to be given in the species parameter dataframe in the columns ppmr_min and ppmr_max.

Value

A vector giving the value of the predation kernel at each of the predator/prey mass ratios in the ppmr argument.

`calibrateBiomass` *Calibrate the model scale to match total observed biomass*

Description

[Experimental] Given a MizerParams object `params` for which biomass observations are available for at least some species via the `biomass_observed` column in the species_params data frame, this function returns an updated MizerParams object which is rescaled with `scaleModel()` so that the total biomass in the model agrees with the total observed biomass.

Usage

```
calibrateBiomass(params)
```

Arguments

`params`	A MizerParams object

Details

Biomass observations usually only include individuals above a certain size. This size should be specified in a biomass_cutoff column of the species parameter data frame. If this is missing, it is assumed that all sizes are included in the observed biomass, i.e., it includes larval biomass.

After using this function the total biomass in the model will match the total biomass, summed over all species. However the biomasses of the individual species will not match observations yet, with some species having biomasses that are too high and others too low. So after this function you may want to use `matchBiomasses()`. This is described in the blog post at https://bit.ly/2YqXESV.

If you have observations of the yearly yield instead of biomasses, you can use `calibrateYield()` instead of this function.

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$biomass_observed <-
    c(0.8, 61, 12, 35, 1.6, 20, 10, 7.6, 135, 60, 30, 78)
species_params(params)$biomass_cutoff <- 10
params2 <- calibrateBiomass(params)
plotBiomassObservedVsModel(params2)
```

`calibrateYield` *Calibrate the model scale to match total observed yield*

Description

[Experimental] Given a MizerParams object `params` for which yield observations are available for at least some species via the `yield_observed` column in the species_params data frame, this function returns an updated MizerParams object which is rescaled with `scaleModel()` so that the total yield in the model agrees with the total observed yield.

Usage

```
calibrateYield(params)
```

Arguments

`params`	A MizerParams object

Details

After using this function the total yield in the model will match the total observed yield, summed over all species. However the yields of the individual species will not match observations yet, with some species having yields that are too high and others too low. So after this function you may want to use `matchYields()`.

If you have observations of species biomasses instead of yields, you can use `calibrateBiomass()` instead of this function.

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$yield_observed <-
    c(0.8, 61, 12, 35, 1.6, 20, 10, 7.6, 135, 60, 30, 78)
gear_params(params)$catchability <-
    c(1.3, 0.065, 0.31, 0.18, 0.98, 0.24, 0.37, 0.46, 0.18, 0.30, 0.27, 0.39)
params2 <- calibrateYield(params)
plotYieldObservedVsModel(params2)
```

compareParams *Compare two MizerParams objects and print out differences*

Description

[Experimental]

Usage

```
compareParams(params1, params2)
```

Arguments

params1	First MizerParams object
params2	Second MizerParams object

Examples

```
## Not run:
sp1 <- NS_species_params
params1 <- newMultispeciesParams(sp1)
sp2 <- sp1
sp2$w_mat[1] <- 10
params2 <- newMultispeciesParams(sp2)
compareParams(params1, params2)

## End(Not run)
```

constantEggRDI *Choose egg production to keep egg density constant*

Description

[Experimental] The new egg production is set to compensate for the loss of individuals from the smallest size class through growth and mortality. The result should not be modified by density dependence, so this should be used together with the `noRDD()` function, see example.

Usage

```
constantEggRDI(params, n, e_growth, mort, ...)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
e_growth	A two dimensional array (species x size) holding the energy available for growth as calculated by mizerEGrowth().
mort	A two dimensional array (species x size) holding the mortality rate as calculated by mizerMort().
...	Unused

See Also

Other functions calculating density-dependent reproduction rate: BevertonHoltRDD(), RickerRDD(), SheperdRDD(), constantRDD(), noRDD()

Examples

```
## Not run:
# choose an example params object
params <- NS_params
# We set the reproduction rate functions
params <- setRateFunction(params, "RDI", "constantEggRDI")
params <- setRateFunction(params, "RDD", "noRDD")
# Now the egg density should stay fixed no matter how we fish
sim <- project(params, effort = 10, progress_bar = FALSE)
# To check that indeed the egg densities have not changed, we first construct
# the indices for addressing the egg densities
no_sp <- nrow(params@species_params)
idx <- (params@w_min_idx - 1) * no_sp + (1:no_sp)
# Now we can check equality between egg densities at the start and the end
all.equal(finalN(sim)[idx], initialN(params)[idx])

## End(Not run)
```

---

constantRDD *Give constant reproduction rate*

Description

[Experimental] Simply returns the value from species_params$constant_reproduction.

Usage

```
constantRDD(rdi, species_params, ...)
```

Arguments

rdi	Vector of density-independent reproduction rates R_{di} for all species.
species_params	A species parameter dataframe. Must contain a column constant_reproduction.
...	Unused

Value

Vector species_params$constant_reproduction

See Also

Other functions calculating density-dependent reproduction rate: BevertonHoltRDD(), RickerRDD(), SheperdRDD(), constantEggRDI(), noRDD()

---

constant_other *Helper function to keep other components constant*

Description

Helper function to keep other components constant

Usage

```
constant_other(params, n_other, component, ...)
```

Arguments

params	MizerParams object
n_other	Abundances of other components
component	Name of the component that is being updated
...	Unused

---

customFunction *Replace a mizer function with a custom version*

Description

[Experimental] This function allows you to make arbitrary changes to how mizer works by allowing you to replace any mizer function with your own version. You should do this only as a last resort, when you find that you can not use the standard mizer extension mechanism to achieve your goal.

Usage

```
customFunction(name, fun)
```

Arguments

name	Name of mizer function to replace
fun	The custom function to use as replacement

Details

If the function you need to overwrite is one of the mizer rate functions, then you should use `setRateFunction()` instead of this function. Similarly you should use `setResource()` to change the resource dynamics and `setReproduction()` to change the density-dependence in reproduction. You should also investigate whether you can achieve your goal by introducing additional ecosystem components with `setComponent()`.

If you find that your goal really does require you to overwrite a mizer function, please also create an issue on the mizer issue tracker at https://github.com/sizespectrum/mizer/issues to describe your goal, because it will be interesting to the mizer community and may motivate future improvements to the mizer functionality.

Note that `customFunction()` only overwrites the function used by the mizer code. It does not overwrite the function that is exported by mizer. This will become clear when you run the code in the Examples section.

This function does not in any way check that your replacement function is compatible with mizer. Calling this function can totally break mizer. However you can always undo the effect by reloading mizer with

```
detach(package:mizer, unload = TRUE)
library(mizer)
```

Examples

```
## Not run:
fake_project <- function(...) "Fake"
customFunction("project", fake_project)
mizer::project(NS_params) # This will print "Fake"
project(NS_params) # This will still use the old project() function
# To undo the effect:
customFunction("project", project)
mizer::project(NS_params) # This will again use the old project()

## End(Not run)
```

---

default_pred_kernel_params

Set defaults for predation kernel parameters

Description

If the predation kernel type has not been specified for a species, then it is set to "lognormal" and the default values are set for the parameters `beta` and `sigma`.

Usage

```
default_pred_kernel_params(object)
```

Arguments

object	Either a MizerParams object or a species parameter data frame

Value

The object with updated columns in the species params data frame.

---

different *Check whether two objects are different*

Description

Check whether two objects are numerically different, ignoring all attributes

Usage

```
different(a, b)
```

Arguments

a	First object
b	Second object

Value

TRUE or FALSE

---

distanceMaxRelRDI *Measure distance between current and previous state in terms of RDI*

Description

[Experimental]

This function can be used in projectToSteady() to decide when sufficient convergence to steady state has been achieved.

Usage

```
distanceMaxRelRDI(params, current, previous)
```

Arguments

params	MizerParams
current	A named list with entries n, n_pp and n_other describing the current state
previous	A named list with entries n, n_pp and n_other describing the previous state

Value

The largest absolute relative change in rdi: max(abs((current_rdi -previous_rdi) / previous_rdi))

See Also

Other distance functions: distanceSSLogN()

---

distanceSSLogN *Measure distance between current and previous state in terms of fish abundances*

Description

[Experimental]

Calculates the sum squared difference between log(N) in current and previous state. This function can be used in projectToSteady() to decide when sufficient convergence to steady state has been achieved.

Usage

```
distanceSSLogN(params, current, previous)
```

Arguments

params	MizerParams
current	A named list with entries n, n_pp and n_other describing the current state
previous	A named list with entries n, n_pp and n_other describing the previous state

Value

The sum of squares of the difference in the logs of the (nonzero) fish abundances n: sum((log(current$n) -log(previous$n))^2)

See Also

Other distance functions: distanceMaxRelRDI()

double_sigmoid_length *Length based double-sigmoid selectivity function*

Description

A hump-shaped selectivity function with a sigmoidal rise and an independent sigmoidal drop-off. This drop-off is what distinguishes this from the function `sigmoid_length()` and it is intended to model the escape of large individuals from the fishing gear.

Usage

```
double_sigmoid_length(w, l25, l50, l50_right, l25_right, species_params, ...)
```

Arguments

`w`	the size of the individual.
`l25`	the length which gives a selectivity of 25%.
`l50`	the length which gives a selectivity of 50%.
`l50_right`	the length which gives a selectivity of 50%.
`l25_right`	the length which gives a selectivity of 25%.
`species_params`	A list with the species params for the current species. Used to get at the length-weight parameters `a` and `b`
`...`	Unused

Details

The selectivity is obtained as the product of two sigmoidal curves, one rising and one dropping. The sigmoidal rise is based on the two parameters `l25` and `l50` which determine the length at which 25% and 50% of the stock is selected respectively. The sigmoidal drop-off is based on the two parameters `l50_right` and `l25_right` which determine the length at which the selectivity curve has dropped back to 50% and 25% respectively.

As the size-based model is weight based, and this selectivity function is length based, it uses the length-weight parameters `a` and `b` to convert between length and weight.

emptyParams *Create empty MizerParams object of the right size*

Description

An internal function. Sets up a valid MizerParams object with all the slots initialised and given dimension names, but with some slots left empty. This function is to be used by other functions to set up full parameter objects.

Usage

```
emptyParams(
  species_params,
  gear_params = data.frame(),
  no_w = 100,
  min_w = 0.001,
  max_w = NA,
  min_w_pp = 1e-12
)
```

Arguments

species_params	A data frame of species-specific parameter values.
gear_params	A data frame with gear-specific parameter values.
no_w	The number of size bins in the consumer spectrum.
min_w	Sets the size of the eggs of all species for which this is not given in the w_min column of the species_params dataframe.
max_w	The largest size of the consumer spectrum. By default this is set to the largest w_inf specified in the species_params data frame.
min_w_pp	The smallest size of the resource spectrum.

Value

An empty but valid MizerParams object

Size grid

A size grid is created so that the log-sizes are equally spaced. The spacing is chosen so that there will be no_w fish size bins, with the smallest starting at min_w and the largest starting at max_w. For the resource spectrum there is a larger set of bins containing additional bins below min_w, with the same log size. The number of extra bins is such that min_w_pp comes to lie within the smallest bin.

Changes to species params

The species_params slot of the returned MizerParams object may differ from the data frame supplied as argument to this function because default values are set for missing parameters.

See Also

See newMultispeciesParams() for a function that fills the slots left empty by this function.

finalN *Size spectra at end of simulation*

Description

Size spectra at end of simulation

Usage

```
finalN(sim)

finalNResource(sim)
```

Arguments

sim	A MizerSim object

Value

For `finalN()`: An array (species x size) holding the consumer number densities at the end of the simulation

For `finalNResource()`: A vector holding the resource number densities at the end of the simulation for all size classes

See Also

`idxFinalT()`

Examples

```
str(finalN(NS_sim))

# This could also be obtained using `N()` and `idxFinalT()`
identical(N(NS_sim)[idxFinalT(NS_sim), , ], finalN(NS_sim))
str(finalNResource(NS_sim))
```

finalNOther *Values of other ecosystem components at end of simulation*

Description

Values of other ecosystem components at end of simulation

Usage

```
finalNOther(sim)
```

Arguments

sim	A MizerSim object

Value

A named list holding the values of other ecosystem components at the end of the simulation

---

gear_params *Gear parameters*

Description

These functions allow you to get or set the gear parameters stored in a MizerParams object. These are used by `setFishing()` to set up the selectivity and catchability and thus together with the fishing effort determine the fishing mortality.

Usage

```
gear_params(params)

gear_params(params) <- value
```

Arguments

params	A MizerParams object
value	A data frame with the gear parameters.

Details

The `gear_params` data has one row for each gear-species pair and one column for each parameter that determines how that gear interacts with that species. For the details see `setFishing()`.

If you change a gear parameter, this will be used to recalculate the `selectivity` and `catchability` arrays by calling `setFishing()`, unless you have previously set these by hand.

See Also

`validGearParams()`

Other functions for setting parameters: `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `setSearchVolume()`, `species_params()`

Examples

```
params <- NS_params
# gears set up in example
gear_params(params)
# setting totally different gears
gear_params(params) <- data.frame(
    gear = c("gear1", "gear2", "gear1"),
    species = c("Cod", "Cod", "Haddock"),
    catchability = c(0.5, 2, 1),
    sel_fun = c("sigmoid_weight", "knife_edge", "sigmoid_weight"),
    sigmoidal_weight = c(1000, NA, 800),
    sigmoidal_sigma = c(100, NA, 100),
    knife_edge_size = c(NA, 1000, NA)
    )
gear_params(params)
# changing an individual entry
gear_params(params)["Cod, gear1", "catchability"] <- 0.8
```

---

getBiomass *Calculate the total biomass of each species within a size range at each time step.*

Description

Calculates the total biomass through time within user defined size limits. The default option is to use the whole size range. You can specify minimum and maximum weight or length range for the species. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used).

Usage

```
getBiomass(sim, ...)
```

Arguments

`sim`	An object of class `MizerSim`.
`...`	Arguments passed on to `get_size_range_array`
	`min_w` Smallest weight in size range. Defaults to smallest weight in the model.
	`max_w` Largest weight in size range. Defaults to largest weight in the model.
	`min_l` Smallest length in size range. If supplied, this takes precedence over `min_w`.
	`max_l` Largest length in size range. If supplied, this takes precedence over `max_w`.

Value

An array (time x species) containing the biomass in grams.

See Also

Other summary functions: `getDiet()`, `getGrowthCurves()`, `getN()`, `getSSB()`, `getYieldGear()`, `getYield()`

Examples

```
biomass <- getBiomass(NS_sim)
biomass["1972", "Herring"]
biomass <- getBiomass(NS_sim, min_w = 10, max_w = 1000)
biomass["1972", "Herring"]
```

`getCommunitySlope` *Calculate the slope of the community abundance*

Description

Calculates the slope of the community abundance through time by performing a linear regression on the logged total numerical abundance at weight and logged weights (natural logs, not log to base 10, are used). You can specify minimum and maximum weight or length range for the species. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used). You can also specify the species to be used in the calculation.

Usage

```
getCommunitySlope(sim, species = NULL, biomass = TRUE, ...)
```

Arguments

`sim`	A MizerSim object
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`biomass`	Boolean. If TRUE (default), the abundance is based on biomass, if FALSE the abundance is based on numbers.
`...`	Arguments passed on to `get_size_range_array` `min_w` Smallest weight in size range. Defaults to smallest weight in the model. `max_w` Largest weight in size range. Defaults to largest weight in the model. `min_l` Smallest length in size range. If supplied, this takes precedence over `min_w`. `max_l` Largest length in size range. If supplied, this takes precedence over `max_w`.

Value

A data.frame with four columns: time step, slope, intercept and the coefficient of determination R^2.

See Also

Other functions for calculating indicators: `getMeanMaxWeight()`, `getMeanWeight()`, `getProportionOfLargeFish()`

Examples

```
# Slope based on biomass, using all species and sizes
slope_biomass <- getCommunitySlope(NS_sim)
slope_biomass[1, ] # in 1976
slope_biomass[idxFinalT(NS_sim), ] # in 2010

# Slope based on numbers, using all species and sizes
slope_numbers <- getCommunitySlope(NS_sim, biomass = FALSE)
slope_numbers[1, ] # in 1976

# Slope based on biomass, using all species and sizes between 10g and 1000g
slope_biomass <- getCommunitySlope(NS_sim, min_w = 10, max_w = 1000)
slope_biomass[1, ] # in 1976

# Slope based on biomass, using only demersal species and
# sizes between 10g and 1000g
dem_species <- c("Dab","Whiting", "Sole", "Gurnard", "Plaice",
                 "Haddock", "Cod", "Saithe")
slope_biomass <- getCommunitySlope(NS_sim, species = dem_species,
                                   min_w = 10, max_w = 1000)
slope_biomass[1, ] # in 1976
```

`getComponent` *Get information about other ecosystem components*

Description

Get information about other ecosystem components

Usage

```
getComponent(params, component)
```

Arguments

`params`	A MizerParams object
`component`	Name of the component of interest. If missing, a list of all components will be returned.

Value

A list with the entries `initial_value`, `dynamics_fun`, `encounter_fun`, `mort_fun`, `component_params` for the requested component. If the requested component does not exist, `NULL` is returned. If no `component` argument is given, then a list of lists for all components is returned.

getCriticalFeedingLevel *Get critical feeding level*

Description

The critical feeding level is the feeding level at which the food intake is just high enough to cover the metabolic costs, with nothing left over for growth or reproduction.

Usage

```
getCriticalFeedingLevel(params)
```

Arguments

params	A MizerParams object

Value

A matrix (species x size) with the critical feeding level

getDiet *Get diet of predator at size, resolved by prey species*

Description

Calculates the rate at which a predator of a particular species and size consumes biomass of each prey species and resource. The diet has units of grams/year.

Usage

```
getDiet(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  proportion = TRUE
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
proportion	If TRUE (default) the function returns the diet as a proportion of the total consumption rate. If FALSE it returns the consumption rate in grams per year.

Details

Returns the rates $D_{ij}(w)$ at which a predator of species i and size w consumes biomass from prey species j. This is calculated from the predation kernel $\phi_i(w, w_p)$, the search volume $\gamma_i(w)$, the feeding level $f_i(w)$, the species interaction matrix θ_{ij} and the prey abundance density $N_j(w_p)$:

$$D_{ij}(w, w_p) = (1 - f_i(w))\gamma_i(w)\theta_{ij} \int N_j(w_p)\phi_i(w, w_p)w_p dw_p.$$

The prey index j runs over all species and the resource. It also runs over any extra ecosystem components in your model for which you have defined an encounter rate function. This encounter rate is multiplied by $1 - f_i(w)$ to give the rate of consumption of biomass from these extra components.

This function performs the same integration as `getEncounter()` but does not aggregate over prey species, and multiplies by $1 - f_i(w)$ to get the consumed biomass rather than the available biomass. Outside the range of sizes for a predator species the returned rate is zero.

Value

An array (predator species x predator size x (prey species + resource + other components))

See Also

`plotDiet()`

Other summary functions: `getBiomass()`, `getGrowthCurves()`, `getN()`, `getSSB()`, `getYieldGear()`, `getYield()`

Examples

```
diet <- getDiet(NS_params)
str(diet)
```

`getEffort` *Fishing effort used in simulation*

Description

Note that the array returned may not be exactly the same as the `effort` argument that was passed in to `project()`. This is because only the saved effort is stored (the frequency of saving is determined by the argument `t_save`).

Usage

```
getEffort(sim)
```

Arguments

`sim`	A MizerSim object

Value

An array (time x gear) that contains the fishing effort by time and gear.

Examples

```
str(getEffort(NS_sim))
```

`getEGrowth` *Get energy rate available for growth*

Description

Calculates the energy rate $g_i(w)$ (grams/year) available by species and size for growth after metabolism, movement and reproduction have been accounted for.

Usage

```
getEGrowth(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Value

A two dimensional array (prey species x prey size)

Your own growth rate function

By default `getEGrowth()` calls `mizerEGrowth()`. However you can replace this with your own alternative growth rate function. If your function is called `"myEGrowth"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "EGrowth", "myEGrowth")
```

Your function will then be called instead of `mizerEGrowth()`, with the same arguments.

See Also

getERepro(), getEReproAndGrowth()

Other rate functions: getEReproAndGrowth(), getERepro(), getEncounter(), getFMortGear(), getFMort(), getFeedingLevel(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the energy at a particular time step
getEGrowth(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)

## End(Not run)
```

---

getEncounter *Get encounter rate*

Description

Returns the rate at which a predator of species i and weight w encounters food (grams/year).

Usage

```
getEncounter(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
...	Unused

Value

A named two dimensional array (predator species x predator size) with the encounter rates.

Predation encounter

The encounter rate $E_i(w)$ at which a predator of species i and weight w encounters food has contributions from the encounter of fish prey and of resource. This is determined by summing over all prey species and the resource spectrum and then integrating over all prey sizes w_p, weighted by predation kernel $\phi(w, w_p)$:

$$E_i(w) = \gamma_i(w) \int \left(\theta_{ip} N_R(w_p) + \sum_j \theta_{ij} N_j(w_p) \right) \phi_i(w, w_p) w_p \, dw_p.$$

Here $N_j(w)$ is the abundance density of species j and $N_R(w)$ is the abundance density of resource. The overall prefactor $\gamma_i(w)$ determines the predation power of the predator. It could be interpreted as a search volume and is set with the `setSearchVolume()` function. The predation kernel $\phi(w, w_p)$ is set with the `setPredKernel()` function. The species interaction matrix θ_{ij} is set with `setInteraction()` and the resource interaction vector θ_{ip} is taken from the `interaction_resource` column in `params@species_params`.

Details

The encounter rate is multiplied by $1 - f_0$ to obtain the consumption rate, where f_0 is the feeding level calculated with `getFeedingLevel()`. This is used by the `project()` function for performing simulations.

The function returns values also for sizes outside the size-range of the species. These values should not be used, as they are meaningless.

If your model contains additional components that you added with `setComponent()` and for which you specified an `encounter_fun` function then the encounters of these components will be included in the returned value.

Your own encounter function

By default `getEncounter()` calls `mizerEncounter()`. However you can replace this with your own alternative encounter function. If your function is called `"myEncounter"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "Encounter", "myEncounter")
```

Your function will then be called instead of `mizerEncounter()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
encounter <- getEncounter(NS_params)
str(encounter)
```

`getERepro` *Get energy rate available for reproduction*

Description

Calculates the energy rate (grams/year) available for reproduction after growth and metabolism have been accounted for.

Usage

```
getERepro(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Value

A two dimensional array (prey species x prey size) holding

$$\psi_i(w) E_{r.i}(w)$$

where $E_{r.i}(w)$ is the rate at which energy becomes available for growth and reproduction, calculated with `getEReproAndGrowth()`, and $\psi_i(w)$ is the proportion of this energy that is used for reproduction. This proportion is taken from the `params` object and is set with `setReproduction()`.

Your own reproduction rate function

By default `getERepro()` calls `mizerERepro()`. However you can replace this with your own alternative reproduction rate function. If your function is called `"myERepro"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "ERepro", "myERepro")
```

Your function will then be called instead of `mizerERepro()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the energy at a particular time step
getERepro(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)

## End(Not run)
```

`getEReproAndGrowth` *Get energy rate available for reproduction and growth*

Description

Calculates the energy rate $E_{r.i}(w)$ (grams/year) available for reproduction and growth after metabolism and movement have been accounted for.

Usage

```
getEReproAndGrowth(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
...	Unused

Value

A two dimensional array (species x size) holding

$$E_{r.i}(w) = \max(0, \alpha_i \, (1 - \texttt{feeding\_level}_i(w)) \, \texttt{encounter}_i(w) - \texttt{metab}_i(w)).$$

Due to the form of the feeding level, calculated by `getFeedingLevel()`, this can also be expressed as

$$E_{r.i}(w) = \max(0, \alpha_i \, \texttt{feeding\_level}_i(w) \, h_i(w) - \texttt{metab}_i(w))$$

where h_i is the maximum intake rate, set with `setMaxIntakeRate()`. The assimilation rate α_i is taken from the species parameter data frame in `params`. The metabolic rate `metab` is taken from `params` and set with `setMetabolicRate()`.

The return value can be negative, which means that the energy intake does not cover the cost of metabolism and movement.

Your own energy rate function

By default `getEReproAndGrowth()` calls `mizerEReproAndGrowth()`. However you can replace this with your own alternative energy rate function. If your function is called `"myEReproAndGrowth"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "EReproAndGrowth", "myEReproAndGrowth")
```

Your function will then be called instead of `mizerEReproAndGrowth()`, with the same arguments.

See Also

The part of this energy rate that is invested into growth is calculated with `getEGrowth()` and the part that is invested into reproduction is calculated with `getERepro()`.

Other rate functions: `getEGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the energy at a particular time step
getEReproAndGrowth(params, n = N(sim)[15, , ],
                   n_pp = NResource(sim)[15, ], t = 15)

## End(Not run)
```

`getESpawning` *Alias for* `getERepro()`

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 1.0

Usage

```
getESpawning(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Value

A two dimensional array (prey species x prey size) holding

$$\psi_i(w) E_{r.i}(w)$$

where $E_{r.i}(w)$ is the rate at which energy becomes available for growth and reproduction, calculated with `getEReproAndGrowth()`, and $\psi_i(w)$ is the proportion of this energy that is used for reproduction. This proportion is taken from the `params` object and is set with `setReproduction()`.

Your own reproduction rate function

By default `getERepro()` calls `mizerERepro()`. However you can replace this with your own alternative reproduction rate function. If your function is called `"myERepro"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "ERepro", "myERepro")
```

Your function will then be called instead of `mizerERepro()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the energy at a particular time step
getERepro(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)

## End(Not run)
```

`getFeedingLevel` *Get feeding level*

Description

Returns the feeding level. By default this function uses `mizerFeedingLevel()` to calculate the feeding level, but this can be overruled via `setRateFunction()`.

Usage

```
getFeedingLevel(object, n, n_pp, n_other, time_range, drop = FALSE, ...)
```

Arguments

`object`	A `MizerParams` object or a `MizerSim` object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`time_range`	A vector of times. Only the range of times is relevant, i.e., all times between the smallest and largest will be selected. The time_range can be character or numeric.
`drop`	If `TRUE` then any dimension of length 1 will be removed from the returned array.
`...`	Unused

Value

If a MizerParams object is passed in, the function returns a two dimensional array (predator species x predator size) based on the abundances also passed in. If a MizerSim object is passed in, the function returns a three dimensional array (time step x predator species x predator size) with the feeding level calculated at every time step in the simulation. If drop = TRUE then the dimension of length 1 will be removed from the returned array.

Feeding level

The feeding level $f_i(w)$ is the proportion of its maximum intake rate at which the predator is actually taking in fish. It is calculated from the encounter rate E_i and the maximum intake rate $h_i(w)$ as

$$f_i(w) = \frac{E_i(w)}{E_i(w) + h_i(w)}.$$

The encounter rate E_i is passed as an argument or calculated with getEncounter(). The maximum intake rate $h_i(w)$ is taken from the params object, and is set with setMaxIntakeRate(). As a consequence of the above expression for the feeding level, $1 - f_i(w)$ is the proportion of the food available to it that the predator actually consumes.

Your own feeding level function

By default getFeedingLevel() calls mizerFeedingLevel(). However you can replace this with your own alternative feeding level function. If your function is called "myFeedingLevel" then you register it in a MizerParams object params with

```
params <- setRateFunction(params, "FeedingLevel", "myFeedingLevel")
```

Your function will then be called instead of mizerFeedingLevel(), with the same arguments.

See Also

Other rate functions: getEGrowth(), getEReproAndGrowth(), getERepro(), getEncounter(), getFMortGear(), getFMort(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
## Not run:
params <- NS_params
# Get initial feeding level
fl <- getFeedingLevel(params)
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the feeding level at all saved time steps
fl <- getFeedingLevel(sim)
# Get the feeding level for years 15 - 20
fl <- getFeedingLevel(sim, time_range = c(15, 20))

## End(Not run)
```

getFMort *Get the total fishing mortality rate from all fishing gears by time, species and size.*

Description

Calculates the total fishing mortality (in units 1/year) from all gears by species and size and possibly time.

Usage

```
getFMort(object, effort, time_range, drop = TRUE)
```

Arguments

object	A MizerParams object or a MizerSim object
effort	The effort of each fishing gear. Only used if the object argument is of class MizerParams. See notes below.
time_range	Subset the returned fishing mortalities by time. The time range is either a vector of values, a vector of min and max time, or a single value. Default is the whole time range. Only used if the object argument is of type MizerSim.
drop	Only used when object is of type MizerSim. Should dimensions of length 1 be dropped, e.g. if your community only has one species it might make presentation of results easier. Default is TRUE.

Details

The total fishing mortality is just the sum of the fishing mortalities imposed by each gear, $\mu_{f.i}(w) = \sum_g F_{g,i,w}$. The fishing mortality for each gear is obtained as catchability x selectivity x effort.

Value

An array. If the effort argument has a time dimension, or object is of class MizerSim, the output array has three dimensions (time x species x size). If the effort argument does not have a time dimension, the output array has two dimensions (species x size).

The effort argument is only used if a MizerParams object is passed in. The effort argument can be a two dimensional array (time x gear), a vector of length equal to the number of gears (each gear has a different effort that is constant in time), or a single numeric value (each gear has the same effort that is constant in time). The order of gears in the effort argument must be the same as in the MizerParams object.

If the object argument is of class MizerSim then the effort slot of the MizerSim object is used and the effort argument is not used.

Your own fishing mortality function

By default `getFMort()` calls `mizerFMort()`. However you can replace this with your own alternative fishing mortality function. If your function is called `"myFMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "FMort", "myFMort")
```

Your function will then be called instead of `mizerFMort()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# Get the total fishing mortality when effort is constant for all
# gears and time:
getFMort(params, effort = 1)
# Get the total fishing mortality when effort is different
# between the four gears but constant in time:
getFMort(params, effort = c(0.5,1,1.5,0.75))
# Get the total fishing mortality when effort is different
# between the four gears and changes with time:
effort <- array(NA, dim = c(20,4))
effort[, 1] <- seq(from = 0, to = 1, length = 20)
effort[, 2] <- seq(from = 1, to = 0.5, length = 20)
effort[, 3] <- seq(from = 1, to = 2, length = 20)
effort[, 4] <- seq(from = 2, to = 1, length = 20)
getFMort(params, effort = effort)
# Get the total fishing mortality using the effort already held in a
# MizerSim object.
sim <- project(params, t_max = 20, effort = 0.5)
getFMort(sim)
getFMort(sim, time_range = c(10, 20))

## End(Not run)
```

---

getFMortGear *Get the fishing mortality by time, gear, species and size*

Description

Calculates the fishing mortality rate $F_{g,i,w}$ by gear, species and size and possibly time (in units 1/year).

Usage

```
getFMortGear(object, effort, time_range)
```

Arguments

object	A MizerParams object or a MizerSim object.
effort	The effort for each fishing gear. See notes below.
time_range	Subset the returned fishing mortalities by time. The time range is either a vector of values, a vector of min and max time, or a single value. Default is the whole time range. Only used if the object argument is of type MizerSim.

Value

An array. If the effort argument has a time dimension, or a MizerSim is passed in, the output array has four dimensions (time x gear x species x size). If the effort argument does not have a time dimension (i.e. it is a vector or a single numeric), the output array has three dimensions (gear x species x size).

Note

Here: fishing mortality = catchability x selectivity x effort.

The effort argument is only used if a MizerParams object is passed in. The effort argument can be a two dimensional array (time x gear), a vector of length equal to the number of gears (each gear has a different effort that is constant in time), or a single numeric value (each gear has the same effort that is constant in time). The order of gears in the effort argument must be the same the same as in the MizerParams object. If the effort argument is not supplied, its value is taken from the @initial_effort slot in the params object.

If the object argument is of class MizerSim then the effort slot of the MizerSim object is used and the effort argument is not used.

See Also

Other rate functions: getEGrowth(), getEReproAndGrowth(), getERepro(), getEncounter(), getFMort(), getFeedingLevel(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
## Not run:
params <-NS_params
# Get the fishing mortality when effort is constant
# for all gears and time:
getFMortGear(params, effort = 1)
# Get the fishing mortality when effort is different
# between the four gears but constant in time:
getFMortGear(params, effort = c(0.5, 1, 1.5, 0.75))
# Get the fishing mortality when effort is different
# between the four gears and changes with time:
effort <- array(NA, dim = c(20, 4))
```

```
effort[, 1] <- seq(from=0, to = 1, length = 20)
effort[, 2] <- seq(from=1, to = 0.5, length = 20)
effort[, 3] <- seq(from=1, to = 2, length = 20)
effort[, 4] <- seq(from=2, to = 1, length = 20)
getFMortGear(params, effort = effort)
# Get the fishing mortality using the effort already held in a MizerSim object.
sim <- project(params, t_max = 20, effort = 0.5)
getFMortGear(sim)
getFMortGear(sim, time_range = c(10, 20))

## End(Not run)
```

`getGrowthCurves` *Get growth curves giving weight as a function of age*

Description

Get growth curves giving weight as a function of age

Usage

```
getGrowthCurves(object, species = NULL, max_age = 20, percentage = FALSE)
```

Arguments

`object`	MizerSim or MizerParams object. If given a MizerSim object, uses the growth rates at the final time of a simulation to calculate the size at age. If given a MizerParams object, uses the initial growth rates instead.
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`max_age`	The age up to which to run the growth curve. Default is 20.
`percentage`	Boolean value. If TRUE, the size is given as a percentage of the maximal size.

Value

An array (species x age) containing the weight in grams.

See Also

Other summary functions: `getBiomass()`, `getDiet()`, `getN()`, `getSSB()`, `getYieldGear()`, `getYield()`

Examples

```
growth_curves <- getGrowthCurves(NS_params, species = c("Cod", "Haddock"))
str(growth_curves)

library(ggplot2)
ggplot(melt(growth_curves)) +
  geom_line(aes(Age, value)) +
  facet_wrap(~ Species, scales = "free") +
  ylab("Size[g]") + xlab("Age[years]")
```

---

getM2 *Alias for* getPredMort()

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 1.0

Usage

```
getM2(object, n, n_pp, n_other, time_range, drop = TRUE, ...)
```

Arguments

object	A MizerParams object or a MizerSim object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
time_range	A vector of times. Only the range of times is relevant, i.e., all times between the smallest and largest will be selected. The time_range can be character or numeric.
drop	If TRUE then any dimension of length 1 will be removed from the returned array.
...	Unused

Value

If a MizerParams object is passed in, the function returns a two dimensional array (prey species x prey size) based on the abundances also passed in. If a MizerSim object is passed in, the function returns a three dimensional array (time step x prey species x prey size) with the predation mortality calculated at every time step in the simulation. Dimensions may be dropped if they have length 1 unless drop = FALSE.

Your own predation mortality function

By default `getPredMort()` calls `mizerPredMort()`. However you can replace this with your own alternative predation mortality function. If your function is called `"myPredMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "PredMort", "myPredMort")
```

Your function will then be called instead of `mizerPredMort()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# With constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get predation mortality at one time step
getPredMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])
# Get predation mortality at all saved time steps
getPredMort(sim)
# Get predation mortality over the years 15 - 20
getPredMort(sim, time_range = c(15, 20))

## End(Not run)
```

---

getM2Background *Alias for* `getResourceMort()`

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 1.0

Usage

```
getM2Background(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
...	Unused

Value

A vector of mortality rate by resource size.

Your own resource mortality function

By default `getResourceMort()` calls `mizerResourceMort()`. However you can replace this with your own alternative resource mortality function. If your function is called `"myResourceMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "ResourceMort", "myResourceMort")
```

Your function will then be called instead of `mizerResourceMort()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`

Examples

```
## Not run:
params <- NS_params
# With constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get resource mortality at one time step
getResourceMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])

## End(Not run)
```

`getMeanMaxWeight` *Calculate the mean maximum weight of the community*

Description

Calculates the mean maximum weight of the community through time. This can be calculated by numbers or biomass. The calculation is the sum of the w_inf * abundance of each species, divided by the total abundance community, where abundance is either in biomass or numbers. You can specify minimum and maximum weight or length range for the species. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used). You can also specify the species to be used in the calculation.

Usage

```
getMeanMaxWeight(sim, species = NULL, measure = "both", ...)
```

Arguments

`sim`	A MizerSim object
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`measure`	The measure to return. Can be 'numbers', 'biomass' or 'both'
`...`	Arguments passed on to `get_size_range_array` `min_w` Smallest weight in size range. Defaults to smallest weight in the model. `max_w` Largest weight in size range. Defaults to largest weight in the model. `min_l` Smallest length in size range. If supplied, this takes precedence over `min_w`. `max_l` Largest length in size range. If supplied, this takes precedence over `max_w`.

Value

Depends on the `measure` argument. If `measure` = "`both`" then you get a matrix with two columns, one with values by numbers, the other with values by biomass at each saved time step. If `measure` = "`numbers`" or "`biomass`" you get a vector of the respective values at each saved time step.

See Also

Other functions for calculating indicators: `getCommunitySlope()`, `getMeanWeight()`, `getProportionOfLargeFish()`

Examples

```
mmw <- getMeanMaxWeight(NS_sim)
years <- c("1967", "2010")
mmw[years, ]
getMeanMaxWeight(NS_sim, species=c("Herring","Sprat","N.pout"))[years, ]
getMeanMaxWeight(NS_sim, min_w = 10, max_w = 5000)[years, ]
```

---

getMeanWeight *Calculate the mean weight of the community*

Description

Calculates the mean weight of the community through time. This is simply the total biomass of the community divided by the abundance in numbers. You can specify minimum and maximum weight or length range for the species. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used). You can also specify the species to be used in the calculation.

Usage

```
getMeanWeight(sim, species = NULL, ...)
```

Arguments

sim	A MizerSim object
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
...	Arguments passed on to get_size_range_array
	min_w Smallest weight in size range. Defaults to smallest weight in the model.
	max_w Largest weight in size range. Defaults to largest weight in the model.
	min_l Smallest length in size range. If supplied, this takes precedence over min_w.
	max_l Largest length in size range. If supplied, this takes precedence over max_w.

Value

A vector containing the mean weight of the community through time

See Also

Other functions for calculating indicators: getCommunitySlope(), getMeanMaxWeight(), getProportionOfLargeFish()

Examples

```
mean_weight <- getMeanWeight(NS_sim)
years <- c("1967", "2010")
mean_weight[years]
getMeanWeight(NS_sim, species = c("Herring", "Sprat", "N.pout"))[years]
getMeanWeight(NS_sim, min_w = 10, max_w = 5000)[years]
```

`getMort` *Get total mortality rate*

Description

Calculates the total mortality rate $\mu_i(w)$ (in units 1/year) on each species by size from predation mortality, background mortality and fishing mortality for a single time step.

Usage

```
getMort(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  effort = getInitialEffort(params),
  t = 0,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`effort`	A numeric vector of the effort by gear or a single numeric effort value which is used for all gears.
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Details

If your model contains additional components that you added with `setComponent()` and for which you specified a `mort_fun` function then the mortality inflicted by these components will be included in the returned value.

Value

A two dimensional array (prey species x prey size).

Your own mortality function

By default `getMort()` calls `mizerMort()`. However you can replace this with your own alternative mortality function. If your function is called `"myMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "Mort", "myMort")
```

Your function will then be called instead of `mizerMort()`, with the same arguments.

See Also

`getPredMort()`, `getFMort()`

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the total mortality at a particular time step
getMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ],
        t = 15, effort = 0.5)

## End(Not run)
```

---

getN *Calculate the number of individuals within a size range*

Description

Calculates the number of individuals within user-defined size limits, for each time and each species in the `MizerSim` object. The default option is to use the whole size range. You can specify minimum and maximum weight or lengths for the species. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used)

Usage

```
getN(sim, ...)
```

Arguments

sim	An object of class MizerSim.
...	Arguments passed on to get_size_range_array
	min_w Smallest weight in size range. Defaults to smallest weight in the model.
	max_w Largest weight in size range. Defaults to largest weight in the model.
	min_l Smallest length in size range. If supplied, this takes precedence over min_w.
	max_l Largest length in size range. If supplied, this takes precedence over max_w.

Value

An array (time x species) containing the total numbers.

See Also

Other summary functions: getBiomass(), getDiet(), getGrowthCurves(), getSSB(), getYieldGear(), getYield()

Examples

```
numbers <- getN(NS_sim)
numbers["1972", "Herring"]
# The above gave a huge number, because that included all the larvae.
# The number of Herrings between 10g and 1kg is much smaller.
numbers <- getN(NS_sim, min_w = 10, max_w = 1000)
numbers["1972", "Herring"]
```

---

getParams *Extract the parameter object underlying a simulation*

Description

Extract the parameter object underlying a simulation

Usage

```
getParams(sim)
```

Arguments

sim	A MizerSim object

Value

The MizerParams object that was used to run the simulation

Examples

```
# This will be identical to the params object that was used to create the
# simulation
sim <- project(NS_params, t_max = 1)
identical(getParams(sim), NS_params)
```

`getPhiPrey` *Get available energy*

Description

[Deprecated]

This is deprecated and is no longer used by the mizer project() method. Calculates the amount $E_{a,i}(w)$ of food exposed to each predator as a function of predator size.

Usage

```
getPhiPrey(object, n, n_pp, ...)
```

Arguments

`object`	An MizerParams object
`n`	A matrix of species abundances (species x size)
`n_pp`	A vector of the background abundance by size
`...`	Other arguments (currently unused)

Value

A two dimensional array (predator species x predator size)

See Also

`project()`

Examples

```
## Not run:
params <-  NS_params
sim <- project(params, t_max = 20, effort = 0.5)
n <- sim@n[21,,]
n_pp <- sim@n_pp[21,]
getPhiPrey(params,n,n_pp)
# ->
getEncounter(params) / getSearchVolume(params)

## End(Not run)
```

`getPredMort` *Get total predation mortality rate*

Description

Calculates the total predation mortality rate $\mu_{p,i}(w_p)$ (in units of 1/year) on each prey species by prey size:

$$\mu_{p.i}(w_p) = \sum_j \texttt{pred\_rate}_j(w_p)\, \theta_{ji}.$$

The predation rate `pred_rate` is returned by `getPredRate()`.

Usage

```
getPredMort(object, n, n_pp, n_other, time_range, drop = TRUE, ...)
```

Arguments

`object`	A `MizerParams` object or a `MizerSim` object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`time_range`	A vector of times. Only the range of times is relevant, i.e., all times between the smallest and largest will be selected. The time_range can be character or numeric.
`drop`	If `TRUE` then any dimension of length 1 will be removed from the returned array.
`...`	Unused

Value

If a `MizerParams` object is passed in, the function returns a two dimensional array (prey species x prey size) based on the abundances also passed in. If a `MizerSim` object is passed in, the function returns a three dimensional array (time step x prey species x prey size) with the predation mortality calculated at every time step in the simulation. Dimensions may be dropped if they have length 1 unless `drop = FALSE`.

Your own predation mortality function

By default `getPredMort()` calls `mizerPredMort()`. However you can replace this with your own alternative predation mortality function. If your function is called `"myPredMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "PredMort", "myPredMort")
```

Your function will then be called instead of `mizerPredMort()`, with the same arguments.

See Also

Other rate functions: getEGrowth(), getEReproAndGrowth(), getERepro(), getEncounter(), getFMortGear(), getFMort(), getFeedingLevel(), getMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
## Not run:
params <- NS_params
# With constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get predation mortality at one time step
getPredMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])
# Get predation mortality at all saved time steps
getPredMort(sim)
# Get predation mortality over the years 15 - 20
getPredMort(sim, time_range = c(15, 20))

## End(Not run)
```

---

getPredRate *Get predation rate*

Description

Calculates the potential rate (in units 1/year) at which a prey individual of a given size w is killed by predators from species j. In formulas

$$\texttt{pred\_rate}_j(w_p) = \int \phi_j(w, w_p)(1 - f_j(w))\gamma_j(w)N_j(w)\, dw.$$

This potential rate is used in getPredMort() to calculate the realised predation mortality rate on the prey individual.

Usage

```
getPredRate(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
...	Unused

Value

A two dimensional array (predator species x prey size), where the prey size runs over fish community plus resource spectrum.

Your own predation rate function

By default `getPredRate()` calls `mizerPredRate()`. However you can replace this with your own alternative predation rate function. If your function is called `"myPredRate"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "PredRate", "myPredRate")
```

Your function will then be called instead of `mizerPredRate()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# With constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the feeding level at one time step
getPredRate(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])

## End(Not run)
```

getProportionOfLargeFish

Calculate the proportion of large fish

Description

Calculates the proportion of large fish through time in the MizerSim class within user defined size limits. The default option is to use the whole size range. You can specify minimum and maximum size ranges for the species and also the threshold size for large fish. Sizes can be expressed as weight or size. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used). You can also specify the species to be used in the calculation. This function can be used to calculate the Large Fish Index. The proportion is based on either abundance or biomass.

Usage

```
getProportionOfLargeFish(
  sim,
  species = NULL,
  threshold_w = 100,
  threshold_l = NULL,
  biomass_proportion = TRUE,
  ...
)
```

Arguments

sim	A MizerSim object
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
threshold_w	the size used as the cutoff between large and small fish. Default value is 100.
threshold_l	the size used as the cutoff between large and small fish.
biomass_proportion	a boolean value. If TRUE the proportion calculated is based on biomass, if FALSE it is based on numbers of individuals. Default is TRUE.
...	Arguments passed on to get_size_range_array min_w Smallest weight in size range. Defaults to smallest weight in the model. max_w Largest weight in size range. Defaults to largest weight in the model. min_l Smallest length in size range. If supplied, this takes precedence over min_w. max_l Largest length in size range. If supplied, this takes precedence over max_w.

Value

A vector containing the proportion of large fish through time

See Also

Other functions for calculating indicators: `getCommunitySlope()`, `getMeanMaxWeight()`, `getMeanWeight()`

Examples

```
lfi <- getProportionOfLargeFish(NS_sim, min_w = 10, max_w = 5000,
                                threshold_w = 500)
years <- c("1972", "2010")
lfi[years]
getProportionOfLargeFish(NS_sim)[years]
getProportionOfLargeFish(NS_sim, species=c("Herring","Sprat","N.pout"))[years]
getProportionOfLargeFish(NS_sim, min_w = 10, max_w = 5000)[years]
getProportionOfLargeFish(NS_sim, min_w = 10, max_w = 5000,
    threshold_w = 500, biomass_proportion = FALSE)[years]
```

---

getRates *Get all rates*

Description

Calls other rate functions in sequence and collects the results in a list.

Usage

```
getRates(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  effort,
  t = 0,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
effort	The effort for each fishing gear
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
...	Unused

Details

By default this function returns a list with the following components:

- encounter from `mizerEncounter()`
- feeding_level from `mizerFeedingLevel()`
- e from `mizerEReproAndGrowth()`
- e_repro from `mizerERepro()`
- e_growth from `mizerEGrowth()`
- pred_rate from `mizerPredRate()`
- pred_mort from `mizerPredMort()`
- f_mort from `mizerFMort()`
- mort from `mizerMort()`
- rdi from `mizerRDI()`
- rdd from `BevertonHoltRDD()`
- resource_mort from `mizerResourceMort()`

However you can replace any of these rate functions by your own rate function if you wish, see `setRateFunction()` for details.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getResourceMort()`

Examples

```
rates <- getRates(NS_params)
names(rates)
identical(rates$encounter, getEncounter(NS_params))
```

---

getRDD *Get density dependent reproduction rate*

Description

Calculates the density dependent rate of egg production R_i (units 1/year) for each species. This is the flux entering the smallest size class of each species. The density dependent rate is the density independent rate obtained with `getRDI()` after it has been put through the density dependence function. This is the Beverton-Holt function `BevertonHoltRDD()` by default, but this can be changed. See `setReproduction()` for more details.

Usage

```
getRDD(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  rdi = getRDI(params, n = n, n_pp = n_pp, n_other = n_other, t = t),
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
rdi	A vector of density-independent reproduction rates for each species. If not specified, rdi is calculated internally using getRDI().
...	Unused

Value

A numeric vector the length of the number of species.

See Also

getRDI()

Other rate functions: getEGrowth(), getEReproAndGrowth(), getERepro(), getEncounter(), getFMortGear(), getFMort(), getFeedingLevel(), getMort(), getPredMort(), getPredRate(), getRDI(), getRates(), getResourceMort()

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the rate at a particular time step
getRDD(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)

## End(Not run)
```

getRDI *Get density independent rate of egg production*

Description

Calculates the density-independent rate of total egg production R_{di} (units 1/year) before density dependence, by species.

Usage

```
getRDI(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
...	Unused

Details

This rate is obtained by taking the per capita rate $E_r(w)\psi(w)$ at which energy is invested in reproduction, as calculated by `getERepro()`, multiplying it by the number of individuals$N(w)$ and integrating over all sizes w and then multiplying by the reproductive efficiency ϵ and dividing by the egg size `w_min`, and by a factor of two to account for the two sexes:

$$R_{di} = \frac{\epsilon}{2w_{min}} \int N(w) E_r(w) \psi(w)\, dw$$

Used by `getRDD()` to calculate the actual, density dependent rate. See `setReproduction()` for more details.

Value

A numeric vector the length of the number of species.

Your own reproduction function

By default getRDI() calls mizerRDI(). However you can replace this with your own alternative reproduction function. If your function is called "myRDI" then you register it in a MizerParams object params with

```
params <- setRateFunction(params, "RDI", "myRDI")
```

Your function will then be called instead of mizerRDI(), with the same arguments. For an example of an alternative reproduction function see constantEggRDI().

See Also

getRDD()

Other rate functions: getEGrowth(), getEReproAndGrowth(), getERepro(), getEncounter(), getFMortGear(), getFMort(), getFeedingLevel(), getMort(), getPredMort(), getPredRate(), getRDD(), getRates(), getResourceMort()

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the density-independent reproduction rate at a particular time step
getRDI(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)

## End(Not run)
```

---

getReproductionLevel *Get reproduction level*

Description

[Experimental] The reproduction level is the ratio between the density-dependent reproduction rate and the maximal reproduction rate.

Usage

```
getReproductionLevel(params)
```

Arguments

params	A MizerParams object

Value

A named vector with the reproduction level for each species.

Examples

```
getReproductionLevel(NS_params)

# The reproduction level can be changed without changing the steady state:
params <- setBevertonHolt(NS_params, reproduction_level = 0.9)
getReproductionLevel(params)

# The result is the ratio of RDD and R_max
identical(getRDD(params) / species_params(params)$R_max,
          getReproductionLevel(params))
```

`getResourceMort` *Get predation mortality rate for resource*

Description

Calculates the predation mortality rate $\mu_p(w)$ on the resource spectrum by resource size (in units 1/year).

Usage

```
getResourceMort(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Value

A vector of mortality rate by resource size.

Your own resource mortality function

By default `getResourceMort()` calls `mizerResourceMort()`. However you can replace this with your own alternative resource mortality function. If your function is called `"myResourceMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "ResourceMort", "myResourceMort")
```

Your function will then be called instead of `mizerResourceMort()`, with the same arguments.

See Also

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`

Examples

```
## Not run:
params <- NS_params
# With constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get resource mortality at one time step
getResourceMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])

## End(Not run)
```

---

getSSB *Calculate the SSB of species*

Description

Calculates the spawning stock biomass (SSB) through time of the species in the `MizerSim` class. SSB is calculated as the total mass of all mature individuals.

Usage

```
getSSB(sim)
```

Arguments

`sim`	An object of class `MizerSim`.

Value

An array (time x species) containing the SSB in grams.

See Also

Other summary functions: `getBiomass()`, `getDiet()`, `getGrowthCurves()`, `getN()`, `getYieldGear()`, `getYield()`

Examples

```
ssb <- getSSB(NS_sim)
ssb[c("1972", "2010"), c("Herring", "Cod")]
```

`getTimes` *Times for which simulation results are available*

Description

Times for which simulation results are available

Usage

```
getTimes(sim)
```

Arguments

`sim`	A MizerSim object

Value

A numeric vectors of the times (in years) at which simulation results have been stored in the MizerSim object.

Examples

```
getTimes(NS_sim)
```

`getYield` *Calculate the yearly yield for each species*

Description

Calculates the yearly yield (biomass fished per year) for each species across all gears at each simulation time step.

Usage

```
getYield(sim)
```

Arguments

sim	An object of class MizerSim.

Value

An array (time x species) containing the total yearly yield in grams.

See Also

getYieldGear()

Other summary functions: getBiomass(), getDiet(), getGrowthCurves(), getN(), getSSB(), getYieldGear()

Examples

```
yield <- getYield(NS_sim)
yield[c("1972", "2010"), c("Herring", "Cod")]
```

---

getYieldGear *Calculate the yearly yield per gear and species*

Description

Calculates the yearly yield (biomass fished per year) per gear and species at each simulation time step.

Usage

```
getYieldGear(sim)
```

Arguments

sim	An object of class MizerSim.

Value

An array (time x gear x species) containing the yearly yield in grams.

See Also

getYield()

Other summary functions: getBiomass(), getDiet(), getGrowthCurves(), getN(), getSSB(), getYield()

Examples

```
yield <- getYieldGear(NS_sim)
yield["1972", "Herring", "Herring"]
# (In this example MizerSim object each species was set up with its own gear)
```

getZ *Alias for* `getMort()`

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 1.0

Usage

```
getZ(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  effort = getInitialEffort(params),
  t = 0,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`effort`	A numeric vector of the effort by gear or a single numeric effort value which is used for all gears.
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Details

If your model contains additional components that you added with `setComponent()` and for which you specified a `mort_fun` function then the mortality inflicted by these components will be included in the returned value.

Value

A two dimensional array (prey species x prey size).

Your own mortality function

By default `getMort()` calls `mizerMort()`. However you can replace this with your own alternative mortality function. If your function is called `"myMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "Mort", "myMort")
```

Your function will then be called instead of `mizerMort()`, with the same arguments.

See Also

`getPredMort()`, `getFMort()`

Other rate functions: `getEGrowth()`, `getEReproAndGrowth()`, `getERepro()`, `getEncounter()`, `getFMortGear()`, `getFMort()`, `getFeedingLevel()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
## Not run:
params <- NS_params
# Project with constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# Get the total mortality at a particular time step
getMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ],
        t = 15, effort = 0.5)

## End(Not run)
```

---

get_f0_default *Get default value for f0*

Description

Fills in any missing values for f0 so that if the prey abundance was described by the power law $\kappa w^{-\lambda}$ then the encounter rate coming from the given `gamma` parameter would lead to the feeding level f_0. This is thus doing the inverse of `get_gamma_default()`. Only for internal use.

Usage

```
get_f0_default(params)
```

Arguments

`params`	A MizerParams object

Details

For species for which no value for `gamma` is specified in the species parameter data frame, the `f0` values is kept as provided in the species parameter data frame or it is set to 0.6 if it is not provided.

Value

A vector with the values of f0 for all species

See Also

Other functions calculating defaults: `get_gamma_default()`, `get_h_default()`, `get_ks_default()`

`get_gamma_default` *Get default value for gamma*

Description

Fills in any missing values for gamma so that if the prey abundance was described by the power law $\kappa w^{-\lambda}$ then the encounter rate would lead to the feeding level f_0. Only for internal use.

Usage

```
get_gamma_default(params)
```

Arguments

`params`	A MizerParams object

Value

A vector with the values of gamma for all species

See Also

Other functions calculating defaults: `get_f0_default()`, `get_h_default()`, `get_ks_default()`

`get_initial_n` *Calculate initial population abundances for the community populations*

Description

This function uses the model parameters and other parameters to calculate initial population abundances for the community populations. These initial abundances should be reasonable guesses at the equilibrium values. The returned population can be passed to the `project` function.

Usage

```
get_initial_n(params, n0_mult = NULL, a = 0.35)
```

Arguments

params	The model parameters. An object of type MizerParams.
n0_mult	Multiplier for the abundance at size 0. Default value is kappa/1000.
a	A parameter with a default value of 0.35.

Value

A matrix (species x size) of population abundances.

Examples

```
## Not run:
params <- newMultispeciesParams(NS_species_params_gears)
init_n <- get_initial_n(params)

## End(Not run)
```

---

get_ks_default *Get default value for* ks

Description

Fills in any missing values for ks so that the critical feeding level needed to sustain the species is as specified in the fc column in the species parameter data frame. If that column is not provided the default critical feeding level $f_c = 0.2$ is used.

Usage

```
get_ks_default(params)
```

Arguments

params	A MizerParams object

Value

A vector with the values of ks for all species

See Also

Other functions calculating defaults: get_f0_default(), get_gamma_default(), get_h_default()

get_phi *Get values from feeding kernel function*

Description

This involves finding the feeding kernel function for each species, using the pred_kernel_type parameter in the species_params data frame, checking that it is valid and all its arguments are contained in the species_params data frame, and then calling this function with the ppmr vector.

Usage

```
get_phi(species_params, ppmr)
```

Arguments

species_params	A species parameter data frame
ppmr	Values of the predator/prey mass ratio at which to evaluate the predation kernel function

Value

An array (species x ppmr) with the values of the predation kernel function

get_required_reproduction *Determine reproduction rate needed for initial egg abundance*

Description

Determine reproduction rate needed for initial egg abundance

Usage

```
get_required_reproduction(params)
```

Arguments

params	A MizerParams object

Value

A vector of reproduction rates for all species

`get_size_range_array` *Get size range array*

Description

Helper function that returns an array (species x size) of boolean values indicating whether that size bin is within the size limits specified by the arguments. Either the size limits can be the same for all species or they can be specified as vectors with one value for each species in the model.

Usage

```
get_size_range_array(
  params,
  min_w = min(params@w),
  max_w = max(params@w),
  min_l = NULL,
  max_l = NULL,
  ...
)
```

Arguments

`params`	MizerParams object
`min_w`	Smallest weight in size range. Defaults to smallest weight in the model.
`max_w`	Largest weight in size range. Defaults to largest weight in the model.
`min_l`	Smallest length in size range. If supplied, this takes precedence over `min_w`.
`max_l`	Largest length in size range. If supplied, this takes precedence over `max_w`.
`...`	Unused

Value

Boolean array (species x size)

Length to weight conversion

If `min_l` is specified there is no need to specify `min_w` and so on. However, if a length is specified (minimum or maximum) then it is necessary for the species parameter data.frame to include the parameters `a` and `b` that determine the relation between length l and weight w by

$$w = al^b.$$

It is possible to mix length and weight constraints, e.g. by supplying a minimum weight and a maximum length, but this must be done the same for all species. The default values are the minimum and maximum weights of the spectrum, i.e., the full range of the size spectrum is used.

get_time_elements *Get_time_elements*

Description

Internal function to get the array element references of the time dimension for the time based slots of a MizerSim object.

Usage

```
get_time_elements(sim, time_range, slot_name = "n")
```

Arguments

sim	A MizerSim object
time_range	A vector of times. Only the range of times is relevant, i.e., all times between the smallest and largest will be selected. The time_range can be character or numeric.
slot_name	Obsolete. Was only needed in early versions of mizer where the effort slot could have different time dimension from the other slots.

Value

Named boolean vector indicating for each time whether it is included in the range or not.

idxFinalT *Time index at end of simulation*

Description

Time index at end of simulation

Usage

```
idxFinalT(sim)
```

Arguments

sim	A MizerSim object

Value

An integer giving the index for extracting the results for the final time step

Examples

```
idx <- idxFinalT(NS_sim)
idx
# This coincides with
length(getTimes(NS_sim))
# and corresponds to the final time
getTimes(NS_sim)[idx]
# We can use this index to extract the result at the final time
identical(N(NS_sim)[idx, , ], finalN(NS_sim))
identical(NResource(NS_sim)[idx, ], finalNResource(NS_sim))
```

`indicator_functions` *Description of indicator functions*

Description

Mizer provides a range of functions to calculate indicators from a MizerSim object.

Details

A list of available indicator functions for MizerSim objects is given in the table below

Function	Returns
`getProportionOfLargeFish()`	A vector with values at each time step.
`getMeanWeight()`	A vector with values at each saved time step.
`getMeanMaxWeight()`	Depends on the measure argument. If measure = "both" then you get a matrix with two col
`getCommunitySlope()`	A data.frame with four columns: time step, slope, intercept and the coefficient of determina

See Also

summary_functions, plotting_functions

`initialN<-` *Initial values for fish spectra*

Description

Values used as starting values for simulations with `project()`.

Usage

```
initialN(params) <- value

initialN(object)
```

Arguments

params	A MizerParams object
value	A matrix with dimensions species x size holding the initial number densities for the fish spectra.
object	An object of class MizerParams or MizerSim

Examples

```
# Doubling abundance of Cod in the initial state of the North Sea model
params <- NS_params
initialN(params)["Cod", ] <- 2 * initialN(params)["Cod", ]
# Calculating the corresponding initial biomass
biomass <- initialN(params)["Cod", ] * dw(NS_params) * w(NS_params)
# Of course this initial state will no longer be a steady state
params <- steady(params)
```

---

initialNOther<- *Initial values for other ecosystem components*

Description

Values used as starting values for simulations with `project()`.

Usage

```
initialNOther(params) <- value

initialNOther(object)
```

Arguments

params	A MizerParams object
value	A named list with the initial values of other ecosystem components
object	An object of class MizerParams or MizerSim

initialNResource<- *Initial value for resource spectrum*

Description

Value used as starting value for simulations with `project()`.

Usage

```
initialNResource(params) <- value

initialNResource(object)
```

Arguments

`params`	A MizerParams object
`value`	A vector with the initial number densities for the resource spectrum
`object`	An object of class MizerParams or MizerSim

Examples

```
# Doubling resource abundance in the initial state of the North Sea model
params <- NS_params
initialNResource(params) <- 2 * initialNResource(params)
# Of course this initial state will no longer be a steady state
params <- steady(params)
```

initial_effort *Initial fishing effort*

Description

The fishing effort is a named vector, specifying for each fishing gear the effort invested into fishing with that gear. The effort value for each gear is multiplied by the catchability and the selectivity to determine the fishing mortality imposed by that gear, see `setFishing()` for more details.

The function also accepts an `effort` that is not yet valid:

Usage

```
initial_effort(params)

initial_effort(params) <- value

validEffortVector(effort, params)
```

Arguments

`params`	A MizerParams object
`value`	The initial fishing effort
`effort`	A vector or scalar.

Details

The initial effort you have set can be overruled when running a simulation by providing an `effort` argument to `project()` which allows you to specify a time-varying effort.

- a scalar, which is then replicated for each gear
- an unnamed vector, which is then assumed to be in the same order as the gears in the params object
- a named vector in which the gear names have a different order than in the params object. This is then sorted correctly.
- a named vector which only supplies values for some of the gears. The effort for the other gears is then set to zero.

An `effort` argument will lead to an error if it is either

- unnamed and of the wrong length
- named but where some names do not match any of the gears
- not numeric

`inter` *Alias for* `NS_interaction`

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 2.3

Usage

```
inter
```

Format

A 12 x 12 matrix.

Source

Blanchard et al.

knife_edge *Weight based knife-edge selectivity function*

Description

A knife-edge selectivity function where weights greater or equal to `knife_edge_size` are selected.

Usage

```
knife_edge(w, knife_edge_size, ...)
```

Arguments

`w`	The size of the individual.
`knife_edge_size`	The weight at which the knife-edge operates.
`...`	Unused

lognormal_pred_kernel *Lognormal predation kernel*

Description

This is the most commonly-used predation kernel. The log of the predator/prey mass ratio is normally distributed.

Usage

```
lognormal_pred_kernel(ppmr, beta, sigma)
```

Arguments

`ppmr`	A vector of predator/prey size ratios
`beta`	The preferred predator/prey size ratio
`sigma`	The width parameter of the log-normal kernel

Details

Writing the predator mass as w and the prey mass as w_p, the feeding kernel is given as

$$\phi_i(w, w_p) = \exp\left[\frac{-(\ln(w/w_p/\beta_i))^2}{2\sigma_i^2}\right]$$

if w/w_p is larger than 1 and zero otherwise. Here β_i is the preferred predator-prey mass ratio and σ_i determines the width of the kernel. These two parameters need to be given in the species parameter dataframe in the columns `beta` and `sigma`.

This function is called from `setPredKernel()` to set up the predation kernel slots in a MizerParams object.

Value

A vector giving the value of the predation kernel at each of the predator/prey mass ratios in the ppmr argument.

`matchBiomasses` *Match biomasses to observations*

Description

[Experimental] The function adjusts the abundances of the species in the model so that their biomasses match with observations.

Usage

```
matchBiomasses(params, species = NULL)
```

Arguments

`params`	A MizerParams object
`species`	The species to be affected. Optional. By default all observed biomasses will be matched. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be affected (TRUE) or not.

Details

The function works by multiplying for each species the abundance density at all sizes by the same factor. This will of course not give a steady state solution, even if the initial abundance densities were at steady state. So after using this function you may want to use `steady()` to run the model to steady state, after which of course the biomasses will no longer match exactly. You could then iterate this process. This is described in the blog post at https://bit.ly/2YqXESV.

Before you can use this function you will need to have added a `biomass_observed` column to your model which gives the observed biomass in grams. For species for which you have no observed biomass, you should set the value in the `biomass_observed` column to 0 or NA.

Biomass observations usually only include individuals above a certain size. This size should be specified in a `biomass_cutoff` column of the species parameter data frame. If this is missing, it is assumed that all sizes are included in the observed biomass, i.e., it includes larval biomass.

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$biomass_observed <-
    c(0.8, 61, 12, 35, 1.6, 20, 10, 7.6, 135, 60, 30, 78)
species_params(params)$biomass_cutoff <- 10
params <- calibrateBiomass(params)
params <- matchBiomasses(params)
plotBiomassObservedVsModel(params)
```

`matchYields` *Match yields to observations*

Description

[Experimental] The function adjusts the abundances of the species in the model so that their yearly yields under the given fishing mortalities match with observations.

Usage

```
matchYields(params, species = NULL)
```

Arguments

`params`	A MizerParams object
`species`	The species to be affected. Optional. By default all observed yields will be matched. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be affected (TRUE) or not.

Details

The function works by multiplying for each species the abundance density at all sizes by the same factor. This will of course not give a steady state solution, even if the initial abundance densities were at steady state. So after using this function you may want to use `steady()` to run the model to steady state, after which of course the yields will no longer match exactly. You could then iterate this process. This is described in the blog post at https://bit.ly/2YqXESV.

Before you can use this function you will need to have added a `yield_observed` column to your model which gives the observed yields in grams per year. For species for which you have no observed biomass, you should set the value in the `yield_observed` column to 0 or NA.

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$yield_observed <-
    c(0.8, 61, 12, 35, 1.6, 20, 10, 7.6, 135, 60, 30, 78)
gear_params(params)$catchability <-
    c(1.3, 0.065, 0.31, 0.18, 0.98, 0.24, 0.37, 0.46, 0.18, 0.30, 0.27, 0.39)
params <- calibrateYield(params)
params <- matchYields(params)
plotYieldObservedVsModel(params)
```

`mizerEGrowth` *Get energy rate available for growth needed to project standard mizer model*

Description

Calculates the energy rate $g_i(w)$ (grams/year) available by species and size for growth after metabolism, movement and reproduction have been accounted for. Used by `project()` for performing simulations. You would not usually call this function directly but instead use `getEGrowth()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerEGrowth(params, n, n_pp, n_other, t, e_repro, e, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`e_repro`	The energy available for reproduction as calculated by `getERepro()`.
`e`	The energy available for reproduction and growth as calculated by `getEReproAndGrowth()`.
`...`	Unused

Value

A two dimensional array (species x size) with the growth rates.

Your own growth rate function

By default `getEGrowth()` calls `mizerEGrowth()`. However you can replace this with your own alternative growth rate function. If your function is called `"myEGrowth"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "EGrowth", "myEGrowth")
```

Your function will then be called instead of `mizerEGrowth()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

---

mizerEncounter *Get encounter rate needed to project standard mizer model*

Description

Calculates the rate $E_i(w)$ at which a predator of species i and weight w encounters food (grams/year). You would not usually call this function directly but instead use `getEncounter()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerEncounter(params, n, n_pp, n_other, t, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`...`	Unused

Value

A named two dimensional array (predator species x predator size) with the encounter rates.

Predation encounter

The encounter rate $E_i(w)$ at which a predator of species i and weight w encounters food has contributions from the encounter of fish prey and of resource. This is determined by summing over all prey species and the resource spectrum and then integrating over all prey sizes w_p, weighted by predation kernel $\phi(w, w_p)$:

$$E_i(w) = \gamma_i(w) \int \left(\theta_{ip} N_R(w_p) + \sum_j \theta_{ij} N_j(w_p) \right) \phi_i(w, w_p) w_p \, dw_p.$$

Here $N_j(w)$ is the abundance density of species j and $N_R(w)$ is the abundance density of resource. The overall prefactor $\gamma_i(w)$ determines the predation power of the predator. It could be interpreted as a search volume and is set with the `setSearchVolume()` function. The predation kernel $\phi(w, w_p)$ is set with the `setPredKernel()` function. The species interaction matrix θ_{ij} is set with `setInteraction()` and the resource interaction vector θ_{ip} is taken from the `interaction_resource` column in `params@species_params`.

Details

The encounter rate is multiplied by $1 - f_0$ to obtain the consumption rate, where f_0 is the feeding level calculated with `getFeedingLevel()`. This is used by the `project()` function for performing simulations.

The function returns values also for sizes outside the size-range of the species. These values should not be used, as they are meaningless.

If your model contains additional components that you added with `setComponent()` and for which you specified an `encounter_fun` function then the encounters of these components will be included in the returned value.

Your own encounter function

By default `getEncounter()` calls `mizerEncounter()`. However you can replace this with your own alternative encounter function. If your function is called `"myEncounter"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "Encounter", "myEncounter")
```

Your function will then be called instead of `mizerEncounter()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`mizerERepro` *Get energy rate available for reproduction needed to project standard mizer model*

Description

Calculates the energy rate (grams/year) available for reproduction after growth and metabolism have been accounted for. You would not usually call this function directly but instead use `getERepro()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerERepro(params, n, n_pp, n_other, t, e, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`e`	A two dimensional array (species x size) holding the energy available for reproduction and growth as calculated by `mizerEReproAndGrowth()`.
`...`	Unused

Value

A two dimensional array (species x size) holding

$$\psi_i(w) E_{r.i}(w)$$

where $E_{r.i}(w)$ is the rate at which energy becomes available for growth and reproduction, calculated with `mizerEReproAndGrowth()`, and $\psi_i(w)$ is the proportion of this energy that is used for reproduction. This proportion is taken from the `params` object and is set with `setReproduction()`.

Your own reproduction rate function

By default `getERepro()` calls `mizerERepro()`. However you can replace this with your own alternative reproduction rate function. If your function is called `"myERepro"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "ERepro", "myERepro")
```

Your function will then be called instead of `mizerERepro()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`mizerEReproAndGrowth` *Get energy rate available for reproduction and growth needed to project standard mizer model*

Description

Calculates the energy rate $E_{r.i}(w)$ (grams/year) available to an individual of species i and size w for reproduction and growth after metabolism and movement have been accounted for. You would not usually call this function directly but instead use `getEReproAndGrowth()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerEReproAndGrowth(
  params,
  n,
  n_pp,
  n_other,
  t,
  encounter,
  feeding_level,
  ...
)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`encounter`	An array (species x size) with the encounter rate as calculated by `getEncounter()`.
`feeding_level`	An array (species x size) with the feeding level as calculated by `getFeedingLevel()`.
`...`	Unused

Value

A two dimensional array (species x size) holding

$$E_{r.i}(w) = \max(0, \alpha_i\,(1 - \texttt{feeding\_level}_i(w))\,\texttt{encounter}_i(w) - \texttt{metab}_i(w)).$$

Due to the form of the feeding level, calculated by `getFeedingLevel()`, this can also be expressed as

$$E_{r.i}(w) = \max(0, \alpha_i\,\texttt{feeding\_level}_i(w)\,h_i(w) - \texttt{metab}_i(w))$$

where h_i is the maximum intake rate, set with `setMaxIntakeRate()`. The assimilation rate α_i is taken from the species parameter data frame in `params`. The metabolic rate `metab` is taken from `params` and set with `setMetabolicRate()`.

The return value can be negative, which means that the energy intake does not cover the cost of metabolism and movement.

Your own energy rate function

By default `getEReproAndGrowth()` calls `mizerEReproAndGrowth()`. However you can replace this with your own alternative energy rate function. If your function is called `"myEReproAndGrowth"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "EReproAndGrowth", "myEReproAndGrowth")
```

Your function will then be called instead of `mizerEReproAndGrowth()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`mizerFeedingLevel` *Get feeding level needed to project standard mizer model*

Description

You would not usually call this function directly but instead use `getFeedingLevel()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerFeedingLevel(params, n, n_pp, n_other, t, encounter, ...)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
encounter	A two dimensional array (predator species x predator size) with the encounter rate.
...	Unused

Value

A two dimensional array (predator species x predator size) with the feeding level.

Feeding level

The feeding level $f_i(w)$ is the proportion of its maximum intake rate at which the predator is actually taking in fish. It is calculated from the encounter rate E_i and the maximum intake rate $h_i(w)$ as

$$f_i(w) = \frac{E_i(w)}{E_i(w) + h_i(w)}.$$

The encounter rate E_i is passed as an argument or calculated with `getEncounter()`. The maximum intake rate $h_i(w)$ is taken from the `params` object, and is set with `setMaxIntakeRate()`. As a consequence of the above expression for the feeding level, $1 - f_i(w)$ is the proportion of the food available to it that the predator actually consumes.

Your own feeding level function

By default `getFeedingLevel()` calls `mizerFeedingLevel()`. However you can replace this with your own alternative feeding level function. If your function is called `"myFeedingLevel"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "FeedingLevel", "myFeedingLevel")
```

Your function will then be called instead of `mizerFeedingLevel()`, with the same arguments.

See Also

The feeding level is used in `mizerEReproAndGrowth()` and in `mizerPredRate()`.

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`mizerFMort` *Get the total fishing mortality rate from all fishing gears*

Description

Calculates the total fishing mortality (in units 1/year) from all gears by species and size. The total fishing mortality is just the sum of the fishing mortalities imposed by each gear, $\mu_{f.i}(w) = \sum_g F_{g,i,w}$. You would not usually call this function directly but instead use `getFMort()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerFMort(params, n, n_pp, n_other, t, effort, e_growth, pred_mort, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`effort`	A vector with the effort for each fishing gear.
`e_growth`	An array (species x size) with the energy available for growth as calculated by `getEGrowth()`. Unused.
`pred_mort`	A two dimensional array (species x size) with the predation mortality as calculated by `getPredMort()`. Unused.
`...`	Unused

Value

An array (species x size) with the fishing mortality.

Your own fishing mortality function

By default `getFMort()` calls `mizerFMort()`. However you can replace this with your own alternative fishing mortality function. If your function is called `"myFMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "FMort", "myFMort")
```

Your function will then be called instead of `mizerFMort()`, with the same arguments.

Note

Here: fishing mortality = catchability x selectivity x effort.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`mizerFMortGear` *Get the fishing mortality needed to project standard mizer model*

Description

Calculates the fishing mortality rate $F_{g,i,w}$ by gear, species and size. This is a helper function for `mizerFMort()`.

Usage

```
mizerFMortGear(params, effort)
```

Arguments

`params`	A MizerParams object
`effort`	A vector with the effort for each fishing gear.

Value

An three dimensional array (gear x species x size) with the fishing mortality

Note

Here: fishing mortality = catchability x selectivity x effort.

See Also

`setFishing()`

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`mizerMort` *Get total mortality rate needed to project standard mizer model*

Description

Calculates the total mortality rate $\mu_i(w)$ (in units 1/year) on each species by size from predation mortality, background mortality and fishing mortality. You would not usually call this function directly but instead use `getMort()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerMort(params, n, n_pp, n_other, t, f_mort, pred_mort, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`f_mort`	A two dimensional array (species x size) with the fishing mortality
`pred_mort`	A two dimensional array (species x size) with the predation mortality
`...`	Unused

Details

If your model contains additional components that you added with `setComponent()` and for which you specified a `mort_fun` function then the mortality inflicted by these components will be included in the returned value.

Value

A named two dimensional array (species x size) with the total mortality rates.

Your own mortality function

By default `getMort()` calls `mizerMort()`. However you can replace this with your own alternative mortality function. If your function is called `"myMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "Mort", "myMort")
```

Your function will then be called instead of `mizerMort()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

`MizerParams` *Alias for* `set_multispecies_model()`

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 1.0

Usage

```
MizerParams(
  species_params,
  interaction = matrix(1, nrow = nrow(species_params), ncol = nrow(species_params)),
  min_w_pp = 1e-10,
  min_w = 0.001,
  max_w = max(species_params$w_inf) * 1.1,
  no_w = 100,
  n = 2/3,
  q = 0.8,
  f0 = 0.6,
  kappa = 1e+11,
  lambda = 2 + q - n,
  r_pp = 10,
  ...
)
```

Arguments

`species_params`	A data frame of species-specific parameter values.
`interaction`	Optional interaction matrix of the species (predator species x prey species). Entries should be numbers between 0 and 1. By default all entries are 1. See "Setting interaction matrix" section below.
`min_w_pp`	The smallest size of the resource spectrum. By default this is set to the smallest value at which any of the consumers can feed.
`min_w`	Sets the size of the eggs of all species for which this is not given in the `w_min` column of the `species_params` dataframe.
`max_w`	The largest size of the consumer spectrum. By default this is set to the largest `w_inf` specified in the `species_params` data frame.
`no_w`	The number of size bins in the consumer spectrum.
`n`	The allometric growth exponent. This can be overruled for individual species by including a `n` column in the `species_params`.

q	Allometric exponent of search volume
f0	Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.
kappa	Coefficient of the intrinsic resource carrying capacity
lambda	Scaling exponent of the intrinsic resource carrying capacity
r_pp	Coefficient of the intrinsic resource birth rate
...	Unused

MizerParams-class *A class to hold the parameters for a size based model.*

Description

Although it is possible to build a MizerParams object by hand it is not recommended and several constructors are available. Dynamic simulations are performed using project() function on objects of this class. As a user you should never need to access the slots inside a MizerParams object directly.

Details

The MizerParams class is fairly complex with a large number of slots, many of which are multidimensional arrays. The dimensions of these arrays is strictly enforced so that MizerParams objects are consistent in terms of number of species and number of size classes.

The MizerParams class does not hold any dynamic information, e.g. abundances or harvest effort through time. These are held in MizerSim objects.

Slots

metadata A list with metadata information. See setMetadata().

mizer_version The package version of mizer (as returned by packageVersion("mizer")) that created or last saved the model.

extensions A named vector of strings where each name is the name of and extension package needed to run the model and each value is a string giving the information that the remotes package needs to install the correct version of the extension package, see https://remotes.r-lib.org/.

time_created A POSIXct date-time object with the creation time.

time_modified A POSIXct date-time object with the last modified time.

w The size grid for the fish part of the spectrum. An increasing vector of weights (in grams) running from the smallest egg size to the largest asymptotic size.

dw The widths (in grams) of the size bins

w_full The size grid for the full size range including the resource spectrum. An increasing vector of weights (in grams) running from the smallest resource size to the largest asymptotic size of fish. The last entries of the vector have to be equal to the content of the w slot.

`dw_full` The width of the size bins for the full spectrum. The last entries have to be equal to the content of the dw slot.

`w_min_idx` A vector holding the index of the weight of the egg size of each species

`maturity` An array (species x size) that holds the proportion of individuals of each species at size that are mature. This enters in the calculation of the spawning stock biomass with `getSSB()`. Set with `setReproduction()`.

`psi` An array (species x size) that holds the allocation to reproduction for each species at size, $\psi_i(w)$. Changed with `setReproduction()`.

`intake_max` An array (species x size) that holds the maximum intake for each species at size. Changed with `setMaxIntakeRate()`.

`search_vol` An array (species x size) that holds the search volume for each species at size. Changed with `setSearchVolume()`.

`metab` An array (species x size) that holds the metabolism for each species at size. Changed with `setMetabolicRate()`.

`mu_b` An array (species x size) that holds the external mortality rate $\mu_{ext.i}(w)$. Changed with `setExtMort()`.

`pred_kernel` An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If this is NA then the following two slots will be used. Changed with `setPredKernel()`.

`ft_pred_kernel_e` An array (species x log of predator/prey size ratio) that holds the Fourier transform of the feeding kernel in a form appropriate for evaluating the encounter rate integral. If this is NA then the `pred_kernel` will be used to calculate the available energy integral. Changed with `setPredKernel()`.

`ft_pred_kernel_p` An array (species x log of predator/prey size ratio) that holds the Fourier transform of the feeding kernel in a form appropriate for evaluating the predation mortality integral. If this is NA then the `pred_kernel` will be used to calculate the integral. Changed with `setPredKernel()`.

`rr_pp` A vector the same length as the w_full slot. The size specific growth rate of the resource spectrum. Changed with `setResource()`.

`cc_pp` A vector the same length as the w_full slot. The size specific carrying capacity of the resource spectrum. Changed with `setResource()`.

`resource_dynamics` Name of the function for projecting the resource abundance density by one timestep. The default is `resource_semichemostat()`. Changed with `setResource()`.

`other_dynamics` A named list of functions for projecting the values of other dynamical components of the ecosystem that may be modelled by a mizer extensions you have installed. The names of the list entries are the names of those components.

`other_encounter` A named list of functions for calculating the contribution to the encounter rate from each other dynamical component.

`other_mort` A named list of functions for calculating the contribution to the mortality rate from each other dynamical components.

`other_params` A list containing the parameters needed by any mizer extensions you may have installed to model other dynamical components of the ecosystem.

`rates_funcs` A named list with the names of the functions that should be used to calculate the rates needed by `project()`. By default this will be set to the names of the built-in rate functions.

`sc` **[Experimental]** The community abundance of the scaling community

`species_params` A data.frame to hold the species specific parameters. See `newMultispeciesParams()` for details.

`gear_params` Data frame with parameters for gear selectivity. See `setFishing()` for details.

`interaction` The species specific interaction matrix, θ_{ij}. Changed with `setInteraction()`.

`selectivity` An array (gear x species x w) that holds the selectivity of each gear for species and size, $S_{g,i,w}$. Changed with `setFishing()`.

`catchability` An array (gear x species) that holds the catchability of each species by each gear, $Q_{g,i}$. Changed with `setFishing()`.

`initial_effort` A vector containing the initial fishing effort for each gear. Changed with `setFishing()`.

`initial_n` An array (species x size) that holds the initial abundance of each species at each weight.

`initial_n_pp` A vector the same length as the w_full slot that describes the initial resource abundance at each weight.

`initial_n_other` A list with the initial abundances of all other ecosystem components. Has length zero if there are no other components.

`resource_params` List with parameters for resource. See `setResource()`.

`A` **[Experimental]** Abundance multipliers.

`linecolour` A named vector of colour values, named by species. Used to give consistent colours in plots.

`linetype` A named vector of linetypes, named by species. Used to give consistent line types in plots.

`ft_mask` An array (species x w_full) with zeros for weights larger than the asymptotic weight of each species. Used to efficiently minimize wrap-around errors in Fourier transform calculations.

See Also

`project()` `MizerSim()` `emptyParams()` `newMultispeciesParams()` `newCommunityParams()` `newTraitParams()`

`mizerPredMort` *Get total predation mortality rate needed to project standard mizer model*

Description

Calculates the total predation mortality rate $\mu_{p,i}(w_p)$ (in units of 1/year) on each prey species by prey size:

$$\mu_{p.i}(w_p) = \sum_j \texttt{pred\_rate}_j(w_p)\, \theta_{ji}.$$

You would not usually call this function directly but instead use `getPredMort()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerPredMort(params, n, n_pp, n_other, t, pred_rate, ...)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
pred_rate	A two dimensional array (predator species x predator size) with the feeding level.
...	Unused

Value

A two dimensional array (prey species x prey size) with the predation mortality

Your own predation mortality function

By default `getPredMort()` calls `mizerPredMort()`. However you can replace this with your own alternative predation mortality function. If your function is called `"myPredMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "PredMort", "myPredMort")
```

Your function will then be called instead of `mizerPredMort()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`, `mizerResourceMort()`

---

mizerPredRate *Get predation rate needed to project standard mizer model*

Description

Calculates the potential rate (in units 1/year) at which a prey individual of a given size w is killed by predators from species j. In formulas

$$\texttt{pred\_rate}_j(w_p) = \int \phi_j(w, w_p)(1 - f_j(w))\gamma_j(w)N_j(w)\, dw.$$

This potential rate is used in the function `mizerPredMort()` to calculate the realised predation mortality rate on the prey individual. You would not usually call this function directly but instead use `getPredRate()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerPredRate(params, n, n_pp, n_other, t, feeding_level, ...)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
feeding_level	An array (species x size) with the feeding level as calculated by getFeedingLevel().
...	Unused

Value

A named two dimensional array (predator species x prey size) with the predation rate, where the prey size runs over fish community plus resource spectrum.

Your own predation rate function

By default getPredRate() calls mizerPredRate(). However you can replace this with your own alternative predation rate function. If your function is called "myPredRate" then you register it in a MizerParams object params with

```
params <- setRateFunction(params, "PredRate", "myPredRate")
```

Your function will then be called instead of mizerPredRate(), with the same arguments.

See Also

Other mizer rate functions: mizerEGrowth(), mizerEReproAndGrowth(), mizerERepro(), mizerEncounter(), mizerFMortGear(), mizerFMort(), mizerFeedingLevel(), mizerMort(), mizerPredMort(), mizerRDI(), mizerRates(), mizerResourceMort()

---

mizerRates *Get all rates needed to project standard mizer model*

Description

Calls other rate functions in sequence and collects the results in a list.

Usage

```
mizerRates(params, n, n_pp, n_other, t = 0, effort, rates_fns, ...)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size).
n_pp	A vector of the resource abundance by size
n_other	A list of abundances for other dynamical components of the ecosystem
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
effort	The effort for each fishing gear
rates_fns	Named list of the functions to call to calculate the rates. Note that this list holds the functions themselves, not their names.
...	Unused

Details

By default this function returns a list with the following components:

- encounter from `mizerEncounter()`
- feeding_level from `mizerFeedingLevel()`
- e from `mizerEReproAndGrowth()`
- e_repro from `mizerERepro()`
- e_growth from `mizerEGrowth()`
- pred_rate from `mizerPredRate()`
- pred_mort from `mizerPredMort()`
- f_mort from `mizerFMort()`
- mort from `mizerMort()`
- rdi from `mizerRDI()`
- rdd from `BevertonHoltRDD()`
- resource_mort from `mizerResourceMort()`

However you can replace any of these rate functions by your own rate function if you wish, see `setRateFunction()` for details.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerResourceMort()`

`mizerRDI` *Get density-independent rate of reproduction needed to project standard mizer model*

Description

Calculates the density-independent rate of total egg production R_{di} (units 1/year) before density dependence, by species. You would not usually call this function directly but instead use `getRDI()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerRDI(params, n, n_pp, n_other, t, e_growth, mort, e_repro, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`e_growth`	An array (species x size) with the energy available for growth as calculated by `getEGrowth()`. Unused.
`mort`	An array (species x size) with the mortality rate as calculated by `getMort()`. Unused.
`e_repro`	An array (species x size) with the energy available for reproduction as calculated by `getERepro()`.
`...`	Unused

Details

This rate is obtained by taking the per capita rate $E_r(w)\psi(w)$ at which energy is invested in reproduction, as calculated by `getERepro()`, multiplying it by the number of individuals$N(w)$ and integrating over all sizes w and then multiplying by the reproductive efficiency ϵ and dividing by the egg size `w_min`, and by a factor of two to account for the two sexes:

$$R_{di} = \frac{\epsilon}{2w_{min}} \int N(w) E_r(w) \psi(w)\, dw$$

Used by `getRDD()` to calculate the actual, density dependent rate. See `setReproduction()` for more details.

Value

A numeric vector with the rate of egg production for each species.

Your own reproduction function

By default `getRDI()` calls `mizerRDI()`. However you can replace this with your own alternative reproduction function. If your function is called `"myRDI"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "RDI", "myRDI")
```

Your function will then be called instead of `mizerRDI()`, with the same arguments. For an example of an alternative reproduction function see `constantEggRDI()`.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRates()`, `mizerResourceMort()`

`mizerResourceMort` *Get predation mortality rate for resource needed to project standard mizer model*

Description

Calculates the predation mortality rate $\mu_p(w)$ on the resource spectrum by resource size (in units 1/year). You would not usually call this function directly but instead use `getResourceMort()`, which then calls this function unless an alternative function has been registered, see below.

Usage

```
mizerResourceMort(params, n, n_pp, n_other, t, pred_rate, ...)
```

Arguments

`params`	A MizerParams object
`n`	A matrix of species abundances (species x size).
`n_pp`	A vector of the resource abundance by size
`n_other`	A list of abundances for other dynamical components of the ecosystem
`t`	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
`pred_rate`	A two dimensional array (predator species x prey size) with the predation rate, where the prey size runs over fish community plus resource spectrum.
`...`	Unused

Value

A vector of mortality rate by resource size.

Your own resource mortality function

By default `getResourceMort()` calls `mizerResourceMort()`. However you can replace this with your own alternative resource mortality function. If your function is called `"myResourceMort"` then you register it in a MizerParams object `params` with

```
params <- setRateFunction(params, "ResourceMort", "myResourceMort")
```

Your function will then be called instead of `mizerResourceMort()`, with the same arguments.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerEReproAndGrowth()`, `mizerERepro()`, `mizerEncounter()`, `mizerFMortGear()`, `mizerFMort()`, `mizerFeedingLevel()`, `mizerMort()`, `mizerPredMort()`, `mizerPredRate()`, `mizerRDI()`, `mizerRates()`

MizerSim *Constructor for the* MizerSim *class*

Description

A constructor for the `MizerSim` class. This is used by `project()` to create `MizerSim` objects of the right dimensions. It is not necessary for users to use this constructor.

Usage

```
MizerSim(params, t_dimnames = NA, t_max = 100, t_save = 1)
```

Arguments

`params`	a MizerParams object
`t_dimnames`	Numeric vector that is used for the time dimensions of the slots. Default = NA.
`t_max`	The maximum time step of the simulation. Only used if t_dimnames = NA. Default value = 100.
`t_save`	How often should the results of the simulation be stored. Only used if t_dimnames = NA. Default value = 1.

Value

An object of type MizerSim

`MizerSim-class` *A class to hold the results of a simulation*

Description

A class that holds the results of projecting a MizerParams object through time using `project()`.

Details

A new `MizerSim` object can be created with the `MizerSim()` constructor, but you will never have to do that because the object is created automatically by `project()` when needed.

As a user you should never have to access the slots of a MizerSim object directly. Instead there are a range of functions to extract the information. `N()` and `NResource()` return arrays with the saved abundances of the species and the resource population at size respectively. `getEffort()` returns the fishing effort of each gear through time. `getTimes()` returns the vector of times at which simulation results were stored and `idxFinalT()` returns the index with which to access specifically the value at the final time in the arrays returned by the other functions. `getParams()` returns the `MizerParams` object that was passed to `project()`. There are also several summary_functions and plotting_functions available to explore the contents of a `MizerSim` object.

The arrays all have named dimensions. The names of the `time` dimension denote the time in years. The names of the `w` dimension are weights in grams rounded to three significant figures. The names of the `sp` dimension are the same as the species name in the order specified in the species_params data frame. The names of the `gear` dimension are the names of the gears, in the same order as specified when setting up the `MizerParams` object.

Extensions of mizer can use the `n_other` slot to store the abundances of other ecosystem components and these extensions should provide their own functions for accessing that information.

The `MizerSim` class has changed since previous versions of mizer. To use a `MizerSim` object created by a previous version, you need to upgrade it with `upgradeSim()`.

Slots

`params` An object of type MizerParams.

`n` Three-dimensional array (time x species x size) that stores the projected community number densities.

`n_pp` An array (time x size) that stores the projected resource number densities.

`n_other` A list array (time x component) that stores the projected values for other ecosystem components.

`effort` An array (time x gear) that stores the fishing effort by time and gear.

N *Time series of size spectra*

Description

Fetch the simulation results for the size spectra over time.

Usage

```
N(sim)

NResource(sim)
```

Arguments

sim	A MizerSim object

Value

For `N()`: A three-dimensional array (time x species x size) with the number density of consumers

For `NResource()`: An array (time x size) with the number density of resource

Examples

```
str(N(NS_sim))
str(NResource(NS_sim))
```

newCommunityParams *Set up parameters for a community-type model*

Description

This functions creates a `MizerParams` object describing a community-type model.

Usage

```
newCommunityParams(
  max_w = 1e+06,
  min_w = 0.001,
  no_w = 100,
  min_w_pp = 1e-10,
  z0 = 0.1,
  alpha = 0.2,
  f0 = 0.7,
  h = 10,
  gamma = NA,
```

```
  beta = 100,
  sigma = 2,
  n = 2/3,
  kappa = 1000,
  lambda = 2.05,
  r_pp = 10,
  knife_edge_size = 1000,
  reproduction
)
```

Arguments

max_w	The maximum size of the community. The w_inf of the species used to represent the community is set to this value.
min_w	The minimum size of the community.
no_w	The number of size bins in the consumer spectrum.
min_w_pp	The smallest size of the resource spectrum. By default this is set to the smallest value at which any of the consumers can feed.
z0	The background mortality of the community.
alpha	The assimilation efficiency of the community.
f0	The average feeding level of individuals who feed on a power-law spectrum. This value is used to calculate the search rate parameter gamma.
h	The coefficient of the maximum food intake rate.
gamma	Volumetric search rate. Estimated using h, f0 and kappa if not supplied.
beta	The preferred predator prey mass ratio.
sigma	The width of the prey preference.
n	The allometric growth exponent. Used as allometric exponent for the maximum intake rate of the community as well as the intrinsic growth rate of the resource.
kappa	Coefficient of the intrinsic resource carrying capacity
lambda	Scaling exponent of the intrinsic resource carrying capacity
r_pp	Coefficient of the intrinsic resource birth rate
knife_edge_size	The size at the edge of the knife-edge-selectivity function.
reproduction	The constant reproduction in the smallest size class of the community spectrum. By default this is set so that the community spectrum is continuous with the resource spectrum.

Details

A community model has several features that distinguish it from a multi-species model:

- Species identities of individuals are ignored. All are aggregated into a single community.
- The resource spectrum only extends to the start of the community spectrum.

- Reproductive rate is constant, independent of the energy invested in reproduction, which is set to 0.
- Standard metabolism is turned off (the parameter `ks` is set to 0). Consequently, the growth rate is now determined solely by the assimilated food

The function has many arguments, all of which have default values.

Fishing selectivity is modelled as a knife-edge function with one parameter, `knife_edge_size`, which determines the size at which species are selected.

The resulting `MizerParams` object can be projected forward using `project()` like any other `MizerParams` object. When projecting the community model it may be necessary to keep a small time step size `dt` of around 0.1 to avoid any instabilities with the solver. You can check for these numerical instabilities by plotting the biomass or abundance through time after the projection.

Value

An object of type `MizerParams`

References

K. H. Andersen,J. E. Beyer and P. Lundberg, 2009, Trophic and individual efficiencies of size-structured communities, Proceedings of the Royal Society, 276, 109-114

See Also

Other functions for setting up models: `newMultispeciesParams()`, `newSingleSpeciesParams()`, `newTraitParams()`

Examples

```
## Not run:
params <- newCommunityParams(f0 = 0.7, z0 = 0.2)
sim <- project(params, t_max = 10)
plotBiomass(sim)
plotSpectra(sim)

## End(Not run)
```

`newMultispeciesParams` *Set up parameters for a general multispecies model*

Description

Sets up a multi-species size spectrum model by filling all slots in the MizerParams object based on user-provided or default parameters. There is a long list of arguments, but almost all of them have sensible default values. The only required argument is the `species_params` data frame. All arguments are described in more details in the sections below the list.

Usage

```
newMultispeciesParams(
  species_params,
  interaction = NULL,
  no_w = 100,
  min_w = 0.001,
  max_w = NA,
  min_w_pp = NA,
  pred_kernel = NULL,
  search_vol = NULL,
  intake_max = NULL,
  metab = NULL,
  p = 0.7,
  ext_mort = NULL,
  z0pre = 0.6,
  z0exp = n - 1,
  maturity = NULL,
  repro_prop = NULL,
  RDD = "BevertonHoltRDD",
  resource_rate = NULL,
  resource_capacity = NULL,
  n = 2/3,
  r_pp = 10,
  kappa = 1e+11,
  lambda = 2.05,
  w_pp_cutoff = 10,
  resource_dynamics = "resource_semichemostat",
  gear_params = NULL,
  selectivity = NULL,
  catchability = NULL,
  initial_effort = NULL,
  info_level = 3,
  z0 = deprecated()
)
```

Arguments

species_params	A data frame of species-specific parameter values.
interaction	Optional interaction matrix of the species (predator species x prey species). Entries should be numbers between 0 and 1. By default all entries are 1. See "Setting interaction matrix" section below.
no_w	The number of size bins in the consumer spectrum.
min_w	Sets the size of the eggs of all species for which this is not given in the w_min column of the species_params dataframe.
max_w	The largest size of the consumer spectrum. By default this is set to the largest w_inf specified in the species_params data frame.

`min_w_pp` The smallest size of the resource spectrum. By default this is set to the smallest value at which any of the consumers can feed.

`pred_kernel` Optional. An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If not supplied, a default is set as described in section "Setting predation kernel".

`search_vol` Optional. An array (species x size) holding the search volume for each species at size. If not supplied, a default is set as described in the section "Setting search volume".

`intake_max` Optional. An array (species x size) holding the maximum intake rate for each species at size. If not supplied, a default is set as described in the section "Setting maximum intake rate".

`metab` Optional. An array (species x size) holding the metabolic rate for each species at size. If not supplied, a default is set as described in the section "Setting metabolic rate".

`p` The allometric metabolic exponent. This is only used if `metab` is not given explicitly and if the exponent is not specified in a `p` column in the `species_params`.

`ext_mort` Optional. An array (species x size) holding the external mortality rate.

`z0pre` If `z0`, the mortality from other sources, is not a column in the species data frame, it is calculated as z0pre * w_inf ^ z0exp. Default value is 0.6.

`z0exp` If `z0`, the mortality from other sources, is not a column in the species data frame, it is calculated as `z0pre * w_inf ^ z0exp`. Default value is `n-1`.

`maturity` Optional. An array (species x size) that holds the proportion of individuals of each species at size that are mature. If not supplied, a default is set as described in the section "Setting reproduction".

`repro_prop` Optional. An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. If not supplied, a default is set as described in the section "Setting reproduction".

`RDD` The name of the function calculating the density-dependent reproduction rate from the density-independent rate. Defaults to "`BevertonHoltRDD()`".

`resource_rate` Optional. Vector of resource intrinsic birth rates

`resource_capacity`
Optional. Vector of resource intrinsic carrying capacity

`n` The allometric growth exponent. This can be overruled for individual species by including a `n` column in the `species_params`.

`r_pp` Coefficient of the intrinsic resource birth rate

`kappa` Coefficient of the intrinsic resource carrying capacity

`lambda` Scaling exponent of the intrinsic resource carrying capacity

`w_pp_cutoff` The upper cut off size of the resource spectrum. The carrying capacity will be set to 0 above this size. Default is 10 g.

`resource_dynamics`
Optional. Name of the function that determines the resource dynamics by calculating the resource spectrum at the next time step from the current state. You only need to specify this if you do not want to use the default `resource_semichemostat()`.

gear_params	A data frame with gear-specific parameter values.
selectivity	Optional. An array (gear x species x size) that holds the selectivity of each gear for species and size, $S_{g,i,w}$.
catchability	Optional. An array (gear x species) that holds the catchability of each species by each gear, $Q_{g,i}$.
initial_effort	Optional. A number or a named numeric vector specifying the fishing effort. If a number, the same effort is used for all gears. If a vector, must be named by gear.
info_level	Controls the amount of information messages that are shown when the function sets default values for parameters.
z0	**[Deprecated]** Use ext_mort instead. Not to be confused with the species_parameter z0.

Value

An object of type MizerParams

Species parameters

The only essential argument is a data frame that contains the species parameters. The data frame is arranged species by parameter, so each column of the parameter data frame is a parameter and each row has the values of the parameters for one of the species in the model.

There are two essential columns that must be included in the species parameter data.frame and that do not have default values: the species column that should hold strings with the names of the species and the w_inf column with the asymptotic sizes of the species in grams.

The species_params dataframe also needs to contain the parameters needed by any predation kernel function or size selectivity function. This will be mentioned in the appropriate sections below.

For all other species parameters, mizer will calculate default values if they are not included in the species parameter data frame. They will be automatically added when the MizerParams object is created. For these parameters you can also specify values for only some species and leave the other entries as NA and the missing values will be set to the defaults. So the species_params data frame saved in the returned MizerParams object will differ from the one you supply because it will have the missing species parameters filled in with default values.

If you are not happy with any of the species parameter values used you can always change them later with species_params<-().

All the parameters will be mentioned in the following sections.

Size grid

A size grid is created so that the log-sizes are equally spaced. The spacing is chosen so that there will be no_w fish size bins, with the smallest starting at min_w and the largest starting at max_w. For the resource spectrum there is a larger set of bins containing additional bins below min_w, with the same log size. The number of extra bins is such that min_w_pp comes to lie within the smallest bin.

Units in mizer

Mizer uses grams to measure weight, centimetres to measure lengths, and years to measure time.

Mizer is agnostic about whether abundances are given as

1. numbers per area,
2. numbers per volume or
3. total numbers for the entire study area.

You should make the choice most convenient for your application and then stick with it. If you make choice 1 or 2 you will also have to choose a unit for area or volume. Your choice will then determine the units for some of the parameters. This will be mentioned when the parameters are discussed in the sections below.

Your choice will also affect the units of the quantities you may want to calculate with the model. For example, the yield will be in grams/year/m^2 in case 1 if you choose m^2 as your measure of area, in grams/year/m^3 in case 2 if you choose m^3 as your unit of volume, or simply grams/year in case 3. The same comment applies for other measures, like total biomass, which will be grams/area in case 1, grams/volume in case 2 or simply grams in case 3. When mizer puts units on axes in plots, it will choose the units appropriate for case 3. So for example in `plotBiomass()` it gives the unit as grams.

You can convert between these choices. For example, if you use case 1, you need to multiply with the area of the ecosystem to get the total quantity. If you work with case 2, you need to multiply by both area and the thickness of the productive layer. In that respect, case 2 is a bit cumbersome. The function `scaleModel()` is useful to change the units you are using.

Setting interaction matrix

You do not need to specify an interaction matrix. If you do not, then the predator-prey interactions are purely determined by the size of predator and prey and totally independent of the species of predator and prey.

The interaction matrix θ_{ij} describes the interaction of each pair of species in the model. This can be viewed as a proxy for spatial interaction e.g. to model predator-prey interaction that is not size based. The values in the interaction matrix are used to scale the encountered food and predation mortality (see on the website the section on predator-prey encounter rate and on predation mortality). The first index refers to the predator species and the second to the prey species.

It is used when calculating the food encounter rate in `getEncounter()` and the predation mortality rate in `getPredMort()`. Its entries are dimensionless numbers.The values are between 0 (species do not overlap and therefore do not interact with each other) to 1 (species overlap perfectly). If all the values in the interaction matrix are set to 1 then predator-prey interactions are determined entirely by size-preference.

This function checks that the supplied interaction matrix is valid and then stores it in the `interaction` slot of the `params` object.

The order of the columns and rows of the `interaction` argument should be the same as the order in the species params data frame in the `params` object. If you supply a named array then the function will check the order and warn if it is different. One way of creating your own interaction matrix is to enter the data using a spreadsheet program and saving it as a .csv file. The data can be read into R using the command `read.csv()`.

The interaction of the species with the resource are set via a column `interaction_resource` in the `species_params` data frame. Again the entries have to be numbers between 0 and 1. By default this column is set to all 1s.

Setting predation kernel

Kernel dependent on predator to prey size ratio

If the `pred_kernel` argument is not supplied, then this function sets a predation kernel that depends only on the ratio of predator mass to prey mass, not on the two masses independently. The shape of that kernel is then determined by the `pred_kernel_type` column in species_params.

The default for `pred_kernel_type` is "lognormal". This will call the function `lognormal_pred_kernel()` to calculate the predation kernel. An alternative pred_kernel type is "box", implemented by the function `box_pred_kernel()`, and "power_law", implemented by the function `power_law_pred_kernel()`. These functions require certain species parameters in the species_params data frame. For the log-normal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`. They are explained in the help pages for the kernel functions. Except for `beta` and `sigma`, no defaults are set for these parameters. If they are missing from the species_params data frame then mizer will issue an error message.

You can use any other string for `pred_kernel_type`. If for example you choose "my" then you need to define a function `my_pred_kernel` that you can model on the existing functions like `lognormal_pred_kernel()`.

When using a kernel that depends on the predator/prey size ratio only, mizer does not need to store the entire three dimensional array in the MizerParams object. Such an array can be very big when there is a large number of size bins. Instead, mizer only needs to store two two-dimensional arrays that hold Fourier transforms of the feeding kernel function that allow the encounter rate and the predation rate to be calculated very efficiently. However, if you need the full three-dimensional array you can calculate it with the `getPredKernel()` function.

Kernel dependent on both predator and prey size

If you want to work with a feeding kernel that depends on predator mass and prey mass independently, you can specify the full feeding kernel as a three-dimensional array (predator species x predator size x prey size).

You should use this option only if a kernel dependent only on the predator/prey mass ratio is not appropriate. Using a kernel dependent on predator/prey mass ratio only allows mizer to use fast Fourier transform methods to significantly reduce the running time of simulations.

The order of the predator species in `pred_kernel` should be the same as the order in the species params dataframe in the `params` object. If you supply a named array then the function will check the order and warn if it is different.

Setting search volume

The search volume $\gamma_i(w)$ of an individual of species i and weight w multiplies the predation kernel when calculating the encounter rate in `getEncounter()` and the predation rate in `getPredRate()`.

The name "search volume" is a bit misleading, because $\gamma_i(w)$ does not have units of volume. It is simply a parameter that determines the rate of predation. Its units depend on your choice, see section "Units in mizer". If you have chosen to work with total abundances, then it is a rate with units 1/year. If you have chosen to work with abundances per m^2 then it has units of m^2/year. If you have chosen to work with abundances per m^3 then it has units of m^3/year.

If the search_vol argument is not supplied, then the search volume is set to

$$\gamma_i(w) = \gamma_i w_i^q.$$

The values of γ_i (the search volume at 1g) and q_i (the allometric exponent of the search volume) are taken from the gamma and q columns in the species parameter dataframe. If the gamma column is not supplied in the species parameter dataframe, a default is calculated by the get_gamma_default() function. Note that only for predators of size $w = 1$ gram is the value of the species parameter γ_i the same as the value of the search volume $\gamma_i(w)$.

Setting maximum intake rate

The maximum intake rate $h_i(w)$ of an individual of species i and weight w determines the feeding level, calculated with getFeedingLevel(). It is measured in grams/year.

If the intake_max argument is not supplied, then the maximum intake rate is set to

$$h_i(w) = h_i w^{n_i}.$$

The values of h_i (the maximum intake rate of an individual of size 1 gram) and n_i (the allometric exponent for the intake rate) are taken from the h and n columns in the species parameter dataframe. If the h column is not supplied in the species parameter dataframe, it is calculated by the get_h_default() function, using the f0 and the k_vb column, if they are supplied.

If h_i is set to Inf, fish of species i will consume all encountered food.

Setting metabolic rate

The metabolic rate is subtracted from the energy income rate to calculate the rate at which energy is available for growth and reproduction, see getEReproAndGrowth(). It is measured in grams/year.

If the metab argument is not supplied, then for each species the metabolic rate $k(w)$ for an individual of size w is set to

$$k(w) = k_s w^p + kw,$$

where $k_s w^p$ represents the rate of standard metabolism and kw is the rate at which energy is expended on activity and movement. The values of k_s, p and k are taken from the ks, p and k columns in the species parameter dataframe. If any of these parameters are not supplied, the defaults are $k = 0$, $p = n$ and

$$k_s = f_c h \alpha w_{mat}^{n-p},$$

where f_c is the critical feeding level taken from the fc column in the species parameter data frame. If the critical feeding level is not specified, a default of $f_c = 0.2$ is used.

Setting external mortality rate

The external mortality is all the mortality that is not due to fishing or predation by predators included in the model. The external mortality could be due to predation by predators that are not explicitly included in the model (e.g. mammals or seabirds) or due to other causes like illness. It is a rate with units 1/year.

The ext_mort argument allows you to specify an external mortality rate that depends on species and body size. You can see an example of this in the Examples section of the help page for setExtMort().

If the ext_mort argument is not supplied, then the external mortality is assumed to depend only on the species, not on the size of the individual: $\mu_{ext.i}(w) = z_{0.i}$. The value of the constant z_0 for each species is taken from the z0 column of the species parameter data frame, if that column exists. Otherwise it is calculated as

$$z_{0.i} = \texttt{z0pre}_i \, w_{inf}^{\texttt{z0exp}}.$$

Setting reproduction

For each species and at each size, the proportion ψ of the available energy that is invested into reproduction is the product of two factors: the proportion maturity of individuals that are mature and the proportion repro_prop of the energy available to a mature individual that is invested into reproduction.

Maturity ogive: If the the proportion of individuals that are mature is not supplied via the maturity argument , then it is set to a sigmoidal maturity ogive that changes from 0 to 1 at around the maturity size:

$$\texttt{maturity}(w) = \left[1 + \left(\frac{w}{w_{mat}}\right)^{-U}\right]^{-1}.$$

(To avoid clutter, we are not showing the species index in the equations, although each species has its own maturity ogive.) The maturity weights are taken from the w_mat column of the species_params data frame. Any missing maturity weights are set to 1/4 of the asymptotic weight in the w_inf column.

The exponent U determines the steepness of the maturity ogive. By default it is chosen as $U = 10$, however this can be overridden by including a column w_mat25 in the species parameter dataframe that specifies the weight at which 25% of individuals are mature, which sets $U = \log(3)/\log(w_{mat}/w_{25})$.

The sigmoidal function given above would strictly reach 1 only asymptotically. Mizer instead sets the function equal to 1 already at the species' maximum size, taken from the compulsory w_inf column in the species parameter data frame. Also, for computational simplicity, any proportion smaller than 1e-8 is set to 0.

Investment into reproduction: If the the energy available to a mature individual that is invested into reproduction is not supplied via the repro_prop argument, it is set to the allometric form

$$\texttt{repro\_prop}(w) = \left(\frac{w}{w_{inf}}\right)^{m-n}.$$

Here n is the scaling exponent of the energy income rate. Hence the exponent m determines the scaling of the investment into reproduction for mature individuals. By default it is chosen to be $m = 1$ so that the rate at which energy is invested into reproduction scales linearly with the size. This default can be overridden by including a column m in the species parameter dataframe. The asymptotic sizes are taken from the compulsory w_inf column in the species parameter data frame.

The total proportion of energy invested into reproduction of an individual of size w is then

$$\psi(w) = \texttt{maturity}(w)\texttt{repro\_prop}(w)$$

Reproductive efficiency: The reproductive efficiency ϵ, i.e., the proportion of energy allocated to reproduction that results in egg biomass, is set through the `erepro` column in the species_params data frame. If that is not provided, the default is set to 1 (which you will want to override). The offspring biomass divided by the egg biomass gives the rate of egg production, returned by `getRDI()`:

$$R_{di} = \frac{\epsilon}{2w_{min}} \int N(w) E_r(w) \psi(w)\, dw$$

Density dependence: The stock-recruitment relationship is an emergent phenomenon in mizer, with several sources of density dependence. Firstly, the amount of energy invested into reproduction depends on the energy income of the spawners, which is density-dependent due to competition for prey. Secondly, the proportion of larvae that grow up to recruitment size depends on the larval mortality, which depends on the density of predators, and on larval growth rate, which depends on density of prey.

Finally, to encode all the density dependence in the stock-recruitment relationship that is not already included in the other two sources of density dependence, mizer puts the the density-independent rate of egg production through a density-dependence function. The result is returned by `getRDD()`. The name of the density-dependence function is specified by the `RDD` argument. The default is the Beverton-Holt function `BevertonHoltRDD()`, which requires an `R_max` column in the species_params data frame giving the maximum egg production rate. If this column does not exist, it is initialised to `Inf`, leading to no density-dependence. Other functions provided by mizer are `RickerRDD()` and `SheperdRDD()` and you can easily use these as models for writing your own functions.

Setting fishing

Gears

In `mizer`, fishing mortality is imposed on species by fishing gears. The total per-capita fishing mortality (1/year) is obtained by summing over the mortality from all gears,

$$\mu_{f.i}(w) = \sum_g F_{g,i}(w),$$

where the fishing mortality $F_{g,i}(w)$ imposed by gear g on species i at size w is calculated as:

$$F_{g,i}(w) = S_{g,i}(w) Q_{g,i} E_g,$$

where S is the selectivity by species, gear and size, Q is the catchability by species and gear and E is the fishing effort by gear.

Selectivity

The selectivity at size of each gear for each species is saved as a three dimensional array (gear x species x size). Each entry has a range between 0 (that gear is not selecting that species at that size) to 1 (that gear is selecting all individuals of that species of that size). This three dimensional array can be specified explicitly via the `selectivity` argument, but usually mizer calculates it from the `gear_params` slot of the MizerParams object.

To allow the calculation of the `selectivity` array, the `gear_params` slot must be a data frame with one row for each gear-species combination. So if for example a gear can select three species, then that gear contributes three rows to the `gear_params` data frame, one for each species it can select. The data frame must have columns `gear`, holding the name of the gear, `species`, holding the

name of the species, and `sel_func`, holding the name of the function that calculates the selectivity curve. Some selectivity functions are included in the package: `knife_edge()`, `sigmoid_length()`, `double_sigmoid_length()`, and `sigmoid_weight()`. Users are able to write their own size-based selectivity function. The first argument to the function must be `w` and the function must return a vector of the selectivity (between 0 and 1) at size.

Each selectivity function may have parameters. Values for these parameters must be included as columns in the gear parameters data.frame. The names of the columns must exactly match the names of the corresponding arguments of the selectivity function. For example, the default selectivity function is `knife_edge()` that a has sudden change of selectivity from 0 to 1 at a certain size. In its help page you can see that the `knife_edge()` function has arguments `w` and `knife_edge_size`. The first argument, `w`, is size (the function calculates selectivity at size). All selectivity functions must have `w` as the first argument. The values for the other arguments must be found in the gear parameters data.frame. So for the `knife_edge()` function there should be a `knife_edge_size` column. Because `knife_edge()` is the default selectivity function, the `knife_edge_size` argument has a default value = `w_mat`.

In case each species is only selected by one gear, the columns of the `gear_params` data frame can alternatively be provided as columns of the `species_params` data frame, if this is more convenient for the user to set up. Mizer will then copy these columns over to create the `gear_params` data frame when it creates the MizerParams object. However changing these columns in the species parameter data frame later will not update the `gear_params` data frame.

Catchability

Catchability is used as an additional factor to make the link between gear selectivity, fishing effort and fishing mortality. For example, it can be set so that an effort of 1 gives a desired fishing mortality. In this way effort can then be specified relative to a 'base effort', e.g. the effort in a particular year.

Catchability is stored as a two dimensional array (gear x species). This can either be provided explicitly via the `catchability` argument, or the information can be provided via a `catchability` column in the `gear_params` data frame.

In the case where each species is selected by only a single gear, the `catchability` column can also be provided in the `species_params` data frame. Mizer will then copy this over to the `gear_params` data frame when the MizerParams object is created.

Effort

The initial fishing effort is stored in the `MizerParams` object. If it is not supplied, it is set to zero. The initial effort can be overruled when the simulation is run with `project()`, where it is also possible to specify an effort that varies through time.

Setting resource dynamics

By default, mizer uses a semichemostat model to describe the resource dynamics in each size class independently. This semichemostat dynamics is implemented by the function `resource_semichemostat()`. You can change the resource dynamics by writing your own function, modelled on `resource_semichemostat()`, and then passing the name of your function in the `resource_dynamics` argument.

The `resource_rate` argument is a vector specifying the intrinsic resource growth rate for each size class. If it is not supplied, then the intrinsic growth rate $r(w)$ at size w is set to

$$r(w) = r_{pp}\, w^{n-1}.$$

The values of r_{pp} and n are taken from the `r_pp` and `n` arguments.

The `resource_capacity` argument is a vector specifying the intrinsic resource carrying capacity for each size class. If it is not supplied, then the intrinsic carrying capacity $c(w)$ at size w is set to

$$c(w) = \kappa\, w^{-\lambda}$$

for all w less than `w_pp_cutoff` and zero for larger sizes. The values of κ and λ are taken from the `kappa` and `lambda` arguments.

See Also

Other functions for setting up models: `newCommunityParams()`, `newSingleSpeciesParams()`, `newTraitParams()`

Examples

```
params <- newMultispeciesParams(NS_species_params)
```

`newSingleSpeciesParams` *Set up parameters for a single species in a power-law background*

Description

[Experimental]

This functions creates a `MizerParams` object with a single species. This species is embedded in a fixed power-law community spectrum

$$N_c(w) = \kappa w^{-\lambda}$$

This community provides the food income for the species. Cannibalism is switched off. The predation mortality arises only from the predators in the power-law community and it is assumed that the predators in the community have the same feeding parameters as the foreground species. The function has many arguments, all of which have default values.

Usage

```
newSingleSpeciesParams(
  species_name = "Target species",
  w_inf = 100,
  w_min = 0.001,
  eta = 10^(-0.6),
  w_mat = w_inf * eta,
  no_w = log10(w_inf/w_min) * 20 + 1,
  n = 3/4,
  p = n,
  lambda = 2.05,
  kappa = 0.005,
```

```
  alpha = 0.4,
  k_vb = 1,
  beta = 100,
  sigma = 1.3,
  f0 = 0.6,
  fc = 0.25,
  ks = NA,
  gamma = NA,
  ext_mort_prop = 0,
  reproduction_level = 0,
  R_factor = deprecated()
)
```

Arguments

species_name	A string with a name for the species. Will be used in plot legends.
w_inf	Asymptotic size of species
w_min	Egg size of species
eta	Ratio between maturity size w_mat and asymptotic size w_inf. Default is 10^(-0.6), approximately 1/4. Ignored if w_mat is supplied explicitly.
w_mat	Maturity size of species. Default value is eta * w_inf.
no_w	The number of size bins in the community spectrum. These bins will be equally spaced on a logarithmic scale. Default value is such that there are 20 bins for each factor of 10 in weight.
n	Scaling exponent of the maximum intake rate.
p	Scaling exponent of the standard metabolic rate. By default this is equal to the exponent n.
lambda	Exponent of the abundance power law.
kappa	Coefficient in abundance power law.
alpha	The assimilation efficiency.
k_vb	The von Bertalanffy growth parameter.
beta	Preferred predator prey mass ratio.
sigma	Width of prey size preference.
f0	Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.
fc	Critical feeding level. Used to determine ks if it is not given explicitly.
ks	Standard metabolism coefficient. If not provided, default will be calculated from critical feeding level argument fc.
gamma	Volumetric search rate. If not provided, default is determined by get_gamma_default() using the value of f0.
ext_mort_prop	The proportion of the total mortality that comes from external mortality, i.e., from sources not explicitly modelled. A number in the interval [0, 1).

reproduction_level
: A number between 0 an 1 that determines the level of density dependence in reproduction, see `setBevertonHolt()`.

R_factor
: **[Deprecated]** Use `reproduction_level = 1 / R_factor` instead.

Details

In addition to setting up the parameters, this function also sets up an initial condition that is close to steady state, under the assumption of no fishing.

Value

An object of type `MizerParams`

See Also

Other functions for setting up models: `newCommunityParams()`, `newMultispeciesParams()`, `newTraitParams()`

Examples

```
params <- newSingleSpeciesParams()
sim <- project(params, t_max = 5, effort = 0)
plotSpectra(sim)
```

---

newTraitParams *Set up parameters for a trait-based multispecies model*

Description

This functions creates a `MizerParams` object describing a trait-based model. This is a simplification of the general size-based model used in `mizer` in which the species-specific parameters are the same for all species, except for the asymptotic size, which is considered the most important trait characterizing a species. Other parameters are related to the asymptotic size. For example, the size at maturity is given by `w_inf * eta`, where `eta` is the same for all species. For the trait-based model the number of species is not important. For applications of the trait-based model see Andersen & Pedersen (2010). See the `mizer` website for more details and examples of the trait-based model.

Usage

```
newTraitParams(
  no_sp = 11,
  min_w_inf = 10,
  max_w_inf = 10^4,
  min_w = 10^(-3),
  max_w = max_w_inf,
  eta = 10^(-0.6),
  min_w_mat = min_w_inf * eta,
  no_w = round(log10(max_w_inf/min_w) * 20 + 1),
```

```
  min_w_pp = 1e-10,
  w_pp_cutoff = min_w_mat,
  n = 2/3,
  p = n,
  lambda = 2.05,
  r_pp = 0.1,
  kappa = 0.005,
  alpha = 0.4,
  h = 40,
  beta = 100,
  sigma = 1.3,
  f0 = 0.6,
  fc = 0.25,
  ks = NA,
  gamma = NA,
  ext_mort_prop = 0,
  reproduction_level = 1/4,
  R_factor = deprecated(),
  gear_names = "knife_edge_gear",
  knife_edge_size = 1000,
  egg_size_scaling = FALSE,
  resource_scaling = FALSE,
  perfect_scaling = FALSE
)
```

Arguments

`no_sp`	The number of species in the model.
`min_w_inf`	The asymptotic size of the smallest species in the community. This will be rounded to lie on a grid point.
`max_w_inf`	The asymptotic size of the largest species in the community. This will be rounded to lie on a grid point.
`min_w`	The size of the the egg of the smallest species. This also defines the start of the community size spectrum.
`max_w`	The largest size in the model. By default this is set to the largest asymptotic size `max_w_inf`. Setting it to something larger only makes sense if you plan to add larger species to the model later.
`eta`	Ratio between maturity size and asymptotic size of a species. Ignored if `min_w_mat` is supplied. Default is 10^(-0.6), approximately 1/4.
`min_w_mat`	The maturity size of the smallest species. Default value is `eta * min_w_inf`. This will be rounded to lie on a grid point.
`no_w`	The number of size bins in the community spectrum. These bins will be equally spaced on a logarithmic scale. Default value is such that there are 20 bins for each factor of 10 in weight.
`min_w_pp`	The smallest size of the resource spectrum. By default this is set to the smallest value at which any of the consumers can feed.

w_pp_cutoff — The largest size of the resource spectrum. Default value is min_w_inf unless perfect_scaling = TRUE when it is Inf.

n — Scaling exponent of the maximum intake rate.

p — Scaling exponent of the standard metabolic rate. By default this is equal to the exponent n.

lambda — Exponent of the abundance power law.

r_pp — Growth rate parameter for the resource spectrum.

kappa — Coefficient in abundance power law.

alpha — The assimilation efficiency.

h — Maximum food intake rate.

beta — Preferred predator prey mass ratio.

sigma — Width of prey size preference.

f0 — Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.

fc — Critical feeding level. Used to determine ks if it is not given explicitly.

ks — Standard metabolism coefficient. If not provided, default will be calculated from critical feeding level argument fc.

gamma — Volumetric search rate. If not provided, default is determined by get_gamma_default() using the value of f0.

ext_mort_prop — The proportion of the total mortality that comes from external mortality, i.e., from sources not explicitly modelled. A number in the interval [0, 1).

reproduction_level — A number between 0 an 1 that determines the level of density dependence in reproduction, see setBevertonHolt().

R_factor — **[Deprecated]** Use reproduction_level = 1 / R_factor instead.

gear_names — The names of the fishing gears for each species. A character vector, the same length as the number of species.

knife_edge_size — The minimum size at which the gear or gears select fish. A single value for each gear or a vector with one value for each gear.

egg_size_scaling — **[Experimental]** If TRUE, the egg size is a constant fraction of the maximum size of each species. This fraction is min_w / min_w_inf. If FALSE, all species have the egg size w_min.

resource_scaling — **[Experimental]** If TRUE, the carrying capacity for larger resource is reduced to compensate for the fact that fish eggs and larvae are present in the same size range.

perfect_scaling — **[Experimental]** If TRUE then parameters are set so that the community abundance, growth before reproduction and death are perfect power laws. In particular all other scaling corrections are turned on.

Details

The function has many arguments, all of which have default values. Of particular interest to the user are the number of species in the model and the minimum and maximum asymptotic sizes.

The characteristic weights of the smallest species are defined by `min_w` (egg size), `min_w_mat` (maturity size) and `min_w_inf` (asymptotic size). The asymptotic sizes of the `no_sp` species are logarithmically evenly spaced, ranging from `min_w_inf` to `max_w_inf`. Similarly the maturity sizes of the species are logarithmically evenly spaced, so that the ratio `eta` between maturity size and asymptotic size is the same for all species. If `egg_size_scaling = TRUE` then also the ratio between asymptotic size and egg size is the same for all species. Otherwise all species have the same egg size.

In addition to setting up the parameters, this function also sets up an initial condition that is close to steady state.

The search rate coefficient `gamma` is calculated using the expected feeding level, `f0`.

The option of including fishing is given, but the steady state may loose its natural stability if too much fishing is included. In such a case the user may wish to include stabilising effects (like `reproduction_level`) to ensure the steady state is stable. Fishing selectivity is modelled as a knife-edge function with one parameter, `knife_edge_size`, which is the size at which species are selected. Each species can either be fished by the same gear (`knife_edge_size` has a length of 1) or by a different gear (the length of `knife_edge_size` has the same length as the number of species and the order of selectivity size is that of the asymptotic size).

The resulting `MizerParams` object can be projected forward using `project()` like any other `MizerParams` object. When projecting the model it may be necessary to reduce `dt` below 0.1 to avoid any instabilities with the solver. You can check this by plotting the biomass or abundance through time after the projection.

Value

An object of type `MizerParams`

See Also

Other functions for setting up models: `newCommunityParams()`, `newMultispeciesParams()`, `newSingleSpeciesParams()`

Examples

```
## Not run:
params <- newTraitParams()
sim <- project(params, t_max = 5, effort = 0)
plotSpectra(sim)

## End(Not run)
```

noRDD *Give density-independent reproduction rate*

Description

Simply returns its `rdi` argument.

Usage

```
noRDD(rdi, ...)
```

Arguments

`rdi`	Vector of density-independent reproduction rates R_{di} for all species.
`...`	Not used.

Value

Vector of density-dependent reproduction rates.

See Also

Other functions calculating density-dependent reproduction rate: `BevertonHoltRDD()`, `RickerRDD()`, `SheperdRDD()`, `constantEggRDI()`, `constantRDD()`

NOther *Time series of other components*

Description

Fetch the simulation results for other components over time.

Usage

```
NOther(sim)
```

Arguments

`sim`	A MizerSim object

Value

A list array (time x component) that stores the projected values for other ecosystem components.

NS_interaction *Example interaction matrix for the North Sea example*

Description

The interaction coefficient between predator and prey species in the North Sea.

Usage

```
NS_interaction
```

Format

A 12 x 12 matrix.

Source

Blanchard et al.

Examples

```
## Not run:
params <- MizerParams(NS_species_params_gears,
                      interaction = NS_inter)
sim = project(params, effort = c(Industrial = 0, Pelagic = 1,
                                 Beam = 0.5, Otter = 0.5))
plot(sim)

## End(Not run)
```

NS_params *Example MizerParams object for the North Sea example*

Description

A MizerParams object created from the `NS_species_params_gears` species parameters and the `inter` interaction matrix together with an initial condition corresponding to the steady state obtained from fishing with an effort `effort = c(Industrial = 0, Pelagic = 1, Beam = 0.5, Otter = 0.5)`.

Usage

```
NS_params
```

Format

A MizerParams object

Source

Blanchard et al.

See Also

Other example parameter objects: NS_sim

Examples

```
## Not run:
sim = project(NS_params, effort = c(Industrial = 0, Pelagic = 1,
                                    Beam = 0.5, Otter = 0.5))
plot(sim)

## End(Not run)
```

NS_sim *Example MizerSim object for the North Sea example*

Description

A MizerSim object containing a simulation with historical fishing mortalities from the North Sea, as created in the tutorial "A Multi-Species Model of the North Sea".

Usage

```
NS_sim
```

Format

A MizerSim object

Source

https://sizespectrum.org/mizer/articles/a_multispecies_model_of_the_north_sea.html

See Also

Other example parameter objects: NS_params

Examples

```
## Not run:
plotBiomass(NS_sim)

## End(Not run)
```

NS_species_params *Example species parameter set based on the North Sea*

Description

This data set is based on species in the North Sea (Blanchard et al.). It is a data.frame that contains all the necessary information to be used by the `MizerParams()` constructor. As there is no gear column, each species is assumed to be fished by a separate gear.

Usage

```
NS_species_params
```

Format

A data frame with 12 rows and 7 columns. Each row is a species.

species Name of the species

w_inf The von Bertalanffy W_infinity parameter

w_mat Size at maturity

beta Size preference ratio

sigma Width of the size-preference

R_max Maximum reproduction rate

k_vb The von Bertalanffy k parameter

Source

Blanchard et al.

Examples

```
## Not run:
params <- MizerParams(NS_species_params)
sim = project(params)
plot(sim)

## End(Not run)
```

NS_species_params_gears *Example species parameter set based on the North Sea with different gears*

Description

This data set is based on species in the North Sea (Blanchard et al.). It is similar to the data set NS_species_params except that this one has an additional column specifying the fishing gear that operates on each species.

Usage

```
NS_species_params_gears
```

Format

A data frame with 12 rows and 8 columns. Each row is a species.

species Name of the species

w_inf The von Bertalanffy W_infinity parameter

w_mat Size at maturity

beta Size preference ratio

sigma Width of the size-preference

R_max Maximum reproduction rate

k_vb The von Bertalanffy k parameter

gear Name of the fishing gear

Source

Blanchard et al.

Examples

```
## Not run:
params <- MizerParams(NS_species_params_gears)
sim = project(params, effort = c(Industrial = 0, Pelagic = 1,
                                 Beam = 0.5, Otter = 0.5))
plot(sim)

## End(Not run)
```

plot,MizerSim,missing-method
Summary plot for MizerSim *objects*

Description

After running a projection, produces 5 plots in the same window: feeding level, abundance spectra, predation mortality and fishing mortality of each species by size; and biomass of each species through time. This method just uses the other plotting functions and puts them all in one window.

Produces 3 plots in the same window: abundance spectra, feeding level and predation mortality of each species through time. This method just uses the other plotting functions and puts them all in one window.

Usage

```
## S4 method for signature 'MizerSim,missing'
plot(x, y, ...)

## S4 method for signature 'MizerParams,missing'
plot(x, y, ...)
```

Arguments

x	An object of class MizerSim
y	Not used
...	For additional arguments see the documentation for plotBiomass(), plotFeedingLevel(),plotSpectra and plotFMort().

Value

A viewport object

A viewport object

See Also

plotting_functions

plotting_functions

Other plotting functions: animateSpectra(), plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Other plotting functions: animateSpectra(), plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plot(sim)
plot(sim, time_range = 10:20) # change time period for size-based plots
plot(sim, min_w = 10, max_w = 1000) # change size range for biomass plot


params <-  NS_params
plot(params)
plot(params, min_w = 10, max_w = 1000) # change size range for biomass plot
```

`plotBiomass` *Plot the biomass of species through time*

Description

After running a projection, the biomass of each species can be plotted against time. The biomass is calculated within user defined size limits (min_w, max_w, min_l, max_l, see `getBiomass()`).

Usage

```
plotBiomass(
  sim,
  species = NULL,
  start_time,
  end_time,
  y_ticks = 6,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
  highlight = NULL,
  return_data = FALSE,
  ...
)

plotlyBiomass(
  sim,
  species = NULL,
  start_time,
  end_time,
  y_ticks = 6,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
```

```
  highlight = NULL,
  ...
)
```

Arguments

sim	An object of class MizerSim
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
start_time	The first time to be plotted. Default is the beginning of the time series.
end_time	The last time to be plotted. Default is the end of the time series.
y_ticks	The approximate number of ticks desired on the y axis
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to refer to the existing minimum or maximum. Any values below 1e-20 are always cut off.
total	A boolean value that determines whether the total biomass from all species is plotted as well. Default is FALSE.
background	A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Arguments passed on to get_size_range_array min_w Smallest weight in size range. Defaults to smallest weight in the model. max_w Largest weight in size range. Defaults to largest weight in the model. min_l Smallest length in size range. If supplied, this takes precedence over min_w. max_l Largest length in size range. If supplied, this takes precedence over max_w.

Value

A ggplot2 object, unless return_data = TRUE, in which case a data frame with the four variables 'Year', 'Biomass', 'Species', 'Legend' is returned.

See Also

plotting_functions, getBiomass()

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
plotBiomass(NS_sim)
plotBiomass(NS_sim, species = c("Sandeel", "Herring"), total = TRUE)
plotBiomass(NS_sim, start_time = 1980, end_time = 1990)

# Returning the data frame
fr <- plotBiomass(NS_sim, return_data = TRUE)
str(fr)
```

---

plotBiomassObservedVsModel

Plotting observed vs. model biomass data

Description

[Experimental] If biomass observations are available for at least some species via the `biomass_observed` column in the species parameter data frame, this function plots the biomass of each species in the model against the observed biomasses. When called with a MizerSim object, the plot will use the model biomasses predicted for the final time step in the simulation.

Usage

```
plotBiomassObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  labels = TRUE,
  show_unobserved = FALSE
)

plotlyBiomassObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  show_unobserved = FALSE
)
```

Arguments

`object`	An object of class MizerParams or MizerSim.

species	The species to be included. Optional. By default all observed biomasses will be included. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be included (TRUE) or not.
ratio	Whether to plot model biomass vs. observed biomass (FALSE) or the ratio of model : observed biomass (TRUE). Default is FALSE.
log_scale	Whether to plot on the log10 scale (TRUE) or not (FALSE). For the non-ratio plot this applies for both axes, for the ratio plot only the x-axis is on the log10 scale. Default is TRUE.
return_data	Whether to return the data frame for the plot (TRUE) or not (FALSE). Default is FALSE.
labels	Whether to show text labels for each species (TRUE) or not (FALSE). Default is TRUE.
show_unobserved	Whether to include also species for which no biomass observation is available. If TRUE, these species will be shown as if their observed biomass was equal to the model biomass.

Details

Before you can use this function you will need to have added a `biomass_observed` column to your model which gives the observed biomass in grams. For species for which you have no observed biomass, you should set the value in the `biomass_observed` column to 0 or NA.

Biomass observations usually only include individuals above a certain size. This size should be specified in a `biomass_cutoff` column of the species parameter data frame. If this is missing, it is assumed that all sizes are included in the observed biomass, i.e., it includes larval biomass.

The total relative error is shown in the caption of the plot, calculated by

$$TRE = \sum_i |1 - \mathrm{ratio_i}|$$

where $\mathrm{ratio_i}$ is the ratio of model biomass / observed biomass for species i.

Value

A ggplot2 object with the plot of model biomass by species compared to observed biomass. If `return_data = TRUE`, the data frame used to create the plot is returned instead of the plot.

Examples

```
# create an example
params <- NS_params
species_params(params)$biomass_observed <-
    c(0.8, 61, 12, 35, 1.6, NA, 10, 7.6, 135, 60, 30, NA)
species_params(params)$biomass_cutoff <- 10
params <- calibrateBiomass(params)

# Plot with default options
plotBiomassObservedVsModel(params)
```

```
# Plot including also species without observations
plotBiomassObservedVsModel(params, show_unobserved = TRUE)

# Show the ratio instead
plotBiomassObservedVsModel(params, ratio = TRUE)

# Run a simulation
params <- matchBiomasses(params)
sim <- project(params, t_max = 10, progress_bar = FALSE)
plotBiomass(sim)

# Plot the biomass comparison at the final time
plotBiomassObservedVsModel(sim)

# The same with no log scaling of axes
plotBiomassObservedVsModel(sim, log_scale = FALSE)
```

`plotDiet` *Plot diet, resolved by prey species, as function of predator at size.*

Description

[Experimental] Plots the proportions with which each prey species contributes to the total biomass consumed by the specified predator species, as a function of the predator's size. These proportions are obtained with `getDiet()`.

Usage

```
plotDiet(object, species = NULL, return_data = FALSE)
```

Arguments

`object`	An object of class MizerSim or MizerParams.
`species`	The name of the predator species for which to plot the diet.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE

Details

Prey species that contribute less than 1 permille to the diet are suppressed in the plot.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w', 'Proportion', 'Prey' is returned.

See Also

getDiet()

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotBiomass(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
plotDiet(NS_params, species = "Cod")

# Returning the data frame
fr <- plotDiet(NS_params, species = "Cod", return_data = TRUE)
str(fr)
```

---

plotFeedingLevel *Plot the feeding level of species by size*

Description

After running a projection, plot the feeding level of each species by size. The feeding level is averaged over the specified time range (a single value for the time range can be used).

Usage

```
plotFeedingLevel(
  object,
  species = NULL,
  time_range,
  highlight = NULL,
  all.sizes = FALSE,
  include_critical = FALSE,
  return_data = FALSE,
  ...
)

plotlyFeedingLevel(
  object,
  species = NULL,
  time_range,
  highlight = NULL,
  include_critical,
  ...
)
```

Arguments

object	An object of class MizerSim or MizerParams.
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a MizerParams object.
highlight	Name or vector of names of the species to be highlighted.
all.sizes	If TRUE, then feeding level is plotted also for sizes outside a species' size range. Default FALSE.
include_critical	If TRUE, then the critical feeding level is also plotted. Default FALSE.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

Details

When called with a MizerSim object, the feeding level is averaged over the specified time range (a single value for the time range can be used to plot a single time step). When called with a MizerParams object the initial feeding level is plotted.

If `include_critical = TRUE` then the critical feeding level (the feeding level at which the intake just covers the metabolic cost) is also plotted, with a thinner line. This line should always stay below the line of the actual feeding level, because the species would stop growing at any point where the feeding level drops to the critical feeding level.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the variables 'w', 'value' and 'Species' is returned. If also `include_critical = TRUE` then the data frame contains a fourth variable 'Type' that distinguishes between 'actual' and 'critical' feeding level.

See Also

plotting_functions, `getFeedingLevel()`

Other plotting functions: `animateSpectra()`, `plot,MizerSim,missing-method`, `plotBiomass()`, `plotDiet()`, `plotFMort()`, `plotGrowthCurves()`, `plotPredMort()`, `plotSpectra()`, `plotYieldGear()`, `plotYield()`, `plotting_functions`

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotFeedingLevel(sim)
```

```
plotFeedingLevel(sim, time_range = 10:20, species = c("Cod", "Herring"),
                 include_critical = TRUE)

# Returning the data frame
fr <- plotFeedingLevel(sim, return_data = TRUE)
str(fr)
```

`plotFMort` *Plot total fishing mortality of each species by size*

Description

After running a projection, plot the total fishing mortality of each species by size. The total fishing mortality is averaged over the specified time range (a single value for the time range can be used to plot a single time step).

Usage

```
plotFMort(
  object,
  species = NULL,
  time_range,
  all.sizes = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)

plotlyFMort(object, species = NULL, time_range, highlight = NULL, ...)
```

Arguments

`object`	An object of class MizerSim or MizerParams.
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`time_range`	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a MizerParams object.
`all.sizes`	If TRUE, then fishing mortality is plotted also for sizes outside a species' size range. Default FALSE.
`highlight`	Name or vector of names of the species to be highlighted.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
`...`	Other arguments (currently unused)

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w', 'value', 'Species' is returned.

See Also

plotting_functions, `getFMort()`

Other plotting functions: `animateSpectra()`, `plot,MizerSim,missing-method`, `plotBiomass()`, `plotDiet()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotPredMort()`, `plotSpectra()`, `plotYieldGear()`, `plotYield()`, `plotting_functions`

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotFMort(sim)
plotFMort(sim, highlight = c("Cod", "Haddock"))

# Returning the data frame
fr <- plotFMort(sim, return_data = TRUE)
str(fr)
```

---

plotGrowthCurves *Plot growth curves giving weight as a function of age*

Description

When the growth curve for only a single species is plotted, horizontal lines are included that indicate the maturity size and the maximum size for that species. If furthermore the species parameters contain the variables a and b for length to weight conversion and the von Bertalanffy parameter k_vb (and optionally t0), then the von Bertalanffy growth curve is superimposed in black.

Usage

```
plotGrowthCurves(
  object,
  species = NULL,
  max_age = 20,
  percentage = FALSE,
  species_panel = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

```
plotlyGrowthCurves(
  object,
  species = NULL,
  max_age = 20,
  percentage = FALSE,
  species_panel = FALSE,
  highlight = NULL
)
```

Arguments

object	MizerSim or MizerParams object. If given a MizerSim object, uses the growth rates at the final time of a simulation to calculate the size at age. If given a MizerParams object, uses the initial growth rates instead.
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
max_age	The age up to which to run the growth curve. Default is 20.
percentage	Boolean value. If TRUE, the size is given as a percentage of the maximal size.
species_panel	**[Experimental]** If TRUE, display all species with their Von Bertalanffy curves as facets (need species and percentage to be set to default). Default FALSE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

Value

A ggplot2 object

See Also

plotting_functions

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotGrowthCurves(sim, percentage = TRUE)
plotGrowthCurves(sim, species = "Cod", max_age = 24)
plotGrowthCurves(sim, species_panel = TRUE)
```

```
# Returning the data frame
fr <- plotGrowthCurves(sim, return_data = TRUE)
str(fr)
```

`plotM2` *Alias for* `plotPredMort()`

Description

[Deprecated] An alias provided for backward compatibility with mizer version <= 1.0

Usage

```
plotM2(
  object,
  species = NULL,
  time_range,
  all.sizes = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

Arguments

`object`	An object of class MizerSim or MizerParams.
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`time_range`	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a MizerParams object.
`all.sizes`	If TRUE, then predation mortality is plotted also for sizes outside a species' size range. Default FALSE.
`highlight`	Name or vector of names of the species to be highlighted.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
`...`	Other arguments (currently unused)

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w', 'value', 'Species' is returned.

See Also

plotting_functions, getPredMort()

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotPredMort(sim)
plotPredMort(sim, time_range = 10:20)

# Returning the data frame
fr <- plotPredMort(sim, return_data = TRUE)
str(fr)
```

---

plotPredMort *Plot predation mortality rate of each species against size*

Description

After running a projection, plot the predation mortality rate of each species by size. The mortality rate is averaged over the specified time range (a single value for the time range can be used to plot a single time step).

Usage

```
plotPredMort(
  object,
  species = NULL,
  time_range,
  all.sizes = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)

plotlyPredMort(object, species = NULL, time_range, highlight = NULL, ...)
```

Arguments

object	An object of class MizerSim or MizerParams.

species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a MizerParams object.
all.sizes	If TRUE, then predation mortality is plotted also for sizes outside a species' size range. Default FALSE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

Value

A ggplot2 object, unless return_data = TRUE, in which case a data frame with the three variables 'w', 'value', 'Species' is returned.

See Also

plotting_functions, getPredMort()

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotSpectra(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotPredMort(sim)
plotPredMort(sim, time_range = 10:20)

# Returning the data frame
fr <- plotPredMort(sim, return_data = TRUE)
str(fr)
```

---

plotSpectra *Plot the abundance spectra*

Description

Plots the number density multiplied by a power of the weight, with the power specified by the power argument.

Usage

```
plotSpectra(
  object,
  species = NULL,
  time_range,
  wlim = c(NA, NA),
  ylim = c(NA, NA),
  power = 1,
  biomass = TRUE,
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  return_data = FALSE,
  ...
)

plotlySpectra(
  object,
  species = NULL,
  time_range,
  wlim = c(NA, NA),
  ylim = c(NA, NA),
  power = 1,
  biomass = TRUE,
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  ...
)
```

Arguments

object	An object of class MizerSim or MizerParams.
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a MizerParams object.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA to refer to the existing minimum or maximum.
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to refer to the existing minimum or maximum. Any values below 1e-20 are always cut off.

power	The abundance is plotted as the number density times the weight raised to power. The default power = 1 gives the biomass density, whereas power = 2 gives the biomass density with respect to logarithmic size bins.
biomass	**[Deprecated]** Only used if power argument is missing. Then biomass = TRUE is equivalent to power=1 and biomass = FALSE is equivalent to power=0
total	A boolean value that determines whether the total over all species in the system is plotted as well. Note that even if the plot only shows a selection of species, the total is including all species. Default is FALSE.
resource	A boolean value that determines whether resource is included. Default is TRUE.
background	A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

Details

When called with a MizerSim object, the abundance is averaged over the specified time range (a single value for the time range can be used to plot a single time step). When called with a MizerParams object the initial abundance is plotted.

Value

A ggplot2 object, unless return_data = TRUE, in which case a data frame with the four variables 'w', 'value', 'Species', 'Legend' is returned.

See Also

plotting_functions

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotYieldGear(), plotYield(), plotting_functions

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotSpectra(sim)
plotSpectra(sim, wlim = c(1e-6, NA))
plotSpectra(sim, time_range = 10:20)
plotSpectra(sim, time_range = 10:20, power = 0)
plotSpectra(sim, species = c("Cod", "Herring"), power = 1)

# Returning the data frame
fr <- plotSpectra(sim, return_data = TRUE)
str(fr)
```

plotting_functions *Description of the plotting functions*

Description

Mizer provides a range of plotting functions for visualising the results of running a simulation, stored in a MizerSim object, or the initial state stored in a MizerParams object. Every plotting function exists in two versions, `plotSomething` and `plotlySomething`. The plotly version is more interactive but not suitable for inclusion in documents.

Details

This table shows the available plotting functions.

Plot	Description
`plotBiomass()`	Plots the total biomass of each species through time. A time range to be plotted can be specified. The
`plotSpectra()`	Plots the abundance (biomass or numbers) spectra of each species and the background community. It
`plotFeedingLevel()`	Plots the feeding level of each species against size.
`plotPredMort()`	Plots the predation mortality of each species against size.
`plotFMort()`	Plots the total fishing mortality of each species against size.
`plotYield()`	Plots the total yield of each species across all fishing gears against time.
`plotYieldGear()`	Plots the total yield of each species by gear against time.
`plotDiet()`	Plots the diet composition at size for a given predator species.
`plotGrowthCurves()`	Plots the size as a function of age.
`plot()`	Produces 5 plots (`plotFeedingLevel()`, `plotBiomass()`, `plotPredMort()`, `plotFMort()` and `plo`

These functions use the ggplot2 package and return the plot as a ggplot object. This means that you can manipulate the plot further after its creation using the ggplot grammar of graphics. The corresponding function names with `plot` replaced by `plotly` produce interactive plots with the help of the plotly package.

While most plot functions take their data from a MizerSim object, some of those that make plots representing data at a single time can also take their data from the initial values in a MizerParams object.

Where plots show results for species, the line colour and line type for each species are specified by the `linecolour` and `linetype` slots in the MizerParams object. These were either taken from a default palette hard-coded into `emptyParams()` or they were specified by the user in the species parameters dataframe used to set up the MizerParams object. The `linecolour` and `linetype` slots hold named vectors, named by the species. They can be overwritten by the user at any time.

Most plots allow the user to select to show only a subset of species, specified as a vector in the `species` argument to the plot function.

The ordering of the species in the legend is the same as the ordering in the species parameter data frame.

See Also

summary_functions, indicator_functions

Other plotting functions: animateSpectra(), plot,MizerSim,missing-method, plotBiomass(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotPredMort(), plotSpectra(), plotYieldGear(), plotYield()

Examples

```
sim <- NS_sim

# Some example plots
plotFeedingLevel(sim)

# Plotting only a subset of species
plotFeedingLevel(sim, species = c("Cod", "Herring"))

# Specifying new colours and linetypes for some species
sim@params@linetype["Cod"] <- "dashed"
sim@params@linecolour["Cod"] <- "red"
plotFeedingLevel(sim, species = c("Cod", "Herring"))

# Manipulating the plot
library(ggplot2)
p <- plotFeedingLevel(sim)
p <- p + geom_hline(aes(yintercept = 0.7))
p <- p + theme_bw()
p
```

---

plotYield *Plot the total yield of species through time*

Description

After running a projection, the total yield of each species across all fishing gears can be plotted against time. The yield is obtained with getYield().

Usage

```
plotYield(
  sim,
  sim2,
  species = NULL,
  total = FALSE,
  log = TRUE,
  highlight = NULL,
  return_data = FALSE,
```

```
  ...
)

plotlyYield(
  sim,
  sim2,
  species = NULL,
  total = FALSE,
  log = TRUE,
  highlight = NULL,
  ...
)
```

Arguments

sim	An object of class MizerSim
sim2	An optional second object of class MizerSim. If this is provided its yields will be shown on the same plot in bolder lines.
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
total	A boolean value that determines whether the total over all species in the system is plotted as well. Note that even if the plot only shows a selection of species, the total is including all species. Default is FALSE.
log	Boolean whether yield should be plotted on a logarithmic axis. Defaults to true.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'Year', 'Yield', 'Species' is returned.

See Also

plotting_functions, `getYield()`

Other plotting functions: `animateSpectra()`, `plot,MizerSim,missing-method`, `plotBiomass()`, `plotDiet()`, `plotFMort()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotPredMort()`, `plotSpectra()`, `plotYieldGear()`, `plotting_functions`

Examples

```
params <- NS_params
```

```
sim <- project(params, effort = 1, t_max = 20, t_save = 0.2, progress_bar = FALSE)
plotYield(sim)
plotYield(sim, species = c("Cod", "Herring"), total = TRUE)

# Comparing with yield from twice the effort
sim2 <- project(params, effort=2, t_max=20, t_save = 0.2, progress_bar = FALSE)
plotYield(sim, sim2, species = c("Cod", "Herring"), log = FALSE)

# Returning the data frame
fr <- plotYield(sim, return_data = TRUE)
str(fr)
```

`plotYieldGear` *Plot the total yield of each species by gear through time*

Description

After running a projection, the total yield of each species by fishing gear can be plotted against time.

Usage

```
plotYieldGear(
  sim,
  species = NULL,
  total = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)

plotlyYieldGear(sim, species = NULL, total = FALSE, highlight = NULL, ...)
```

Arguments

`sim`	An object of class MizerSim
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`total`	A boolean value that determines whether the total over all species in the system is plotted as well. Note that even if the plot only shows a selection of species, the total is including all species. Default is FALSE.
`highlight`	Name or vector of names of the species to be highlighted.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
`...`	Other arguments (currently unused)

Details

This plot is pretty easy to do by hand. It just gets the biomass using the `getYieldGear()` method and plots using the ggplot2 package. You can then fiddle about with colours and linetypes etc. Just look at the source code for details.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the four variables 'Year', 'Yield', 'Species' and 'Gear' is returned.

See Also

plotting_functions, `getYieldGear()`

Other plotting functions: `animateSpectra()`, `plot,MizerSim,missing-method`, `plotBiomass()`, `plotDiet()`, `plotFMort()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotPredMort()`, `plotSpectra()`, `plotYield()`, `plotting_functions`

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 0.2, progress_bar = FALSE)
plotYieldGear(sim)
plotYieldGear(sim, species = c("Cod", "Herring"), total = TRUE)

# Returning the data frame
fr <- plotYieldGear(sim, return_data = TRUE)
str(fr)
```

---

plotYieldObservedVsModel

Plotting observed vs. model yields

Description

[Experimental] If yield observations are available for at least some species via the `yield_observed` column in the species parameter data frame, this function plots the yield of each species in the model against the observed yields. When called with a MizerSim object, the plot will use the model yields predicted for the final time step in the simulation.

Usage

```
plotYieldObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
```

```
  log_scale = TRUE,
  return_data = FALSE,
  labels = TRUE,
  show_unobserved = FALSE
)

plotlyYieldObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  show_unobserved = FALSE
)
```

Arguments

`object`	An object of class MizerParams or MizerSim.
`species`	The species to be included. Optional. By default all observed yields will be included. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be included (TRUE) or not.
`ratio`	Whether to plot model yield vs. observed yield (FALSE) or the ratio of model : observed yield (TRUE). Default is FALSE.
`log_scale`	Whether to plot on the log10 scale (TRUE) or not (FALSE). For the non-ratio plot this applies for both axes, for the ratio plot only the x-axis is on the log10 scale. Default is TRUE.
`return_data`	Whether to return the data frame for the plot (TRUE) or not (FALSE). Default is FALSE.
`labels`	Whether to show text labels for each species (TRUE) or not (FALSE). Default is TRUE.
`show_unobserved`	Whether to include also species for which no yield observation is available. If TRUE, these species will be shown as if their observed yield was equal to the model yield.

Details

Before you can use this function you will need to have added a `yield_observed` column to your model which gives the observed yield in grams per year. For species for which you have no observed yield, you should set the value in the `yield_observed` column to 0 or NA.

The total relative error is shown in the caption of the plot, calculated by

$$TRE = \sum_i |1 - \mathrm{ratio_i}|$$

where $\mathrm{ratio_i}$ is the ratio of model yield / observed yield for species i.

Value

A ggplot2 object with the plot of model yield by species compared to observed yield. If `return_data = TRUE`, the data frame used to create the plot is returned instead of the plot.

Examples

```
# create an example
params <- NS_params
species_params(params)$yield_observed <-
    c(0.8, 61, 12, 35, 1.6, NA, 10, 7.6, 135, 60, 30, NA)
params <- calibrateYield(params)

# Plot with default options
plotYieldObservedVsModel(params)

# Plot including also species without observations
plotYieldObservedVsModel(params, show_unobserved = TRUE)

# Show the ratio instead
plotYieldObservedVsModel(params, ratio = TRUE)

# Run a simulation
params <- matchYields(params)
sim <- project(params, t_max = 10, progress_bar = FALSE)
plotBiomass(sim)

# Plot the yield comparison at the final time
plotYieldObservedVsModel(sim)

# The same with no log scaling of axes
plotYieldObservedVsModel(sim, log_scale = FALSE)
```

---

power_law_pred_kernel *Power-law predation kernel*

Description

This predation kernel is a power-law, with sigmoidal cut-offs at large and small predator/prey mass ratios.

Usage

```
power_law_pred_kernel(
  ppmr,
  kernel_exp,
  kernel_l_l,
  kernel_u_l,
  kernel_l_r,
  kernel_u_r
)
```

Arguments

ppmr	A vector of predator/prey size ratios at which to evaluate the predation kernel.
kernel_exp	The exponent of the power law
kernel_l_l	The location of the left, rising sigmoid
kernel_u_l	The shape of the left, rising sigmoid
kernel_l_r	The location of the right, falling sigmoid
kernel_u_r	The shape of the right, falling sigmoid

Details

The return value is calculated as

```
ppmr^kernel_exp / (1 + (exp(kernel_l_l) / ppmr)^kernel_u_l) / (1 + (ppmr / exp(kernel_l_r))^kernel_u_r)
```

The parameters need to be given as columns in the species parameter dataframe.

Value

A vector giving the value of the predation kernel at each of the predator/prey mass ratios in the ppmr argument.

---

project *Project size spectrum forward in time*

Description

Runs the size spectrum model simulation. The function returns an object of type MizerSim that can then be explored with a range of summary_functions, indicator_functions and plotting_functions.

Usage

```
project(
  object,
  effort,
  t_max = 100,
  dt = 0.1,
  t_save = 1,
  t_start = 0,
  initial_n,
  initial_n_pp,
  append = TRUE,
  progress_bar = TRUE,
  ...
)
```

Arguments

object	Either a MizerParams object or a MizerSim object (which contains a MizerParams object).
effort	The effort of each fishing gear through time. See notes below.
t_max	The number of years the projection runs for. The default value is 100. This argument is ignored if an array is used for the effort argument. See notes below.
dt	Time step of the solver. The default value is 0.1.
t_save	The frequency with which the output is stored. The default value is 1. This argument is ignored if an array is used for the effort argument. See notes below.
t_start	The the year of the start of the simulation. The simulation will cover the period from t_start to t_start + t_max. Defaults to 0. Ignored if an array is used for the effort argument or a MizerSim for the object argument.
initial_n	**[Deprecated]** The initial abundances of species. Instead of using this argument you should set initialN(params) to the desired value.
initial_n_pp	**[Deprecated]** The initial abundances of resource. Instead of using this argument you should set initialNResource(params) to the desired value.
append	A boolean that determines whether the new simulation results are appended to the previous ones. Only relevant if object is a MizerSim object. Default = TRUE.
progress_bar	Either a boolean value to determine whether a progress bar should be shown in the console, or a shiny Progress object to implement a progress bar in a shiny app.
...	Other arguments will be passed to rate functions.

Value

An object of class MizerSim.

Note

The effort argument specifies the level of fishing effort during the simulation. If it is not supplied, the initial effort stored in the params object is used. The effort can be specified in three different ways:

- A single numeric value. This specifies the effort of all fishing gears which is constant through time (i.e. all the gears have the same constant effort).
- A numerical vector which has the same length as the number of fishing gears. The vector must be named and the names must correspond to the gear names in the MizerParams object. The values in the vector specify the constant fishing effort of each of the fishing gears, i.e. the effort is constant through time but each gear may have a different fishing effort.
- A numerical array with dimensions time x gear. This specifies the fishing effort of each gear at each time step. The first dimension, time, must be named numerically and increasing. The second dimension of the array must be named and the names must correspond to the gear

names in the MizerParams argument. The value for the effort for a particular time is used during the interval from that time to the next time in the array.

If effort is specified as an array then the smallest time in the array is used as the initial time for the simulation. Otherwise the initial time is set to the final time of the previous simulation if object is a MizerSim object or to t_start otherwise. Also, if the effort is an array then the t_max and t_save arguments are ignored and the simulation times will be taken from the effort array.

If the object argument is of class MizerSim then the initial values for the simulation are taken from the final values in the MizerSim object and the corresponding arguments to this function will be ignored.

Examples

```
## Not run:
params <-  NS_params
# With constant fishing effort for all gears for 20 time steps
sim <- project(params, t_max = 20, effort = 0.5)
# With constant fishing effort which is different for each gear
effort <- c(Industrial = 0, Pelagic = 1, Beam = 0.5, Otter = 0.5)
sim <- project(params, t_max = 20, effort = effort)
# With fishing effort that varies through time for each gear
gear_names <- c("Industrial","Pelagic","Beam","Otter")
times <- seq(from = 1, to = 10, by = 1)
effort_array <- array(NA, dim = c(length(times), length(gear_names)),
    dimnames = list(time = times, gear = gear_names))
effort_array[,"Industrial"] <- 0.5
effort_array[,"Pelagic"] <- seq(from = 1, to = 2, length = length(times))
effort_array[,"Beam"] <- seq(from = 1, to = 0, length = length(times))
effort_array[,"Otter"] <- seq(from = 1, to = 0.5, length = length(times))
sim <- project(params, effort = effort_array)

## End(Not run)
```

---

projectToSteady *Project to steady state*

Description

[Experimental]

Run the full dynamics, as in project(), but stop once the change has slowed down sufficiently, in the sense that the distance between states at successive time steps is less than tol. You determine how the distance is calculated.

Usage

```
projectToSteady(
  params,
  effort = params@initial_effort,
```

```
  distance_func = distanceSSLogN,
  t_per = 1.5,
  t_max = 100,
  dt = 0.1,
  tol = 0.1 * t_per,
  return_sim = FALSE,
  progress_bar = TRUE,
  ...
)
```

Arguments

params	A MizerParams object
effort	The fishing effort to be used throughout the simulation. This must be a vector or list with one named entry per fishing gear.
distance_func	A function that will be called after every t_per years with both the previous and the new state and that should return a number that in some sense measures the distance between the states. By default this uses the function distanceSSLogN() that you can use as a model for your own distance function.
t_per	The simulation is broken up into shorter runs of t_per years, after each of which we check for convergence. Default value is 1.5. This should be chosen as an odd multiple of the timestep dt in order to be able to detect period 2 cycles.
t_max	The maximum number of years to run the simulation. Default is 100.
dt	The time step to use in project().
tol	The simulation stops when the relative change in the egg production RDI over t_per years is less than tol for every species.
return_sim	If TRUE, the function returns the MizerSim object holding the result of the simulation run. If FALSE (default) the function returns a MizerParams object with the "initial" slots set to the steady state.
progress_bar	A shiny progress object to implement a progress bar in a shiny app. Default FALSE.
...	Further arguments will be passed on to your distance function.

See Also

distanceSSLogN(), distanceMaxRelRDI()

---

project_simple *Project abundances by a given number of time steps into the future*

Description

This is an internal function used by the user-facing project() function. It is of potential interest only to mizer extension authors.

Usage

```
project_simple(
  params,
  n = params@initial_n,
  n_pp = params@initial_n_pp,
  n_other = params@initial_n_other,
  effort = params@initial_effort,
  t = 0,
  dt = 0.1,
  steps,
  resource_dynamics_fn = get(params@resource_dynamics),
  other_dynamics_fns = lapply(params@other_dynamics, get),
  rates_fns = lapply(params@rates_funcs, get),
  ...
)
```

Arguments

`params`	A MizerParams object.
`n`	An array (species x size) with the number density at start of simulation.
`n_pp`	A vector (size) with the resource number density at start of simulation.
`n_other`	A named list with the abundances of other components at start of simulation.
`effort`	The fishing effort to be used throughout the simulation. This must be a vector or list with one named entry per fishing gear.
`t`	Time at the start of the simulation.
`dt`	Size of time step.
`steps`	The number of time steps by which to project.
`resource_dynamics_fn`	The function for the resource dynamics. See Details.
`other_dynamics_fns`	List with the functions for the dynamics of the other components. See Details.
`rates_fns`	List with the functions for calculating the rates. See Details.
`...`	Other arguments that are passed on to the rate functions.

Details

The function does not check its arguments because it is meant to be as fast as possible to allow it to be used in a loop. For example, it is called in `project()` once for every saved value. The function also does not save its intermediate results but only returns the result at time `t + dt * steps`. During this time it uses the constant fishing effort `effort`.

The functional arguments can be calculated from slots in the `params` object with

```
resource_dynamics_fn <- get(params@resource_dynamics)
other_dynamics_fns <- lapply(params@other_dynamics, get)
rates_fns <- lapply(params@rates_funcs, get)
```

The reason the function does not do that itself is to shave 20 microseconds of its running time, which pays when the function is called hundreds of times in a row.

This function is also used in `steady()`. In between calls to `project_simple()` the `steady()` function checks whether the values are still changing significantly, so that it can stop when a steady state has been approached. Mizer extension packages might have a similar need to run a simulation repeatedly for short periods to run some other code in between. Because this code may want to use the values of the rates at the final time step, these too are included in the returned list.

Value

List with the final values of `n`, `n_pp` and `n_other`, `rates`.

`removeSpecies` *Remove species*

Description

[Experimental]

This function simply removes all entries from the MizerParams object that refer to the selected species. It does not recalculate the steady state for the remaining species or retune their reproductive efficiency.

Usage

```
removeSpecies(params, species)
```

Arguments

`params`	A mizer params object for the original system.
`species`	The species to be removed. A vector of species names, or a numeric vector of species indices, or a logical vector indicating for each species whether it is to be removed (TRUE) or not.

Value

An object of type MizerParams

Examples

```
## Not run:
params <- NS_params
species_params(params)$species
params <- removeSpecies(params, c("Cod", "Haddock"))
species_params(params)$species

## End(Not run)
```

renameSpecies *Rename species*

Description

[Experimental]

Changes the names of species in a MizerParams object. This involves for example changing the species dimension names of rate arrays appropriately.

Usage

```
renameSpecies(params, replace)
```

Arguments

params	A mizer params object
replace	A named character vector, with new names as values, and old names as names.

Value

An object of type MizerParams

Examples

```
replace <- c(Cod = "Kabeljau", Haddock = "Schellfisch")
params <- renameSpecies(NS_params, replace)
species_params(params)$species
```

resource_constant *Keep resource abundance constant*

Description

This function can be used instead of the standard `resource_semichemostat()` in order to keep the resource spectrum constant over time.

Usage

```
resource_constant(params, n_pp, ...)
```

Arguments

params	A MizerParams object
n_pp	A vector of the resource abundance by size
...	Unused

Value

Vector containing resource spectrum at next timestep

Examples

```
## Not run:
params <- newMultispeciesParams(NS_species_params_gears, NS_interaction,
                                resource_dynamics = "resource_constant")

## End(Not run)
```

---

resource_params *Resource parameters*

Description

These functions allow you to get or set the resource parameters stored in a MizerParams object. The resource parameters are stored as a named list with the slot names `r_pp`, `kappa`, `lambda`, `n`, `w_pp_cutoff`. For their meaning see Details below. If you change these parameters then this will recalculate the resource rate and the resource capacity, unless you have set custom values for these. If you have specified a different resource dynamics function that requires additional parameters, then these should also be added to the `resource_params` list.

Usage

```
resource_params(params)

resource_params(params) <- value
```

Arguments

`params`	A MizerParams object
`value`	A named list of resource parameters.

Details

The resource parameters `r_pp` and `n` are used to set the intrinsic replenishment rate $r_R(w)$ for the resource at size w to

$$r_R(w) = r_{pp}\, w^{n-1}.$$

The resource parameters `kappa`, `lambda` and `w_pp_cutoff` are used to set the intrinsic resource carrying capacity capacity $c_R(w)$ at size w is set to

$$c_R(w) = \kappa\, w^{-\lambda}$$

for all w less than `w_pp_cutoff` and zero for larger sizes.

If you use the default semichemostat dynamics for the resource then these rates enter the equation for the resource abundance density as

$$\frac{\partial N_R(w,t)}{\partial t} = r_R(w)\Big[c_R(w) - N_R(w,t)\Big] - \mu_R(w,t)N_R(w,t)$$

where the mortality $\mu_R(w,t)$ is due to predation by consumers and is calculate with `getResourceMort()`.

You can however set up different resource dynamics with `resource_dynamics<-()`.

See Also

Other functions for setting parameters: `gear_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `setSearchVolume()`, `species_params()`

Examples

```
resource_params(NS_params)
# Doubling the replenishment rate
params <- NS_params
resource_params(params)$r_pp <- 2 * resource_params(params)$r_pp
```

`resource_semichemostat`

Project resource using semichemostat model

Description

This function calculates the resource abundance at time `t + dt` from all abundances and rates at time `t`.

Usage

```
resource_semichemostat(
  params,
  n,
  n_pp,
  n_other,
  rates,
  t,
  dt,
  resource_rate,
  resource_capacity,
  ...
)
```

Arguments

params	A MizerParams object
n	A matrix of species abundances (species x size)
n_pp	A vector of the resource abundance by size
n_other	A list with the abundances of other components
rates	A list of rates as returned by mizerRates()
t	The current time
dt	Time step
resource_rate	Resource replenishment rate
resource_capacity	Resource carrying capacity
...	Unused

Details

The time evolution of the resource spectrum is described by a semi-chemostat equation

$$\frac{\partial N_R(w,t)}{\partial t} = r_R(w)\Big[c_R(w) - N_R(w,t)\Big] - \mu_R(w,t)N_R(w,t)$$

Here $r_R(w)$ is the resource regeneration rate and $c_R(w)$ is the carrying capacity in the absence of predation. These parameters are changed with setResource(). The mortality $\mu_R(w,t)$ is due to predation by consumers and is calculate with getResourceMort().

This function uses the analytic solution of the above equation, keeping the mortality fixed during the timestep.

It is also possible to implement other resource dynamics, as described in the help page for setResource().

Value

Vector containing resource spectrum at next timestep

Examples

```
## Not run:
params <- newMultispeciesParams(NS_species_params_gears, NS_interaction,
                                resource_dynamics = "resource_semichemostat")

## End(Not run)
```

RickerRDD *Ricker function to calculate density-dependent reproduction rate*

Description

[Experimental] Takes the density-independent rates R_{di} of egg production and returns reduced, density-dependent rates R_{dd} given as

$$R_{dd} = R_{di} \exp(-bR_{di})$$

Usage

```
RickerRDD(rdi, species_params, ...)
```

Arguments

rdi	Vector of density-independent reproduction rates R_{di} for all species.
species_params	A species parameter dataframe. Must contain a column ricker_b holding the coefficient b.
...	Unused

Value

Vector of density-dependent reproduction rates.

See Also

Other functions calculating density-dependent reproduction rate: BevertonHoltRDD(), SheperdRDD(), constantEggRDI(), constantRDD(), noRDD()

saveParams *Save a MizerParams object to file, and restore it*

Description

[Experimental] saveParams() saves a MizerParams object to a file. This can then be restored with readParams().

Usage

```
saveParams(params, file)

readParams(file)
```

Arguments

params	A MizerParams object
file	The name of the file or a connection where the MizerParams object is saved to or read from.

Details

Issues a warning if the model you are saving relies on some custom functions. Before saving a model you may want to set its metadata with `setMetadata()`.

---

scaleModel *Change scale of the model*

Description

[Experimental]

The abundances in mizer and some rates depend on the size of the area to which they refer. So they could be given per square meter or per square kilometer or for an entire study area or any other choice of yours. This function allows you to change the scale of the model by automatically changing the abundances and rates accordingly.

Usage

```
scaleModel(params, factor)
```

Arguments

params	A MizerParams object
factor	The factor by which the scale is multiplied

Details

If you rescale the model by a factor c then this function makes the following rescalings in the params object:

- The initial abundances are rescaled by c.
- The search volume is rescaled by $1/c$.
- The resource carrying capacity is rescaled by c
- The maximum reproduction rate R_{max} is rescaled by c.

The effect of this is that the dynamics of the rescaled model are identical to those of the unscaled model, in the sense that it does not matter whether one first calls `scaleModel()` and then runs a simulation with `project()` or whether one first runs a simulation and then rescales the resulting abundances.

Note that if you use non-standard resource dynamics or other components then you may need to rescale additional parameters that appear in those dynamics.

In practice you will need to use some observations to set the scale for your model. If you have biomass observations you can use `calibrateBiomass()`, if you have yearly yields you can use `calibrateYield()`.

Value

The rescaled MizerParams object

`setBevertonHolt` *Set Beverton-Holt density dependence*

Description

[Experimental] Takes a MizerParams object `params` with arbitrary density dependence and returns a MizerParams object with Beverton-Holt density-dependence in such a way that the energy invested into reproduction by the mature individuals leads to the reproduction rate that is required to maintain the given egg abundance. Hence if you have tuned your `params` object to describe a particular steady state, then setting the Beverton-Holt density dependence with this function will leave you with the exact same steady state. By specifying one of the parameters `erepro`, `R_max` or `reproduction_level` you pick the desired reproduction curve. More details of these parameters are provided below.

Usage

```
setBevertonHolt(
  params,
  R_factor = deprecated(),
  erepro,
  R_max,
  reproduction_level
)
```

Arguments

`params`	A MizerParams object
`R_factor`	**[Deprecated]** Use `reproduction_level = 1 / R_factor` instead.
`erepro`	Reproductive efficiency for each species. See details.
`R_max`	Maximum reproduction rate. See details.
`reproduction_level`	Sets `R_max` so that the reproduction rate at the initial state is `R_max * reproduction_level`.

Details

With Beverton-Holt density dependence the relation between the energy invested into reproduction and the number of eggs hatched is determined by two parameters: the reproductive efficiency `erepro` and the maximum reproduction rate `R_max`.

If no maximum is imposed on the reproduction rate ($R_{max} = \infty$) then the resulting density-independent reproduction rate R_{di} is proportional to the total rate E_R at which energy is invested into reproduction,

$$R_{di} = \frac{\text{erepro}}{2w_{min}} E_R,$$

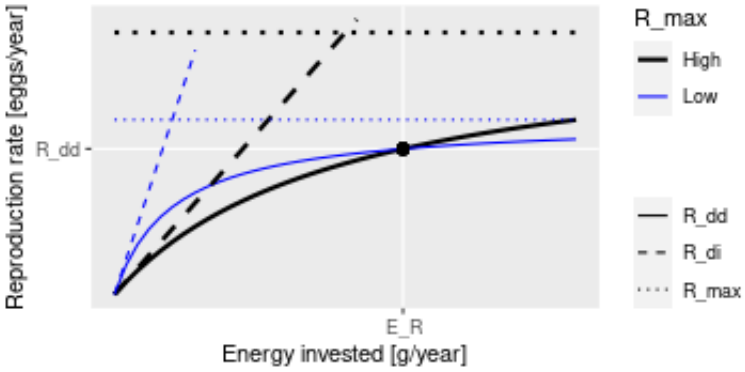
where the proportionality factor is given by the reproductive efficiency `erepro` divided by the egg size `w_min` to convert energy to egg number and divided by 2 to account for the two sexes.

Imposing a finite maximum reproduction rate R_{max} leads to a non-linear relationship between energy invested and eggs hatched. This density-dependent reproduction rate R_{dd} is given as

$$R_{dd} = R_{di} \frac{R_{max}}{R_{di} + R_{max}}.$$

(All quantities in the above equations are species-specific but we dropped the species index for simplicity.)

The following plot illustrates the Beverton-Holt density dependence in the reproduction rate for two different choices of parameters.



This plot shows that a given energy E_R invested into reproduction can lead to the same reproduction rate R_{dd} with different choices of the parameters `R_max` and `erepro`. `R_max` determines the asymptote of the curve and `erepro` its initial slope. A higher `R_max` coupled with a lower `erepro` (black curves) can give the same value as a lower `R_max` coupled with a higher `erepro` (blue curves).

For the given initial state in the MizerParams object `params` one can calculate the energy E_R that is invested into reproduction by the mature individuals and the reproduction rate R_{dd} that is required to keep the egg abundance constant. These two values determine the location of the black dot in the above graph. You then only need one parameter to select one curve from the family of Beverton-Holt curves going through that point. This parameter can be `erepro` or `R_max`. Instead of `R_max` you can alternatively specify the `reproduction_level` which is the ratio between the density-dependent reproduction rate R_{dd} and the maximal reproduction rate R_{max}.

If you do not provide a value for any of the reproduction parameter arguments, then `erepro` will be set to the value it has in the current species parameter data frame. If you do provide one of the reproduction parameters, this can be either a vector with one value for each species, or a named

vector where the names determine which species are affected, or a single unnamed value that is then used for all species. Any species for which the given value is NA will remain unaffected.

The values for R_max must be larger than R_{dd} and can range up to Inf. If a smaller value is requested a warning is issued and the value is increased to the value required for a reproduction level of 0.99.

The values for the reproduction_level must be positive and less than 1. The values for erepro must be large enough to allow the required reproduction rate. If a smaller value is requested a warning is issued and the value is increased to the smallest possible value. The values for erepro should also be smaller than 1 to be physiologically sensible, but this is not enforced by the function.

As can be seen in the graph above, choosing a lower value for R_max or a higher value for erepro means that near the steady state the reproduction will be less sensitive to a change in the energy invested into reproduction and hence less sensitive to changes in the spawning stock biomass or its energy income. As a result the species will also be less sensitive to fishing, leading to a higher F_MSY.

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$erepro
# Attempting to set the same erepro for all species
params <- setBevertonHolt(params, erepro = 0.1)
t(species_params(params)[, c("erepro", "R_max")])
# Setting erepro for some species
params <- setBevertonHolt(params, erepro = c("Gurnard" = 0.6, "Plaice" = 0.95))
t(species_params(params)[, c("erepro", "R_max")])
# Setting R_max
R_max <- 1e17 * species_params(params)$w_inf^-1
params <- setBevertonHolt(NS_params, R_max = R_max)
t(species_params(params)[, c("erepro", "R_max")])
# Setting reproduction_level
params <- setBevertonHolt(params, reproduction_level = 0.3)
t(species_params(params)[, c("erepro", "R_max")])
```

---

setColours *Set line colours and line types to be used in mizer plots*

Description

[Experimental] Used for setting the colour and type of lines representing "Total", "Resource", "Fishing", "Background" and possibly other categories in plots.

Usage

```
setColours(params, colours)

getColours(params)

setLinetypes(params, linetypes)

getLinetypes(params)
```

Arguments

params	A MizerParams object
colours	A named list or named vector of line colours.
linetypes	A named list or named vector of linetypes.

Details

Colours for names that already had a colour set for them will be overwritten by the colour you specify. Colours for names that did not yet have a colour will be appended to the list of colours.

Do not use this for setting the colours or linetypes of species, because those are determined by setting the `linecolour` and `linetype` variables in the species parameter data frame.

You can use the same colours in your own ggplot2 plots by adding `scale_colour_manual(values = getColours(params))` to your plot. Similarly you can use the linetypes with `scale_linetype_manual(values = getLinetypes(params))`.

Value

`setColours`: The MizerParams object with updated line colours

`getColours()`: A named vector of colours

`setLinetypes()`: The MizerParams object with updated linetypes

`getLinetypes()`: A named vector of linetypes

Examples

```
params <- setColours(NS_params, list("Resource" = "red", "Total" = "#0000ff"))
params <- setLinetypes(NS_params, list("Total" = "dotted"))
# Set colours and linetypes for species
species_params(params)["Cod", "linecolour"] <- "black"
species_params(params)["Cod", "linetype"] <- "dashed"
plotSpectra(params, total = TRUE)
getColours(params)
getLinetypes(params)
```

`setComponent` *Add a dynamical ecosystem component*

Description

By default, mizer models any number of size-resolved consumer species and a single size-resolved resource spectrum. Your model may require additional components, like for example detritus or carrion or multiple resources or .... This function allows you to set up such components.

Usage

```
setComponent(
  params,
  component,
  initial_value,
  dynamics_fun,
  encounter_fun,
  mort_fun,
  component_params
)

removeComponent(params, component)
```

Arguments

`params`	A MizerParams object
`component`	Name of the component
`initial_value`	Initial value of the component
`dynamics_fun`	Name of function to calculate value at the next time step
`encounter_fun`	Name of function to calculate contribution to encounter rate. Optional.
`mort_fun`	Name of function to calculate contribution to the mortality rate. Optional.
`component_params`	Object holding the parameters needed by the component functions. This could for example be a named list of parameters. Optional.

Details

The component can be a number, a vector, an array, a list, or any other data structure you like.

If you set a component with a new name, the new component will be added to the existing components. If you set a component with an existing name, that component will be overwritten. You can remove a component with `removeComponent()`.

Value

The updated MizerParams object

`setExtMort` *Set external mortality rate*

Description

Set external mortality rate

Usage

```
setExtMort(
  params,
  ext_mort = NULL,
  z0pre = 0.6,
  z0exp = -1/4,
  reset = FALSE,
  z0 = deprecated(),
  ...
)

getExtMort(params)

ext_mort(params)

ext_mort(params) <- value
```

Arguments

`params`	MizerParams
`ext_mort`	Optional. An array (species x size) holding the external mortality rate.
`z0pre`	If `z0`, the mortality from other sources, is not a column in the species data frame, it is calculated as z0pre * w_inf ^ z0exp. Default value is 0.6.
`z0exp`	If `z0`, the mortality from other sources, is not a column in the species data frame, it is calculated as `z0pre * w_inf ^ z0exp`. Default value is `n-1`.
`reset`	**[Experimental]** If set to TRUE, then the external mortality rate will be reset to the value calculated from the `z0` parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
`z0`	**[Deprecated]** Use `ext_mort` instead. Not to be confused with the species_parameter `z0`.
`...`	Unused
`value`	ext_mort

Value

`setExtMort()`: A MizerParams object with updated external mortality rate.

`getExtMort()` or equivalently `ext_mort()`: An array (species x size) with the external mortality.

Setting external mortality rate

The external mortality is all the mortality that is not due to fishing or predation by predators included in the model. The external mortality could be due to predation by predators that are not explicitly included in the model (e.g. mammals or seabirds) or due to other causes like illness. It is a rate with units 1/year.

The `ext_mort` argument allows you to specify an external mortality rate that depends on species and body size. You can see an example of this in the Examples section of the help page for `setExtMort()`.

If the `ext_mort` argument is not supplied, then the external mortality is assumed to depend only on the species, not on the size of the individual: $\mu_{ext.i}(w) = z_{0.i}$. The value of the constant z_0 for each species is taken from the `z0` column of the species parameter data frame, if that column exists. Otherwise it is calculated as

$$z_{0.i} = \texttt{z0pre}_i \, w_{inf}^{\texttt{z0exp}}.$$

See Also

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `setSearchVolume()`, `species_params()`

Examples

```
## Not run:
params <- newMultispeciesParams(NS_species_params)

#### Setting allometric death rate ######################

# Set coefficient for each species. Here we choose 0.1 for each species
z0pre <- rep(0.1, nrow(species_params(params)))

# Multiply by power of size with exponent, here chosen to be -1/4
# The outer() function makes it an array species x size
allo_mort <- outer(z0pre, w(params)^(-1/4))

# Change the external mortality rate in the params object
ext_mort(params) <- allo_mort

## End(Not run)
```

---

setFishing *Set fishing parameters*

Description

Set fishing parameters

Usage

```
setFishing(
  params,
  selectivity = NULL,
  catchability = NULL,
  reset = FALSE,
  initial_effort = NULL,
  ...
)

getCatchability(params)

catchability(params)

catchability(params) <- value

getSelectivity(params)

selectivity(params)

selectivity(params) <- value

getInitialEffort(params)
```

Arguments

`params`	A MizerParams object
`selectivity`	Optional. An array (gear x species x size) that holds the selectivity of each gear for species and size, $S_{g,i,w}$.
`catchability`	Optional. An array (gear x species) that holds the catchability of each species by each gear, $Q_{g,i}$.
`reset`	**[Experimental]** If set to TRUE, then both `catchability` and `selectivity` will be reset to the values calculated from the gear parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the gear parameters will take place only if no custom value has been set.
`initial_effort`	Optional. A number or a named numeric vector specifying the fishing effort. If a number, the same effort is used for all gears. If a vector, must be named by gear.
`...`	Unused
`value`	.

Value

`setFishing()`: A MizerParams object with updated fishing parameters.

`getCatchability()` or equivalently `catchability()`: An array (gear x species) that holds the catchability of each species by each gear, $Q_{g,i}$. The names of the dimensions are "gear, "sp".

`getSelectivity()` or equivalently `selectivity()`: An array (gear x species x size) that holds the selectivity of each gear for species and size, $S_{g,i,w}$. The names of the dimensions are "gear, "sp", "w".

`getInitialEffort()` or equivalently `initial_effort()`: A named vector with the initial fishing effort for each gear.

Setting fishing

Gears

In `mizer`, fishing mortality is imposed on species by fishing gears. The total per-capita fishing mortality (1/year) is obtained by summing over the mortality from all gears,

$$\mu_{f.i}(w) = \sum_g F_{g,i}(w),$$

where the fishing mortality $F_{g,i}(w)$ imposed by gear g on species i at size w is calculated as:

$$F_{g,i}(w) = S_{g,i}(w) Q_{g,i} E_g,$$

where S is the selectivity by species, gear and size, Q is the catchability by species and gear and E is the fishing effort by gear.

Selectivity

The selectivity at size of each gear for each species is saved as a three dimensional array (gear x species x size). Each entry has a range between 0 (that gear is not selecting that species at that size) to 1 (that gear is selecting all individuals of that species of that size). This three dimensional array can be specified explicitly via the `selectivity` argument, but usually mizer calculates it from the `gear_params` slot of the MizerParams object.

To allow the calculation of the `selectivity` array, the `gear_params` slot must be a data frame with one row for each gear-species combination. So if for example a gear can select three species, then that gear contributes three rows to the `gear_params` data frame, one for each species it can select. The data frame must have columns `gear`, holding the name of the gear, `species`, holding the name of the species, and `sel_func`, holding the name of the function that calculates the selectivity curve. Some selectivity functions are included in the package: `knife_edge()`, `sigmoid_length()`, `double_sigmoid_length()`, and `sigmoid_weight()`. Users are able to write their own size-based selectivity function. The first argument to the function must be `w` and the function must return a vector of the selectivity (between 0 and 1) at size.

Each selectivity function may have parameters. Values for these parameters must be included as columns in the gear parameters data.frame. The names of the columns must exactly match the names of the corresponding arguments of the selectivity function. For example, the default selectivity function is `knife_edge()` that a has sudden change of selectivity from 0 to 1 at a certain size. In its help page you can see that the `knife_edge()` function has arguments `w` and `knife_edge_size`. The first argument, `w`, is size (the function calculates selectivity at size). All selectivity functions must have `w` as the first argument. The values for the other arguments must be found in the gear parameters data.frame. So for the `knife_edge()` function there should be a `knife_edge_size` column. Because `knife_edge()` is the default selectivity function, the `knife_edge_size` argument has a default value = `w_mat`.

In case each species is only selected by one gear, the columns of the `gear_params` data frame can alternatively be provided as columns of the `species_params` data frame, if this is more convenient

for the user to set up. Mizer will then copy these columns over to create the gear_params data frame when it creates the MizerParams object. However changing these columns in the species parameter data frame later will not update the gear_params data frame.

Catchability

Catchability is used as an additional factor to make the link between gear selectivity, fishing effort and fishing mortality. For example, it can be set so that an effort of 1 gives a desired fishing mortality. In this way effort can then be specified relative to a 'base effort', e.g. the effort in a particular year.

Catchability is stored as a two dimensional array (gear x species). This can either be provided explicitly via the catchability argument, or the information can be provided via a catchability column in the gear_params data frame.

In the case where each species is selected by only a single gear, the catchability column can also be provided in the species_params data frame. Mizer will then copy this over to the gear_params data frame when the MizerParams object is created.

Effort

The initial fishing effort is stored in the MizerParams object. If it is not supplied, it is set to zero. The initial effort can be overruled when the simulation is run with project(), where it is also possible to specify an effort that varies through time.

See Also

gear_params()

Other functions for setting parameters: gear_params(), resource_params(), setExtMort(), setInitialValues(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setParams(), setPredKernel(), setReproduction(), setResource(), setSearchVolume(), species_params()

Examples

```
str(getCatchability(NS_params))
str(getSelectivity(NS_params))
str(getInitialEffort(NS_params))
```

---

setInitialValues *Set initial values to final values of a simulation*

Description

Takes the final values from a simulation in a MizerSim object and stores them as initial values in a MizerParams object.

Usage

```
setInitialValues(params, sim)
```

Arguments

params	A MizerParams() object
sim	A MizerSim object.

Value

The params object with updated initial values and initial effort, taken from the values at the final time of the simulation in sim. Because of the way the R language works, setInitialValues() does not make the changes to the params object that you pass to it but instead returns a new params object. So to affect the change you call the function in the form params <-setInitialValues(params,sim).

See Also

Other functions for setting parameters: gear_params(), resource_params(), setExtMort(), setFishing(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setParams(), setPredKernel(), setReproduction(), setResource(), setSearchVolume(), species_params()

Examples

```
## Not run:
params <- NS_params
sim <- project(params, t_max = 20, effort = 0.5)
params <- setInitialValues(params, sim)

## End(Not run)
```

---

setInteraction *Set species interaction matrix*

Description

Set species interaction matrix

Usage

```
setInteraction(params, interaction = NULL)

getInteraction(params)
```

Arguments

params	MizerParams object
interaction	Optional interaction matrix of the species (predator species x prey species). Entries should be numbers between 0 and 1. By default all entries are 1. See "Setting interaction matrix" section below.

Value

`setInteraction`: A MizerParams object with updated interaction matrix

`getInteraction()`: The interaction matrix (predator species x prey species)

Setting interaction matrix

You do not need to specify an interaction matrix. If you do not, then the predator-prey interactions are purely determined by the size of predator and prey and totally independent of the species of predator and prey.

The interaction matrix θ_{ij} describes the interaction of each pair of species in the model. This can be viewed as a proxy for spatial interaction e.g. to model predator-prey interaction that is not size based. The values in the interaction matrix are used to scale the encountered food and predation mortality (see on the website the section on predator-prey encounter rate and on predation mortality). The first index refers to the predator species and the second to the prey species.

It is used when calculating the food encounter rate in `getEncounter()` and the predation mortality rate in `getPredMort()`. Its entries are dimensionless numbers.The values are between 0 (species do not overlap and therefore do not interact with each other) to 1 (species overlap perfectly). If all the values in the interaction matrix are set to 1 then predator-prey interactions are determined entirely by size-preference.

This function checks that the supplied interaction matrix is valid and then stores it in the `interaction` slot of the `params` object.

The order of the columns and rows of the `interaction` argument should be the same as the order in the species params data frame in the `params` object. If you supply a named array then the function will check the order and warn if it is different. One way of creating your own interaction matrix is to enter the data using a spreadsheet program and saving it as a .csv file. The data can be read into R using the command `read.csv()`.

The interaction of the species with the resource are set via a column `interaction_resource` in the `species_params` data frame. Again the entries have to be numbers between 0 and 1. By default this column is set to all 1s.

See Also

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `setSearchVolume()`, `species_params()`

Examples

```
params <- newTraitParams(no_sp = 3)
inter <- getInteraction(params)
inter[1, 2:3] <- 0
params <- setInteraction(params, interaction = inter)
getInteraction(params)
```

`setMaxIntakeRate` *Set maximum intake rate*

Description

Set maximum intake rate

Usage

```
setMaxIntakeRate(params, intake_max = NULL, reset = FALSE, ...)

getMaxIntakeRate(params)

intake_max(params)

intake_max(params) <- value
```

Arguments

`params`	MizerParams
`intake_max`	Optional. An array (species x size) holding the maximum intake rate for each species at size. If not supplied, a default is set as described in the section "Setting maximum intake rate".
`reset`	**[Experimental]** If set to TRUE, then the intake rate will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
`...`	Unused
`value`	intake_max

Value

`setReproduction()`: A MizerParams object with updated maximum intake rate.

`getMaxIntakeRate()` or equivalently `intake_max()`: An array (species x size) with the maximum intake rate.

Setting maximum intake rate

The maximum intake rate $h_i(w)$ of an individual of species i and weight w determines the feeding level, calculated with `getFeedingLevel()`. It is measured in grams/year.

If the `intake_max` argument is not supplied, then the maximum intake rate is set to

$$h_i(w) = h_i w^{n_i}.$$

The values of h_i (the maximum intake rate of an individual of size 1 gram) and n_i (the allometric exponent for the intake rate) are taken from the `h` and `n` columns in the species parameter

dataframe. If the h column is not supplied in the species parameter dataframe, it is calculated by the get_h_default() function, using the f0 and the k_vb column, if they are supplied.

If h_i is set to Inf, fish of species i will consume all encountered food.

See Also

Other functions for setting parameters: gear_params(), resource_params(), setExtMort(), setFishing(), setInitialValues(), setInteraction(), setMetabolicRate(), setParams(), setPredKernel(), setReproduction(), setResource(), setSearchVolume(), species_params()

---

setMetabolicRate *Set metabolic rate*

Description

Sets the rate at which energy is used for metabolism and activity

Usage

```
setMetabolicRate(params, metab = NULL, p = NULL, reset = FALSE, ...)

getMetabolicRate(params)

metab(params)

metab(params) <- value
```

Arguments

params	MizerParams
metab	Optional. An array (species x size) holding the metabolic rate for each species at size. If not supplied, a default is set as described in the section "Setting metabolic rate".
p	The allometric metabolic exponent. This is only used if metab is not given explicitly and if the exponent is not specified in a p column in the species_params.
reset	**[Experimental]** If set to TRUE, then the metabolic rate will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
...	Unused
value	metab

Value

setMetabolicRate(): A MizerParams object with updated metabolic rate.

getMetabolicRate() or equivalently metab(): An array (species x size) with the metabolic rate.

Setting metabolic rate

The metabolic rate is subtracted from the energy income rate to calculate the rate at which energy is available for growth and reproduction, see `getEReproAndGrowth()`. It is measured in grams/year.

If the `metab` argument is not supplied, then for each species the metabolic rate $k(w)$ for an individual of size w is set to

$$k(w) = k_s w^p + kw,$$

where $k_s w^p$ represents the rate of standard metabolism and kw is the rate at which energy is expended on activity and movement. The values of k_s, p and k are taken from the `ks`, `p` and `k` columns in the species parameter dataframe. If any of these parameters are not supplied, the defaults are $k = 0$, $p = n$ and

$$k_s = f_c h \alpha w_{mat}^{n-p},$$

where f_c is the critical feeding level taken from the `fc` column in the species parameter data frame. If the critical feeding level is not specified, a default of $f_c = 0.2$ is used.

See Also

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `setSearchVolume()`, `species_params()`

`setMetadata` *Set metadata for a model*

Description

[Experimental] Setting metadata is particularly important for sharing your model with others. All metadata fields are optional and you can also add other fields of your own choosing. If you set a value for a field that already existed, the old value will be overwritten.

Usage

```
setMetadata(params, title, description, authors, url, doi, ...)

getMetadata(params)
```

Arguments

`params`	The MizerParams object for the model
`title`	A string with the title for the model
`description`	A string with a description of the model. This could for example contain information about any publications using the model.
`authors`	An author entry or a list of author entries, where each author entry could either be just a name or could itself be a list with fields like `name`, `orcid`, possibly `email`.

`url`	A URL where more information about the model can be found. This could be a blog post on the mizer blog, for example.
`doi`	The digital object identifier for your model. To create a doi you can use online services like https://zenodo.org/ or https://figshare.com.
`...`	Additional metadata fields that you would like to add

Details

In addition to the metadata fields you can set by hand, there are four fields that are set automatically by mizer:

- `mizer_version` The version string of the mizer version under which the model was last saved. Can be compared to the current version which is obtained with `packageVersion("mizer")`. The purpose of this field is that if the model is not working as expected in the current version of mizer, you can go back to the older version under which presumably it was working.
- `extensions` A named vector of strings where each name is the name of and extension package needed to run the model and each value is a string giving the information that the remotes package needs to install the correct version of the extension package, see https://remotes.r-lib.org/. This field is set by the extension packages.
- `time_created` A POSIXct date-time object with the creation time.
- `time_modified` A POSIXct date-time object with the last modified time.

Value

`setMetadata()`: The MizerParams object with updated metadata

`getMetadata()`: A list with all metadata entries that have been set, including at least `mizer_version`, `extensions`, `time_created` and `time_modified`.

`setParams` *Set or change any model parameters*

Description

This is a convenient wrapper function calling each of the following functions

- `setPredKernel()`
- `setSearchVolume()`
- `setInteraction()`
- `setMaxIntakeRate()`
- `setMetabolicRate()`
- `setExtMort()`
- `setReproduction()`
- `setFishing()`
- `setResource()`

See the Details section below for a discussion of how to use this function.

Usage

```
setParams(params, interaction = NULL, ...)
```

Arguments

params	A MizerParams object
interaction	Optional interaction matrix of the species (predator species x prey species). Entries should be numbers between 0 and 1. By default all entries are 1. See "Setting interaction matrix" section below.
...	Arguments passed on to setPredKernel, setSearchVolume, setMaxIntakeRate, setMetabolicRate, setExtMort, setReproduction, setFishing, setResource

pred_kernel Optional. An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If not supplied, a default is set as described in section "Setting predation kernel".

search_vol Optional. An array (species x size) holding the search volume for each species at size. If not supplied, a default is set as described in the section "Setting search volume".

intake_max Optional. An array (species x size) holding the maximum intake rate for each species at size. If not supplied, a default is set as described in the section "Setting maximum intake rate".

metab Optional. An array (species x size) holding the metabolic rate for each species at size. If not supplied, a default is set as described in the section "Setting metabolic rate".

p The allometric metabolic exponent. This is only used if metab is not given explicitly and if the exponent is not specified in a p column in the species_params.

ext_mort Optional. An array (species x size) holding the external mortality rate.

z0pre If z0, the mortality from other sources, is not a column in the species data frame, it is calculated as z0pre * w_inf ^ z0exp. Default value is 0.6.

z0exp If z0, the mortality from other sources, is not a column in the species data frame, it is calculated as z0pre * w_inf ^ z0exp. Default value is n-1.

z0 **[Deprecated]** Use ext_mort instead. Not to be confused with the species_parameter z0.

maturity Optional. An array (species x size) that holds the proportion of individuals of each species at size that are mature. If not supplied, a default is set as described in the section "Setting reproduction".

repro_prop Optional. An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. If not supplied, a default is set as described in the section "Setting reproduction".

RDD The name of the function calculating the density-dependent reproduction rate from the density-independent rate. Defaults to "BevertonHoltRDD()".

selectivity Optional. An array (gear x species x size) that holds the selectivity of each gear for species and size, $S_{g,i,w}$.

catchability Optional. An array (gear x species) that holds the catchability of each species by each gear, $Q_{g,i}$.

`initial_effort` Optional. A number or a named numeric vector specifying the fishing effort. If a number, the same effort is used for all gears. If a vector, must be named by gear.

`resource_rate` Optional. Vector of resource intrinsic birth rates

`resource_capacity` Optional. Vector of resource intrinsic carrying capacity

`r_pp` Coefficient of the intrinsic resource birth rate

`n` Allometric growth exponent for resource

`kappa` Coefficient of the intrinsic resource carrying capacity

`lambda` Scaling exponent of the intrinsic resource carrying capacity

`w_pp_cutoff` The upper cut off size of the resource spectrum. The carrying capacity will be set to 0 above this size. Default is 10 g.

`resource_dynamics` Optional. Name of the function that determines the resource dynamics by calculating the resource spectrum at the next time step from the current state. You only need to specify this if you do not want to use the default `resource_semichemostat()`.

Details

If you are not happy with the assumptions that mizer makes by default about the shape of the model functions, for example if you want to change one of the allometric scaling assumptions, you can do this by providing your choice as an array in the appropriate argument to `setParams()`. The sections below discuss all the model functions that you can change this way.

Because of the way the R language works, `setParams` does not make the changes to the `params` object that you pass to it but instead returns a new params object. So to affect the change you call the function in the form `params <-setParams(params,...)`.

Usually, if you are happy with the way mizer calculates its model functions from the species parameters and only want to change the values of some species parameters, you would make those changes in the `species_params` data frame contained in the `params` object using `species_params<-()`. Here is an example which assumes that you have have a MizerParams object `params` in which you just want to change the `gamma` parameter of the third species:

```
species_params(params)$gamma[[3]] <- 1000
```

Internally that will actually call `setParams()` to recalculate any of the other parameters that are affected by the change in the species parameter.

`setParams()` will use the species parameters in the `params` object to recalculate the values of all the model functions except those for which you have set custom values.

Value

A MizerParams object

Units in mizer

Mizer uses grams to measure weight, centimetres to measure lengths, and years to measure time.

Mizer is agnostic about whether abundances are given as

1. numbers per area,
2. numbers per volume or
3. total numbers for the entire study area.

You should make the choice most convenient for your application and then stick with it. If you make choice 1 or 2 you will also have to choose a unit for area or volume. Your choice will then determine the units for some of the parameters. This will be mentioned when the parameters are discussed in the sections below.

Your choice will also affect the units of the quantities you may want to calculate with the model. For example, the yield will be in grams/year/m^2 in case 1 if you choose m^2 as your measure of area, in grams/year/m^3 in case 2 if you choose m^3 as your unit of volume, or simply grams/year in case 3. The same comment applies for other measures, like total biomass, which will be grams/area in case 1, grams/volume in case 2 or simply grams in case 3. When mizer puts units on axes in plots, it will choose the units appropriate for case 3. So for example in `plotBiomass()` it gives the unit as grams.

You can convert between these choices. For example, if you use case 1, you need to multiply with the area of the ecosystem to get the total quantity. If you work with case 2, you need to multiply by both area and the thickness of the productive layer. In that respect, case 2 is a bit cumbersome. The function `scaleModel()` is useful to change the units you are using.

Setting interaction matrix

You do not need to specify an interaction matrix. If you do not, then the predator-prey interactions are purely determined by the size of predator and prey and totally independent of the species of predator and prey.

The interaction matrix θ_{ij} describes the interaction of each pair of species in the model. This can be viewed as a proxy for spatial interaction e.g. to model predator-prey interaction that is not size based. The values in the interaction matrix are used to scale the encountered food and predation mortality (see on the website the section on predator-prey encounter rate and on predation mortality). The first index refers to the predator species and the second to the prey species.

It is used when calculating the food encounter rate in `getEncounter()` and the predation mortality rate in `getPredMort()`. Its entries are dimensionless numbers.The values are between 0 (species do not overlap and therefore do not interact with each other) to 1 (species overlap perfectly). If all the values in the interaction matrix are set to 1 then predator-prey interactions are determined entirely by size-preference.

This function checks that the supplied interaction matrix is valid and then stores it in the `interaction` slot of the `params` object.

The order of the columns and rows of the `interaction` argument should be the same as the order in the species params data frame in the `params` object. If you supply a named array then the function will check the order and warn if it is different. One way of creating your own interaction matrix is to enter the data using a spreadsheet program and saving it as a .csv file. The data can be read into R using the command `read.csv()`.

The interaction of the species with the resource are set via a column `interaction_resource` in the `species_params` data frame. Again the entries have to be numbers between 0 and 1. By default this column is set to all 1s.

Setting predation kernel

Kernel dependent on predator to prey size ratio

If the `pred_kernel` argument is not supplied, then this function sets a predation kernel that depends only on the ratio of predator mass to prey mass, not on the two masses independently. The shape of that kernel is then determined by the `pred_kernel_type` column in species_params.

The default for `pred_kernel_type` is "lognormal". This will call the function `lognormal_pred_kernel()` to calculate the predation kernel. An alternative pred_kernel type is "box", implemented by the function `box_pred_kernel()`, and "power_law", implemented by the function `power_law_pred_kernel()`. These functions require certain species parameters in the species_params data frame. For the log-normal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`. They are explained in the help pages for the kernel functions. Except for `beta` and `sigma`, no defaults are set for these parameters. If they are missing from the species_params data frame then mizer will issue an error message.

You can use any other string for `pred_kernel_type`. If for example you choose "my" then you need to define a function `my_pred_kernel` that you can model on the existing functions like `lognormal_pred_kernel()`.

When using a kernel that depends on the predator/prey size ratio only, mizer does not need to store the entire three dimensional array in the MizerParams object. Such an array can be very big when there is a large number of size bins. Instead, mizer only needs to store two two-dimensional arrays that hold Fourier transforms of the feeding kernel function that allow the encounter rate and the predation rate to be calculated very efficiently. However, if you need the full three-dimensional array you can calculate it with the `getPredKernel()` function.

Kernel dependent on both predator and prey size

If you want to work with a feeding kernel that depends on predator mass and prey mass independently, you can specify the full feeding kernel as a three-dimensional array (predator species x predator size x prey size).

You should use this option only if a kernel dependent only on the predator/prey mass ratio is not appropriate. Using a kernel dependent on predator/prey mass ratio only allows mizer to use fast Fourier transform methods to significantly reduce the running time of simulations.

The order of the predator species in `pred_kernel` should be the same as the order in the species params dataframe in the `params` object. If you supply a named array then the function will check the order and warn if it is different.

Setting search volume

The search volume $\gamma_i(w)$ of an individual of species i and weight w multiplies the predation kernel when calculating the encounter rate in `getEncounter()` and the predation rate in `getPredRate()`.

The name "search volume" is a bit misleading, because $\gamma_i(w)$ does not have units of volume. It is simply a parameter that determines the rate of predation. Its units depend on your choice, see section "Units in mizer". If you have chosen to work with total abundances, then it is a rate with units 1/year. If you have chosen to work with abundances per m^2 then it has units of m^2/year. If you have chosen to work with abundances per m^3 then it has units of m^3/year.

If the `search_vol` argument is not supplied, then the search volume is set to

$$\gamma_i(w) = \gamma_i w_i^q.$$

The values of γ_i (the search volume at 1g) and q_i (the allometric exponent of the search volume) are taken from the gamma and q columns in the species parameter dataframe. If the gamma column is not supplied in the species parameter dataframe, a default is calculated by the get_gamma_default() function. Note that only for predators of size $w = 1$ gram is the value of the species parameter γ_i the same as the value of the search volume $\gamma_i(w)$.

Setting maximum intake rate

The maximum intake rate $h_i(w)$ of an individual of species i and weight w determines the feeding level, calculated with getFeedingLevel(). It is measured in grams/year.

If the intake_max argument is not supplied, then the maximum intake rate is set to

$$h_i(w) = h_i w^{n_i}.$$

The values of h_i (the maximum intake rate of an individual of size 1 gram) and n_i (the allometric exponent for the intake rate) are taken from the h and n columns in the species parameter dataframe. If the h column is not supplied in the species parameter dataframe, it is calculated by the get_h_default() function, using the f0 and the k_vb column, if they are supplied.

If h_i is set to Inf, fish of species i will consume all encountered food.

Setting metabolic rate

The metabolic rate is subtracted from the energy income rate to calculate the rate at which energy is available for growth and reproduction, see getEReproAndGrowth(). It is measured in grams/year.

If the metab argument is not supplied, then for each species the metabolic rate $k(w)$ for an individual of size w is set to

$$k(w) = k_s w^p + kw,$$

where $k_s w^p$ represents the rate of standard metabolism and kw is the rate at which energy is expended on activity and movement. The values of k_s, p and k are taken from the ks, p and k columns in the species parameter dataframe. If any of these parameters are not supplied, the defaults are $k = 0$, $p = n$ and

$$k_s = f_c h \alpha w_{mat}^{n-p},$$

where f_c is the critical feeding level taken from the fc column in the species parameter data frame. If the critical feeding level is not specified, a default of $f_c = 0.2$ is used.

Setting external mortality rate

The external mortality is all the mortality that is not due to fishing or predation by predators included in the model. The external mortality could be due to predation by predators that are not explicitly included in the model (e.g. mammals or seabirds) or due to other causes like illness. It is a rate with units 1/year.

The ext_mort argument allows you to specify an external mortality rate that depends on species and body size. You can see an example of this in the Examples section of the help page for setExtMort().

If the ext_mort argument is not supplied, then the external mortality is assumed to depend only on the species, not on the size of the individual: $\mu_{ext.i}(w) = z_{0.i}$. The value of the constant z_0 for each species is taken from the z0 column of the species parameter data frame, if that column exists. Otherwise it is calculated as

$$z_{0.i} = \texttt{z0pre}_i \, w_{inf}^{\texttt{z0exp}}.$$

Setting reproduction

For each species and at each size, the proportion ψ of the available energy that is invested into reproduction is the product of two factors: the proportion `maturity` of individuals that are mature and the proportion `repro_prop` of the energy available to a mature individual that is invested into reproduction.

Maturity ogive: If the the proportion of individuals that are mature is not supplied via the `maturity` argument , then it is set to a sigmoidal maturity ogive that changes from 0 to 1 at around the maturity size:

$$\texttt{maturity}(w) = \left[1 + \left(\frac{w}{w_{mat}}\right)^{-U}\right]^{-1}.$$

(To avoid clutter, we are not showing the species index in the equations, although each species has its own maturity ogive.) The maturity weights are taken from the `w_mat` column of the species_params data frame. Any missing maturity weights are set to 1/4 of the asymptotic weight in the `w_inf` column.

The exponent U determines the steepness of the maturity ogive. By default it is chosen as $U = 10$, however this can be overridden by including a column `w_mat25` in the species parameter dataframe that specifies the weight at which 25% of individuals are mature, which sets $U = \log(3)/\log(w_{mat}/w_{25})$.

The sigmoidal function given above would strictly reach 1 only asymptotically. Mizer instead sets the function equal to 1 already at the species' maximum size, taken from the compulsory `w_inf` column in the species parameter data frame. Also, for computational simplicity, any proportion smaller than `1e-8` is set to `0`.

Investment into reproduction: If the the energy available to a mature individual that is invested into reproduction is not supplied via the `repro_prop` argument, it is set to the allometric form

$$\texttt{repro\_prop}(w) = \left(\frac{w}{w_{inf}}\right)^{m-n}.$$

Here n is the scaling exponent of the energy income rate. Hence the exponent m determines the scaling of the investment into reproduction for mature individuals. By default it is chosen to be $m = 1$ so that the rate at which energy is invested into reproduction scales linearly with the size. This default can be overridden by including a column `m` in the species parameter dataframe. The asymptotic sizes are taken from the compulsory `w_inf` column in the species parameter data frame.

The total proportion of energy invested into reproduction of an individual of size w is then

$$\psi(w) = \texttt{maturity}(w)\texttt{repro\_prop}(w)$$

Reproductive efficiency: The reproductive efficiency ϵ, i.e., the proportion of energy allocated to reproduction that results in egg biomass, is set through the `erepro` column in the species_params data frame. If that is not provided, the default is set to 1 (which you will want to override). The offspring biomass divided by the egg biomass gives the rate of egg production, returned by `getRDI()`:

$$R_{di} = \frac{\epsilon}{2w_{min}} \int N(w) E_r(w) \psi(w)\, dw$$

Density dependence: The stock-recruitment relationship is an emergent phenomenon in mizer, with several sources of density dependence. Firstly, the amount of energy invested into reproduction depends on the energy income of the spawners, which is density-dependent due to competition for prey. Secondly, the proportion of larvae that grow up to recruitment size depends on the larval mortality, which depends on the density of predators, and on larval growth rate, which depends on density of prey.

Finally, to encode all the density dependence in the stock-recruitment relationship that is not already included in the other two sources of density dependence, mizer puts the the density-independent rate of egg production through a density-dependence function. The result is returned by `getRDD()`. The name of the density-dependence function is specified by the `RDD` argument. The default is the Beverton-Holt function `BevertonHoltRDD()`, which requires an `R_max` column in the species_params data frame giving the maximum egg production rate. If this column does not exist, it is initialised to `Inf`, leading to no density-dependence. Other functions provided by mizer are `RickerRDD()` and `SheperdRDD()` and you can easily use these as models for writing your own functions.

Setting fishing

Gears

In `mizer`, fishing mortality is imposed on species by fishing gears. The total per-capita fishing mortality (1/year) is obtained by summing over the mortality from all gears,

$$\mu_{f.i}(w) = \sum_g F_{g,i}(w),$$

where the fishing mortality $F_{g,i}(w)$ imposed by gear g on species i at size w is calculated as:

$$F_{g,i}(w) = S_{g,i}(w) Q_{g,i} E_g,$$

where S is the selectivity by species, gear and size, Q is the catchability by species and gear and E is the fishing effort by gear.

Selectivity

The selectivity at size of each gear for each species is saved as a three dimensional array (gear x species x size). Each entry has a range between 0 (that gear is not selecting that species at that size) to 1 (that gear is selecting all individuals of that species of that size). This three dimensional array can be specified explicitly via the `selectivity` argument, but usually mizer calculates it from the `gear_params` slot of the MizerParams object.

To allow the calculation of the `selectivity` array, the `gear_params` slot must be a data frame with one row for each gear-species combination. So if for example a gear can select three species, then that gear contributes three rows to the `gear_params` data frame, one for each species it can select. The data frame must have columns `gear`, holding the name of the gear, `species`, holding the name of the species, and `sel_func`, holding the name of the function that calculates the selectivity curve. Some selectivity functions are included in the package: `knife_edge()`, `sigmoid_length()`, `double_sigmoid_length()`, and `sigmoid_weight()`. Users are able to write their own size-based selectivity function. The first argument to the function must be `w` and the function must return a vector of the selectivity (between 0 and 1) at size.

Each selectivity function may have parameters. Values for these parameters must be included as columns in the gear parameters data.frame. The names of the columns must exactly match the

names of the corresponding arguments of the selectivity function. For example, the default selectivity function is `knife_edge()` that a has sudden change of selectivity from 0 to 1 at a certain size. In its help page you can see that the `knife_edge()` function has arguments `w` and `knife_edge_size`. The first argument, `w`, is size (the function calculates selectivity at size). All selectivity functions must have `w` as the first argument. The values for the other arguments must be found in the gear parameters data.frame. So for the `knife_edge()` function there should be a `knife_edge_size` column. Because `knife_edge()` is the default selectivity function, the `knife_edge_size` argument has a default value = `w_mat`.

In case each species is only selected by one gear, the columns of the `gear_params` data frame can alternatively be provided as columns of the `species_params` data frame, if this is more convenient for the user to set up. Mizer will then copy these columns over to create the `gear_params` data frame when it creates the MizerParams object. However changing these columns in the species parameter data frame later will not update the `gear_params` data frame.

Catchability

Catchability is used as an additional factor to make the link between gear selectivity, fishing effort and fishing mortality. For example, it can be set so that an effort of 1 gives a desired fishing mortality. In this way effort can then be specified relative to a 'base effort', e.g. the effort in a particular year.

Catchability is stored as a two dimensional array (gear x species). This can either be provided explicitly via the `catchability` argument, or the information can be provided via a `catchability` column in the `gear_params` data frame.

In the case where each species is selected by only a single gear, the `catchability` column can also be provided in the `species_params` data frame. Mizer will then copy this over to the `gear_params` data frame when the MizerParams object is created.

Effort

The initial fishing effort is stored in the `MizerParams` object. If it is not supplied, it is set to zero. The initial effort can be overruled when the simulation is run with `project()`, where it is also possible to specify an effort that varies through time.

Setting resource dynamics

By default, mizer uses a semichemostat model to describe the resource dynamics in each size class independently. This semichemostat dynamics is implemented by the function `resource_semichemostat()`. You can change the resource dynamics by writing your own function, modelled on `resource_semichemostat()`, and then passing the name of your function in the `resource_dynamics` argument.

The `resource_rate` argument is a vector specifying the intrinsic resource growth rate for each size class. If it is not supplied, then the intrinsic growth rate $r(w)$ at size w is set to

$$r(w) = r_{pp}\, w^{n-1}.$$

The values of r_{pp} and n are taken from the `r_pp` and `n` arguments.

The `resource_capacity` argument is a vector specifying the intrinsic resource carrying capacity for each size class. If it is not supplied, then the intrinsic carrying capacity $c(w)$ at size w is set to

$$c(w) = \kappa\, w^{-\lambda}$$

for all w less than `w_pp_cutoff` and zero for larger sizes. The values of κ and λ are taken from the `kappa` and `lambda` arguments.

See Also

Other functions for setting parameters: gear_params(), resource_params(), setExtMort(), setFishing(), setInitialValues(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setPredKernel(), setReproduction(), setResource(), setSearchVolume(), species_params()

---

setPredKernel *Set predation kernel*

Description

The predation kernel determines the distribution of prey sizes that a predator feeds on. It is used in getEncounter() when calculating the rate at which food is encountered and in getPredRate() when calculating the rate at which a prey is predated upon. The predation kernel can be a function of the predator/prey size ratio or it can be a function of the predator size and the prey size separately. Both types can be set up with this function.

Usage

```
setPredKernel(params, pred_kernel = NULL, reset = FALSE, ...)

getPredKernel(params)

pred_kernel(params)

pred_kernel(params) <- value
```

Arguments

params	A MizerParams object
pred_kernel	Optional. An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If not supplied, a default is set as described in section "Setting predation kernel".
reset	**[Experimental]** If set to TRUE, then the predation kernel will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
...	Unused
value	pred_kernel

Value

setPredKernel(): A MizerParams object with updated predation kernel.

getPredKernel() or equivalently pred_kernel(): An array (predator species x predator_size x prey_size)

Setting predation kernel

Kernel dependent on predator to prey size ratio

If the `pred_kernel` argument is not supplied, then this function sets a predation kernel that depends only on the ratio of predator mass to prey mass, not on the two masses independently. The shape of that kernel is then determined by the `pred_kernel_type` column in species_params.

The default for `pred_kernel_type` is "lognormal". This will call the function `lognormal_pred_kernel()` to calculate the predation kernel. An alternative pred_kernel type is "box", implemented by the function `box_pred_kernel()`, and "power_law", implemented by the function `power_law_pred_kernel()`. These functions require certain species parameters in the species_params data frame. For the log-normal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`. They are explained in the help pages for the kernel functions. Except for `beta` and `sigma`, no defaults are set for these parameters. If they are missing from the species_params data frame then mizer will issue an error message.

You can use any other string for `pred_kernel_type`. If for example you choose "my" then you need to define a function `my_pred_kernel` that you can model on the existing functions like `lognormal_pred_kernel()`.

When using a kernel that depends on the predator/prey size ratio only, mizer does not need to store the entire three dimensional array in the MizerParams object. Such an array can be very big when there is a large number of size bins. Instead, mizer only needs to store two two-dimensional arrays that hold Fourier transforms of the feeding kernel function that allow the encounter rate and the predation rate to be calculated very efficiently. However, if you need the full three-dimensional array you can calculate it with the `getPredKernel()` function.

Kernel dependent on both predator and prey size

If you want to work with a feeding kernel that depends on predator mass and prey mass independently, you can specify the full feeding kernel as a three-dimensional array (predator species x predator size x prey size).

You should use this option only if a kernel dependent only on the predator/prey mass ratio is not appropriate. Using a kernel dependent on predator/prey mass ratio only allows mizer to use fast Fourier transform methods to significantly reduce the running time of simulations.

The order of the predator species in `pred_kernel` should be the same as the order in the species params dataframe in the `params` object. If you supply a named array then the function will check the order and warn if it is different.

See Also

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setReproduction()`, `setResource()`, `setSearchVolume()`, `species_params()`

Examples

```
## Not run:
## Set up a MizerParams object
params <-  NS_params

## If you change predation kernel parameters after setting up a model,
#  this will be used to recalculate the kernel
```

```
species_params(params)["Cod", "beta"] <- 200

## You can change to a different predation kernel type
species_params(params)$ppmr_max <- 4000
species_params(params)$ppmr_min <- 200
species_params(params)$pred_kernel_type <- "box"
plot(w_full(params), getPredKernel(params)["Cod", 100, ], type="l", log="x")

## If you need a kernel that depends also on prey size you need to define
# it yourself.
pred_kernel <- getPredKernel(params)
pred_kernel["Herring", , ] <- sweep(pred_kernel["Herring", , ], 2,
                                    params@w_full, "*")
params<- setPredKernel(params, pred_kernel = pred_kernel)

## End(Not run)
```

`setRateFunction` *Set own rate function to replace mizer rate function*

Description

If the way mizer calculates a fundamental rate entering the model is not flexible enough for you (for example if you need to introduce time dependence) then you can write your own functions for calculating that rate and use `setRateFunction()` to register it with mizer.

Usage

```
setRateFunction(params, rate, fun)

getRateFunction(params, rate)

other_params(params)

other_params(params) <- value
```

Arguments

`params`	A MizerParams object
`rate`	Name of the rate for which a new function is to be set.
`fun`	Name of the function to use to calculate the rate.
`value`	Values for other parameters

Details

At each time step during a simulation with the `project()` function, mizer needs to calculate the instantaneous values of the various rates. By default it calls the `mizerRates()` function which creates a list with the following components:

- encounter from mizerEncounter()
- feeding_level from mizerFeedingLevel()
- pred_rate from mizerPredRate()
- pred_mort from mizerPredMort()
- f_mort from mizerFMort()
- mort from mizerMort()
- resource_mort from mizerResourceMort()
- e from mizerEReproAndGrowth()
- e_repro from mizerERepro()
- e_growth from mizerEGrowth()
- rdi from mizerRDI()
- rdd from BevertonHoltRDD()

For each of these you can substitute your own function. So for example if you have written your own function for calculating the total mortality rate and have called it myMort and have a mizer model stored in a MizerParams object called params that you want to run with your new mortality rate, then you would call

```
params <- setRateFunction(params, "Mort", "myMort")
```

In general if you want to replace a function mizerSomeRateFunc() with a function myVersionOfThis() you would call

```
params <- setRateFunction(params, "SomeRateFunc", "myVersionOfThis")
```

In some extreme cases you may need to swap out the entire mizerRates() function for your own function called myRates(). That you can do with

```
params <- setRateFunction(params, "Rates", "myRates")
```

Your new rate functions may need their own model parameters. These you can store in other_params(params). For example

```
other_params(params)$my_param <- 42
```

Note that your own rate functions need to be defined in the global environment or in a package. If they are defined within a function then mizer will not find them.

Value

For setRateFunction(): An updated MizerParams object

For getRateFunction(): The name of the registered rate function for the requested rate, or the list of all rate functions if called without rate argument.

For other_params(): A named list with all the parameters for which you have set values.

`setReproduction` *Set reproduction parameters*

Description

Sets the proportion of the total energy available for reproduction and growth that is invested into reproduction as a function of the size of the individual and sets additional density dependence.

Usage

```
setReproduction(
  params,
  maturity = NULL,
  repro_prop = NULL,
  reset = FALSE,
  RDD = NULL,
  ...
)

getMaturityProportion(params)

maturity(params)

maturity(params) <- value

getReproductionProportion(params)

repro_prop(params)

repro_prop(params) <- value
```

Arguments

`params`	A MizerParams object
`maturity`	Optional. An array (species x size) that holds the proportion of individuals of each species at size that are mature. If not supplied, a default is set as described in the section "Setting reproduction".
`repro_prop`	Optional. An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. If not supplied, a default is set as described in the section "Setting reproduction".
`reset`	**[Experimental]** If set to TRUE, then both `maturity` and `repro_prop` will be reset to the value calculated from the species parameters, even if they were previously overwritten with custom values. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom values have been set.

RDD	The name of the function calculating the density-dependent reproduction rate from the density-independent rate. Defaults to "BevertonHoltRDD()".
...	Unused
value	.

Value

setReproduction(): A MizerParams object with updated reproduction parameters.

getMaturityProportion() or equivalently 'maturity(): An array (species x size) that holds the proportion of individuals of each species at size that are mature.

getReproductionProportion() or equivalently repro_prop(): An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. For sizes where the maturity proportion is zero, also the reproduction proportion is returned as zero.

Setting reproduction

For each species and at each size, the proportion ψ of the available energy that is invested into reproduction is the product of two factors: the proportion maturity of individuals that are mature and the proportion repro_prop of the energy available to a mature individual that is invested into reproduction.

Maturity ogive: If the the proportion of individuals that are mature is not supplied via the maturity argument , then it is set to a sigmoidal maturity ogive that changes from 0 to 1 at around the maturity size:

$$\texttt{maturity}(w) = \left[1 + \left(\frac{w}{w_{mat}}\right)^{-U}\right]^{-1}.$$

(To avoid clutter, we are not showing the species index in the equations, although each species has its own maturity ogive.) The maturity weights are taken from the w_mat column of the species_params data frame. Any missing maturity weights are set to 1/4 of the asymptotic weight in the w_inf column.

The exponent U determines the steepness of the maturity ogive. By default it is chosen as $U = 10$, however this can be overridden by including a column w_mat25 in the species parameter dataframe that specifies the weight at which 25% of individuals are mature, which sets $U = \log(3)/\log(w_{mat}/w_{25})$.

The sigmoidal function given above would strictly reach 1 only asymptotically. Mizer instead sets the function equal to 1 already at the species' maximum size, taken from the compulsory w_inf column in the species parameter data frame. Also, for computational simplicity, any proportion smaller than 1e-8 is set to 0.

Investment into reproduction: If the the energy available to a mature individual that is invested into reproduction is not supplied via the repro_prop argument, it is set to the allometric form

$$\texttt{repro\_prop}(w) = \left(\frac{w}{w_{inf}}\right)^{m-n}.$$

Here n is the scaling exponent of the energy income rate. Hence the exponent m determines the scaling of the investment into reproduction for mature individuals. By default it is chosen to be $m = 1$ so that the rate at which energy is invested into reproduction scales linearly with the size. This default can be overridden by including a column `m` in the species parameter dataframe. The asymptotic sizes are taken from the compulsory `w_inf` column in the species parameter data frame.

The total proportion of energy invested into reproduction of an individual of size w is then

$$\psi(w) = \texttt{maturity}(w)\texttt{repro\_prop}(w)$$

Reproductive efficiency: The reproductive efficiency ϵ, i.e., the proportion of energy allocated to reproduction that results in egg biomass, is set through the `erepro` column in the species_params data frame. If that is not provided, the default is set to 1 (which you will want to override). The offspring biomass divided by the egg biomass gives the rate of egg production, returned by `getRDI()`:

$$R_{di} = \frac{\epsilon}{2w_{min}} \int N(w) E_r(w) \psi(w)\, dw$$

Density dependence: The stock-recruitment relationship is an emergent phenomenon in mizer, with several sources of density dependence. Firstly, the amount of energy invested into reproduction depends on the energy income of the spawners, which is density-dependent due to competition for prey. Secondly, the proportion of larvae that grow up to recruitment size depends on the larval mortality, which depends on the density of predators, and on larval growth rate, which depends on density of prey.

Finally, to encode all the density dependence in the stock-recruitment relationship that is not already included in the other two sources of density dependence, mizer puts the the density-independent rate of egg production through a density-dependence function. The result is returned by `getRDD()`. The name of the density-dependence function is specified by the `RDD` argument. The default is the Beverton-Holt function `BevertonHoltRDD()`, which requires an `R_max` column in the species_params data frame giving the maximum egg production rate. If this column does not exist, it is initialised to `Inf`, leading to no density-dependence. Other functions provided by mizer are `RickerRDD()` and `SheperdRDD()` and you can easily use these as models for writing your own functions.

See Also

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setResource()`, `setSearchVolume()`, `species_params()`

Examples

```
# Plot maturity and reproduction ogives for Cod in North Sea model
maturity <- getMaturityProportion(NS_params)["Cod", ]
repro_prop <- getReproductionProportion(NS_params)["Cod", ]
df <- data.frame(Size = w(NS_params),
                 Reproduction = repro_prop,
                 Maturity = maturity,
                 Total = maturity * repro_prop)
```

```
dff <- melt(df, id.vars = "Size",
            variable.name = "Type",
            value.name = "Proportion")
library(ggplot2)
ggplot(dff) + geom_line(aes(x = Size, y = Proportion, colour = Type))
```

---

setResource *Set up resource*

Description

Sets the intrinsic resource growth rate and the intrinsic resource carrying capacity as well as the name of the function used to simulate the resource dynamics

Usage

```
setResource(
  params,
  resource_rate = NULL,
  resource_capacity = NULL,
  reset = FALSE,
  r_pp = resource_params(params)[["r_pp"]],
  kappa = resource_params(params)[["kappa"]],
  lambda = resource_params(params)[["lambda"]],
  n = resource_params(params)[["n"]],
  w_pp_cutoff = resource_params(params)[["w_pp_cutoff"]],
  resource_dynamics = NULL,
  ...
)

getResourceRate(params)

resource_rate(params)

resource_rate(params) <- value

getResourceCapacity(params)

resource_capacity(params)

resource_capacity(params) <- value

getResourceDynamics(params)

resource_dynamics(params)

resource_dynamics(params) <- value
```

Arguments

params	A MizerParams object
resource_rate	Optional. Vector of resource intrinsic birth rates
resource_capacity	Optional. Vector of resource intrinsic carrying capacity
reset	**[Experimental]** If set to TRUE, then both resource_rate and resource_capacity will be reset to the value calculated from the resource parameters, even if they were previously overwritten with custom values. If set to FALSE (default) then a recalculation from the resource parameters will take place only if no custom values have been set.
r_pp	Coefficient of the intrinsic resource birth rate
kappa	Coefficient of the intrinsic resource carrying capacity
lambda	Scaling exponent of the intrinsic resource carrying capacity
n	Allometric growth exponent for resource
w_pp_cutoff	The upper cut off size of the resource spectrum. The carrying capacity will be set to 0 above this size. Default is 10 g.
resource_dynamics	Optional. Name of the function that determines the resource dynamics by calculating the resource spectrum at the next time step from the current state. You only need to specify this if you do not want to use the default resource_semichemostat().
...	Unused
value	.

Value

setResource: A MizerParams object with updated resource parameters

Setting resource dynamics

By default, mizer uses a semichemostat model to describe the resource dynamics in each size class independently. This semichemostat dynamics is implemented by the function resource_semichemostat(). You can change the resource dynamics by writing your own function, modelled on resource_semichemostat(), and then passing the name of your function in the resource_dynamics argument.

The resource_rate argument is a vector specifying the intrinsic resource growth rate for each size class. If it is not supplied, then the intrinsic growth rate $r(w)$ at size w is set to

$$r(w) = r_{pp}\, w^{n-1}.$$

The values of r_{pp} and n are taken from the r_pp and n arguments.

The resource_capacity argument is a vector specifying the intrinsic resource carrying capacity for each size class. If it is not supplied, then the intrinsic carrying capacity $c(w)$ at size w is set to

$$c(w) = \kappa\, w^{-\lambda}$$

for all w less than w_pp_cutoff and zero for larger sizes. The values of κ and λ are taken from the kappa and lambda arguments.

See Also

resource_params()

Other functions for setting parameters: gear_params(), resource_params(), setExtMort(), setFishing(), setInitialValues(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setParams(), setPredKernel(), setReproduction(), setSearchVolume(), species_params()

---

setRmax *Alias for* setBevertonHolt()

Description

[Deprecated]

An alias provided for backward compatibility with mizer version <= 2.0.4

Usage

```
setRmax(params, R_factor = deprecated(), erepro, R_max, reproduction_level)
```

Arguments

params	A MizerParams object
R_factor	**[Deprecated]** Use reproduction_level = 1 / R_factor instead.
erepro	Reproductive efficiency for each species. See details.
R_max	Maximum reproduction rate. See details.
reproduction_level	Sets R_max so that the reproduction rate at the initial state is R_max * reproduction_level.

Details

With Beverton-Holt density dependence the relation between the energy invested into reproduction and the number of eggs hatched is determined by two parameters: the reproductive efficiency erepro and the maximum reproduction rate R_max.

If no maximum is imposed on the reproduction rate ($R_{max} = \infty$) then the resulting density-independent reproduction rate R_{di} is proportional to the total rate E_R at which energy is invested into reproduction,

$$R_{di} = \frac{\text{erepro}}{2w_{min}} E_R,$$

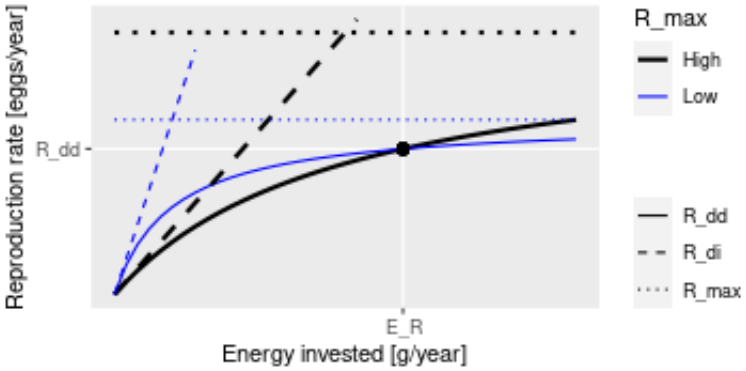
where the proportionality factor is given by the reproductive efficiency erepro divided by the egg size w_min to convert energy to egg number and divided by 2 to account for the two sexes.

Imposing a finite maximum reproduction rate R_{max} leads to a non-linear relationship between energy invested and eggs hatched. This density-dependent reproduction rate R_{dd} is given as

$$R_{dd} = R_{di} \frac{R_{max}}{R_{di} + R_{max}}.$$

(All quantities in the above equations are species-specific but we dropped the species index for simplicity.)

The following plot illustrates the Beverton-Holt density dependence in the reproduction rate for two different choices of parameters.



This plot shows that a given energy E_R invested into reproduction can lead to the same reproduction rate R_{dd} with different choices of the parameters `R_max` and `erepro`. `R_max` determines the asymptote of the curve and `erepro` its initial slope. A higher `R_max` coupled with a lower `erepro` (black curves) can give the same value as a lower `R_max` coupled with a higher `erepro` (blue curves).

For the given initial state in the MizerParams object `params` one can calculate the energy E_R that is invested into reproduction by the mature individuals and the reproduction rate R_{dd} that is required to keep the egg abundance constant. These two values determine the location of the black dot in the above graph. You then only need one parameter to select one curve from the family of Beverton-Holt curves going through that point. This parameter can be `erepro` or `R_max`. Instead of `R_max` you can alternatively specify the `reproduction_level` which is the ratio between the density-dependent reproduction rate R_{dd} and the maximal reproduction rate R_{max}.

If you do not provide a value for any of the reproduction parameter arguments, then `erepro` will be set to the value it has in the current species parameter data frame. If you do provide one of the reproduction parameters, this can be either a vector with one value for each species, or a named vector where the names determine which species are affected, or a single unnamed value that is then used for all species. Any species for which the given value is `NA` will remain unaffected.

The values for `R_max` must be larger than R_{dd} and can range up to `Inf`. If a smaller value is requested a warning is issued and the value is increased to the value required for a reproduction level of 0.99.

The values for the `reproduction_level` must be positive and less than 1. The values for `erepro` must be large enough to allow the required reproduction rate. If a smaller value is requested a warning is issued and the value is increased to the smallest possible value. The values for `erepro` should also be smaller than 1 to be physiologically sensible, but this is not enforced by the function.

As can be seen in the graph above, choosing a lower value for `R_max` or a higher value for `erepro` means that near the steady state the reproduction will be less sensitive to a change in the energy invested into reproduction and hence less sensitive to changes in the spawning stock biomass or its energy income. As a result the species will also be less sensitive to fishing, leading to a higher F_MSY.

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$erepro
# Attempting to set the same erepro for all species
params <- setBevertonHolt(params, erepro = 0.1)
t(species_params(params)[, c("erepro", "R_max")])
# Setting erepro for some species
params <- setBevertonHolt(params, erepro = c("Gurnard" = 0.6, "Plaice" = 0.95))
t(species_params(params)[, c("erepro", "R_max")])
# Setting R_max
R_max <- 1e17 * species_params(params)$w_inf^-1
params <- setBevertonHolt(NS_params, R_max = R_max)
t(species_params(params)[, c("erepro", "R_max")])
# Setting reproduction_level
params <- setBevertonHolt(params, reproduction_level = 0.3)
t(species_params(params)[, c("erepro", "R_max")])
```

---

setSearchVolume *Set search volume*

Description

Set search volume

Usage

```
setSearchVolume(params, search_vol = NULL, reset = FALSE, ...)

getSearchVolume(params)

search_vol(params)

search_vol(params) <- value
```

Arguments

params	MizerParams
search_vol	Optional. An array (species x size) holding the search volume for each species at size. If not supplied, a default is set as described in the section "Setting search volume".
reset	**[Experimental]** If set to TRUE, then the search volume will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
...	Unused
value	search_vol

Value

`setSearchVolume()`: A MizerParams object with updated search volume.

`getSearchVolume()` or equivalently `search_vol()`: An array (species x size) holding the search volume

Setting search volume

The search volume $\gamma_i(w)$ of an individual of species i and weight w multiplies the predation kernel when calculating the encounter rate in `getEncounter()` and the predation rate in `getPredRate()`.

The name "search volume" is a bit misleading, because $\gamma_i(w)$ does not have units of volume. It is simply a parameter that determines the rate of predation. Its units depend on your choice, see section "Units in mizer". If you have chosen to work with total abundances, then it is a rate with units 1/year. If you have chosen to work with abundances per m^2 then it has units of m^2/year. If you have chosen to work with abundances per m^3 then it has units of m^3/year.

If the `search_vol` argument is not supplied, then the search volume is set to

$$\gamma_i(w) = \gamma_i w_i^q.$$

The values of γ_i (the search volume at 1g) and q_i (the allometric exponent of the search volume) are taken from the `gamma` and `q` columns in the species parameter dataframe. If the `gamma` column is not supplied in the species parameter dataframe, a default is calculated by the `get_gamma_default()` function. Note that only for predators of size $w = 1$ gram is the value of the species parameter γ_i the same as the value of the search volume $\gamma_i(w)$.

See Also

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `species_params()`

---

set_community_model *Deprecated function for setting up parameters for a community-type model*

Description

[Deprecated]

This function has been deprecated in favour of the function `newCommunityParams()` that sets better default values.

Usage

```
set_community_model(
  max_w = 1e+06,
  min_w = 0.001,
  min_w_pp = 1e-10,
```

```
  z0 = 0.1,
  alpha = 0.2,
  h = 10,
  beta = 100,
  sigma = 2,
  q = 0.8,
  n = 2/3,
  kappa = 1000,
  lambda = 2 + q - n,
  f0 = 0.7,
  r_pp = 10,
  gamma = NA,
  knife_edge_size = 1000,
  knife_is_min = TRUE,
  recruitment = kappa * min_w^-lambda,
  rec_mult = 1,
  ...
)
```

Arguments

max_w	The maximum size of the community. The w_inf of the species used to represent the community is set to this value. The default value is 1e6.
min_w	The minimum size of the community. Default value is 1e-3.
min_w_pp	The smallest size of the resource spectrum.
z0	The background mortality of the community. Default value is 0.1.
alpha	The assimilation efficiency of the community. Default value 0.2
h	The maximum food intake rate. Default value is 10.
beta	The preferred predator prey mass ratio. Default value is 100.
sigma	The width of the prey preference. Default value is 2.0.
q	The search volume exponent. Default value is 0.8.
n	The scaling of the intake. Default value is 2/3.
kappa	The carrying capacity of the resource spectrum. Default value is 1000.
lambda	The exponent of the resource spectrum. Default value is 2 + q - n.
f0	The average feeding level of individuals who feed on a power-law spectrum. This value is used to calculate the search rate parameter gamma (see the package vignette). Default value is 0.7.
r_pp	Growth rate parameter for the resource spectrum. Default value is 10.
gamma	Volumetric search rate. Estimated using h, f0 and kappa if not supplied.
knife_edge_size	The size at the edge of the knife-selectivity function. Default value is 1000.
knife_is_min	Is the knife-edge selectivity function selecting above (TRUE) or below (FALSE) the edge. Default is TRUE.

recruitment	The constant recruitment in the smallest size class of the community spectrum. This should be set so that the community spectrum continues the resource spectrum. Default value = kappa * min_w^-lambda.
rec_mult	Additional multiplier for the constant recruitment. Default value is 1.
...	Other arguments to pass to the MizerParams constructor.

Details

This functions creates a MizerParams object so that community-type models can be easily set up and run. A community model has several features that distinguish it from the food-web type models. Only one 'species' is resolved, i.e. one 'species' is used to represent the whole community. The resource spectrum only extends to the start of the community spectrum. Recruitment to the smallest size in the community spectrum is constant and set by the user. As recruitment is constant, the proportion of energy invested in reproduction (the slot psi of the returned MizerParams object) is set to 0. Standard metabolism has been turned off (the parameter ks is set to 0). Consequently, the growth rate is now determined solely by the assimilated food (see the package vignette for more details).

The function has many arguments, all of which have default values. The main arguments that the users should be concerned with are z0, recruitment, alpha and f0 as these determine the average growth rate of the community.

Fishing selectivity is modelled as a knife-edge function with one parameter, knife_edge_size, which determines the size at which species are selected.

The resulting MizerParams object can be projected forward using project() like any other MizerParams object. When projecting the community model it may be necessary to keep a small time step size dt of around 0.1 to avoid any instabilities with the solver. You can check for these numerical instabilities by plotting the biomass or abundance through time after the projection.

Value

An object of type MizerParams

References

K. H. Andersen,J. E. Beyer and P. Lundberg, 2009, Trophic and individual efficiencies of size-structured communities, Proceedings of the Royal Society, 276, 109-114

Examples

```
## Not run:
params <- set_community_model(f0=0.7, z0=0.2, recruitment=3e7)
# This is now achieved with
params <- newCommunityParams(f0 = 0.7, z0 = 0.2)
sim <- project(params, effort = 0, t_max = 100, dt=0.1)
plotBiomass(sim)
plotSpectra(sim)

## End(Not run)
```

`set_multispecies_model` *Deprecated obsolete function for setting up multispecies parameters*

Description

[Deprecated]

This function has been deprecated in favour of the function `newMultispeciesParams()` that sets better default values.

Usage

```
set_multispecies_model(
  species_params,
 interaction = matrix(1, nrow = nrow(species_params), ncol = nrow(species_params)),
  min_w_pp = 1e-10,
  min_w = 0.001,
  max_w = max(species_params$w_inf) * 1.1,
  no_w = 100,
  n = 2/3,
  q = 0.8,
  f0 = 0.6,
  kappa = 1e+11,
  lambda = 2 + q - n,
  r_pp = 10,
  ...
)
```

Arguments

`species_params`	A data frame of species-specific parameter values.
`interaction`	Optional interaction matrix of the species (predator species x prey species). Entries should be numbers between 0 and 1. By default all entries are 1. See "Setting interaction matrix" section below.
`min_w_pp`	The smallest size of the resource spectrum. By default this is set to the smallest value at which any of the consumers can feed.
`min_w`	Sets the size of the eggs of all species for which this is not given in the `w_min` column of the `species_params` dataframe.
`max_w`	The largest size of the consumer spectrum. By default this is set to the largest `w_inf` specified in the `species_params` data frame.
`no_w`	The number of size bins in the consumer spectrum.
`n`	The allometric growth exponent. This can be overruled for individual species by including a `n` column in the `species_params`.
`q`	Allometric exponent of search volume

f0	Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.
kappa	Coefficient of the intrinsic resource carrying capacity
lambda	Scaling exponent of the intrinsic resource carrying capacity
r_pp	Coefficient of the intrinsic resource birth rate
...	Unused

`set_species_param_default` *Set a species parameter to a default value*

Description

If the species parameter does not yet exist in the species parameter data frame, then create it and fill it with the default. Otherwise use the default only to fill in any NAs. Optionally gives a message if the parameter did not already exist.

Usage

```
set_species_param_default(object, parname, default, message = NULL)
```

Arguments

object	Either a MizerParams object or a species parameter data frame
parname	A string with the name of the species parameter to set
default	A single default value or a vector with one default value for each species
message	A string with a message to be issued when the parameter did not already exist

Value

The object with an updated column in the species params data frame.

`set_trait_model` *Deprecated function for setting up parameters for a trait-based model*

Description

[Deprecated]

This function has been deprecated in favour of the function `newTraitParams()` that sets better default values.

Usage

```
set_trait_model(
  no_sp = 10,
  min_w_inf = 10,
  max_w_inf = 1e+05,
  no_w = 100,
  min_w = 0.001,
  max_w = max_w_inf * 1.1,
  min_w_pp = 1e-10,
  w_pp_cutoff = 1,
  k0 = 50,
  n = 2/3,
  p = 0.75,
  q = 0.9,
  eta = 0.25,
  r_pp = 4,
  kappa = 0.005,
  lambda = 2 + q - n,
  alpha = 0.6,
  ks = 4,
  z0pre = 0.6,
  h = 30,
  beta = 100,
  sigma = 1.3,
  f0 = 0.5,
  gamma = NA,
  knife_edge_size = 1000,
  gear_names = "knife_edge_gear",
  ...
)
```

Arguments

no_sp	The number of species in the model. The default value is 10. The more species, the longer takes to run.
min_w_inf	The asymptotic size of the smallest species in the community.
max_w_inf	The asymptotic size of the largest species in the community.
no_w	The number of size bins in the community spectrum.
min_w	The smallest size of the community spectrum.
max_w	Obsolete argument because the maximum size of the consumer spectrum is set to max_w_inf.
min_w_pp	Obsolete argument because the smallest resource size is set to the smallest size at which the consumers feed.
w_pp_cutoff	The cut off size of the resource spectrum. Default value is 1.
k0	Multiplier for the maximum recruitment. Default value is 50.
n	Scaling of the intake. Default value is 2/3.

p	Scaling of the standard metabolism. Default value is 0.75.
q	Exponent of the search volume. Default value is 0.9.
eta	Factor to calculate w_mat from asymptotic size.
r_pp	Growth rate parameter for the resource spectrum. Default value is 4.
kappa	Coefficient in abundance power law. Default value is 0.005.
lambda	Exponent of the abundance power law. Default value is (2+q-n).
alpha	The assimilation efficiency of the community. The default value is 0.6
ks	Standard metabolism coefficient. Default value is 4.
z0pre	The coefficient of the background mortality of the community. z0 = z0pre * w_inf ^ (n-1). The default value is 0.6.
h	Maximum food intake rate. Default value is 30.
beta	Preferred predator prey mass ratio. Default value is 100.
sigma	Width of prey size preference. Default value is 1.3.
f0	Expected average feeding level. Used to set gamma, the factor for the search volume. The default value is 0.5.
gamma	Volumetric search rate. Estimated using h, f0 and kappa if not supplied.
knife_edge_size	The minimum size at which the gear or gears select species. Must be of length 1 or no_sp.
gear_names	The names of the fishing gears. A character vector, the same length as the number of species. Default is 1 - no_sp.
...	Other arguments to pass to the MizerParams constructor.

Details

This functions creates a MizerParams object so that trait-based-type models can be easily set up and run. The trait-based size spectrum model can be derived as a simplification of the general size-based model used in mizer. The species-specific parameters are the same for all species, except for the asymptotic size, which is considered the most important trait characterizing a species. Other parameters are related to the asymptotic size. For example, the size at maturity is given by w_inf * eta, where eta is the same for all species. For the trait-based model the number of species is not important. For applications of the trait-based model see Andersen & Pedersen (2010). See the mizer vignette for more details and examples of the trait-based model.

The function has many arguments, all of which have default values. Of particular interest to the user are the number of species in the model and the minimum and maximum asymptotic sizes. The asymptotic sizes of the species are spread evenly on a logarithmic scale within this range.

The stock recruitment relationship is the default Beverton-Holt style. The maximum recruitment is calculated using equilibrium theory (see Andersen & Pedersen, 2010) and a multiplier, k0. Users should adjust k0 to get the spectra they want.

The factor for the search volume, gamma, is calculated using the expected feeding level, f0.

Fishing selectivity is modelled as a knife-edge function with one parameter, knife_edge_size, which is the size at which species are selected. Each species can either be fished by the same gear (knife_edge_size has a length of 1) or by a different gear (the length of knife_edge_size has

the same length as the number of species and the order of selectivity size is that of the asymptotic size).

The resulting `MizerParams` object can be projected forward using `project` like any other `MizerParams` object. When projecting the community model it may be necessary to reduce `dt` to 0.1 to avoid any instabilities with the solver. You can check this by plotting the biomass or abundance through time after the projection.

Value

An object of type `MizerParams`

References

K. H. Andersen and M. Pedersen, 2010, Damped trophic cascades driven by fishing in model marine ecosystems. Proceedings of the Royal Society V, Biological Sciences, 1682, 795-802.

`SheperdRDD` *Sheperd function to calculate density-dependent reproduction rate*

Description

[Experimental] Takes the density-independent rates R_{di} of egg production and returns reduced, density-dependent rates R_{dd} given as

$$R_{dd} = \frac{R_{di}}{1 + (b\, R_{di})^c}$$

Usage

```
SheperdRDD(rdi, species_params, ...)
```

Arguments

`rdi`	Vector of density-independent reproduction rates R_{di} for all species.
`species_params`	A species parameter dataframe. Must contain columns `sheperd_b` and `sheperd_c` with the parameters b and c.
`...`	Unused

Value

Vector of density-dependent reproduction rates.

See Also

Other functions calculating density-dependent reproduction rate: `BevertonHoltRDD()`, `RickerRDD()`, `constantEggRDI()`, `constantRDD()`, `noRDD()`

sigmoid_length *Length based sigmoid selectivity function*

Description

A sigmoid shaped selectivity function. Based on two parameters `l25` and `l50` which determine the length at which 25% and 50% of the stock is selected respectively. As the size-based model is weight based, and this selectivity function is length based, it uses the length-weight parameters `a` and `b` to convert between length and weight.

Usage

```
sigmoid_length(w, l25, l50, species_params, ...)
```

Arguments

`w`	the size of the individual.
`l25`	the length which gives a selectivity of 25%.
`l50`	the length which gives a selectivity of 50%.
`species_params`	A list with the species params for the current species. Used to get at the length-weight parameters `a` and `b`
`...`	Unused

sigmoid_weight *Weight based sigmoidal selectivity function*

Description

A sigmoidal selectivity function with 50% selectivity at weight `sigmoidal_weight` and width `sigmoidal_sigma`.

Usage

```
sigmoid_weight(w, sigmoidal_weight, sigmoidal_sigma, ...)
```

Arguments

`w`	The size of the individual.
`sigmoidal_weight`	The weight at which the knife-edge operates.
`sigmoidal_sigma`	The width of the selection function
`...`	Unused

species_params *Species parameters*

Description

These functions allow you to get or set the species parameters stored in a MizerParams object.

Usage

```
species_params(params)

species_params(params) <- value
```

Arguments

params	A MizerParams object
value	A data frame with the species parameters

Details

The species_params data frame holds species-specific parameters. The data frame has one row for each species and one column for each species parameter. There are a lot of species parameters and we will list them all below, but most of them have sensible default values. The only required columns are species for the species name and w_inf for its asymptotic size. However if you have information about the values of other parameters then you should include them in the species_params data frame.

Species parameters for setting up size-dependent parameters:

There are some species parameters that are used to set up the size-dependent parameters that are used in the mizer model:

- gamma and q are used to set the search volume, see setSearchVolume().
- h and n are used to set the maximum intake rate, see setMaxIntakeRate().
- k, ks and p are used to set activity and basic metabolic rate, see setMetabolicRate().
- z0 is used to set the external mortality rate, see setExtMort().
- w_mat, w_mat25, w_inf and m are used to set the allocation to reproduction, see setReproduction().
- pred_kernel_type specifies the shape of the predation kernel. The default is a "lognormal", for other options see the "Setting predation kernel" section in the help for setPredKernel().
- beta and sigma are parameters of the lognormal predation kernel, see lognormal_pred_kernel(). There will be other parameters if you are using other predation kernel functions.

When you change one of the above species parameters in an already existing MizerParams object using species_params<-(), the new value will be used to update the corresponding size-dependent rates automatically, unless you have set those size-dependent rates manually, in which case the corresponding species parameters will be ignored.

Species parameters used in model directly:

There are some species parameters that are used directly in the model rather than being used for setting up size-dependent parameters:

- `alpha` is the assimilation efficiency, the proportion of the consumed biomass that can be used for growth, metabolism and reproduction, see the help for `getEReproAndGrowth()`.
- `w_min` is the egg size.
- `interaction_resource` sets the interaction strength with the resource, see "Predation encounter" section in the help for `getEncounter()`.
- `erepro` is the reproductive efficiency, the proportion of the energy invested into reproduction that is converted to egg biomass, see `getRDI()`.
- `Rmax` is the parameter in the Beverton-Holt density dependence added to the reproduction, see `setBevertonHolt()`. There will be other such parameters if you use other density dependence functions, see the "Density dependence" section in the help for `setReproduction()`.

Two parameters are used only by functions that need to convert between weight and length:

- `a` and `b` are the parameters in the allometric weight-length relationship $w = al^b$.

Species parameters to calculate defaults for others:

Not all of species parameters have to be specified by the user. If they are missing, `newMultispeciesParams()` will give them default values, sometimes by using other species parameters. The parameters that are only used to calculate default values for other parameters are:

- `k_vb` and `t0` are the von Bertalanffy growth parameters and are used together with the length-weight relationship exponent `b` and the egg size `w_min` to get a default value for the coefficient of the maximum intake rate `h`, see `get_h_default()`.
- `f0` is the feeding level and is used to get a default value for the coefficient of the search volume `gamma`, see `get_gamma_default()`.
- `fc` is the critical feeding level below which the species can not maintain itself. This is used to get a default value for the coefficient of the metabolic rate `ks`, see `get_ks_default()`.

Note that these parameters will only be used when setting up a new model with `newMultispeciesParams()`. Changing them later will have no effect because the default for the other parameters will not be recalculated.

Species parameters containing observations:

There are other species parameters that are used in tuning the model to observations:

- `biomass_observed` and `biomass_cutoff` allow you to specify for each species the total observed biomass above some cutoff size. This is used by `calibrateBiomass()` and `matchBiomasses()`.
- `yield_observed` allows you to specify for each species the total annual fisheries yield. This is used by `calibrateYield()` and `matchYields()`.

Species parameters influencing plots:

Finally there are two species parameters that control the way the species are represented in plots:

- `linecolour` specifies the colour and can be any valid R colour value.
- `linetype` specifies the line type ("solid", "dashed", "dotted", "dotdash", "longdash", "twodash" or "blank")

Species parameters related to fishing gears:

Other species-specific information that is related to how the species is fished is specified in a gear parameter data frame, see `gear_params()`. However in the case where each species is caught by only a single gear, this information can also optionally be provided as columns in the `species_params` data frame and `newMultispeciesParams()` will transfer them to the `gear_params` data frame. However changing these parameters later in the species parameter data frame will have no effect.

Your own species parameters:

You are allowed to include additional columns in the `species_params` data frame. They will simply be ignored by mizer but will be stored in the MizerParams object, in case your own code makes use of them.

See Also

`validSpeciesParams()`

Other functions for setting parameters: `gear_params()`, `resource_params()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setResource()`, `setSearchVolume()`

`steady` *Set initial values to a steady state for the model*

Description

The steady state is found by running the dynamics while keeping reproduction and other components constant until the size spectra no longer change much (or until time `t_max` is reached, if earlier). Then the reproduction parameters are set to values that give the level of reproduction observed in that steady state.

Usage

```
steady(
  params,
  t_max = 100,
  t_per = 1.5,
  dt = 0.1,
  tol = 0.1 * dt,
  return_sim = FALSE,
  preserve = c("reproduction_level", "erepro", "R_max"),
  progress_bar = TRUE
)
```

Arguments

params	A MizerParams object
t_max	The maximum number of years to run the simulation. Default is 100.
t_per	The simulation is broken up into shorter runs of t_per years, after each of which we check for convergence. Default value is 1.5. This should be chosen as an odd multiple of the timestep dt in order to be able to detect period 2 cycles.
dt	The time step to use in project().
tol	The simulation stops when the relative change in the egg production RDI over t_per years is less than tol for every species.
return_sim	If TRUE, the function returns the MizerSim object holding the result of the simulation run. If FALSE (default) the function returns a MizerParams object with the "initial" slots set to the steady state.
preserve	**[Experimental]** Specifies whether the reproduction_level should be preserved (default) or the maximum reproduction rate R_max or the reproductive efficiency erepro. See setBevertonHolt() for an explanation of the reproduction_level.
progress_bar	A shiny progress object to implement a progress bar in a shiny app. Default FALSE.

Examples

```
## Not run:
params <- newTraitParams()
species_params(params)$gamma[5] <- 3000
params <- steady(params)
plotSpectra(params)

## End(Not run)
```

---

summary,MizerParams-method

Summarize MizerParams object

Description

Outputs a general summary of the structure and content of the object

Usage

```
## S4 method for signature 'MizerParams'
summary(object, ...)
```

Arguments

object	A MizerParams object.
...	Other arguments (currently not used).

Examples

```
summary(NS_params)
```

---

summary,MizerSim-method *Summarize MizerSim object*

Description

Outputs a general summary of the structure and content of the object

Usage

```
## S4 method for signature 'MizerSim'
summary(object, ...)
```

Arguments

object	A MizerSim object.
...	Other arguments (currently not used).

Examples

```
summary(NS_sim)
```

---

summary_functions *Description of summary functions*

Description

Mizer provides a range of functions to summarise the results of a simulation.

Details

A list of available summary functions is given in the table below.

Function	Returns	Description
getDiet()	Three dimensional array (predator x size x prey)	Diet of predator at size, resolved by prey speci
getSSB()	Two dimensional array (time x species)	Total Spawning Stock Biomass (SSB) of each
getBiomass()	Two dimensional array (time x species)	Total biomass of each species through time.
getN()	Two dimensional array (time x species)	Total abundance of each species through time.
getFeedingLevel()	Three dimensional array (time x species x size)	Feeding level of each species by size through t
getM2	Three dimensional array (time x species x size)	The predation mortality imposed on each spec
getFMort()	Three dimensional array (time x species x size)	Total fishing mortality on each species by size
getFMortGear()	Four dimensional array (time x gear x species x size)	Fishing mortality on each species by each gea
getYieldGear()	Three dimensional array (time x gear x species)	Total yield by gear and species through time.
getYield()	Two dimensional array (time x species)	Total yield of each species across all gears thr

See Also

indicator_functions, plotting_functions

`truncated_lognormal_pred_kernel`
Truncated lognormal predation kernel

Description

This is like the `lognormal_pred_kernel()` but with an imposed maximum predator/prey mass ratio

Usage

```
truncated_lognormal_pred_kernel(ppmr, beta, sigma)
```

Arguments

`ppmr`	A vector of predator/prey size ratios
`beta`	The preferred predator/prey size ratio
`sigma`	The width parameter of the log-normal kernel

Details

Writing the predator mass as w and the prey mass as w_p, the feeding kernel is given as

$$\phi_i(w, w_p) = \exp\left[\frac{-(\ln(w/w_p/\beta_i))^2}{2\sigma_i^2}\right]$$

if w/w_p is between 1 and $\beta_i \exp(3\sigma_i)$ and zero otherwise. Here β_i is the preferred predator-prey mass ratio and σ_i determines the width of the kernel. These two parameters need to be given in the species parameter dataframe in the columns `beta` and `sigma`.

This function is called from `setPredKernel()` to set up the predation kernel slots in a MizerParams object.

Value

A vector giving the value of the predation kernel at each of the predator/prey mass ratios in the `ppmr` argument.

upgradeParams *Upgrade MizerParams object from earlier mizer versions*

Description

Occasionally during the development of new features for mizer, the MizerParams object gains extra slots. MizerParams objects created in older versions of mizer are then no longer valid in the new version because of the missing slots. You need to upgrade them with

```
params <- upgradeParams(params)
```

where `params` should be replaced by the name of your MizerParams object. This function adds the missing slots and fills them with default values. Any object from version 0.4 onwards can be upgraded. Any old MizerSim objects should be similarly updated with `upgradeSim()`. This function uses `newMultispeciesParams()` to create a new MizerParams object using the parameters extracted from the old MizerParams object.

Usage

```
upgradeParams(params)
```

Arguments

`params`	An old MizerParams object to be upgraded

Value

The upgraded MizerParams object

Backwards compatibility

The internal numerics in mizer have changed over time, so there may be small discrepancies between the results obtained with the upgraded object in the new version and the original object in the old version. If it is important for you to reproduce the exact results then you should install the version of mizer with which you obtained the results. You can do this with

```
remotes::install_github("sizespectrum/mizer", ref = "v0.2")
```

where you should replace "v0.2" with the version number you require. You can see the list of available releases at https://github.com/sizespectrum/mizer/tags.

If you only have a serialised version of the old object, for example created via `saveRDS()`, and you get an error when trying to read it in with `readRDS()` then unfortunately you will need to install the old version of mizer first to read the params object into your workspace, then switch to the current version and then call `upgradeParams()`. You can then save the new version again with `saveRDS()`.

See Also

`validParams()`

`upgradeSim` *Upgrade MizerSim object from earlier mizer versions*

Description

Occasionally, during the development of new features for mizer, the MizerSim class or the MizerParams class gains extra slots. MizerSim objects created in older versions of mizer are then no longer valid in the new version because of the missing slots. You need to upgrade them with

```
sim <- upgradeSim(sim)
```

where `sim` should be replaced by the name of your MizerSim object.

Usage

```
upgradeSim(sim)
```

Arguments

`sim`	An old MizerSim object to be upgraded

Details

This function adds the missing slots and fills them with default values. It calls `upgradeParams()` to upgrade the MizerParams object inside the MizerSim object. Any object from version 0.4 onwards can be upgraded.

Value

The upgraded MizerSim object

Backwards compatibility

The internal numerics in mizer have changed over time, so there may be small discrepancies between the results obtained with the upgraded object in the new version and the original object in the old version. If it is important for you to reproduce the exact results then you should install the version of mizer with which you obtained the results. You can do this with

```
remotes::install_github("sizespectrum/mizer", ref = "v0.2")
```

where you should replace "v0.2" with the version number you require. You can see the list of available releases at https://github.com/sizespectrum/mizer/tags.

If you only have a serialised version of the old object, for example created via `saveRDS()`, and you get an error when trying to read it in with `readRDS()` then unfortunately you will need to install the old version of mizer first to read the params object into your workspace, then switch to the current version and then call `upgradeParams()`. You can then save the new version again with `saveRDS()`.

validGearParams *Check validity of gear parameters and set defaults*

Description

The function returns a valid gear parameter data frame that can be used by `setFishing()` or it gives an error message.

Usage

```
validGearParams(gear_params, species_params)
```

Arguments

`gear_params`	Gear parameter data frame
`species_params`	Species parameter data frame

Details

The gear_params data frame is allowed to have zero rows, but if it has rows, then the following requirements apply:

- There must be columns `species` and `gear` and any species - gear pair is allowed to appear at most once. Any species that appears must also appear in the `species_params` data frame.
- There must be a `sel_func` column. If a selectivity function is not supplied, it will be set to "knife_edge".
- There must be a `catchability` column. If a catchability is not supplied, it will be set to 1.
- All the parameters required by the selectivity functions must be provided.

If gear_params is empty, then this function tries to find the necessary information in the species_params data frame. This restricts each species to be fished by only one gear. Defaults are used for information that can not be found in the species_params dataframe, as follows:

- If there is no `gear` column or it is NA then a new gear named after the species is introduced.
- If there is no `sel_func` column or it is NA then `knife_edge` is used.
- If there is no `catchability` column or it is NA then this is set to 1.
- If the selectivity function is `knife_edge` and no `knife_edge_size` is provided, it is set to `w_mat`.

The row names of the returned data frame are of the form "species, gear".

For backwards compatibility, when `gear_params` is `NULL` and there is no gear information in `species_params`, then a gear called `knife_edge_gear` is set up with a `knife_edge` selectivity for each species and a `knive_edge_size` equal to `w_mat`. Catchability is set to 1 for all species.

Value

A valid gear parameter data frame

See Also

gear_params()

---

validParams *Validate MizerParams object and upgrade if necessary*

Description

Validate MizerParams object and upgrade if necessary

Usage

```
validParams(params)
```

Arguments

params	The MizerParams object to validate

Value

A valid MizerParams object

---

validSpeciesParams *Validate species parameter data frame*

Description

Check validity of species parameters and set defaults for missing but required parameters

Usage

```
validSpeciesParams(species_params)
```

Arguments

species_params	The user-supplied species parameter data frame

Value

A valid species parameter data frame

This function throws an error if

- the `species` column does not exist or contains duplicates
- the `w_inf` column does not exist or contains NAs or is not numeric

It sets default values if any of the following are missing or NA

- `w_mat` is set to `w_inf/4`
- `w_min` is set to `0.001`
- `alpha` is set to `0.6`
- `interaction_resource` is set to `1`

Any `w_mat` that is given that is not smaller than `w_inf` is set to `w_inf / 4`.

Any `w_mat25` that is given that is not smaller than `w_mat` is set to `w_mat * 3^(-0.1)`.

The row names of the returned data frame will be the species names. If `species_params` was provided as a tibble it is converted back to an ordinary data frame.

---

valid_species_arg *Helper function to assure validity of species argument*

Description

If the species argument contains invalid species, then these are ignored but a warning is issued.

Usage

```
valid_species_arg(object, species = NULL, return.logical = FALSE)
```

Arguments

`object`	A MizerSim or MizerParams object from which the species should be selected.
`species`	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
`return.logical`	Whether the return value should be a logical vector. Default FALSE.

Value

A vector of species names, in the same order as specified in the 'species' argument. If 'return.logical = TRUE' then a logical vector is returned instead, with length equal to the number of species, with TRUE entry for each selected species.

w *Size bins*

Description

Functions to fetch information about the size bins used in the model described by `params`.

Usage

```
w(params)

w_full(params)

dw(params)

dw_full(params)
```

Arguments

`params`	A MizerParams object

Details

To represent the continuous size spectrum in the computer, the size variable is discretized into a vector `w` of discrete weights, providing a grid of sizes spanning the range from the smallest egg size to the largest asymptotic size. These grid values divide the full size range into a finite number of size bins. The size bins should be chosen small enough to avoid the discretisation errors from becoming too big. You can fetch this vector with `w()` and the vector of bin widths with `dw()`.

The weight grid is set up to be logarithmically spaced, so that `w[j]=w[1]*10^(j*dx)` for some fixed `dx`. This means that the bin widths increase with size: `dw[j] = w[j] * (10^dx -1)`. This grid is set up automatically when creating a MizerParams object.

Because the resource spectrum spans a larger range of sizes, these sizes are discretized into a different vector of weights `w_full`. This usually starts at a much smaller size than `w`, but also runs up to the same largest size, so that the last entries of `w_full` have to coincide with the entries of `w`. The logarithmic spacing for `w_full` is the same as that for `w`, so that again `w_full[j]=w_full[1]*10^(j*dx)`. The function `w_full()` gives the vector of sizes and `dw_full()` gives the vector of bin widths.

You will need these vectors when converting number densities to numbers. For example the size spectrum of a species is stored as a vector of values that represent the *density* of fish in each size bin rather than the *number* of fish. The number of fish in the size bin between `w[j]` and `w[j+1]=w[j]+dw[j]` is obtained as `N[j]*dw[j]`.

The vector `w` can be used for example to convert the number of individuals in a size bin into the biomass in the size bin. The biomass in the `j`th bin is `biomass[j] = N[j] * dw[j] * w[j]`.

Of course all these calculations with discrete sizes and size bins are only giving approximations to the continuous values, and these approximations get better the smaller the size bins are, i.e., the more size bins are used. However using more size bins also slows down the calculations, so there is a trade-off. This is why the functions setting up MizerParams objects allow you to choose the number of size bins `no_w`.

Value

w() returns a vector with the sizes at the start of each size bin of the consumer spectrum.

w_full() returns a vector with the sizes at the start of each size bin of the resource spectrum, which typically starts at smaller sizes than the consumer spectrum.

dw() returns a vector with the widths of the size bins of the consumer spectrum.

dw_full() returns a vector with the widths of the size bins of the resource spectrum.

Examples

```
str(w(NS_params))
str(dw(NS_params))
str(w_full(NS_params))
str(dw_full(NS_params))

# Calculating the biomass of Cod in each bin in the North Sea model
biomass <- initialN(NS_params)["Cod", ] * dw(NS_params) * w(NS_params)
# Summing to get total biomass
sum(biomass)
```

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