Package: mizer (via r-universe)

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Title Dynamic Multi-Species Size Spectrum Modelling

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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.

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'rate_functions.R' 'sim_rates.R' 'sizeIntegral.R'
'summary_methods.R' 'indicator_functions.R' 'plots.R'
'plotBiomassObservedVsModel.R' 'plotYieldObservedVsModel.R'
'animateSpectra.R' 'newMultispeciesParams.R'
'wrapper_functions.R' 'newSingleSpeciesParams.R' 'steady.R'
'steadyState.R' 'scanModel.R' 'scan_setters.R' 'plotYieldVsF.R'
'extension.R' 'data.R' 'RcppExports.R' 'deprecated.R'
'get_initial_n.R' 'compareParams.R' 'customFunction.R'
'manipulate_species.R' 'observations.R' 'calibrate.R'
'scaleRates.R' 'match.R' 'matchGrowth.R'
'steadySingleSpecies.R' 'steadyNewton.R' 'getSteadyResidual.R'
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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:
   - `newSingleSpeciesParams()`
   - `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.

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See Also

Useful links:

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

---

addPlot *Add lines to an existing plot*

Description

[Experimental] `addPlot()` adds another set of values to an existing ggplot, for example to compare the same rate before and after a model change. There are methods for all the mizer array classes. Each checks whether the existing plot uses a compatible x variable, and warns if the y variable or y-axis units appear to differ.

Usage

```
addPlot(
  plot,
  x,
  species = NULL,
  total = FALSE,
  background = TRUE,
  colour = NULL,
  linetype = "dashed",
  linewidth = 0.8,
  alpha = 1,
  ...
)
```

Arguments

`plot`	A ggplot2 object to which the new values should be added.
`x`	An object containing the values to add. Can be an `ArraySpeciesBySize`, `ArrayTimeBySpecies`, `ArrayTimeBySpeciesBySize`, `ArrayResourceBySize` or `ArrayTimeByResourceBySize` object.
`species`	Character vector of species to include. `NULL` (default) means all species. A resource array holds a single spectrum, so this argument is not used by the resource methods, which warn if it is set.
`total`	A boolean value that determines whether the total is plotted as well. The total is the total of everything the array holds, every species and every size, whatever is drawn. Default is `FALSE`. Not used by the resource methods, which warn if it is set.

background — A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE. Not used by the resource methods, which warn if it is set.

colour — Optional fixed colour for the added lines. If NULL, the species colours from the existing plot are used. Because a resource array is a single line whose "Resource" level may be missing from the existing plot's colour scale, the resource methods instead default to the fixed resource colour from getColours().

linetype — Optional fixed line type for the added lines. If NULL, the species line types from the existing plot are used.

linewidth — Width of the added lines.

alpha — Transparency of the added lines.

... — Further arguments used by only some of the methods:

For the ArraySpeciesBySize**,** ArrayTimeBySpeciesBySize**,** ArrayResourceBySize **and** ArrayTimeByResourceBySize **methods:**

wlim A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use NA to refer to the existing minimum or maximum.

For the ArraySpeciesBySize **and** ArrayTimeBySpeciesBySize **methods:**

all.sizes If FALSE (default), values outside a species' size range (w_min to w_max) are removed.

llim A numeric vector of length two providing lower and upper limits for the length (x) axis when size_axis = "l". Use NA to refer to the existing minimum or maximum.

size_axis Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship of each species, or of the resource, see resource_params().

per_log_size For an array that holds a density, whether to plot it per logarithmic size (TRUE) rather than per size (FALSE). The default, NULL, plots the density as it stands. Unlike size_axis this needs no weight-length relationship, so it is available for the resource classes too. An error for an array that does not hold a density.

For ArrayTimeBySpecies **methods:**

tlim A numeric vector of length two providing lower and upper limits for the time axis, e.g. c(1980, 2000). Use NA to apply no limit at that end. Default is c(NA, NA).

ylim A numeric vector of length two providing lower and upper limits for the value (y) axis.

For the ArrayTimeBySpeciesBySize **and** ArrayTimeByResourceBySize **methods:**

time The time to display. Default (NULL) is the final time step.

Value

A ggplot2 object.

See Also

Other plotting functions: animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
p <- plot(getEncounter(NS_params), species = "Cod")
addPlot(p, getEncounter(NS_params), species = "Cod")

pr <- plot(getResourceMort(NS_params))
addPlot(pr, getResourceMort(NS_params))
```

---

addSpecies *Add new species*

Description

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,
  steady = TRUE,
  info_level = default_info_level(),
  ...
)
```

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 any new fishing gear introduced in gear_params. Not needed if the added species are only fished by already existing gear. Should not include effort values for existing gear. New gear for which no effort is set via this vector will have an initial effort of 0.

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.

steady — If TRUE (default), runs steadySingleSpecies() to initialise the new species at their single-species steady state and retuning their reproductive efficiencies. Set to FALSE when the caller (e.g. an extension package using NextMethod()) needs to make further changes to the params object before that steady-state calculation can be run successfully.

info_level — Controls the amount of information messages that are shown when the function sets default values for parameters. Higher levels lead to more messages. Set to 0 to suppress all such messages.

... — Currently unused.

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 tuneSteadyState(). The new species will have a reproduction level of 1/4, this can then be changed with reproduction_level<-().

Value

An object of type MizerParams

See Also

removeSpecies(), renameSpecies()

Examples

```
params <- newTraitParams()
species_params <- data.frame(
    species = "Mullet",
    w_max = 173,
    w_mat = 15,
    beta = 283,
    sigma = 1.8,
```

```
    h = 30,
    a = 0.0085,
    b = 3.11
)
params <- addSpecies(params, species_params)
plotSpectra(params)
```

---

adjustSizeGrid *Adjust the size grid*

Description

This function adjusts the size grid in a MizerParams object to the desired minimum and maximum size. It can both expand and truncate the grid. If the grid is truncated, any data outside the new grid is discarded. A warning is issued if there is non-negligible biomass in the discarded size bins.

Usage

```
adjustSizeGrid(params, ...)

## S3 method for class 'MizerParams'
adjustSizeGrid(
  params,
  new_min_w = min(params@species_params$w_min),
  new_max_w = max(params@species_params$w_max),
  new_min_w_pp = min(params@w_full),
  preserve_species = params@species_params$species,
  tol = 1e-06,
  ...
)
```

Arguments

params	A MizerParams object.
...	Additional arguments.
new_min_w	The new minimum size in the grid. Defaults to the minimum egg size of all species.
new_max_w	The new maximum size in the grid. Defaults to the maximum asymptotic size of all species.
new_min_w_pp	The new minimum size of the resource spectrum. Defaults to the current minimum of `w_full`.
preserve_species	A vector of species names for which all rate arrays should be copied over to the new params object rather than being re-calculated from the species parameters. If missing, all species are preserved.

`tol`	A numeric value specifying the tolerance for truncation losses. The following checks are made separately for each species and a warning is raised, listing the affected species, if the lost fraction exceeds this value for any of them: the fraction of the species' biomass lost, the fraction of the diet of the smallest individuals of the species lost to resource truncation, and the fraction of the diet of the largest individuals of the species lost to resource truncation. Defaults to `1e-6`.

Value

A new MizerParams object with the updated size grid.

`age_mat` *Calculate age at maturity*

Description

Uses the size-dependent growth rate and the size at maturity to calculate the age at maturity.

Usage

```
age_mat(params, ...)
```

Arguments

`params`	A MizerParams object
`...`	Currently unused.

Details

Using that by definition of the growth rate $g(w) = dw/dt$ we have that

$$\mathrm{age}_{\mathrm{mat}} = \int_0^{w_{mat}} \frac{dw}{g(w)}$$

In the implementation this integral is approximated on the model size grid by summing `dw / g(w)` over all size bins with `w < w_mat`.

Value

A named vector. The names are the species names and the values are the ages at maturity.

Examples

```
age_mat(NS_params)
```

age_mat_vB — *Calculate age at maturity from von Bertalanffy growth parameters*

Description

This is not a good way to determine the age at maturity because the von Bertalanffy growth curve is not reliable for larvae and juveniles. However this was used in previous versions of mizer and is supplied for backwards compatibility.

Usage

```
age_mat_vB(object, ...)
```

Arguments

`object`	A MizerParams object or a species_params data frame
`...`	Currently unused.

Details

Uses the age at maturity that is implied by the von Bertalanffy growth curve specified by the `w_inf`, `k_vb`, `t0`, `a` and `b` parameters in the species_params data frame.

If any of `k_vb` is missing for a species, the function returns NA for that species. Default values of `b = 3` and `t0 = 0` are used if these are missing. If `w_inf` is missing, `w_max` is used instead.

Value

A named vector. The names are the species names and the values are the ages at maturity.

animate — *Animate size-dependent quantities through time*

Description

Creates an interactive plotly animation in which a play button steps through time, drawing one line per species at each frame.

Usage

```
animate(
  x,
  species = NULL,
  log_x = TRUE,
  log_y = TRUE,
  log = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  ylim = c(NA, NA),
  tlim = c(NA, NA),
  size_axis = c("w", "l"),
  per_log_size = NULL,
  total = FALSE,
  background = TRUE,
  frame_duration = 500,
  transition_duration = frame_duration,
  easing = "linear",
  ...
)

animateSpectra(sim, ...)
```

Arguments

x	A MizerSim, ArrayTimeBySpeciesBySize or ArrayTimeByResourceBySize object.
species	Name or vector of names of the species to be plotted. By default all species are plotted. Not used by the ArrayTimeByResourceBySize method, which warns if it is set.
log_x	If TRUE (default), use a log10 x-axis for body size.
log_y	If TRUE (default), use a log10 y-axis.
log	A character string specifying which axes to log-transform: "x", "y", "xy" or "". If supplied, this overrides log_x and log_y.
wlim	A numeric vector of length two providing lower and upper limits for the body-size (x) axis. Use NA to refer to the existing minimum or maximum.
llim	A numeric vector of length two providing lower and upper limits for the length (x) axis when size_axis = "l". Use NA to refer to the existing minimum or maximum.
ylim	A numeric vector of length two providing lower and upper limits for the value (y) axis. Use NA to refer to the existing minimum or maximum. Limits are applied as Plotly axis ranges, so points outside the limits are clipped by the viewport rather than removed from the animation frames.
tlim	A numeric vector of length two providing lower and upper limits for the animated time window, e.g. c(1997, 2007). Use NA to apply no limit at that end. Default is c(NA, NA).

size_axis
: Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship of each species, or of the resource, see resource_params(). Number and biomass densities are transformed to match the chosen axis.

per_log_size
: Whether to animate a density per logarithmic size (TRUE) rather than per size (FALSE). Unlike size_axis this needs no weight-length relationship, so the ArrayTimeByResourceBySize method takes it too. The two kinds of x read the default NULL differently. For an array it means animating the density as it stands, and asking for it on an array that does not hold a density is an error. For a MizerSim it means FALSE unless power says otherwise, since there the argument chooses the plotted quantity together with biomass and power, in the same way as in plotSpectra().

total
: A boolean value that determines whether the total is plotted as an additional trace called "Total". The total is the total of everything the object holds, whatever is drawn: for a MizerSim every species and the resource, for an array every species it holds. Default is FALSE. Not used by the ArrayTimeByResourceBySize method, which warns if it is set.

background
: A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE. Not used by the ArrayTimeByResourceBySize method, which warns if it is set.

frame_duration
: Duration in milliseconds for which each saved frame is displayed. Default is 500.

transition_duration
: Duration in milliseconds of the interpolation between frames. Use transition_duration = 0 to step directly from one saved frame to the next. Default is frame_duration.

easing
: The Plotly easing function to use when interpolating between frames. Default is "linear". Available options are "linear", "quad", "cubic", "sin", "exp", "circle", "elastic", "back", "bounce", and each of those with suffix "-in", "-out", or "-in-out" appended, for example "cubic-in-out".

...
: Further arguments used by only some of the methods:

  For MizerSim methods:

  biomass Whether to animate the biomass density (TRUE, the default) or the number density (FALSE).

  power The abundance is plotted as the number density times the weight raised to power. An alternative to biomass and per_log_size, with which it must agree if they are given as well. See plotSpectra() for details.

  resource A boolean value that determines whether resource is included. If TRUE, the resource spectrum is plotted as an additional trace called "Resource". Default is TRUE.

sim
: A MizerSim object.

Details

The function dispatches on the class of x:

- MizerSim — animates the community abundance spectra (number density or biomass density vs body size). Resource, background species, and a community total can be added via the

resource, background, and total arguments. The total is the total of everything the model holds, whatever is drawn. The biomass and per_log_size arguments choose the plotted quantity in the same way as in plotSpectra(), and the power argument is available as the same alternative to them. Both axes are log10 by default and can each be switched to linear with log_x = FALSE or log_y = FALSE.

- ArrayTimeBySpeciesBySize — animates any per-species, size-resolved quantity returned by a MizerSim accessor, such as getFMort(), getFeedingLevel(), or getPredMort(). Both axes are log10 by default and can each be switched to linear with log_x = FALSE or log_y = FALSE. Background species and a total can be added via the background and total arguments. The total is the total over every species the array holds, whatever is drawn.
- ArrayTimeByResourceBySize — animates the size-resolved resource quantity returned by NResource() on a MizerSim object. There is only a single resource spectrum, so species, total and background do nothing and warn if set.

Species linecolours and linetypes follow params@linecolour and params@linetype.

animateSpectra() is retained as a backward-compatible alias.

Value

A plotly object with one animated line trace per plotted group. Use the play button or the slider to step through time.

See Also

Other plotting functions: addPlot(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
# Animate biomass density spectra, showing only sizes above 0.1 g
animate(NS_sim, power = 2, wlim = c(0.1, NA), tlim = c(1997, 2007))

# Animate fishing mortality through time
animate(getFMort(NS_sim))

# Animate feeding level for two species only
animate(getFeedingLevel(NS_sim), species = c("Cod", "Herring"))

# Animate the resource spectrum
animate(NResource(NS_sim))
```

ArrayResourceBySize *S3 class for resource size spectra*

Description

[Experimental] Several functions in mizer return a vector over the full size grid holding a resource-related quantity such as the resource number density, the resource mortality, the intrinsic resource birth rate or carrying capacity. The `ArrayResourceBySize` class wraps these vectors to provide convenient `print()`, `summary()`, `plot()`, and `as.data.frame()` methods.

Usage

```
ArrayResourceBySize(
  x,
  value_name = NULL,
  units = NULL,
  type = NULL,
  params = NULL
)

is.ArrayResourceBySize(x)
```

Arguments

`x`	A numeric vector over the full size grid. For `is.ArrayResourceBySize()`, any object to test.
`value_name`	A string giving the human-readable name for the value.
`units`	A string giving the units (e.g. "1/year").
`type`	The kind of quantity the values are, see `ArraySpeciesBySize()` and array_types.
`params`	A `MizerParams` object. Used for the resource colour and the size grid in the `plot()` method.

Details

An `ArrayResourceBySize` object behaves just like a regular numeric vector for arithmetic operations and subsetting. It carries three lightweight attributes:

- `value_name` – a human-readable name for the value (e.g. "Resource mortality").
- `units` – the units of the value (e.g. "1/year").
- `params` – the `MizerParams` object that the value was computed from.

Value

An `ArrayResourceBySize` object (inherits from `numeric`).

`is.ArrayResourceBySize()` returns `TRUE` if `x` is an `ArrayResourceBySize` object, `FALSE` otherwise.

See Also

print(), summary(), as.data.frame(), plot(), plot2(), plotRelative(), addPlot()

Examples

```
mort <- getResourceMort(NS_params)
is.ArrayResourceBySize(mort)
summary(mort)
plot(mort)
```

ArraySpeciesBySize *S3 class for species x size rate arrays*

Description

Many functions in mizer return two-dimensional arrays (species x size) holding rates like encounter rate, feeding level, growth rate, mortality etc. The ArraySpeciesBySize class wraps these arrays to provide convenient print(), summary(), plot(), and as.data.frame() methods.

Usage

```
ArraySpeciesBySize(
  x,
  value_name = NULL,
  units = NULL,
  type = NULL,
  params = NULL,
  representation = c("point", "average")
)

is.ArraySpeciesBySize(x)
```

Arguments

x	A matrix (species x size). For is.ArraySpeciesBySize(), any object to test.
value_name	A string giving the human-readable name for the value.
units	A string giving the units (e.g. "g/year", "1/year").
type	The kind of quantity the values are, see array_types: "value" (the default) for a rate or an amount, "density" for an amount per gram of body weight, "proportion" for a fraction. This is what tells plot() to multiply a density by the appropriate Jacobian when it is plotted against a length axis (size_axis = "l"), and to show a proportion against the whole of the interval from 0 to 1. The default, NULL, treats a value_name of "Number density" or units of "1/g" as a density, the way mizer recognised one before this attribute existed.

params	A MizerParams object. Used for species colours, linetypes, and size ranges in the plot() method.
representation	Either "point" (the default) for a quantity sampled at the grid nodes, or "average" for a finite-volume bin average. A bin-averaged quantity is drawn at the geometric bin centre rather than the left bin edge, but only when the model uses second-order bin-averaging (second_order_w[["bin_average"]]), so default plots are unchanged.

Details

An ArraySpeciesBySize object behaves just like a regular matrix for arithmetic operations and subsetting. It carries a few lightweight attributes:

- value_name – a human-readable name for the value (e.g. "Encounter rate").
- units – the units of the rate (e.g. "g/year").
- type – the kind of quantity the values are.

Value

An ArraySpeciesBySize object (inherits from matrix and array).

is.ArraySpeciesBySize() returns TRUE if x is an ArraySpeciesBySize object, FALSE otherwise.

See Also

print(), summary(), as.data.frame(), plot()

Examples

```
enc <- getEncounter(NS_params)
is.ArraySpeciesBySize(enc)
summary(enc)
```

ArrayTimeByResourceBySize

S3 class for time x resource-size arrays

Description

[Experimental] The NResource() function returns a two-dimensional array (time x size) holding the resource number density through time. The ArrayTimeByResourceBySize class wraps this array to provide convenient print(), summary(), plot(), and as.data.frame() methods.

Usage

```
ArrayTimeByResourceBySize(
  x,
  value_name = NULL,
  units = NULL,
  type = NULL,
  params = NULL
)

is.ArrayTimeByResourceBySize(x)
```

Arguments

x	A matrix (time x size). For `is.ArrayTimeByResourceBySize()`, any object to test.
value_name	A string giving the human-readable name for the value.
units	A string giving the units (e.g. "1/g").
type	The kind of quantity the values are, see `ArraySpeciesBySize()` and array_types.
params	A `MizerParams` object. Used for the resource colour and the size grid in the `plot()` method.

Details

An `ArrayTimeByResourceBySize` object behaves just like a regular matrix for arithmetic operations and subsetting. It carries these lightweight attributes:

- `value_name` – a human-readable name for the value (e.g. "Number density").
- `units` – the units of the value (e.g. "1/g").
- `params` – the `MizerParams` object that the value was computed from.

Value

An `ArrayTimeByResourceBySize` object (inherits from `matrix` and `array`).

`is.ArrayTimeByResourceBySize()` returns `TRUE` if `x` is an `ArrayTimeByResourceBySize` object, `FALSE` otherwise.

See Also

`print()`, `summary()`, `as.data.frame()`, `plot()`, `plot2()`, `plotRelative()`, `addPlot()`, `animate()`

Examples

```
nr <- NResource(NS_sim)
is.ArrayTimeByResourceBySize(nr)
summary(nr)
plot(nr)
```

ArrayTimeBySpecies *S3 class for time x species arrays*

Description

Some functions in mizer return two-dimensional arrays (time x species) holding quantities like biomass, abundance, or yield rate through time. The `ArrayTimeBySpecies` class wraps these arrays to provide convenient `print()`, `summary()`, `plot()`, and `as.data.frame()` methods.

Usage

```
ArrayTimeBySpecies(
  x,
  value_name = NULL,
  units = NULL,
  type = NULL,
  params = NULL
)

is.ArrayTimeBySpecies(x)
```

Arguments

`x`	A matrix (time x species). For `is.ArrayTimeBySpecies()`, any object to test.
`value_name`	A string giving the human-readable name for the value.
`units`	A string giving the units (e.g. "g", "g/year").
`type`	The kind of quantity the values are, see `ArraySpeciesBySize()` and array_types.
`params`	A `MizerParams` object holding the model that created the values.

Details

An `ArrayTimeBySpecies` object behaves just like a regular matrix for arithmetic operations and subsetting. It carries these lightweight attributes:

- `value_name` – a human-readable name for the value (e.g. "Biomass").
- `units` – the units of the value (e.g. "g", "g/year").
- `params` – the `MizerParams` object that created the values.

Value

An `ArrayTimeBySpecies` object (inherits from `matrix` and `array`).

`is.ArrayTimeBySpecies()` returns `TRUE` if `x` is an `ArrayTimeBySpecies` object, `FALSE` otherwise.

See Also

`print()`, `summary()`, `as.data.frame()`, `plot()`

Examples

```
bio <- getBiomass(NS_sim)
is.ArrayTimeBySpecies(bio)
summary(bio)
```

ArrayTimeBySpeciesBySize

S3 class for time x species x size arrays

Description

Some functions in mizer return three-dimensional arrays (time x species x size) holding quantities like fishing mortality, feeding level, or predation mortality through time. The `ArrayTimeBySpeciesBySize` class wraps these arrays to provide convenient `print()`, `summary()`, `plot()`, `animate()`, and `as.data.frame()` methods.

Usage

```
ArrayTimeBySpeciesBySize(
  x,
  value_name = NULL,
  units = NULL,
  type = NULL,
  params = NULL,
  representation = c("point", "average")
)

is.ArrayTimeBySpeciesBySize(x)
```

Arguments

`x`	A 3D array (time x species x size). For `is.ArrayTimeBySpeciesBySize()`, any object to test.
`value_name`	A string giving the human-readable name for the value.
`units`	A string giving the units (e.g. "1/year").
`type`	The kind of quantity the values are, see `ArraySpeciesBySize()` and array_types.
`params`	A `MizerParams` object. Used for species colours, linetypes, and size ranges in the `plot()` and `animateSpectra()` methods.
`representation`	Either `"point"` (the default) for a quantity sampled at the grid nodes, or `"average"` for a finite-volume bin average, which is then drawn at the geometric bin centre when the model uses second-order bin-averaging (`second_order_w[["bin_average"]]`). See `ArraySpeciesBySize()`.

Details

An ArrayTimeBySpeciesBySize object behaves just like a regular array for arithmetic operations and subsetting. It carries these lightweight attributes:

- value_name – a human-readable name for the value (e.g. "Fishing mortality").
- units – the units of the value (e.g. "1/year").
- type – the kind of quantity the values are.
- params – the MizerParams object that the value was computed from.

Value

An ArrayTimeBySpeciesBySize object (inherits from array).

is.ArrayTimeBySpeciesBySize() returns TRUE if x is an ArrayTimeBySpeciesBySize object, FALSE otherwise.

See Also

print(), summary(), as.data.frame(), plot(), animateSpectra()

Examples

```
fmort <- getFMort(NS_sim)
is.ArrayTimeBySpeciesBySize(fmort)
summary(fmort)
plot(fmort, time = 2007)
```

---

as.data.frame *Convert mizer arrays to data frames*

Description

The as.data.frame() methods for mizer array classes turn matrix- and array-like results into tidy long-form data frames, with one row per observed combination of species, size and/or time. The numeric result is always stored in a column called value.

Usage

```
## S3 method for class 'ArraySpeciesBySize'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
## S3 method for class 'ArrayTimeBySpecies'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
## S3 method for class 'ArrayTimeBySpeciesBySize'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

x	An ArraySpeciesBySize, ArrayTimeBySpecies or ArrayTimeBySpeciesBySize object.
row.names	Optional and included only for compatibility with the base generic. NULL or a character vector giving the row names for the data frame.
optional	Optional and included only for compatibility with the base generic. A logical value. If TRUE, setting row names and converting column names (to syntactic names) is optional.
...	Further arguments. They are currently ignored by the mizer methods.

Details

The returned columns are:

- ArraySpeciesBySize: w, value, Species.
- ArrayTimeBySpecies: time, value, Species.
- ArrayTimeBySpeciesBySize: time, Species, w, value.

If the original object has non-numeric or missing dimension names, sequential indices are used for the time or w columns. Species names are taken from the row, column or dimension names of the original object.

Value

A data frame in long format.

See Also

print(), summary(), str(), plot(), ArraySpeciesBySize(), ArrayTimeBySpecies(), ArrayTimeBySpeciesBySize()

Examples

```
enc <- getEncounter(NS_params)
head(as.data.frame(enc))

biomass <- getBiomass(NS_sim)
head(as.data.frame(biomass))
```

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()`

`bin_average_weight` *Bin-average the weight of a size-spectrum integral*

Description

[Experimental] Prepares the weight $K(w)$ of an integral over the size spectrum so that the integral is evaluated with the quadrature scheme the model is actually using. Use this when writing your own indicator or diagnostic function; the built-in summary and indicator functions call it for you.

Usage

```
bin_average_weight(K, params)
```

Arguments

`K`	A numeric vector of weights indexed over the size grid, or a numeric array whose last dimension runs over the size grid (e.g. a species-by-size matrix or a gear-by-species-by-size array).
`params`	A MizerParams object whose `second_order_w` slot controls the gating.

Details

An integral $\int N(w)K(w)\,dw$ is discretised on mizer's finite-volume grid as $\sum_j N_j \bar{K}_j \Delta w_j$, where N_j is the cell average of the density over bin $[w_j, w_{j+1}]$. Only the weight is approximated: N_j is already a cell average and Δw_j is exact, so **neither the abundance nor the bin widths should ever be passed through this function**.

Whether the point weight $K(w_j)$ is replaced by the bin average

$$\bar{K}_j = \frac{1}{\Delta w_j} \int_{w_j}^{w_{j+1}} K(w)\,dw \approx \tfrac{1}{2}\big(K(w_j) + K(w_{j+1})\big)$$

is controlled by the `bin_average` entry of the model's `second_order_w()` slot. When it is `FALSE` (the default) `K` is returned unchanged, so an indicator written with this function reproduces the left-edge Riemann sums of previous mizer versions byte-for-byte. When it is `TRUE` the trapezoidal bin average is returned, which is uniformly second order and exact whenever K is linear in w (e.g. the first moment $K = w$, for which it equals $(w_{j+1}^2 - w_j^2)/(2\Delta w_j)$).

Because the gating happens inside, always call this rather than averaging unconditionally: a hard-coded bin average silently changes the results of models that are on the default scheme.

If `K` is a product of several size-dependent factors, average the **product** and not the individual factors — the average of a product is not the product of the averages. Spawning stock biomass, for example, averages `maturity * w` as a single weight.

The top bin has no right-hand neighbour on the grid, so its weight is left unaveraged (one-sided); the density there is negligible, so this does not affect the second-order accuracy of the totals.

Value

The weight K, bin-averaged when params@second_order_w[["bin_average"]] is TRUE, otherwise returned unchanged.

See Also

second_order_w(), get_size_range_array(), encounter_kernel()

Examples

```
# Biomass of each species above 10g -- what getBiomass() does internally.
params <- NS_params
K <- get_size_range_array(params, min_w = 10)   # species x size, 0/1
K <- sweep(K, 2, params@w, "*")                 # weight by w to get biomass
K <- bin_average_weight(K, params)              # gated on second_order_w
rowSums(sweep(initialN(params) * K, 2, params@dw, "*"))
```

---

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 inclusive and zero otherwise. ppmr_min must be strictly smaller than ppmr_max. 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.

See Also

setPredKernel()

Other predation kernel: gaussian_mixture_pred_kernel(), lognormal_pred_kernel(), power_law_pred_kernel(), truncated_lognormal_pred_kernel()

Examples

```
params <- NS_params
# Set all required paramters before changing 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), pred_kernel(params)["Cod", 10, ], type="l", log="x")
```

---

calc_selectivity *Calculate selectivity from gear parameters*

Description

This function calculates the selectivity for each gear, species and size from the gear parameters. It is called by setFishing() when the selectivity is not set by the user. The returned array is initialised to zero, so gear-species combinations that are not listed in gear_params(params) remain zero. For each listed combination the function named in sel_func is called with w = params@w, the corresponding species parameters, and the selectivity parameters from the matching row in gear_params(params).

Usage

```
calc_selectivity(params)
```

Arguments

params	A MizerParams object

Value

An array (gear x species x size) with the selectivity values

Bin-averaged selectivity

By default the selectivity is point-sampled at the grid nodes params@w, i.e. at the left edge of each size bin. This is only first-order accurate in the bin size when the selectivity is used in the finite-volume update of the size spectrum. When the bin_average entry of the second_order_w() slot is TRUE, each selectivity function is instead integrated over its size bin, so that selectivity[g, i, j] holds the bin average

$$\bar{S}_{g,i,j} = \frac{1}{\Delta w_j} \int_{w_j}^{w_{j+1}} S_{g,i}(w)\, dw.$$

The integral is evaluated with a composite-midpoint rule on a log-spaced sub-grid of each bin, mirroring the bin-integrated predation kernel. This lifts the fishing mortality towards second order at no extra runtime cost (the integration happens once here, the rate functions are unchanged). A welcome side effect is that a knife-edge gear then gets the exact fraction of the straddling bin that lies above the knife edge, removing a grid artefact.

Examples

```
params <- NS_params
str(calc_selectivity(params))
calc_selectivity(params)["Pelagic", "Herring", ]
```

`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
`...`	Additional arguments passed to the method.

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://blog.mizer.sizespectrum.org/posts/2021-08-20-a-5-step-recipe-for-tuning-the-model-steady-state/.

Value

A MizerParams object. If no non-missing observed biomass values are provided, the original object is returned unchanged.

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)
```

`calibrateNumber` *Calibrate the model scale to match total observed number*

Description

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

Usage

```
calibrateNumber(params, ...)
```

Arguments

`params`	A MizerParams object
`...`	Additional arguments passed to the method.

Details

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

After using this function the total number in the model will match the total number, summed over all species. However the numbers of the individual species will not match observations yet, with some species having numbers that are too high and others too low. So after this function you may want to use `matchNumbers()`. This is described in the blog post at https://blog.mizer.sizespectrum.org/posts/2021-08-20-a-5-step-recipe-for-tuning-the-model-steady-state/.

Value

A MizerParams object. If no non-missing observed number values are provided, the original object is returned unchanged.

Examples

```
params <- NS_params
species_params(params)$number_observed <-
    c(0.8, 61, 12, 35, 1.6, 20, 10, 7.6, 135, 60, 30, 78)
species_params(params)$number_cutoff <- 10
params2 <- calibrateNumber(params)
```

---

coerceToExtensionClass

Coerce a mizer object to its extension class

Description

Coerces a `MizerParams` or `MizerSim` object to the S3 class hierarchy corresponding to the object's own extension list. For `MizerSim`, the extension names are read from the embedded `MizerParams` object.

Usage

```
coerceToExtensionClass(object, extensions = objectExtensions(object))
```

Arguments

`object`	A `MizerParams` or `MizerSim` object.
`extensions`	Optional extension list or vector. Defaults to the extensions stored in `object`, or in `object$params` for `MizerSim`.

Details

This is infrastructure for extension package authors. Ordinary users should load saved models with `readParams()` or `readSim()`; `validParams()` and `validSim()` repair the class vector of an object that is already in memory.

Value

The same object coerced to the appropriate S3 class vector, or to the base class for an empty extension list.

See Also

"Creating a mizer extension package": Creating a mizer extension package

Other extension tools: `NOther()`, `initialNOther<-()`, `other_mort()`, `recordExtension()`, `setComponent()`, `setRateFunction()`

compareParams *Compare two MizerParams objects and print out differences*

Description

Compare two MizerParams objects and print out differences

Usage

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

Arguments

params1	First MizerParams object
params2	Second MizerParams object
...	Additional arguments passed to the method.

Value

Invisibly returns a character vector of difference messages, one element per difference. As a side effect, prints the differences in a human-readable format.

Examples

```
params1 <- NS_params
params2 <- params1
species_params(params2)$w_mat[1] <- 10
# Keep this example focused on the model parameter.
params2@time_modified <- params1@time_modified
compareParams(params1, params2)
```

completeSpeciesParams *Alias for* validSpeciesParams()

Description

[Superseded]

An alias provided for backward compatibility with mizer version <= 2.5.2

Usage

```
completeSpeciesParams(species_params, check_misspellings = TRUE)
```

Arguments

`species_params` The user-supplied species parameter data frame

`check_misspellings`
Whether to report column names that look like misspellings of standard species parameter names. `TRUE` by default.

`validSpeciesParams()` first calls `validGivenSpeciesParams()` but then goes further by adding default values for species parameters that were not provided. It only sets defaults for those species parameters that are not owned by a single rate-setting function, namely those that are read by several of them (`n`), that are used only when projecting (`alpha`), that determine the size grid (`w_min`, `w_max`), that are needed for the length-weight conversion (`a`, `b`) or that are used only for reporting (`is_background`). The function sets default values if any of the following species parameters are missing or NA:

- `w_max` is set to `1.5 * w_inf` (it is only a computational boundary)
- `w_repro_max` is set to `w_inf`
- `w_mat` is set to `w_inf/4`
- `w_min` is set to `0.001`
- `alpha` is set to `0.6`
- `n` is set to `3/4`
- `a` is set to `0.01`
- `b` is set to `3`
- `is_background` is set to `FALSE`

All other species parameters are given their default values by the rate-setting function that uses them, so that each default has a single home. For example `p` and `k` are set by `setMetabolicRate()`, `z_ext`, `d` and `z0` by `setExtMort()`, `E_ext` by `setExtEncounter()`, `D_ext` by `setExtDiffusion()`, `interaction_resource` by `setInteraction()`, `beta` and `sigma` by `setPredKernel()`, `q` and `gamma` by `setSearchVolume()`, and `erepro`, `m`, `w_mat25` and `R_max` by `setReproduction()`. These columns are therefore absent from the data frame returned by `validSpeciesParams()` but present in the species parameters of a `MizerParams` object, because `setParams()` calls all the rate-setting functions.

Note that the species parameters returned by these functions are not guaranteed to produce a viable model. More checks of the parameters are performed by the individual rate-setting functions (see `setParams()` for the list of these functions).

Details

`validGivenSpeciesParams()` checks the validity of the given species parameters. It throws an error if

- the `species` column does not exist or contains duplicates
- the asymptotic size `w_inf` is not specified for all species (but see the backwards-compatibility note below)

If a weight-based parameter is missing but the corresponding length-based parameter is given, as well as the a and b parameters for length-weight conversion, then the weight-based parameters are added. If both length and weight are given, then weight is used and an info_about_default condition is signalled if the two are inconsistent.

The required maximum-size parameter is w_inf, the von Bertalanffy asymptotic size of an average individual. For backwards compatibility, if no w_inf column is given, its values are taken from the w_repro_max column if that is present, or otherwise from the w_max column, and an informational message is issued. (w_repro_max is preferred over w_max because in earlier versions of mizer it was the size at which growth stopped and is therefore the closest analogue to the asymptotic size.)

Some inconsistencies in the size parameters are resolved as follows:

- Any w_mat that is not smaller than w_inf is set to w_inf / 4.
- Any w_mat25 that is not smaller than w_mat is marked as missing, as is the corresponding l_mat25, so that the default is used instead.
- Any w_min that is not smaller than w_mat is set to 0.001 or w_mat /10, whichever is smaller.
- Any w_repro_max that is not larger than w_mat is set to 4 * w_mat.

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.

The function tests for some typical misspellings of parameter names, like wrong capitalisation or missing underscores and issues a warning if it detects such a name. Pass check_misspellings = FALSE to skip that test, as mizer does when it re-validates a table it has already checked, so that the report is made once, when the column is introduced.

Value

For validSpeciesParams(): A valid species parameter data frame with additional parameters with default values.

For validGivenSpeciesParams(): A valid species parameter data frame without additional parameters.

See Also

species_params(), validGearParams(), validParams(), validSim()

---

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

Value

The current value of the component

---

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, diffusion, ...)
```

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()`.
diffusion	A two dimensional array (species x size) holding the diffusion rate as calculated by `mizerDiffusion()`.
...	Unused

Value

Vector with the value for each species

See Also

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

Examples

```
# 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])
```

`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()`

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 `resource_dynamics()<-` 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)
```

Value

No return value, called for side effects

See Also

"Extending mizer": guide to extending 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_info_level` *The default level of information that mizer gives*

Description

[Experimental] Returns the `mizer_info_level` option if it is set and `fallback` otherwise. This is the default of the `info_level` argument of the functions that report information, so that `options(mizer_info_level = 0)` quietens mizer as a whole, including the functions that have no `info_level` argument of their own, such as `species_params<-()` and the rate setters.

Usage

```
default_info_level(fallback = 3)
```

Arguments

`fallback`	The level to use when the option is not set. Defaults to 3, which reports everything.

Details

Extension packages should use this as the default of their own `info_level` argument, so that a constructor or setter of theirs follows the option like mizer's own do:

```
newFooParams <- function(species_params, ...,
                         info_level = default_info_level()) {
    newMultispeciesParams(species_params, info_level = info_level, ...)
}
```

Take the argument explicitly like that rather than hard-coding a value in the call, which would make a user's own `info_level` collide with it.

Value

A single number, or `NA` to leave the reporting to a handler further out.

Examples

```
default_info_level()

# Setting the option changes what every reporting function defaults to.
old <- options(mizer_info_level = 1)
default_info_level()
options(old)
```

`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.

`defaults_edition` *Default editions*

Description

Function to set and get which edition of default choices is being used.

Usage

```
defaults_edition(edition = NULL)
```

Arguments

`edition`	NULL or a numerical value.

Details

The mizer functions for creating new models make a lot of choices for default values for parameters that are not provided by the user. Sometimes we find better ways to choose the defaults and update mizer accordingly. When we do this, we will increase the edition number.

If you call `defaults_edition()` without an argument it returns the currently active edition. Otherwise it sets the active edition to the given value.

Users who want their existing code for creating models not to change behaviour when run with future versions of mizer should explicitly set the desired defaults edition at the top of their code.

The most recent edition is edition 2. It will become the default in the next release. The current default is edition 1. The following defaults are changed in edition 2:

- `catchability` = 0.3 instead of 1
- `initial effort` = 1 instead of 0
- gamma is set to ensure a feeding level of `f0` for larvae with the current value of `interaction_resource` instead of interaction_resource = 1‘.
- `initial_n` is set using `get_steady_state_n()` instead of the rather arbitrary old choice.
- In `setReproduction()`, `psi` is no longer forced to 1 above `w_repro_max`; its value is determined entirely by the maturity ogive and the reproductive proportion.

Value

If `edition` is `NULL`, the currently active edition number. If `edition` is supplied, the function sets the global `mizer_defaults_edition` option, emits a message, and returns the supplied value invisibly.

`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

Details

We use this helper function in particular to see if a new value for a slot in MizerParams is different from the existing value in order to give the appropriate messages.

Value

TRUE or FALSE

---

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

Description

[Experimental]

This function can be used in `projectUntilSettled()` 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))`. A species with zero rdi in both states, such as one that is absent from the model, has not changed and contributes zero. A species whose rdi has risen from zero makes the result infinite.

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 `projectUntilSettled()` to decide when sufficient convergence to steady state has been achieved.

Only the size classes that hold fish are measured. A class whose density is zero in either state has no log to take, and one holding a negligible share of its species' biomass has a log that never stops moving: above a size where growth stops the density decays exponentially, so `log(n)` falls by the same amount between every pair of states, for ever. Left in the sum, a single such class holding 10^{-92} g of fish can hold the distance above any tolerance indefinitely and stop `projectUntilSettled()` from ever converging, while the biomass drift correctly reports a fixed point. Excluding it changes nothing for a model that does not have one, because the classes that hold the fish are exactly the classes that are kept.

Usage

```
distanceSSLogN(
  params,
  current,
  previous,
  biomass_share_cutoff = steady_share_cutoff(),
  ...
)
```

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
`biomass_share_cutoff`	**[Experimental]** A finite number between 0 and 1, inclusive, giving the share of a species' biomass that a size class must hold in the current state to be measured. `0` measures every class with a nonzero density in both states, which is what this function did before mizer 3.3.
`...`	Unused. Accepted because `projectUntilSettled()` forwards its own `...` to both the rate functions and the distance function, so an argument meant for one arrives at the other.

Value

The sum of squares of the difference in the logs of the fish abundances `n`, over the size classes that hold fish in both states: `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`	Vector of sizes.
`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

You would not usually call this function directly. Instead, set the `sel_func` column in `gear_params()` to `"double_sigmoid_length"` and provide the `l25`, `l50`, `l50_right` and `l25_right` values as additional columns. `setFishing()` will then call this function automatically when calculating the selectivity array.

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. The selectivity is given by the function

$$S(l) = \frac{1}{1 + \exp\left(\log(3)\frac{l50 - l}{l50 - l25}\right)} \frac{1}{1 + \exp\left(\log(3)\frac{l50_{right} - l}{l50_{right} - l25_{right}}\right)}$$

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.

$$l = \left(\frac{w}{a}\right)^{1/b}$$

Value

Vector of selectivities at the given sizes. Requires `l25 < l50 < l50_right < l25_right`.

See Also

`gear_params()` for setting the selectivity parameters.

Other selectivity functions: `knife_edge()`, `knife_edge_length()`, `sigmoid_length()`, `sigmoid_weight()`

Examples

```
# Hump-shaped selectivity: rises from l25=10 to l50=15,
# then drops back to 50% at l50_right=40 and 25% at l25_right=50
sp <- list(a = 0.01, b = 3)
w <- c(1, 10, 100, 500, 1000)
double_sigmoid_length(w, l25 = 10, l50 = 15,
                      l50_right = 40, l25_right = 50,
                      species_params = sp)
```

---

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_max` 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.

---

encounter_kernel *The predation kernel as used by the encounter quadrature*

Description

[Experimental] Returns the kernel array $\Phi_i(w_k, w_p)$ for which

$$E_i(w_k) = \gamma_i(w_k) \sum_p \Phi_i(w_k, w_p) N_i^{eff}(w_p) w_p \Delta w_p$$

reproduces exactly the available energy computed by `mizerEncounter()`, where N^{eff} is the interaction-weighted prey density. It is the kernel that any summary function must use if its result is to be consistent with `getEncounter()`.

Usage

```
encounter_kernel(params)
```

Arguments

`params`	A MizerParams object.

Details

On the default first-order path this is just the point-sampled kernel returned by `pred_kernel()`. When second-order bin-averaging is switched on (see `second_order_w()`) the two differ: `setPredKernel()` then builds the Fourier-transformed kernel from the kernel *integrated over the prey bin*, divided by $\beta - 1$ so that the plain point weight $w_p \Delta w_p$ carried by the prey vector is cancelled. Those bin-integrated weights are recovered here from `params@ft_pred_kernel_e` by an inverse Fourier transform, which costs one FFT and keeps this helper automatically in step with whatever quadrature `setPredKernel()` used.

Pair it with the **plain point prey weight** `params@w_full * params@dw_full`. That weight is a normalisation which the kernel construction is built to cancel, not a first-order quadrature weight, so it must not be passed through `bin_average_weight()`: doing so applies the prey-bin integral twice. A summary function that instead pairs the point-sampled `pred_kernel()` with a bin-averaged prey weight double-counts that quadrature; that was the bug behind issue #474.

Value

An array (predator species x predator size x prey size).

See Also

`pred_kernel()` for the point-sampled kernel used for plotting and for supplying a custom kernel, `second_order_w()`, `bin_average_weight()`

---

expandSizeGrid *Expand the size grid*

Description

[Deprecated] This function expands the size grid in a MizerParams object to the desired min and max size, preserving all existing species. The function is deprecated because you can achieve the same more flexibly with `adjustSizeGrid()`.

Usage

```
expandSizeGrid(params, ...)

## S3 method for class 'MizerParams'
expandSizeGrid(
  params,
  new_min_w = min(params@w),
  new_max_w = max(params@w),
  preserve_species = params@species_params$species,
  ...
)
```

Arguments

`params`	A MizerParams object.
`...`	Additional arguments (currently unused).
`new_min_w`	The new minimum size in the grid. Defaults to the current minimum.
`new_max_w`	The new maximum size in the grid. Defaults to the current maximum.
`preserve_species`	A vector of species names for which all rate arrays should be copied over to the new params object rather than being re-calculated from the species parameters. If missing, all species are preserved.

Value

A new MizerParams object with the updated size grid.

---

finalN — *Size spectra at end of simulation*

Description

Size spectra at end of simulation

Usage

```
finalN(sim)

finalNResource(sim)

idxFinalT(sim)
```

Arguments

`sim`	A MizerSim object

Value

For `finalN()`: An `ArraySpeciesBySize` object (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

For `idxFinalT()`: An integer giving the index for extracting the results for the final time step

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))
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))
```

---

findSteadyState *Find the steady state of a model*

Description

[Experimental]

Puts the model onto a steady state of its own dynamics, changing no parameter: the reproduction rate, the resource and the consumer spectra all settle together at whatever the parameters you already have imply.

Usage

```
findSteadyState(
  params,
  solver = c("project", "newton"),
  effort = params@initial_effort,
  info_level = default_info_level(),
  ...
)
```

Arguments

params	A MizerParams object
solver	The solver to use: "project" to run the dynamics until they settle, "newton" to solve the steady-state equation directly. See *Choosing a solver*.
effort	The fishing effort to use throughout. By default the initial effort stored in params.
info_level	Controls the amount of information messages that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().

... Arguments for the chosen solver.

With `solver = "project"`: `distance_func`, `t_max`, `t_check`, `dt`, `distance_tol`, `residual_tol`, `amplitude_tol`, `amp_rel_tol`, `extinction_threshold`, `progress_bar` and `method`, all as described in `projectUntilSettled()`. There is no `t_save`, because no trajectory is returned.

With `solver = "newton"`: `extinction_floor` (default `1e-6`), the relative abundance below which a species counts as extinct, plus `solver_tol`, `maxit`, `jacobian`, `global` and `verbose` as described in `tuneSteadyState()`.

Details

This is the counterpart of `tuneSteadyState()`, which instead holds the reproduction rate and the resource at the values you supplied and adjusts `erepro`/`R_max` and `cc_pp` to make those values steady. Use this function when the parameters are the thing you want to keep — when asking what state a given model settles into, for instance under a changed fishing effort — and `tuneSteadyState()` while calibrating.

Nothing being held fixed means the search has more ways to end badly. With `solver = "project"` the run can settle on a limit cycle or drive a species extinct rather than reach a fixed point, and with either solver reproduction can collapse. Check the `"convergence"` attribute rather than assuming a fixed point was reached; see the section below.

Value

A `MizerParams` object with the initial state replaced by the steady state found and no parameter changed. It carries a `"convergence"` attribute describing the solution found; see `projectUntilSettled()`.

Choosing a solver

`solver = "project"` (the default) runs the dynamics until they settle, via `projectUntilSettled()`, and takes the final state. It is exactly that function with the trajectory thrown away; call `projectUntilSettled()` instead if you want to watch the approach.

`solver = "newton"` solves the steady-state equation directly with a Newton-type root finder from the `nleqslv` package, so it converges even when the steady state is dynamically **unstable**, where the time-stepping solver diverges away from it. This is the natural entry point for a stability analysis with `getStability()`.

The Newton solver treats the resource densities as unknowns alongside the fish and appends the resource steady-state equation to the system, so the resource density and the feeding levels it implies are self-consistent even where consumers are satiated. That equation is written for the default semichemostat resource dynamics, so `solver = "newton"` stops with an error for any other `resource_dynamics`; use `solver = "project"` there.

The Newton iteration also needs the residual $F(N)$ to be continuous. A custom rate function registered with `setRateFunction()` that jumps as a function of the abundances makes F discontinuous, and where the equilibrium lies on the switching threshold there is no root at all, because neither branch is in equilibrium there. The solver then stalls (`nleqslv` termination code 3) and returns an iterate pinned to the threshold. See Discontinuous rate functions.

It also respects the active transport scheme: if the experimental second-order scheme is enabled (see `second_order_w()`) it solves the steady-state equation of that scheme. With the van Leer

reconstruction the residual is only Lipschitz, so the iteration converges to a fixed point of the dynamics but not to machine precision. The unlimited "centred" reconstruction admits an undamped odd-even mode at a steady state with no physical diffusion, giving an ill-conditioned steady-state Jacobian for which the solver is not expected to converge.

What you get back may not be a steady state

The stopping criterion is a proxy. It says that two states t_per years apart differ by less than distance_tol on whatever scale the criterion is measured on; it does not say that the state reached is a fixed point. There are four ways the returned object can fail to be one:

- the run converged on its own scale while the biomasses are still visibly drifting (termination = "distance_tolerance");
- the run reached t_max without converging (termination = "time_limit");
- the run settled on a limit cycle (termination = "cycle_detected"), in which case the state stored is one point on that cycle;
- the run stopped because a species was going extinct (termination = "extinction").

So treat the result as a claim to be checked rather than as a guarantee:

```
attr(params, "convergence")$attractor  # "fixed_point", "limit_cycle" or NA
attr(params, "convergence")$residual   # largest biomass drift, in 1/year
isSteady(params)                       # TRUE if within tolerance
summary(params)                        # includes the biomass-drift verdict
plot(getSteadyResidual(params))        # which species, and at which sizes
```

attractor is the field that answers the question: it is "fixed_point" only where the measured biomass drift is within residual_tol, so it cannot be satisfied by a distance function that has merely gone quiet. termination says how the run ended and converged whether the solver met its own criterion; neither is a claim about the state. The last line says *where* the model is not steady, which is the one to reach for when it is not: a model that is off steady state is usually off in one species or one part of the size range, and the plot names it. See getSteadyResidual() for why the verdict is phrased in terms of biomass drift rather than the largest per-capita rate.

The messages this function prints say the same thing — a converged run whose biomasses are still moving reports the drift and adds "Reduce the tolerance on the distance function to converge further." — but they are suppressed by info_level = 0, so in a script the "convergence" attribute is the reliable check.

Finally, a genuine fixed point need not be a *stable* one. Use getStability() to find out, and solver = "newton" to converge onto a fixed point that the dynamics themselves would run away from.

See Also

tuneSteadyState(), projectUntilSettled(), isSteady(), getSteadyResidual(), getStability()

Examples

```
params <- findSteadyState(NS_params, solver = "newton")
plotSpectra(params)
```

frozen_rate_params *Which parameters feed which frozen array*

Description

A lookup table used by `signal_frozen_changes()` to decide whether a change the user made can take effect. Each entry is named after a slot of MizerParams that can be frozen and gives the quantity as the user knows it, the call that unfreezes it, the parameters that the setter and its default calculations read, and what kind of parameters those are.

Usage

```
frozen_rate_params()
```

Details

The list of parameters does not have to be exhaustive, and deliberately is not: it names the parameters that the setter reads directly together with the main inputs of the default calculations for those parameters. A parameter that is missing simply means that the user is not warned, and is left with the message that the setter itself gives, see `signal_not_recalculated()`. Listing a parameter that in fact has no influence is the worse mistake, because it warns about a change that did take effect.

Value

A named list of lists with entries `quantity`, `reset_call`, `params` and `derived_from`.

gaussian_mixture_pred_kernel *Gaussian-mixture predation kernel*

Description

[Experimental] A predation kernel for which the log predator/prey mass ratio follows a mixture of Gaussian distributions.

Usage

```
gaussian_mixture_pred_kernel(ppmr, kernel_p, kernel_mean, kernel_sd)
```

Arguments

`ppmr`	A vector of predator/prey mass ratios.
`kernel_p`	A numeric vector of relative component proportions.
`kernel_mean`	A numeric vector of component means on the log predator/prey mass-ratio scale.
`kernel_sd`	A numeric vector of positive component standard deviations.

Details

Writing the predator mass as w, the prey mass as w_p, and $x = \ln(w/w_p)$, the feeding kernel is

$$\phi_i(w, w_p) = \sum_j a_{ij} \exp\left[-\frac{(x-\mu_{ij})^2}{2\sigma_{ij}^2}\right], \qquad a_{ij} = \frac{p_{ij}/\sigma_{ij}}{\sum_k p_{ik}/\sigma_{ik}}.$$

for predator/prey mass ratios greater than or equal to one, and zero for smaller ratios.

This is proportional to the Gaussian-mixture probability density with mixing proportions p_{ij}, means μ_{ij}, and standard deviations σ_{ij}. The scaling makes the sum of the component peak heights equal to one. Consequently the kernel is at most one, and a one-component mixture is identical to `lognormal_pred_kernel()` with `beta = exp(kernel_mean)` and `sigma = kernel_sd`.

The three component parameters are vectors of equal length. When this function is selected in a species parameter data frame, they should be held in the list-columns `kernel_p`, `kernel_mean`, and `kernel_sd`. The values in `kernel_p` must be non-negative with at least one positive value, but they do not need to sum to one because they are normalised by the function.

Value

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

See Also

`setPredKernel()`

Other predation kernel: `box_pred_kernel()`, `lognormal_pred_kernel()`, `power_law_pred_kernel()`, `truncated_lognormal_pred_kernel()`

Examples

```
ppmr <- exp(seq(0, 12, length.out = 200))
phi <- gaussian_mixture_pred_kernel(
    ppmr,
    kernel_p = c(0.3, 0.7),
    kernel_mean = c(4, 8),
    kernel_sd = c(0.8, 1.5)
)
plot(ppmr, phi, type = "l", log = "x")
```

`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(object)

gear_params(object) <- value

is.gear_params(x)
```

Arguments

object	A MizerParams object, a MizerSim object or a data frame
value	A data frame with the new gear parameters.
x	An object to test with `is.gear_params()`.

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. The columns are:

- `species` The name of the species
- `gear` The name of the gear
- `catchability` A number specifying how strongly this gear selects this species.
- `sel_func` The name of the function that calculates the selectivity curve.
- One column for each selectivity parameter needed by the selectivity functions.

For the details see `setFishing()`.

There can optionally also be a column `yield_observed` that allows you to specify for each gear and species the total annual fisheries yield in grams per year. This is used by `plotYieldObservedVsModel()`, which adds the yields up over the gears to get the observed yield of each species, see `get_yield_observed()`.

The fishing effort, which is also needed to determine the fishing mortality exerted by a gear is not set via the `gear_params` data frame but is set with `initial_effort()` or is specified when calling `project()`.

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.
`gear_params<-` automatically sets the row names to contain the species name and the gear name, separated by a comma and a space. The last example below illustrates how this facilitates changing an individual gear parameter.

Value

Data frame with gear parameters

`is.gear_params()` returns `TRUE` if `x` is a `gear_params` object, `FALSE` otherwise.

See Also

Other functions for setting parameters: `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

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_func = 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
```

---

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.

See the Target Feeding Level section of the "Calculation of Default Parameter Values" vignette for the mathematical derivation.

The available energy is measured with the predation part of mizer's own encounter rate, `mizerEncounter()`. It is a property of the species parameters and of the resource power law rather than of the model's dynamics, so external encounter and contributions registered with `other_encounter()` (including component encounter functions) are excluded. The measurement also deliberately does not go through the extension dispatch chain, nor through an encounter function registered with `setRateFunction()`.

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 fish feeding on a resource spectrum described by the power law $\kappa w^{-\lambda}$ achieve a feeding level f_0. Only for internal use.

Usage

```
get_gamma_default(params)
```

Arguments

`params`	A MizerParams object

Details

See the Search Volume Coefficient section of the "Calculation of Default Parameter Values" vignette for the mathematical derivation.

The available energy is measured with the predation part of mizer's own encounter rate, `mizerEncounter()`. It is a property of the species parameters and of the resource power law rather than of the model's dynamics, so external encounter and contributions registered with `other_encounter()` (including component encounter functions) are excluded. The measurement also deliberately does not go through the extension dispatch chain, nor through an encounter function registered with `setRateFunction()`.

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_h_default *Get default value for h*

Description

Sets h so that the species reaches maturity size w_mat at the maturity age age_mat if it feeds at feeding level f0.

Usage

```
get_h_default(params)
```

Arguments

params	A MizerParams object or a species parameter data frame

Details

If age_mat is missing in the species parameter data frame, then it is calculated from the von Bertalanffy growth curve parameters k_vb and (optionally t0) taken from the species parameter data frame. This is not reliable and a warning is issued.

If no growth information is given at all for a species, the default is set to h = 30.

See the Maximum Intake Rate Coefficient section of the "Calculation of Default Parameter Values" vignette for the mathematical derivation.

Value

A vector with the values of h for all species

See Also

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

get_initial_n *Calculate initial population abundances*

Description

This function uses the model parameters and other parameters to calculate initial values for the species number densities. These initial abundances are currently quite arbitrary and not close to the steady state. We intend to improve this in the future.

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 when using defaults edition 1. If not supplied, `kappa / 1000` is used. This argument is ignored for defaults edition 2 and later.
`a`	A parameter with a default value of 0.35.

Value

An `ArraySpeciesBySize` object (species x size) of population abundances.

Examples

```
init_n <- get_initial_n(NS_params)
```

`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

Details

See the Standard Metabolic Rate Coefficient section of the "Calculation of Default Parameter Values" vignette for the mathematical derivation.

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_size_range_array — *Get size range array*

Description

Helper function that returns an array (species x size) of logical 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

A logical array (species x size), with dimnames `sp` and `w`.

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_steady_state_n` *Calculate steady state abundance*

Description

This function calculates the steady state abundance by solving the transport equation with given growth and mortality rates. It sets up a tri-diagonal system and solves it.

Usage

```
get_steady_state_n(
  params,
  g,
  mu,
  D,
  N0,
  max_iterations = 500,
  tol = 1e-10,
  relax = 0.3
)
```

Arguments

params	A MizerParams object
g	A matrix of growth rates (species x size)
mu	A matrix of mortality rates (species x size)
D	A matrix of diffusion rates (species x size)
N0	A vector with the abundance at the smallest size for each species
max_iterations	Maximum number of Picard iterations used when a flux limiter is active.
tol	Relative convergence tolerance for the Picard iteration.
relax	Under-relaxation factor in (0, 1] for the Picard iteration when a flux limiter is active.

Details

The spatial discretisation of the advective flux is read from the `flux` entry of the `second_order_w` slot of `params`. With a second-order flux scheme active the steady state must match the one that `project()` converges to. Because the limiter depends on the solution, the steady state is then found by an under-relaxed Picard iteration: the limiter is frozen at the current iterate, the resulting tridiagonal system is solved, and the iterate is updated towards that solution, repeating until it converges. (At `dt = 1` the limited operator is not diagonally dominant, so the plain fixed-point map only stalls; under-relaxation makes it converge.)

The returned abundance is held at zero above each species' `w_max`, the same upper boundary condition that `project()` imposes (via `zero_above_support()` in `project_n()`) and that the Newton solver solves on. Without this the bottom-up solve would carry density above `w_max` whenever growth is still positive there or diffusion pushes density past it.

Value

A matrix with the steady state abundance

---

get_time_elements *Get array indices for a time range in a MizerSim object*

Description

Internal helper to select the saved time points whose times lie between the smallest and largest values in `time_range`, inclusive.

Usage

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

Arguments

sim	A MizerSim object.
time_range	A numeric or character vector of times. Only the range of values matters, so all saved times between min(time_range) and max(time_range) are selected.
slot_name	Obsolete, kept only for backward compatibility with early versions where different time-based slots could have different time grids. Leave at the default.

Value

A named logical vector, with one entry for each saved time in sim, indicating whether that time lies in the requested range.

---

get_yield_observed *Observed yield of each species*

Description

The observed yield lives in the yield_observed column of the gear parameter data frame, see gear_params(), where it is given for each gear-species pair. This function adds the observations up over the gears to give the total observed yield of each species. With the gear argument you can restrict the sum to a subset of the gears.

Usage

```
get_yield_observed(params, gear = NULL)
```

Arguments

params	A MizerParams object
gear	The gears whose observations are to be added up. Optional. By default all gears are included. A vector of gear names.

Details

Older models, and the examples in older versions of mizer, put yield_observed into the species parameter data frame instead. That is still accepted: a species that has no observation among the gear parameters takes its value from the species parameters. Where both tables give a value for a species, the gear parameters win. The species parameter observation is a total over all gears, so it is ignored when gear selects only some of the gears.

Value

A numeric vector with one entry for each species, named by species, holding the observed yield in grams per year, or NA for species without an observation. NULL if the observations are not available: if neither the gear parameters nor the species parameters have a yield_observed column, or, when gear is given, if the gear parameters have no such column.

`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 size range starting at the size specified by the `biomass_cutoff` species parameter, if it is set, or else the full size range of each species. 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(object, use_cutoff = FALSE, ...)
```

Arguments

`object`	An object of class `MizerParams` or `MizerSim`.
`use_cutoff`	If TRUE, the `biomass_cutoff` column in the species parameters is used as the minimum weight for each species (ignoring any size range arguments in `...`). If FALSE (default), the specified size range arguments are used, if provided, or the full size range of the species is used.
`...`	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`.

Details

When no size range arguments are provided, the function checks if the `biomass_cutoff` column exists in the species parameters. If it does, those values are used as the minimum weight for each species. For species with NA values in `biomass_cutoff`, the default minimum weight (smallest weight in the model) is used.

Value

If called with a MizerParams object, a named vector with the biomass in grams for each species in the model. If called with a MizerSim object, an `ArrayTimeBySpecies` object (time x species) containing the biomass in grams at each time step for all species.

See Also

Other summary functions: getDiet(), getGrowthCurves(), getN(), getSSB(), getSteadyResidual(), getTrophicLevel(), getTrophicLevelBySpecies(), getYield(), getYieldGear()

Examples

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

# If species_params contains a `biomass_cutoff`` column, it can be used
# as the minimum weight when use_cutoff = TRUE
species_params(NS_sim@params)$biomass_cutoff <- 10
biomass <- getBiomass(NS_sim, use_cutoff = TRUE)  # Uses biomass_cutoff as min_w
biomass["1972", "Herring"]
```

---

getCommunitySlope *Calculate the slope of the community abundance*

Description

Calculates the slope of the community abundance 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(object, species = NULL, biomass = TRUE, ...)
```

Arguments

object	A MizerSim or MizerParams 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 columns slope, intercept and the coefficient of determination R^2 (and a time step column when called with a `MizerSim` object).

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

getCommunitySlope(NS_params)
```

---

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

An `ArraySpeciesBySize` object (species x size) with the critical feeding level

Examples

```
str(getFeedingLevel(NS_params))
```

---

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, resource, and other components of the ecosystem. Returns either the rates in grams/year or the proportion of the total consumption rate.

Usage

```
getDiet(object, proportion = TRUE, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`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.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

For a MizerSim object:

`time_range` The time range over which to return the diet. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Details

The rates $D_{ij}(w)$ at which a predator of species i and size w consumes biomass from prey species j are 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.

Extra columns are added for the external encounter rate and for any extra ecosystem components in your model for which you have defined an encounter rate function. These encounter rates are 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. Summing the result of `getDiet(proportion = FALSE)` over prey therefore reproduces `getEncounter(params) * (1 - getFeedingLevel(params))`, whichever quadrature scheme the model uses (see `second_order_w()`).

Value

- `MizerParams`: An array (predator species x predator size x (prey species + resource + other components)). Dimnames are "predator", "w", and "prey".
- `MizerSim`: A four-dimensional array (time x predator species x predator size x prey) with the diet at each selected saved time step. If `drop = TRUE` then dimensions of length 1 are removed.

See Also

`plotDiet()`

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

Examples

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

# For a MizerSim the diet is returned at each saved time step
sim <- project(NS_params, t_max = 20, effort = 0.5)
# Diet at the saved time steps over years 15 - 20
diet <- getDiet(sim, time_range = c(15, 20))
str(diet)
```

`getDiffusion` *Get diffusion rate from predation*

Description

Calculates the diffusion rate $D_i(w)$ (grams^2/year) for each species. This diffusion rate has two components:

1. The diffusion due to the variability in prey sizes. This is the diffusion term from the jump-growth equation.
2. Any externally specified diffusion, which is added via `setExtDiffusion()`

Usage

```
getDiffusion(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Details

The diffusion due to the variability in prey sizes 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 $\phi(w, w_p)$:

$$D_{pred.i}(w) = (1 - f_i(w))\,\gamma_i(w) \int \left(\theta_{ip} N_R(w_p) + \sum_j \theta_{ij} N_j(w_p) \right) \phi_i(w, w_p)(\alpha_i w_p)^2 \, dw_p.$$

This has the same form as the rate at which the predator absorbs prey biomass, except that the factor $\alpha_i w_p$, the increase in the predator's mass from eating a prey of mass w_p, is squared. 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 `species_params()`. $f(w)$ is the feeding level calculated with `getFeedingLevel()`, and α_i is the proportion of the consumed food that is absorbed, taken from the `alpha` column in `species_params()`. The total diffusion rate is $D_i(w) = D_{pred.i}(w) + D_{ext.i}(w)$, where $D_{ext.i}(w)$ is the external diffusion.

The diffusion integral is normally evaluated efficiently with a fast Fourier transform, which assumes that the predation kernel depends only on the ratio of predator to prey size. If a custom predation kernel that depends on predator and prey size separately has been set with `setPredKernel()`, the integral is instead evaluated by direct summation over the full predation kernel, as in `getEncounter()`.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (predator species x predator size) with the diffusion rates.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x predator species x predator size) with the diffusion rates at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

References

Datta, S., Delius, G. W. and Law, R. (2010). A jump-growth model for predator-prey dynamics: derivation and application to marine ecosystems. Bulletin of Mathematical Biology, 72(6):1361–1382

See Also

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

`getDiscreteStability` *Analyse the stability of mizer's numerical time step*

Description

[Experimental] Computes the eigenvalues μ_i of the linearised one-step-ahead map at the steady state stored in `params@initial_n`, for a given step size `dt`. These describe how mizer's numerical scheme, rather than the model, behaves near the steady state: the map does not amplify perturbations when the spectral radius $\max_i |\mu_i|$ is less than 1.

Usage

```
getDiscreteStability(params, effort = params@initial_effort, h = 1e-04, dt = 1)
```

Arguments

`params`	A MizerParams object whose `initial_n` holds the steady state to analyse. Typically the output of `findSteadyState()`.
`effort`	The fishing effort to use. By default the initial effort stored in `params`.
`h`	Relative step size for centred finite differences. Default `1e-4`. The result should not depend on this choice. If it does, the dynamics are not smooth at the state being analysed — see the section below.
`dt`	The time step size of the one-step map. Default `1`.

Details

This is the numerical counterpart of `getStability()`, which analyses the model itself and involves no time step at all. Use `getStability()` to ask whether the steady state of the *model* is stable, and this function to ask what mizer's solver does at a particular `dt`. The two can disagree, and that disagreement is the point: the implicit transport solve damps oscillations artificially, so a physically unstable steady state can have a spectral radius below 1 at a large `dt`, and the simulation then sits at a state the model does not actually hold.

The map that is linearised:

One step is what `project()` takes with `method = "euler"`: the rates are evaluated at the state at the start of the step, and the resulting transport problem is solved implicitly,

$$A(N^t, n^t_{pp})\, N^{t+1} = S(N^t, n^t_{pp}),$$

with the same `project_n_loop()` C++ Thomas solver and the same spatial scheme (`second_order_w()`) as the regular dynamics.

Because the rates are evaluated at the *input* state, the step is not fully implicit, and the discrete eigenvalues therefore cannot be converted into continuous-time eigenvalues by any exact algebraic relation. That conversion is what `getStability()` avoids by differentiating the rates of change themselves.

The resource is advanced by the model's own `resource_dynamics` function, the one `project()` calls. Nothing is substituted for it: the map that is differentiated here reproduces a single `project(method = "euler")` step exactly, which is what makes the spectral radius a statement about mizer's solver rather than about a nearby scheme.

Value

A named list with the following components:

`discrete_eigenvalues` Complex vector of the eigenvalues μ_i of the one-step map, sorted by decreasing modulus.

`spectral_radius` $\max_i |\mu_i|$. Less than 1 means the numerical scheme is stable at this `dt`.

`stable` Logical: `TRUE` when `spectral_radius < 1`.

`dt` The step size the map was evaluated at.

`n_active` Dimension of the Jacobian.

`leading_eigenvectors` The eigenvectors of the two largest-modulus eigenvalues, in the same shape as for `getStability()`.

`params` The validated `params` object the analysis was made at.

Requires smooth dynamics

The finite-difference Jacobian is only meaningful if the rates of change are differentiable at N^*. A custom rate function registered with `setRateFunction()` that jumps as a function of the abundances breaks this in two ways. If the state sits on the switching threshold, some perturbations straddle it and pick up the jump, and the reported eigenvalues then vary wildly with `h`. If the state is near but not on the threshold, no perturbation crosses it, and the function silently returns the stability of the single branch the state happens to lie on — which can read as `stable` for a model whose simulations never settle.

Re-running with a different `h` is the cheapest check: if the answer moves, do not trust it. See Discontinuous rate functions.

See Also

`getStability()`, `findSteadyState()`

`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(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Details

The growth rate is calculated as the difference between the energy available for reproduction and growth (obtainable with `getEReproAndGrowth()`) and the energy used for reproduction (obtainable with `getERepro()`), but is set to 0 if the result would be negative.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (species x size) with the somatic growth rates (grams/year).
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x species x size) with the growth rates at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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: getDiffusion(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
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
growth <- getEGrowth(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)
# Growth rate at this time for Sprat of size 2g
growth["Sprat", "2"]
```

---

getEncounter *Get encounter rate*

Description

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

Usage

```
getEncounter(object, ...)
```

Arguments

object	A MizerParams or MizerSim object.
...	Additional arguments that depend on the class of object.

For a MizerParams object:

- n A matrix of species abundances (species x size). Defaults to the initial abundances stored in object.
- n_pp A vector of the resource abundance by size. Defaults to the initial resource abundance stored in object.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (predator species x predator size) with the encounter rates.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x predator species x predator size) with the encounter rates at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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.

Extension hook

projectEncounter() is the S3 generic used by extension-aware projections. Extension packages can add methods for their extension classes and call NextMethod() to compose encounter-rate changes. The MizerParams method contains the standard mizer calculation and is also exported as mizerEncounter() for compatibility.

Your own encounter function

By default getEncounter() calls mizerEncounter() on models without extensions. 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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), 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(object, ...)
```

Arguments

object	A MizerParams or MizerSim object.
...	Additional arguments that depend on the class of object.

For a MizerParams object:

n A matrix of species abundances (species x size). Defaults to the initial abundances stored in object.

n_pp A vector of the resource abundance by size. Defaults to the initial resource abundance stored in object.

n_other A named list of the abundances of other dynamical components. Defaults to the initial values stored in object.

t The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

time_range The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

drop If TRUE then any dimension of length 1 is removed from the returned array.

Value

- MizerParams: An ArraySpeciesBySize object (species x size) holding

$$\psi_i(w)\max(0, E_{r.i}(w))$$

  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. Negative values of $E_{r.i}(w)$ are clipped to 0 before multiplying by $\psi_i(w)$. This proportion is taken from the params object and is set with setReproduction().
- MizerSim: An ArrayTimeBySpeciesBySize object (time step x species x size) with the energy for reproduction at every time step. If drop = TRUE then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
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
erepro <- getERepro(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)
# Rate at this time for Sprat of size 2g
erepro["Sprat", "2"]
```

`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(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (species x size) with the energy rate $E_{r.i}(w)$ available for growth and reproduction (grams/year).
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x species x size) with the energy rate at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getERepro(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
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
e <- getEReproAndGrowth(params, n = N(sim)[15, , ],
                        n_pp = NResource(sim)[15, ], t = 15)
# Rate at this time for Sprat of size 2g
e["Sprat", "2"]
```

---

getESpawning *Alias for* getERepro()

Description

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

Usage

```
getESpawning(object, ...)
```

Arguments

object — A MizerParams or MizerSim object.

... — Additional arguments that depend on the class of object.

For a MizerParams object:

n A matrix of species abundances (species x size). Defaults to the initial abundances stored in object.

n_pp A vector of the resource abundance by size. Defaults to the initial resource abundance stored in object.

n_other A named list of the abundances of other dynamical components. Defaults to the initial values stored in object.

t The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

time_range The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

drop If TRUE then any dimension of length 1 is removed from the returned array.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (species x size) holding

$$\psi_i(w)\max(0, E_{r.i}(w))$$

  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. Negative values of $E_{r.i}(w)$ are clipped to 0 before multiplying by $\psi_i(w)$. This proportion is taken from the `params` object and is set with `setReproduction()`.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x species x size) with the energy for reproduction at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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: `getDiffusion()`, `getEGrowth()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `getFlux()`, `getFluxGradient()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
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
erepro <- getERepro(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)
# Rate at this time for Sprat of size 2g
erepro["Sprat", "2"]
```

---

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, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (predator species x predator size) with the feeding level.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x predator species x predator size) with the feeding level at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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: `getDiffusion()`, `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFlux()`, `getFluxGradient()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
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))
```

---

getFlux *Get flux into size bins*

Description

Calculates the flux $J_i(w)$ (numbers/year) entering each size class from the one below it. This is composed of an advective flux from somatic growth and a diffusive flux from the redistribution of individuals.

Usage

```
getFlux(object, ..., power = 0)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

t The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

time_range The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

drop If TRUE then any dimension of length 1 is removed from the returned array.

power The flux at weight w is multiplied by w raised to power. The default power = 0 gives the flux of individuals (numbers/year), whereas power = 1 gives the flux of biomass (grams/year).

Details

At the recruitment size, the flux is simply the recruitment rate $R_{dd,i}$ (see getRDD()). For sizes below the recruitment size the flux is zero.

The flux at weight w is multiplied by w raised to the power given by the power argument, similar to the power argument of plotSpectra(). The default power = 0 returns the flux of individuals (numbers/year). With power = 1 the result is the flux of biomass (grams/year).

Value

- MizerParams: An ArraySpeciesBySize object (species x size) with the flux entering each size class. The units are numbers/year when power = 0 and g^power/year otherwise.
- MizerSim: An ArrayTimeBySpeciesBySize object (time step x species x size) with the flux at every time step. If drop = TRUE then dimensions of length 1 will be removed.

See Also

getEGrowth(), getRDD()

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

Examples

```
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 flux at a particular time step
flux <- getFlux(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ], t = 15)
# Flux for Sprat of size 2g
flux["Sprat", "2"]
```

`getFluxGradient` *Get flux gradient*

Description

[Experimental] Calculates the flux divergence $(J_{j+1} - J_j)/\Delta w_j$ that appears as the second term in the discretised size-spectrum transport equation

$$\frac{\partial N_j}{\partial t} + \frac{J_{j+1} - J_j}{\Delta w_j} = -\mu_j N_j.$$

The bin-boundary fluxes J_j are obtained from `getFlux()`, which uses the advective-flux scheme stored in the `flux` entry of the `second_order_w` slot of `params`. The flux leaving the largest size class through the upper boundary (J_{K+1}) is evaluated with the same scheme using the boundary condition $N_{K+1} = 0$.

Usage

```
getFluxGradient(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (species x size) giving the flux divergence in each size bin, in units of g^{-1} year^{-1}.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x species x size) with the flux divergence at every saved time step. If `drop = TRUE` then dimensions of length 1 will be removed.

See Also

getFlux(), second_order_w()

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

Examples

```
params <- NS_params
fg <- getFluxGradient(params)
sim <- project(params, t_max = 5)
fg_sim <- getFluxGradient(sim)
```

---

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. See setFishing() for details of how fishing gears are set up.

Usage

```
getFMort(object, ...)
```

Arguments

object — A MizerParams or MizerSim object.

... — Additional arguments that depend on the class of object.

For a MizerParams object:

effort The effort of each fishing gear. See notes below. Defaults to the initial effort stored in object.

n A matrix of species abundances (species x size). Defaults to the initial abundances stored in object.

n_pp A vector of the resource abundance by size. Defaults to the initial resource abundance stored in object.

n_other A named list of the abundances of other dynamical components. Defaults to the initial values stored in object.

t The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

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. Defaults to the whole time range of the simulation.

drop Should dimensions of length 1 be dropped, e.g. if your community only has one species it might make presentation of results easier. Defaults to TRUE.

Details

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

Value

- MizerParams with vector effort: An ArraySpeciesBySize object (species x size) with the fishing mortality rates.
- MizerParams with time-dimensioned effort or MizerSim: An ArrayTimeBySpeciesBySize object (time x 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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
params <- NS_params
# Get the total fishing mortality in the initial state
F <- getFMort(params, effort = 1)
str(F)
# Get the initial total fishing mortality when effort is different
# between the four gears:
F <- 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)
F <- getFMort(params, effort = effort)
str(F)
# Get the total fishing mortality using the effort already held in a
# MizerSim object.
sim <- project(params, t_max = 20, effort = 0.5)
F <- getFMort(sim)
F <- getFMort(sim, time_range = c(10, 20))
```

`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, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`effort` The effort for each fishing gear. See notes below. Defaults to the initial effort stored in `object`.

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`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. Defaults to the whole time range of the simulation.

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: `getDiffusion()`, `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFeedingLevel()`, `getFlux()`, `getFluxGradient()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`, `getResourceMort()`

Examples

```
params <-NS_params
# Get the fishing mortality in initial state
F <- getFMortGear(params, effort = 1)
str(F)
# Get the initial fishing mortality when effort is different
# between the four gears:
F <- 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)
F <- getFMortGear(params, effort = effort)
str(F)
# Get the fishing mortality using the effort already held in a MizerSim object.
sim <- project(params, t_max = 20, effort = 0.5)
F <- getFMortGear(sim)
F <- getFMortGear(sim, time_range = c(10, 20))
```

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(), getSteadyResidual(), getTrophicLevel(), getTrophicLevelBySpecies(), getYield(), getYieldGear()

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

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

Usage

```
getM2(object, ...)
```

Arguments

object	A MizerParams or MizerSim object.
...	Additional arguments that depend on the class of object. **For a MizerParams object:** n A matrix of species abundances (species x size). Defaults to the initial abundances stored in object. n_pp A vector of the resource abundance by size. Defaults to the initial resource abundance stored in object. n_other A named list of the abundances of other dynamical components. Defaults to the initial values stored in object. t The time for which to do the calculation. Defaults to 0. **For a MizerSim object:** time_range The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation. drop If TRUE then any dimension of length 1 is removed from the returned array.

Value

- MizerParams: An ArraySpeciesBySize object (prey species x prey size) with the predation mortality rates.
- MizerSim: An ArrayTimeBySpeciesBySize object (time step x prey species x prey size) with the predation mortality at every time step. If drop = TRUE then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
params <- NS_params
# Predation mortality in initial state
M2 <- getPredMort(params)
str(M2)
# 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
M2 <- getPredMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])
# Get predation mortality at all saved time steps
M2 <- getPredMort(sim)
str(M2)
# Get predation mortality over the years 15 - 20
M2 <- getPredMort(sim, time_range = c(15, 20))
```

---

getM2Background *Alias for* getResourceMort()

Description

[Superseded] 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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates()

Examples

```
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, ])
```

---

getMeanMaxWeight *Calculate the mean maximum weight of the community*

Description

Calculates the mean maximum weight of the community. 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(object, species = NULL, measure = "both", ...)
```

Arguments

`object`	A MizerSim or MizerParams 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 (or a named vector with two entries for `MizerParams`). If `measure` = "`numbers`" or "`biomass`" you get a vector of the respective values at each saved time step (or a single value for `MizerParams`).

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, ]
getMeanMaxWeight(NS_params)
```

`getMeanWeight` *Calculate the mean size of the community*

Description

`getMeanWeight()` calculates the mean weight of the community. This is simply the total biomass of the community divided by the abundance in numbers. `getMeanLength()` calculates the mean length of the community, i.e. the total length of all individuals divided by their number, where the length of an individual of weight w of species i is obtained from the length-weight relationship $w = a_i l^{b_i}$ with the species parameters a and b.

Usage

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

getMeanLength(object, species = NULL, ...)
```

Arguments

object	A MizerSim or MizerParams 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.

Details

The length-weight parameters a and b are taken from the species parameter data frame, where they are given the defaults a = 0.01 and b = 3 when a model is created. getMeanLength() gives an error if a model is so old that it has no such columns.

You can specify minimum and maximum weight or length for the included size range. 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.

You will usually want to give a minimum size. Over the full size range the community is dominated in numbers by the smallest individuals, so both means describe the larvae rather than the fish, and in the case of getMeanLength() they do so with a length-weight relationship that was fitted to observed fish and is being extrapolated far below the sizes it describes. A minimum size also makes the indicator comparable to one calculated from survey data, which sees only the sizes the gear catches.

Value

A vector containing the mean weight (in grams) or the mean length (in cm) of the community through time, or a single value if called with a MizerParams object.

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]
getMeanWeight(NS_params)

mean_length <- getMeanLength(NS_sim)
mean_length[years]
# Only a couple of centimetres, because the larvae outnumber everything
# else. Give a minimum size to get an indicator about fish:
getMeanLength(NS_sim, min_l = 10)[years]
getMeanLength(NS_sim, min_w = 10, max_w = 5000)[years]
getMeanLength(NS_sim, species = c("Herring", "Sprat", "N.pout"),
              min_l = 10)[years]
getMeanLength(NS_sim@params, min_l = 10)
```

---

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(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`effort` A numeric vector of the effort by gear or a single numeric effort value which is used for all gears. Defaults to the initial effort stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

time_range The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

drop If TRUE then any dimension of length 1 is removed from the returned array.

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

- MizerParams: An ArraySpeciesBySize object (species x size) with the total mortality rates.
- MizerSim: An ArrayTimeBySpeciesBySize object (time step x species x size) with the total mortality rates at every time step. If drop = TRUE then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
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
mort <- getMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ],
                t = 15, effort = 0.5)
# Mortality rate at this time for Sprat of size 2g
mort["Sprat", "2"]
```

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

Description

Calculates the number of individuals within user-defined size limits. 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(object, ...)
```

Arguments

object	An object of class `MizerParams` or `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

If called with a MizerParams object, a named vector with the numbers for each species in the model. If called with a MizerSim object, a `ArrayTimeBySpecies` object (time x species) containing the numbers at each time step for all species.

See Also

Other summary functions: `getBiomass()`, `getDiet()`, `getGrowthCurves()`, `getSSB()`, `getSteadyResidual()`, `getTrophicLevel()`, `getTrophicLevelBySpecies()`, `getYield()`, `getYieldGear()`

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"]
```

`getOscillationModeSim` *Construct a MizerSim of the leading oscillatory mode*

Description

[Experimental] Using the leading complex eigenvector from `getStability()`, constructs a MizerSim object covering one period of that oscillation in the linear approximation. The result can be inspected with all standard mizer plotting functions (e.g. `plotBiomass()`, `plotSpectra()`).

Usage

```
getOscillationModeSim(x, amplitude = 0.1, t_save = 0.1, ...)
```

Arguments

`x`	A MizerParams object at a steady state, typically the output of `findSteadyState()`, or the list returned by `getStability()`.
`amplitude`	Largest relative swing in species biomass across the cycle, $\max_i \max_t |B_i(t) - B_i^*|/B_i^*$. Default `0.1`, meaning the most strongly oscillating species departs 10 % from its steady biomass.
`t_save`	The time interval between saved time steps in the returned MizerSim. Defaults to `0.1`. The final interval is shorter when `t_save` does not divide the period, so that the cycle closes.
`...`	Additional arguments forwarded to `getStability()` when `x` is a `MizerParams` object.

Details

The object shows the *shape* of the mode — which species swing, how far, and in what phase relative to each other and to the resource. Whether the model actually settles onto this oscillation is a separate question, answered by the real part of the eigenvalue: it is a limit cycle only where that real part is zero, at a Hopf bifurcation.

Mathematical background:

An oscillatory mode is a complex-conjugate pair of eigenvalues $\lambda = \sigma \pm i\omega$ of the Jacobian, with period $T = 2\pi/|\omega|$. `getStability()` returns the pair with the largest σ as `leading_oscillatory_eigenvalue` and its eigenvector as `leading_oscillatory_eigenvector`. The linearised perturbation of the full state $x = (N, n_{pp})$ is

$$\delta x(t) = A \ \mathrm{Re}[e^{i\omega t}\,\mathbf{v}],$$

where $\mathbf{v}$ is that eigenvector and A is chosen so that the largest *relative swing in species biomass* equals `amplitude`. Biomass is a linear functional of the abundance, so

$$B_i(t) = B_i^* + A \ \mathrm{Re}[e^{i\omega t} c_i], \qquad c_i = \int v_i(w)\, w\, dw,$$

and species i departs from its steady biomass by at most $A|c_i|$. A is set so that $\max_i A|c_i|/B_i^*$ is `amplitude`: no species' biomass moves further than that fraction from its steady value, and

the one that oscillates hardest moves exactly that far. The integral uses `sizeIntegral()`, so it follows the model's own quadrature scheme and agrees with `getBiomass()` bin for bin.

The cap is on the species that swings hardest rather than on the community total, because species oscillating out of phase cancel in the total: a modest total swing can be produced by wild swings in the individual species.

The state at each time is

$$x(t) = \max(x^* + \delta x(t),\ 0).$$

Because the cap is on biomass, an individual size class can still be driven negative while the biomass it belongs to moves only a little — a cohort trough is a much larger relative excursion than the biomass integral over it. That clipping is reported when it happens, and means the picture is no longer the linear mode.

The fish and resource blocks of $\mathbf{v}$ carry a single common normalisation, so the same A drives both and the resource oscillates with the amplitude and phase *the mode gives it* — generally neither in step with the fish nor slaved to them. `amplitude` is set on the fish biomass, so how far the resource moves is a property of the mode rather than something you choose.

The growth of the mode is deliberately dropped: $e^{\sigma t}$ is omitted so that the oscillation closes after one period. That is exact only at a Hopf bifurcation, where $\sigma = 0$; away from it the returned object shows the *shape* of the oscillation, not its envelope. σ is recorded in the result's `sim_params` as `growth_rate`, and it is the number to look at before calling what you are seeing a cycle.

The returned MizerSim has times running from 0 to exactly T (the period, in years). The saved times are spaced `t_save` apart, except for the last interval, which is shortened when `t_save` does not divide T. Ending exactly at T is what makes the cycle close: the phase factor $e^{i\omega T}$ is 1, so the final state is the first state again.

Value

A MizerSim object whose time axis spans one period $[0, T]$ of the linearised oscillatory mode.

See Also

`getStability()`, `findSteadyState()`

`getParams` *Extract the model state from a simulation*

Description

A `MizerParams` object describes the state of the ecosystem: its species parameters, size grid, rate functions, *and* the current abundances stored in the `initial_n`, `initial_n_pp`, `initial_n_other`, and `initial_effort` slots. These functions extract that state from a `MizerSim` object.

Usage

```
getParams(sim, time_range, geometric_mean = FALSE)

initialParams(sim)

finalParams(sim)
```

Arguments

`sim`	A `MizerSim` object.
`time_range`	The time range to average the abundances over. Can be a vector of values, a vector of min and max time, or a single value. Only the range of times is relevant, i.e., all times between the smallest and largest will be selected. Default is the final time step.
`geometric_mean`	**[Experimental]** If `TRUE`, the average of the abundances over the time range is a geometric mean instead of the default arithmetic mean. This does not affect the average of the effort or of other components, which is always arithmetic.

Details

`getParams()` returns the state averaged over a chosen `time_range`, or at a single time point. When no `time_range` is given, the state at the final time step is returned.

`initialParams()` returns the state at the initial time of the simulation, i.e., the `MizerParams` object that the simulation started from.

`finalParams()` returns the state at the *last* saved time step. It is a convenience wrapper around `getParams()` with no `time_range` argument.

The abundances set by `getParams()` are averages over the selected time range. By default this is an arithmetic mean; set `geometric_mean = TRUE` to use a geometric mean instead (this does not affect the effort or other components, which are always averaged arithmetically).

Value

A `MizerParams` object with `initial_n`, `initial_n_pp`, `initial_n_other`, and `initial_effort` set to the values from the selected time of the simulation.

Examples

```
sim <- project(NS_params, t_max = 20, effort = 0.5)
# State at a specific time
params_10 <- getParams(sim, time_range = 10)
# State averaged over the last 10 years
params_avg <- getParams(sim, time_range = c(10, 20))
# State at the start and at the end of the simulation
params_start <- initialParams(sim)
params_end <- finalParams(sim)
```

`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) equal to `getEncounter(object, n, n_pp) / search_vol(object)`.

See Also

`project()`

---

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, ...)
```

Arguments

object	A MizerParams or MizerSim object.
...	Additional arguments that depend on the class of `object`. **For a MizerParams object:** `n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`. `n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`. `n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

t The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

time_range The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

drop If TRUE then any dimension of length 1 is removed from the returned array.

Value

- MizerParams: An ArraySpeciesBySize object (prey species x prey size) with the predation mortality rates.
- MizerSim: An ArrayTimeBySpeciesBySize object (time step x prey species x prey size) with the predation mortality at every time step. If drop = TRUE then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
params <- NS_params
# Predation mortality in initial state
M2 <- getPredMort(params)
str(M2)
# 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
M2 <- getPredMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ])
# Get predation mortality at all saved time steps
M2 <- getPredMort(sim)
str(M2)
# Get predation mortality over the years 15 - 20
M2 <- getPredMort(sim, time_range = c(15, 20))
```

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(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

Value

- `MizerParams`: An `ArraySpeciesBySize` object (predator species x prey size), where the prey size runs over fish community plus resource spectrum.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x predator species x prey size) with the predation rates at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
params <- NS_params
# Predation rate in initial state
pred_rate <- getPredRate(params)
str(pred_rate)
# 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
pred_rate <- getPredRate(params, n = N(sim)[15, , ],
                         n_pp = NResource(sim)[15, ], t = 15)
```

---

getProportionOfLargeFish

Calculate the proportion of large fish

Description

Calculates the proportion of large fish in a MizerSim or MizerParams object 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 length. Lengths take precedence over weights (i.e. if both min_l and min_w are supplied, only min_l will be used, and if threshold_l is supplied it takes precedence over threshold_w). 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(
  object,
  species = NULL,
  threshold_w = 100,
  threshold_l = NULL,
  biomass_proportion = TRUE,
  ...
)
```

Arguments

`object` A MizerSim or MizerParams 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 weight used as the cutoff between large and small fish. Default value is 100.

`threshold_l` The length used as the cutoff between large and small fish. If supplied, this takes precedence over `threshold_w`.

`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, or a single value if called with a `MizerParams` object.

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]
getProportionOfLargeFish(NS_params)
```

---

getRates *Get all rates*

Description

Calls other rate functions in sequence and collects the results in a list. The rates returned are encounter, feeding level, energy for growth and reproduction, predation rate, predation mortality, and resource mortality. The purpose of this function is to provide a convenient way to get all the rates at once, and to ensure that they are all calculated at the same time step with the same inputs. The rates are returned in a list with the same names as the rate functions that calculate them, so for example the encounter rate is returned in the list element named "encounter" and is calculated with the getEncounter() function.

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

When mizer needs to calculate the rates during a simulation it does not use this function but instead the faster `projectRates()`.

See Also

Other rate functions: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), 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(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

`rdi` A vector of density-independent reproduction rates for each species. If not specified, it is calculated internally using getRDI().

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

Value

- `MizerParams`: A numeric vector the length of the number of species.
- `MizerSim`: An `ArrayTimeBySpecies` object (time x species).

See Also

`getRDI()`

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

Examples

```
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)
```

---

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(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

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

- MizerParams: A numeric vector the length of the number of species.
- MizerSim: An ArrayTimeBySpecies object (time x 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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getMort(), getPredMort(), getPredRate(), getRDD(), getRates(), getResourceMort()

Examples

```
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)
```

getRequiredRDD — *Determine reproduction rate needed for initial egg abundance*

Description

Determine reproduction rate needed for initial egg abundance

Usage

```
getRequiredRDD(params, ...)
```

Arguments

params	A MizerParams object
...	Unused.

Value

A vector of reproduction rates for all species

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: `getDiffusion()`, `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `getFlux()`, `getFluxGradient()`, `getMort()`, `getPredMort()`, `getPredRate()`, `getRDD()`, `getRDI()`, `getRates()`

Examples

```
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, ])
```

getSimParams — *Extract the projection parameters used to produce a simulation*

Description

Returns the named list of arguments passed to `project()` or `projectUntilSettled()` when producing this `MizerSim` object, such as `method` and `dt`. Returns an empty list for simulations produced by older versions of mizer.

Usage

```
getSimParams(sim)
```

Arguments

`sim`	A MizerSim object

Value

A named list of projection parameters.

Examples

```
sim <- project(NS_params, t_max = 0.1, dt = 0.05, method = "predictor-corrector")
getSimParams(sim)
```

getSSB — *Calculate the SSB of species*

Description

Calculates the spawning stock biomass (SSB) for each species. For a `MizerSim` object this is returned for every saved time; for a `MizerParams` object it is calculated from the initial state. SSB is the total mass of all mature individuals.

Usage

```
getSSB(object)
```

Arguments

`object`	An object of class `MizerParams` or `MizerSim`.

Value

If called with a MizerParams object, a named vector with the SSB in grams for each species in the model. If called with a MizerSim object, a `ArrayTimeBySpecies` object (time x species) containing the SSB in grams at each time step for all species.

See Also

Other summary functions: getBiomass(), getDiet(), getGrowthCurves(), getN(), getSteadyResidual(), getTrophicLevel(), getTrophicLevelBySpecies(), getYield(), getYieldGear()

Examples

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

---

getStability *Analyse the dynamic stability of a mizer steady state*

Description

[Experimental] Computes the eigenvalues of the linearised dynamics at the steady state stored in `params@initial_n`. These eigenvalues determine whether the steady state is dynamically stable and, where the spectrum contains a complex pair, the period at which the model oscillates.

Usage

```
getStability(params, effort = params@initial_effort, h = 1e-04)
```

Arguments

`params`	A MizerParams object whose `initial_n` holds the steady state to analyse. Typically the output of `findSteadyState()`.
`effort`	The fishing effort to use. By default the initial effort stored in `params`.
`h`	Relative step size for centred finite differences. Default `1e-4`. The result should not depend on this choice. If it does, the dynamics are not smooth at the state being analysed — see the section below.

Details

Mathematical background:

Mizer discretises the size axis but not time: on the size grid the model is a system of ordinary differential equations

$$\frac{dN}{dt} = F(N, n_{pp}),$$

where F collects the divergence of the growth flux, the mortality sink and the reproductive influx at the egg size, assembled with the spatial scheme configured via `second_order_w()`. `getStability()` differentiates F directly, by centred finite differences in each state variable, and returns the eigenvalues λ_i of the resulting Jacobian $J = \partial F / \partial N$. The steady state is **stable** when all of them satisfy $\mathrm{Re}(\lambda_i) < 0$ and **unstable** when at least one exceeds 0.

No time step enters this calculation. The eigenvalues are a property of the model, not of any solver: they describe the continuous-time dynamics of the semi-discretised model, and are what a

simulation with a small enough time step converges to. The stability of the numerical step itself is a separate question, answered by `getDiscreteStability()`.

A complex-conjugate pair $\lambda = \sigma \pm i\omega$ is an oscillatory mode: a perturbation along it rings with period

$$T = \frac{2\pi}{|\omega|} \text{ years},$$

growing or decaying as $e^{\sigma t}$. The pair with the largest σ is returned as `leading_oscillatory_eigenvalue`, with its period and eigenvector.

That is a statement about the mode, not about a bifurcation. A **Hopf bifurcation** is the event of such a pair *crossing* the imaginary axis, and a single spectrum cannot show a crossing: the leading oscillatory mode of a comfortably stable model can sit far to the left, ringing only as a transient on the way back to the fixed point. Establishing a Hopf bifurcation means watching σ pass through zero as a parameter is varied, which is what `scanModel()` is for. Only then is T the period of an emerging limit cycle; otherwise it is the period of a damped (or growing) oscillation.

What is in the Jacobian:

The resource is a state variable of the system like any other: fish and resource cells are perturbed independently, giving the full coupled Jacobian. Its eigenvalues include both the slow fish modes and a cluster of fast resource-relaxation modes, at $\lambda \approx -(r_{pp} + \mu_R)$. Any resource dynamics function is supported: the semichemostat derivative is written down analytically, and anything else is differenced over a short step.

Components registered with `setComponent()` are *not* state variables here. They are held at their stored values while the fish and the resource are perturbed, so the spectrum is that of the consumer-resource subsystem with the components frozen. This is exact when a component is a fixed input, and a good approximation when it is much faster or much slower than the fish, but it is not the full model, and mizer says so with a warning when it meets one. Giving extension components an explicit residual and Jacobian is the work that would lift this restriction.

Reproduction is a state-dependent rate like any other: the reproduction function stored in `params@rates_funcs$RDD` is evaluated at each perturbed state, so the feedback from the spectra back onto the influx of eggs is part of the Jacobian, exactly as it is part of `project()`. There is no option to pin the reproduction rate at its value at the fixed point. A model in which reproduction really is constant expresses that as a model: with `rates_funcs$RDD = "constantRDD"` the derivative of the reproduction rate is zero and the pinned Jacobian is what the analysis returns.

This is why the stability of a steady state depends on the reproduction parameters even though the steady state itself does not. `setBevertonHolt()` moves along a family of `erepro`/`R_max` pairs that all leave the same fixed point, but they do not all leave the same dynamics: at a `reproduction_level()` near 1 the reproduction rate barely responds to the energy invested in it, approaching the constant-reproduction case, while at a level near 0 it follows that energy proportionally. The two ends can differ in their verdict, so the analysis has to read the model rather than take an argument.

Numerical details:

The Jacobian is computed numerically using a multiplicative (relative) finite-difference step $h \cdot N^*$. Where a cell sits at exactly zero and so has no scale of its own, the step is floored at the local scale of the spectrum, interpolated from the nonzero neighbours, so that the cell still gets a resolved derivative rather than a column of rounding error.

Every state at which the rates are evaluated satisfies $N \geq 0$: where a centred step would push a cell negative — which can only happen for a cell at (or below) the floor described above —

the column is differenced forwards from the unperturbed state instead. At the boundary of the physical cone the one-sided derivative is the appropriate object anyway, since the dynamics never visit the states a centred step would sample. A rate function registered with `setRateFunction()` therefore never has to be defined at negative abundances. Such columns are first order in `h` rather than second, so they respond slightly more to a change of `h` than the rest.

Value

A named list with the following components:

`eigenvalues` Complex vector of the continuous-time eigenvalues λ_i, sorted by decreasing real part.

`max_real_part` The largest real part of the eigenvalues: $\max_i \mathrm{Re}(\lambda_i)$. Greater than 0 means unstable.

`stable` Logical: `TRUE` when `max_real_part < 0`.

`dominant_period` The period (in years) of the dominant eigenvalue: `2*pi / abs(Im(lambda_1))`. `Inf` for a real dominant eigenvalue (monotone dynamics).

`oscillation_period` Period (in years) of the oscillatory mode below, $2\pi/|\omega|$; `NULL` when no complex eigenvalue exists. It is the period at which the model rings, and only at a Hopf bifurcation — where the real part is zero — the period of a limit cycle.

`leading_oscillatory_eigenvalue` The complex eigenvalue with the largest real part, or `NULL` when there is none. Its real part is the rate at which that oscillation grows, so a strongly negative one means the ringing is a transient, not a cycle the model settles onto.

`leading_oscillatory_eigenvector` Its eigenvector, as a list with `$fish`, a complex `(n_species, n_sizes)` matrix, and `$resource`, a complex vector of length `n_w_full`. This is the mode `getOscillationModeSim()` draws, and it is not in general one of `leading_eigenvectors`: the dominant mode of the system can be real while the dominant *oscillatory* mode is well down the spectrum.

`n_active` Dimension of the Jacobian: the number of active fish cells plus all resource cells.

`leading_eigenvectors` The eigenvectors of the two eigenvalues with the largest real part, reshaped back into the state space: a list with `$fish`, a complex array of shape `(n_species, n_sizes, 2)` with the same species and size dimnames as `params@initial_n`, and `$resource`, a complex matrix of shape `(n_w_full, 2)`. Each eigenvector is normalised by a single scalar covering both blocks, so that the relative amplitude and phase between fish and resource are those of the mode. The scalar is chosen so that the largest perturbation *relative to the steady state*, $|v_i|/x_i^*$, is 1 somewhere in the state: an absolute normalisation would be set entirely by the resource, whose densities dwarf the fish abundances. `Mod(fish[, , 1]) / initialN(params)` is therefore the relative amplitude pattern, peaking at 1 in whichever cell swings hardest. The real and imaginary parts of eigenvector 1 span the two-dimensional oscillation plane of the dominant mode.

`params` The validated `params` object the analysis was made at.

Requires smooth dynamics

The finite-difference Jacobian is only meaningful if the rates of change are differentiable at N^*. A custom rate function registered with `setRateFunction()` that jumps as a function of the abundances breaks this in two ways. If the state sits on the switching threshold, some perturbations straddle it and pick up the jump, and the reported eigenvalues then vary wildly with `h`. If the state is

near but not on the threshold, no perturbation crosses it, and the function silently returns the stability of the single branch the state happens to lie on — which can read as `stable` for a model whose simulations never settle.

Re-running with a different `h` is the cheapest check: if the answer moves, do not trust it. See Discontinuous rate functions.

See Also

`findSteadyState()`, `getDiscreteStability()`, `getOscillationModeSim()`

`getSteadyResidual` *How far a model is from its steady state*

Description

[Experimental] Returns the rate at which the abundances would change if the model were projected forward from its current initial state, resolved by species and by size. At a steady state this is zero, so it answers the question that every calibration workflow otherwise has to remember to ask: *is this model still at its steady state?*

Usage

```
getSteadyResidual(
  params,
  effort = params@initial_effort,
  dt = 1e-04,
  measure = c("biomass", "per_capita")
)
```

Arguments

`params`	A MizerParams object.
`effort`	The fishing effort at which to evaluate the residual. By default the initial effort stored in `params`, which is the effort the model's steady state belongs to.
`dt`	The step length used for the resource and other components, whose dynamics functions are only available as one-step maps. Smaller is more accurate. Not used for the consumers, whose rate is exact.
`measure`	**[Experimental]** Which rate of change to report. `"biomass"` (the default) gives the contribution of each size class to the relative rate of change of its species' biomass, which sums over sizes to the drift that `isSteady()` judges a model by. `"per_capita"` gives the rate of change of each size class relative to its own density. See the sections above.

Details

There are two ways to say how fast a size class is changing, and `measure` selects between them. Both are in units of 1/year.

`measure = "biomass"`**, the default:**

How much of its species' biomass each size class is adding or removing per year:

$$C_i(w) = \frac{1}{B_i}\,\frac{dN_i(w)}{dt}\,w\,\Delta w, \qquad B_i = \int N_i(w)\,w\,dw.$$

The bin weight $w\,\Delta w$ is the one `sizeIntegral()` uses for a biomass, so it follows whichever quadrature scheme the model is on (see `second_order_w()`), and the values **add up over sizes to the relative rate of change of the species' biomass**:

```
rowSums(getSteadyResidual(params))    # (dB_i/dt) / B_i, one per species
```

That total is the number `isSteady()`, the `summary()` line of a MizerParams object and `project(check_steady = TRUE)` all judge a model by, and it is the drift that would actually show up in `plotBiomass()`. This array therefore says *where* a model is unsteady in the same currency that mizer uses to decide *whether* it is, and a size class can only be conspicuous in it if it is moving enough biomass to matter.

That last property is why this is the default. A size class near the egg size turns over in hours, and one above the size where growth stops decays exponentially towards zero for ever; both carry enormous *per-capita* rates while holding no mass at all. Weighting by biomass gives them the weight they deserve, which is none, with no need for a threshold below which a class is declared to hold nothing.

`measure = "per_capita"`**:**

The rate of change of each size class relative to its own density,

$$R_i(w) = \frac{1}{N_i(w)}\,\frac{dN_i(w)}{dt}.$$

A value of `0.05` means that size class would grow by about 5% over the first year of a projection, and `-0.05` that it would shrink by about that much. This is the scale-free reading. It shows a size class whose growth and mortality are out of balance even when the class holds a millionth of its species' biomass, which is a real statement about the structure of a model, but not one about whether anything observable is moving.

Do not reduce this measure to `max(abs(...))`. Its extremes belong to the fastest-relaxing cells, which are exactly the ones holding no mass: on `NS_params` the largest per-capita rate is 1.2/year, in a cell holding 2e-8 of its species' biomass, while the biomass drift is 0.014/year and the model counts as settled. Under the second-order scheme this is severe enough to reverse the ordering between a converged model and one that has just been knocked off its steady state.

How the rates are obtained:

For the consumers `dN/dt` is exact, not a finite-difference approximation: the backward-Euler transport coefficients used by `project()` satisfy $AN - S = -dt\,dN/dt$ identically, so evaluating them at `dt = 1` gives the instantaneous rate with no time-discretisation error. The resource and other components have arbitrary user-supplied dynamics functions, so their rates are obtained by taking one short step of length `dt`, accurate to $O(dt)$.

Everything is evaluated at the model's own stored state — `initialN()`, `initialNResource()`, `initialNOther()` — using the model's own reproduction function and its own `resource_dynamics`. Nothing is substituted or held fixed. The number therefore answers exactly "if I called `project()` now, would anything move?", which is why it works for every model rather than only for the semichemostat resource that `findSteadyState(solver = "newton")` requires.

Reading the result:

The returned array is an ArraySpeciesBySize object, so it prints, summarises and plots itself:

```
res <- getSteadyResidual(params)
rowSums(res)                  # the biomass drift of each species
plot(res)                     # which species, and at which sizes
```

The plot is the diagnostic one: a model that is off steady state is usually off in one species, or one part of the size range, and the plot says which. Mizer's size grid is logarithmic, so the bin widths are proportional to `w` and the default measure keeps the shape of a density per unit of log size when drawn against a logarithmic size axis: equal areas under the curve are equal contributions to the drift.

With `measure = "per_capita"` a size class with no fish in it has no relative rate of change — it is `0/0` — and is returned as `NA`, so pass `na.rm = TRUE` to any summary. The default measure needs no such exception: `dN/dt` is perfectly well defined in a class with no fish in it, which can be filling up, and its contribution to the biomass drift is reported like any other.

Value

An ArraySpeciesBySize object (species x size) of rates in 1/year: with `measure = "biomass"`, contributions to each species' relative rate of biomass change, which sum over sizes to that rate and are `NA` only for a species with no biomass at all; with `measure = "per_capita"`, per-capita rates of change, `NA` where the size class holds no fish. It carries two further attributes:

`resource` The same measure for the resource, a numeric vector over `w_full`.

`other` A named list with one entry per other component, holding its per-capita rate of change, or `NA` for a component whose state is not numeric. These are reported but not folded into the biomass drift that `isSteady()` judges a model by: mizer does not know what a component's state is measured in, so it cannot form a biomass for it.

See Also

`isSteady()`, `tuneSteadyState()`, `findSteadyState()`, `getStability()`

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

Examples

```
# The relative rate of change of each species' biomass, in 1/year
rowSums(getSteadyResidual(NS_params))

# Matching biomasses moves the model off its steady state, and the plot
# shows which species and which sizes have moved.
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)
plot(getSteadyResidual(params))
```

`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 vector of the times (in years) at which simulation results have been stored in the MizerSim object.

Examples

```
getTimes(NS_sim)
```

`getTrophicLevel` *Get trophic level of individuals at size*

Description

[Experimental] Calculates the trophic level of individuals of each species at each size, assuming the system is in a steady state. The trophic level of an individual is defined as 1 more than the consumption-rate-weighted average trophic level of all the prey it has consumed during its lifetime up to the current size. The resource is given a size-dependent trophic level (see below).

Usage

```
getTrophicLevel(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  w_R = 1e-10,
  beta_R = 1000,
  ...
)
```

Arguments

params	A MizerParams object.
n	A matrix of species abundances (species x size). Defaults to the initial abundances stored in params.
n_pp	A vector of the resource abundance by size. Defaults to the initial resource abundance stored in params.
n_other	A named list of the abundances of other dynamical components. Defaults to the initial values stored in params.
w_R	An average size (in grams) of primary producers in the resource spectrum, used to set the size-dependent resource trophic level. Defaults to 1e-10.
beta_R	An average predator/prey mass ratio for the resource spectrum, used to set the size-dependent resource trophic level. Must be greater than 1. Defaults to 1000.
...	Unused

Details

In the traditional non-size-resolved approach, all individuals of a species have the same diet composition D_{ij}, defined as the proportion of total biomass intake of species i that comes from species j. The trophic levels then satisfy

$$T_i = 1 + \sum_j D_{ij}\, T_j,$$

which is solved as a linear system $(I - D)\,\mathbf{T} = \mathbf{1}$.

In mizer, diet composition changes as an individual grows, so we must integrate over the individual's lifetime. Assuming a steady state so that the growth rate $g_i(w)$ and prey densities depend only on size and not on time, we can replace the integral over time since birth by an integral over weight using $dt = dw/g_i(w)$. The trophic level $T_i(w)$ of an individual of species i at weight w is then

$$T_i(w) = 1 + \frac{\int_{w_0}^{w} \frac{1}{g_i(w')} \sum_j \int r_{ij}(w', w_p)\, T_j(w_p)\, dw_p\, dw'}{\int_{w_0}^{w} \frac{1}{g_i(w')} \sum_j \int r_{ij}(w', w_p)\, dw_p\, dw'},$$

where w_0 is the egg size and $r_{ij}(w, w_p)$ is the rate at which a predator of species i at weight w consumes biomass from prey species j at weight w_p:

$$r_{ij}(w, w_p) = \theta_{ij}\, \gamma_i(w)\, (1 - f_i(w))\, \phi_i(w/w_p)\, N_j(w_p)\, w_p.$$

The sum over j runs over all species and the resource. The resource is assigned a size-dependent trophic level

$$T_R(w) = \max\left(1,\ 1 + \frac{\log(w/w_R)}{\log(\beta_R)}\right),$$

where w_R is an average size of primary producers (which therefore have trophic level 1) and β_R is an average predator/prey mass ratio for the resource (for example zooplankton). This adds one trophic level for each factor of β_R increase in resource size, with a floor at 1 so that the resource trophic level never drops below the primary-producer level. Both the numerator and the denominator (which equals the total biomass consumed over the predator's lifetime from egg size to current weight w) therefore include the resource.

This equation can be viewed as a linear system $(I - D)\,\mathbf{T} = \mathbf{1}$ in which the entries of $\mathbf{T}$ are indexed by (i, w) and the matrix D encodes the lifetime-integrated diet composition. The system is solved iteratively from small to large sizes, exploiting the fact that prey are typically much smaller than the predator (large predator-to-prey mass ratio), so that the trophic levels of all relevant prey sizes are already known when computing $T_i(w)$.

Value

An `ArraySpeciesBySize` object (species x size) with the trophic level of individuals at each size. Entries below the egg size of each species are `NA`.

See Also

`getTrophicLevelBySpecies()`

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

Examples

```
tl <- getTrophicLevel(NS_params)
plot(tl)
```

`getTrophicLevelBySpecies`

Get mean trophic level of each species

Description

[Experimental] Calculates the consumption-rate-weighted mean trophic level of each species, defined as

$$T_i = \frac{\int r_i(w)\, N_i(w)\, T_i(w)\, dw}{\int r_i(w)\, N_i(w)\, dw},$$

where $r_i(w) = (1 - f_i(w))\, E_i(w)$ is the consumption rate of an individual of species i at weight w, $N_i(w)$ is the abundance density, and $T_i(w)$ is the size-resolved trophic level from `getTrophicLevel()`. As in `getTrophicLevel()`, the resource is given a size-dependent trophic level controlled by the `w_R` and `beta_R` arguments.

Usage

```
getTrophicLevelBySpecies(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  w_R = 1e-10,
  beta_R = 1000,
  ...
)
```

Arguments

params	A MizerParams object.
n	A matrix of species abundances (species x size). Defaults to the initial abundances stored in params.
n_pp	A vector of the resource abundance by size. Defaults to the initial resource abundance stored in params.
n_other	A named list of the abundances of other dynamical components. Defaults to the initial values stored in params.
w_R	An average size (in grams) of primary producers in the resource spectrum, used to set the size-dependent resource trophic level. Defaults to 1e-10.
beta_R	An average predator/prey mass ratio for the resource spectrum, used to set the size-dependent resource trophic level. Must be greater than 1. Defaults to 1000.
...	Unused

Value

A named vector with the mean trophic level for each species.

See Also

getTrophicLevel()

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

Examples

```
getTrophicLevelBySpecies(NS_params)
```

getYield *Calculate the rate at which biomass of each species is fished*

Description

This yield rate is given in grams per year. It is calculated at each time step saved in the MizerSim object.

Usage

```
getYield(object)
```

Arguments

object	An object of class MizerParams or MizerSim.

Details

The yield rate $y_i(t)$ for species i at time t is defined as

$$y_i(t) = \int \mu_{f.i}(w,t) N_i(w,t) w dw$$

where $\mu_{f.i}(w,t)$ is the fishing mortality of an individual of species i and weight w at time t and $N_i(w,t)$ is the abundance density of such individuals. The factor of w converts the abundance density into a biomass density and the integral aggregates the contribution from all sizes.

The total catch in a time period from t_1 to t_2 is the integral of the yield rate over that period:

$$C = \int_{t_1}^{t2} y_i(t) dt$$

In practice, as the yield rate is only available at the saved times, one can only approximate this integral by averaging over the available yield rates during the time period and multiplying by the time period. The less the yield changes between the saved values, the more accurate this approximation is. So the approximation can be improved by saving simulation results at smaller intervals, using the t_save argument to project(). But this is only a concern if abundances change quickly during the time period of interest.

Value

If called with a MizerParams object, a named numeric vector with the yield rate in grams per year for each species in the model. If called with a MizerSim object, an ArrayTimeBySpecies object (time x species) containing the yield rate in grams per year at each saved time step.

See Also

getYieldGear()

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

Examples

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

# Running simulation for another year, saving intermediate time steps
params <- finalParams(NS_sim)
sim <- project(params, t_save = 0.1, t_max = 1,
               t_start = 2010, progress_bar = FALSE)
# The yield rate for Herring decreases during the year
getYield(sim)[, "Herring"]
# We approximate the total catch in the year by averaging over the year
sum(getYield(sim)[1:10, "Herring"] / 10)
```

---

getYieldGear — *Calculate the rate at which biomass of each species is fished by each gear*

Description

This yield rate is given in grams per year. It is calculated at each time step saved in the MizerSim object.

Usage

```
getYieldGear(object)
```

Arguments

object	An object of class MizerParams or MizerSim.

Details

For details of how the yield rate is defined see the help page of getYield().

Value

If called with a MizerParams object, an array (gear x species) with the yield rate in grams per year from each gear for each species in the model. If called with a MizerSim object, an array (time x gear x species) containing the yield rate at each time step.

See Also

getYield()

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

Examples

```
yield <- getYieldGear(NS_sim)
dim(yield)
yield["1972", , "Herring"]
```

---

getZ *Alias for* `getMort()`

Description

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

Usage

```
getZ(object, ...)
```

Arguments

`object` A MizerParams or MizerSim object.

`...` Additional arguments that depend on the class of `object`.

For a MizerParams object:

`n` A matrix of species abundances (species x size). Defaults to the initial abundances stored in `object`.

`n_pp` A vector of the resource abundance by size. Defaults to the initial resource abundance stored in `object`.

`n_other` A named list of the abundances of other dynamical components. Defaults to the initial values stored in `object`.

`effort` A numeric vector of the effort by gear or a single numeric effort value which is used for all gears. Defaults to the initial effort stored in `object`.

`t` The time for which to do the calculation. Defaults to 0.

For a MizerSim object:

`time_range` The time range over which to return the rates. Either a vector of values, a vector of min and max time, or a single value. Defaults to the whole time range of the simulation.

`drop` If `TRUE` then any dimension of length 1 is removed from the returned array.

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

- `MizerParams`: An `ArraySpeciesBySize` object (species x size) with the total mortality rates.
- `MizerSim`: An `ArrayTimeBySpeciesBySize` object (time step x species x size) with the total mortality rates at every time step. If `drop = TRUE` then dimensions of length 1 will be removed.

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: getDiffusion(), getEGrowth(), getERepro(), getEReproAndGrowth(), getEncounter(), getFMort(), getFMortGear(), getFeedingLevel(), getFlux(), getFluxGradient(), getPredMort(), getPredRate(), getRDD(), getRDI(), getRates(), getResourceMort()

Examples

```
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
mort <- getMort(params, n = N(sim)[15, , ], n_pp = NResource(sim)[15, ],
                t = 15, effort = 0.5)
# Mortality rate at this time for Sprat of size 2g
mort["Sprat", "2"]
```

---

indicator_functions *Description of indicator functions*

Description

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

Details

When called with a MizerSim object, these functions return a time series of values. When called with a MizerParams object, they return a single value calculated from the initial abundances stored in the params object.

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

Function	Returns
getProportionOfLargeFish()	A vector with values at each time step (or a single value for MizerParams).
getMeanWeight()	A vector with values at each saved time step (or a single value for MizerParams).
getMeanLength()	A vector with values at each saved time step (or a single value for MizerParams).

`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

`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 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.

Usage

```
initial_effort(params)

initial_effort(params) <- value
```

Arguments

`params`	A MizerParams object
`value`	A vector or scalar with the initial fishing effort, see Details below.

Details

A valid effort vector is a named vector with one effort value for each gear. However you can also supply the effort value in different ways:

- 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 the default effort returned by `validEffortVector()`, which depends on the defaults edition.

These conversions are done by the function `validEffortVector()`.

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

Value

A named effort vector ordered by gear.

Examples

```
str(initial_effort(NS_params))
```

`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

Value

An `ArraySpeciesBySize` object with dimensions species x size holding the initial number densities for the fish spectra.

See Also

`initialNResource()`, `initialNOther()`

Examples

```
# Doubling abundance of Cod in the initial state of the North Sea model
params <- NS_params
initialN(params)["Cod", ] <- 2 * initialN(params)["Cod", ]
```

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

Value

A named list with the initial values of other ecosystem components

See Also

`initialNResource()`, `initialN()`

Other extension tools: `NOther()`, `coerceToExtensionClass()`, `other_mort()`, `recordExtension()`, `setComponent()`, `setRateFunction()`

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

Value

A vector with the initial number densities for the resource spectrum

See Also

initialN(), initialNOther()

Examples

```
# Doubling resource abundance in the initial state of the North Sea model
params <- NS_params
initialNResource(params) <- 2 * initialNResource(params)
```

---

inter *Alias for* NS_interaction

Description

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

Usage

```
inter
```

Format

A 12 x 12 matrix.

Source

Blanchard et al.

isSteady *Check whether a model is at steady state*

Description

[Experimental] Returns TRUE if the model is at its steady state (within a specified tolerance), FALSE otherwise.

Usage

```
isSteady(params, tol = 0.05, effort = params@initial_effort, ...)
```

Arguments

params	A MizerParams object or an extension thereof.
tol	Tolerance for the relative rate of biomass change in 1/year. Defaults to 0.05 (5% change per year).
effort	The fishing effort at which to evaluate steadiness. By default the initial effort stored in params.
...	Additional arguments passed to methods.

Details

Steadiness is judged by computing the relative rate of change of biomass across all consumer species and the resource (see getSteadyResidual()). If the largest biomass drift is less than or equal to tol, the model is considered to be at steady state.

Value

TRUE if the model's biomass drift is within tol, FALSE otherwise.

Components are not included

Components registered with setComponent() are deliberately left out of this judgement. Their state can be any object at all, so mizer does not know what currency its entries are in and cannot form a biomass for them; and tuneSteadyState(), findSteadyState() and getStability() all hold them fixed, so a criterion that included them could be one that no mizer function is able to satisfy.

A model can therefore be isSteady() while a component of it is still changing. If your model has components with dynamics of their own, check them as well: attr(getSteadyResidual(params), "other") holds their rates of change, and mizer names any that are moving whenever it reports on the model's steady state. To settle them along with everything else, project the model with projectUntilSettled(), which advances the components like every other state variable.

See Also

getSteadyResidual(), tuneSteadyState(), findSteadyState()

Examples

```
isSteady(NS_params)


# Moving a species abundance off its steady state makes isSteady() FALSE
params <- NS_params
initialN(params)[1, ] <- initialN(params)[1, ] * 2
isSteady(params)
```

`knife_edge` *Weight based knife-edge selectivity function*

Description

A knife-edge selectivity function where weights greater or equal to `knife_edge_size` are fully selected and no fish smaller than this size are selected.

Usage

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

Arguments

`w`	Vector of sizes.
`knife_edge_size`	The weight at which the knife-edge operates.
`...`	Unused

Details

You would not usually call this function directly. Instead, set the `sel_func` column in `gear_params()` to `"knife_edge"` and provide `knife_edge_size` as an additional column. `setFishing()` will then call this function automatically when calculating the selectivity array.

Value

Vector of selectivities at the given sizes.

See Also

`gear_params()` for setting the `knife_edge_size` parameter.

Other selectivity functions: `double_sigmoid_length()`, `knife_edge_length()`, `sigmoid_length()`, `sigmoid_weight()`

Examples

```
knife_edge(w = c(1, 10, 100, 1000), knife_edge_size = 100)
```

knife_edge_length *Length based knife-edge selectivity function*

Description

A knife-edge selectivity function where individuals with a length greater or equal to `knife_edge_length` are fully selected and no fish shorter than this length are selected.

Usage

```
knife_edge_length(w, knife_edge_length, species_params, ...)
```

Arguments

`w`	Vector of sizes (weights).
`knife_edge_length`	The length at which the knife-edge operates.
`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

You would not usually call this function directly. Instead, set the `sel_func` column in `gear_params()` to `"knife_edge_length"` and provide `knife_edge_length` as an additional column. `setFishing()` will then call this function automatically when calculating the selectivity array.

As the mizer model is weight based, and this selectivity function is length based, it uses the length-weight parameters `a` and `b` to convert the cut-off length to a weight:

$$w_{\text{cut}} = a \cdot l_{\text{cut}}^{b}$$

Value

Vector of selectivities at the given sizes.

See Also

`gear_params()` for setting the `knife_edge_length` parameter.

Other selectivity functions: `double_sigmoid_length()`, `knife_edge()`, `sigmoid_length()`, `sigmoid_weight()`

Examples

```
# Knife-edge at 20 cm using length-weight parameters a = 0.01, b = 3
sp <- list(a = 0.01, b = 3)
knife_edge_length(w = c(1, 10, 100, 1000), knife_edge_length = 20,
                  species_params = sp)
```

`l2w` *Length-weight conversion*

Description

For each species, convert between length and weight using the relationship

$$w_i = a_i l_i^{b_i}$$

or

$$l_i = (w_i/a_i)^{1/b_i}$$

where `a` and `b` are taken from the species parameter data frame and i is the species index.

Usage

```
l2w(l, species_params)

w2l(w, species_params)
```

Arguments

`l`	Lengths in cm. Either a single number used for all species or a vector with one number for each species.
`species_params`	A species parameter data frame or a MizerParams object.
`w`	Weights in grams. Either a single number used for all species or a vector with one number for each species.

Details

This is useful for converting a length-based species parameter to a weight-based species parameter.

Value

A vector with one entry for each species. `l2w()` returns a vector of weights in grams and `w2l()` returns a vector of lengths in cm.

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.

See Also

`setPredKernel()`

Other predation kernel: `box_pred_kernel()`, `gaussian_mixture_pred_kernel()`, `power_law_pred_kernel()`, `truncated_lognormal_pred_kernel()`

Examples

```
params <- NS_params
plot(w_full(params), pred_kernel(params)["Cod", 10, ], type="l", log="x")
# The restriction that the kernel is zero for w/w_p < 1 is more
# noticeable for larger sigma
species_params(params)$sigma <- 4
plot(w_full(params), pred_kernel(params)["Cod", 10, ], type="l", log="x")
```

---

markBackground *Designate species as background species*

Description

Marks the specified set of species as background species by setting the `is_background` column in their species parameters to `TRUE`. Background species are handled differently in plots (displayed in grey) and their abundances can be automatically adjusted to keep the community close to the Sheldon spectrum (see `adjustBackgroundSpecies()` in the mizerExperimental package).

Usage

```
markBackground(object, species = NULL)
```

Arguments

`object`	An object of class MizerParams or 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.

Value

An object of the same class as the `object` argument

See Also

`removeBackgroundSpecies()`

Examples

```
params <- markBackground(NS_params,
                         species = c("Sprat", "Sandeel", "N.pout"))
any(species_params(params)$is_background)
```

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, info_level = default_info_level(), ...)
```

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.
info_level	Controls the amount of information messages that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.
...	Additional arguments passed to the method.

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 `tuneSteadyState()` 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://blog.mizer.sizespectrum.org/posts/2021-08-20-a-5-step-recipe-for-tuning-the-model-steady-state/.

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)
```

`matchGrowth` *Adjust model to produce observed growth*

Description

[Experimental] Scales the search volume, the maximum consumption rate, the metabolic rate and the external encounter rate all by the same factor in order to achieve a growth rate that allows individuals to reach their maturity size by their maturity age while keeping the feeding level and the critical feeding level unchanged. Then recalculates the size spectra using `steadySingleSpecies()`.

Usage

```
matchGrowth(
  params,
  species = NULL,
  keep = c("egg", "biomass", "number"),
  info_level = default_info_level(),
  ...
)
```

Arguments

`params`	A MizerParams object
`species`	The species to be affected. Optional. By default all species for which growth information is available will be affected. 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.
`keep`	A string determining which quantity is to be kept constant. The choices are "egg" which keeps the egg density constant, "biomass" which keeps the total biomass of the species constant and "number" which keeps the total number of individuals constant.
`info_level`	Controls the amount of information messages that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.
`...`	Additional arguments passed to the method.

Details

Maturity size and age are taken from the `w_mat` and `age_mat` columns in the species_params data frame. If `age_mat` is missing, mizer calculates it from the von Bertalanffy growth curve parameters using `age_mat_vB()`. If those are not available either for a species, the growth rate for that species will not be changed.

Value

A modified MizerParams object with rescaled search volume, maximum consumption rate and metabolic rate and rescaled species parameters `gamma`,`h`, `ks` and `k`.

Examples

```
# Rescale rates so all species reach maturity by their maturity age.
# The search volume gamma is adjusted to achieve the correct growth rate.
species_params(NS_params)["Cod", "gamma"]
params <- matchGrowth(NS_params)
species_params(params)["Cod", "gamma"]
age_mat(params)["Cod"]
```

---

matchNumbers *Match numbers to observations*

Description

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

Usage

```
matchNumbers(params, species = NULL, info_level = default_info_level(), ...)
```

Arguments

`params`	A MizerParams object
`species`	The species to be affected. Optional. By default all observed numbers 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.
`info_level`	Controls the amount of information messages that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.
`...`	Additional arguments passed to the method.

Details

The function works by multiplying for each species the number density at all sizes by the same factor. This will of course not give a steady state solution, even if the initial number densities were at steady state. So after using this function you may want to use `tuneSteadyState()` to run the model to steady state, after which of course the numbers will no longer match exactly. You could then iterate this process. This is described in the blog post at https://blog.mizer.sizespectrum.org/posts/2021-08-20-a-5-step-recipe-for-tuning-the-model-steady-state/.

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

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

Value

A MizerParams object

Examples

```
params <- NS_params
species_params(params)$number_observed <-
    c(0.8, 61, 12, 35, 1.6, 20, 10, 7.6, 135, 60, 30, 78)
species_params(params)$number_cutoff <- 10
params <- calibrateNumber(params)
params <- matchNumbers(params)
```

---

mizerDiffusion *Calculate diffusion rate*

Description

Calculates the diffusion rate $D_i(w)$ (grams^2/year) for each species. This diffusion rate has two components:

1. The diffusion due due to the variability in prey sizes. This is the diffusion term from the jump-growth equation.
2. Any externally specified diffusion, which is added via `setExtDiffusion()`

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

Usage

```
projectDiffusion(params, n, n_pp, n_other, t = 0, feeding_level, ...)

## S3 method for class 'MizerParams'
projectDiffusion(params, n, n_pp, n_other, t = 0, feeding_level, ...)

mizerDiffusion(params, n, n_pp, n_other, t = 0, 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
t	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions.)
feeding_level	An array (species x size) with the feeding level. If not provided, it is calculated from the given abundances.
...	Unused

Value

A two dimensional array (species x size) holding the diffusion rate.

---

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

```
projectEGrowth(params, n, n_pp, n_other, t = 0, e_repro, e, ...)

## S3 method for class 'MizerParams'
projectEGrowth(params, n, n_pp, n_other, t = 0, e_repro, e, ...)

mizerEGrowth(params, n, n_pp, n_other, t = 0, 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

Details

The growth rate is calculated as the difference between the energy available for reproduction and growth (obtainable with getEReproAndGrowth()) and the energy used for reproduction (obtainable with getERepro()), but is set to 0 if the result would be negative.

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: mizerERepro(), mizerEReproAndGrowth(), mizerEncounter(), mizerFMort(), mizerFMortGear(), mizerFeedingLevel(), mizerMort(), mizerPredMort(), mizerPredRate(), mizerRDI(), mizerRates(), mizerResourceMort()

mizerEncounter *Get encounter rate during projection*

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

```
projectEncounter(params, n, n_pp, n_other, t = 0, ...)

## S3 method for class 'MizerParams'
projectEncounter(params, n, n_pp, n_other, t = 0, ...)

mizerEncounter(params, n, n_pp, n_other, 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.

Extension hook

`projectEncounter()` is the S3 generic used by extension-aware projections. Extension packages can add methods for their extension classes and call `NextMethod()` to compose encounter-rate changes. The `MizerParams` method contains the standard mizer calculation and is also exported as `mizerEncounter()` for compatibility.

Your own encounter function

By default `getEncounter()` calls `mizerEncounter()` on models without extensions. 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()`, `mizerERepro()`, `mizerEReproAndGrowth()`, `mizerFMort()`, `mizerFMortGear()`, `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

```
projectERepro(params, n, n_pp, n_other, t = 0, e, ...)

## S3 method for class 'MizerParams'
projectERepro(params, n, n_pp, n_other, t = 0, e, ...)

mizerERepro(params, n, n_pp, n_other, t = 0, 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

$$\psi_i(w)\max(0, E_{r.i}(w))$$

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. Negative entries in e are clipped to 0 before multiplying by $\psi_i(w)$. 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()`, `mizerFMort()`, `mizerFMortGear()`, `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

```
projectEReproAndGrowth(
  params,
  n,
  n_pp,
  n_other,
  t = 0,
  encounter,
  feeding_level,
  ...
)

## S3 method for class 'MizerParams'
projectEReproAndGrowth(
  params,
  n,
  n_pp,
  n_other,
  t = 0,
  encounter,
  feeding_level,
  ...
)

mizerEReproAndGrowth(
  params,
  n,
  n_pp,
  n_other,
  t = 0,
  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

$$E_{r.i}(w) = \alpha_i \left(1 - \texttt{feeding_level}_i(w)\right) \texttt{encounter}_i(w) - \texttt{metab}_i(w).$$

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

$$E_{r.i}(w) = \alpha_i \, \texttt{feeding_level}_i(w) \, h_i(w) - \texttt{metab}_i(w)$$

where h_i is the maximum intake rate, set with setMaxIntakeRate(). However this function is using the first equation above so that it works also when the maximum intake rate is infinite, i.e., there is no satiation. 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(), mizerFMort(), mizerFMortGear(), 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

```
projectFeedingLevel(params, n, n_pp, n_other, t = 0, encounter, ...)

## S3 method for class 'MizerParams'
projectFeedingLevel(params, n, n_pp, n_other, t = 0, encounter, ...)

mizerFeedingLevel(params, n, n_pp, n_other, t = 0, 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()`, `mizerERepro()`, `mizerEReproAndGrowth()`, `mizerEncounter()`, `mizerFMort()`, `mizerFMortGear()`, `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

```
projectFMort(params, n, n_pp, n_other, t = 0, effort, e_growth, pred_mort, ...)

## S3 method for class 'MizerParams'
projectFMort(params, n, n_pp, n_other, t = 0, effort, e_growth, pred_mort, ...)

mizerFMort(params, n, n_pp, n_other, t = 0, 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(), mizerERepro(), mizerEReproAndGrowth(), 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

A 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(), mizerERepro(), mizerEReproAndGrowth(), 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

```
projectMort(params, n, n_pp, n_other, t = 0, f_mort, pred_mort, ...)

## S3 method for class 'MizerParams'
projectMort(params, n, n_pp, n_other, t = 0, f_mort, pred_mort, ...)

mizerMort(params, n, n_pp, n_other, t = 0, 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()`, `mizerERepro()`, `mizerEReproAndGrowth()`, `mizerEncounter()`, `mizerFMort()`, `mizerFMortGear()`, `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 = NULL,
  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). 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_max 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, but must still be finite and in the interval (0, 1).
kappa	The coefficient κ of the resource carrying capacity power law $c_R(w) = \kappa\, w^{-\lambda}$, which also sets the initial resource abundance. See resource_params().
lambda	Used to set power-law exponent for resource capacity if the resource_capacity argument is given as a single number.
r_pp	**[Deprecated]**. Use resource_rate argument instead.
...	Further arguments passed to newMultispeciesParams().

Details

If species_params contains a w_inf column then it is copied to w_max. If max_w is not supplied then it is set to 1.1 * max(species_params$w_max). The supplied min_w_pp is shifted up by one grid step before being passed to newMultispeciesParams() to compensate for the fact that newer mizer versions extend the full size grid below min_w_pp.

Missing legacy columns in species_params are filled as follows: gear = species, k = 0, alpha = 0.6, erepro = 1, sel_func = "knife_edge", knife_edge_size = w_mat if needed, catchability = 1, ks = h * 0.2, and m = 1. If h is missing it is calculated from k_vb, alpha, f0 and w_max. If gamma is missing it is calculated from f0, h, beta, sigma, lambda and kappa.

Value

A MizerParams object

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 upgraded the model.

extensions Describes the extension chain needed to run the model. The entries are named by extension identifier (also the S3 extension class name) and ordered in S3 dispatch order, from outermost to innermost extension. It is either a named character vector whose values are requirement strings (version strings, installation specifications, or NA_character_), or a named list whose entries are length-2 character vectors c(requirement = ..., version = ...). The version records the version of the extension package that last upgraded the object (NA if unknown) and is used by needs_upgrading(). Use recordExtension() to write entries rather than modifying the slot directly.

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 maximum 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 maximum 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()`.

`ext_encounter` An array (species x size) that holds the external encounter rate $E_{ext.i}(w)$. Changed with `setExtEncounter()`.

`ext_diffusion` An array (species x size) that holds the external rate at which the abundance density is redistributed over body size due to mixing, beyond the deterministic growth dynamics. Changed with `ext_diffusion()`.

`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()`.

`ft_pred_kernel_d` 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-diffusion integral (used when `use_predation_diffusion` is `TRUE`). It differs from `ft_pred_kernel_e` only when `second_order_w[["bin_average"]]` is `TRUE`, where it carries the extra power of prey size that the diffusion integrand needs; otherwise it equals `ft_pred_kernel_e`. Changed with `setPredKernel()`.

`rr_pp` A vector the same length as the w_full slot. The size specific growth rate of the resource spectrum.

`cc_pp` A vector the same length as the w_full slot. The size specific carrying capacity of the resource spectrum.

`resource_dynamics` Name of the function for projecting the resource abundance density by one timestep.

`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 `species_params()` for details.

`given_species_params` A data.frame to hold the species parameters that were given explicitly rather than obtained by default calculations.

`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.

`A` **[Deprecated]** Formerly used to flag background species via `NA` values. Replaced by the `is_background` column in `species_params`. Will be removed in a future version.

`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 maximum weight of each species. Used to efficiently minimize wrap-around errors in Fourier transform calculations.

`use_predation_diffusion` A logical flag controlling whether predation-induced diffusion is included when calculating rates with `mizerDiffusion()`. Defaults to `FALSE` to preserve the behaviour of previous mizer versions. Set to `TRUE` to enable the diffusion term from the jump-growth equation.

`second_order_w` A named list with entry `flux` (the advective flux scheme: `"upwind"`, `"van_leer"`, or `"centred"`) and logical entry `bin_average` (controls whether bin-averaging is used for rates). Both default to the first-order setting to preserve the behaviour of previous mizer versions.

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

```
projectPredMort(params, n, n_pp, n_other, t = 0, pred_rate, ...)

## S3 method for class 'MizerParams'
projectPredMort(params, n, n_pp, n_other, t = 0, pred_rate, ...)

mizerPredMort(params, n, n_pp, n_other, t = 0, 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 prey size runs over fish community plus resource spectrum.
...	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(), mizerERepro(), mizerEReproAndGrowth(), mizerEncounter(), mizerFMort(), mizerFMortGear(), 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

```
projectPredRate(params, n, n_pp, n_other, t = 0, feeding_level, ...)

## S3 method for class 'MizerParams'
projectPredRate(params, n, n_pp, n_other, t = 0, feeding_level, ...)

mizerPredRate(params, n, n_pp, n_other, t = 0, 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(), mizerERepro(), mizerEReproAndGrowth(), mizerEncounter(), mizerFMort(), mizerFMortGear(), 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.

projectRates() is an S3 generic used by extension-aware projections to calculate all rates. Models without extensions keep using mizerRates() directly. The base method mirrors mizerRates() but calls migrated projection hooks directly, starting with projectEncounter().

Usage

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

projectRates(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.

Value

List of rates.

See Also

Other mizer rate functions: `mizerEGrowth()`, `mizerERepro()`, `mizerEReproAndGrowth()`, `mizerEncounter()`, `mizerFMort()`, `mizerFMortGear()`, `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

```
projectRDI(
  params,
  n,
  n_pp,
  n_other,
  t = 0,
  e_growth,
  mort,
  e_repro,
  diffusion = NULL,
  ...
)

## S3 method for class 'MizerParams'
projectRDI(
  params,
  n,
  n_pp,
  n_other,
  t = 0,
  e_growth,
  mort,
  e_repro,
  diffusion = NULL,
  ...
)

mizerRDI(
  params,
  n,
  n_pp,
  n_other,
  t = 0,
  e_growth,
  mort,
```

```
  e_repro,
  diffusion = NULL,
  ...
)
```

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().
diffusion	An array (species x size) with the diffusion rate as calculated by getDiffusion(). Unused by the default function but supplied to custom RDI functions.
...	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(), mizerERepro(), mizerEReproAndGrowth(), mizerEncounter(), mizerFMort(), mizerFMortGear(), 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

```
projectResourceMort(params, n, n_pp, n_other, t = 0, pred_rate, ...)

## S3 method for class 'MizerParams'
projectResourceMort(params, n, n_pp, n_other, t = 0, pred_rate, ...)

mizerResourceMort(params, n, n_pp, n_other, t = 0, 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(), mizerERepro(), mizerEReproAndGrowth(), mizerEncounter(), mizerFMort(), mizerFMortGear(), mizerFeedingLevel(), mizerMort(), mizerPredMort(), mizerPredRate(), mizerRDI(), mizerRates()

MizerScan *S3 class for the result of a parameter scan*

Description

[Experimental] scanModel() varies one aspect of a model over a range of values and measures a quantity on the attractor the model settles on at each of them. It returns its result as a MizerScan object, which is a data frame carrying, in addition, everything that plot() needs to draw it.

Usage

```
MizerScan(
  x,
  scan_name = NULL,
  scan_units = NULL,
  value_name = NULL,
  value_units = NULL,
  type = NULL,
  params = NULL,
  reference_lines = NULL,
  settings = NULL
)

is.MizerScan(x)
```

Arguments

x	A data frame with at least three columns, laid out as described above. For is.MizerScan(), any object to test.
scan_name	A string naming the quantity that was varied.
scan_units	A string giving its units, for example "1/year".

value_name	A string naming the quantity that was measured.
value_units	A string giving its units, for example "g/year".
type	The kind of quantity the measured values are, see array_types.
params	The MizerParams object the scan started from.
reference_lines	An optional named numeric vector of x positions to mark with vertical lines.
settings	An optional list recording the settings used.

Details

A MizerScan object behaves like an ordinary data frame with one row for each combination of scanned value and series. Its columns are, in order:

1 The scanned value. The column is named after the scan_name, so for example a scan over fishing effort has a column called "Fishing effort". Use names(scan)[[1]] rather than hard-coding it.

2 The measured quantity, averaged over the attractor. Named after the value_name.

Species The series the row refers to. Named Species whatever the series are, because that is the column that mizer's colour and line-type machinery reads.

ymin**,** ymax The smallest and largest value over the sampling window. On a fixed point these both equal the value; on a limit cycle they give the range of the oscillation.

attractor What the state reached at this scan value is: "fixed_point", "limit_cycle" or NA for neither. This is the column that says whether the value in this row can be read as an equilibrium.

termination**,** converged Why the run at this scan value stopped, and whether the solver met its own criterion. Both come from the "convergence" attribute that projectUntilSettled() attaches to its result, and neither is a claim about the state — see attractor for that.

period The period of the limit cycle in years, or NA.

residual How far the state still is from a fixed point: the largest absolute relative rate of biomass change, in 1/year, taken from the "convergence" attribute that projectUntilSettled() attaches to its result and described there. It is a biomass-weighted aggregate over each species' size classes, not the largest cellwise value of getSteadyResidual().

The first three columns are the x, y and grouping variable in that order, which is the layout plotDataFrame() expects.

It also carries these attributes:

- scan_name, scan_units – name and units of the quantity that was varied, used for the x-axis label.
- value_name, value_units – name and units of the quantity that was measured, used for the y-axis label.
- type – the kind of quantity the values are, see array_types.
- params – the MizerParams object the scan started from, used for species colours and line types.

- `reference_lines` – an optional named numeric vector of positions on the x axis to mark with vertical lines, for example `c(F_MSY = 0.32)`.
- `at_max`, `max_value` – for each series, the scanned value at which the measured quantity is largest, and the value it takes there. See the section below.
- `settings` – a list recording the settings the scan was run with.

Value

A `MizerScan` object, which inherits from `data.frame`.

`is.MizerScan()` returns `TRUE` if `x` is a `MizerScan` object, `FALSE` otherwise.

Where the maximum is

The `at_max` attribute holds, for each series, the scanned value at which that series' measured quantity is largest. On a yield-versus-fishing-mortality scan that is F_{MSY}; on a scan over fishing effort it is the effort that maximises the quantity being plotted. `max_value` holds the value attained there.

This is the largest value **among those that were scanned**, not the maximum of the underlying curve. It is therefore only as good as the grid you gave in `scan_values`, and the way to sharpen it is to scan a finer grid near the maximum, not to interpolate a coarse one. Subsetting a `MizerScan` with `[` recomputes both attributes from the rows that remain, so they never go stale.

Limitations

Because the object is a data frame subclass, its attributes survive base R subsetting with `[` but are dropped by functions that rebuild the data frame, including `dplyr::filter()`, `dplyr::mutate()`, `subset()` and `transform()`. A scan that has lost its attributes can no longer be plotted. Subset with `[`, or rebuild the object with `MizerScan()`.

See Also

`scanModel()`, `plot.MizerScan()`

Other scan functions: `plot.MizerScan()`, `plotYieldVsF()`, `scanEffort()`, `scanModel()`

Examples

```
scan <- scanModel(NS_params, scan_values = c(0, 0.5, 1),
                  set_func = scanEffort(), species = "Cod")
scan
summary(scan)
attr(scan, "at_max")
```

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()` extracts the ecosystem state as a `MizerParams` object with initial abundances set to values from the simulation; `finalParams()` and `initialParams()` are convenient shorthands for the final and

initial time steps. 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 `validSim()`.

Slots

`params` An object of type MizerParams. If this params object uses extensions, the `MizerSim` object uses the same extension chain, which can be inspected with `getMetadata(params)$extensions`; `MizerSim` has no separate extension record.

`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.

`sim_params` A named list of the parameters passed to `project()` or `projectUntilSettled()` to produce this simulation, such as `method` and `dt`.

`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()`: An `ArrayTimeBySpeciesBySize` object (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))
```

---

needs_upgrading — *Determine whether a MizerParams or MizerSim object needs to be upgraded*

Description

Looks at the mizer version that was used to last update the object and returns TRUE if changes since that version require an upgrade of the object. You would not usually have to call this function. Upgrades are initiated automatically by `validParams` and `validSim` when necessary.

Usage

```
needs_upgrading(object)
```

Arguments

`object`	A MizerParams or MizerSim object

Value

TRUE or FALSE

---

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

Description

This functions creates a `MizerParams` object describing a community-type model. The function has many arguments, all of which have default values.

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,
  second_order_w = FALSE,
  info_level = default_info_level(2)
)
```

Arguments

max_w	The maximum size of the community. The w_max 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. Must be finite and in the interval [0, 1).
h	The coefficient of the maximum food intake rate.
gamma	Volumetric search rate. Passed through to newMultispeciesParams(), which estimates it from h, f0, and kappa if it is left as NA.
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	The coefficient κ of the resource carrying capacity power law $c_R(w) = \kappa\, w^{-\lambda}$, which also sets the initial resource abundance. See resource_params().

lambda — Used to set power-law exponent for resource capacity if the `resource_capacity` argument is given as a single number.

r_pp — Growth rate parameter for the resource spectrum.

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 to the rate required to maintain the constructed initial egg abundance.

second_order_w — **[Experimental]** Selects the second-order numerical scheme for the new model. Accepts the same values as the `second_order_w()` setter: a single logical (`TRUE` switches on both second-order flux and bin-averaging), a single flux scheme name (`"upwind"`, `"van_leer"` or `"centred"`), or a named vector with entries `flux` and/or `bin_average`. The `bin_average` choice is applied *before* the resource and abundance power laws are constructed, so they are built bin-averaged from the start (unlike setting `second_order_w()` on an existing object). The `flux` scheme governs time projection only, so the robust first-order upwind scheme is used for the construction-time steady-state solve and the chosen scheme is then activated for the returned model. Defaults to `FALSE` (the first-order behaviour of previous mizer).

info_level — Controls the amount of information messages that are shown when the function sets default values for parameters. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.

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

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

Because this constructor does not yet set up stochastic growth by diffusion, the size grid is not extended beyond the community's maximum size `max_w` (so that `w_max = w_repro_max`), rather than leaving the headroom that `newMultispeciesParams()` uses to accommodate stochastic growth. This will be revisited once these constructors gain a diffusion parameter, see https://github.com/sizespectrum/mizer/issues/339.

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

```
params <- newCommunityParams()
sim <- project(params, t_max = 10)
plotBiomass(sim)
plotSpectra(sim, power = 2)

# More satiation. More mortality
params <- newCommunityParams(f0 = 0.8, z0 = 0.4)
sim <- project(params, t_max = 10)
plotBiomass(sim)
plotSpectra(sim, power = 2)
```

---

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,
  ext_encounter = NULL,
  maturity = NULL,
  repro_prop = NULL,
  RDD = "BevertonHoltRDD",
  kappa = 1e+11,
  n = 2/3,
  resource_rate = 10,
  resource_capacity = kappa,
  lambda = 2.05,
  w_pp_cutoff = 10,
  resource_dynamics = "resource_semichemostat",
  gear_params = NULL,
  selectivity = NULL,
  catchability = NULL,
  initial_effort = NULL,
  second_order_w = FALSE,
  info_level = default_info_level(),
  z0 = deprecated(),
  r_pp = deprecated()
)
```

Arguments

species_params	A data frame of species-specific parameter values.
interaction	Optional interaction matrix of the species (predator species x prey species). 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_max 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 can be overruled for individual species by including a `p` column in the `species_params`.

`ext_mort` Optional. An array (species x size) holding the external mortality rate. If not supplied, a default is set as described in the section "Setting external mortality rate".

`z0pre` If `z0`, the mortality from other sources, is not present in `given_species_params()`, it is calculated as `z0pre * w_inf ^ z0exp`. Default value is 0.6.

`z0exp` The exponent used with `z0pre` to calculate non-given `z0`. Default value is `n - 1`.

`ext_encounter` Optional. An array (species x size) holding the external encounter rate. If not supplied, a default is calculated from the `E_ext` and `n` species parameters as described in the section "Setting external encounter rate".

`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 the energy available for growth and reproduction 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()`".

`kappa` The coefficient κ of the resource carrying capacity power law $c_R(w) = \kappa\, w^{-\lambda}$, which also sets the initial resource abundance. See `resource_params()`.

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

`resource_rate` Optional. A vector of per-capita resource birth rate for each size class or a single number giving the coefficient in the power-law for this rate, see "Setting resource dynamics" below. Must be strictly positive.

`resource_capacity` Optional. Vector of resource intrinsic carrying capacities or coefficient in the power-law for the capacity, see "Setting resource dynamics" below. The resource capacity must not be smaller than the resource abundance.

`lambda` Used to set power-law exponent for resource capacity if the `resource_capacity` argument is given as a single number.

`w_pp_cutoff` The upper cut off size of the resource spectrum power law used when `resource_capacity` is given as a single number. When changing `w_pp_cutoff` without providing `resource_capacity`, the cutoff can only be decreased. In that case, both the carrying capacity and the initial resource abundance will be cut off at the new value. To increase the cutoff, you must also provide the `resource_capacity` for the extended range.

`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.

`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.

`second_order_w` **[Experimental]** Selects the second-order numerical scheme for the new model. Accepts the same values as the `second_order_w()` setter: a single logical (`TRUE` switches on both second-order flux and bin-averaging), a single flux scheme name (`"upwind"`, `"van_leer"` or `"centred"`), or a named vector with entries `flux` and/or `bin_average`. The `bin_average` choice is applied *before* the resource and abundance power laws are constructed, so they are built bin-averaged from the start (unlike setting `second_order_w()` on an existing object). The `flux` scheme governs time projection only, so the robust first-order upwind scheme is used for the construction-time steady-state solve and the chosen scheme is then activated for the returned model. Defaults to `FALSE` (the first-order behaviour of previous mizer).

`info_level` Controls the amount of information messages that are shown when the function sets default values for parameters. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.

`z0` **[Deprecated]** Use `ext_mort` instead. Not to be confused with the species_parameter `z0`.

`r_pp` **[Deprecated]**. Use `resource_rate` argument instead.

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 von Bertalanffy asymptotic sizes of the species in grams. (You could alternatively specify the corresponding length in cm in an `l_inf` column.) The computational upper size boundary `w_max` is not essential; if it is missing it defaults to `1.5 * w_inf`. For backwards compatibility, if `w_inf` is missing it is taken from the `w_repro_max` or `w_max` column instead.

The `species_params dataframe` also needs to contain the parameters needed by any predation kernel function (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.

Setting initial values

The initial values for the species number densities are set using the function `get_initial_n()`. These are quite arbitrary and not very close to the steady state abundances. We intend to improve this in the future.

The initial resource number density $N_R(w)$ is set to a power law with coefficient `kappa` (κ) and exponent `-lambda` ($-\lambda$):

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

for all w less than `w_pp_cutoff` and zero for sizes at or above `w_pp_cutoff`.

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} modifies the interaction of each pair of species in the model. This can be used for example to allow for different spatial overlap among the species. 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.

The interaction matrix is used when calculating the food encounter rate in `getEncounter()` and the predation mortality rate in `getPredMort()`. Its entries are dimensionless numbers. If all the values in the interaction matrix are equal 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 message if it is different before ignoring the supplied dimnames. If you supply only column names then these are also used as the row names. 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 then 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. 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. Alternative pred_kernel types are "box", implemented by `box_pred_kernel()`, "power_law", implemented by `power_law_pred_kernel()`, and "gaussian_mixture", implemented by `gaussian_mixture_pred_kernel()`. These functions require certain species parameters in the species_params data frame. For the lognormal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`, and for the Gaussian mixture they are the list-columns `kernel_p`, `kernel_mean`, and `kernel_sd`. 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 `pred_kernel()` 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. If the `q` column is not supplied, a default of `lambda - 2 + n` is used. 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 $\gamma_i(w)$.

If the `search_vol` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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. If the `n` column is not supplied, a default of $n_i = 3/4$ is used.

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

If the `intake_max` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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.

If the `metab` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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 taken from the species parameters as

$$\mu_{ext.i}(w) = z_{0.i} + z_{ext.i} w^{d_i}.$$

The value of the constant z_0 for each species is taken from the `z0` column of `given_species_params()` if it is present there. Otherwise it is recalculated, even if a value from an earlier calculation is still present in `species_params`, as

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

When `z0pre` or `z0exp` is supplied explicitly and used to calculate non-given `z0`, the resulting values are recorded in `given_species_params()`. Values calculated from the defaults `z0pre = 0.6` and

z0exp = n - 1 are not recorded there. If either argument is supplied but cannot be used because z0 is given for every species or because ext_mort was supplied, a warning is issued. Missing values of z_ext are set to 0 and missing values of d are set to n - 1.

By default the power law is evaluated at the left bin edges w_j (point sampling). If the bin_average entry of the second_order_w slot is TRUE (see second_order_w()), then the $z_{ext} w^d$ term is instead replaced by its exact average over each bin $[w_j, w_{j+1}]$,

$$\frac{z_{ext}}{\Delta w_j} \int_{w_j}^{w_{j+1}} w^d \, dw = z_{ext} \, \frac{w_{j+1}^{d+1} - w_j^{d+1}}{(d+1)\,\Delta w_j},$$

(with the limiting form $z_{ext} \ln(w_{j+1}/w_j)/\Delta w_j$ when $d = -1$). This is the consistent choice in the finite-volume scheme, where the external mortality multiplies the bin-averaged abundance. The bin-averaging is applied only to the auto-calculated power-law default; a user-supplied ext_mort array is left untouched.

Setting external encounter rate

The external encounter rate is the rate at which a predator encounters food that is not explicitly modelled. It is a rate with units mass/year.

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

If the ext_encounter argument is not supplied, then the external encounter rate is calculated as a power law:

$$E_{ext.i}(w) = E_{ext.i} \, w^{n_i}.$$

The coefficient $E_{ext.i}$ is taken from the E_ext column of the species parameter data frame, which defaults to 0. The exponent n_i is taken from the n column of the species parameter data frame.

If the ext_encounter slot has a comment and reset = FALSE, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

Setting external diffusion rate

The external diffusion rate allows you to impose additional diffusion beyond the predation-driven diffusion that can be internally modelled by mizer.

The ext_diffusion argument allows you to specify a diffusion rate that depends on species and body size.

If the ext_diffusion argument is not supplied, then the external diffusion rate is calculated as a power law:

$$D_{ext.i}(w) = D_{ext.i} \, w^{n_i+1}.$$

The coefficient $D_{ext.i}$ is taken from the D_ext column of the species parameter data frame, which defaults to 0. The exponent $n_i + 1$ uses the n column of the species parameter data frame.

If the ext_diffusion slot has a comment and reset = FALSE, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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. There is a size `w_repro_max` at which a typical mature individual invests all of its available energy into reproduction. This is **not** a hard ceiling on size: not all individuals are mature at `w_repro_max`, and diffusion in the growth process allows some individuals to grow beyond it, so fish larger than `w_repro_max` can exist. If you have not specified the `w_repro_max` column in the species parameter data frame, then the von Bertalanffy asymptotic size `w_inf` is used instead.

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 size 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 $U = \log(3)/\log(w_{mat}/w_{mat25})$.

The sigmoidal function given above would strictly reach 0 only asymptotically and thus have some (negligible) amount of reproduction at arbitrarily small size. 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

$$\texttt{repro_prop}(w) = \min\left(\left(\frac{w}{w_{\texttt{repro_max}}}\right)^{m-n}, 1\right).$$

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 sizes w_{repro_max} are taken from the `w_repro_max` column in the species parameter data frame, if it exists, or otherwise from the `w_inf` column.

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

$$\psi(w) = \texttt{maturity}(w)\texttt{repro_prop}(w)$$

In mizer edition 1, at sizes above `w_repro_max` the value of ψ is additionally forced to 1, so that all available energy is invested into reproduction and growth stops. In edition 2 and above this forcing is not applied, and ψ is determined entirely by the maturity ogive and the reproductive proportion.

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.

The most commonly-used selectivity function is sigmoid_length(). It has a smooth transition from 0 to 1 at a certain size. The sigmoid_length() function has the two parameters l50 and l25 that are the lengths in cm at which 50% or 25% of the fish are selected by the gear. If you choose this selectivity function then the l50 and l25 columns must be included in the gear parameters data.frame.

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

The resource_dynamics argument allows you to choose the resource dynamics function. 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 that to use a logistic model implemented by `resource_logistic()` or you can use `resource_constant()` which keeps the resource constant or you can write your own function.

Both the `resource_semichemostat()` and the `resource_logistic()` dynamics are parametrised in terms of a size-dependent birth rate $r_R(w)$ and a size-dependent capacity c_R. The help pages of these functions give the details.

The `resource_rate` argument can be a vector (with the same length as `w_full(params)`) specifying the intrinsic resource birth rate for each size class. Alternatively it can be a single number that is used as the coefficient in a power law: then the intrinsic birth rate $r_R(w)$ at size w is set to

$$r_R(w) = r_R w^{n-1}.$$

The power-law exponent n is taken from the `n` argument.

The `resource_capacity` argument can be a vector specifying the intrinsic resource carrying capacity for each size class. Alternatively it can be a single number that is used as the coefficient in a truncated power law: then the intrinsic carrying capacity $c_R(w)$ at size w is set to

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

for all w less than `w_pp_cutoff` and zero for larger sizes. The power-law exponent λ is taken from the `lambda` argument.

The values for `lambda`, `n` and `w_pp_cutoff` are stored in a list in the `resource_params` slot of the MizerParams object so that they can be re-used automatically in the future. If you specify `resource_rate` or `resource_capacity` as a single number, that coefficient is likewise stored, as `r_pp` and `kappa` respectively. That list can be accessed with `resource_params()`.

The resource power law also determines defaults for species search volume. Changing `lambda` recalculates any `q` and `gamma` values that mizer calculated, and changing `kappa` (by supplying a scalar `resource_capacity`) recalculates any calculated `gamma`. Species-specific values that you supplied explicitly remain unchanged.

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_max = 100,
  w_min = 0.001,
  eta = 10^(-0.6),
  w_mat = w_max * eta,
  no_w = log10(w_max/w_min) * 20 + 1,
  n = 3/4,
  p = n,
  lambda = 2.05,
  kappa = 0.005,
  alpha = 0.4,
  h = 30,
  beta = 100,
  sigma = 1.3,
  f0 = 0.6,
  fc = 0.25,
  ks = NA,
  gamma = NA,
  ext_mort_prop = 0,
  reproduction_level = 0,
  second_order_w = FALSE,
  info_level = default_info_level(),
  R_factor = deprecated(),
  w_inf = deprecated(),
  k_vb = deprecated()
)
```

Arguments

`species_name`	A string with a name for the species. Will be used in plot legends.
`w_max`	Maximum size of species
`w_min`	Egg size of species

eta	Ratio between maturity size w_mat and maximum size w_max. 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_max.
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.
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, but must still be finite and in the interval (0, 1).
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 and 1 that determines the level of density dependence in reproduction, see reproduction_level<-().
second_order_w	**[Experimental]** Selects the second-order numerical scheme for the new model, applied before the resource and abundance power laws are constructed so that they are built bin-averaged from the start. Accepts the same values as the second_order_w() setter. Defaults to FALSE. See newMultispeciesParams().
info_level	Controls the amount of information messages that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().
R_factor	**[Deprecated]** Use reproduction_level = 1 / R_factor instead.
w_inf	**[Deprecated]** The argument has been renamed to w_max.
k_vb	**[Deprecated]** The von Bertalanffy growth parameter.

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.

The function rounds `no_w` to the nearest integer and increases it if necessary so that there are at least 5 size bins per factor 10 in body size. It requires `w_min < w_mat < w_max`, `ext_mort_prop` in `[0, 1)`, positive values for `n`, `lambda`, `kappa`, `alpha`, `h`, `beta`, `sigma` and `f0`, and `fc` between 0 and `f0` if `fc` is supplied. If `gamma` is supplied then `f0` is ignored after its value has been validated. The function stops if the resulting feeding level is not sufficient to maintain the species.

The returned model has a single foreground species with cannibalism switched off and a fixed power-law background community that provides both food and predation mortality. The initial species spectrum is scaled so that its maximum abundance is half the background abundance at the corresponding size, and `erepro` is then adjusted so the initial state satisfies the egg boundary condition.

The diffusion rate is set to `0`. Because growth is therefore deterministic, no individual grows beyond `w_repro_max`, the size at which all available energy is invested into reproduction. The upper boundary of the size grid is therefore placed at that size, so that `w_max = w_repro_max`, instead of the `1.5 * w_repro_max` headroom that `newMultispeciesParams()` leaves to accommodate the stochastic growth produced by diffusion. This choice will be revisited once these constructors gain a diffusion parameter, see https://github.com/sizespectrum/mizer/issues/339.

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 maximum size, which is considered the most important trait characterizing a species. Other parameters are related to the maximum size. For example, the size at maturity is given by `w_max * 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_max = 10,
  max_w_max = 10^4,
  min_w = 10^(-3),
  max_w = max_w_max,
  eta = 10^(-0.6),
  min_w_mat = min_w_max * eta,
  no_w = round(log10(max_w_max/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,
  second_order_w = FALSE,
  min_w_inf = deprecated(),
  max_w_inf = deprecated(),
  info_level = default_info_level(2)
)
```

Arguments

no_sp	The number of species in the model.
min_w_max	The maximum size of the smallest species in the community. This will be rounded to lie on a grid point.
max_w_max	The maximum 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 maximum size max_w_max. 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 maximum 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_max. 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 cutoff used when truncating the constructed resource spectrum. Resource abundance is retained only up to the largest grid point below this value. If perfect_scaling = TRUE, the constructed initial resource spectrum is not truncated.

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, but must still be finite and in the interval (0, 1).

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 and 1 that determines the level of density dependence in reproduction, see reproduction_level<-().

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

gear_names — The names of the fishing gears for each species. Either a single name used for all species or a character vector of length no_sp.

knife_edge_size
: The minimum size at which the gear or gears select fish. Either a single value used for all species or a vector of length no_sp.

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_max. 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.

second_order_w
: **[Experimental]** Selects the second-order numerical scheme for the new model, applied before the resource and abundance power laws are constructed so that they are built bin-averaged from the start. Accepts the same values as the second_order_w() setter. Defaults to FALSE. See newMultispeciesParams().

min_w_inf
: **[Deprecated]** The argument has been renamed to min_w_max to make it clearer that it refers to the maximum size of a species not the von Bertalanffy asymptotic size parameter.

max_w_inf
: **[Deprecated]** The argument has been renamed to max_w_max.

info_level
: Controls the amount of information messages that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().

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 sizes.

The characteristic weights of the smallest species are defined by min_w (egg size), min_w_mat (maturity size) and min_w_max (maximum size). The maximum sizes of the no_sp species are logarithmically evenly spaced, ranging from min_w_max to max_w_max. Similarly the maturity sizes of the species are logarithmically evenly spaced, so that the ratio eta between maturity size and maximum size is the same for all species. If egg_size_scaling = TRUE then also the ratio between maximum 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 diffusion rate is set to 0. Because growth is therefore deterministic, no individual grows beyond w_repro_max, the size at which all available energy is invested into reproduction. The upper boundary of the size grid is therefore placed at that size, so that w_max = w_repro_max, instead of the 1.5 * w_repro_max headroom that newMultispeciesParams() leaves to accommodate the stochastic

growth produced by diffusion. This choice will be revisited once these constructors gain a diffusion parameter, see https://github.com/sizespectrum/mizer/issues/339.

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 maximum 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

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

`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)

finalNOther(sim)
```

Arguments

sim	A MizerSim object

Value

For NOther: A list array indexed by time and component that stores the projected values for other ecosystem components.

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

See Also

Other extension tools: coerceToExtensionClass(), initialNOther<-(), other_mort(), recordExtension(), setComponent(), setRateFunction()

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

```
params <- newMultispeciesParams(NS_species_params_gears,
                                interaction = NS_interaction)
```

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

```
sim = project(NS_params, effort = c(Industrial = 0, Pelagic = 1,
                                    Beam = 0.5, Otter = 0.5))
plot(sim)
```

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

```
plotBiomass(NS_sim)
```

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_max Computational upper size boundary, defaulting to `1.5 * w_inf`.

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

w_inf The von Bertalanffy asymptotic size. This is the required maximum-size parameter.

Source

Blanchard et al.

Examples

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

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_max Computational upper size boundary, defaulting to `1.5 * w_inf`.

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

w_inf The von Bertalanffy asymptotic size. This is the required maximum-size parameter.

gear Name of the fishing gear

Source

Blanchard et al.

Examples

```
params <- MizerParams(NS_species_params_gears)
```

`other_mort` *Extra contributions to the mortality and encounter rates*

Description

Besides the rates that mizer calculates itself, a model can carry extra contributions to the mortality rate and to the encounter rate. Each contribution is an R function, registered here by name, that mizer calls at every time step: `getMort()` adds the result of every function listed in `other_mort(params)` to the mortality rate and `getEncounter()` adds the result of every function listed in `other_encounter(params)` to the encounter rate.

Usage

```
other_mort(params)

other_mort(params) <- value

other_encounter(params)

other_encounter(params) <- value
```

Arguments

`params`	A MizerParams object
`value`	A named list of function names, or `NULL` to remove all contributions that do not belong to a component. You choose the names, but they must be unique and must not clash with the name of a component.

Details

Use these when the extra contribution depends on the state of the model, as a starvation mortality or a density-dependent mortality does. A contribution that is simply a fixed array is better set with `ext_mort()` or `ext_encounter()`, which is what mizer's own external mortality and external encounter use.

Assigning `NULL` to an entry removes that contribution:

```
other_mort(params)[["starvation"]] <- NULL
```

Value

A named list with the names of the functions contributing to the rate, excluding any that belong to a component.

How your function is called

Each registered function is called as

```
fun(params, n, n_pp, n_other, t, component, ...)
```

and has to return an array with the same dimensions as the rate it contributes to, that is species x size. The `component` argument holds the name under which the function is registered, so a single implementation can serve several entries. Always give your function a `...` argument so that it tolerates being passed arguments it does not use.

Make sure the function depends *continuously* on the abundances, for the reasons set out in `setRateFunction()`.

Contributions belonging to a component

A component set up with `setComponent()` can contribute to these rates through that function's `mort_fun` and `encounter_fun` arguments. Such an entry belongs to its component: `setComponent()` sets it, `removeComponent()` removes it and `getComponent()` reports it. The accessors here therefore leave those entries alone. `other_mort()` and `other_encounter()` list only the contributions that do not belong to a component, and assigning through them preserves the ones that do. This mirrors `other_params()`, which likewise hides the parameters belonging to a component, and it makes it impossible to wipe out a component's contribution by assigning a whole list.

See Also

`setComponent()`, `other_params()`, `ext_mort()`, `ext_encounter()`

Other extension tools: `NOther()`, `coerceToExtensionClass()`, `initialNOther<-()`, `recordExtension()`, `setComponent()`, `setRateFunction()`

Examples

```
# An extra mortality that grows with the total biomass in the community.
# Like any custom rate function it has to live in the global environment
# or in a package, so that mizer can find it by name.
crowdingMort <- function(params, n, n_pp, n_other, t, component, ...) {
```

```
    biomass <- sum(n %*% (params@w * params@dw))
    # Same dimensions as the mortality rate: species x size
    0 * params@mu_b + 1e-14 * biomass
}
params <- NS_params
other_mort(params)[["crowding"]] <- "crowdingMort"
other_mort(params)

# The contribution is included in the mortality rate
range(getMort(params) - getMort(NS_params))

# and can be removed again
other_mort(params)[["crowding"]] <- NULL
other_mort(params)
```

---

plot *Plot mizer arrays*

Description

Many mizer functions return values that depend on species and either size or time. `plot()` creates a ggplot2 figure with one line for each species showing the values against size or against time (depending on the type of output). `plotHover()` creates an interactive version of the same figure.

Details

This works because the mizer functions that give values that depend on species and size return an `ArraySpeciesBySize` object and those that give values that depend on species and time return an `ArrayTimeBySpecies` object. These objects have attributes that store the name of the value, its units, and a reference to the `MizerParams` object that the value was computed from. This allows the plots to be automatically labelled and coloured appropriately.

The resource classes `ArrayResourceBySize` and `ArrayTimeByResourceBySize` work the same way, except that they hold a single spectrum rather than one per species.

To compare two mizer arrays in a single plot, use `plot2()`. To show the relative difference between two arrays, use `plotRelative()`. To add an array to an existing plot, use `addPlot()`. All three, and `animate()`, have methods for every mizer array class.

All methods return a ggplot2 object, unless `return_data = TRUE`, in which case they return the underlying data frame instead. `plotHover()` returns a plotly object.

Arguments used by all methods:

`species` Character vector of species to include. `NULL` (default) means all species.

`highlight` Name or vector of names of the species to be highlighted.

`total` A boolean value that determines whether the total is plotted as well. The total is the total of everything the array holds, every species and every size, whatever is drawn. 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`.

`return_data` If `TRUE`, return the data frame instead of the plot.

`log_x` If `TRUE`, use a log10 x-axis. The default depends on the method; see its own help page.

`log_y` If `TRUE`, use a log10 y-axis. The default depends on the method; see its own help page.

`log` Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.

`ylim` A numeric vector of length two providing lower and upper limits for the value (y) axis. Use `NA` to refer to the existing minimum or maximum.

`y_ticks` The approximate number of ticks desired on the y axis.

Additional arguments for `plot.ArraySpeciesBySize()` and `plot.ArrayTimeBySpeciesBySize()`:

`all.sizes` If `FALSE` (default), values outside a species' size range (`w_min` to `w_max`) are removed.

`wlim` A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use `NA` to refer to the existing minimum or maximum.

`llim` A numeric vector of length two providing lower and upper limits for the length (x) axis when `size_axis = "l"`. Use `NA` to refer to the existing minimum or maximum.

`size_axis` Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship. Densities are transformed to match the chosen axis.

`per_log_size` For an array that holds a density, whether to plot it per logarithmic size (`TRUE`) rather than per size (`FALSE`). The default, `NULL`, plots the density as it stands. Unlike `size_axis` this needs no weight-length relationship, so it is available for the resource classes too. An error for an array that does not hold a density.

Additional argument for `plot.ArrayTimeBySpecies()`:

`tlim` A numeric vector of length two providing lower and upper limits for the time axis, e.g. `c(1980, 2000)`. Use `NA` to apply no limit at that end. Default is `c(NA, NA)`.

Additional argument for `plot.ArrayTimeBySpeciesBySize()` and `plot.ArrayTimeByResourceBySize()`:

`time` The time to display. Default (`NULL`) is the final time step.

See the individual method help pages for each method's exact arguments and defaults: `plot.ArraySpeciesBySize()`, `plot.ArrayTimeBySpecies()`, `plot.ArrayTimeBySpeciesBySize()`, `plot.ArrayResourceBySize()`, `plot.ArrayTimeByResourceBySize()`.

See Also

Other plotting functions: `addPlot()`, `animate()`, `plot2()`, `plotBiomass()`, `plotCDF()`, `plotCDF2()`, `plotDiet()`, `plotFMort()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotMizerParams`, `plotMizerSim`, `plotPredMort()`, `plotRelative()`, `plotSpectra()`, `plotSpectra2()`, `plotSpectraRelative()`, `plotYield()`, `plotYieldGear()`, `plotYieldVsF()`, `plotting_functions`

Examples

```
plot(getEncounter(NS_params))
plot(getFeedingLevel(NS_params), species = c("Cod", "Herring"))
plot(getPredMort(NS_params), species = c("Cod", "Herring"),
     size_axis = "l")
plot(getBiomass(NS_sim))
plot(getBiomass(NS_sim), species = c("Cod", "Herring"), total = TRUE)
plot(getYield(NS_sim), species = c("Cod", "Herring"))
plot(getFMort(NS_sim), time = 2010)
plot(getResourceMort(NS_params))
plot(initialNResource(NS_params))
plot(NResource(NS_sim))
```

---

plot.MizerScan *Plot method for* MizerScan *objects*

Description

[Experimental] Draws the result of a scanModel() run: the measured quantity against the quantity that was scanned, with a band showing the range the quantity takes over the attractor wherever that attractor is not a fixed point.

Usage

```
## S3 method for class 'MizerScan'
plot(
  x,
  species = NULL,
  style = c("ribbon", "envelope", "line"),
  highlight = NULL,
  log_x = FALSE,
  log_y = TRUE,
  log = NULL,
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  y_ticks = 6,
  reference_lines = TRUE,
  mark_max = FALSE,
  show_unsettled = TRUE,
  return_data = FALSE,
  ...
)
```

Arguments

x	A MizerScan object.

species	The species to show. By default all series in the scan.
style	One of "ribbon" (default: the average as a line inside the band), "envelope" (lines along the edges of the band, no average) or "line" (no band).
highlight	Name or vector of names of the species to be highlighted with a thicker line.
log_x, log_y, log	Whether to use logarithmic axes, see parsePlotLog().
xlim, ylim	Numeric vectors of length two giving the axis limits. Use NA to refer to the existing minimum or maximum.
y_ticks	The approximate number of ticks desired on the y axis.
reference_lines	Whether to draw the reference lines stored in the scan, or a named numeric vector of x positions to draw instead.
mark_max	Whether to mark, for each series, the scanned value at which the measured quantity is largest. See MizerScan().
show_unsettled	Whether to mark the scan values where the model did not settle onto an attractor.
return_data	Whether to return the data frame used for the plot instead of the plot itself.
...	Unused.

Details

A model that settles on a fixed point contributes a single value, so the band has zero width there. A model that settles on a limit cycle contributes the average over one period as the line and the range over that period as the band, so a Hopf bifurcation shows up as the scan value at which the band opens up.

Scan values where the model reached neither a fixed point nor a limit cycle within the time allowed are marked with a cross, because the value plotted there is only an average over the last few years of a run that was still changing.

Value

A ggplot2 object, unless return_data = TRUE, in which case the data frame used for the plot is returned.

See Also

scanModel(), MizerScan(), plotting_functions

Other scan functions: MizerScan(), plotYieldVsF(), scanEffort(), scanModel()

Examples

```
scan <- scanModel(NS_params, scan_values = seq(0, 1, 0.25),
                  set_func = scanEffort(), species = c("Cod", "Herring"))
plot(scan)
plot(scan, style = "envelope", mark_max = TRUE)
```

plot2 *Compare two mizer arrays in a single plot*

Description

plot2() compares two compatible mizer array objects in a single ggplot. Colours identify species or groups, and linetype identifies which object the values came from.

Usage

```
plot2(
  x,
  y,
  name1 = "First",
  name2 = "Second",
  species = NULL,
  log_x,
  log_y,
  log = NULL,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
  highlight = NULL,
  y_ticks = 6,
  ...
)
```

Arguments

x	The first of two compatible mizer array objects to compare. Can be an ArraySpeciesBySize, ArrayTimeBySpecies, ArrayTimeBySpeciesBySize, ArrayResourceBySize or ArrayTimeByResourceBySize object.
y	The second mizer array object, compatible with x.
name1, name2	Labels for the two objects, used in the linetype legend.
species	Character vector of species to include. NULL (default) means all species. A resource array holds a single spectrum, so this argument is not used by the resource methods, which warn if it is set.
log_x	If TRUE, use a log10 x-axis. Default is TRUE for size spectra and FALSE for time series.
log_y	If TRUE, use a log10 y-axis. Default is FALSE for ArraySpeciesBySize and TRUE for ArrayTimeBySpecies and for the resource classes.
log	Character string specifying which axes should use log10 scales, in the same form as the base plot() argument. For example, "x", "y", "xy" or "". If supplied, this overrides log_x and log_y.

`ylim` A numeric vector of length two providing lower and upper limits for the value (y) axis. Use `NA` to refer to the existing minimum or maximum.

`total` A boolean value that determines whether the total is plotted as well. The total is the total of everything the array holds, every species and every size, whatever is drawn. Default is `FALSE`. Not used by the resource methods, which warn if it is set.

`background` A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is `TRUE`. Not used by the resource methods, which warn if it is set.

`highlight` Name or vector of names of the species to be highlighted with a thicker line.

`y_ticks` The approximate number of ticks desired on the y axis.

`...` Further arguments used by only some of the methods:

For the `ArraySpeciesBySize`, `ArrayTimeBySpeciesBySize`, `ArrayResourceBySize` and `ArrayTimeByResourceBySize` methods:

`wlim` A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use `NA` to refer to the existing minimum or maximum.

For the `ArraySpeciesBySize` and `ArrayTimeBySpeciesBySize` methods:

`all.sizes` If `FALSE` (default), values outside a species' size range (`w_min` to `w_max`) are removed.

`llim` A numeric vector of length two providing lower and upper limits for the length (x) axis when `size_axis = "l"`. Use `NA` to refer to the existing minimum or maximum.

`size_axis` Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship of each species, or of the resource, see `resource_params()`.

`per_log_size` For an array that holds a density, whether to plot it per logarithmic size (`TRUE`) rather than per size (`FALSE`). The default, `NULL`, plots the density as it stands. Unlike `size_axis` this needs no weight-length relationship, so it is available for the resource classes too. An error for an array that does not hold a density.

For `ArrayTimeBySpecies` methods:

`tlim` A numeric vector of length two providing lower and upper limits for the time axis, e.g. `c(1980, 2000)`. Use `NA` to apply no limit at that end. Default is `c(NA, NA)`.

For the `ArrayTimeBySpeciesBySize` and `ArrayTimeByResourceBySize` methods:

`time` The time to display. Default (`NULL`) is the final time step.

Value

A ggplot2 object.

See Also

Other plotting functions: addPlot(), animate(), plot, plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
plot2(getEncounter(NS_params), getEncounter(NS_params))
plot2(getResourceMort(NS_params), getResourceMort(NS_params))
```

---

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 (see getBiomass()).

Usage

```
plotBiomass(
  object,
  species = NULL,
  tlim = c(NA, NA),
  y_ticks = 6,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
  highlight = NULL,
  log = NULL,
  return_data = FALSE,
  log_x = FALSE,
  log_y = TRUE,
  use_cutoff = FALSE,
  ...
)
```

Arguments

object	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.

tlim	A numeric vector of length two providing lower and upper limits for the time axis, e.g. c(1980, 2000). Use NA to apply no limit at that end. Default is c(NA, NA).
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.
log	Character string specifying which axes should use log10 scales, in the same form as the base plot() argument. For example, "x", "y", "xy" or "". If supplied, this overrides log_x and log_y. For backward compatibility, TRUE and FALSE are interpreted as setting only log_y.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
log_x	If TRUE, use a log10 x-axis. Default is FALSE.
log_y	If TRUE, use a log10 y-axis. Default is TRUE.
use_cutoff	If TRUE, the biomass_cutoff column in the species parameters is used as the minimum weight for each species.
...	Arguments setting the size range over which the biomass is calculated (see getBiomass()): 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: addPlot(), animate(), plot, plot2(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
plotBiomass(NS_sim)
plotBiomass(NS_sim, species = c("Sandeel", "Herring"), total = TRUE)
plotBiomass(NS_sim, tlim = c(1980, 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. `ratio` defaults to `FALSE`.

Usage

```
plotBiomassObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  labels = TRUE,
  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.

`...` For `plotlyBiomassObservedVsModel()`, additional arguments passed to `plotHover()`. Otherwise unused.

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, ratio = FALSE)

# Plot including also species without observations
plotBiomassObservedVsModel(params, show_unobserved = TRUE, ratio = FALSE)

# Show the ratio instead
plotBiomassObservedVsModel(params, ratio = TRUE)
```

plotCDF *Plot cumulative abundance or biomass distributions*

Description

plotCDF() plots the cumulative distribution over body size from small to large sizes. It uses the same spectra data preparation as plotSpectra(): the number density is multiplied by w^power and then integrated over size. With normalise = TRUE, each curve is divided by its final value so that it ends at 1.

Usage

```
plotCDF(
  object,
  species = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  ylim = c(NA, NA),
  power = NULL,
  biomass = NULL,
  per_log_size = NULL,
  total = FALSE,
  resource = FALSE,
  background = TRUE,
  highlight = NULL,
  normalise = TRUE,
  log_x = TRUE,
  log_y = FALSE,
  log = NULL,
  size_axis = c("w", "l"),
  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.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA for the default: the lower default is min(params@w) / 100 when resource = TRUE (to show some resource below the fish grid) or min(params@w) when resource = FALSE; the upper default is max(params@w_full). Data is filtered to this range and the axis limits are set accordingly.

`llim` A numeric vector of length two providing lower and upper limits for the length axis when `size_axis = "l"`. Use `NA` to auto-scale to the data range. Data is filtered to this range and the axis limits are set accordingly.

`ylim` A numeric vector of length two providing lower and upper limits for the y axis. Use NA to auto-scale to the data range. Values below 1e-20 are always filtered out from the data regardless of `ylim[1]`. Data above `ylim[2]` is filtered and the upper axis limit is set accordingly.

`power` The number density is multiplied by the weight raised to `power` before being integrated. An alternative to the `biomass` argument, with which it must agree if that is given as well. The default is `power = 1`, the cumulative biomass.

`biomass` Whether to plot the cumulative biomass (`TRUE`, the default) or the cumulative abundance (`FALSE`).

`per_log_size` Only `FALSE` (the default) is accepted; see Details.

`total` A boolean value that determines whether the total is plotted as well. The total is the total of everything the object holds — every species and the resource — whatever is drawn, so it does not move when `species`, `resource` or `background` change. Default is FALSE.

`resource` A boolean value that determines whether resource is included. 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 by being plotted with thicker lines.

`normalise` If `TRUE` (default), plot the cumulative proportion. If `FALSE`, plot the cumulative abundance, biomass, or other unnormalised integral.

`log_x` If `TRUE` (default), use a log10 x-axis.

`log_y` If `TRUE`, use a log10 y-axis. Default is `FALSE`.

`log` Character string specifying which axes should use a log10 scale, in the same form as the base `plot()` argument. If supplied, this overrides `log_x` and `log_y`.

`size_axis` Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship.

`return_data` A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.

`...` Further arguments used by only some of the methods:

For `MizerSim` methods:

- `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.
- `geometric_mean`: **[Experimental]** If `TRUE` then the average of the abundances over the time range is a geometric mean instead of the default arithmetic mean.

Details

Unlike for plotSpectra(), the only choice that matters here is biomass: whether to accumulate numbers or biomass. Whether a density is expressed with respect to size or with respect to logarithmic size makes no difference to its integral, because the change of variable cancels the factor of the weight, and so plotCDF() does not accept per_log_size = TRUE.

plotlyCDF() is the interactive plotly version. To compare cumulative distributions from two objects, use plotCDF2().

Value

A ggplot2 object, unless return_data = TRUE, in which case a data frame with the four variables 'w' (or 'l' if size_axis = "l"), 'value', 'Species', 'Legend' is returned. plotlyCDF() returns a plotly object.

See Also

plotSpectra(), plotCDF2()

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
plotCDF(NS_params, species = c("Cod", "Herring"))
plotCDF(NS_sim, power = 0, normalise = FALSE)
```

---

plotCDF2 — *Compare cumulative abundance or biomass distributions from two objects*

Description

plotCDF2() compares cumulative distributions from two MizerParams or MizerSim objects in a single plot. Colours identify species or groups and linetype identifies the object.

Usage

```
plotCDF2(
  object1,
  object2,
  name1 = "First",
  name2 = "Second",
  species = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
```

```
  ylim = c(NA, NA),
  power = NULL,
  biomass = NULL,
  per_log_size = NULL,
  total = FALSE,
  resource = FALSE,
  background = TRUE,
  highlight = NULL,
  normalise = TRUE,
  log_x = TRUE,
  log_y = FALSE,
  log = NULL,
  size_axis = c("w", "l"),
  ...
)
```

Arguments

object1	First MizerParams or MizerSim object.
object2	Second MizerParams or MizerSim object.
name1, name2	Labels for the two objects, used in the linetype legend.
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.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA for the default: the lower default is min(params@w) / 100 when resource = TRUE (to show some resource below the fish grid) or min(params@w) when resource = FALSE; the upper default is max(params@w_full). Data is filtered to this range and the axis limits are set accordingly.
llim	A numeric vector of length two providing lower and upper limits for the length axis when size_axis = "l". Use NA to auto-scale to the data range. Data is filtered to this range and the axis limits are set accordingly.
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to auto-scale to the data range. Values below 1e-20 are always filtered out from the data regardless of ylim[1]. Data above ylim[2] is filtered and the upper axis limit is set accordingly.
power	The number density is multiplied by the weight raised to power before being integrated. An alternative to the biomass argument, with which it must agree if that is given as well. The default is power = 1, the cumulative biomass.
biomass	Whether to plot the cumulative biomass (TRUE, the default) or the cumulative abundance (FALSE).
per_log_size	Only FALSE (the default) is accepted; see Details.
total	A boolean value that determines whether the total is plotted as well. The total is the total of everything the object holds — every species and the resource — whatever is drawn, so it does not move when species, resource or background change. Default is FALSE.

resource	A boolean value that determines whether resource is included. 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 by being plotted with thicker lines.
normalise	If TRUE (default), plot the cumulative proportion. If FALSE, plot the cumulative abundance, biomass, or other unnormalised integral.
log_x	If TRUE (default), use a log10 x-axis.
log_y	If TRUE, use a log10 y-axis. Default is FALSE.
log	Character string specifying which axes should use a log10 scale, in the same form as the base plot() argument. If supplied, this overrides log_x and log_y.
size_axis	Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship.
...	Additional arguments passed to plotCDF() for preparing the cumulative distribution data, for example time_range or geometric_mean for MizerSim objects.

Details

plotlyCDF2() is the interactive plotly version.

Value

A ggplot2 object. plotlyCDF2() returns a plotly object.

See Also

plotSpectra(), plotCDF()

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
sim1 <- project(NS_params, t_max = 10, progress_bar = FALSE)
sim2 <- project(NS_params, effort = 0.5, t_max = 10, progress_bar = FALSE)
plotCDF2(sim1, sim2, "Original", "Effort = 0.5")
```

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,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  size_axis = c("w", "l"),
  return_data = FALSE,
  log_x = TRUE,
  log_y = FALSE,
  log = 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.
`wlim`	A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use `NA` to auto-scale to the data range.
`llim`	A numeric vector of length two providing lower and upper limits for the length (x) axis when `size_axis = "l"`. Use `NA` to auto-scale to the data range.
`size_axis`	Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
`log_x`	If `TRUE` (default), use a log10 x-axis.
`log_y`	If `TRUE`, use a log10 y-axis. Default is `FALSE`.
`log`	Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.

... Further arguments used by only some of the methods:

For `MizerSim` methods:

- `time_range`: The time range (either a vector of values, a vector of min and max time, or a single value) over which to average the diet. The consumption rates are averaged over this range and then normalised to proportions. Default is the final time step.

Details

Prey species that contribute less than 1 permille to the diet are suppressed in the plot. The plot only extends to predator sizes where the predator has a meaningful abundance (defined as having a biomass density greater than 0.1% of its maximum biomass density).

If more than one predator species is selected, then the plot contains one facet for each species.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the four variables 'Predator', 'w' (or 'l' if `size_axis = "l"`), 'Proportion', 'Prey' is returned.

`plotlyDiet()` returns a plotly object.

See Also

`getDiet()`

Other plotting functions: `addPlot()`, `animate()`, `plot`, `plot2()`, `plotBiomass()`, `plotCDF()`, `plotCDF2()`, `plotFMort()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotMizerParams`, `plotMizerSim`, `plotPredMort()`, `plotRelative()`, `plotSpectra()`, `plotSpectra2()`, `plotSpectraRelative()`, `plotYield()`, `plotYieldGear()`, `plotYieldVsF()`, `plotting_functions`

Examples

```
plotDiet(NS_params, species = "Cod")
plotDiet(NS_params, species = 5:9)

# 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,
  all.sizes = FALSE,
  highlight = NULL,
  include_critical = FALSE,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  size_axis = c("w", "l"),
  return_data = FALSE,
  log_x = TRUE,
  log_y = FALSE,
  log = 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.
`all.sizes`	If TRUE, then feeding level is plotted also for sizes outside a species' size range. Default FALSE.
`highlight`	Name or vector of names of the species to be highlighted.
`include_critical`	If TRUE, then the critical feeding level is also plotted. Default FALSE.
`wlim`	A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use `NA` to auto-scale to the data range.
`llim`	A numeric vector of length two providing lower and upper limits for the length (x) axis when `size_axis = "l"`. Use `NA` to auto-scale to the data range.
`size_axis`	Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
`log_x`	If `TRUE` (default), use a log10 x-axis.
`log_y`	If `TRUE`, use a log10 y-axis. Default is `FALSE`.
`log`	Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.
`...`	Further arguments used by only some of the methods: **For `MizerSim` methods:**

time_range The time range (either a vector of values, a vector of min and max time, or a single value) to average the feeding level over. Default is the final time step.

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' (or 'l' if size_axis = "l"), '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: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), 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,
  all.sizes = FALSE,
  highlight = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  size_axis = c("w", "l"),
  return_data = FALSE,
  log_x = TRUE,
  log_y = FALSE,
  log = 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.
`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.
`wlim`	A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use `NA` to auto-scale to the data range.
`llim`	A numeric vector of length two providing lower and upper limits for the length (x) axis when `size_axis = "l"`. Use `NA` to auto-scale to the data range.
`size_axis`	Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
`log_x`	If `TRUE` (default), use a log10 x-axis.
`log_y`	If `TRUE`, use a log10 y-axis. Default is `FALSE`.
`log`	Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.

... Further arguments used by only some of the methods:

For `MizerSim` **methods:**

`time_range` The time range (either a vector of values, a vector of min and max time, or a single value) to average the fishing mortality over. Default is the final time step.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w' (or 'l' if `size_axis = "l"`), 'value', 'Species' is returned.

See Also

plotting_functions, `getFMort()`

Other plotting functions: `addPlot()`, `animate()`, `plot`, `plot2()`, `plotBiomass()`, `plotCDF()`, `plotCDF2()`, `plotDiet()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotMizerParams`, `plotMizerSim`, `plotPredMort()`, `plotRelative()`, `plotSpectra()`, `plotSpectra2()`, `plotSpectraRelative()`, `plotYield()`, `plotYieldGear()`, `plotYieldVsF()`, `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*

Description

[Experimental] The growth curves represent the average age of all the living fish of a species as a function of their size. So it would be natural to plot size on the x-axis. But to follow the usual convention from age-based models, we plot size on the y-axis and age on the x-axis.

Usage

```
plotGrowthCurves(
  object,
  species = NULL,
  max_age = 20,
  percentage = FALSE,
  species_panel = FALSE,
```

```
  highlight = NULL,
  size_at_age = NULL,
  return_data = FALSE,
  log_x = FALSE,
  log_y = FALSE,
  log = 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.
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	If TRUE (default), and `percentage = FALSE`, display all species as facets. Otherwise puts all species into a single panel.
highlight	Name or vector of names of the species to be highlighted.
size_at_age	A data frame with observed size at age data to be plotted on top of growth curve graphs. Should contain columns `species` (species name as used in the model), `age` (in years) and either `weight` (in grams) or `length` (in cm). If both `weight` and `length` are provided, only `weight` is used.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
log_x	If `TRUE`, use a log10 x-axis. Default is `FALSE`.
log_y	If `TRUE`, use a log10 y-axis. Default is `FALSE`.
log	Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.
...	Unused.

Details

In each panel for a single species, a horizontal line is included that indicate the maturity size of the species and a vertical line indicating its maturity age.

If size at age data is passed via the `size_at_age` argument, this is plotted on top of the growth curve. When comparing this to the growth curves, you need to remember that the growth curves should only represent the average age at each size. So a scatter in the x-direction around the curve is to be expected.

If the species parameters contain the variables `a` and `b` for length to weight conversion and the von Bertalanffy parameter `k_vb`, `w_inf` (and optionally `t0`), then the von Bertalanffy growth curve is superimposed in black. Note that the von Bertalanffy curve (which approximates the average length at each age) should not be compared directly to the mizer growth curves (which approximate the average age at each length).

Value

A ggplot2 object

See Also

plotting_functions

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), 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)
```

---

plotHover.ArraySpeciesBySize

Create a hover-enabled plotly plot from a mizer object

Description

Creates an interactive plotly version of a mizer plot. Can be called on any mizer array object (such as those returned by getEncounter(), getBiomass(), etc.) or on any mizer_plot object returned by the named plot functions such as plotBiomass(), plotSpectra(), etc.

Usage

```
## S3 method for class 'ArrayTimeBySpecies'
plotHover(x, ...)

## S3 method for class 'MizerScan'
plotHover(x, ...)

plotHover(x, ...)
```

Arguments

x	A mizer_plot, ArraySpeciesBySize, ArrayTimeBySpecies, or ArrayTimeBySpeciesBySize object.
...	Arguments passed to the corresponding plot() method for mizer array objects, or to plotly::ggplotly() for mizer_plot objects.

Value

A plotly object.

See Also

plot(), plotBiomass(), plotSpectra(), plotting_functions

Examples

```
plotHover(getEncounter(NS_params))


plotHover(getBiomass(NS_sim))


plotHover(getFMort(NS_sim))


plotHover(getResourceMort(NS_params))


plotHover(NResource(NS_sim))
```

---

plotM2 *Alias for* plotPredMort()

Description

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

Usage

```
plotM2(
  object,
  species = NULL,
  all.sizes = FALSE,
  highlight = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  size_axis = c("w", "l"),
```

```
  return_data = FALSE,
  log_x = TRUE,
  log_y = FALSE,
  log = 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.
`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.
`wlim`	A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use `NA` to auto-scale to the data range.
`llim`	A numeric vector of length two providing lower and upper limits for the length (x) axis when `size_axis = "l"`. Use `NA` to auto-scale to the data range.
`size_axis`	Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship.
`return_data`	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
`log_x`	If `TRUE` (default), use a log10 x-axis.
`log_y`	If `TRUE`, use a log10 y-axis. Default is `FALSE`.
`log`	Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.
`...`	Further arguments used by only some of the methods: **For `MizerSim` methods:** `time_range` The time range (either a vector of values, a vector of min and max time, or a single value) to average the predation mortality over. Default is the final time step.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w' (or 'l' if `size_axis = "l"`), 'value', 'Species' is returned.

See Also

plotting_functions, `getPredMort()`

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), 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)
```

---

plotMizerParams *Summary plot for* MizerParams *objects*

Description

Produces 3 plots in the same window: abundance spectra, feeding level and predation mortality of each species against size. This method just puts the plots generated by plotFeedingLevel(), plotPredMort() and plotSpectra() all in one window.

Usage

```
## S3 method for class 'MizerParams'
plot(x, ...)
```

Arguments

x	An object of class MizerParams
...	Arguments passed on to the individual plotting functions plotFeedingLevel(), plotSpectra() and plotPredMort(). The arguments that describe the plotted spectrum (power, biomass, per_log_size and resource) go to plotSpectra() only, because they mean nothing to a rate.

Value

A viewport object

See Also

plotting_functions

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
params <-  NS_params
plot(params)
```

---

plotMizerSim *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 puts the plots generated by plotBiomass(), plotFeedingLevel(), plotSpectra(), plotPredMort() and plotFMort() all in one window.

Usage

```
## S3 method for class 'MizerSim'
plot(x, ...)
```

Arguments

x	An object of class MizerSim
...	Arguments passed on to the individual plotting functions plotBiomass(), plotFeedingLevel(), plotSpectra(), plotPredMort() and plotFMort(). The arguments that describe the plotted spectrum (power, biomass, per_log_size and resource) go to plotSpectra() only, because they mean nothing to a rate.

Value

A viewport object

See Also

plotting_functions

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
params <-  NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plot(sim)
```

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,
  all.sizes = FALSE,
  highlight = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  size_axis = c("w", "l"),
  return_data = FALSE,
  log_x = TRUE,
  log_y = FALSE,
  log = 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.
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.
wlim	A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use NA to auto-scale to the data range.
llim	A numeric vector of length two providing lower and upper limits for the length (x) axis when size_axis = "l". Use NA to auto-scale to the data range.
size_axis	Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default is FALSE.
log_x	If TRUE (default), use a log10 x-axis.

`log_y` If TRUE, use a log10 y-axis. Default is FALSE.

`log` Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, "x", "y", "xy" or "". If supplied, this overrides `log_x` and `log_y`.

`...` Further arguments used by only some of the methods:

For `MizerSim` methods:

`time_range` The time range (either a vector of values, a vector of min and max time, or a single value) to average the predation mortality over. Default is the final time step.

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w' (or 'l' if `size_axis = "l"`), 'value', 'Species' is returned.

See Also

plotting_functions, `getPredMort()`

Other plotting functions: `addPlot()`, `animate()`, `plot`, `plot2()`, `plotBiomass()`, `plotCDF()`, `plotCDF2()`, `plotDiet()`, `plotFMort()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotMizerParams`, `plotMizerSim`, `plotRelative()`, `plotSpectra()`, `plotSpectra2()`, `plotSpectraRelative()`, `plotYield()`, `plotYieldGear()`, `plotYieldVsF()`, `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)
```

`plotRelative` *Plot relative difference between two mizer arrays*

Description

`plotRelative()` plots the difference between two compatible mizer array objects relative to their average. If the values in the first object are N_1 and the values in the second are N_2, it plots

$$2(N_2 - N_1)/(N_1 + N_2).$$

Usage

```
plotRelative(
  x,
  y,
  species = NULL,
  log_x,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
  highlight = NULL,
  ...
)
```

Arguments

x	The first of two compatible mizer array objects to compare. Can be an ArraySpeciesBySize, ArrayTimeBySpecies, ArrayTimeBySpeciesBySize, ArrayResourceBySize or ArrayTimeByResourceBySize object.
y	The second mizer array object, compatible with x.
species	Character vector of species to include. NULL (default) means all species. A resource array holds a single spectrum, so this argument is not used by the resource methods, which warn if it is set.
log_x	If TRUE, use a log10 x-axis. Default is TRUE for size spectra and FALSE for time series.
ylim	A numeric vector of length two providing lower and upper limits for the value (y) axis.
total	A boolean value that determines whether the total is plotted as well. The total is the total of everything the array holds, every species and every size, whatever is drawn. Default is FALSE. Not used by the resource methods, which warn if it is set.
background	A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE. Not used by the resource methods, which warn if it is set.
highlight	Name or vector of names of the species to be highlighted with a thicker line.
...	Further arguments used by only some of the methods:

For the ArraySpeciesBySize**,** ArrayTimeBySpeciesBySize**,** ArrayResourceBySize **and** ArrayTimeByResourceBySize **methods:**

wlim A numeric vector of length two providing lower and upper limits for the weight (x) axis. Use NA to refer to the existing minimum or maximum.

For the ArraySpeciesBySize **and** ArrayTimeBySpeciesBySize **methods:**

all.sizes If FALSE (default), values outside a species' size range (w_min to w_max) are removed.

llim A numeric vector of length two providing lower and upper limits for the length (x) axis when size_axis = "l". Use NA to refer to the existing minimum or maximum.

size_axis Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship of each species, or of the resource, see resource_params().

per_log_size For an array that holds a density, whether to express it per logarithmic size (TRUE) rather than per size (FALSE). The default, NULL, leaves the density as it stands. An error for an array that does not hold a density.

For ArrayTimeBySpecies **methods:**

tlim A numeric vector of length two providing lower and upper limits for the time axis, e.g. c(1980, 2000). Use NA to apply no limit at that end. Default is c(NA, NA).

For the ArrayTimeBySpeciesBySize **and** ArrayTimeByResourceBySize **methods:**

time The time to display. Default (NULL) is the final time step.

Value

A ggplot2 object.

See Also

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
params <- NS_params
given_species_params(params)["Cod", "w_mat"] <- 1200
plotRelative(getEGrowth(NS_params), getEGrowth(params),
             wlim = c(500, 2000), log_x = FALSE, species = "Cod")

# The same works for the resource
params2 <- setResource(NS_params,
                       resource_capacity = 2 * resource_capacity(NS_params))
plotRelative(resource_capacity(NS_params), resource_capacity(params2))
```

---

plotSpectra *Plot abundance and biomass spectra*

Description

plotSpectra() plots either a number density or a biomass density, either with respect to size or with respect to logarithmic size. Those two choices are made with the biomass and per_log_size arguments. 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. With `size_axis = "l"`, densities are converted from per unit weight to per unit length; densities with respect to logarithmic size are instead converted between logarithmic weight and logarithmic length intervals.

Usage

```
plotSpectra(
  object,
  species = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  ylim = c(NA, NA),
  power = NULL,
  biomass = NULL,
  per_log_size = NULL,
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  log_x = TRUE,
  log_y = TRUE,
  log = NULL,
  size_axis = c("w", "l"),
  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.
`wlim`	A numeric vector of length two providing lower and upper limits for the w axis. Use NA for the default: the lower default is `min(params@w) / 100` when `resource = TRUE` (to show some resource below the fish grid) or `min(params@w)` when `resource = FALSE`; the upper default is `max(params@w_full)`. Data is filtered to this range and the axis limits are set accordingly.
`llim`	A numeric vector of length two providing lower and upper limits for the length axis when `size_axis = "l"`. Use `NA` to auto-scale to the data range. Data is filtered to this range and the axis limits are set accordingly.
`ylim`	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to auto-scale to the data range. Values below 1e-20 are always filtered out from the data regardless of `ylim[1]`. Data above `ylim[2]` is filtered and the upper axis limit is set accordingly.
`power`	The abundance is plotted as the number density times the weight raised to `power`. An alternative to the `biomass` and `per_log_size` arguments, with which it must

agree if they are given as well; see Details. The default is `power = 1`, the biomass density.

`biomass` Whether to plot the biomass density (`TRUE`, the default) or the number density (`FALSE`).

`per_log_size` Whether to plot the density with respect to logarithmic size (`TRUE`) or with respect to size (`FALSE`, the default).

`total` A boolean value that determines whether the total is plotted as well. The total is the total of everything the object holds — every species and the resource — whatever is drawn, so it does not move when `species`, `resource` or `background` change. 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 by being plotted with thicker lines.

`log_x` If `TRUE` (default), use a log10 x-axis.

`log_y` If `TRUE` (default), use a log10 y-axis.

`log` Character string specifying which axes should use log10 scales, in the same form as the base `plot()` argument. For example, `"x"`, `"y"`, `"xy"` or `""`. If supplied, this overrides `log_x` and `log_y`.

`size_axis` Whether to plot size as weight (`"w"`, default) or length (`"l"`), using the allometric weight-length relationship. Spectrum densities and their units are transformed to match the chosen axis.

`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

`...` Further arguments used by only some of the methods:

For `MizerSim` methods:

- `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.
- `geometric_mean`: **[Experimental]** If `TRUE` then the average of the abundances over the time range is a geometric mean instead of the default arithmetic mean.

Details

The plotted quantity is the number density multiplied by `w^power`, where the power is the sum of the two choices above: a biomass density carries one factor of the weight and a density with respect to logarithmic size carries another:

	`per_log_size = FALSE`	`per_log_size = TRUE`
`biomass = FALSE`	`power = 0`	`power = 1`
`biomass = TRUE`	`power = 1`	`power = 2`

The power argument can still be given instead, and is the only way to ask for a power that is not the sum of the two flags. But note that power on its own does not distinguish the two entries with power = 1: it is taken to mean the biomass density with respect to weight, which is what determines the y-axis label and the Jacobian used for a length axis. Supplying power together with a flag that contradicts it is an error.

The log_x argument only controls how the size axis is displayed; it does not change the density on the y-axis. In particular, showing weight on a logarithmic axis does not by itself convert a density per unit weight into a density per logarithmic weight interval. That choice is made with per_log_size, and the conversion from weight to length then uses the logarithmic Jacobian, irrespective of the value of log_x.

plotlySpectra() is the interactive plotly version. To compare spectra from two objects use plotSpectra2(). To show relative differences use plotSpectraRelative().

Value

A ggplot2 object, unless return_data = TRUE, in which case a data frame with the four variables 'w' (or 'l' if size_axis = "l"), 'value', 'Species', 'Legend' is returned. plotlySpectra() returns a plotly object.

See Also

plotting_functions

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), 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, biomass = FALSE)
plotSpectra(sim, species = c("Cod", "Herring"), per_log_size = TRUE)
plotSpectra(sim, species = c("Cod", "Herring"), size_axis = "l")

# Returning the data frame
fr <- plotSpectra(sim, return_data = TRUE)
str(fr)
```

plotSpectra2 *Compare abundance and biomass spectra from two objects*

Description

plotSpectra2() compares the abundance spectra from two MizerParams or MizerSim objects in a single plot. Colours identify species or groups and linetype identifies the object.

Usage

```
plotSpectra2(
  object1,
  object2,
  name1 = "First",
  name2 = "Second",
  species = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  ylim = c(NA, NA),
  power = NULL,
  biomass = NULL,
  per_log_size = NULL,
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  log_x = TRUE,
  log_y = TRUE,
  log = NULL,
  size_axis = c("w", "l"),
  ...
)
```

Arguments

object1	First MizerParams or MizerSim object.
object2	Second MizerParams or MizerSim object.
name1, name2	Labels for the two objects, used in the linetype legend.
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.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA for the default: the lower default is min(params@w) / 100 when resource = TRUE (to show some resource below the fish grid) or min(params@w) when resource = FALSE; the upper default is max(params@w_full). Data is filtered to this range and the axis limits are set accordingly.

llim	A numeric vector of length two providing lower and upper limits for the length axis when size_axis = "l". Use NA to auto-scale to the data range. Data is filtered to this range and the axis limits are set accordingly.
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to auto-scale to the data range. Values below 1e-20 are always filtered out from the data regardless of ylim[1]. Data above ylim[2] is filtered and the upper axis limit is set accordingly.
power	The abundance is plotted as the number density times the weight raised to power. An alternative to the biomass and per_log_size arguments, with which it must agree if they are given as well; see Details. The default is power = 1, the biomass density.
biomass	Whether to plot the biomass density (TRUE, the default) or the number density (FALSE).
per_log_size	Whether to plot the density with respect to logarithmic size (TRUE) or with respect to size (FALSE, the default).
total	A boolean value that determines whether the total is plotted as well. The total is the total of everything the object holds — every species and the resource — whatever is drawn, so it does not move when species, resource or background change. 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 by being plotted with thicker lines.
log_x	If TRUE (default), use a log10 x-axis.
log_y	If TRUE (default), use a log10 y-axis.
log	Character string specifying which axes should use log10 scales, in the same form as the base plot() argument. For example, "x", "y", "xy" or "". If supplied, this overrides log_x and log_y.
size_axis	Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship. Spectrum densities and their units are transformed to match the chosen axis.
...	Additional arguments passed to plotSpectra() for preparing the spectra data, for example time_range or geometric_mean for MizerSim objects.

Details

plotlySpectra2() is the interactive plotly version.

Value

A ggplot2 object. plotlySpectra2() returns a plotly object.

See Also

plotting_functions, plotSpectra(), plotSpectraRelative()

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
sim1 <- project(NS_params, t_max = 10, progress_bar = FALSE)
sim2 <- project(NS_params, effort = 0.5, t_max = 10, progress_bar = FALSE)
plotSpectra2(sim1, sim2, "Original", "Effort = 0.5")
```

---

plotSpectraRelative *Plot relative difference between abundance spectra*

Description

plotSpectraRelative() plots the difference between the spectra relative to their average. If we denote the number density from the first object as $N_1(w)$ and that from the second object as $N_2(w)$, then this plot shows

$$2(N_2(w) - N_1(w))/(N_2(w) + N_1(w)).$$

Note that it does not matter whether the relative difference is calculated for number density, biomass density, or biomass density in log weight, because the factors of w by which the densities differ cancel out in the relative difference.

Usage

```
plotSpectraRelative(
  object1,
  object2,
  species = NULL,
  wlim = c(NA, NA),
  llim = c(NA, NA),
  ylim = c(NA, NA),
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  log_x = TRUE,
  size_axis = c("w", "l"),
  ...
)
```

Arguments

object1	First MizerParams or MizerSim object.
object2	Second MizerParams or 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.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA for the default: the lower default is min(params@w) / 100 when resource = TRUE (to show some resource below the fish grid) or min(params@w) when resource = FALSE; the upper default is max(params@w_full). Data is filtered to this range and the axis limits are set accordingly.
llim	A numeric vector of length two providing lower and upper limits for the length axis when size_axis = "l". Use NA to auto-scale to the data range. Data is filtered to this range and the axis limits are set accordingly.
ylim	A numeric vector of length two providing lower and upper limits for the y axis (the relative difference). Use NA to refer to the existing minimum or maximum.
total	A boolean value that determines whether the total is plotted as well. The total is the total of everything the object holds — every species and the resource — whatever is drawn, so it does not move when species, resource or background change. 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 by being plotted with thicker lines.
log_x	If TRUE (default), use a log10 x-axis.
size_axis	Whether to plot size as weight ("w", default) or length ("l"), using the allometric weight-length relationship. Spectrum densities and their units are transformed to match the chosen axis.
...	Additional arguments passed to plotSpectra() for preparing the spectra data, for example time_range or geometric_mean for MizerSim objects.

Details

plotlySpectraRelative() is the interactive plotly version.

Value

A ggplot2 object. plotlySpectraRelative() returns a plotly object.

See Also

plotting_functions, plotSpectra(), plotSpectra2()

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotYield(), plotYieldGear(), plotYieldVsF(), plotting_functions

Examples

```
sim1 <- project(NS_params, t_max = 10, progress_bar = FALSE)
sim2 <- project(NS_params, effort = 0.5, t_max = 10, progress_bar = FALSE)
plotSpectraRelative(sim1, sim2)
```

---

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.

Details

The quickest way to make a standard plot is often to call plot() directly. mizer provides plot() methods for MizerSim and MizerParams objects, and also for the array classes returned by many summary and rate functions:

- plot(<MizerSim>) produces a five-panel summary plot with plotFeedingLevel(), plotBiomass(), plotPredMort(), plotFMort() and plotSpectra().
- plot(<MizerParams>) produces a three-panel summary plot with plotFeedingLevel(), plotPredMort() and plotSpectra() from the initial state.
- plot(<ArrayTimeBySpecies>) plots any time-by-species array, such as those returned by getBiomass(), getSSB(), getYield() and getN() on a MizerSim, as lines of value against time.
- plot(<ArraySpeciesBySize>) plots any species-by-size array, such as those returned by getEncounter(), getFeedingLevel(), getPredMort(), getFMort() and search_vol(), as lines of value against body size.
- plot(<ArrayTimeBySpeciesBySize>) plots a time slice from a time-by-species-by-size array, such as those returned by getFMort() or getPredMort() on a MizerSim.
- plot(<ArrayResourceBySize>) plots a resource array, such as those returned by getResourceMort(), against body size.
- plot(<ArrayTimeByResourceBySize>) plots a time slice from a time-by-resource array, such as that returned by NResource() on a MizerSim, against body size.

The same array objects can be passed to plotHover() to produce hover-enabled plotly versions, for example plotHover(getBiomass(sim)) or plotHover(getEncounter(params)). To add another compatible array to an existing ggplot, use addPlot(). To compare two compatible mizer arrays directly, use plot2(). To plot cumulative distributions over body size, use plotCDF(). To visualise how spectra or rates change through time, use animate() on a MizerSim or an ArrayTimeBySpeciesBySize object.

The named plotting functions give more specialised control. This table shows the available named plotting functions.

Plot	Description
plotBiomass()	Plots the total biomass of each species through time. A time range to be plotted can be s
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.
plotSpectra()	Plots the abundance (biomass or numbers) spectra of each species and the background c
plotCDF()	Plots cumulative distributions of abundance or biomass over size.
plotCDF2()	Compares cumulative distributions from two simulations or parameter objects in one plo
plotSpectra2()	Compares the spectra from two simulations or parameter objects in one plot.
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.
plotGrowthCurves()	Plots the size as a function of age.
plotDiet()	Plots the diet composition at size for a given predator species.
plotBiomassObservedVsModel()	Compares observed biomass with model biomass.
plotYieldObservedVsModel()	Compares observed yield with model yield.
animate()	Animates spectra or rate arrays through time. The older animateSpectra() name is reta

The static plotting functions use ggplot2 and return a ggplot object. This means that you can manipulate the plot further after its creation using the ggplot grammar of graphics. The named high-level plot functions have plotly counterparts, for example plotlyBiomass() or plotlySpectra(), for interactive exploration. Generic and compositional plotting APIs, such as plot(), plot2(), plotRelative() and addPlot(), do not have separate plotly wrappers. Use plotHover() on the ggplot object they return.

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: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotYieldVsF()

Examples

```
sim <- NS_sim

# Generic plot methods
plot(sim)
plot(getBiomass(sim), species = c("Cod", "Herring"))
plotHover(getBiomass(sim))

# Named plot functions
plotFeedingLevel(sim)

# Plotting only a subset of species
plotFeedingLevel(sim, species = c("Cod", "Herring"))

# Adding another compatible array to an existing plot
p <- plot(getBiomass(sim), species = "Cod")
addPlot(p, getBiomass(sim), species = "Herring", linetype = "dashed")

# 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(
  object,
  sim2 = NULL,
  species = NULL,
  total = FALSE,
  log_x = FALSE,
  log_y = TRUE,
  log = NULL,
  ylim = c(NA, NA),
  tlim = c(NA, NA),
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

Arguments

object	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 yield from all species is plotted as well. Default is FALSE.
log_x	If TRUE, use a log10 x-axis. Default is FALSE.
log_y	If TRUE, use a log10 y-axis. Default is TRUE.
log	Character string specifying which axes should use log10 scales, in the same form as the base plot() argument. For example, "x", "y", "xy" or "". If supplied, this overrides log_x and log_y. For backward compatibility, TRUE and FALSE are interpreted as setting only log_y.
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.
tlim	A numeric vector of length two providing lower and upper limits for the time axis, e.g. c(1980, 2000). Use NA to apply no limit at that end. Default is c(NA, NA).
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 is FALSE.
...	Arguments passed to getYield().

Value

A ggplot2 object, unless `return_data = TRUE`, in which case a data frame with the three variables 'Year', 'Yield', 'Species' is returned. If `sim2` is supplied, the data frame also has a 'Simulation' variable.

See Also

plotting_functions, `getYield()`

Other plotting functions: `addPlot()`, `animate()`, `plot`, `plot2()`, `plotBiomass()`, `plotCDF()`, `plotCDF2()`, `plotDiet()`, `plotFMort()`, `plotFeedingLevel()`, `plotGrowthCurves()`, `plotMizerParams`, `plotMizerSim`, `plotPredMort()`, `plotRelative()`, `plotSpectra()`, `plotSpectra2()`, `plotSpectraRelative()`, `plotYieldGear()`, `plotYieldVsF()`, `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(
  object,
  species = NULL,
  gears = NULL,
  total = FALSE,
  log_x = FALSE,
  log_y = TRUE,
  log = NULL,
  ylim = c(NA, NA),
  tlim = c(NA, NA),
```

```
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

Arguments

object	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.
gears	A vector of gear names to be included in the plot. Default is all gears.
total	A boolean value that determines whether the total yield from all species is plotted as well. Default is FALSE.
log_x	If TRUE, use a log10 x-axis. Default is FALSE.
log_y	If TRUE, use a log10 y-axis. Default is TRUE.
log	Character string specifying which axes should use log10 scales, in the same form as the base plot() argument. For example, "x", "y", "xy" or "". If supplied, this overrides log_x and log_y. For backward compatibility, TRUE and FALSE are interpreted as setting only log_y.
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.
tlim	A numeric vector of length two providing lower and upper limits for the time axis, e.g. c(1980, 2000). Use NA to apply no limit at that end. Default is c(NA, NA).
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 is FALSE.
...	Arguments passed to getYieldGear().

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: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldVsF(), 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, 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,
  gear = NULL,
  ...
)
```

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.
`gear`	The gears to be included. Optional. By default the catch of all gears is included. A vector of gear names. Only species caught by the selected gears are shown.
`...`	For `plotlyYieldObservedVsModel()`, additional arguments passed to `plotHover()`. Otherwise unused.

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. Its home is the gear parameter data frame, see `gear_params()`, where you give the yield for each gear-species pair and this function adds them up over the gears. For backwards compatibility a `yield_observed` column in the species parameter data frame is also accepted, see `get_yield_observed()`. For species for which you have no observed yield, you should set the value in the `yield_observed` column to 0 or NA.

If a species is caught by several gears, both the model yield and the observed yield are summed over the gears. With the `gear` argument you can restrict the comparison to a subset of the gears, in which case only the catch of those gears enters on both axes. Because the species parameter data frame only holds the yield summed over all gears, the observations then have to come from the gear parameters.

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
# In this model each species is caught by a single gear, so there is one
# row in the gear parameters for each species, in the same order.
# Species without an observation get NA.
gear_params(params)$yield_observed <-
    c(NA, NA, NA, 3e11, 4e9, 4e10, 5e10, NA, 2e11, 6e10, 3e11, NA)

# 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)

# If several gears catch the same species, their yields are added up.
# Give Cod a second gear that takes a quarter of the observed yield.
gp <- gear_params(params)
gp["Cod, Otter", "yield_observed"] <- 3e11 * 0.75
extra <- gp["Cod, Otter", ]
extra$gear <- "Gillnet"
extra$yield_observed <- 3e11 * 0.25
gear_params(params) <- rbind(gp, extra)

# Compare only the catch of the Otter gear against its observation
plotYieldObservedVsModel(params, gear = "Otter")
```

`plotYieldVsF` *Plot the yield of a species against the fishing mortality on it*

Description

[Experimental]

Varies the fishing mortality on one species over a range of values, leaving the fishing on every other species unchanged, and plots the long-term yield of that species against it. The fishing mortality at which the yield is largest is F_{MSY}, and is marked on the plot by default.

This is `scanModel()` with `scanFishingMortality()` as its setter and `getYield()` as the quantity it measures. Use `scanModel()` directly to vary something other than the fishing mortality on a single species, to measure something other than the yield, or to follow more than one species at once.

At each fishing mortality the model is projected until it settles, and what is plotted depends on what it settled on. At a fixed point the yield is read straight off the settled state. On a limit cycle it is averaged over exactly one period, and the band around the line shows the range the yield covers over that cycle, so an oscillation is displayed rather than silently averaged away. Fishing mortalities

at which the model settled on neither are marked with a cross and should not be relied on; raise `t_max` for those.

The scan starts from the fishing mortality the model currently sits at and works outwards in both directions, each arm warm-starting from the attractor reached at the previous value.

Usage

```
plotYieldVsF(
  params,
  species,
  F_range,
  F_min = 0,
  F_max = 1.5,
  no_steps = 16,
  gear = NULL,
  style = "ribbon",
  mark_max = TRUE,
  reference_lines = TRUE,
  log_y = FALSE,
  log = NULL,
  return_data = FALSE,
  progress_bar = interactive(),
  ...
)
```

Arguments

`params` A MizerParams object.

`species` The name of the species whose fishing mortality is varied. Only one species at a time.

`F_range` A numeric vector of fishing mortalities for the x-axis. If missing it is built as `seq(F_min, F_max, length.out = no_steps)`.

`F_min, F_max, no_steps` Used to build `F_range` when that is missing.

`gear` The name of the gear whose fishing mortality on the species is varied. Only needed when several gears catch the species; if NULL (default), the fishing mortality from all of them is replaced. See `scanFishingMortality()`.

`style` How the range covered on a limit cycle is drawn, see `plot.MizerScan()`. The default `"ribbon"` draws the average as a line inside the band.

`mark_max` Whether to mark the fishing mortality at which the yield is largest, which is F_{MSY}. Default TRUE.

`reference_lines` Whether to draw reference lines (the current fishing mortality as "Current F", and the `F_MSY` species parameter if the species has one) as vertical lines. See `plot.MizerScan()`.

log_y, log	Whether to use a logarithmic y-axis, see parsePlotLog(). Unlike most mizer plots this defaults to FALSE, because the yield is exactly zero at zero fishing mortality and a logarithmic axis would drop the point that anchors the curve.
return_data	If TRUE the MizerScan object underlying the plot is returned instead of the plot. Default FALSE.
progress_bar	If TRUE a text progress bar is shown while the fishing mortalities are swept. Defaults to interactive().
...	Further arguments are passed on to scanModel().

Value

A ggplot2 object, or, if return_data = TRUE, the MizerScan object holding the data. The fishing mortality giving the largest yield is available from that object as attr(scan, "at_max").

See Also

scanModel(), scanFishingMortality(), plot.MizerScan(), getYield()

Other plotting functions: addPlot(), animate(), plot, plot2(), plotBiomass(), plotCDF(), plotCDF2(), plotDiet(), plotFMort(), plotFeedingLevel(), plotGrowthCurves(), plotMizerParams, plotMizerSim, plotPredMort(), plotRelative(), plotSpectra(), plotSpectra2(), plotSpectraRelative(), plotYield(), plotYieldGear(), plotting_functions

Other scan functions: MizerScan(), plot.MizerScan(), scanEffort(), scanModel()

Examples

```
plotYieldVsF(NS_params, "Cod", F_max = 1.5, no_steps = 8)

# The fishing mortality that maximises the yield
scan <- plotYieldVsF(NS_params, "Cod", F_max = 1.5, no_steps = 8,
                     return_data = TRUE)
attr(scan, "at_max")
```

---

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.

See Also

setPredKernel()

Other predation kernel: box_pred_kernel(), gaussian_mixture_pred_kernel(), lognormal_pred_kernel(), truncated_lognormal_pred_kernel()

Examples

```
params <- NS_params
# Set all required paramters before changing kernel type
species_params(params)["Cod", "kernel_exp"] <- -0.8
species_params(params)["Cod", "kernel_l_l"] <- 4.6
species_params(params)["Cod", "kernel_u_l"] <- 3
species_params(params)["Cod", "kernel_l_r"] <- 12.5
species_params(params)["Cod", "kernel_u_r"] <- 4.3
species_params(params)["Cod", "pred_kernel_type"] <- "power_law"
plot(w_full(params), pred_kernel(params)["Cod", 10, ], type="l", log="x")
```

print *Print mizer objects*

Description

Mizer supplies `print()` methods for the array-like objects returned by many rate and summary functions. These methods print a compact preview of the underlying matrix, array or vector: a header reporting the value name, dimensions and units, followed by the actual values, truncated to fit the console when the array is large. Species are truncated to a leading subset, sizes to an evenly log-spaced sample spanning the full size range (because size grids are uniform in log-space, this shows small, medium and large individuals rather than just the smallest), and time series to a representative sample of time steps that always includes the first and last. A trailing note reports how much was omitted. A three-dimensional `ArrayTimeBySpeciesBySize()` object is previewed via its final time slice, matching the default behaviour of `plot()` for that class.

Usage

```
## S3 method for class 'ArraySpeciesBySize'
print(x, ...)
## S3 method for class 'ArrayTimeBySpecies'
print(x, ...)
## S3 method for class 'ArrayTimeBySpeciesBySize'
print(x, ...)
## S3 method for class 'summary.ArraySpeciesBySize'
print(x, ...)
## S3 method for class 'summary.ArrayTimeBySpecies'
print(x, ...)
## S3 method for class 'summary.ArrayTimeBySpeciesBySize'
print(x, ...)
```

Arguments

x	The object to print.
...	Further arguments. They are currently ignored by the mizer methods.

Details

For full numeric access, use the object itself as an ordinary matrix, array or vector, or convert it to a long data frame with `as.data.frame()`.

Value

The printed object, invisibly.

See Also

`summary()`, `as.data.frame()`, `plot()`, `ArraySpeciesBySize()`, `ArrayTimeBySpecies()`, `ArrayTimeBySpeciesBySize(`

Examples

```
enc <- getEncounter(NS_params)
print(enc)

biomass <- getBiomass(NS_sim)
print(biomass)
```

`print.mizer_plot` *Print a mizer plot*

Description

Suppresses the uninformative ggplot2 warning about log transformations introducing infinite values, which occurs when zero values are present on a logged axis.

Usage

```
## S3 method for class 'mizer_plot'
print(x, ...)
```

Arguments

`x`	A `mizer_plot` object.
`...`	Further arguments passed to the ggplot2 print method.

Value

The plot object, invisibly.

`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,
  callback = NULL,
  method = c("euler", "predictor_corrector", "tr_bdf2"),
  check_steady = FALSE,
  ...
)
```

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. When an effort array is supplied, this argument can be used to extend the simulation beyond the times specified in the effort array. See notes below.
`dt`	Time step of the solver. The default value is 0.1. When `object` is a `MizerSim`, defaults to the value used to produce that simulation.
`t_save`	The frequency with which the output is stored. The default value is 1. 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.
`callback`	A function to be called at each saved time step of the simulation. The callback function is called with the `MizerSim` object, the current time index, and any additional arguments passed to `project()` via `...`.

`method` The numerical method to use for the consumer density update.

`"euler"` uses the first-order semi-implicit Euler update.

`"tr_bdf2"` uses the L-stable, second-order TR-BDF2 method and is the recommended second-order method. `"second_order"` is accepted as an easier-to-remember alias for it, matching the name of the spatial second-order option `second_order_w()`.

`"predictor_corrector"` is superseded by `"tr_bdf2"`. It is also second order and costs the same, but its Crank-Nicolson corrector is only A-stable, so it rings at large time steps where TR-BDF2 does not. It is retained for backwards compatibility and for comparison. `"predictor-corrector"` is accepted as an alias for it.

The two second-order methods treat the nonlinear rates identically. The Crank-Nicolson update in `"predictor_corrector"` is only the *corrector*, applied to the transport operator with those rates frozen, so the method does not inherit Crank-Nicolson's stability properties for the full nonlinear dynamics. The same holds for the L-stability of `"tr_bdf2"`; see the section "Custom rates must depend continuously on abundance" below.

Aliases are resolved to the canonical name, so `getSimParams()` reports `"tr_bdf2"` even when `"second_order"` was supplied.

When `object` is a `MizerSim`, defaults to the value used to produce that simulation. A warning is issued if `append = TRUE` and the supplied value differs from the stored one.

`check_steady` **[Experimental]** If `TRUE`, warn when the model is not at its steady state before the projection starts, which catches the common mistake of forgetting to re-run `tuneSteadyState()` after a `match. . . /calibrate. . .` step. Default `FALSE`, because projecting a model away from its steady state is a perfectly normal thing to do. It is meant for a `MizerParams` object; when continuing from a `MizerSim` the starting state is deliberately wherever the previous run ended, so there is nothing to check. The check is made at the effort stored in the params object rather than at the `effort` supplied here, so that running a fishing scenario at a new effort — which legitimately starts away from the steady state of that new effort — does not warn. See `getSteadyResidual()`.

`...` Other arguments will be passed to rate functions.

Value

An object of class MizerSim.

Advective flux scheme

The spatial discretisation of the growth (advection) term is controlled by the `flux` entry of the `second_order_w` slot of the params object, not by an argument to `project()`. With the default (`"upwind"`) the first-order upwind flux is used. Setting it to `"van_leer"` (for example with `second_order_w(params) <- TRUE`) switches on a flux-limited (van Leer, TVD) deferred correction that removes the leading numerical diffusion $\approx g\, w\, \log \beta$ of the upwind flux while keeping the density update a tridiagonal solve and preserving positivity. The correction is most useful on coarse logarithmic grids and pairs naturally with the second-order time methods. Because it changes the

discrete steady state, the choice lives in the params object alongside the steady state rather than being a per-run argument. See `second_order_w()`.

Custom rates must depend continuously on abundance

All three methods are *semi-implicit*: the densities are solved for implicitly, but the rates that build the transport operator are frozen at values computed from earlier states. The second-order methods gain their extra order by evaluating the rates twice — at the start of the step and from a provisional prediction of its end — and averaging. That average is only second order if the rates vary smoothly along the trajectory.

A custom rate function registered with `setRateFunction()` that depends discontinuously on the abundances therefore defeats all three methods alike, including the L-stable `"tr_bdf2"`, whose damping applies to the frozen linear operator and not to the rates. The result is a trajectory that keeps changing as `dt` is refined. See the Discontinuous rate functions article for the symptoms and the remedy.

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 four 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 named vector whose names match with existing gear names. The values in the vector specify the constant fishing effort for those fishing gears, i.e. the effort is constant through time. The effort for gears that are not included in the effort vector is set to the default effort value, which is 1 in defaults edition 2 and later and 0 in earlier defaults editions. Missing (`NA`) effort entries are replaced in the same way.
- A numerical vector which has the same length as the number of fishing gears. The values in the vector specify the constant fishing effort of each of the fishing gears, with the ordering assumed to be the same as in the MizerParams object.
- 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` object. 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.

When an effort array is provided, the `t_max` argument can be used to extend the simulation beyond the last time specified in the effort array. In this case, the effort values from the last time in the array will be used for the extended period. The `t_save` argument can be used to specify the frequency at which simulation results are saved. If `t_save` is not supplied, the results will be saved at the times specified in the effort array. If both `t_max` and `t_save` are provided with an effort array, effort values will be interpolated (using step function) or extrapolated (using the last known value)

as needed for the new time points. The `t_start` argument continues to be ignored when an effort array is supplied.

Note that if `t_max` or `t_save` are specified, the time grid for the simulation is resampled based on `t_save`. This means that if the time points in the `effort` array are irregular and do not align with the new grid, those specific time points may be lost and the effort values at the new grid points will be calculated via interpolation.

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

```
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)
# Extend a simulation beyond the effort array times
# Effort values from the final time are used for the extension
sim <- project(params, effort = effort_array, t_max = 15)
# Control save times with an effort array using t_save
sim <- project(params, effort = effort_array, t_save = 2)
```

`project_n` *Project values for first time step of Euler method*

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_n(
  params,
  r,
  n,
  dt,
  a,
  b,
  c,
  S,
  idx,
  w_min_idx_array_ref,
  no_sp,
  no_w,
  flux_limiter = "none"
)

project_n_no_diffusion(
  params,
  r,
  n,
  dt,
  a,
  b,
  S,
  idx,
  w_min_idx_array_ref,
  no_sp,
  no_w
)
```

Arguments

params	A MizerParams object.
r	A list of rates as returned by `mizerRates()`.
n	An array (species x size) with the number density at the current time step.
dt	Time step.
a	A matrix (species x size) used in the solver (transport term).
b	A matrix (species x size) used in the solver (diagonal term).
c	A matrix (species x size) used in the solver (transport term).
S	A matrix (species x size) used in the solver (source term).
idx	Index vector for size bins (excluding the first one).
w_min_idx_array_ref	Index vector for the start of the size spectrum for each species.
no_sp	Number of species.

no_w	Number of size bins.
flux_limiter	Name of the flux limiter used for a deferred high-order correction of the upwind advective flux, or "none" for plain first-order upwind. See project().

Details

The function calculates the abundance at the next time step using the McKendrick-von Foerster equation:

$$\frac{\partial N}{\partial t} + \frac{\partial}{\partial w}\left(gN - \frac{1}{2}\frac{\partial(DN)}{\partial w}\right) = -\mu N$$

which is solved using a semi-implicit upwind finite volume scheme.

Value

The updated abundance density matrix n.

See Also

project, mizerRates

---

project_n_2 *Project values with a predictor-corrector method*

Description

This is an experimental second-order time stepping variant of project_n(). It first predicts the new consumer densities with project_n(), optionally recalculates rates from that prediction, and then applies a Crank-Nicolson corrector using midpoint rates.

Usage

```
project_n_2(
  params,
  r,
  n,
  dt,
  a,
  b,
  c,
  S,
  idx,
  w_min_idx_array_ref,
  no_sp,
  no_w,
  rates_fns = NULL,
  n_pp = NULL,
  n_other = NULL,
```

```
  t = 0,
  effort = NULL,
  r_hat = NULL,
  r_mid = NULL,
  n_hat = NULL,
  flux_limiter = "none",
  ...
)
```

Arguments

params	A MizerParams object.
r	A list of rates as returned by `mizerRates()`.
n	An array (species x size) with the number density at the current time step.
dt	Time step.
a	A matrix (species x size) used in the solver (transport term).
b	A matrix (species x size) used in the solver (diagonal term).
c	A matrix (species x size) used in the solver (transport term).
S	A matrix (species x size) used in the solver (source term).
idx	Index vector for size bins (excluding the first one).
w_min_idx_array_ref	Index vector for the start of the size spectrum for each species.
no_sp	Number of species.
no_w	Number of size bins.
rates_fns	Optional named list of rate functions, as used by `mizerRates()`. If supplied together with `n_pp`, `n_other` and `effort`, provisional end-of-step rates are calculated from the predicted densities.
n_pp	Resource abundance used when recalculating provisional rates.
n_other	Other ecosystem components used when recalculating provisional rates.
t	Current time.
effort	Fishing effort used when recalculating provisional rates.
r_hat	Optional provisional end-of-step rates. If supplied, these are used instead of recalculating them.
r_mid	Optional midpoint rates. If supplied, these are used directly in the Crank-Nicolson corrector.
n_hat	Optional provisional end-of-step densities. When supplied with a flux limiter, the limiter is frozen at the midpoint field `(n + n_hat) / 2`; otherwise it falls back to the start-of-step `n`.
flux_limiter	Name of the flux limiter used for a deferred high-order correction of the upwind advective flux, or `"none"` for plain first-order upwind. See `project()`.
...	Further arguments passed to the rate functions.

Details

If the rate recalculation arguments are not supplied, the corrector uses the supplied rates as fixed rates. In that case the corrector is second order only for the frozen-rate transport problem, not for the full nonlinear mizer dynamics.

Value

The updated abundance density matrix `n`.

See Also

`project_n`

`project_n_tr_bdf2` *Project values with the TR-BDF2 method*

Description

This is an L-stable, second-order time stepping variant of `project_n()`. It takes one TR-BDF2 step, consisting of a trapezoidal (Crank-Nicolson) stage over the first part of the time step followed by a second-order backward differentiation (BDF2) stage over the remainder.

Usage

```
project_n_tr_bdf2(
  params,
  r,
  n,
  dt,
  a,
  b,
  c,
  S,
  idx,
  w_min_idx_array_ref,
  no_sp,
  no_w,
  rates_fns = NULL,
  n_pp = NULL,
  n_other = NULL,
  t = 0,
  effort = NULL,
  r_hat = NULL,
  r_mid = NULL,
  n_hat = NULL,
  flux_limiter = "none",
  ...
)
```

Arguments

params	A MizerParams object.
r	A list of rates as returned by mizerRates().
n	An array (species x size) with the number density at the current time step.
dt	Time step.
a	A matrix (species x size) used in the solver (transport term).
b	A matrix (species x size) used in the solver (diagonal term).
c	A matrix (species x size) used in the solver (transport term).
S	A matrix (species x size) used in the solver (source term).
idx	Index vector for size bins (excluding the first one).
w_min_idx_array_ref	Index vector for the start of the size spectrum for each species.
no_sp	Number of species.
no_w	Number of size bins.
rates_fns	Optional named list of rate functions, as used by mizerRates(). If supplied together with n_pp, n_other and effort, provisional end-of-step rates are calculated from the predicted densities.
n_pp	Resource abundance used when recalculating provisional rates.
n_other	Other ecosystem components used when recalculating provisional rates.
t	Current time.
effort	Fishing effort used when recalculating provisional rates.
r_hat	Optional provisional end-of-step rates. If supplied, these are used instead of recalculating them.
r_mid	Optional midpoint rates. If supplied, these are used directly to build the TR-BDF2 operator.
n_hat	Optional provisional end-of-step densities. When supplied with a flux limiter, the limiter is frozen at the midpoint field (n + n_hat) / 2; otherwise it falls back to the start-of-step n.
flux_limiter	Name of the flux limiter used for a deferred high-order correction of the upwind advective flux, or "none" for plain first-order upwind. See project().
...	Further arguments passed to the rate functions.

Details

The nonlinear rates are handled exactly as in project_n_2(): a provisional Euler predictor gives end-of-step rates, which are averaged with the start-of-step rates to obtain second-order-accurate midpoint rates r_mid. Both TR-BDF2 stages then use this single frozen operator.

With the standard parameter $\gamma = 2 - \sqrt{2}$ both stages share the same implicit coefficient $\alpha\,\Delta t$ with $\alpha = \gamma/2 = 1 - 1/\sqrt{2}$, so the operator $I - \alpha\,\Delta t\,L$ is assembled once with get_transport_coefs() and each stage is a single tridiagonal solve with project_n_loop(), exactly as in project_n() and project_n_2(). Unlike the Crank-Nicolson corrector in project_n_2(), TR-BDF2 is L-stable and therefore damps the stiff modes that cause Crank-Nicolson to oscillate at large time steps.

If the rate recalculation arguments are not supplied, the step uses the supplied rates as fixed rates. In that case the method is second order only for the frozen-rate transport problem, not for the full nonlinear mizer dynamics, but it remains L-stable.

Value

The updated abundance density matrix `n`.

See Also

`project_n`, `project_n_2`

`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,
  n_pp,
  n_other,
  effort,
  t,
  dt,
  steps,
  resource_dynamics_fn,
  other_dynamics_fns,
  rates_fns,
  method = c("euler", "predictor_corrector", "tr_bdf2"),
  ...
)
```

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.
`method`	The numerical method to use for the consumer density update. See `project()`.
`...`	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 by the steady-state finders. 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 from the final update step, these too are included in the returned list.

Value

List with the final values of `n`, `n_pp`, and `n_other`, together with `rates`, the rates calculated at the start of the final update step.

projectRDD — *Get density-dependent reproduction rate during projection*

Description

S3 generic used by extension-aware projections to calculate the density-dependent reproduction rate. The base method calls the selected density-dependence function in `params@rates_funcs$RDD`.

Usage

```
projectRDD(params, rdi, species_params = params@species_params, t = 0, ...)

## S3 method for class 'MizerParams'
projectRDD(params, rdi, species_params = params@species_params, t = 0, ...)
```

Arguments

`params`	A MizerParams object.
`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.
`t`	The time for which to do the calculation.
`...`	Unused

Value

Vector of density-dependent reproduction rates.

projectUntilSettled — *Project the dynamics until they settle*

Description

[Experimental]

Run the full dynamics, as in `project()`, but stop once the run has settled: either the change has slowed down sufficiently, in the sense that the distance between states `t_check` years apart is less than `distance_tol` and the state has stopped drifting, or the run has been recognised as being on a limit cycle. You determine how the distance is calculated.

Nothing is held fixed, so the run can only ever end up on an attractor of the dynamics, and that need not be a fixed point: besides a limit cycle it may stop on a species going extinct, or simply at `t_max`. "Settled" is therefore the most this function claims; the state it leaves behind is not necessarily a steady state. See the section below on how to check, and use `findSteadyState()` if what you want is the steady state itself rather than the trajectory leading to it.

Usage

```
projectUntilSettled(
  params,
  effort = params@initial_effort,
  distance_func = distanceSSLogN,
  t_check = 15 * dt,
  t_max = 100,
  dt = 0.1,
  t_save = 1,
  distance_tol = 0.1 * t_check,
  residual_tol = steady_residual_tol(),
  amplitude_tol = 0.01,
  amp_rel_tol = 0.1,
  extinction_threshold = 1e-06,
  progress_bar = TRUE,
  info_level = default_info_level(),
  method = c("euler", "predictor_corrector", "tr_bdf2"),
  ...
)
```

Arguments

params	A MizerParams object
effort	The fishing effort to be used throughout the simulation. This is validated by `validEffortVector()` and can therefore be `NULL`, a single numeric value used for all gears, an unnamed numeric vector with one entry per gear, or a named numeric vector for some or all gears.
distance_func	A function that will be called at every check 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_check	The interval in years at which the run pauses to check whether it has settled, and hence also the interval over which `distance_func` measures change. Must be a positive multiple of `dt`. The default `15 * dt` is an odd multiple of the time step, which is what lets a period-2 cycle be seen; you should rarely need to change it.
t_max	The maximum number of years to run the simulation. Default is 100.
dt	The time step to use in `project()`.
t_save	The interval in years at which the state is stored in the returned `MizerSim`, as in `project()`. Must be a positive multiple of `dt`, but need bear no relation to `t_check`. Default is 1. The state the run settles on is always the final time point, even when the run stops between two saves.
distance_tol	The run stops when the number returned by `distance_func` for two states `t_check` years apart drops below `distance_tol`, provided the drift criterion below is also met. Its meaning therefore depends on the distance function you supply. It was called `tol` before mizer 3.3.

residual_tol **[Experimental]** The largest relative rate of biomass change, in 1/year, that a state may have and still be called a fixed point. This is the criterion of isSteady() and is measured with getSteadyResidual(), so it has the same meaning for every model and every distance function. Default 0.05.

It is a backstop against a distance function that has gone quiet while the model is still moving, not the main line of defence against a cycle: an oscillation of relative amplitude A and period T drifts at up to $2\pi A/T$ per year, which for a small amplitude_tol can be below any sensible residual_tol. Cycles that small are caught by the cycle detection above, which is why that runs unconditionally.

amplitude_tol **[Experimental]** The minimum relative biomass amplitude for a persistent oscillation to be reported as a limit cycle rather than treated as an (effectively steady) fixed point. This is a fraction of mean biomass and is kept separate from distance_tol (which measures convergence to a fixed point on a different scale). Default 0.01.

amp_rel_tol **[Experimental]** Maximum relative change of amplitude between successive periods for the cycle to count as settled. Default 0.01.

extinction_threshold **[Experimental]** A species is treated as going extinct, stopping the run, once its reproduction rate (RDD) falls below this fraction of its value at the start of the run. For example the default 1e-6 treats a species as extinct once its reproduction has collapsed to a millionth of its initial level. Because it is relative to the initial reproduction, a species that is present but starts with zero reproduction is flagged immediately, and (in tuneSteadyState(), where reproduction is held constant) a healthy species is never flagged. A species with no fish at the start is not tested.

progress_bar A shiny progress object to implement a progress bar in a shiny app. Default FALSE.

info_level Controls the amount of information messages that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().

method The numerical method to use for the consumer density update. See project().

... Further arguments will be passed on to your distance function.

Value

A MizerSim object containing the states saved every t_save years, with the state the run settled on as its final time point. That last interval is shorter than the others when the run stops between two saves. Use finalParams() to extract that final state as a MizerParams object, or call findSteadyState() instead, which returns it directly.

The returned object carries an attribute "convergence" describing the solution the run settled on, a named list with entries. The first three answer three different questions and should not be read as one:

termination Why the run stopped: "residual_tolerance" (both convergence criteria were met), "distance_tolerance" (the distance function was satisfied but the state is still drifting — reachable with a loose residual_tol, and from the superseded steady(), which stops on

the distance criterion alone), "cycle_detected" (a limit cycle), "time_limit" (still changing at t_max) or "extinction" (a species died out). The steady-state finders can also return "solver_converged" and "solver_failed" from the Newton solver.

converged Logical, TRUE when the run stopped on a criterion of its own rather than running out of time or losing a species. This is a statement about the numerics, not about the state.

attractor What the state that was reached actually is: "fixed_point" when the biomass drift is within residual_tol, "limit_cycle" when a cycle was detected, and NA when it is neither — a run stopped in mid-flight, or a species on its way out. This is the entry to test before treating a result as a steady state.

distance The final value returned by distance_func.

residual The largest absolute relative rate of biomass change, in 1/year, at the state that was reached. For each consumer species this is $(dB_i/dt)/B_i$, a biomass-weighted aggregate over its size classes; the resource is treated the same way and the other components contribute their own relative rates. Unlike distance, which compares two states t_check apart on whatever scale the distance function uses, this measures how far the state actually is from being a fixed point.

years The number of years simulated. NA for a direct solve.

period For a limit cycle, its period in years; otherwise NA.

amplitude For a limit cycle, the largest per-species relative peak-to-trough biomass amplitude; otherwise NA.

extinct Character vector naming any species that went extinct during the run, or character(0) if none.

How the run is organised

The dynamics are advanced with time step dt exactly as in project(). Every t_check years the function pauses to decide whether to stop, so t_check sets how often the stopping criteria are evaluated and also the interval over which change is measured. You should not normally need to set it: it defaults to 15 * dt, which is an odd multiple of the time step for the reason given below. The run ends at the latest after t_max years.

Independently of that, the state is stored in the returned MizerSim every t_save years, exactly as in project(), and a cheap scalar summary of the state (the biomass of each species) is recorded after every time step. That finely resolved series is what the limit-cycle detection works on, so that a cycle can be found and its period measured even when that period bears no simple relation to t_check. The three intervals are independent of each other; t_check and t_save need only be multiples of dt.

At each check the following tests are made, in this order.

1. Extinction:

If the reproduction rate (RDD) of any species has fallen below extinction_threshold times its value at the start of the run, or has become NA, that species is deemed to be on its way to extinction. A warning naming the affected species is issued and the run stops with termination = "extinction". Because the criterion is relative to the initial reproduction, a species that is present but starts with zero reproduction is flagged immediately, whereas in tuneSteadyState(), where reproduction is held constant, a healthy species is never flagged. A species with no fish at the start of the run is not tested: it stays absent while the others settle, as it does with the Newton solver of findSteadyState().

2. Limit cycle:

The recorded biomass series is examined to see whether the run has settled onto a limit cycle. If it has, the run stops with `termination = "cycle_detected"` and the period and amplitude of the cycle are reported.

It is made at every check, whether or not the state looks converged by the measure below. A cycle whose period divides `t_check` puts the two states that the distance function compares at the same phase, so it would otherwise be reported as a fixed point of zero width. The detection works on the biomass series sampled at every time step instead, which is blind to `t_check`.

3. Convergence to a fixed point:

Two things have to hold for the run to stop on a fixed point.

First, `distance_func` is called with the state at the previous check and the state at the current one, i.e. with two states `t_check` years apart, and the number it returns must be less than `distance_tol`. What "distance" means is entirely up to that function: the default `distanceSSLogN()` uses the sum of squared changes in log abundance, while `tuneSteadyState()` instead passes `distanceMaxRelRDI()`, which uses the largest relative change in egg production.

Second, the state actually reached must be a fixed point: the largest relative rate of biomass change there, as measured by `getSteadyResidual()`, must be at most `residual_tol`. The distance criterion on its own says only that the state stopped moving on the scale of the distance function, which is a different question — a distance function can be insensitive to the very motion that is left. When the distance criterion is met but the drift is not, the run carries on rather than declaring a fixed point.

When both hold the run stops with `termination = "residual_tolerance"`. That is deliberately not called `"steady"`: `residual_tol` is a working tolerance rather than a proof, and the `residual` entry of the `"convergence"` attribute reports the drift that was actually reached.

Even so, `t_check` should be an *odd* multiple of `dt`, which is why it defaults to `15 * dt`. A period-2 cycle (period `2 * dt`), the most common numerical oscillation, is otherwise sampled at the same phase at every check, and its amplitude can sit below `amplitude_tol` where the cycle detection deliberately ignores it.

If none of the three checks fires before `t_max` is reached, the run stops with `termination = "time_limit"`. In every case the outcome is recorded in the `"convergence"` attribute of the returned object, described under *Value* below.

How a limit cycle is detected

The detection uses the community-total biomass, on a log scale and with its mean removed, as a scalar signal, sampled after every time step. At least 20 steps are needed before any cycle can be reported.

1. **Candidate period.** The autocorrelation function of the signal is computed up to a lag of half the length of the series, and the first local maximum with an autocorrelation above `0.5` is taken as the candidate period. If there is no such peak, or the peak is at a lag of one sample, no cycle is reported.
2. **Enough history.** The series must cover at least three full candidate periods. Otherwise the check is deferred to a later block, when more history has accumulated.
3. **Amplitude.** For each of the last three period-long windows, the amplitude is measured as the largest over species of the relative peak-to-trough biomass range `(max - min) / mean`. The

amplitude in the most recent window must exceed amplitude_tol; a smaller oscillation is considered negligible and the state is left to be treated as a fixed point.

4. **Settled.** The amplitudes of the three successive windows must agree with each other to within amp_rel_tol, and the most recent amplitude must not be smaller than the oldest by more than amp_rel_tol.

The last condition is what distinguishes a genuine limit cycle from a slowly decaying spiral towards a stable fixed point: the spiral loses amplitude from one period to the next, the cycle does not. The distinction is necessarily imperfect when the decay is extremely slow, because over any finite run such a spiral is indistinguishable from a cycle. If you need a definitive answer, use getStability() on the fixed point found by findSteadyState(), which works out the eigenvalues of the linearised dynamics instead of watching a trajectory.

The reported period is a multiple of dt, so it is only resolved to that accuracy; reduce dt if you need the period more precisely.

What you get back may not be a steady state

The stopping criterion is a proxy. It says that two states t_per years apart differ by less than distance_tol on whatever scale the criterion is measured on; it does not say that the state reached is a fixed point. There are four ways the returned object can fail to be one:

- the run converged on its own scale while the biomasses are still visibly drifting (termination = "distance_tolerance");
- the run reached t_max without converging (termination = "time_limit");
- the run settled on a limit cycle (termination = "cycle_detected"), in which case the state stored is one point on that cycle;
- the run stopped because a species was going extinct (termination = "extinction").

So treat the result as a claim to be checked rather than as a guarantee:

```
attr(params, "convergence")$attractor  # "fixed_point", "limit_cycle" or NA
attr(params, "convergence")$residual   # largest biomass drift, in 1/year
isSteady(params)                       # TRUE if within tolerance
summary(params)                        # includes the biomass-drift verdict
plot(getSteadyResidual(params))        # which species, and at which sizes
```

attractor is the field that answers the question: it is "fixed_point" only where the measured biomass drift is within residual_tol, so it cannot be satisfied by a distance function that has merely gone quiet. termination says how the run ended and converged whether the solver met its own criterion; neither is a claim about the state. The last line says *where* the model is not steady, which is the one to reach for when it is not: a model that is off steady state is usually off in one species or one part of the size range, and the plot names it. See getSteadyResidual() for why the verdict is phrased in terms of biomass drift rather than the largest per-capita rate.

The messages this function prints say the same thing — a converged run whose biomasses are still moving reports the drift and adds "Reduce the tolerance on the distance function to converge further." — but they are suppressed by info_level = 0, so in a script the "convergence" attribute is the reliable check.

Finally, a genuine fixed point need not be a *stable* one. Use `getStability()` to find out, and `solver = "newton"` to converge onto a fixed point that the dynamics themselves would run away from.

See Also

`findSteadyState()`, `tuneSteadyState()`, `isSteady()`, `getSteadyResidual()`, `distanceSSLogN()`, `distanceMaxRelRDI()`, `getStability()`

`reconcileSpeciesParams` *Reconcile the species parameters with the given species parameters*

Description

[Experimental] Records among the given species parameters every value in `species_params(params)` that mizer would otherwise change when it recalculates the species parameters, so that the model's species parameters become a fixed point: no recalculation, however often repeated, moves them again. Called automatically by `readParams()`.

Usage

```
reconcileSpeciesParams(params, info_level = default_info_level())
```

Arguments

`params`	A MizerParams object.
`info_level`	Controls the amount of information messages and warnings that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.

Details

Mizer distinguishes between the species parameters that were given explicitly and the ones it calculated itself, see `species_params()`. Only the given ones are protected: whenever the species parameters are recalculated – which every use of `species_params<-()` triggers – the calculated ones are derived afresh from the given ones.

A value that was written straight into the `species_params` slot, with for example `params@species_params$h[1] <- 20`, is therefore not protected and the next parameter change undoes it without saying so. Models saved before mizer kept track of the given species parameters, and models built by code that changes the slot directly without also calling `record_given_species_params()`, can hold many such values.

This function repairs such a model. It works out what the species parameters would look like if they were recalculated from the given species parameters now, compares that against the species parameters the model actually holds, and records the entries that differ among the given species parameters. It then repeats that with the enlarged record, and keeps going until a recalculation reproduces the species parameters exactly.

The repetition is what makes the result a fixed point. Recording one value generally changes what a recalculation gives for the parameters mizer derives from it, so a single pass is not enough. If you had set h by hand, for instance, the model's gamma was derived from the old h; the first pass records h, and only the second notices that gamma would now be derived afresh from your new h and records it too. Once the loop finishes, nothing in species_params() moves again, no matter how many times the species parameters are recalculated.

The comparison is made entry by entry, so a parameter is recorded only for the species whose value differs, and only where the model actually holds a value: an NA in species_params() is not a value the user put there and is never recorded. A value that a recalculation already reproduces is left calculated and goes on responding to changes in the parameters it is derived from.

The model is not changed by this function: no species parameter value, and no rate array, is touched. Only the record of where the values came from is.

Value

The MizerParams object with the additional given species parameters recorded.

The price of the fixed point

Freezing the model as it stands means recording values that mizer calculated rather than values you supplied – the gamma of the example is mizer's own, derived from an h that is no longer in the model. That is deliberate: it is the gamma the model's rate arrays were built from, and the alternative is to let a load or an unrelated parameter change silently alter the model.

The cost is that such a parameter no longer responds to the parameters it was derived from. To hand one back to mizer's calculation, clear its entry to NA in given_species_params(params), as for any other given species parameter.

See Also

species_params(), given_species_params(), record_given_species_params()

Examples

```
params <- NS_params
# Write a value straight into the species parameter slot, bypassing the
# record of the values the user has supplied.
params@species_params$w_mat25[1] <- species_params(params)$w_mat25[1] / 2
# Mizer does not know that this value was given, so a recalculation would
# undo it.
is.null(given_species_params(params)$w_mat25)

params <- reconcileSpeciesParams(params)
# Now it is recorded, for the one species whose value differs.
given_species_params(params)$w_mat25
```

record_given_species_params

Record the species parameters that have changed

Description

[Experimental] Compares the new species parameters in `value` against the old ones in `old_sp` and records the entries that have changed in the given species parameter data frame `given`. This is the change detection used by `species_params<-()`, exported so that code which updates the species parameters by other means can record its changes the same way.

Usage

```
record_given_species_params(given, value, old_sp)
```

Arguments

`given`	The given species parameter data frame to record into, usually `given_species_params(params)`.
`value`	A data frame holding the new species parameters.
`old_sp`	A data frame holding the species parameters as they were before the change. Must have one row per species, in the same order as `value` and `given`.

Details

Mizer distinguishes between the species parameters that were given explicitly and those that it calculated itself, see `species_params()`. Only the given ones are protected: whenever the species parameters are recalculated – which every use of `species_params<-()` triggers – the calculated ones are derived afresh from the given ones. So code that computes a species parameter and writes it into the `species_params` slot directly has its work silently undone by the next parameter change, unless the value is also recorded among the given species parameters.

The usual way to record a parameter is to set it with `species_params<-()`, which also rebuilds the species parameters and recalculates all the rates that depend on them. This function is the recording step on its own, for the case where the caller has already updated the affected rates itself, for example an optimiser that fits a species parameter and the rate array it determines together. Rebuilding and recalculating would then be wasted work, and can even undo the caller's own adjustment.

Only the values that have actually changed are recorded. This matters: recording an unchanged value would turn a calculated species parameter into a given one and thereby stop it from responding to changes in the parameters it is derived from. The comparison is made entry by entry, so a parameter is protected only for the species whose value changed. `NA` is compared as a value rather than as an unknown, so `NA` staying `NA` does not count as a change. A column that is not present in `old_sp` at all is taken to be new and is recorded in full.

Value

The updated `given` data frame.

See Also

species_params(), given_species_params()

Examples

```
params <- NS_params
sp_before <- species_params(params)
given_before <- given_species_params(params)

# Set a species parameter and the rate it determines, without going through
# `species_params<-()` and its recalculation of every other rate.
params@species_params$ks[1] <- species_params(params)$ks[1] * 2
params@metab[1, ] <- params@metab[1, ] * 2

# Record the change so that it is not recalculated away later
params@given_species_params <-
    record_given_species_params(given_species_params(params),
                                species_params(params), sp_before)

# Only the entry that changed has been recorded
given_species_params(params)$ks == given_before$ks
```

---

recordExtension *Record an extension and its version stamp on a mizer object*

Description

Writes an entry for name into the object's extension metadata, converting it to the versioned list form. Existing entries (and their version stamps) are preserved, keeping their position in the chain. A genuinely new entry is prepended to the front of the list.

Usage

```
recordExtension(params, name, version = NULL, requirement = NULL)
```

Arguments

params	A MizerParams object.
name	The extension identifier (package/class name).
version	Optional version string to stamp. If NULL (default) the existing stamp is preserved.
requirement	Optional requirement string (e.g. "sizespectrum/mizerMR" or "1.0.0").

Details

This is infrastructure for extension package authors. An extension constructor normally calls recordExtension() and then coerceToExtensionClass(). Ordinary model users do not need either call.

Value

The `params` object with updated extension metadata.

See Also

"Creating a mizer extension package": Creating a mizer extension package

Other extension tools: `NOther()`, `coerceToExtensionClass()`, `initialNOther<-()`, `other_mort()`, `setComponent()`, `setRateFunction()`

---

removeBackgroundSpecies

Remove all background species

Description

Removes all species that have been marked as background species with `markBackground()`.

Usage

```
removeBackgroundSpecies(params)
```

Arguments

`params`	A MizerParams object

Details

This is just a shorthand for `removeSpecies(params, species_params(params)$is_background)`

Value

A MizerParams object with background species removed

See Also

`markBackground()`

Examples

```
params <- markBackground(NS_params,
                         species = c("Sprat", "Sandeel", "N.pout"))
params <- removeBackgroundSpecies(params)
species_params(params)$species
```

removeSpecies *Remove species*

Description

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.
...	Currently unused.

Details

If a gear was targeting only the removed species, then this function will NOT remove that gear. If you want to also remove that gear then you can do that by calling `setFishing()`.

Value

An object of type MizerParams

See Also

`addSpecies()`, `renameSpecies()`

Examples

```
params <- NS_params
species_params(params)$species
params <- removeSpecies(params, c("Cod", "Haddock"))
species_params(params)$species
```

renameGear — *Rename gears*

Description

Changes the names of gears in a MizerParams object. This involves for example changing the gear dimension names of selectivity and catchability arrays appropriately.

Usage

```
renameGear(params, replace, ...)
```

Arguments

params	A mizer params object
replace	A named character vector, with new names as values, and old names as names.
...	Currently unused.

Value

An object of type MizerParams

See Also

renameSpecies()

Examples

```
replace <- c(Industrial = "Trawl", Otter = "Beam_Trawl")
params <- renameGear(NS_params, replace)
gear_params(params)$gear
```

renameSpecies — *Rename species*

Description

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.
...	Currently unused.

Value

An object of type MizerParams

See Also

renameGear()

Examples

```
replace <- c(Cod = "Kabeljau", Haddock = "Schellfisch")
params <- renameSpecies(NS_params, replace)
species_params(params)$species
```

---

resource_constant *Keep resource abundance constant*

Description

If you set your resource dynamics to use this function then the resource abundances are kept 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

Details

To set your model to keep the resource constant over time you do

```
resource_dynamics(params) <- "resource_constant"
```

where you should replace `params` with the name of the variable holding your MizerParams object.

Value

Vector containing the resource number density in each size class at the next timestep

See Also

setResource()

Other resource dynamics functions: resource_logistic(), resource_semichemostat()

Examples

```
params <- NS_params
resource_dynamics(params) <- "resource_constant"
```

---

resource_logistic *Project resource using logistic model*

Description

If you set your resource dynamics to use this function then the time evolution of the resource spectrum is described by a logistic equation

$$\frac{\partial N_R(w,t)}{\partial t} = r_R(w)N_R(w)\Big[1 - \frac{N_R(w,t)}{c_R(w)}\Big] - \mu_R(w,t)N_R(w,t)$$

Usage

```
resource_logistic(
  params,
  n,
  n_pp,
  n_other,
  rates,
  t,
  dt,
  resource_rate,
  resource_capacity,
  ...
)

balance_resource_logistic(params, 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

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 to calculate the resource abundance at time t + dt from all abundances and rates at time t, keeping the mortality fixed during the timestep.

To set your model to use logistic dynamics for the resource you do

```
params <- setResource(params,
                      resource_dynamics = "resource_logistic",
                      resource_level = 0.5)
```

where you should replace params with the name of the variable holding your MizerParams object. You can of course choose any value between 0 and 1 for the resource level.

The balance_resource_logistic() function is called by setResource() to determine the values of the resource parameters that are needed to make the replenishment rate at each size equal the consumption rate at that size, as calculated by getResourceMort(). It should be called with exactly one of resource_rate or resource_capacity and returns a named list with values for both. If resource_rate is supplied it must be at least as large as the current mortality at each size. If resource_capacity is supplied it must be not be less than the current resource abundance. Where it equals the current resource abundance and there is positive consumption, it is nudged upwards slightly to avoid division by zero.

Value

Vector containing the resource number density in each size class at the next timestep

See Also

setResource()

Other resource dynamics functions: resource_constant(), resource_semichemostat()

resource_params *Resource parameters*

Description

The recommended way to change the resource dynamics parameters is to use `setResource()`. The `resource_params` list contains values that are helpful in setting up the actual size-dependent parameters with `setResource()`. If you have specified a custom 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_params` list will at least contain the slots `kappa`, `lambda`, `w_pp_cutoff` and `n`.

The resource parameter `n` is the exponent for the power-law form for the replenishment rate $r_R(w)$:

$$r_R(w) = r_R\, w^{n-1}.$$

The resource parameter `lambda` (λ) is the exponent for the power-law form for the carrying capacity $c_R(w)$ and `w_pp_cutoff` is its cutoff value:

$$c_R(w) = c_R w^{-\lambda}$$

for all w less than `w_pp_cutoff` and zero for larger sizes.

The resource parameter `kappa` (κ) is the coefficient c_R of the carrying capacity in the power law above, so

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

for all w less than `w_pp_cutoff` and zero for larger sizes. Changing `kappa` therefore rescales the carrying capacity. It has a second role in that the same expression also set the initial resource abundance when the model was created:

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

Unlike the carrying capacity, however, the initial resource abundance is **not** updated when you subsequently change `kappa` (or call `setResource()`).

The resource parameters `a` and `b` give the allometric weight-length relationship $w = al^b$ of the resource, with w in grams and l in centimetres. They feed none of the rates; they exist so that the

resource can be shown on the length-based plots (`size_axis = "l"`) alongside the species. They default to the equivalent spherical diameter of an organism with the density of water, $a = \pi/6$ and $b = 3$, which is the convention plankton ecology uses for a composite of many taxa. This is a different convention from the one the species use, so the resource and the species each sit on the length axis at their own; see resource_length_defaults.

Assigning to `resource_params` only rebuilds the size-dependent resource rate and capacity arrays from these scalars (leaving any arrays you have set manually untouched). Changing `lambda` also recalculates any `q` and `gamma` species parameters that mizer calculated, and changing `kappa` recalculates any calculated `gamma`; values you supplied explicitly are preserved. It does **not** balance the resource, i.e. it does not adjust one of the rate or capacity to keep the resource at the steady state where it replenishes at the rate at which it is consumed. This mirrors the way the species parameters feed the species rates. If you want to preserve the steady state after changing a resource scalar, call `setResource()` with the appropriate argument (which balances by default).

Value

A named list of resource parameters.

See Also

`setResource()`

`resource_semichemostat`

Project resource using semichemostat model

Description

If you set your resource dynamics to use this function then the time evolution of the resource spectrum is described by a semi-chemostat equation

$$\frac{\partial N_R(w,t)}{\partial t} = r_R(w)\Big[c_R(w) - N_R(w,t)\Big] - \mu_R(w,t)N_R(w,t)$$

Usage

```
resource_semichemostat(
  params,
  n,
  n_pp,
  n_other,
  rates,
  t,
  dt,
  resource_rate,
  resource_capacity,
  ...
```

```
)

balance_resource_semichemostat(params, 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

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 to calculate the resource abundance at time t + dt from all abundances and rates at time t, keeping the mortality fixed during the timestep.

To set your model to use semichemostat dynamics for the resource you do

```
params <- setResource(params,
                      resource_dynamics = "resource_semichemostat",
                      resource_level = 0.5)
```

where you should replace params with the name of the variable holding your MizerParams object. You can of course choose any value between 0 and 1 for the resource level.

The balance_resource_semichemostat() function is called by setResource() to determine the values of the resource parameters that are needed to make the replenishment rate at each size equal the consumption rate at that size, as calculated by getResourceMort(). It should be called with only one of resource_rate or resource_capacity and returns a named list with values for both. If resource_rate is supplied it must be positive wherever the current resource mortality is positive. If resource_capacity is supplied it must not be less than the current resource abundance. Where it equals the current resource abundance and there is positive consumption, it is nudged upwards slightly to avoid division by zero.

Value

Vector containing the resource number density in each size class at the next timestep

See Also

setResource()

Other resource dynamics functions: resource_constant(), resource_logistic()

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 and restore mizer objects*

Description

saveParams() saves a MizerParams object to a file. This can then be restored with readParams(). saveSim() and readSim() provide the same lifecycle for MizerSim objects.

Usage

```
saveParams(params, file)

readParams(file, install_extensions = FALSE)

saveSim(sim, file)

readSim(file, install_extensions = FALSE)
```

Arguments

params	A MizerParams object
file	The name of the file or a connection where the object is saved to or read from.
install_extensions	Logical. Should readParams() or readSim() attempt to install missing extension packages before loading them?
sim	A MizerSim object

Details

While these functions ultimately use saveRDS() and readRDS(), they do extra work to make the saved file more robust and more portable, so you should always prefer them over calling saveRDS()/readRDS() directly on a mizer object.

The complete S3 class vector is stored with the object, including any extension classes.

Value

saveParams() and saveSim() return NULL invisibly. readParams() returns a MizerParams object. readSim() returns a MizerSim object.

What saveParams() and saveSim() do beyond saveRDS()

- They **validate** the object before writing it, so a corrupted or inconsistent object is caught at save time rather than when you next try to use it.
- They **check that the required extension packages are installed** and stop with an informative error if they are not, so you do not save a file that you would be unable to read back.

- They **warn if the model relies on custom functions** (custom rate, dynamics, selectivity or predation-kernel functions that are not provided by mizer or a registered extension package). Such functions are not stored in the file, so to share the model you also need to share an R script or R Markdown file defining them.

Before saving a model you may want to set its metadata with `setMetadata()`.

What `readParams()` and `readSim()` do beyond `readRDS()`

- They **upgrade** an object saved by an older version of mizer to the current structure (see `upgradeParams()`), so that models saved years ago still load correctly.
- They **load the extension packages** that the model needs and, optionally, install any that are missing (see `install_extensions`), before revalidating the object.
- `readParams()` **reconciles the species parameters**, see `reconcileSpeciesParams()`. A model may hold species parameter values that were written straight into the `species_params` slot and that mizer would therefore undo at the next recalculation. Those values are recorded as given species parameters instead, so that they survive.

See Also

The guide to using mizer extension packages

Examples

```
# Save params to a temporary file and read them back
tmp <- tempfile(fileext = ".rds")
saveParams(NS_params, file = tmp)
params <- readParams(tmp)
identical(params, NS_params)

# Save and read back a simulation
tmp2 <- tempfile(fileext = ".rds")
saveSim(NS_sim, file = tmp2)
sim <- readSim(tmp2)
identical(sim, NS_sim)
```

`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 kilometre 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
...	Additional arguments passed to the method.

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 observed numbers you can use `calibrateNumber()`.

Value

The rescaled MizerParams object

---

scaleRates *Rescale all rates in a mizer model*

Description

[Experimental] Multiplies all rates in the model by a given factor. Rescaling all rates by a factor f is equivalent to rescaling time by f: it speeds up (or slows down) all dynamics without affecting the steady state of each species, provided the resource spectrum is held at its steady-state value.

Usage

```
scaleRates(params, factor, ...)
```

Arguments

params	A MizerParams object
factor	The positive factor by which all rates are multiplied.
...	Currently unused.

Details

The following rates and their associated species parameters are rescaled:

- Search volume (search_vol slot and gamma species parameter)
- Maximum intake rate (intake_max slot and h species parameter)
- Metabolic rate (metab slot and ks, k species parameters)
- External mortality (mu_b slot and z0, z_ext, z0pre species parameters)
- External encounter rate (ext_encounter slot and E_ext species parameter)
- External diffusion (ext_diffusion slot and D_ext species parameter)
- Catchability (catchability slot and catchability column in gear_params)
- Maximum reproduction rate (R_max species parameter)
- Resource growth rate (rr_pp slot)

Both the rate arrays stored in the MizerParams slots and the associated species parameters in species_params and given_species_params are rescaled, so that the parameters remain consistent with the rate arrays.

Value

The MizerParams object with all rates rescaled by factor.

See Also

scaleModel()

---

scanEffort *Setters for scanning a model*

Description

[Experimental] These functions build the set_func that scanModel() uses to apply each scan value to the model. Each returns a function of (params, value) that returns a modified MizerParams object, carrying attributes that let scanModel() label the axis and mark reference lines without being told.

Usage

```
scanEffort(gear = NULL)

scanFishingMortality(species, gear = NULL)

scanSpeciesParam(species, parameter)
```

Arguments

gear	For scanEffort(), the name of the gear whose effort is scanned, or NULL (default) to scan the effort of every gear together. For scanFishingMortality(), the name of the gear whose fishing mortality on the target species is scanned. Only needed when several gears catch the species; if NULL, the fishing mortality from all of them is replaced.
species	The name of the target species.
parameter	The name of the species parameter to scan.

Details

You are not restricted to these. Any function of (params, value) returning a MizerParams will do, as long as it is **idempotent**: with continuation = TRUE it is applied to the object it returned at the previous scan value, so applying it twice must give the same thing as applying it once. Setting a value is idempotent; appending something is not, which is why scanFishingMortality() checks whether its gear is already there.

scanEffort() Scans the fishing effort. With gear = NULL the same effort is applied to every gear, which is what a bifurcation diagram over fishing effort needs.

scanFishingMortality() Scans the fishing mortality on one species while leaving the fishing on every other species alone. It does this by adding a temporary gear that catches only the target species with catchability 1, so that its effort *is* the fishing mortality, and switching off the catchability of the gears it replaces. If several gears catch the species you can name the one whose mortality is to be varied, and the others go on fishing unchanged. The added gear is given a name the model is not already using, so a model that happens to have a gear called "scan" is not disturbed.

scanSpeciesParam() Scans any species parameter. It assigns to species_params(), so the value is recorded as a given one and the change propagates through to the rates that depend on it. The parameter has to be one the model already has; add the column first if it is not.

Value

A function of (params, value) returning a MizerParams object.

See Also

scanModel()

Other scan functions: MizerScan(), plot.MizerScan(), plotYieldVsF(), scanModel()

Examples

```
# The fishing mortality on Cod alone, leaving the other species alone
plot(scanModel(NS_params, scan_values = seq(0, 1.2, 0.3),
               set_func = scanFishingMortality("Cod"),
               value_func = getYield, species = "Cod"))
```

---

scanModel *Scan a model over a range of values*

Description

[Experimental] Varies one aspect of a model over a range of values and measures a quantity at each of them. At every value the model is projected until it settles onto an attractor, and the quantity is measured on that attractor rather than at whatever state the projection happened to stop at.

Usage

```
scanModel(
  params,
  scan_values,
  set_func,
  value_func = getBiomass,
  species = NULL,
  scan_name = NULL,
  scan_units = NULL,
  value_name = NULL,
  value_units = NULL,
  reference_lines = NULL,
  current_scan_value = NULL,
  continuation = TRUE,
  distance_func = distanceSSLogN,
  distance_tol = 0.001,
  residual_tol = steady_residual_tol(),
  t_check = 15 * dt,
  t_max = 100,
  dt = 0.1,
  amplitude_tol = 0.01,
  amp_rel_tol = 0.1,
  extinction_threshold = 1e-06,
  method = c("euler", "predictor_corrector", "tr_bdf2"),
  t_sample = 10,
  sample_all = FALSE,
  progress_bar = interactive(),
  info_level = 0,
  ...
)
```

Arguments

- `params` — An object of class `MizerParams`.
- `scan_values` — A numeric vector of values to scan over.
- `set_func` — A function of `(params, value)` returning a modified `MizerParams` object. Several are provided: `scanEffort()`, `scanFishingMortality()` and `scanSpeciesParam()`.
- `value_func` — A function of a `MizerSim` returning the quantity to measure. Defaults to `getBiomass()`.
- `species` — The species to keep in the result. By default all of the series that `value_func` returns.
- `scan_name` — A string naming the quantity that is varied, used for the x-axis label and as the name of the first column of the result. Taken from `set_func` when it supplies one.
- `scan_units` — A string giving the units of that quantity.
- `value_name` — A string naming the quantity that is measured, used for the y-axis label and as the name of the second column of the result. Taken from what `value_func` returns when it supplies one.
- `value_units` — A string giving the units of that quantity.
- `reference_lines` — An optional named numeric vector of positions on the x axis for `plot.MizerScan()` to mark with vertical dashed lines, for example `c(F_MSY = 0.32)`. Taken from `set_func` when it supplies one.
- `current_scan_value` — The value at which the model currently sits. When given, the scan works outwards from it in both directions so that every projection starts from a neighbouring attractor rather than from a distant state, and each of the two directions begins again at the model as it was given. Pass `"auto"` to ask `set_func` for it. By default the values are scanned in the order given, which is also how you trace a hysteresis branch deliberately: pass a decreasing `scan_values`.
- `continuation` — Whether each scan value should start from the attractor reached at the previous one. Default TRUE.
- `distance_func` — A function that will be called at every convergence check with both the previous and the new state and that should return a number measuring the distance between them. See `distanceSSLogN()`.
- `distance_tol` — The projection at each scan value stops once the number returned by `distance_func` for two states `t_check` years apart drops below `distance_tol`. The default is tighter than the one `projectUntilSettled()` uses on its own, because a scan produces a curve, and a loosely converged point does not average away: it shows up as a kink in the curve and as spurious width in the band. Loosen it to go faster, and use the `residual` column of the result to check whether that cost you anything.
- `residual_tol` — The largest relative rate of biomass change, in 1/year, at which a scan point may still be recorded as a fixed point. See `projectUntilSettled()`. A point that meets `distance_tol` but not this is not sampled as a single value, which would draw it as a band of zero width.

`t_check`	The interval in years at which convergence is checked, see `projectUntilSettled()`. Must be a positive multiple of `dt`; the default `15 * dt` is an odd multiple, which is what lets a period-2 cycle be seen.
`t_max`	The longest time to project at each scan value.
`dt`	The time step to use.
`amplitude_tol`	The minimum relative biomass amplitude for a persistent oscillation to count as a limit cycle rather than a fixed point.
`amp_rel_tol`	Maximum relative change of amplitude between successive periods for a cycle to count as settled.
`extinction_threshold`	A species is treated as going extinct once its reproduction rate falls below this fraction of its value at the start of the projection.
`method`	The numerical method to use, see `project()`.
`t_sample`	The number of years over which to average when the model has settled onto neither a fixed point nor a limit cycle.
`sample_all`	Whether to run the sampling projection even at a fixed point, where it is not otherwise needed. Set this if `value_func` needs more than one time step.
`progress_bar`	Whether to show a text progress bar over the scan values.
`info_level`	Controls how much the projections say for themselves. Defaults to 0, because a scan makes one projection per scan value and summarises them itself; raise it when investigating why one of them behaved oddly.
`...`	Further arguments are passed on to `distance_func`.

Details

You say what to vary by giving a function that changes the model, and what to measure by giving a function that computes a quantity from a simulation. So a yield-versus-fishing-mortality curve, a bifurcation diagram over fishing effort and a scan over the resource carrying capacity are all the same function call with different arguments.

This is a generic function with a method for objects of class MizerParams.

Value

An object of class MizerScan, which is a data frame with one row per scan value and series, carrying the metadata that `plot()` needs.

What is measured, and where

At each scan value the model is projected with `projectUntilSettled()`, which stops as soon as it recognises that the model has settled onto a fixed point or onto a limit cycle, and reports which of the two happened. What happens next depends on that answer:

A fixed point The state does not change, so there is nothing to average. The quantity is read off the settled state with no further projection at all, and the reported minimum and maximum are equal to it.

A limit cycle The model is projected for **exactly one period** of the detected cycle and the quantity is averaged over it, which is its long-term average. The minimum and maximum over the cycle are reported too.

Neither The model did not settle within `t_max` years, or a species went extinct. The quantity is averaged over the last `t_sample` years and the scan values concerned are named in a message, because those points should not be relied on.

Averaging over exactly one period is both faster and more accurate than averaging over a fixed number of years. A window that is not a whole number of periods leaves a residue of the oscillation in the average, which shows up as a jagged curve. The window is rounded to a whole number of time steps, so it can differ from the true period by up to `dt/2`; if you need the average more accurately, reduce `dt` rather than lengthening the window, because a longer window that is not a whole number of periods is worse, not better.

Writing the two functions

`set_func(params, value)` takes a `MizerParams` object and one entry of `scan_values` and returns a modified `MizerParams`. It must be **idempotent** — `set_func(set_func(p, v), v)` must give the same thing as `set_func(p, v)` — because with `continuation = TRUE` it is applied to the object it returned at the previous scan value. Setting something is idempotent; appending something is not, so a function that adds a gear must check whether the gear is already there. See `scanFishingMortality()` for a worked example.

There is no `effort` argument, because there does not need to be one: `project()` and `projectUntilSettled()` both take the fishing effort from `params@initial_effort`, so a `set_func()` that changes the effort is all it takes to scan over effort, and a scan over something else never has to mention fishing at all.

`value_func(sim)` takes a `MizerSim` and returns either a time by series matrix, as `getBiomass()`, `getYield()`, `getSSB()`, `getN()` and `sizeIntegral()` all do, or a plain numeric vector over time, as `getMeanWeight()` does. When it returns a matrix carrying `value_name` and `units` attributes — which all of mizer's `MizerSim` methods do — those are used for the y-axis label unless you override them.

Note that at a fixed point `value_func()` is handed a simulation with a single time step, so a function that needs more than one time step will not work there. Set `sample_all = TRUE` to force the sampling projection at every scan value.

Neither function can be given extra arguments through `...`, which is reserved for `distance_func`. Use a closure instead, for example `value_func = function(sim) getBiomass(sim, min_w = 10)`.

See Also

`MizerScan()`, `plot.MizerScan()`, `scanEffort()`, `scanFishingMortality()`, `scanSpeciesParam()`, `plotYieldVsF()`

Other scan functions: `MizerScan()`, `plot.MizerScan()`, `plotYieldVsF()`, `scanEffort()`

Examples

```
# A bifurcation diagram over fishing effort
scan <- scanModel(NS_params, scan_values = seq(0, 2, 0.25),
                  set_func = scanEffort(), value_func = getYield)
plot(scan, style = "envelope")
```

```
# A yield curve for a single species, and the F at which it is largest
cod <- scanModel(NS_params, scan_values = seq(0, 1.2, 0.2),
                 set_func = scanFishingMortality("Cod"),
                 value_func = getYield, species = "Cod")
plot(cod, mark_max = TRUE, log_y = FALSE)
attr(cod, "at_max")

# Scanning something that has nothing to do with fishing
kappa <- resource_params(NS_params)$kappa
plot(scanModel(NS_params, scan_values = kappa * c(0.5, 1, 2),
               set_func = function(params, value) {
                   resource_params(params)$kappa <- value
                   params
               },
               scan_name = "Resource capacity", scan_units = "g"),
     log_x = TRUE)
```

`second_order_w` *Get or set the second_order_w flags*

Description

[Experimental] Controls whether mizer uses numerical methods that are precise to second order in Δw.

Usage

```
second_order_w(params)

second_order_w(params) <- value
```

Arguments

`params`	A MizerParams object.
`value`	A single logical value (`TRUE` or `FALSE`) which sets both entries, a single flux scheme name (`"upwind"`, `"van_leer"` or `"centred"`) which sets only `flux`, or a named vector with entries `flux` (logical or scheme name) and/or `bin_average` (logical).

Details

The slot is a named list with entries:

`flux` The advective-flux reconstruction scheme used in the numerical solver. `"upwind"` is the first-order upwind scheme. `"van_leer"` is the second-order scheme with the total-variation- diminishing van Leer limiter, which keeps abundances non-negative. `"centred"` is the second-order scheme with the unlimited centred flux, which is genuinely second order even at extrema but

is not monotonicity-preserving (it can produce small over/undershoots and is best used with some physical diffusion).

`bin_average` Logical. Controls whether bin-averaging is used for quantities that need it in order to be second-order precise in bin size. When `FALSE`, point-sampling at the left bin edge is used.

When `flux` is `"upwind"` and `bin_average` is `FALSE` (the defaults), mizer preserves the behaviour of previous mizer versions. Setting both to their second-order values gives a consistently second-order model.

The setter accepts a single logical value (which sets both entries), a single scheme name (which sets only `flux`), or a named vector to set individual entries. The setter re-runs `setParams()` to rebuild precomputed arrays when `bin_average` is changed.

Value

`second_order_w()`: A named list with entries `flux` (character) and `bin_average` (logical).
`second_order_w<-`: A MizerParams object with the `second_order_w` flags updated and, when `bin_average` is changed, all model parameters recalculated via `setParams()`.

`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

```
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)
```

---

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.

This wrapper keeps the legacy defaults and also fills in several columns in species_params if they are missing, using the same rules as older mizer versions.

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 = NULL,
  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). 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_max 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, but must still be finite and in the interval (0, 1).
kappa	The coefficient κ of the resource carrying capacity power law $c_R(w) = \kappa\, w^{-\lambda}$, which also sets the initial resource abundance. See resource_params().
lambda	Used to set power-law exponent for resource capacity if the resource_capacity argument is given as a single number.
r_pp	**[Deprecated]**. Use resource_rate argument instead.
...	Further arguments passed to newMultispeciesParams().

Details

If species_params contains a w_inf column then it is copied to w_max. If max_w is not supplied then it is set to 1.1 * max(species_params$w_max). The supplied min_w_pp is shifted up by one grid step before being passed to newMultispeciesParams() to compensate for the fact that newer mizer versions extend the full size grid below min_w_pp.

Missing legacy columns in species_params are filled as follows: gear = species, k = 0, alpha = 0.6, erepro = 1, sel_func = "knife_edge", knife_edge_size = w_mat if needed, catchability = 1, ks = h * 0.2, and m = 1. If h is missing it is calculated from k_vb, alpha, f0 and w_max. If gamma is missing it is calculated from f0, h, beta, sigma, lambda and kappa.

Value

A MizerParams object

---

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. The signal has class info_about_default.

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	Maximum size of the consumer size grid passed to MizerParams(). Default value is max_w_inf * 1.1.
min_w_pp	Smallest size on the resource size grid passed to MizerParams(). Default value is 1e-10.
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_max * 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.

`setBevertonHolt` *Set Beverton-Holt reproduction without changing the steady state*

Description

Takes a MizerParams object `params` with arbitrary density dependence in reproduction 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,
  erepro,
  R_max,
  reproduction_level,
  info_level = default_info_level(),
  ...
)

reproduction_level(params)

reproduction_level(params) <- value
```

Arguments

params	A MizerParams object
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.
info_level	Controls the amount of information messages and warnings that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().
...	Unused • R_factor: Legacy alternative for specifying reproduction_level = 1 / R_factor.
value	A number between 0 and 1, or a vector of numbers, giving the reproduction level for each species.

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,

$$R_{di} = \frac{\text{erepro}}{2w_{min}} E_R,$$

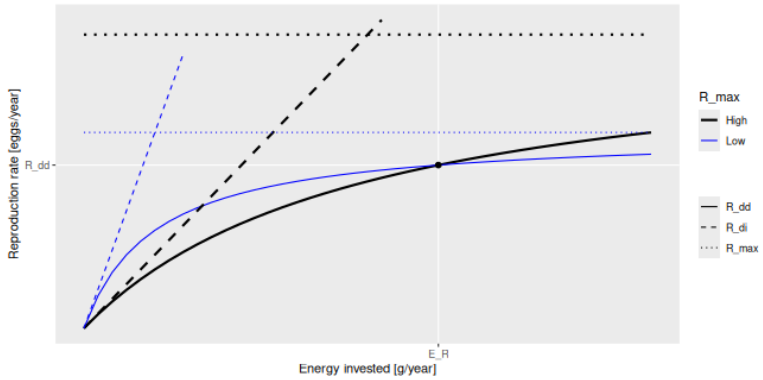
where the proportionality factor is given by the reproductive efficiency erepro divided by the egg size w_min to convert energy to egg number and divided by 2 to account for the two sexes.

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 non-negative 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.

A species that is absent from the initial state, with zero abundance at all sizes, has no reproduction whatever its parameters, so every Beverton-Holt curve keeps it at its steady state. For such a species a given `erepro` or `R_max` is used as it is and the other parameter is left unchanged. Its reproduction level is zero whatever its `R_max`, so a non-zero `reproduction_level` cannot be set for it: its parameters are then left unchanged and a warning is issued.

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

`reproduction_level()`: A named vector with the reproduction level for each species.

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_max^-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")])

# Inspecting reproduction level
reproduction_level(NS_params)

# The reproduction level can be changed without changing the steady state:
reproduction_level(params) <- 0.9
reproduction_level(params)
```

`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", "External" 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.

If a name coincides with the name of a species, the `linecolour` (for `setColours()`) or `linetype` (for `setLinetypes()`) entry for that species in `species_params` and `given_species_params` is updated as well, so that the choice persists with the species. Alternatively you can set the `linecolour` and `linetype` variables in the species parameter data frame directly, see the example below.

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, either via setColours()/
# setLinetypes() or directly via the species parameter data frame
params <- setColours(params, list("Cod" = "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,
  colour = "grey",
  linetype = "solid"
)

removeComponent(params, component)

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.
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.
colour	Line colour to use for the component in plots. Defaults to "grey".
linetype	Line type to use for the component in plots. Defaults to "solid".

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, the initial_value and dynamics_fun are overwritten, while the optional encounter_fun, mort_fun and component_params are only changed if the corresponding arguments are supplied. You can remove a component with removeComponent().

Value

The updated MizerParams object

For getComponent: 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.

See Also

"Extending mizer": guide to extending mizer

Other extension tools: `NOther()`, `coerceToExtensionClass()`, `initialNOther<-()`, `other_mort()`, `recordExtension()`, `setRateFunction()`

`setExtDiffusion` *Set external diffusion rate*

Description

You will usually not need to call this function directly. Instead change the `D_ext` and `n` species parameters with `given_species_params(params) <-` and let mizer recalculate the external diffusion rate for you. Call `setExtDiffusion()` directly only if you want to impose a different functional form for the size dependence of the external diffusion rate. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setExtDiffusion(params, ext_diffusion = NULL, reset = FALSE, ...)

ext_diffusion(params)

ext_diffusion(params) <- value
```

Arguments

`params`	MizerParams
`ext_diffusion`	Optional. An array (species x size) holding the external diffusion rate. If not supplied, a default is calculated from the `D_ext` and `n` species parameters as described in the section "Setting external diffusion rate".
`reset`	If set to TRUE, then the external diffusion 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`	ext_diffusion

Value

`setExtDiffusion()`: A MizerParams object with updated external diffusion rate.

`ext_diffusion()`: An `ArraySpeciesBySize` object (species x size) with the external diffusion rate.

Setting external diffusion rate

The external diffusion rate allows you to impose additional diffusion beyond the predation-driven diffusion that can be internally modelled by mizer.

The `ext_diffusion` argument allows you to specify a diffusion rate that depends on species and body size.

If the `ext_diffusion` argument is not supplied, then the external diffusion rate is calculated as a power law:

$$D_{ext.i}(w) = D_{ext.i}\, w^{n_i+1}.$$

The coefficient $D_{ext.i}$ is taken from the `D_ext` column of the species parameter data frame, which defaults to 0. The exponent $n_i + 1$ uses the `n` column of the species parameter data frame.

If the `ext_diffusion` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

See Also

Other functions for setting parameters: `gear_params()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

---

setExtEncounter *Set external encounter rate*

Description

You will usually not need to call this function directly. Instead change the `E_ext` and `n` species parameters with `given_species_params(params) <-` and let mizer recalculate the external encounter rate for you. Call `setExtEncounter()` directly only if you want to impose a different functional form for the size dependence of the external encounter rate. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setExtEncounter(params, ext_encounter = NULL, reset = FALSE, ...)

ext_encounter(params)

ext_encounter(params) <- value
```

Arguments

`params`	MizerParams
`ext_encounter`	Optional. An array (species x size) holding the external encounter rate. If not supplied, a default is calculated from the `E_ext` and `n` species parameters as described in the section "Setting external encounter rate".

reset	If set to TRUE, then the external encounter 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	ext_encounter

Value

`setExtEncounter()`: A MizerParams object with updated external encounter rate.

`ext_encounter()`: An `ArraySpeciesBySize` object (species x size) with the external encounter rate.

Setting external encounter rate

The external encounter rate is the rate at which a predator encounters food that is not explicitly modelled. It is a rate with units mass/year.

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

If the `ext_encounter` argument is not supplied, then the external encounter rate is calculated as a power law:

$$E_{ext.i}(w) = E_{ext.i}\, w^{n_i}.$$

The coefficient $E_{ext.i}$ is taken from the `E_ext` column of the species parameter data frame, which defaults to 0. The exponent n_i is taken from the `n` column of the species parameter data frame.

If the `ext_encounter` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

Examples

```
params <- newMultispeciesParams(NS_species_params)

#### Setting allometric encounter rate #######################

# Set coefficient for each species. Here we choose 0.1 for each species
encounter_pre <- rep(0.1, nrow(species_params(params)))

# Multiply by power of size with exponent, here chosen to be 3/4
# The outer() function makes it an array species x size
allo_encounter <- outer(encounter_pre, w(params)^(3/4))
```

```
# Change the external encounter rate in the params object
ext_encounter(params) <- allo_encounter
```

---

setExtMort *Set external mortality rate*

Description

You will usually not need to call this function directly. Instead change the z0, z_ext and d species parameters with given_species_params(params) <- and let mizer recalculate the external mortality rate for you. Call setExtMort() directly only if you want to impose a different functional form for the size dependence of the external mortality. See vignette("guide-change-parameters") for a full explanation of when to reach for which level of the model.

Usage

```
setExtMort(
  params,
  ext_mort = NULL,
  z0pre = 0.6,
  z0exp = params@resource_params$n - 1,
  reset = FALSE,
  z0 = deprecated(),
  ...
)

ext_mort(params)

ext_mort(params) <- value
```

Arguments

params	MizerParams
ext_mort	Optional. An array (species x size) holding the external mortality rate. If not supplied, a default is set as described in the section "Setting external mortality rate".
z0pre	If z0, the mortality from other sources, is not present in given_species_params(), it is calculated as z0pre * w_inf ^ z0exp. Default value is 0.6.
z0exp	The exponent used with z0pre to calculate non-given z0. Default value is n - 1.
reset	If set to TRUE, then the external mortality 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.
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.

`ext_mort()`: An `ArraySpeciesBySize` object (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 taken from the species parameters as

$$\mu_{ext.i}(w) = z_{0.i} + z_{ext.i} w^{d_i}.$$

The value of the constant z_0 for each species is taken from the `z0` column of `given_species_params()` if it is present there. Otherwise it is recalculated, even if a value from an earlier calculation is still present in `species_params`, as

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

When `z0pre` or `z0exp` is supplied explicitly and used to calculate non-given `z0`, the resulting values are recorded in `given_species_params()`. Values calculated from the defaults `z0pre = 0.6` and `z0exp = n - 1` are not recorded there. If either argument is supplied but cannot be used because `z0` is given for every species or because `ext_mort` was supplied, a warning is issued. Missing values of `z_ext` are set to 0 and missing values of `d` are set to `n - 1`.

By default the power law is evaluated at the left bin edges w_j (point sampling). If the `bin_average` entry of the `second_order_w` slot is `TRUE` (see `second_order_w()`), then the $z_{ext} w^d$ term is instead replaced by its exact average over each bin $[w_j, w_{j+1}]$,

$$\frac{z_{ext}}{\Delta w_j} \int_{w_j}^{w_{j+1}} w^d \, dw = z_{ext} \, \frac{w_{j+1}^{d+1} - w_j^{d+1}}{(d+1)\,\Delta w_j},$$

(with the limiting form $z_{ext} \ln(w_{j+1}/w_j)/\Delta w_j$ when $d = -1$). This is the consistent choice in the finite-volume scheme, where the external mortality multiplies the bin-averaged abundance. The bin-averaging is applied only to the auto-calculated power-law default; a user-supplied `ext_mort` array is left untouched.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

Examples

```
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
```

---

setFishing *Set fishing parameters*

Description

Set fishing parameters

Usage

```
setFishing(
  params,
  selectivity = NULL,
  catchability = NULL,
  reset = FALSE,
  initial_effort = NULL,
  ...
)

catchability(params)

catchability(params) <- value

selectivity(params)

selectivity(params) <- value
```

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`	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`	The array to assign

Value

`setFishing()`: A MizerParams object with updated fishing parameters.

`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".

`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".

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.

The most commonly-used selectivity function is sigmoid_length(). It has a smooth transition from 0 to 1 at a certain size. The sigmoid_length() function has the two parameters l50 and l25 that are the lengths in cm at which 50% or 25% of the fish are selected by the gear. If you choose this selectivity function then the l50 and l25 columns must be included in the gear parameters data.frame.

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(), setExtDiffusion(), setExtEncounter(), setExtMort(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setParams(), setPredKernel(), setReproduction(), setSearchVolume(), species_params(), use_predation_diffusion()

Examples

```
# Halve the initial fishing effort for all gears
params <- setFishing(NS_params, initial_effort = 0.5)
initial_effort(params)
str(catchability(NS_params))
str(selectivity(NS_params))
```

`setInitialValues` *Set initial values to values from a simulation*

Description

[Deprecated] This function is deprecated. Use `getParams()`, `initialParams()`, or `finalParams()` instead. These functions return a `MizerParams` object with the ecosystem state extracted from a simulation.

Usage

```
setInitialValues(params, sim, time_range, geometric_mean = FALSE, ...)
```

Arguments

`params`	A `MizerParams` object in which to set the initial values
`sim`	A `MizerSim` object from which to take the values.
`time_range`	The time range to average the abundances over. Can be a vector of values, a vector of min and max time, or a single value. Only the range of times is relevant, i.e., all times between the smallest and largest will be selected. Default is the final time step.
`geometric_mean`	**[Experimental]** If TRUE then the average of the abundances over the time range is a geometric mean instead of the default arithmetic mean. This does not affect the average of the effort or of other components, which is always arithmetic.
`...`	Additional arguments passed to the method.

Details

[Deprecated]

Value

The `params` object with updated initial values and initial effort.

Examples

```
params <- NS_params
sim <- project(params, t_max = 20, effort = 0.5)
params <- setInitialValues(params, sim)
```

`setInteraction` *Set species interaction matrix*

Description

Set species interaction matrix

Usage

```
setInteraction(params, interaction = NULL, ...)

interaction_matrix(params)

interaction_matrix(params) <- value
```

Arguments

`params`	MizerParams object
`interaction`	Optional interaction matrix of the species (predator species x prey species). By default all entries are 1. See "Setting interaction matrix" section below.
`...`	Unused
`value`	An interaction matrix

Value

`setInteraction`: A MizerParams object with updated interaction matrix

`interaction_matrix()`: 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} modifies the interaction of each pair of species in the model. This can be used for example to allow for different spatial overlap among the species. 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.

The interaction matrix is used when calculating the food encounter rate in `getEncounter()` and the predation mortality rate in `getPredMort()`. Its entries are dimensionless numbers. If all the values in the interaction matrix are equal 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 message if it is different before ignoring the supplied dimnames. If you supply only column names then these are also used as the row names. 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 then 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. By default this column is set to all 1s.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

Examples

```
params <- newTraitParams(no_sp = 3)
inter <- interaction_matrix(params)
inter[1, 2:3] <- 0
params <- setInteraction(params, interaction = inter)
interaction_matrix(params)
```

---

setMaxIntakeRate *Set maximum intake rate*

Description

You will usually not need to call this function directly. Instead change the `h` and `n` species parameters with `given_species_params(params) <-` and let mizer recalculate the maximum intake rate for you. Call `setMaxIntakeRate()` directly only if you want to impose a different functional form for the size dependence of the intake rate. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setMaxIntakeRate(params, intake_max = NULL, reset = FALSE, ...)

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	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

`setMaxIntakeRate()`: A MizerParams object with updated maximum intake rate.

`intake_max()`: An `ArraySpeciesBySize` object (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. If the `n` column is not supplied, a default of $n_i = 3/4$ is used.

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

If the `intake_max` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

Examples

```
# Inspect the current maximum intake rate
intake_max(NS_params)["Cod", 1:5]

# Increase intake rate for Cod by 50%
im <- intake_max(NS_params)
im["Cod", ] <- im["Cod", ] * 1.5
params <- setMaxIntakeRate(NS_params, intake_max = im)
intake_max(params)["Cod", 1:5]
```

setMetabolicRate *Set metabolic rate*

Description

Sets the rate at which energy is used for metabolism and activity. You will usually not need to call this function directly. Instead change the k, ks and p species parameters with `given_species_params(params) <-` and let mizer recalculate the metabolic rate for you. Call `setMetabolicRate()` directly only if you want to impose a different functional form for the size dependence of the metabolic rate. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setMetabolicRate(object, metab = NULL, p = deprecated(), reset = FALSE, ...)

metab(params)

metab(params) <- value
```

Arguments

object	A MizerParams object
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	**[Deprecated]** The allometric metabolic exponent. Set the p column in the species parameters instead, with `species_params(params)$p <- value`. This argument never took effect on a `MizerParams` object because such an object always has a p column already, and the argument was only used to fill in a missing one.
reset	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
params	A MizerParams object
value	metab

Value

`setMetabolicRate()`: A MizerParams object with updated metabolic rate.

`metab()`: An `ArraySpeciesBySize` object (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.

If the `metab` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

Examples

```
# Inspect the current metabolic rate
metab(NS_params)["Cod", 1:5]

# Reset metabolic rate from species parameters
params <- setMetabolicRate(NS_params, reset = TRUE)
metab(params)["Cod", 1:5]
```

---

setMetadata *Set metadata for a model*

Description

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 = NULL,
  description = NULL,
  authors = NULL,
  url = NULL,
  doi = NULL,
  ...
)

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 created or last upgraded. 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 list with one entry for each extension package needed to run the model. Each entry records the installation `requirement` and the package `version` whose object layout is in use. This field is set by extension packages with `recordExtension()` and can be inspected with `getMetadata(params)$extensions`.
- `time_created` A POSIXct date-time object with the creation time.
- `time_modified` A POSIXct date-time object with the last modified time.

Setting the metadata with this function does not count as a modification of the object, so the `time_modified` field will not be updated.

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`.

Examples

```
params <- setMetadata(NS_params,
    title = "North Sea model",
    description = "A multi-species model of the North Sea fish community.",
    authors = list(list(name = "Finlay Scott", email = "finlay@example.com")),
    my_own_filed = "something that doesn't fit elsewhere")
getMetadata(params)$title
getMetadata(params)$authors[[1]]$name
```

---

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()`
- `setExtEncounter()`
- `setExtDiffusion()`
- `setReproduction()`
- `setFishing()`

Note that `setResource()` is **not** among them: the resource rate, capacity and dynamics are not changed by `setParams()` and have to be set with `setResource()`. Passing a resource argument to `setParams()` gives an error rather than being silently ignored. See the Details section below for a discussion of how to use this function.

Usage

```
setParams(
  object,
  interaction = NULL,
  info_level = default_info_level(),
  ...,
  reset = FALSE
)
```

Arguments

`object` A MizerParams object

`interaction` Optional interaction matrix of the species (predator species x prey species). By default all entries are 1. See "Setting interaction matrix" section below.

`info_level` Controls the amount of information messages that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`. Note that the report that a change cannot take effect because the rate array it feeds has been set manually is a warning rather than a message, but it too is silenced by `info_level = 0`.

`...` Arguments passed on to `setPredKernel`, `setSearchVolume`, `setMaxIntakeRate`, `setMetabolicRate`, `setExtMort`, `setExtEncounter`, `setExtDiffusion`, `setReproduction`, `setFishing`

`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".

`value` pred_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".

`ext_mort` Optional. An array (species x size) holding the external mortality rate. If not supplied, a default is set as described in the section "Setting external mortality rate".

`z0pre` If `z0`, the mortality from other sources, is not present in `given_species_params()`, it is calculated as `z0pre * w_inf ^ z0exp`. Default value is 0.6.

`z0exp` The exponent used with `z0pre` to calculate non-given `z0`. Default value is `n - 1`.

`z0` **[Deprecated]** Use `ext_mort` instead. Not to be confused with the species_parameter `z0`.

`ext_encounter` Optional. An array (species x size) holding the external encounter rate. If not supplied, a default is calculated from the `E_ext` and `n` species parameters as described in the section "Setting external encounter rate".

`ext_diffusion` Optional. An array (species x size) holding the external diffusion rate. If not supplied, a default is calculated from the `D_ext` and `n` species parameters as described in the section "Setting external diffusion rate".

`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 the energy available for growth and reproduction 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.

`reset` If set to TRUE then all the rate arrays that `setParams()` sets are recalculated from the species parameters, even if they had previously been overwritten with custom values. The default is FALSE, in which case arrays that have been set manually are left alone. This is passed on to each of the setter functions listed above, so it thaws all of them at once. To thaw only one of them, call that setter with `reset = TRUE` instead.

Details

If you are not happy with the assumptions that mizer makes by default about the size-dependence of parameters, 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 the size-dependent parameters 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 parameter arrays 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} modifies the interaction of each pair of species in the model. This can be used for example to allow for different spatial overlap among the species. 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.

The interaction matrix is used when calculating the food encounter rate in `getEncounter()` and the predation mortality rate in `getPredMort()`. Its entries are dimensionless numbers. If all the values in the interaction matrix are equal 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 message if it is different before ignoring the supplied dimnames. If you supply only column names then these are also used as the row names. 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 then 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. 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. Alternative pred_kernel types are "box", implemented by `box_pred_kernel()`, "power_law", implemented by `power_law_pred_kernel()`, and "gaussian_mixture", implemented by `gaussian_mixture_pred_kernel()`. These functions require certain species parameters in the species_params data frame. For the lognormal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`, and for the Gaussian mixture they are the list-columns `kernel_p`, `kernel_mean`, and `kernel_sd`. 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 `pred_kernel()` 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. If the q column is not supplied, a default of lambda - 2 + n is used. 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 $\gamma_i(w)$.

If the search_vol slot has a comment and reset = FALSE, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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. If the n column is not supplied, a default of $n_i = 3/4$ is used.

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

If the intake_max slot has a comment and reset = FALSE, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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.

If the metab slot has a comment and reset = FALSE, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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 taken from the species parameters as

$$\mu_{ext.i}(w) = z_{0.i} + z_{ext.i} w^{d_i}.$$

The value of the constant z_0 for each species is taken from the `z0` column of `given_species_params()` if it is present there. Otherwise it is recalculated, even if a value from an earlier calculation is still present in `species_params`, as

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

When `z0pre` or `z0exp` is supplied explicitly and used to calculate non-given `z0`, the resulting values are recorded in `given_species_params()`. Values calculated from the defaults `z0pre = 0.6` and `z0exp = n - 1` are not recorded there. If either argument is supplied but cannot be used because `z0` is given for every species or because `ext_mort` was supplied, a warning is issued. Missing values of `z_ext` are set to 0 and missing values of `d` are set to `n - 1`.

By default the power law is evaluated at the left bin edges w_j (point sampling). If the `bin_average` entry of the `second_order_w` slot is `TRUE` (see `second_order_w()`), then the $z_{ext} w^d$ term is instead replaced by its exact average over each bin $[w_j, w_{j+1}]$,

$$\frac{z_{ext}}{\Delta w_j} \int_{w_j}^{w_{j+1}} w^d \, dw = z_{ext} \, \frac{w_{j+1}^{d+1} - w_j^{d+1}}{(d+1)\,\Delta w_j},$$

(with the limiting form $z_{ext} \ln(w_{j+1}/w_j)/\Delta w_j$ when $d = -1$). This is the consistent choice in the finite-volume scheme, where the external mortality multiplies the bin-averaged abundance. The bin-averaging is applied only to the auto-calculated power-law default; a user-supplied `ext_mort` array is left untouched.

Setting external encounter rate

The external encounter rate is the rate at which a predator encounters food that is not explicitly modelled. It is a rate with units mass/year.

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

If the `ext_encounter` argument is not supplied, then the external encounter rate is calculated as a power law:

$$E_{ext.i}(w) = E_{ext.i} \, w^{n_i}.$$

The coefficient $E_{ext.i}$ is taken from the `E_ext` column of the species parameter data frame, which defaults to 0. The exponent n_i is taken from the `n` column of the species parameter data frame.

If the `ext_encounter` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

Setting external diffusion rate

The external diffusion rate allows you to impose additional diffusion beyond the predation-driven diffusion that can be internally modelled by mizer.

The `ext_diffusion` argument allows you to specify a diffusion rate that depends on species and body size.

If the `ext_diffusion` argument is not supplied, then the external diffusion rate is calculated as a power law:

$$D_{ext.i}(w) = D_{ext.i}\, w^{n_i+1}.$$

The coefficient $D_{ext.i}$ is taken from the `D_ext` column of the species parameter data frame, which defaults to 0. The exponent $n_i + 1$ uses the `n` column of the species parameter data frame.

If the `ext_diffusion` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

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. There is a size `w_repro_max` at which a typical mature individual invests all of its available energy into reproduction. This is **not** a hard ceiling on size: not all individuals are mature at `w_repro_max`, and diffusion in the growth process allows some individuals to grow beyond it, so fish larger than `w_repro_max` can exist. If you have not specified the `w_repro_max` column in the species parameter data frame, then the von Bertalanffy asymptotic size `w_inf` is used instead.

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 size 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 $U = \log(3)/\log(w_{mat}/w_{mat25})$.

The sigmoidal function given above would strictly reach 0 only asymptotically and thus have some (negligible) amount of reproduction at arbitrarily small size. 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

$$\texttt{repro_prop}(w) = \min\left(\left(\frac{w}{w_{\texttt{repro_max}}}\right)^{m-n}, 1\right).$$

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 sizes w_{repro_max} are taken from the `w_repro_max` column in the species parameter data frame, if it exists, or otherwise from the `w_inf` column.

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

$$\psi(w) = \texttt{maturity}(w)\texttt{repro_prop}(w)$$

In mizer edition 1, at sizes above `w_repro_max` the value of ψ is additionally forced to 1, so that all available energy is invested into reproduction and growth stops. In edition 2 and above this forcing is not applied, and ψ is determined entirely by the maturity ogive and the reproductive proportion.

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`.

The most commonly-used selectivity function is `sigmoid_length()`. It has a smooth transition from 0 to 1 at a certain size. The `sigmoid_length()` function has the two parameters `l50` and `l25` that are the lengths in cm at which 50% or 25% of the fish are selected by the gear. If you choose this selectivity function then the `l50` and `l25` columns must be included in the gear parameters data.frame.

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

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

`setPredKernel` *Set predation kernel*

Description

You will usually not need to call this function directly. Instead change the relevant species parameters (`pred_kernel_type`, and, depending on its value, the parameters required by the selected kernel) with `given_species_params(params) <-` and let mizer recalculate the predation kernel for you. Call `setPredKernel()` directly only if you want to supply the full kernel array yourself. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setPredKernel(params, pred_kernel = NULL, reset = FALSE, ...)

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`	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

Details

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.

Value

`setPredKernel()`: A MizerParams object with updated predation kernel.

`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. Alternative pred_kernel types are "box", implemented by `box_pred_kernel()`, "power_law", implemented by `power_law_pred_kernel()`, and "gaussian_mixture", implemented by `gaussian_mixture_pred_kernel()`. These functions require certain species parameters in the species_params data frame. For the lognormal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`, and for the Gaussian mixture they are the list-columns `kernel_p`, `kernel_mean`, and `kernel_sd`. 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 `pred_kernel()` 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.

Higher-order quadrature

When the predation kernel depends only on the predator/prey mass ratio, the encounter and predation rates are evaluated as convolutions using the fast Fourier transform. By default mizer point-samples the kernel at the grid nodes, which is a first-order (rectangle-rule) quadrature. When the `bin_average` entry of the `second_order_w` slot is `TRUE`, the kernel is instead integrated over each logarithmic size bin when building the Fourier-transformed kernels. This finite-volume consistent quadrature lifts the encounter and predation rates towards second order at no extra runtime cost, because the integration is performed once here and the rate functions themselves are unchanged. The predation kernel is additionally averaged over the prey bin (a trapezoid fold), so that the predation rate returned by `getPredRate()` is the prey-bin average that the predation-mortality sink needs to be second order. The default remains the first-order scheme so that existing models are unaffected. Enable it with `second_order_w(params) <- TRUE` (see `second_order_w()`), which also turns on the other bin-averaged rate quadratures so the whole model stays consistent. See the `vignette("fft")` for the mathematical details.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setReproduction()`, `setSearchVolume()`, `species_params()`, `use_predation_diffusion()`

Examples

```
## 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), pred_kernel(params)["Cod", 100, ], type="l", log="x")

## If you need a kernel that depends also on prey size you need to define
# it yourself.
pk <- pred_kernel(params)
pk["Herring", , ] <- sweep(pk["Herring", , ], 2,
                           params@w_full, "*")
params<- setPredKernel(params, pred_kernel = pk)
```

---

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`	A named list of user-defined parameters to store in `other_params(params)`.

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()`
- `diffusion` from `mizerDiffusion()`
- `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()`: The user-defined parameters stored in `other_params(params)`, or `NULL` if none have been set. This excludes any component-specific parameters stored via `setComponent()`.

Avoid rates that jump as a function of abundance

Make sure your rate function depends **continuously** on the abundances `n`, `n_pp` and `n_other`. It is tempting to write a rate that switches abruptly on the state of the model — a fishery that closes when a stock falls below a limit reference point, a predator that switches diet when its preferred prey becomes scarce, a mortality that kicks in below a critical condition. Such a rate breaks the assumption underlying every one of mizer's time-stepping methods, which freeze the rates during each density update and so cannot see a threshold being crossed within a step.

The symptoms are quiet: mizer issues no warning, but the trajectory keeps changing as you refine `dt`, the Newton solver stalls, and `getStability()` reports a confident but meaningless answer. Choosing the L-stable `method = "tr_bdf2"` in `project()` does not help, because the difficulty lies in the frozen rates rather than in the linear solve.

The remedy is to give the switch a finite width, using a linear ramp between two thresholds or a logistic transition, which is usually the more realistic model anyway. Rates built with `max()` or `min()` are continuous but not differentiable; these are much less troublesome, costing some accuracy but not correctness. See the Discontinuous rate functions article for the full story, the diagnostics and the fix.

See Also

"Extending mizer": guide to extending mizer; Discontinuous rate functions

Other extension tools: `NOther()`, `coerceToExtensionClass()`, `initialNOther<-()`, `other_mort()`, `recordExtension()`, `setComponent()`

---

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. You will usually not need to call this function directly. Instead change the `w_mat`, `w_mat25`, `w_repro_max` and `m` species parameters with `given_species_params(params) <-` and let mizer recalculate the maturity ogive and reproduction allocation for you. Call `setReproduction()` directly only if you want to impose different functional forms for these. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setReproduction(
  params,
  maturity = NULL,
  repro_prop = NULL,
  reset = FALSE,
  RDD = NULL,
  ...
)

maturity(params)

maturity(params) <- value

repro_prop(params)

repro_prop(params) <- value

psi(params)
```

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 the energy available for growth and reproduction 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	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	The desired new value for the respective parameter.

Value

setReproduction(): A MizerParams object with updated reproduction parameters.

maturity(): An ArraySpeciesBySize object (species x size) that holds the proportion of individuals of each species at size that are mature.

repro_prop(): An ArraySpeciesBySize object (species x size) that holds the proportion of the energy available for growth and reproduction 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. There is a size w_repro_max at which a typical mature individual invests all of its available energy into reproduction. This is **not** a hard ceiling on size: not all individuals are mature at w_repro_max, and diffusion in the growth process allows some individuals to grow beyond it, so fish larger than w_repro_max can exist. If you have not specified the w_repro_max column in the species parameter data frame, then the von Bertalanffy asymptotic size w_inf is used instead.

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:

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

(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 size 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 $U = \log(3)/\log(w_{mat}/w_{mat25})$.

The sigmoidal function given above would strictly reach 0 only asymptotically and thus have some (negligible) amount of reproduction at arbitrarily small size. 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

$$\texttt{repro_prop}(w) = \min\left(\left(\frac{w}{w_{\texttt{repro_max}}}\right)^{m-n}, 1\right).$$

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 sizes w_{repro_max} are taken from the `w_repro_max` column in the species parameter data frame, if it exists, or otherwise from the `w_inf` column.

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

$$\psi(w) = \texttt{maturity}(w)\texttt{repro_prop}(w)$$

In mizer edition 1, at sizes above `w_repro_max` the value of ψ is additionally forced to 1, so that all available energy is invested into reproduction and growth stops. In edition 2 and above this forcing is not applied, and ψ is determined entirely by the maturity ogive and the reproductive proportion.

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(), setExtDiffusion(), setExtEncounter(), setExtMort(), setFishing(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setParams(), setPredKernel(), setSearchVolume(), species_params(), use_predation_diffusion()

Examples

```
# Plot maturity and reproduction ogives for Cod in North Sea model
mat <- maturity(NS_params)["Cod", ]
rp <- repro_prop(NS_params)["Cod", ]
df <- data.frame(Size = w(NS_params),
                 Reproduction = rp,
                 Maturity = mat,
                 Total = mat * rp)
dff <- reshape2::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 resource dynamics*

Description

Sets the intrinsic resource birth rate and the intrinsic resource carrying capacity as well as the name of the function used to simulate the resource dynamics. By default, the birth rate and the carrying capacity are changed together in such a way that the resource replenishes at the same rate at which it is consumed. So you should only provide either the `resource_rate` or the `resource_capacity` (or `resource_level`) because the other is determined by the requirement that the resource replenishes at the same rate at which it is consumed.

Usage

```
setResource(
  params,
  resource_rate = NULL,
  resource_capacity = NULL,
  resource_level = NULL,
  resource_dynamics = NULL,
  lambda = resource_params(params)[["lambda"]],
  n = resource_params(params)[["n"]],
  w_pp_cutoff = resource_params(params)[["w_pp_cutoff"]],
  balance = NULL,
  reset = FALSE,
  ...
)
```

```
resource_rate(params)

resource_rate(params, balance = NULL) <- value

resource_capacity(params)

resource_capacity(params, balance = NULL) <- value

resource_level(params)

resource_level(params, balance = NULL) <- value

resource_dynamics(params)

resource_dynamics(params, balance = NULL) <- value
```

Arguments

`params` A MizerParams object

`resource_rate` Optional. A vector of per-capita resource birth rate for each size class or a single number giving the coefficient in the power-law for this rate, see "Setting resource dynamics" below. Must be strictly positive.

`resource_capacity` Optional. Vector of resource intrinsic carrying capacities or coefficient in the power-law for the capacity, see "Setting resource dynamics" below. The resource capacity must not be smaller than the resource abundance.

`resource_level` Optional. The ratio between the current resource number density and the resource capacity. Either a number used at all sizes or a vector specifying a value for each size. Must be greater than 0 and at most 1, except at sizes where the resource is zero, where it can be `NaN`. This determines the resource capacity, so do not specify both this and `resource_capacity`.

`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.

`lambda` Used to set power-law exponent for resource capacity if the `resource_capacity` argument is given as a single number.

`n` Used to set power-law exponent for resource rate if the `resource_rate` argument is given as a single number.

`w_pp_cutoff` The upper cut off size of the resource spectrum power law used when `resource_capacity` is given as a single number. When changing `w_pp_cutoff` without providing `resource_capacity`, the cutoff can only be decreased. In that case, both the carrying capacity and the initial resource abundance will be cut off at the new value. To increase the cutoff, you must also provide the `resource_capacity` for the extended range.

`balance` By default, if possible, the resource parameters are set so that the resource replenishes at the same rate at which it is consumed. In this case you should only

specify either the resource rate or the resource capacity (or resource level) because the other is then determined automatically. Set to FALSE if you do not want the balancing.

`reset` If set to TRUE, then the resource capacity and birth rate will be reset to the values 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.

`...` Unused

`value` The desired new value for the respective parameter.

Details

You would usually set the resource dynamics only after having finished the calibration of the steady state. Then setting the resource dynamics with this function will preserve that steady state, unless you explicitly choose to set `balance = FALSE`. Your choice of the resource dynamics only affects the dynamics around the steady state. The higher the resource rate or the lower the resource capacity the less sensitive the model will be to changes in the competition for resource.

If you provide the `resource_level` then that sets the `resource_capacity` to the current resource number density divided by the resource level. So in that case you should not specify `resource_capacity` as well.

If you provide none of the arguments `resource_level`, `resource_rate` or `resource_capacity`, and you do not change any of the resource parameters, then the resource rate is kept at its previous value and, when balancing, the capacity is recalculated from it. If instead you change one of the resource parameters (`kappa`, `lambda`, `n` or `w_pp_cutoff`) or set `reset = TRUE`, the rate and capacity are recalculated from the resource parameters (and then balanced, unless `balance = FALSE`).

Value

`setResource`: A MizerParams object with updated resource parameters

A vector with the intrinsic resource birth rate for each size class.

A vector with the intrinsic resource capacity for each size class.

A vector with the ratio between the current resource number density and the resource capacity for each size class.

The name of the function that determines the resource dynamics.

Setting resource dynamics

The `resource_dynamics` argument allows you to choose the resource dynamics function. 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 that to use a logistic model implemented by `resource_logistic()` or you can use `resource_constant()` which keeps the resource constant or you can write your own function.

Both the `resource_semichemostat()` and the `resource_logistic()` dynamics are parametrised in terms of a size-dependent birth rate $r_R(w)$ and a size-dependent capacity c_R. The help pages of these functions give the details.

The resource_rate argument can be a vector (with the same length as w_full(params)) specifying the intrinsic resource birth rate for each size class. Alternatively it can be a single number that is used as the coefficient in a power law: then the intrinsic birth rate $r_R(w)$ at size w is set to

$$r_R(w) = r_R w^{n-1}.$$

The power-law exponent n is taken from the n argument.

The resource_capacity argument can be a vector specifying the intrinsic resource carrying capacity for each size class. Alternatively it can be a single number that is used as the coefficient in a truncated power law: then the intrinsic carrying capacity $c_R(w)$ at size w is set to

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

for all w less than w_pp_cutoff and zero for larger sizes. The power-law exponent λ is taken from the lambda argument.

The values for lambda, n and w_pp_cutoff are stored in a list in the resource_params slot of the MizerParams object so that they can be re-used automatically in the future. If you specify resource_rate or resource_capacity as a single number, that coefficient is likewise stored, as r_pp and kappa respectively. That list can be accessed with resource_params().

The resource power law also determines defaults for species search volume. Changing lambda recalculates any q and gamma values that mizer calculated, and changing kappa (by supplying a scalar resource_capacity) recalculates any calculated gamma. Species-specific values that you supplied explicitly remain unchanged.

See Also

setParams()

Examples

```
params <- NS_params
resource_dynamics(params)
resource_dynamics(params) <- "resource_constant"
```

---

setRmax *Alias for* setBevertonHolt()

Description

[Superseded]

An alias provided for backward compatibility with mizer version <= 2.0.4

Usage

```
setRmax(
  params,
  erepro,
  R_max,
  reproduction_level,
  info_level = default_info_level(),
  ...
)
```

Arguments

params	A MizerParams object
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.
info_level	Controls the amount of information messages and warnings that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().
...	Unused • R_factor: Legacy alternative for specifying reproduction_level = 1 / R_factor.

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,

$$R_{di} = \frac{\text{erepro}}{2w_{min}} E_R,$$

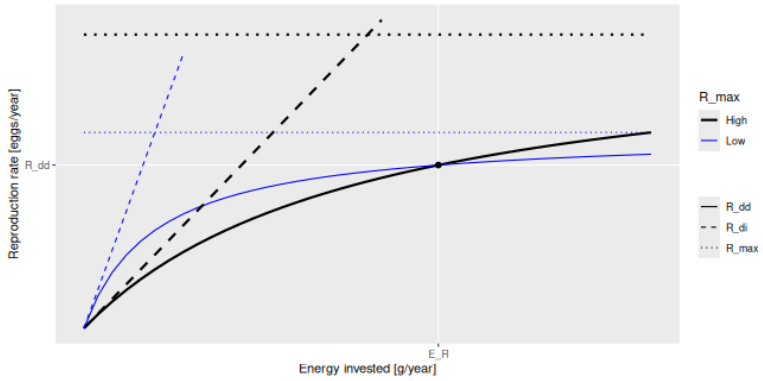
where the proportionality factor is given by the reproductive efficiency erepro divided by the egg size w_min to convert energy to egg number and divided by 2 to account for the two sexes.

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 non-negative 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.

A species that is absent from the initial state, with zero abundance at all sizes, has no reproduction whatever its parameters, so every Beverton-Holt curve keeps it at its steady state. For such a species a given `erepro` or `R_max` is used as it is and the other parameter is left unchanged. Its reproduction level is zero whatever its `R_max`, so a non-zero `reproduction_level` cannot be set for it: its parameters are then left unchanged and a warning is issued.

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

`reproduction_level()`: A named vector with the reproduction level for each species.

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_max^-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")])

# Inspecting reproduction level
reproduction_level(NS_params)

# The reproduction level can be changed without changing the steady state:
reproduction_level(params) <- 0.9
reproduction_level(params)
```

---

setSearchVolume *Set search volume*

Description

You will usually not need to call this function directly. Instead change the `gamma` and `q` species parameters with `given_species_params(params) <-` and let mizer recalculate the search volume for you. Call `setSearchVolume()` directly only if you want to impose a different functional form for the size dependence of the search volume. See `vignette("guide-change-parameters")` for a full explanation of when to reach for which level of the model.

Usage

```
setSearchVolume(params, search_vol = NULL, reset = FALSE, ...)

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`	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.

`search_vol()`: An `ArraySpeciesBySize` object (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. If the `q` column is not supplied, a default of `lambda - 2 + n` is used. 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 $\gamma_i(w)$.

If the `search_vol` slot has a comment and `reset = FALSE`, then a recalculation from the species parameters is suppressed and a message is issued if the recalculated values would differ from the stored ones.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `species_params()`, `use_predation_diffusion()`

Examples

```
# Inspect the current search volume
search_vol(NS_params)["Cod", 1:5]

# Double the search volume for all species
sv <- search_vol(NS_params) * 2
params <- setSearchVolume(NS_params, search_vol = sv)
search_vol(params)["Cod", 1:5]
```

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

Details

With $b = 1/R_{max}$ and $c = 1$ this reduces to the Beverton-Holt reproduction rate, see BevertonHoltRDD().

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.

Usage

```
sigmoid_length(w, l25, l50, species_params, ...)
```

Arguments

`w`	Vector of sizes.
`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

Details

You would not usually call this function directly. Instead, set the `sel_func` column in `gear_params()` to `"sigmoid_length"` and provide the `l25` and `l50` values as additional columns. `setFishing()` will then call this function automatically when calculating the selectivity array.

The selectivity is given by the logistic function

$$S(l) = \frac{1}{1 + \exp\left(\log(3)\frac{l50-l}{l50-l25}\right)}$$

As the mizer 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

$$l = \left(\frac{w}{a}\right)^{1/b}$$

Value

Vector of selectivities at the given sizes.

See Also

`gear_params()` for setting the selectivity parameters.

Other selectivity functions: `double_sigmoid_length()`, `knife_edge()`, `knife_edge_length()`, `sigmoid_weight()`

Examples

```
# Selectivity at weight given l25 = 10 cm, l50 = 15 cm
# using length-weight parameters a = 0.01, b = 3
sp <- list(a = 0.01, b = 3)
w <- c(1, 10, 100, 500, 1000)
sigmoid_length(w, l25 = 10, l50 = 15, species_params = sp)
```

`sigmoid_weight` *Weight based sigmoidal selectivity function*

Description

A sigmoidal selectivity function with 50% selectivity at weight `sigmoidal_weight` $= w_{\text{sigmoid}}$ and width `sigmoidal_sigma` $= \sigma$.

$$S(w) = \left(1 + \left(\frac{w}{w_{\text{sigmoid}}}\right)^{-\sigma}\right)^{-1}$$

Usage

```
sigmoid_weight(w, sigmoidal_weight, sigmoidal_sigma, ...)
```

Arguments

`w`	Vector of sizes.
`sigmoidal_weight`	The weight at which selectivity is 50%.
`sigmoidal_sigma`	The width of the selection function.
`...`	Unused

Details

You would not usually call this function directly. Instead, set the `sel_func` column in `gear_params()` to `"sigmoid_weight"` and provide `sigmoidal_weight` and `sigmoidal_sigma` as additional columns. `setFishing()` will then call this function automatically when calculating the selectivity array.

Value

Vector of selectivities at the given sizes.

See Also

`gear_params()` for setting the selectivity parameters.

Other selectivity functions: `double_sigmoid_length()`, `knife_edge()`, `knife_edge_length()`, `sigmoid_length()`

Examples

```
sigmoid_weight(w = c(1, 10, 100, 1000),
               sigmoidal_weight = 100, sigmoidal_sigma = 3)
```

---

signal_frozen *Signal that a change the user made cannot take effect*

Description

A rate array that has been set by hand is protected by a comment, see the "Setting or changing rates" section in `setParams()`. Mizer then no longer calculates it from the species parameters, so a change to one of the species parameters that feeds it has no effect on the model. This function raises the condition that tells the user so.

Usage

```
signal_frozen(var, message)
```

Arguments

`var`	A string naming the quantity the report is about.
`message`	The message to give the user.

Details

The condition is raised at severity `"warning"`, see `signal_info()`, so that it survives the `suppressMessages()` that `species_params<-()` runs over its recalculation. It also carries the class `info_about_frozen` for code that wants to catch this kind of report in particular.

Only signal this when the user has actually asked for something that is not happening. The mere fact that a frozen array differs from what the formula would give is not enough: mizer freezes arrays itself when it builds the trait-based and community models, and those arrays differ from the formula for the lifetime of the model. See `signal_frozen_changes()`, which decides this from the species parameters the user changed.

Value

`NULL` invisibly. Called for its side effect of signalling.

signal_frozen_changes *Signal the changes to species parameters that cannot take effect*

Description

Goes through the rate arrays that can be frozen, see `frozen_rate_params()`, and raises a `signal_frozen()` condition for each frozen array that one of the changed species parameters feeds. This is what turns "the model no longer follows the species parameters" into a warning the user sees at the moment they make the change. It is one of the diagnostics that only `given_species_params<-()` gives, see there.

Usage

```
signal_frozen_changes(params, changed)
```

Arguments

params	A MizerParams object, holding the rate arrays as they are, that is, before the change is applied.
changed	A character vector with the names of the species parameters that the user changed.

Value

`NULL` invisibly. Called for its side effect of signalling.

signal_gear_params_changes *Signal a gear parameter changed through the given species parameters*

Description

Mizer looks for the gear parameters in the gear parameter table, which is read only when the model is built, so changing one of them through the species parameters does not reach the model. This is one of the diagnostics that only `given_species_params<-()` gives; `species_params<-()` stays quiet, see there.

Usage

```
signal_gear_params_changes(changed)
```

Arguments

changed	A named list with one entry per changed column, or a character vector of the changed column names.

Details

yield_observed is the exception. It belongs in gear_params(), which gives the observed yield per gear and species, and that is where it should be set, which is what this reports. But it feeds no rate, so a value in the species parameters is not lost: get_yield_observed() falls back to it for any species that has no observation among the gear parameters.

Value

NULL invisibly. Called for its side effect of signalling.

---

signal_ignored_changes

Signal the changes that are ignored because another parameter was given

---

Description

Some species parameters are only used to calculate a default for another one: f0 for gamma, fc for ks, age_mat for h, and k_vb for h or age_mat. Once the other one has been given, the model no longer consults them, so changing them has no effect. This raises a warning about that. It is one of the diagnostics that only given_species_params<-() gives, see there.

Usage

```
signal_ignored_changes(given, changed)
```

Arguments

given	The given species parameters, as they are before the change.
changed	A named list with one logical vector per changed column, saying which species were given a value, as built by given_species_params<-().

Details

Only a value that is there can be ignored, so this is asked about the species that were *given* a value, not about every species whose value changed: clearing a value to NA is a change, but not one this has anything to say about.

Value

NULL invisibly. Called for its side effect of signalling.

signal_info *Signal information about a choice mizer made*

Description

[Experimental] Raises the condition that `with_info_level()` collects. This is the way for mizer, and for anything extending it, to tell the user about a default it filled in, an input it adjusted or an instruction it could not carry out, without deciding on its own how loudly to say it: the handler installed by whichever function the user actually called does that.

Usage

```
signal_info(
  var,
  message,
  level = 3,
  severity = c("info", "warning"),
  unhandled = c("drop", "show"),
  class = character()
)
```

Arguments

`var`	A string naming the quantity the report is about.
`message`	The message to give the user.
`level`	How important the report is. Level 1 is important enough to survive `info_level = 1`, level 3 is chatter that only the default `info_level = 3` shows.
`severity`	`"info"` to report as a message, `"warning"` to report as a warning. Use `"warning"` when the user asked for something that is not happening, because a message can be, and on the `species_params<-()` path is, suppressed.
`unhandled`	What to do when no handler is collecting, for example because a rate setter was called directly rather than through `setParams()`. `"drop"` says nothing, which suits chatter that only makes sense as part of a report about a whole model. `"show"` reports it there and then, at the same severity: a message for `"info"` and a warning for `"warning"`.
`class`	Further classes to give the condition, for code that wants to catch a particular kind of report.

Details

Progress reports are the one thing that does not belong here: they have to appear while the work is going on, and these are collected and given at the end.

Value

`NULL` invisibly. Called for its side effect of signalling.

Examples

```
# With nothing collecting, a `"drop"` report says nothing at all ...
signal_info("h", "Using a default for `h`.")

# ... whereas `unhandled = "show"` reports it there and then.
signal_info("h", "Using a default for `h`.", unhandled = "show")

# Normally it is raised inside a call whose body is wrapped in
# `with_info_level()`, which is what decides whether to show it.
with_info_level(signal_info("h", "Using a default for `h`."))
```

---

signal_not_recalculated

Signal that a rate array was not recalculated because it is frozen

---

Description

[Experimental] Raised by the rate setters when they leave a frozen array alone although the species parameters say that it should have a different value. It is reported as a message, and `info_level = 0` silences it along with the other information. Where no handler is collecting, for example when a rate setter is called directly rather than via `setParams()`, it is shown anyway, because it may then be all the user hears. The stronger `signal_frozen()` warning is raised elsewhere, by whoever knows that the user asked for a change, see `signal_frozen_changes()`.

Usage

```
signal_not_recalculated(
  var,
  quantity,
  reset_call,
  derived_from = "species parameters"
)
```

Arguments

`var`	A string naming the slot that was not recalculated.
`quantity`	A string naming the quantity for the user, for example "metabolic rate".
`reset_call`	A string with the call that recalculates the quantity, for example "setMetabolicRate(params, reset = TRUE)".
`derived_from`	A string naming the parameters that the quantity would have been calculated from.

Value

`NULL` invisibly. Called for its side effect of signalling.

Examples

```
with_info_level(
    signal_not_recalculated("metab", "metabolic rate",
                            "setMetabolicRate(params, reset = TRUE)")
)
```

---

signal_removed_species_params
Signal that species parameter columns have been removed

Description

A column that is absent from the table assigned to `species_params<-()` or `given_species_params<-()` is one the user no longer supplies. Mizer calculates afresh those it knows how to calculate, and the rest leave the model altogether. This reports the ones that leave the given species parameters, whether or not mizer puts a calculated value back.

Usage

```
signal_removed_species_params(withdrawn)
```

Arguments

`withdrawn`	A character vector of the withdrawn column names. Nothing is signalled when it is empty.

Details

The report is made at level 3, so it is visible in ordinary use and silent from `info_level` 1 downwards: removing a column is what the user asked for, not something that went differently from how they asked. It carries the class `info_about_removed` for code that wants to catch it in particular.

Value

`NULL` invisibly. Called for its side effect of signalling.

`sizeIntegral` *Integrate a quantity over the size spectrum*

Description

[Experimental] Calculates

$$\int_{w_{min}}^{w_{max}} N_i(w)\, K_i(w)\, dw$$

for each species i, using the quadrature scheme that the model is actually using. This is the recommended way to write your own summary or indicator function: it selects the size range, applies the bin-averaging appropriate to the model's `second_order_w()` setting and wraps the result in the appropriate mizer array class, so that none of those rules need to be remembered. The built-in summary functions like `getBiomass()`, `getN()`, `getSSB()` and `getYield()` are all implemented with it.

Usage

```
sizeIntegral(
  object,
  weighting = 1,
  n = NULL,
  ...,
  value_name = NULL,
  units = NULL
)
```

Arguments

`object`	A `MizerParams` or a `MizerSim` object.
`weighting`	The weighting factor $K(w)$ of the integral, evaluated on the size grid. See the section "The weighting factor" below. Defaults to 1.
`n`	The abundance density. Either a species x size matrix or a time x species x size array. Defaults to the initial abundance `initialN(object)` for a `MizerParams` object and to the saved abundances `object@n` for a `MizerSim` object.
`...`	Arguments passed to `get_size_range_array()` to select the size range to integrate over, i.e. `min_w`, `max_w`, `min_l` and `max_l`.
`value_name`	A string giving a human-readable name for the value, used when the result is wrapped in a mizer array class.
`units`	A string giving the units of the result, used when the result is wrapped in a mizer array class.

Value

The value of the integral, see the section "Shape of the result" above.

The weighting factor

The weighting factor $K(w)$ is supplied already evaluated on the size grid. It can be

- a single number (the default `weighting = 1` integrates the abundance density itself, giving numbers),
- a vector with one value for each size bin, which is then used for all species,
- a matrix (species x size), for example `params@maturity`,
- an array with further dimensions in front, for example the gear x species x size array returned by `getFMortGear()` or the time x species x size array returned by `getFMort(sim)`. Those extra dimensions are carried through to the result.

If the weighting factor is a product of several size-dependent factors, pass the whole product: bin-averaging is applied to the product as a single weighting factor, which is not the same as averaging the factors separately.

Do **not** include the bin widths `params@dw` in the weighting factor and do not bin-average it yourself; `sizeIntegral()` does both.

Shape of the result

The size dimension is integrated out. The remaining dimensions are those of `n` together with any extra dimensions of `weighting`, so

- with a `MizerParams` object and a species x size weighting the result is a named vector with one value per species,
- with a `MizerSim` object it is an ArrayTimeBySpecies object (time x species),
- with a gear x species x size weighting the extra `gear` dimension is kept, giving a gear x species array (or time x gear x species for a `MizerSim`).

Dimensions of `weighting` other than the last two are matched to the dimensions of `n` by the names of their dimnames, so a weighting whose first dimension is named `"time"` is lined up with the times of the simulation rather than producing an outer product.

See Also

`get_size_range_array()`, `bin_average_weight()`, `second_order_w()`

Examples

```
# The biomass of each species, i.e. what getBiomass() does
sizeIntegral(NS_params, weighting = NS_params@w)

# ... restricted to a size range
sizeIntegral(NS_params, weighting = NS_params@w, min_w = 10, max_w = 1000)

# The numbers of individuals larger than 10g
sizeIntegral(NS_params, min_w = 10)

# Spawning stock biomass: the weighting is the product maturity * w
K <- sweep(NS_params@maturity, 2, NS_params@w, "*")
```

```
sizeIntegral(NS_params, weighting = K)

# An indicator through time, ready to plot
biomass <- sizeIntegral(NS_sim, weighting = NS_params@w,
                        value_name = "Biomass", units = "g")
biomass[c("1972", "2010"), c("Herring", "Cod")]
```

---

species_params *Species parameters*

Description

These functions allow you to get or set the species-specific parameters stored in a MizerParams object.

Usage

```
species_params(object, ...)

species_params(object, recalculate = TRUE) <- value

is.species_params(x)

given_species_params(object, ...)

is.given_species_params(x)

given_species_params(object) <- value

calculated_species_params(params)
```

Arguments

`object` A MizerParams object, a MizerSim object or a data frame

`...` Other arguments passed to methods. The methods for a data frame accept:

strict Whether to raise an error, rather than correct silently, for the inconsistencies that can be corrected. Used internally.

check_misspellings Whether to report column names that look like misspellings of standard species parameter names. `TRUE` by default. Mizer passes `FALSE` when it re-validates a table whose columns it has already checked, so that the report is made once, when the column is introduced, rather than again on every rebuild.

`recalculate` Whether `species_params<-()` should be allowed to re-derive calculated species parameters and rates that depend on a changed parameter. Defaults to `TRUE`; mizer still skips the rebuild when all changes are to columns with no cached dependants. See the section "Setting species parameters without recalculation" below before setting it to `FALSE`.

value	A data frame with the new species parameters.
x	An object to test with `is.species_params()` or `is.given_species_params()`.
params	A MizerParams object.

Details

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 von Bertalanffy asymptotic size. However if you have information about the values of other parameters then you should provide them.

Three species parameters describe maximum sizes and play distinct roles:

- `w_inf` is the von Bertalanffy asymptotic size of an average individual. It is the required maximum-size parameter and is used to set default values for `w_max`, `w_repro_max` and `w_mat`.
- `w_repro_max` is the size at which a typical mature individual invests all of its available energy into reproduction, see `setReproduction()`. It is not a hard ceiling on size and defaults to `w_inf`.
- `w_max` is purely a computational boundary: it sets the upper end of the size grid and the range of plots. It defaults to `1.5 * w_inf`. For backwards compatibility, if `w_inf` is not supplied it is taken from `w_repro_max` or `w_max` instead.

Mizer distinguishes between the species parameters that you have given explicitly and the species parameters that have been calculated by mizer or set to default values. You can retrieve the given species parameters with `given_species_params()` and the calculated ones with `calculated_species_params()`. You get all species_params with `species_params()`.

When you change species parameters with `species_params<-()`, mizer automatically detects which parameters you have changed. It records these changed parameters in `given_species_params` so that they are protected against being overwritten by future recalculations. It then re-calculates the quantities that depend on the changed parameters. Changes to observation, direct-runtime or other custom columns that base mizer does not use to build a cached quantity do not trigger that recalculation. Unknown columns on an extension object retain the conservative recalculation path because an extension setter may use them.

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`, `z_ext` and `d` are used to set the external mortality rate, see `setExtMort()`.
- `E_ext` and `n` are used to set the external encounter rate, see `setExtEncounter()`.
- `D_ext` and `n` are used to set the external diffusion rate, see `setExtDiffusion()`.
- `w_mat`, `w_mat25`, `w_repro_max` 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(). The Gaussian-mixture kernel instead uses the list-columns kernel_p, kernel_mean, and kernel_sd, see gaussian_mixture_pred_kernel(). There will be other parameters if you are using other predation kernel functions.

When you change one of the above species parameters using species_params<-() or given_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. Mizer warns you when that happens, because the value is then in the species parameter table without having any effect on the model. The warning names the call that puts the rate back under the control of the species parameters.

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().
- R_max 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 $w = al^b$.

If you have supplied the a and b parameters, then you can replace weight parameters like w_inf, w_max, w_mat, w_mat25, w_repro_max and w_min by their corresponding length parameters l_inf, l_max, l_mat, l_mat25, l_repro_max and l_min.

You can also keep both, and change either of them later. Mizer keeps the two consistent by the rule that the one you gave last wins, and if you gave both at the same time the weight wins. So on a model set up with lengths you can still set w_mat with species_params<-() and mizer will update l_mat to match, and if you set l_mat it will update w_mat as always. When you supply a length and a weight together that do not agree, mizer uses the weight and warns you that it has changed the length to match.

The rule is applied when a species parameter data frame is put into a model. A data frame that you have taken out of a model and are editing on its own is left exactly as you write it: no conversions, no checks and no warnings until you assign it back with species_params<-() or given_species_params<-(), which is when mizer can tell which values you changed. A data frame that was never in a model, for example one you pass to validSpeciesParams(), carries no such history, so a length and a weight that disagree there count as given at the same time and the weight wins.

The parameters that are only used to calculate default values for other parameters are:

- 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 ks of the metabolic rate, see get_ks_default().
- age_mat is the age at maturity and is used to get a default value for the coefficient h of the maximum intake rate, see get_h_default().
- If age_mat is not supplied, mizer used the von Bertalanffy parameters k_vb, w_inf and t0 as well as the weight-length exponent b to determine it. This is unreliable and is therefore not recommended.

Changing these parameters with species_params<-() will trigger a recalculation of the downstream parameters, provided they are not protected by being explicitly given.

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().

The total annual fisheries yield is not a species parameter but a gear parameter, because it is observed for each gear separately, see gear_params(). For backwards compatibility mizer still accepts a yield_observed column in the species parameter data frame, see get_yield_observed().

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")

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 species parameters and newMultispeciesParams() will transfer them to the gear_params data frame. However changing these parameters later in the species parameter data frames will have no effect.

You are allowed to include additional columns in the species parameter data frames. They will simply be ignored by mizer but will be stored in the MizerParams object, in case your own code makes use of them.

Value

species_params(): Data frame containing all species parameters currently stored in the model.
species_params<-(): Updates the given_species_params with any parameters you have changed, and recalculates the full species parameter table and model parameters when a changed column has cached dependants. A column that value does not have is one you no longer supply and is removed from the given species parameters, see the section "Removing a species parameter column" below. With recalculate = FALSE it only does the recording and stores the parameters you supplied, see the section "Setting species parameters without recalculation" below.

given_species_params(): Data frame containing the species parameter values that were supplied explicitly by the user.
given_species_params<-(): Replaces the authoritative table of parameters that are to count as explicit user input. Every non-NA entry in value is recorded as given, even when it is numerically equal to the value currently in species_params(). This lets you protect a calculated value against future recalculation. An NA entry, or removal of a column, hands a previously given parameter

back to mizer's calculation – and where there is no mizer calculation to hand it back to, removing the column removes the parameter from the model, see the section "Removing a species parameter column" below. Dependent quantities are recalculated only when the replacement can change them; merely marking the current value as given does not rebuild the model.

This setter also warns when a change you asked for cannot take effect, namely when the parameter is overridden by another one you have already given (`f0` by `gamma`, `fc` by `ks`, `age_mat` by `h`), when the rate array it feeds has been set by hand and so is no longer calculated, or when it is a gear parameter that mizer reads from `gear_params()` instead. `species_params<-()` stays quiet about all three. `given_species_params<-()` has no `recalculate` argument; where you need to record values without recalculating, use `species_params<-()` or `record_given_species_params()`.

`calculated_species_params()`: Data frame containing only those species parameter entries that are not explicit user input. Columns that would consist entirely of `NA` values are dropped.

`is.species_params()` returns `TRUE` if `x` is a `species_params` object, `FALSE` otherwise.

`is.given_species_params()` returns `TRUE` if `x` is a `given_species_params` object, `FALSE` otherwise.

Extracting a column with `$`

`species_params(params)$w_mat` returns the column as a vector named after the species. Unlike `$` on an ordinary data frame, it does **not** partially match the column name. Partial matching is dangerous here because so many species parameter names are prefixes of others: in a model without length-weight parameters `species_params(params)$a` used to return the `alpha` column and `$b` the `beta` column, complete with species names, so code converting weights to lengths silently got the assimilation efficiency and the preferred predator/prey mass ratio instead. Writing was never partially matched, so reads and writes disagreed about which column `$b` meant.

A name that is not a column now gives `NULL`, so `is.null(species_params(params)$foo)` is a reliable way of testing whether a parameter is present. If the name would have partially matched a column under the old behaviour you also get a warning naming that column, because that is exactly the case where existing code changes its meaning. The same holds for `gear_params()`.

Removing a species parameter column

A column that is missing from the table you assign is one you no longer supply, and mizer takes it out of the given species parameters. What happens next depends on whether mizer knows how to produce the parameter itself: one that it calculates comes straight back as a calculated value, while one that it knows nothing about leaves the model altogether. Both setters work this way, so either of these removes a custom column:

```
species_params(params)$my_col <- NULL
given_species_params(params)$my_col <- NULL
```

and either of these hands a parameter you had given back to mizer, exactly as setting it to `NA` in the given species parameters does:

```
species_params(params)$gamma <- NULL
given_species_params(params)$gamma <- NULL
```

This is how an extension package withdraws a species parameter it added when the user switches the extension off, without reaching into the species_params slot. Mizer reports the removal at info_level 3, see setParams().

Because the whole table is compared, assigning a table with only some of the model's columns withdraws all the others. There is not much room for surprise: species_params<-() validates what you give it, so a table without species and one of w_inf, w_max or w_repro_max is an error rather than a partial update. Still, edit the table you got from the accessor rather than building a new one from a handful of columns.

Setting species parameters without recalculation

species_params(params, recalculate = FALSE) <- value records the values you changed among the given species parameters, so that they are not calculated away later, and stores value as the species parameters. It then stops there: the calculated species parameters are not re-derived from the given ones, no missing parameters are filled in with their default values, and none of the size-dependent rates are recalculated. Your species parameters are stored as you supplied them, after the same checks and length-to-weight conversions that writing into the species_params slot would trigger.

This is for code that has worked out a species parameter *together with* the rate array that the parameter determines, for example an optimiser that fits ks and the matching metab, or z_ext and the matching mu_b. There the recalculation is not just wasted work but would overwrite the rates the caller has just set.

The object you get back is only as consistent as you make it. Mizer will not check that the species parameters you supplied agree with the rate arrays in the object, nor that they agree with the other species parameters that are normally derived from them. Unless you are setting the affected rates yourself, use the default recalculate = TRUE.

See Also

validSpeciesParams(), setParams()

Other functions for setting parameters: gear_params(), setExtDiffusion(), setExtEncounter(), setExtMort(), setFishing(), setInteraction(), setMaxIntakeRate(), setMetabolicRate(), setParams(), setPredKernel(), setReproduction(), setSearchVolume(), use_predation_diffusion()

---

steadySingleSpecies — *Set initial abundances to solution of steady-state equation with current rates*

Description

[Experimental] This first calculates growth and death rates that arise from the current initial abundances. Then it solves the steady-state equation with these growth and death rates and the current abundance at the smallest size. It sets the initial abundances of the selected species to this solution.

Usage

```
steadySingleSpecies(
  params,
  species = NULL,
  keep = c("egg", "biomass", "number"),
  info_level = default_info_level()
)
```

Arguments

params	A MizerParams 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.
keep	A string determining which quantity is to be kept constant. The choices are "egg" which keeps the egg density constant, "biomass" which keeps the total biomass of the species constant and "number" which keeps the total number of individuals constant.
info_level	Controls the amount of information messages and warnings that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.

Details

The function only changes the initial abundances. It does not adjust the reproduction parameters or any other parameters. Therefore the result of applying this function is of course not a steady state, because after changing the abundances of the selected species the growth, death and reproduction rates will have changed.

If the `keep` argument is supplied, the solution for the selected species are rescaled to keep the specified quantity at the value they had before calling this function. The biomass is counted above the `biomass_cutoff` species parameter, if there is one. A species that had none of the quantity is not rescaled, because there is nothing to keep: it is absent, or it lies entirely below its biomass cutoff. If its solution does have some of the quantity, a warning says so. The function stops with an error if the solution for a species has none of a quantity that the species did have.

Value

A MizerParams object in which the initial abundances of the selected species are changed to their single-species steady state abundances.

Examples

```
# Set initial abundance of Cod to its single-species steady state
params <- steadySingleSpecies(NS_params, species = "Cod")
```

str *Display the structure of mizer objects*

Description

Mizer provides `str()` methods for `MizerParams()` and `MizerSim()` objects, as well as `ArraySpeciesBySize()`, `ArrayTimeBySpecies()` and `ArrayTimeBySpeciesBySize()` objects. These methods produce a clean, compact overview of the object's structure without polluting the console with large amounts of internal data.

Usage

```
## S3 method for class 'ArraySpeciesBySize'
str(object, ...)
## S3 method for class 'ArrayTimeBySpecies'
str(object, ...)
## S3 method for class 'ArrayTimeBySpeciesBySize'
str(object, ...)
## S3 method for class 'MizerSim'
str(object, max.level = NA, ...)
## S3 method for class 'MizerParams'
str(object, max.level = NA, ...)
```

Arguments

`object`	The object to display the structure of.
`max.level`	Maximum level of nesting to print. Defaults to `NA` (no limit).
`...`	Further arguments. They are passed to the default `str()` method.

Value

`NULL`, invisibly.

See Also

`print()`, `as.data.frame()`, `summary()`, `plot()`, `MizerParams()`, `MizerSim()`, `ArraySpeciesBySize()`, `ArrayTimeBySpecies()`, `ArrayTimeBySpeciesBySize()`

Examples

```
str(NS_params)
str(NS_sim)
str(getEncounter(NS_params))
```

summary *Summarise mizer objects*

Description

Mizer provides summary() methods for model objects and for the specialised array classes returned by many mizer functions.

Usage

```
## S3 method for class 'ArraySpeciesBySize'
summary(object, all.sizes = FALSE, ...)
## S3 method for class 'ArrayTimeBySpecies'
summary(object, ...)
## S3 method for class 'ArrayTimeBySpeciesBySize'
summary(object, all.sizes = FALSE, ...)
## S3 method for class 'MizerSim'
summary(object, ...)
## S3 method for class 'MizerParams'
summary(object, ...)
```

Arguments

object	The object to summarise.
all.sizes	If FALSE (the default), values outside a species' size range (w_min to w_max) are left out, as in plot(). Only for the classes with a size dimension.
...	Further arguments. They are currently ignored by the mizer methods.

Details

For a MizerParams() object, summary() prints the model metadata, size grids, selected species parameters and fishing gear details. For a MizerSim() object, it first prints the parameter summary and then reports the simulated time period and output interval.

For ArraySpeciesBySize(), ArrayTimeBySpecies() and ArrayTimeBySpeciesBySize() objects, summary() returns a small list with the value name, units, dimensions and a per-species data frame containing minimum, mean and maximum values. Printing that summary object gives the same compact table in a human-readable form.

For the two classes that have a size dimension, those values are taken over each species' own size range, from its w_min to its w_max, which is the range plot() draws. A rate array is defined on the whole size grid, but the values outside a species' range describe an animal that does not exist — the encounter rate a 40 kg Sprat would have — and they are usually the extreme ones, so a summary that included them reported the size grid rather than the species. Pass all.sizes = TRUE for the whole grid.

Value

For `MizerParams()` and `MizerSim()`, the object is returned invisibly. For array objects, a list of class `summary.ArraySpeciesBySize`, `summary.ArrayTimeBySpecies` or `summary.ArrayTimeBySpeciesBySize`.

See Also

`print()`, `as.data.frame()`, `str()`, `MizerParams()`, `MizerSim()`, `ArraySpeciesBySize()`, `ArrayTimeBySpecies()`, `ArrayTimeBySpeciesBySize()`

Examples

```
summary(NS_params)
summary(NS_sim)
summary(getEncounter(NS_params))
summary(getFMort(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 siz
`getTrophicLevel()`	`ArraySpeciesBySize` (species x size)	Trophic level of indivi
`getTrophicLevelBySpecies()`	Named vector (species)	Consumption-rate-wei
`getSSB()`	Two dimensional array (time x species)	Total Spawning Stock
`getBiomass()`	Two dimensional array (time x species)	Total biomass of each
`getN()`	Two dimensional array (time x species)	Total abundance of ea
`getFeedingLevel()`	Three dimensional array (time x species x size)	Feeding level of each
`getM2`	Three dimensional array (time x species x size)	The predation mortalit
`getFMort()`	Three dimensional array (time x species x size)	Total fishing mortality
`getFMortGear()`	Four dimensional array (time x gear x species x size)	Fishing mortality on e
`getYieldGear()`	Three dimensional array (time x gear x species)	Total yield by gear an
`getYield()`	Two dimensional array (time x species)	Total yield of each spe
`sizeIntegral()`	Named vector (species) or two dimensional array (time x species)	Any integral over the

Writing your own summary function

The entry point is `sizeIntegral()`. It selects the size range, applies the bin-averaging appropriate to the model's `second_order_w()` setting and wraps the result in the right mizer array class, so a summary function built on it is automatically consistent with the quadrature the model is actually using. Pass the whole weighting factor $K(w)$ evaluated on the size grid, but neither the bin widths `params@dw` nor any bin-averaging of your own: `sizeIntegral()` supplies both.

If your quantity involves the predation kernel, take the kernel from `encounter_kernel()` rather than from `pred_kernel()`, and pair it with the plain point prey weight `params@w_full * params@dw_full`. That weight is a normalisation which the kernel construction is built to cancel, not a quadrature weight, so it is the one place where you must *not* bin-average. Pairing the point-sampled `pred_kernel()` with a bin-averaged prey weight applies the prey-bin integral twice.

See Also

indicator_functions, plotting_functions

---

superseded_accessors *Superseded* `get`*-prefixed aliases for values stored in a model*

Description

[Superseded]

Each of these functions is an alias for a function with a shorter name that returns exactly the same thing. The shorter name is the one that also has a replacement function (`catchability(params) <- value` and friends), so that is the name to use:

Superseded	Use instead
`getCatchability()`	`catchability()`
`getSelectivity()`	`selectivity()`
`getInitialEffort()`	`initial_effort()`
`getInteraction()`	`interaction_matrix()`
`getResourceDynamics()`	`resource_dynamics()`
`getResourceLevel()`	`resource_level()`
`getResourceRate()`	`resource_rate()`
`getResourceCapacity()`	`resource_capacity()`
`getPredKernel()`	`pred_kernel()`
`getSearchVolume()`	`search_vol()`
`getMaxIntakeRate()`	`intake_max()`
`getMetabolicRate()`	`metab()`
`getExtMort()`	`ext_mort()`
`getExtEncounter()`	`ext_encounter()`
`getMaturityProportion()`	`maturity()`
`getReproductionProportion()`	`repro_prop()`
`getReproductionLevel()`	`reproduction_level()`

The `get` prefix is reserved for the functions that *calculate* a rate from the current state of a model, like `getEncounter()` or `getFMort()`. The functions above only read back a value that is already stored in the MizerParams object, which is what the bare names say.

The old names are however not going away. They are plain aliases: they do not warn and they will keep working, so existing code and old scripts run unchanged. They are not used anywhere inside mizer and should not be used in new code.

Usage

```
getCatchability(params)

getSelectivity(params)

getInitialEffort(params)

getInteraction(params)

getResourceDynamics(params)

getResourceLevel(params)

getResourceRate(params)

getResourceCapacity(params)

getPredKernel(params)

getSearchVolume(params)

getMaxIntakeRate(params)

getMetabolicRate(params)

getExtMort(params)

getExtEncounter(params)

getMaturityProportion(params)

getReproductionProportion(params)

getReproductionLevel(params)
```

Arguments

`params`	A MizerParams object

Value

The same as the function it is an alias for.

`superseded_steady` *Superseded names for the steady-state finders*

Description

[Superseded]

Neither of these names says what distinguishes the two functions, and `projectToSteady()` returns a different class depending on an argument. Both have been replaced:

Superseded	Use instead
`steady()`	`tuneSteadyState()`
`projectToSteady()`	`findSteadyState()`, or `projectUntilSettled()` for the trajectory

The distinction the new names carry is what each one holds fixed. `tuneSteadyState()` holds the inputs to the fish dynamics — the reproduction rate and the resource — at the values you supply while the spectra settle, and then adjusts the parameters that generate them (`erepro`/`R_max` and `cc_pp`) so that those held values are steady too. That is what `steady()` always did. `findSteadyState()` changes no parameter and lets reproduction, the resource and the spectra settle together, which is what `projectToSteady()` did.

Each of the two also gained a `solver` argument, so the same job can be done either by running the dynamics (`solver = "project"`, the default and the old behaviour) or by solving the steady-state equation directly with a Newton-type root finder (`solver = "newton"`), which converges even at a dynamically unstable steady state.

The `return_sim` argument is gone from the new functions: `tuneSteadyState()` and `findSteadyState()` always return a `MizerParams` object and `projectUntilSettled()` always returns a `MizerSim`.

The old names are however not going away. They are thin wrappers that reproduce the old behaviour exactly, `return_sim` included: they do not warn and they will keep working, so existing code and old scripts run unchanged. They are not used anywhere inside mizer and should not be used in new code.

Usage

```
steady(
  params,
  t_max = 100,
  t_per = 1.5,
  dt = 0.1,
  t_save = dt,
  tol = 0.1 * dt,
  amplitude_tol = 0.01,
  amp_rel_tol = 0.01,
```

```
  extinction_threshold = 1e-06,
  return_sim = FALSE,
  preserve = c("reproduction_level", "erepro", "R_max"),
  progress_bar = TRUE,
  info_level = default_info_level(),
  method = c("euler", "predictor_corrector", "tr_bdf2")
)

projectToSteady(
  params,
  effort = params@initial_effort,
  distance_func = distanceSSLogN,
  t_per = 1.5,
  t_max = 100,
  dt = 0.1,
  t_save = dt,
  tol = 0.1 * t_per,
  amplitude_tol = 0.01,
  amp_rel_tol = 0.1,
  extinction_threshold = 1e-06,
  return_sim = FALSE,
  progress_bar = TRUE,
  info_level = default_info_level(),
  method = c("euler", "predictor_corrector", "tr_bdf2"),
  ...
)
```

Arguments

params	A MizerParams object
t_max	The maximum number of years to run the simulation. Default is 100.
t_per	The interval in years at which convergence is checked, and hence also the interval at which the trajectory is saved when `return_sim = TRUE`. In `projectUntilSettled()` these two roles have been separated into `t_check` and `t_save`.
dt	The time step to use in `project()`.
t_save	Has no effect. It briefly controlled how finely the biomass series used for limit-cycle detection was sampled; that series is now sampled at every time step, which is what its default `dt` gave.
tol	The simulation stops when the relative change in the egg production RDI over t_per years is less than tol for every species.
amplitude_tol	**[Experimental]** The minimum relative biomass amplitude for a persistent oscillation to be reported as a limit cycle rather than treated as an (effectively steady) fixed point. This is a fraction of mean biomass and is kept separate from `distance_tol` (which measures convergence to a fixed point on a different scale). Default `0.01`.
amp_rel_tol	**[Experimental]** Maximum relative change of amplitude between successive periods for the cycle to count as settled. Default `0.01`.

extinction_threshold
: **[Experimental]** A species is treated as going extinct, stopping the run, once its reproduction rate (RDD) falls below this fraction of its value at the start of the run. For example the default `1e-6` treats a species as extinct once its reproduction has collapsed to a millionth of its initial level. Because it is relative to the initial reproduction, a species that is present but starts with zero reproduction is flagged immediately, and (in `tuneSteadyState()`, where reproduction is held constant) a healthy species is never flagged. A species with no fish at the start is not tested.

return_sim
: If TRUE, the function returns the MizerSim object holding the result of the simulation run, saved at intervals of `t_per`. 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.

info_level
: Controls the amount of information messages that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.

method
: The numerical method to use for the consumer density update. See `project()`.

effort
: The fishing effort to use throughout. By default the initial effort stored in `params`.

distance_func
: A function that will be called at every check 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.

...
: Further arguments will be passed on to your distance function.

Value

A `MizerParams` object, or a `MizerSim` object if `return_sim = TRUE`, in either case carrying the `"convergence"` attribute described in `projectUntilSettled()`.

See Also

`tuneSteadyState()`, `findSteadyState()`, `projectUntilSettled()`

---

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.

See Also

`setPredKernel()`

Other predation kernel: `box_pred_kernel()`, `gaussian_mixture_pred_kernel()`, `lognormal_pred_kernel()`, `power_law_pred_kernel()`

Examples

```
params <- NS_params
species_params(params)$pred_kernel_type <- "truncated_lognormal"
plot(w_full(params), pred_kernel(params)["Cod", 10, ], type="l", log="x")
```

tuneSteadyState *Tune a model so that the state it is in becomes a steady state*

Description

[Experimental]

Solves for the consumer size spectra while holding the reproduction rate (RDD), the resource and any other components at the values stored in `params`, and then adjusts the parameters that generate those held values so that they are steady too. This is the function to use while setting up and calibrating a model: holding the inputs to the fish dynamics fixed is what makes the search reliable.

Usage

```
tuneSteadyState(
  params,
  solver = c("project", "newton"),
  effort = params@initial_effort,
  preserve = c("reproduction_level", "erepro", "R_max"),
  info_level = default_info_level(),
  ...
)
```

Arguments

`params`	A MizerParams object
`solver`	The solver to use: `"project"` to run the dynamics until they settle, `"newton"` to solve the steady-state equation directly. See *Choosing a solver*.
`effort`	The fishing effort to use throughout. By default the initial effort stored in `params`.
`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`.
`info_level`	Controls the amount of information messages that are shown. Higher levels lead to more messages, `info_level = 0` gives silence. The default is taken from the `mizer_info_level` option, see `default_info_level()`.
`...`	Arguments for the chosen solver. With `solver = "project"`: `t_max`, `t_check`, `dt`, `distance_tol`, `residual_tol`, `amplitude_tol`, `amp_rel_tol`, `extinction_threshold`, `progress_bar` and `method`, all as described in `projectUntilSettled()`. There is no `t_save`, because no trajectory is returned. Note that `distance_tol` here defaults to `0.1 * dt` and measures the largest relative change in egg production, because the distance function is `distanceMaxRelRDI()`. `residual_tol` is judged on the model as the search sees it, with reproduction, the resource and the other components pinned; the residual reported in the result is measured again on the model that is actually returned.

With solver = "newton": solver_tol (default 1e-6), a tolerance on the per-capita rate of change passed to nleqslv::nleqslv(). It was called residual_tol before mizer 3.3, a name that now belongs to the biomass drift criterion above; maxit (default 200); jacobian, either "update" (default, the Jacobian is computed once and then updated cheaply each iteration — nleqslv's "Broyden") or "recompute" (a numerical Jacobian at every iteration — nleqslv's "Newton"); global, the globalisation strategy (default "dbldog", a robust double-dogleg trust region); and verbose to trace the iterations.

Details

Concretely, three things are held fixed during the search and two parameters are re-derived afterwards:

- The reproduction rate is pinned at getRDD(params). Afterwards, if the model uses Beverton-Holt reproduction, setBevertonHolt() restores the density dependence so that it reproduces exactly that rate at the new spectra. Use preserve to say which of the reproduction parameters should be kept as it was.
- The resource abundance is held at initialNResource(params). Afterwards the resource capacity cc_pp is recomputed so that this abundance is a steady state of the resource under the new spectra. If the capacity had been set by hand (frozen), it is rebalanced and thereby unfrozen.
- Other components are held constant throughout and are not adjusted.

So the model you get back is at a fixed point of the *full* dynamics, with reproduction and the resource free, and getStability() can be applied to it directly. Contrast findSteadyState(), which changes no parameter and instead lets the reproduction rate and the resource move to wherever the parameters you already have put them.

Holding those inputs fixed is what makes the search reliable, but it does not make the result certain: the state that is stored is only as close to a fixed point as the solver's tolerance allowed, and with solver = "project" the run may instead have stopped on a limit cycle or on a species going extinct. Check the result rather than assuming it; see the section below.

Value

A MizerParams object with the initial state replaced by the steady state found, and with erepro/R_max and cc_pp adjusted as described above. It carries a "convergence" attribute describing the solution found; see projectUntilSettled(). Check it: convergence is not guaranteed.

Choosing a solver

solver = "project" (the default) runs the dynamics until they settle, via projectUntilSettled(), using distanceMaxRelRDI() as its distance function. It needs no extra packages and works with any resource dynamics.

solver = "newton" solves the steady-state equation directly with a Newton-type root finder from the nleqslv package. It converges even when the steady state is dynamically **unstable**, where the time-stepping solver cannot, and it discovers the support of the steady state automatically. It starts from the spectra in initialN(params), so a reasonable initial guess still matters — for example the spectra from a nearby stable parameterisation, or the (diverging) output of solver = "project".

Because the resource is held fixed either way, `solver = "newton"` here does not need the resource to be a semichemostat, unlike in `findSteadyState()` where the resource is one of the unknowns.

What you get back may not be a steady state

The stopping criterion is a proxy. It says that two states `t_per` years apart differ by less than `distance_tol` on whatever scale the criterion is measured on; it does not say that the state reached is a fixed point. There are four ways the returned object can fail to be one:

- the run converged on its own scale while the biomasses are still visibly drifting (`termination = "distance_tolerance"`);
- the run reached `t_max` without converging (`termination = "time_limit"`);
- the run settled on a limit cycle (`termination = "cycle_detected"`), in which case the state stored is one point on that cycle;
- the run stopped because a species was going extinct (`termination = "extinction"`).

So treat the result as a claim to be checked rather than as a guarantee:

```
attr(params, "convergence")$attractor  # "fixed_point", "limit_cycle" or NA
attr(params, "convergence")$residual   # largest biomass drift, in 1/year
isSteady(params)                       # TRUE if within tolerance
summary(params)                        # includes the biomass-drift verdict
plot(getSteadyResidual(params))        # which species, and at which sizes
```

`attractor` is the field that answers the question: it is `"fixed_point"` only where the measured biomass drift is within `residual_tol`, so it cannot be satisfied by a distance function that has merely gone quiet. `termination` says how the run ended and `converged` whether the solver met its own criterion; neither is a claim about the state. The last line says *where* the model is not steady, which is the one to reach for when it is not: a model that is off steady state is usually off in one species or one part of the size range, and the plot names it. See `getSteadyResidual()` for why the verdict is phrased in terms of biomass drift rather than the largest per-capita rate.

The messages this function prints say the same thing — a converged run whose biomasses are still moving reports the drift and adds "Reduce the tolerance on the distance function to converge further." — but they are suppressed by `info_level = 0`, so in a script the `"convergence"` attribute is the reliable check.

Finally, a genuine fixed point need not be a *stable* one. Use `getStability()` to find out, and `solver = "newton"` to converge onto a fixed point that the dynamics themselves would run away from.

See Also

`findSteadyState()`, `projectUntilSettled()`, `steadySingleSpecies()`, `isSteady()`, `getSteadyResidual()`, `getStability()`

Examples

```
params <- newTraitParams()
species_params(params)$gamma[5] <- 3000
params <- tuneSteadyState(params)
plotSpectra(params)
```

---

use_predation_diffusion

Get or set the use_predation_diffusion flag

Description

Controls whether predation-induced diffusion is included when calculating rates with `mizerDiffusion()`. When `FALSE` (the default), the predation-driven diffusion term is omitted, preserving the behaviour of previous mizer versions. Set to `TRUE` to enable the diffusion term from the jump-growth equation.

Usage

```
use_predation_diffusion(params)

use_predation_diffusion(params) <- value
```

Arguments

`params`	A MizerParams object.
`value`	A single logical value (`TRUE` or `FALSE`).

Value

`use_predation_diffusion()`: A single logical value.
`use_predation_diffusion<-`: A MizerParams object with the `use_predation_diffusion` flag updated.

See Also

Other functions for setting parameters: `gear_params()`, `setExtDiffusion()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`

valid_gears_arg *Helper function to assure validity of gears argument*

Description

If the gears argument contains invalid gears, then these are ignored but a warning is issued.

Usage

```
valid_gears_arg(object, gears = NULL, error_on_empty = FALSE)
```

Arguments

object	A MizerSim or MizerParams object from which the gears should be selected.
gears	The gears to be selected. Optional. By default all gears are selected. A vector of gear names.
error_on_empty	Whether to throw an error if there are zero valid gears. Default FALSE.

Value

A vector of gear names in the same order as supplied in gears, with invalid names removed. If gears is NULL, all gears are returned in the order stored in the model.

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,
  error_on_empty = 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.
`error_on_empty`	Whether to throw an error if there are zero valid species. 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.

`validEffortVector` *Make a valid effort vector*

Description

Make a valid effort vector

Usage

```
validEffortVector(effort, params)
```

Arguments

`effort`	A vector or scalar with the initial fishing effort, see Details below.
`params`	A MizerParams object.

Details

A valid effort vector is a named vector with one effort value for each gear. However you can also supply the effort value in different ways:

- 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 the default effort returned by `validEffortVector()`, which depends on the defaults edition.

These conversions are done by the function `validEffortVector()`.

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

See Also

`initial_effort()`

`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".

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 0.3 for all species.

Value

A valid gear parameter data frame

See Also

gear_params()

---

validParams *Validate MizerParams object and upgrade if necessary*

Description

Checks that the given MizerParams object is valid and upgrades it if necessary.

Usage

```
validParams(params, info_level = default_info_level())
```

Arguments

params	The MizerParams object to validate
info_level	Controls the amount of information messages and warnings that are shown. Higher levels lead to more messages, info_level = 0 gives silence. The default is taken from the mizer_info_level option, see default_info_level().

Details

It is possible to render a MizerParams object invalid by manually changing its slots. This function checks that the object is valid and if not it attempts to upgrade it to a valid object or gives an error message. If the object is valid then it is returned unchanged. The function reports an error if any of the rate arrays contain any non-finite numbers (except for the maximum intake rate that is allowed to be infinite).

Value

A valid MizerParams object

Cost of repeated calls

Because `validParams()` returns an already-valid object unchanged, it is safe to call it at the start of any function that takes a MizerParams object. To make that cheap, the repair work (rebuilding the species parameter tables and the `w_min_idx` and `ft_mask` slots, and checking the structural validity of the object) is skipped for an object that has already been through it. Mizer recognises such an object by a fingerprint calculated from the contents of the slots that the repair and the validity checks depend on. The fingerprint is recalculated on every call, so it cannot become stale: any change to any of those slots, made by any route, gives a new fingerprint and triggers the full validation.

The checks for non-finite values in the rate arrays are always performed, because the fingerprint does not cover the values in those arrays.

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 this function. It 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 `validSim()`.

This function uses `newMultispeciesParams()` to create a new MizerParams object using the parameters extracted from the old 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 `validParams()`. You can then save the new version again with `saveParams()`.

---

validSim — *Validate MizerSim object and upgrade if necessary*

Description

Checks that the given MizerSim object is valid and upgrades it if necessary. It also validates the embedded `MizerParams-class()` object with `validParams()`. If any entries of the consumer abundance array `sim@n` are non-finite, a warning is issued and the simulation is truncated at the last time step where `sim@n` is still finite.

Usage

```
validSim(sim)
```

Arguments

sim	The MizerSim object to validate

Details

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 this function.

This function adds the missing slots and fills them with default values. It also calls `validParams()` to upgrade the MizerParams object inside the MizerSim object. Any object from version 0.4 onwards can be upgraded.

Value

A valid 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 `validParams()`. You can then save the new version again with `saveParams()`.

---

validSpeciesParams *Validate species parameter data frame*

Description

These functions check the validity of a species parameter frame and, where necessary, make corrections. `validGivenSpeciesParams()` only checks and corrects the given species parameters but does not add default values for species parameters that were not provided. `validSpeciesParams()` first calls `validGivenSpeciesParams()` but then goes further by adding default values for species parameters that were not provided.

Usage

```
validSpeciesParams(species_params, check_misspellings = TRUE)

validGivenSpeciesParams(species_params, check_misspellings = TRUE)
```

Arguments

species_params The user-supplied species parameter data frame

check_misspellings

Whether to report column names that look like misspellings of standard species parameter names. TRUE by default.

validSpeciesParams() first calls validGivenSpeciesParams() but then goes further by adding default values for species parameters that were not provided. It only sets defaults for those species parameters that are not owned by a single rate-setting function, namely those that are read by several of them (n), that are used only when projecting (alpha), that determine the size grid (w_min, w_max), that are needed for the length-weight conversion (a, b) or that are used only for reporting (is_background). The function sets default values if any of the following species parameters are missing or NA:

- w_max is set to 1.5 * w_inf (it is only a computational boundary)
- w_repro_max is set to w_inf
- w_mat is set to w_inf/4
- w_min is set to 0.001
- alpha is set to 0.6
- n is set to 3/4
- a is set to 0.01
- b is set to 3
- is_background is set to FALSE

All other species parameters are given their default values by the rate-setting function that uses them, so that each default has a single home. For example p and k are set by setMetabolicRate(), z_ext, d and z0 by setExtMort(), E_ext by setExtEncounter(), D_ext by setExtDiffusion(), interaction_resource by setInteraction(), beta and sigma by setPredKernel(), q and gamma by setSearchVolume(), and erepro, m, w_mat25 and R_max by setReproduction(). These columns are therefore absent from the data frame returned by validSpeciesParams() but present in the species parameters of a MizerParams object, because setParams() calls all the rate-setting functions.

Note that the species parameters returned by these functions are not guaranteed to produce a viable model. More checks of the parameters are performed by the individual rate-setting functions (see setParams() for the list of these functions).

Details

validGivenSpeciesParams() checks the validity of the given species parameters. It throws an error if

- the species column does not exist or contains duplicates
- the asymptotic size w_inf is not specified for all species (but see the backwards-compatibility note below)

If a weight-based parameter is missing but the corresponding length-based parameter is given, as well as the a and b parameters for length-weight conversion, then the weight-based parameters are added. If both length and weight are given, then weight is used and an info_about_default condition is signalled if the two are inconsistent.

The required maximum-size parameter is w_inf, the von Bertalanffy asymptotic size of an average individual. For backwards compatibility, if no w_inf column is given, its values are taken from the w_repro_max column if that is present, or otherwise from the w_max column, and an informational message is issued. (w_repro_max is preferred over w_max because in earlier versions of mizer it was the size at which growth stopped and is therefore the closest analogue to the asymptotic size.)

Some inconsistencies in the size parameters are resolved as follows:

- Any w_mat that is not smaller than w_inf is set to w_inf / 4.
- Any w_mat25 that is not smaller than w_mat is marked as missing, as is the corresponding l_mat25, so that the default is used instead.
- Any w_min that is not smaller than w_mat is set to 0.001 or w_mat /10, whichever is smaller.
- Any w_repro_max that is not larger than w_mat is set to 4 * w_mat.

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.

The function tests for some typical misspellings of parameter names, like wrong capitalisation or missing underscores and issues a warning if it detects such a name. Pass check_misspellings = FALSE to skip that test, as mizer does when it re-validates a table it has already checked, so that the report is made once, when the column is introduced.

Value

For validSpeciesParams(): A valid species parameter data frame with additional parameters with default values.

For validGivenSpeciesParams(): A valid species parameter data frame without additional parameters.

See Also

species_params(), validGearParams(), validParams(), validSim()

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 maximum 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)
```

`with_info_level` *Collect and report the information signals raised while setting parameters*

Description

[Experimental] While mizer sets up or changes a model it raises conditions of class `info_about_default` to tell the user about the choices it made on their behalf and about the instructions it could not carry out. This function evaluates `expr` with a calling handler that collects those conditions and reports them together once `expr` has finished, so that the user gets one report rather than a stream of messages.

Usage

```
with_info_level(expr, info_level = default_info_level(), except = character())
```

Arguments

`expr`	The expression to evaluate. It is evaluated in the calling environment, so assignments made in it have the same effect as they would have without this wrapper.
`info_level`	The level of information to report, or `NA` to leave the reporting to a handler further out. Defaults to `default_info_level()`, which consults the `mizer_info_level` option.
`except`	A character vector of `vars` not to report on, for a caller that is going to say the same thing itself. Everything else raised inside `expr` is reported as usual.

Details

Each condition carries three fields, see signal_info():

- var names the quantity the report is about.
- level says how important it is, a low level meaning important and a high level meaning chatter. Only conditions with level at most info_level are reported.
- severity says how to report it: "info" conditions become a single message() and "warning" conditions a single warning().

The severity matters because species_params<-() runs suppressMessages() over its recalculation to quieten the routine chatter. A report that the user needs to see even there — that an instruction of theirs had no effect — must therefore be a warning, see signal_frozen().

Identical reports are collapsed, so a quantity that is reported on twice in the same call takes up one line, but two different things said about the same quantity are both kept.

Value

The value of expr.

Nesting

Handlers nest by themselves: while one is collecting, any handler installed further in steps aside and lets the outer one do the reporting. A function can therefore wrap its body in with_info_level() without knowing whether its caller has already done so, which is what allows every entry point to install a handler. info_level = NA asks for the same thing explicitly, for the rare case where a function wants to leave the reporting to a caller that has not installed a handler yet.

The reporting happens on exit, so a function can wrap its whole body even though it returns from the middle of it.

Silence is the exception to "the outermost handler decides": info_level = 0 drops the reports raised inside it even when a handler further out is collecting, so that a function can build something quietly as part of a larger job that does report.

Examples

```
# Wrap the body of a function that reports, and everything raised inside it
# is collected and given together once the call has finished.
myConstructor <- function(x, info_level = default_info_level()) {
    with_info_level(info_level = info_level, {
        signal_info("h", "No `h` provided, using a default.", level = 1)
        signal_info("gamma", "Calculating `gamma` from `f0`.")
        x
    })
}
myConstructor(1)

# `info_level = 1` keeps only the report that was marked important.
myConstructor(1, info_level = 1)

# `info_level = 0` is silence.
myConstructor(1, info_level = 0)
```

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