

# Package ‘mizer’

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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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**License** GPL-3

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'species\_params.R' 'setColours.R' 'setInteraction.R'  
'setPredKernel.R' 'setSearchVolume.R' 'setMaxIntakeRate.R'  
'setMetabolicRate.R' 'setMetadata.R' 'setExtMort.R'  
'setExtEncounter.R' 'setReproduction.R' 'setResource.R'  
'setFishing.R' 'setInitialValues.R' 'setBevertonHolt.R'  
'upgrade.R' 'selectivity\_funcs.R' 'pred\_kernel\_funcs.R'  
'resource\_dynamics.R' 'resource\_semichemostat.R'  
'resource\_logistic.R' 'project.R' 'mizer-package.R'  
'project\_methods.R' 'rate\_functions.R' 'summary\_methods.R'  
'plots.R' 'plotBiomassObservedVsModel.R'  
'plotYieldObservedVsModel.R' 'animateSpectra.R'  
'newMultispeciesParams.R' 'wrapper\_functions.R'  
'newSingleSpeciesParams.R' 'steady.R' 'extension.R' 'data.R'  
'RcppExports.R' 'deprecated.R' 'get\_initial\_n.R'  
'compareParams.R' 'customFunction.R' 'manipulate\_species.R'

'calibrate.R' 'match.R' 'matchGrowth.R' 'steadySingleSpecies.R'  
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mizer-package	<i>mizer: Multi-species size-based modelling in R</i>
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## 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>

---

addSpecies

*Add new species*

---

**Description****[Experimental]**

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

**Usage**

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

**Arguments**

<code>params</code>	A mizer params object for the original system.
<code>species_params</code>	Data frame with the species parameters of the new species we want to add to the system.
<code>gear_params</code>	Data frame with the gear parameters for the new species. If not provided then the new species will not be fished.
<code>initial_effort</code>	A named vector with the effort for any new fishing gear introduced in <code>gear_params</code> . 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.
<code>interaction</code>	Interaction matrix. A square matrix giving either the interaction coefficients between all species or only those between the new species. In the latter case all interaction between an old and a new species are set to 1. If this argument is missing, all interactions involving a new species are set to 1.

**Details**

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

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

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

**Value**

An object of type `MizerParams`

**See Also**

`removeSpecies()`

**Examples**

```
params <- newTraitParams()
species_params <- data.frame(
  species = "Mullet",
  w_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)

```

---

age\_mat *Calculate age at maturity*

---

### Description

Uses the growth rate and the size at maturity to calculate the age at maturity

### Usage

```
age_mat(params)
```

### Arguments

params            A MizerParams object

### Details

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

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

### 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

**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.

---

animateSpectra            *Animation of the abundance spectra*

---

**Description**

[Experimental]

**Usage**

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

**Arguments**

`sim`            A MizerSim object

`species`        Name or vector of names of the species to be plotted. By default all species are plotted.

`time_range`    The time range to animate over. Either a vector of values or a vector of min and max time. Default is the entire time range of the simulation.

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

`ylim`           A numeric vector of length two providing lower and upper limits for the y axis. Use NA to refer to the existing minimum or maximum. Any values below  $1e-20$  are always cut off.

power	The abundance is plotted as the number density times the weight raised to power. The default power = 1 gives the biomass density, whereas power = 2 gives the biomass density with respect to logarithmic size bins.
total	A boolean value that determines whether the total over all species in the system is plotted as well. Default is FALSE.
resource	A boolean value that determines whether resource is included. Default is TRUE.

**Value**

A plotly object

**See Also**

Other plotting functions: [plot,MizerParams,missing-method,plot,MizerSim,missing-method,plotBiomass\(\),plotDiet\(\),plotFMort\(\),plotFeedingLevel\(\),plotGrowthCurves\(\),plotPredMort\(\),plotSpectra\(\),plotYield\(\),plotYieldGear\(\),plotting\\_functions](#)

**Examples**

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

---

BevertonHoltRDD	<i>Beverton Holt function to calculate density-dependent reproduction rate</i>
-----------------	--

---

**Description**

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

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

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

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

Vector of density-dependent reproduction rates.

**See Also**

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

---

box_pred_kernel	<i>Box predation kernel</i>
-----------------	-----------------------------

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

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

**See Also**

[setPredKernel\(\)](#)

Other predation 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), getPredKernel(params)["Cod", 10, ], type="l", log="x")

```

---

calc_selectivity	<i>Calculate selectivity from gear parameters</i>
------------------	---

---

**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.

**Usage**

```
calc_selectivity(params)
```

**Arguments**

params            A MizerParams object

**Value**

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

**Examples**

```

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

```

---

calibrateBiomass	<i>Calibrate the model scale to match total observed biomass</i>
------------------	--

---

**Description**

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

**Usage**

```
calibrateBiomass(params)
```

**Arguments**

params            A MizerParams object

**Details**

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

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

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

**Value**

A MizerParams object

**Examples**

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

---

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

## 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://bit.ly/2YqXESV>.

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

## 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
params2 <- calibrateNumber(params)
```

---

calibrateYield	<i>Calibrate the model scale to match total observed yield</i>
----------------	--

---

## Description

**[Deprecated]**

## Usage

```
calibrateYield(params)
```

## Arguments

params            A MizerParams object

## Details

This function has been deprecated and will be removed in the future unless you have a use case for it. If you do have a use case for it, please let the developers know by creating an issue at <https://github.com/sizespectrum/mizer/issues>.

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

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

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

## Value

A MizerParams object

## Examples

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

---

compareParams

*Compare two MizerParams objects and print out differences*

---

## Description

**[Experimental]**

## Usage

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

## Arguments

params1	First MizerParams object
params2	Second MizerParams object

## Value

String describing the differences

## Examples

```
params1 <- NS_params
params2 <- params1
species_params(params2)$w_mat[1] <- 10
compareParams(params1, params2)
```



---

completeSpeciesParams *Alias for validSpeciesParams()*

---

## Description

### [Deprecated]

An alias provided for backward compatibility with mizer version  $\leq 2.5.2$

## Usage

```
completeSpeciesParams(species_params)
```

## Arguments

species\_params The user-supplied species parameter data frame

## Details

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

- the species column does not exist or contains duplicates
- the maximum size is not specified for all species

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 a warning is issued if the two are inconsistent.

If a w\_inf column is given but no w\_max then the value from w\_inf is used. This is for backwards compatibility. But note that the von Bertalanffy parameter w\_inf is not the maximum size of the largest individual, but the asymptotic size of an average individual.

Some inconsistencies in the size parameters are resolved as follows:

- Any w\_mat that is not smaller than w\_max is set to w\_max / 4.
- Any w\_mat25 that is not smaller than w\_mat is set to NA.
- 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.

validSpeciesParams() first calls validateGivenSpeciesParams() but then goes further by adding default values for species parameters that were not provided. The function sets default values if any of the following species parameters are missing or NA:

- `w_repro_max` is set to `w_max`
- `w_mat` is set to `w_max/4`
- `w_min` is set to `0.001`
- `alpha` is set to `0.6`
- `interaction_resource` is set to `1`
- `n` is set to `3/4`

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).

### 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\(\)](#)

---

constantEggRDI	<i>Choose egg production to keep egg density constant</i>
----------------	---

---

### Description

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

### Usage

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

### Arguments

<code>params</code>	A <code>MizerParams</code> object
<code>n</code>	A matrix of species abundances (species x size).
<code>e_growth</code>	A two dimensional array (species x size) holding the energy available for growth as calculated by <a href="#">mizerEGrowth()</a> .
<code>mort</code>	A two dimensional array (species x size) holding the mortality rate as calculated by <a href="#">mizerMort()</a> .
<code>...</code>	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\(\)](#)

---

constant_other	<i>Helper function to keep other components constant</i>
----------------	--

---

**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

---

customFunction	<i>Replace a mizer function with a custom version</i>
----------------	---

---

**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

**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)
```

---

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

**Value**

The current edition number.

---

default\_pred\_kernel\_params

*Set defaults for predation kernel parameters*

---

**Description**

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

**Usage**

`default_pred_kernel_params(object)`

**Arguments**

object            Either a MizerParams object or a species parameter data frame

**Value**

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

---

different	<i>Check whether two objects are different</i>
-----------	--

---

**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

---

distanceMaxReIRDI	<i>Measure distance between current and previous state in terms of RDI</i>
-------------------	--

---

**Description****[Experimental]**

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

**Usage**

```
distanceMaxReIRDI(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:  $\max(\text{abs}((\text{current\_rdi} - \text{previous\_rdi}) / \text{previous\_rdi}))$

**See Also**

Other distance functions: [distanceSSLogN\(\)](#)

---

distanceSSLogN	<i>Measure distance between current and previous state in terms of fish abundances</i>
----------------	--

---

**Description****[Experimental]**

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

**Usage**

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

**Arguments**

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

**Value**

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

**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

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.

**See Also**

[gear\\_params\(\)](#) for setting the selectivity parameters.

Other selectivity functions: [knife\\_edge\(\)](#), [sigmoid\\_length\(\)](#), [sigmoid\\_weight\(\)](#)

emptyParams

*Create empty MizerParams object of the right size***Description**

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

**Usage**

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

**Arguments**

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

---

finalN	<i>Size spectra at end of simulation</i>
--------	--

---

**Description**

Size spectra at end of simulation

**Usage**

```
finalN(sim)
```

```
finalNResource(sim)
```

```
idxFinalT(sim)
```

**Arguments**

`sim`                    A `MizerSim` object

**Value**

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

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

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))

```

---

finalNOther	<i>Values of other ecosystem components at end of simulation</i>
-------------	--

---

### Description

Values of other ecosystem components at end of simulation

### Usage

```
finalNOther(sim)
```

### Arguments

sim                    A MizerSim object

### Value

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

---

gear_params	<i>Gear parameters</i>
-------------	------------------------

---

### Description

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

### Usage

```

gear_params(params)

gear_params(params) <- value

```

### Arguments

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

## Details

The gear\_params data has one row for each gear-species pair and one column for each parameter that determines how that gear interacts with that species. 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.

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

## See Also

[validGearParams\(\)](#)

Other functions for setting parameters: [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

## Examples

```
params <- NS_params

# gears set up in example
gear_params(params)

# setting totally different gears
gear_params(params) <- data.frame(
  gear = c("gear1", "gear2", "gear1"),
  species = c("Cod", "Cod", "Haddock"),
  catchability = c(0.5, 2, 1),
  sel_fun = c("sigmoid_weight", "knife_edge", "sigmoid_weight"),
  sigmoidal_weight = c(1000, NA, 800),
  sigmoidal_sigma = c(100, NA, 100),
```

```

      knife_edge_size = c(NA, 1000, NA)
    )
  gear_params(params)

  # changing an individual entry
  gear_params(params)["Cod, gear1", "catchability"] <- 0.8

```

---

getBiomass	<i>Calculate the total biomass of each species within a size range at each time step.</i>
------------	---

---

### Description

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

### Usage

```
getBiomass(object, ...)
```

### Arguments

<code>object</code>	An object of class <code>MizerParams</code> or <code>MizerSim</code> .
<code>...</code>	Arguments passed on to <a href="#">get_size_range_array</a>
<code>min_w</code>	Smallest weight in size range. Defaults to smallest weight in the model.
<code>max_w</code>	Largest weight in size range. Defaults to largest weight in the model.
<code>min_l</code>	Smallest length in size range. If supplied, this takes precedence over <code>min_w</code> .
<code>max_l</code>	Largest length in size range. If supplied, this takes precedence over <code>max_w</code> .

### Value

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

### See Also

Other summary functions: [getDiet\(\)](#), [getGrowthCurves\(\)](#), [getN\(\)](#), [getSSB\(\)](#), [getYield\(\)](#), [getYieldGear\(\)](#)

**Examples**

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

---

getCommunitySlope      *Calculate the slope of the community abundance*

---

**Description**

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

**Usage**

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

**Arguments**

<code>sim</code>	A <a href="#">MizerSim</a> object
<code>species</code>	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.
<code>biomass</code>	Boolean. If TRUE (default), the abundance is based on biomass, if FALSE the abundance is based on numbers.
<code>...</code>	Arguments passed on to <a href="#">get_size_range_array</a>
<code>min_w</code>	Smallest weight in size range. Defaults to smallest weight in the model.
<code>max_w</code>	Largest weight in size range. Defaults to largest weight in the model.
<code>min_l</code>	Smallest length in size range. If supplied, this takes precedence over <code>min_w</code> .
<code>max_l</code>	Largest length in size range. If supplied, this takes precedence over <code>max_w</code> .

**Value**

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

**See Also**

Other functions for calculating indicators: [getMeanMaxWeight\(\)](#), [getMeanWeight\(\)](#), [getProportionOfLargeFish\(\)](#)

**Examples**

```

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

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

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

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

```

---

getComponent

*Get information about other ecosystem components*


---

**Description**

Get information about other ecosystem components

**Usage**

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

**Arguments**

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

**Value**

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



---

```
getCriticalFeedingLevel
```

*Get critical feeding level*

---

**Description**

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

**Usage**

```
getCriticalFeedingLevel(params)
```

**Arguments**

params            A MizerParams object

**Value**

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

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

**Arguments**

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

**Details**

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  $\theta_{ij}$  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.

**Value**

An array (predator species x predator size x (prey species + resource + other components)). Dimnames are "prey", "w", and "predator".

**See Also**

[plotDiet\(\)](#)

Other summary functions: [getBiomass\(\)](#), [getGrowthCurves\(\)](#), [getN\(\)](#), [getSSB\(\)](#), [getYield\(\)](#), [getYieldGear\(\)](#)

**Examples**

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

---

getEffort	<i>Fishing effort used in simulation</i>
-----------	--

---

**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**

<code>sim</code>	A MizerSim object
------------------	-------------------

**Value**

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

**Examples**

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

---

getEGrowth	<i>Get energy rate available for growth</i>
------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A two dimensional array (prey species x prey size)

**Your own growth rate function**

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

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

Your function will then be called instead of [mizerEGrowth\(\)](#), with the same arguments.

**See Also**

[getERepro\(\)](#), [getEReproAndGrowth\(\)](#)

Other rate functions: [getERepro\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFMortGear\(\)](#), [getFeedingLevel\(\)](#), [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	<i>Get encounter rate</i>
--------------	---------------------------

---

### Description

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

### Usage

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

### Arguments

params	A <a href="#">MizerParams</a> 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  $\theta_{ij}$  is set with `setInteraction()` and the resource interaction vector  $\theta_{ip}$  is taken from the `interaction_resource` column in `params@species_params`.

### Details

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

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

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

### Your own encounter function

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

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

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

### See Also

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

### Examples

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

---

getERepro

*Get energy rate available for reproduction*

---

### Description

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

**Usage**

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

**Arguments**

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

**Value**

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

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

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

**Your own reproduction rate function**

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

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

Your function will then be called instead of [mizerERepro\(\)](#), with the same arguments.

**See Also**

Other rate functions: [getEGrowth\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFMortGear\(\)](#), [getFeedingLevel\(\)](#), [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(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)

```

**Arguments**

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

**Value**

A two dimensional array (species x size) holding

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



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

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

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

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

### Your own energy rate function

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

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

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

### See Also

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

Other rate functions: `getEGrowth()`, `getERepro()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `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

**[Deprecated]** An alias provided for backward compatibility with `mizer` version  $\leq 1.0$

**Usage**

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

**Arguments**

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

**Value**

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

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

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

**Your own reproduction rate function**

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

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

Your function will then be called instead of [mizerERepro\(\)](#), with the same arguments.

**See Also**

Other rate functions: [getEGrowth\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFMortGear\(\)](#), [getFeedingLevel\(\)](#), [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	<i>Get feeding level</i>
-----------------	--------------------------

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

### Feeding level

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

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

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

### Your own feeding level function

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

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

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

### See Also

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `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))
```

---

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, effort, time_range, drop = TRUE)
```

**Arguments**

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

**Details**

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

**Value**

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

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

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

**Your own fishing mortality function**

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

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

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

**See Also**

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMortGear()`, `getFeedingLevel()`, `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, effort, time_range)
```

**Arguments**

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

**Value**

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

**Note**

Here: fishing mortality = catchability x selectivity x effort.

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

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

**See Also**

Other rate functions: [getEGrowth\(\)](#), [getERepro\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFeedingLevel\(\)](#), [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 <a href="#">MizerSim</a> object, uses the growth rates at the final time of a simulation to calculate the size at age. If given a <a href="#">MizerParams</a> 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\(\)](#), [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**

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

**Usage**

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



**Arguments**

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

**Value**

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

**Your own predation mortality function**

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

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

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

**See Also**

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `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

**[Deprecated]** An alias provided for backward compatibility with mizer version  $\leq 1.0$

## Usage

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

## Arguments

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

## Value

A vector of mortality rate by resource size.

## Your own resource mortality function

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

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

Your function will then be called instead of [mizerResourceMort\(\)](#), with the same arguments.

**See Also**

Other rate functions: [getEGrowth\(\)](#), [getERepro\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFMortGear\(\)](#), [getFeedingLevel\(\)](#), [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, ])
```

---

<code>getMeanMaxWeight</code>	<i>Calculate the mean maximum weight of the community</i>
-------------------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

<code>sim</code>	A <a href="#">MizerSim</a> object
<code>species</code>	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.
<code>measure</code>	The measure to return. Can be 'numbers', 'biomass' or 'both'
<code>...</code>	Arguments passed on to <a href="#">get_size_range_array</a>
	<code>min_w</code> Smallest weight in size range. Defaults to smallest weight in the model.
	<code>max_w</code> Largest weight in size range. Defaults to largest weight in the model.
	<code>min_l</code> Smallest length in size range. If supplied, this takes precedence over <code>min_w</code> .
	<code>max_l</code> Largest length in size range. If supplied, this takes precedence over <code>max_w</code> .

**Value**

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

**See Also**

Other functions for calculating indicators: [getCommunitySlope\(\)](#), [getMeanWeight\(\)](#), [getProportionOfLargeFish\(\)](#)

**Examples**

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

---

getMeanWeight

*Calculate the mean weight of the community*

---

**Description**

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

**Usage**

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

**Arguments**

sim	A <a href="#">MizerSim</a> 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 <a href="#">get_size_range_array</a>
min_w	Smallest weight in size range. Defaults to smallest weight in the model.
max_w	Largest weight in size range. Defaults to largest weight in the model.
min_l	Smallest length in size range. If supplied, this takes precedence over min_w.
max_l	Largest length in size range. If supplied, this takes precedence over max_w.

**Value**

A vector containing the mean weight of the community through time

**See Also**

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

**Examples**

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

---

getMort

*Get total mortality rate*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

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

**Your own mortality function**

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

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

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

**See Also**

`getPredMort()`, `getFMort()`

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `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 <a href="#">get_size_range_array</a>
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 vector with the numbers for each species in the model. If called with a MizerSim object, an array (time x species) containing the numbers at each time step for all species.

**See Also**

Other summary functions: [getBiomass\(\)](#), [getDiet\(\)](#), [getGrowthCurves\(\)](#), [getSSB\(\)](#), [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"]
```

---

getParams

*Extract the parameter object underlying a simulation*


---

**Description**

Extract the parameter object underlying a simulation

**Usage**

```
getParams(sim)
```

**Arguments**

sim	A MizerSim object
-----	-------------------

**Value**

The MizerParams object that was used to run the simulation

**Examples**

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

---

getPhiPrey

*Get available energy*

---

**Description****[Deprecated]**

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

**Usage**

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

**Arguments**

object	An <a href="#">MizerParams</a> object
n	A matrix of species abundances (species x size)
n_pp	A vector of the background abundance by size
...	Other arguments (currently unused)

**Value**

A two dimensional array (predator species x predator size)

**See Also**

[project\(\)](#)

**Examples**

```
params <- NS_params
sim <- project(params, t_max = 20, effort = 0.5)
n <- sim@n[21,,]
n_pp <- sim@n_pp[21,]
getPhiPrey(params,n,n_pp)
# ->
getEncounter(params) / getSearchVolume(params)
```



---

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:

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

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

### Usage

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

### Arguments

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

### Value

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

### Your own predation mortality function

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

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

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

**See Also**

Other rate functions: [getEGrowth\(\)](#), [getERepro\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFMortGear\(\)](#), [getFeedingLevel\(\)](#), [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

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

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

**Usage**

```

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

```



---

```
getProportionOfLargeFish
```

*Calculate the proportion of large fish*

---

### Description

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

### Usage

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

### Arguments

<code>sim</code>	A <a href="#">MizerSim</a> object
<code>species</code>	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.
<code>threshold_w</code>	the size used as the cutoff between large and small fish. Default value is 100.
<code>threshold_l</code>	the size used as the cutoff between large and small fish.
<code>biomass_proportion</code>	a boolean value. If TRUE the proportion calculated is based on biomass, if FALSE it is based on numbers of individuals. Default is TRUE.
<code>...</code>	Arguments passed on to <a href="#">get_size_range_array</a>
<code>min_w</code>	Smallest weight in size range. Defaults to smallest weight in the model.
<code>max_w</code>	Largest weight in size range. Defaults to largest weight in the model.
<code>min_l</code>	Smallest length in size range. If supplied, this takes precedence over <code>min_w</code> .
<code>max_l</code>	Largest length in size range. If supplied, this takes precedence over <code>max_w</code> .

**Value**

A vector containing the proportion of large fish through time

**See Also**

Other functions for calculating indicators: [getCommunitySlope\(\)](#), [getMeanMaxWeight\(\)](#), [getMeanWeight\(\)](#)

**Examples**

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

---

getRates

*Get all rates*


---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

- encounter from [mizerEncounter\(\)](#)
- feeding\_level from [mizerFeedingLevel\(\)](#)
- e from [mizerEReproAndGrowth\(\)](#)
- e\_repro from [mizerERepro\(\)](#)
- e\_growth from [mizerEGrowth\(\)](#)
- pred\_rate from [mizerPredRate\(\)](#)
- pred\_mort from [mizerPredMort\(\)](#)
- f\_mort from [mizerFMort\(\)](#)
- mort from [mizerMort\(\)](#)
- rdi from [mizerRDI\(\)](#)
- rdd from [BevertonHoltRDD\(\)](#)
- resource\_mort from [mizerResourceMort\(\)](#)

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

**Value**

List of rates.

**See Also**

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

**Examples**

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

---

getRDD

*Get density dependent reproduction rate*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A numeric vector the length of the number of species.

**See Also**

[getRDI\(\)](#)

Other rate functions: [getEGrowth\(\)](#), [getERepro\(\)](#), [getEReproAndGrowth\(\)](#), [getEncounter\(\)](#), [getFMort\(\)](#), [getFMortGear\(\)](#), [getFeedingLevel\(\)](#), [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(
  params,
  n = initialN(params),
  n_pp = initialNResource(params),
  n_other = initialNOther(params),
  t = 0,
  ...
)
```

### Arguments

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

### Details

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

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

Used by [getRDD\(\)](#) to calculate the actual, density dependent rate. See [setReproduction\(\)](#) for more details.

### Value

A numeric vector the length of the number of species.



**Your own reproduction function**

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

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

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

**See Also**

`getRDD()`

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `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)
```

---

`getReproductionLevel` *Get reproduction level*

---

**Description**

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

**Usage**

```
getReproductionLevel(params)
```

**Arguments**

`params` A `MizerParams` object

**Value**

A named vector with the reproduction level for each species.

**Examples**

```

getReproductionLevel(NS_params)

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

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

```

---

getResourceMort	<i>Get predation mortality rate for resource</i>
-----------------	--

---

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

**Value**

A vector of mortality rate by resource size.

### Your own resource mortality function

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

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

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

### See Also

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `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, ])
```

---

getSSB

*Calculate the SSB of species*

---

### Description

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

### Usage

```
getSSB(object)
```

### Arguments

object            An object of class MizerParams or MizerSim'.

### Value

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

**See Also**

Other summary functions: [getBiomass\(\)](#), [getDiet\(\)](#), [getGrowthCurves\(\)](#), [getN\(\)](#), [getYield\(\)](#), [getYieldGear\(\)](#)

**Examples**

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

---

getTimes	<i>Times for which simulation results are available</i>
----------	---

---

**Description**

Times for which simulation results are available

**Usage**

```
getTimes(sim)
```

**Arguments**

sim                    A MizerSim object

**Value**

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

**Examples**

```
getTimes(NS_sim)
```

---

getYield	<i>Calculate the rate at which biomass of each species is fished</i>
----------	--

---

**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:

$$C = \int_{t_1}^{t_2} y_i(t) dt$$

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

**See Also**

`getYieldGear()`

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

**Examples**

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

# Running simulation for another year, saving intermediate time steps
params <- setInitialValues(getParams(NS_sim), 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 get the total catch in the year by averaging over the year
sum(getYield(sim)[1:10, "Herring"] / 10)
```

---

getYieldGear	<i>Calculate the rate at which biomass of each species is fished by each gear</i>
--------------	---

---

### 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\(\)](#), [getYield\(\)](#)

### Examples

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

---

getZ	<i>Alias for getMort()</i>
------	----------------------------

---

### Description

**[Deprecated]** An alias provided for backward compatibility with mizer version  $\leq 1.0$

### Usage

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

### Arguments

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

### Details

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

### Value

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

### Your own mortality function

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

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

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

### See Also

`getPredMort()`, `getFMort()`

Other rate functions: `getEGrowth()`, `getERepro()`, `getEReproAndGrowth()`, `getEncounter()`, `getFMort()`, `getFMortGear()`, `getFeedingLevel()`, `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"]
```

---

get_f0_default	<i>Get default value for f0</i>
----------------	---------------------------------

---

### Description

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

### Usage

```
get_f0_default(params)
```

### Arguments

`params`            A MizerParams object

### Details

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



**Value**

A vector with the values of  $f_0$  for all species

**See Also**

Other functions calculating defaults: [get\\_gamma\\_default\(\)](#), [get\\_h\\_default\(\)](#), [get\\_ks\\_default\(\)](#)

---

get_gamma_default	<i>Get default value for gamma</i>
-------------------	------------------------------------

---

**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

**Value**

A vector with the values of gamma for all species

**See Also**

Other functions calculating defaults: [get\\_f0\\_default\(\)](#), [get\\_h\\_default\(\)](#), [get\\_ks\\_default\(\)](#)

---

get_initial_n	<i>Calculate initial population abundances</i>
---------------	--

---

**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 <a href="#">MizerParams</a> .
n0_mult	Multiplier for the abundance at size 0. Default value is kappa/1000.
a	A parameter with a default value of 0.35.

**Value**

A matrix (species x size) of population abundances.

**Examples**

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

---

get_ks_default	<i>Get default value for ks</i>
----------------	---------------------------------

---

**Description**

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

**Usage**

```
get_ks_default(params)
```

**Arguments**

params	A MizerParams object
--------	----------------------

**Value**

A vector with the values of ks for all species

**See Also**

Other functions calculating defaults: [get\\_f0\\_default\(\)](#), [get\\_gamma\\_default\(\)](#), [get\\_h\\_default\(\)](#)

---

get_phi	<i>Get values from feeding kernel function</i>
---------	--

---

**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**

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

**Value**

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

---

get_required_reproduction	<i>Determine reproduction rate needed for initial egg abundance</i>
---------------------------	---

---

**Description**

Determine reproduction rate needed for initial egg abundance

**Usage**

```
get_required_reproduction(params)
```

**Arguments**

<code>params</code>	A <code>MizerParams</code> object
---------------------	-----------------------------------

**Value**

A vector of reproduction rates for all species

---

get\_size\_range\_array *Get size range array*

---

### Description

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

### Usage

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

### Arguments

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

### Value

Boolean array (species x size)

### Length to weight conversion

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

$$w = al^b.$$

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

---

get\_time\_elements      *Get\_time\_elements*

---

### Description

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

### Usage

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

### Arguments

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

### Value

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

---

indicator\_functions      *Description of indicator functions*

---

### Description

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

### Details

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

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

### See Also

[summary\\_functions](#), [plotting\\_functions](#)

---

initialN<-	<i>Initial values for fish spectra</i>
------------	--

---

**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**

A matrix 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", ]
# Calculating the corresponding initial biomass
biomass <- initialN(params)["Cod", ] * dw(NS_params) * w(NS_params)
# Of course this initial state will no longer be a steady state
params <- steady(params)
```

---

`initialNOther<-`      *Initial values for other ecosystem components*

---

**Description**

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

**Usage**

```
initialNOther(params) <- value
initialNOther(object)
```

**Arguments**

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

**Value**

A named list with the initial values of other ecosystem components

**See Also**

[initialNResource\(\)](#), [initialN\(\)](#)

---

`initialNResource<-`      *Initial value for resource spectrum*

---

**Description**

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

**Usage**

```
initialNResource(params) <- value
initialNResource(object)
```

**Arguments**

<code>params</code>	A <code>MizerParams</code> object
<code>value</code>	A vector with the initial number densities for the resource spectrum
<code>object</code>	An object of class <code>MizerParams</code> or <code>MizerSim</code>

**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)
# Of course this initial state will no longer be a steady state
params <- steady(params)
```

---

<code>initial_effort</code>	<i>Initial fishing effort</i>
-----------------------------	-------------------------------

---

**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

validEffortVector(effort, params)
```

**Arguments**

<code>params</code>	A MizerParams object
<code>value</code>	A vector or scalar with the initial fishing effort, see Details below.
<code>effort</code>	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 zero.

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

Effort vector

---

inter

*Alias for NS\_interaction*

---

## Description

**[Deprecated]** An alias provided for backward compatibility with mizer version  $\leq 2.3$

## Usage

inter

## Format

A 12 x 12 matrix.

## Source

Blanchard et al.

---

knife_edge	<i>Weight based knife-edge selectivity function</i>
------------	---

---

### 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

### 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\(\)](#), [sigmoid\\_length\(\)](#), [sigmoid\\_weight\(\)](#)

---

l2w	<i>Length-weight conversion</i>
-----	---------------------------------

---

### 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, params)
```

```
w2l(w, params)
```

**Arguments**

l	Lengths in cm. Either a single number used for all species or a vector with one number for each 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. If any a or b parameters are missing the default values  $a = 0.01$  and  $b = 3$  are used for the missing values.

**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  $\beta_i$  is the preferred predator-prey mass ratio and  $\sigma_i$  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\(\)](#), [power\\_law\\_pred\\_kernel\(\)](#), [truncated\\_lognormal\\_pred\\_kernel\(\)](#)

**Examples**

```
params <- NS_params
plot(w_full(params), getPredKernel(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), getPredKernel(params)["Cod", 10, ], type="l", log="x")
```

---

matchBiomasses

*Match biomasses to observations*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

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

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

## Value

A `MizerParams` object

## Examples

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

---

matchGrowth

*Adjust model to produce observed growth*

---

## Description

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"))
```

## Arguments

<code>params</code>	A <code>MizerParams</code> object
<code>species</code>	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.
<code>keep</code>	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.

**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`.

---

<code>matchNumbers</code>	<i>Match numbers to observations</i>
---------------------------	--------------------------------------

---

**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)
```

**Arguments**

<code>params</code>	A <code>MizerParams</code> object
<code>species</code>	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.

**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 `steady()` 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://bit.ly/2YqXESV>.

Before you can use this function you will need to have added a `number_observed` column to your model which gives the observed number in grams. 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)
```

---

matchYields

*Match yields to observations*

---

**Description**

**[Deprecated]** This function has been deprecated and will be removed in the future unless you have a use case for it. If you do have a use case for it, please let the developers know by creating an issue at <https://github.com/sizespectrum/mizer/issues>.

**Usage**

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

**Arguments**

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

**Details**

If you want to match the yields to observations, you should use the `matchYield()` function from the `mizerExperimental` package instead, which adjusts the catchability to match the yield rather than by adjusting the biomass.

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

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

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

**Value**

A MizerParams object

**Examples**

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

---

mizerEGrowth	<i>Get energy rate available for growth needed to project standard mizer model</i>
--------------	--

---

**Description**

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

**Usage**

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

**Arguments**

params	A <a href="#">MizerParams</a> 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 <code>getERepro()</code> .
e	The energy available for reproduction and growth as calculated by <code>getEReproAndGrowth()</code> .
...	Unused

**Value**

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



### Your own growth rate function

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

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

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

### See Also

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

---

mizerEncounter	<i>Get encounter rate needed to project standard mizer model</i>
----------------	--

---

### Description

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

### Usage

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

### Arguments

<code>params</code>	A <code>MizerParams</code> object
<code>n</code>	A matrix of species abundances (species x size).
<code>n_pp</code>	A vector of the resource abundance by size
<code>n_other</code>	A list of abundances for other dynamical components of the ecosystem
<code>t</code>	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
<code>...</code>	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  $\theta_{ij}$  is set with `setInteraction()` and the resource interaction vector  $\theta_{ip}$  is taken from the `interaction_resource` column in `params@species_params`.

### Details

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

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

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

### Your own encounter function

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

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

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

### See Also

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

---

mizerERepro	<i>Get energy rate available for reproduction needed to project standard mizer model</i>
-------------	--

---

### Description

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

### Usage

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

### Arguments

params	A <a href="#">MizerParams</a> 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 <code>mizerEReproAndGrowth()</code> .
...	Unused

### Value

A two dimensional array (species x size) holding

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

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

### Your own reproduction rate function

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

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

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

**See Also**

Other mizer rate functions: [mizerEGrowth\(\)](#), [mizerEReproAndGrowth\(\)](#), [mizerEncounter\(\)](#), [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**

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

**Arguments**

params	A <a href="#">MizerParams</a> 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 <a href="#">getEncounter()</a> .
feeding_level	An array (species x size) with the feeding level as calculated by <a href="#">getFeedingLevel()</a> .
...	Unused

**Value**

A two dimensional array (species x size) holding

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

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

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

where  $h_i$  is the maximum intake rate, set with `setMaxIntakeRate()`. The assimilation rate  $\alpha_i$  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()`

---

<code>mizerFeedingLevel</code>	<i>Get feeding level needed to project standard mizer model</i>
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---

**Description**

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

**Usage**

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

**Arguments**

params	A <a href="#">MizerParams</a> 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	<i>Get the total fishing mortality rate from all fishing gears</i>
------------	--

---

### Description

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

### Usage

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

### Arguments

params	A <a href="#">MizerParams</a> 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 <a href="#">getEGrowth()</a> . Unused.
pred_mort	A two dimensional array (species x size) with the predation mortality as calculated by <a href="#">getPredMort()</a> . 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 <a href="#">MizerParams</a> object
effort	A vector with the effort for each fishing gear.

**Value**

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

**Note**

Here: fishing mortality = catchability x selectivity x effort.

**See Also**

[setFishing\(\)](#)

Other mizer rate functions: [mizerEGrowth\(\)](#), [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

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

### Arguments

params	A <a href="#">MizerParams</a> 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	<i>Alias for set_multispecies_model()</i>
-------------	---

---

**Description**

**[Deprecated]** An alias provided for backward compatibility with mizer version  $\leq 1.0$

**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**

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

q	Allometric exponent of search volume
f $\theta$	Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.
kappa	The coefficient of the initial resource abundance power-law.
lambda	Used to set power-law exponent for resource capacity if the resource_capacity argument is given as a single number.
r_pp	<b>[Deprecated]</b> . Use resource_rate argument instead.
...	Unused

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

time\_created A POSIXct date-time object with the creation time.

time\_modified A POSIXct date-time object with the last modified time.

w The size grid for the fish part of the spectrum. An increasing vector of weights (in grams) running from the smallest egg size to the largest 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()`.
- `pred_kernel` An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If this is NA then the following two slots will be used. Changed with `setPredKernel()`.
- `ft_pred_kernel_e` An array (species x log of predator/prey size ratio) that holds the Fourier transform of the feeding kernel in a form appropriate for evaluating the encounter rate integral. If this is NA then the `pred_kernel` will be used to calculate the available energy integral. Changed with `setPredKernel()`.
- `ft_pred_kernel_p` An array (species x log of predator/prey size ratio) that holds the Fourier transform of the feeding kernel in a form appropriate for evaluating the predation mortality integral. If this is NA then the `pred_kernel` will be used to calculate the integral. Changed with `setPredKernel()`.
- `rr_pp` A vector the same length as the `w_full` slot. The size specific growth rate of the resource spectrum.
- `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,  $\theta_{ij}$ . 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` **[Experimental]** Abundance multipliers.
- `linecolour` A named vector of colour values, named by species. Used to give consistent colours in plots.
- `linetype` A named vector of linetypes, named by species. Used to give consistent line types in plots.
- `ft_mask` An array (species x `w_full`) with zeros for weights larger than the maximum weight of each species. Used to efficiently minimize wrap-around errors in Fourier transform calculations.

**See Also**

[project\(\)](#) [MizerSim\(\)](#) [emptyParams\(\)](#) [newMultispeciesParams\(\)](#) [newCommunityParams\(\)](#) [newTraitParams\(\)](#)

---

mizerPredMort	<i>Get total predation mortality rate needed to project standard mizer model</i>
---------------	--

---

### Description

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

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

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

### Usage

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

### Arguments

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

### Value

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

### Your own predation mortality function

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

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

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

**See Also**

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

---

mizerPredRate	<i>Get predation rate needed to project standard mizer model</i>
---------------	--

---

**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

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

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

**Usage**

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

**Arguments**

params	A <a href="#">MizerParams</a> 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 <a href="#">getFeedingLevel()</a> .
...	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.

### Usage

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

### Arguments

<code>params</code>	A <a href="#">MizerParams</a> object
<code>n</code>	A matrix of species abundances (species x size).
<code>n_pp</code>	A vector of the resource abundance by size
<code>n_other</code>	A list of abundances for other dynamical components of the ecosystem
<code>t</code>	The time for which to do the calculation (Not used by standard mizer rate functions but useful for extensions with time-dependent parameters.)
<code>effort</code>	The effort for each fishing gear
<code>rates_fns</code>	Named list of the functions to call to calculate the rates. Note that this list holds the functions themselves, not their names.
<code>...</code>	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	<i>Get density-independent rate of reproduction needed to project standard mizer model</i>
----------	--

---

**Description**

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

**Usage**

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

**Arguments**

params	A <a href="#">MizerParams</a> 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 <a href="#">getEGrowth()</a> . Unused.
mort	An array (species x size) with the mortality rate as calculated by <a href="#">getMort()</a> . Unused.
e_repro	An array (species x size) with the energy available for reproduction as calculated by <a href="#">getERepro()</a> .
...	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  $\epsilon$  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	<i>Get predation mortality rate for resource needed to project standard mizer model</i>
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---

### Description

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

### Usage

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

### Arguments

params	A <a href="#">MizerParams</a> 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\(\)](#)

---

MizerSim	<i>Constructor for the MizerSim class</i>
----------	---

---

### 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

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

### Value

An object of type [MizerSim](#)

---

MizerSim-class	<i>A class to hold the results of a simulation</i>
----------------	--

---

### Description

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

### Details

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

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

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

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

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

### Slots

`params` An object of type `MizerParams`.

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

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

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

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

---

 N

*Time series of size spectra*


---

### Description

Fetch the simulation results for the size spectra over time.

### Usage

```
N(sim)
```

```
NResource(sim)
```

### Arguments

`sim` A `MizerSim` object

### Value

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

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

### Examples

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

---

needs_upgrading	<i>Determine whether a MizerParams or MizerSim object needs to be upgraded</i>
-----------------	--

---

**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	<i>Set up parameters for a community-type model</i>
--------------------	---

---

**Description**

This function 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
)

```

### 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.
h	The coefficient of the maximum food intake rate.
gamma	Volumetric search rate. Estimated using h, f0 and kappa if not supplied.
beta	The preferred predator prey mass ratio.
sigma	The width of the prey preference.
n	The allometric growth exponent. Used as allometric exponent for the maximum intake rate of the community as well as the intrinsic growth rate of the resource.
kappa	The coefficient of the initial resource abundance power-law.
lambda	Used to set power-law exponent for resource capacity if the resource_capacity argument is given as a single number.
r_pp	<b>[Deprecated]</b> . Use resource_rate argument instead.
knife_edge_size	The size at the edge of the knife-edge-selectivity function.
reproduction	The constant reproduction in the smallest size class of the community spectrum. By default this is set so that the community spectrum is continuous with the resource spectrum.

### Details

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

- Species identities of individuals are ignored. All are aggregated into a single community.
- The resource spectrum only extends to the start of the community spectrum.
- Reproductive rate is constant, independent of the energy invested in reproduction, which is set to 0.
- Standard metabolism is turned off (the parameter ks is set to 0). Consequently, the growth rate is now determined solely by the assimilated food

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

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

### Value

An object of type `MizerParams`

### References

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

### See Also

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

### Examples

```
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,
  info_level = 3,
  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 is only used if metab is not given explicitly and if the exponent is not specified in a p column in the species_params.
ext_mort	Optional. An array (species x size) holding the external mortality rate. 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 a column in the species data frame, it is calculated as $z0pre * w\_max ^ z0exp$ . Default value is 0.6.
z0exp	If z0, the mortality from other sources, is not a column in the species data frame, it is calculated as $z0pre * w\_max ^ z0exp$ . Default value is n-1.
ext_encounter	Optional. An array (species x size) holding the external encounter rate. If not supplied, the external encounter rate is left unchanged. Initially is set to 0.
maturity	Optional. An array (species x size) that holds the proportion of individuals of each species at size that are mature. If not supplied, a default is set as described in the section "Setting reproduction".
repro_prop	Optional. An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. If not supplied, a default is set as described in the section "Setting reproduction".
RDD	The name of the function calculating the density-dependent reproduction rate from the density-independent rate. Defaults to " <a href="#">BevertonHoltRDD()</a> ".
kappa	The coefficient of the initial resource abundance power-law.
n	The allometric growth exponent. This can be overruled for individual species by including a n column in the species_params.
resource_rate	Optional. Vector of resource intrinsic birth rates or coefficient in the power-law for the birth rate, see Details. Must be strictly positive.
resource_capacity	Optional. Vector of resource intrinsic carrying capacities or coefficient in the power-law for the capacity, see Details. The resource capacity must be larger 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 only if resource_capacity is given as a single number.
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.
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.
z0	<b>[Deprecated]</b> Use ext_mort instead. Not to be confused with the species_parameter z0.
r_pp	<b>[Deprecated]</b> . 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\_max column with the maximum sizes of the species in grams. (You could alternatively specify the maximum length in cm in an l\_max column.)

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 ( $\kappa$ ) and exponent `-lambda` ( $-\lambda$ ):

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

for all  $w$  less than `w_pp_cutoff` and zero for larger sizes.

### 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  $\theta_{ij}$  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 warn if it is different. One way of creating your own interaction matrix is to enter the data using a spreadsheet program and saving it as a `.csv` file. The data can 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. An alternative `pred_kernel` type is "box", implemented by the function `box_pred_kernel()`, and "power\_law", implemented by the function `power_law_pred_kernel()`. These functions require certain species parameters in the `species_params` data frame. For the lognormal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`. They are explained in the help pages for the kernel functions. Except for `beta` and `sigma`, no defaults are set for these parameters. If they are missing from the `species_params` data frame then `mizer` will issue an error message.

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

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

### Kernel dependent on both predator and prey size

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

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

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

### Setting search volume

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

The name "search volume" is a bit misleading, because  $\gamma_i(w)$  does not have units of volume. It is simply a parameter that determines the rate of predation. Its units depend on your choice, see section "Units in mizer". If you have chosen to work with total abundances, then it is a rate with units 1/year. If you have chosen to work with abundances per m<sup>2</sup> then it has units of m<sup>2</sup>/year. If you have chosen to work with abundances per m<sup>3</sup> then it has units of m<sup>3</sup>/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  $\gamma_i$  (the search volume at 1g) and  $q_i$  (the allometric exponent of the search volume) are taken from the `gamma` and `q` columns in the species parameter dataframe. If the `gamma` column is not supplied in the species parameter dataframe, a default is calculated by the `get_gamma_default()` function. Note that only for predators of size  $w = 1$  gram is the value of the species parameter  $\gamma_i$  the same as the value of the search volume  $\gamma_i(w)$ .

### Setting maximum intake rate

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

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

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

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

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

### Setting metabolic rate

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

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

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

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

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

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

### Setting external mortality rate

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

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

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

$$z_{0,i} = z_{0pre,i} w_{inf}^{z_{0exp}}.$$

### 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\(\)](#).

### Setting reproduction

For each species and at each size, the proportion  $\psi$  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 all the energy is invested into reproduction and therefore all growth stops. There can be no fish larger than `w_repro_max`. If you have not specified the `w_repro_max` column in the species parameter data frame, then the maximum size `w_max` 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:

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

(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 maximum weight in the `w_max` 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 1 only asymptotically. Mizer instead sets the function equal to 1 already at a size taken from the `w_repro_max` column in the species parameter data frame, if it exists, or otherwise from the `w_max` column. Also, for computational simplicity, any proportion smaller than  $1e-8$  is set to  $\emptyset$ .

**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

$$\text{repro\_prop}(w) = \left( \frac{w}{w_{mat_{max}}} \right)^{m-n}.$$

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

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

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

**Reproductive efficiency:** The reproductive efficiency  $\epsilon$ , 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 has a 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 150 and 125 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 150 and 125 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

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.

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 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 growth rate for each size class. Alternatively it can be a single number, which is then used as the coefficient in a power law: then the intrinsic growth 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, which is then used as the coefficient in a truncated power law: then the intrinsic growth rate  $c_R(w)$  at size  $w$  is set to

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

for all  $w$  less than `w_pp_cutoff` and zero for larger sizes. The power-law exponent  $\lambda$  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. That list can be accessed with `resource_params()`. It also holds the coefficient `kappa` that describes the steady-state resource abundance.

### 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 function 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,
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.
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 <code>get_gamma_default()</code> using the value of $f_0$ .
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 <code>setBevertonHolt()</code> .
R_factor	<b>[Deprecated]</b> Use <code>reproduction_level = 1 / R_factor</code> instead.
w_inf	<b>[Deprecated]</b> The argument has been renamed to <code>w_max</code> .
k_vb	<b>[Deprecated]</b> 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.

### 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 function 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,
  min_w_inf = deprecated(),
  max_w_inf = deprecated()
)

```

**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 $\eta * \text{min\_w\_max}$ . 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 largest size of the resource spectrum. Default value is min_w_max unless perfect_scaling = TRUE when it is Inf.
n	Scaling exponent of the maximum intake rate.
p	Scaling exponent of the standard metabolic rate. By default this is equal to the exponent n.
lambda	Exponent of the abundance power law.
r_pp	Growth rate parameter for the resource spectrum.
kappa	Coefficient in abundance power law.
alpha	The assimilation efficiency.
h	Maximum food intake rate.
beta	Preferred predator prey mass ratio.
sigma	Width of prey size preference.
f0	Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.
fc	Critical feeding level. Used to determine ks if it is not given explicitly.
ks	Standard metabolism coefficient. If not provided, default will be calculated from critical feeding level argument fc.
gamma	Volumetric search rate. If not provided, default is determined by <code>get_gamma_default()</code> 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 <code>setBevertonHolt()</code> .
R_factor	<b>[Deprecated]</b> Use <code>reproduction_level = 1 / R_factor</code> instead.
gear_names	The names of the fishing gears for each species. A character vector, the same length as the number of species.
knife_edge_size	The minimum size at which the gear or gears select fish. A single value for each gear or a vector with one value for each gear.

egg_size_scaling	<b>[Experimental]</b> If TRUE, the egg size is a constant fraction of the maximum size of each species. This fraction is $\text{min\_w} / \text{min\_w\_max}$ . If FALSE, all species have the egg size $w_{\text{min}}$ .
resource_scaling	<b>[Experimental]</b> 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	<b>[Experimental]</b> 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.
min_w_inf	<b>[Deprecated]</b> The argument has been renamed to $\text{min\_w\_max}$ to make it clearer that it refers to the maximum size of a species not the von Bertalanffy asymptotic size parameter.
max_w_inf	<b>[Deprecated]</b> The argument has been renamed to $\text{max\_w\_max}$ .

## 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  $\text{min\_w}$  (egg size),  $\text{min\_w\_mat}$  (maturity size) and  $\text{min\_w\_max}$  (maximum size). The maximum sizes of the  $\text{no\_sp}$  species are logarithmically evenly spaced, ranging from  $\text{min\_w\_max}$  to  $\text{max\_w\_max}$ . 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  $\text{egg\_size\_scaling} = \text{TRUE}$  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,  $f\theta$ .

The option of including fishing is given, but the steady state may lose its natural stability if too much fishing is included. In such a case the user may wish to include stabilising effects (like  $\text{reproduction\_level}$ ) to ensure the steady state is stable. Fishing selectivity is modelled as a knife-edge function with one parameter,  $\text{knife\_edge\_size}$ , which is the size at which species are selected. Each species can either be fished by the same gear ( $\text{knife\_edge\_size}$  has a length of 1) or by a different gear (the length of  $\text{knife\_edge\_size}$  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  $\text{dt}$  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	<i>Time series of other components</i>
--------	--

---

**Description**

Fetch the simulation results for other components over time.

**Usage**

```
NOther(sim)
```

**Arguments**

sim                    A MizerSim object

**Value**

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

---

NS_interaction	<i>Example interaction matrix for the North Sea example</i>
----------------	---

---

**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 <- MizerParams(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  $\text{effort} = c(\text{Industrial} = 0, \text{Pelagic} = 1, \text{Beam} = 0.5, \text{Otter} = 0.5)$ .

### 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](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	<i>Example species parameter set based on the North Sea</i>
-------------------	---

---

**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** Maximum size.

**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

**Source**

Blanchard et al.

**Examples**

```
params <- MizerParams(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** Maximum size.

**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

**gear** Name of the fishing gear

## Source

Blanchard et al.

## Examples

```
params <- MizerParams(NS_species_params_gears)
```

---

plot,MizerParams,missing-method

*Summary plot for MizerParams objects*

---

## Description

Produces 3 plots in the same window: abundance spectra, feeding level and predation mortality of each species through time. This method just uses the other plotting functions and puts them all in one window.

## Usage

```
## S4 method for signature 'MizerParams,missing'  
plot(x, y, ...)
```

## Arguments

x	An object of class <a href="#">MizerParams</a>
y	Not used
...	For additional arguments see the documentation for <a href="#">plotFeedingLevel()</a> , <a href="#">plotSpectra()</a> , <a href="#">plotPredMort()</a>

## Value

A viewport object

## See Also

[plotting\\_functions](#)

Other plotting functions: [animateSpectra\(\)](#),[plot,MizerSim,missing-method](#),[plotBiomass\(\)](#),[plotDiet\(\)](#),[plotFMort\(\)](#),[plotFeedingLevel\(\)](#),[plotGrowthCurves\(\)](#),[plotPredMort\(\)](#),[plotSpectra\(\)](#),[plotYield\(\)](#),[plotYieldGear\(\)](#),[plotting\\_functions](#)

## Examples

```
params <- NS_params  
plot(params)
```

---

plot,MizerSim,missing-method

*Summary plot for MizerSim objects*

---

## Description

After running a projection, produces 5 plots in the same window: feeding level, abundance spectra, predation mortality and fishing mortality of each species by size; and biomass of each species through time. This method just uses the other plotting functions and puts them all in one window.

## Usage

```
## S4 method for signature 'MizerSim,missing'  
plot(x, y, ...)
```

## Arguments

x	An object of class <a href="#">MizerSim</a>
y	Not used
...	For additional arguments see the documentation for <a href="#">plotBiomass()</a> , <a href="#">plotFeedingLevel()</a> , <a href="#">plotSpectra()</a> and <a href="#">plotFMort()</a> .

## Value

A viewport object

## See Also

[plotting\\_functions](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

## Examples

```
params <- NS_params  
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)  
plot(sim)
```

---

plotBiomass

*Plot the biomass of species through time*


---

### Description

After running a projection, the biomass of each species can be plotted against time. The biomass is calculated within user defined size limits (`min_w`, `max_w`, `min_l`, `max_l`, see `getBiomass()`).

### Usage

```
plotBiomass(
  sim,
  species = NULL,
  start_time,
  end_time,
  y_ticks = 6,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

```
plotlyBiomass(
  sim,
  species = NULL,
  start_time,
  end_time,
  y_ticks = 6,
  ylim = c(NA, NA),
  total = FALSE,
  background = TRUE,
  highlight = NULL,
  ...
)
```

### Arguments

<code>sim</code>	An object of class <code>MizerSim</code>
<code>species</code>	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.
<code>start_time</code>	The first time to be plotted. Default is the beginning of the time series.
<code>end_time</code>	The last time to be plotted. Default is the end of the time series.



y_ticks	The approximate number of ticks desired on the y axis
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to refer to the existing minimum or maximum. Any values below 1e-20 are always cut off.
total	A boolean value that determines whether the total biomass from all species is plotted as well. Default is FALSE.
background	A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Arguments passed on to <a href="#">get_size_range_array</a>
	min_w Smallest weight in size range. Defaults to smallest weight in the model.
	max_w Largest weight in size range. Defaults to largest weight in the model.
	min_l Smallest length in size range. If supplied, this takes precedence over min_w.
	max_l Largest length in size range. If supplied, this takes precedence over max_w.

### Value

A ggplot2 object, unless return\_data = TRUE, in which case a data frame with the four variables 'Year', 'Biomass', 'Species', 'Legend' is returned.

### See Also

[plotting\\_functions](#), [getBiomass\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot](#), [MizerParams](#), [missing-method](#), [plot](#), [MizerSim](#), [missing-method](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

### Examples

```
plotBiomass(NS_sim)
plotBiomass(NS_sim, species = c("Sandeel", "Herring"), total = TRUE)
plotBiomass(NS_sim, start_time = 1980, end_time = 1990)

# Returning the data frame
fr <- plotBiomass(NS_sim, return_data = TRUE)
str(fr)
```

---

```
plotBiomassObservedVsModel
```

*Plotting observed vs. model biomass data*

---

### Description

**[Experimental]** If biomass observations are available for at least some species via the `biomass_observed` column in the species parameter data frame, this function plots the biomass of each species in the model against the observed biomasses. When called with a `MizerSim` object, the plot will use the model biomasses predicted for the final time step in the simulation.

### Usage

```
plotBiomassObservedVsModel(
  object,
  species = NULL,
  ratio = TRUE,
  log_scale = TRUE,
  return_data = FALSE,
  labels = TRUE,
  show_unobserved = FALSE
)
```

```
plotlyBiomassObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  show_unobserved = FALSE
)
```

### Arguments

<code>object</code>	An object of class <a href="#">MizerParams</a> or <a href="#">MizerSim</a> .
<code>species</code>	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.
<code>ratio</code>	Whether to plot model biomass vs. observed biomass (FALSE) or the ratio of model : observed biomass (TRUE). Default is TRUE.
<code>log_scale</code>	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.
<code>return_data</code>	Whether to return the data frame for the plot (TRUE) or not (FALSE). Default is FALSE.

labels	Whether to show text labels for each species (TRUE) or not (FALSE). Default is TRUE.
show_unobserved	Whether to include also species for which no biomass observation is available. If TRUE, these species will be shown as if their observed biomass was equal to the model biomass.

## Details

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

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

The total relative error is shown in the caption of the plot, calculated by

$$TRE = \sum_i |1 - \text{ratio}_i|$$

where  $\text{ratio}_i$  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)
```

---

plotDiet *Plot diet, resolved by prey species, as function of predator at size.*

---

### Description

**[Experimental]** Plots the proportions with which each prey species contributes to the total biomass consumed by the specified predator species, as a function of the predator's size. These proportions are obtained with `getDiet()`.

### Usage

```
plotDiet(object, species = NULL, return_data = FALSE)
```

### Arguments

object	An object of class <a href="#">MizerSim</a> or <a href="#">MizerParams</a> .
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_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE

### Details

Prey species that contribute less than 1 permille to the diet are suppressed in the plot.

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', 'Proportion', 'Prey' is returned.

### See Also

[getDiet\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method,plot,MizerSim,missing-method,plotBiomass\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [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,
  time_range,
  highlight = NULL,
  all.sizes = FALSE,
  include_critical = FALSE,
  return_data = FALSE,
  ...
)
```

```
plotlyFeedingLevel(
  object,
  species = NULL,
  time_range,
  highlight = NULL,
  include_critical,
  ...
)
```

### Arguments

object	An object of class <a href="#">MizerSim</a> or <a href="#">MizerParams</a> .
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a <a href="#">MizerParams</a> object.
highlight	Name or vector of names of the species to be highlighted.
all.sizes	If TRUE, then feeding level is plotted also for sizes outside a species' size range. Default FALSE.

<code>include_critical</code>	If TRUE, then the critical feeding level is also plotted. Default FALSE.
<code>return_data</code>	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
<code>...</code>	Other arguments (currently unused)

### Details

When called with a [MizerSim](#) object, the feeding level is averaged over the specified time range (a single value for the time range can be used to plot a single time step). When called with a [MizerParams](#) object the initial feeding level is plotted.

If `include_critical = TRUE` then the critical feeding level (the feeding level at which the intake just covers the metabolic cost) is also plotted, with a thinner line. This line should always stay below the line of the actual feeding level, because the species would stop growing at any point where the feeding level drops to the critical feeding level.

### Value

A `ggplot2` object, unless `return_data = TRUE`, in which case a data frame with the variables 'w', 'value' and 'Species' is returned. If also `include_critical = TRUE` then the data frame contains a fourth variable 'Type' that distinguishes between 'actual' and 'critical' feeding level.

### See Also

[plotting\\_functions](#), [getFeedingLevel\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method](#), [plot,MizerSim,missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

### Examples

```
params <- NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotFeedingLevel(sim)
plotFeedingLevel(sim, time_range = 10:20, species = c("Cod", "Herring"),
  include_critical = TRUE)

# Returning the data frame
fr <- plotFeedingLevel(sim, return_data = TRUE)
str(fr)
```

plotFMort

*Plot total fishing mortality of each species by size***Description**

After running a projection, plot the total fishing mortality of each species by size. The total fishing mortality is averaged over the specified time range (a single value for the time range can be used to plot a single time step).

**Usage**

```
plotFMort(
  object,
  species = NULL,
  time_range,
  all.sizes = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

```
plotlyFMort(object, species = NULL, time_range, highlight = NULL, ...)
```

**Arguments**

object	An object of class <a href="#">MizerSim</a> or <a href="#">MizerParams</a> .
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a <a href="#">MizerParams</a> object.
all.sizes	If TRUE, then fishing mortality is plotted also for sizes outside a species' size range. Default FALSE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

**Value**

A `ggplot2` object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w', 'value', 'Species' is returned.

**See Also**

[plotting\\_functions](#), [getFMort\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method](#), [plot,MizerSim,missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [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**

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,
  ...
)
```

```
plotlyGrowthCurves(
  object,
  species = NULL,
  max_age = 20,
  percentage = FALSE,
  species_panel = FALSE,
```



```

    highlight = NULL
  )

```

### Arguments

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

For legacy reasons, 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. This was implemented before we understood that the von Bertalanffy curves (which approximates the average length at each age) should not be compared to the mizer growth curves (which approximate the average age at each length).

### Value

A `ggplot2` object

**See Also**

[plotting\\_functions](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method,plot,MizerSim,missing-method,plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

**Examples**

```
params <- NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotGrowthCurves(sim, percentage = TRUE)
plotGrowthCurves(sim, species = "Cod", max_age = 24)
plotGrowthCurves(sim, species_panel = TRUE)

# Returning the data frame
fr <- plotGrowthCurves(sim, return_data = TRUE)
str(fr)
```

---

plotM2

*Alias for plotPredMort()*

---

**Description**

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

**Usage**

```
plotM2(
  object,
  species = NULL,
  time_range,
  all.sizes = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

**Arguments**

**object** An object of class [MizerSim](#) or [MizerParams](#).

**species** The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.

time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a <a href="#">MizerParams</a> object.
all_sizes	If TRUE, then predation mortality is plotted also for sizes outside a species' size range. Default FALSE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

**Value**

A `ggplot2` object, unless `return_data = TRUE`, in which case a data frame with the three variables 'w', 'value', 'Species' is returned.

**See Also**

[plotting\\_functions](#), [getPredMort\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot](#), [MizerParams](#), [missing-method](#), [plot](#), [MizerSim](#), [missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

**Examples**

```
params <- NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotPredMort(sim)
plotPredMort(sim, time_range = 10:20)

# Returning the data frame
fr <- plotPredMort(sim, return_data = TRUE)
str(fr)
```

---

plotPredMort

*Plot predation mortality rate of each species against size*


---

**Description**

After running a projection, plot the predation mortality rate of each species by size. The mortality rate is averaged over the specified time range (a single value for the time range can be used to plot a single time step).

**Usage**

```
plotPredMort(
  object,
  species = NULL,
  time_range,
  all.sizes = FALSE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

```
plotlyPredMort(object, species = NULL, time_range, highlight = NULL, ...)
```

**Arguments**

object	An object of class <a href="#">MizerSim</a> or <a href="#">MizerParams</a> .
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a <a href="#">MizerParams</a> object.
all.sizes	If TRUE, then predation mortality is plotted also for sizes outside a species' size range. Default FALSE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

**Value**

A ggplot2 object, unless return\_data = TRUE, in which case a data frame with the three variables 'w', 'value', 'Species' is returned.

**See Also**

[plotting\\_functions](#), [getPredMort\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method](#), [plot,MizerSim,missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

**Examples**

```
params <- NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotPredMort(sim)
```

```
plotPredMort(sim, time_range = 10:20)

# Returning the data frame
fr <- plotPredMort(sim, return_data = TRUE)
str(fr)
```

---

plotSpectra

*Plot the abundance spectra*

---

### Description

Plots the number density multiplied by a power of the weight, with the power specified by the power argument.

### Usage

```
plotSpectra(
  object,
  species = NULL,
  time_range,
  geometric_mean = FALSE,
  wlim = c(NA, NA),
  ylim = c(NA, NA),
  power = 1,
  biomass = TRUE,
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  return_data = FALSE,
  ...
)
```

```
plotlySpectra(
  object,
  species = NULL,
  time_range,
  geometric_mean = FALSE,
  wlim = c(NA, NA),
  ylim = c(NA, NA),
  power = 1,
  biomass = TRUE,
  total = FALSE,
  resource = TRUE,
  background = TRUE,
  highlight = NULL,
  ...
)
```

**Arguments**

object	An object of class <a href="#">MizerSim</a> or <a href="#">MizerParams</a> .
species	The species to be selected. Optional. By default all target species are selected. A vector of species names, or a numeric vector with the species indices, or a logical vector indicating for each species whether it is to be selected (TRUE) or not.
time_range	The time range (either a vector of values, a vector of min and max time, or a single value) to average the abundances over. Default is the final time step. Ignored when called with a <a href="#">MizerParams</a> object.
geometric_mean	<b>[Experimental]</b> If TRUE then the average of the abundances over the time range is a geometric mean instead of the default arithmetic mean.
wlim	A numeric vector of length two providing lower and upper limits for the w axis. Use NA to refer to the existing minimum or maximum.
ylim	A numeric vector of length two providing lower and upper limits for the y axis. Use NA to refer to the existing minimum or maximum. Any values below 1e-20 are always cut off.
power	The abundance is plotted as the number density times the weight raised to power. The default power = 1 gives the biomass density, whereas power = 2 gives the biomass density with respect to logarithmic size bins.
biomass	<b>[Deprecated]</b> Only used if power argument is missing. Then biomass = TRUE is equivalent to power=1 and biomass = FALSE is equivalent to power=0
total	A boolean value that determines whether the total over all species in the system is plotted as well. Note that even if the plot only shows a selection of species, the total is including all species. Default is FALSE.
resource	A boolean value that determines whether resource is included. Default is TRUE.
background	A boolean value that determines whether background species are included. Ignored if the model does not contain background species. Default is TRUE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

**Details**

When called with a [MizerSim](#) object, the abundance is averaged over the specified time range (a single value for the time range can be used to plot a single time step). When called with a [MizerParams](#) object the initial abundance is plotted.

**Value**

A ggplot2 object, unless return\_data = TRUE, in which case a data frame with the four variables 'w', 'value', 'Species', 'Legend' is returned.

**See Also**[plotting\\_functions](#)

Other plotting functions: [animateSpectra\(\)](#), [plot](#), [MizerParams](#), [missing-method](#), [plot](#), [MizerSim](#), [missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

**Examples**

```

params <- NS_params
sim <- project(params, effort=1, t_max=20, t_save = 2, progress_bar = FALSE)
plotSpectra(sim)
plotSpectra(sim, wlim = c(1e-6, NA))
plotSpectra(sim, time_range = 10:20)
plotSpectra(sim, time_range = 10:20, power = 0)
plotSpectra(sim, species = c("Cod", "Herring"), power = 1)

# Returning the data frame
fr <- plotSpectra(sim, return_data = TRUE)
str(fr)

```

---

plotting_functions	<i>Description of the plotting functions</i>
--------------------	--

---

**Description**

Mizer provides a range of plotting functions for visualising the results of running a simulation, stored in a MizerSim object, or the initial state stored in a MizerParams object. Every plotting function exists in two versions, `plotSomething` and `plotlySomething`. The `plotly` version is more interactive but not suitable for inclusion in documents.

**Details**

This table shows the available plotting functions.

Plot	Description
<a href="#">plotBiomass()</a>	Plots the total biomass of each species through time. A time range to be plotted can be specified. The
<a href="#">plotSpectra()</a>	Plots the abundance (biomass or numbers) spectra of each species and the background community. It
<a href="#">plotFeedingLevel()</a>	Plots the feeding level of each species against size.
<a href="#">plotPredMort()</a>	Plots the predation mortality of each species against size.
<a href="#">plotFMort()</a>	Plots the total fishing mortality of each species against size.
<a href="#">plotYield()</a>	Plots the total yield of each species across all fishing gears against time.
<a href="#">plotYieldGear()</a>	Plots the total yield of each species by gear against time.
<a href="#">plotDiet()</a>	Plots the diet composition at size for a given predator species.
<a href="#">plotGrowthCurves()</a>	Plots the size as a function of age.
<a href="#">plot()</a>	Produces 5 plots ( <a href="#">plotFeedingLevel()</a> , <a href="#">plotBiomass()</a> , <a href="#">plotPredMort()</a> , <a href="#">plotFMort()</a> and <a href="#">plot</a>

These functions use the `ggplot2` package and return the plot as a `ggplot` object. This means that you can manipulate the plot further after its creation using the `ggplot` grammar of graphics. The corresponding function names with `plot` replaced by `plotly` produce interactive plots with the help of the `plotly` package.

While most plot functions take their data from a `MizerSim` object, some of those that make plots representing data at a single time can also take their data from the initial values in a `MizerParams` object.

Where plots show results for species, the line colour and line type for each species are specified by the `linecolour` and `linetype` slots in the `MizerParams` object. These were either taken from a default palette hard-coded into `emptyParams()` or they were specified by the user in the species parameters dataframe used to set up the `MizerParams` object. The `linecolour` and `linetype` slots hold named vectors, named by the species. They can be overwritten by the user at any time.

Most plots allow the user to select to show only a subset of species, specified as a vector in the `species` argument to the plot function.

The ordering of the species in the legend is the same as the ordering in the species parameter dataframe.

### See Also

[summary\\_functions](#), [indicator\\_functions](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method](#), [plot,MizerSim,missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotYieldGear\(\)](#)

### Examples

```
sim <- NS_sim

# Some example plots
plotFeedingLevel(sim)

# Plotting only a subset of species
plotFeedingLevel(sim, species = c("Cod", "Herring"))

# Specifying new colours and linetypes for some species
sim@params@linetype["Cod"] <- "dashed"
sim@params@linecolour["Cod"] <- "red"
plotFeedingLevel(sim, species = c("Cod", "Herring"))

# Manipulating the plot
library(ggplot2)
p <- plotFeedingLevel(sim)
p <- p + geom_hline(aes(yintercept = 0.7))
p <- p + theme_bw()
p
```



---

`plotYield`*Plot the total yield of species through time*

---

### Description

After running a projection, the total yield of each species across all fishing gears can be plotted against time. The yield is obtained with `getYield()`.

### Usage

```
plotYield(  
  sim,  
  sim2,  
  species = NULL,  
  total = FALSE,  
  log = TRUE,  
  highlight = NULL,  
  return_data = FALSE,  
  ...  
)
```

```
plotlyYield(  
  sim,  
  sim2,  
  species = NULL,  
  total = FALSE,  
  log = TRUE,  
  highlight = NULL,  
  ...  
)
```

### Arguments

<code>sim</code>	An object of class <code>MizerSim</code>
<code>sim2</code>	An optional second object of class <code>MizerSim</code> . If this is provided its yields will be shown on the same plot in bolder lines.
<code>species</code>	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.
<code>total</code>	A boolean value that determines whether the total over all species in the system is plotted as well. Note that even if the plot only shows a selection of species, the total is including all species. Default is FALSE.
<code>log</code>	Boolean whether yield should be plotted on a logarithmic axis. Defaults to true.
<code>highlight</code>	Name or vector of names of the species to be highlighted.

return\_data     A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE

...             Other arguments (currently unused)

### Value

A ggplot2 object, unless return\_data = TRUE, in which case a data frame with the three variables 'Year', 'Yield', 'Species' is returned.

### See Also

[plotting\\_functions](#), [getYield\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot,MizerParams,missing-method](#), [plot,MizerSim,missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYieldGear\(\)](#), [plotting\\_functions](#)

### Examples

```
params <- NS_params
sim <- project(params, effort = 1, t_max = 20, t_save = 0.2, progress_bar = FALSE)
plotYield(sim)
plotYield(sim, species = c("Cod", "Herring"), total = TRUE)

# Comparing with yield from twice the effort
sim2 <- project(params, effort=2, t_max=20, t_save = 0.2, progress_bar = FALSE)
plotYield(sim, sim2, species = c("Cod", "Herring"), log = FALSE)

# Returning the data frame
fr <- plotYield(sim, return_data = TRUE)
str(fr)
```

---

plotYieldGear

*Plot the total yield of each species by gear through time*

---

### Description

After running a projection, the total yield of each species by fishing gear can be plotted against time.

### Usage

```
plotYieldGear(
  sim,
  species = NULL,
  gears = NULL,
  total = FALSE,
  highlight = NULL,
  return_data = FALSE,
```

```

    ...
  )

  plotlyYieldGear(sim, species = NULL, total = FALSE, highlight = NULL, ...)

```

### Arguments

sim	An object of class <a href="#">MizerSim</a>
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 over all species in the system is plotted as well. Note that even if the plot only shows a selection of species, the total is including all species. Default is FALSE.
highlight	Name or vector of names of the species to be highlighted.
return_data	A boolean value that determines whether the formatted data used for the plot is returned instead of the plot itself. Default value is FALSE
...	Other arguments (currently unused)

### Details

This plot is pretty easy to do by hand. It just gets the biomass using the [getYieldGear\(\)](#) method and plots using the [ggplot2](#) package. You can then fiddle about with colours and linetypes etc. Just look at the source code for details.

### Value

A [ggplot2](#) object, unless `return_data = TRUE`, in which case a data frame with the four variables 'Year', 'Yield', 'Species' and 'Gear' is returned.

### See Also

[plotting\\_functions](#), [getYieldGear\(\)](#)

Other plotting functions: [animateSpectra\(\)](#), [plot](#), [MizerParams](#), [missing-method](#), [plot](#), [MizerSim](#), [missing-method](#), [plotBiomass\(\)](#), [plotDiet\(\)](#), [plotFMort\(\)](#), [plotFeedingLevel\(\)](#), [plotGrowthCurves\(\)](#), [plotPredMort\(\)](#), [plotSpectra\(\)](#), [plotYield\(\)](#), [plotting\\_functions](#)

### Examples

```

params <- NS_params
sim <- project(params, effort=1, t_max=20, t_save = 0.2, progress_bar = FALSE)
plotYieldGear(sim)
plotYieldGear(sim, species = c("Cod", "Herring"), total = TRUE)

# Returning the data frame
fr <- plotYieldGear(sim, return_data = TRUE)

```

```
str(fr)
```

---

```
plotYieldObservedVsModel
```

*Plotting observed vs. model yields*

---

### Description

**[Experimental]** If yield observations are available for at least some species via the `yield_observed` column in the species parameter data frame, this function plots the yield of each species in the model against the observed yields. When called with a `MizerSim` object, the plot will use the model yields predicted for the final time step in the simulation.

### Usage

```
plotYieldObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  labels = TRUE,
  show_unobserved = FALSE
)

plotlyYieldObservedVsModel(
  object,
  species = NULL,
  ratio = FALSE,
  log_scale = TRUE,
  return_data = FALSE,
  show_unobserved = FALSE
)
```

### Arguments

<code>object</code>	An object of class <a href="#">MizerParams</a> or <a href="#">MizerSim</a> .
<code>species</code>	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.
<code>ratio</code>	Whether to plot model yield vs. observed yield (FALSE) or the ratio of model : observed yield (TRUE). Default is FALSE.
<code>log_scale</code>	Whether to plot on the log10 scale (TRUE) or not (FALSE). For the non-ratio plot this applies for both axes, for the ratio plot only the x-axis is on the log10 scale. Default is TRUE.

return_data	Whether to return the data frame for the plot (TRUE) or not (FALSE). Default is FALSE.
labels	Whether to show text labels for each species (TRUE) or not (FALSE). Default is TRUE.
show_unobserved	Whether to include also species for which no yield observation is available. If TRUE, these species will be shown as if their observed yield was equal to the model yield.

### Details

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

The total relative error is shown in the caption of the plot, calculated by

$$TRE = \sum_i |1 - \text{ratio}_i|$$

where  $\text{ratio}_i$  is the ratio of model yield / observed yield for species  $i$ .

### Value

A `ggplot2` object with the plot of model yield by species compared to observed yield. If `return_data = TRUE`, the data frame used to create the plot is returned instead of the plot.

### Examples

```
# create an example
params <- NS_params
species_params(params)$yield_observed <-
  c(0.8, 61, 12, 35, 1.6, NA, 10, 7.6, 135, 60, 30, NA)
params <- calibrateYield(params)

# Plot with default options
plotYieldObservedVsModel(params)

# Plot including also species without observations
plotYieldObservedVsModel(params, show_unobserved = TRUE)

# Show the ratio instead
plotYieldObservedVsModel(params, ratio = TRUE)
```

---

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

$$\text{ppmr}^{\text{kernel\_exp}} / (1 + (\exp(\text{kernel\_l\_l}) / \text{ppmr})^{\text{kernel\_u\_l}}) / (1 + (\text{ppmr} / \exp(\text{kernel\_l\_r}))^{\text{kernel\_u\_r}})$$

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\(\)](#), [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", "kernel_type"] <- "power_law"
plot(w_full(params), getPredKernel(params)["Cod", 10, ], type="l", log="x")

```

---

project

*Project size spectrum forward in time*

---

## Description

Runs the size spectrum model simulation. The function returns an object of type [MizerSim](#) that can then be explored with a range of [summary\\_functions](#), [indicator\\_functions](#) and [plotting\\_functions](#).

## Usage

```

project(
  object,
  effort,
  t_max = 100,
  dt = 0.1,
  t_save = 1,
  t_start = 0,
  initial_n,
  initial_n_pp,
  append = TRUE,
  progress_bar = TRUE,
  ...
)

```

## Arguments

object	Either a <a href="#">MizerParams</a> object or a <a href="#">MizerSim</a> object (which contains a <a href="#">MizerParams</a> object).
effort	The effort of each fishing gear through time. See notes below.
t_max	The number of years the projection runs for. The default value is 100. This argument is ignored if an array is used for the <code>effort</code> argument. See notes below.
dt	Time step of the solver. The default value is 0.1.
t_save	The frequency with which the output is stored. The default value is 1. This argument is ignored if an array is used for the <code>effort</code> argument. See notes below.

<code>t_start</code>	The the year of the start of the simulation. The simulation will cover the period from <code>t_start</code> to <code>t_start + t_max</code> . Defaults to 0. Ignored if an array is used for the <code>effort</code> argument or a <code>MizerSim</code> for the <code>object</code> argument.
<code>initial_n</code>	<b>[Deprecated]</b> The initial abundances of species. Instead of using this argument you should set <code>initialN(params)</code> to the desired value.
<code>initial_n_pp</code>	<b>[Deprecated]</b> The initial abundances of resource. Instead of using this argument you should set <code>initialNResource(params)</code> to the desired value.
<code>append</code>	A boolean that determines whether the new simulation results are appended to the previous ones. Only relevant if <code>object</code> is a <code>MizerSim</code> object. Default = <code>TRUE</code> .
<code>progress_bar</code>	Either a boolean value to determine whether a progress bar should be shown in the console, or a shiny <code>Progress</code> object to implement a progress bar in a shiny app.
<code>...</code>	Other arguments will be passed to rate functions.

**Value**

An object of class `MizerSim`.

**Note**

The `effort` argument specifies the level of fishing effort during the simulation. If it is not supplied, the initial effort stored in the `params` object is used. The effort can be specified in 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 0.
- 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. Also, if the `effort` is an array then the `t_max` and `t_save` arguments are ignored and the simulation times will be taken from the `effort` array.

If the `object` argument is of class `MizerSim` then the initial values for the simulation are taken from the final values in the `MizerSim` object and the corresponding arguments to this function will be ignored.



**Examples**

```

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)

```

---

projectToSteady

*Project to steady state*


---

**Description****[Experimental]**

Run the full dynamics, as in [project\(\)](#), but stop once the change has slowed down sufficiently, in the sense that the distance between states at successive time steps is less than `tol`. You determine how the distance is calculated.

**Usage**

```

projectToSteady(
  params,
  effort = params@initial_effort,
  distance_func = distanceSSLogN,
  t_per = 1.5,
  t_max = 100,
  dt = 0.1,
  tol = 0.1 * t_per,
  return_sim = FALSE,
  progress_bar = TRUE,
  ...
)

```

**Arguments**

`params`            A [MizerParams](#) object

effort	The fishing effort to be used throughout the simulation. This must be a vector or list with one named entry per fishing gear.
distance_func	A function that will be called after every <code>t_per</code> years with both the previous and the new state and that should return a number that in some sense measures the distance between the states. By default this uses the function <a href="#">distanceSSLogN()</a> that you can use as a model for your own distance function.
t_per	The simulation is broken up into shorter runs of <code>t_per</code> years, after each of which we check for convergence. Default value is 1.5. This should be chosen as an odd multiple of the timestep <code>dt</code> in order to be able to detect period 2 cycles.
t_max	The maximum number of years to run the simulation. Default is 100.
dt	The time step to use in <code>project()</code> .
tol	The simulation stops when the relative change in the egg production RDI over <code>t_per</code> years is less than <code>tol</code> for every species.
return_sim	If TRUE, the function returns the MizerSim object holding the result of the simulation run, saved at intervals of <code>t_per</code> . If FALSE (default) the function returns a MizerParams object with the "initial" slots set to the steady state.
progress_bar	A shiny progress object to implement a progress bar in a shiny app. Default FALSE.
...	Further arguments will be passed on to your distance function.

**Value**

A MizerParams or a MizerSim object

**See Also**

[distanceSSLogN\(\)](#), [distanceMaxRelRDI\(\)](#)

---

project_simple	<i>Project abundances by a given number of time steps into the future</i>
----------------	---

---

**Description**

This is an internal function used by the user-facing `project()` function. It is of potential interest only to mizer extension authors.

**Usage**

```
project_simple(
  params,
  n = params@initial_n,
  n_pp = params@initial_n_pp,
  n_other = params@initial_n_other,
  effort = params@initial_effort,
  t = 0,
```

```

    dt = 0.1,
    steps,
    resource_dynamics_fn = get(params@resource_dynamics),
    other_dynamics_fns = lapply(params@other_dynamics, get),
    rates_fns = lapply(params@rates_funcs, get),
    ...
  )

```

### Arguments

params	A MizerParams object.
n	An array (species x size) with the number density at start of simulation.
n_pp	A vector (size) with the resource number density at start of simulation.
n_other	A named list with the abundances of other components at start of simulation.
effort	The fishing effort to be used throughout the simulation. This must be a vector or list with one named entry per fishing gear.
t	Time at the start of the simulation.
dt	Size of time step.
steps	The number of time steps by which to project.
resource_dynamics_fn	The function for the resource dynamics. See Details.
other_dynamics_fns	List with the functions for the dynamics of the other components. See Details.
rates_fns	List with the functions for calculating the rates. See Details.
...	Other arguments that are passed on to the rate functions.

### Details

The function does not check its arguments because it is meant to be as fast as possible to allow it to be used in a loop. For example, it is called in `project()` once for every saved value. The function also does not save its intermediate results but only returns the result at time  $t + dt * steps$ . During this time it uses the constant fishing effort `effort`.

The functional arguments can be calculated from slots in the `params` object with

```

resource_dynamics_fn <- get(params@resource_dynamics)
other_dynamics_fns <- lapply(params@other_dynamics, get)
rates_fns <- lapply(params@rates_funcs, get)

```

The reason the function does not do that itself is to shave 20 microseconds of its running time, which pays when the function is called hundreds of times in a row.

This function is also used in `steady()`. In between calls to `project_simple()` the `steady()` function checks whether the values are still changing significantly, so that it can stop when a steady state has been approached. Mizer extension packages might have a similar need to run a simulation repeatedly for short periods to run some other code in between. Because this code may want to use the values of the rates at the final time step, these too are included in the returned list.

**Value**

List with the final values of `n`, `n_pp` and `n_other`, `rates`.

---

<code>removeSpecies</code>	<i>Remove species</i>
----------------------------	-----------------------

---

**Description****[Experimental]**

This function simply removes all entries from the `MizerParams` object that refer to the selected species. It does not recalculate the steady state for the remaining species or retune their reproductive efficiency.

**Usage**

```
removeSpecies(params, species)
```

**Arguments**

<code>params</code>	A mizer params object for the original system.
<code>species</code>	The species to be removed. A vector of species names, or a numeric vector of species indices, or a logical vector indicating for each species whether it is to be removed (TRUE) or not.

**Value**

An object of type `MizerParams`

**Examples**

```
params <- NS_params
species_params(params)$species
params <- removeSpecies(params, c("Cod", "Haddock"))
species_params(params)$species
```

---

renameSpecies	<i>Rename species</i>
---------------	-----------------------

---

**Description****[Experimental]**

Changes the names of species in a MizerParams object. This involves for example changing the species dimension names of rate arrays appropriately.

**Usage**

```
renameSpecies(params, replace)
```

**Arguments**

params	A mizer params object
replace	A named character vector, with new names as values, and old names as names.

**Value**

An object of type [MizerParams](#)

**Examples**

```
replace <- c(Cod = "Kabeljau", Haddock = "Schellfisch")
params <- renameSpecies(NS_params, replace)
species_params(params)$species
```

---

resource_constant	<i>Keep resource abundance constant</i>
-------------------	---

---

**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 <a href="#">MizerParams</a> 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 resource spectrum at next timestep

**See Also**

Other resource dynamics: [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

$$\frac{\partial N_R(w,t)}{\partial t} = r_R(w)N_R(w) \left[ 1 - \frac{N_R(w,t)}{c_R(w)} \right] - \mu_R(w,t)N_R(w,t)$$

**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 <a href="#">MizerParams</a> 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 <a href="#">mizerRates()</a>
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 only one of resource\_rate or resource\_capacity should and will return a named list with the values for both.

**Value**

Vector containing resource spectrum at next timestep

**See Also**

Other resource dynamics: [resource\\_constant\(\)](#), [resource\\_semichemostat\(\)](#)

---

resource_params	<i>Resource parameters</i>
-----------------	----------------------------

---

### 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` ( $\lambda$ ) 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` ( $\kappa$ ) determines the initial resource abundance:

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

for all  $w$  less than `w_pp_cutoff` and zero for larger sizes.

### Value

A named list of resource parameters.



---

 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

$$\frac{\partial N_R(w, t)}{\partial t} = r_R(w) [c_R(w) - N_R(w, t)] - \mu_R(w, t) N_R(w, t)$$

### 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 <a href="#">MizerParams</a> 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 <a href="#">mizerRates()</a>
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` should and will return a named list with the values for both.

**Value**

Vector containing resource spectrum at next timestep

**See Also**

Other resource dynamics: `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**

<code>rdi</code>	Vector of density-independent reproduction rates $R_{di}$ for all species.
<code>species_params</code>	A species parameter dataframe. Must contain a column <code>ricker_b</code> holding the coefficient $b$ .
<code>...</code>	Unused

**Value**

Vector of density-dependent reproduction rates.

**See Also**

Other functions calculating density-dependent reproduction rate: [BevertonHoltRDD\(\)](#), [SheperdRDD\(\)](#), [constantEggRDI\(\)](#), [constantRDD\(\)](#), [noRDD\(\)](#)

---

saveParams	<i>Save a MizerParams object to file, and restore it</i>
------------	--

---

**Description**

**[Experimental]** `saveParams()` saves a `MizerParams` object to a file. This can then be restored with `readParams()`.

**Usage**

```
saveParams(params, file)
```

```
readParams(file)
```

**Arguments**

params	A <code>MizerParams</code> object
file	The name of the file or a connection where the <code>MizerParams</code> object is saved to or read from.

**Details**

Issues a warning if the model you are saving relies on some custom functions. Before saving a model you may want to set its metadata with [setMetadata\(\)](#).

**Value**

NULL invisibly

---

`scaleModel`*Change scale of the model*

---

## Description

### [Experimental]

The abundances in mizer and some rates depend on the size of the area to which they refer. So they could be given per square meter or per square kilometer or for an entire study area or any other choice of yours. This function allows you to change the scale of the model by automatically changing the abundances and rates accordingly.

## Usage

```
scaleModel(params, factor)
```

## Arguments

<code>params</code>	A MizerParams object
<code>factor</code>	The factor by which the scale is multiplied

## Details

If you rescale the model by a factor  $c$  then this function makes the following rescalings in the `params` object:

- The initial abundances are rescaled by  $c$ .
- The search volume is rescaled by  $1/c$ .
- The resource carrying capacity is rescaled by  $c$
- The maximum reproduction rate  $R_{max}$  is rescaled by  $c$ .

The effect of this is that the dynamics of the rescaled model are identical to those of the unscaled model, in the sense that it does not matter whether one first calls `scaleModel()` and then runs a simulation with `project()` or whether one first runs a simulation and then rescales the resulting abundances.

Note that if you use non-standard resource dynamics or other components then you may need to rescale additional parameters that appear in those dynamics.

In practice you will need to use some observations to set the scale for your model. If you have biomass observations you can use `calibrateBiomass()`, if you have yearly yields you can use `calibrateYield()`.

## Value

The rescaled MizerParams object

---

setBevertonHolt	<i>Set Beverton-Holt reproduction without changing the steady state</i>
-----------------	---

---

## Description

**[Experimental]** 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,
  R_factor = deprecated(),
  erepro,
  R_max,
  reproduction_level
)
```

## Arguments

<code>params</code>	A MizerParams object
<code>R_factor</code>	<b>[Deprecated]</b> Use <code>reproduction_level = 1 / R_factor</code> instead.
<code>erepro</code>	Reproductive efficiency for each species. See details.
<code>R_max</code>	Maximum reproduction rate. See details.
<code>reproduction_level</code>	Sets <code>R_max</code> so that the reproduction rate at the initial state is <code>R_max * reproduction_level</code> .

## 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,

$$R_{di} = \frac{erepro}{2w_{min}} E_R,$$

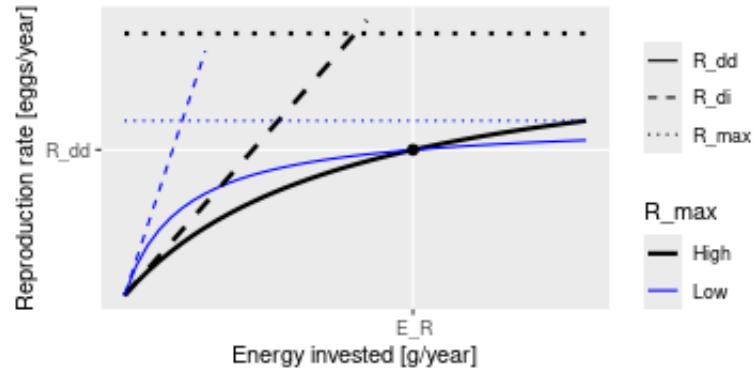
where the proportionality factor is given by the reproductive efficiency `erepro` divided by the egg size `w_min` to convert energy to egg number and divided by 2 to account for the two sexes.

Imposing a finite maximum reproduction rate  $R_{max}$  leads to a non-linear relationship between energy invested and eggs hatched. This density-dependent reproduction rate  $R_{dd}$  is given as

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

(All quantities in the above equations are species-specific but we dropped the species index for simplicity.)

The following plot illustrates the Beverton-Holt density dependence in the reproduction rate for two



different choices of parameters.

This plot shows that a given energy  $E_R$  invested into reproduction can lead to the same reproduction rate  $R_{dd}$  with different choices of the parameters  $R_{max}$  and  $erepro$ .  $R_{max}$  determines the asymptote of the curve and  $erepro$  its initial slope. A higher  $R_{max}$  coupled with a lower  $erepro$  (black curves) can give the same value as a lower  $R_{max}$  coupled with a higher  $erepro$  (blue curves).

For the given initial state in the MizerParams object `params` one can calculate the energy  $E_R$  that is invested into reproduction by the mature individuals and the reproduction rate  $R_{dd}$  that is required to keep the egg abundance constant. These two values determine the location of the black dot in the above graph. You then only need one parameter to select one curve from the family of Beverton-Holt curves going through that point. This parameter can be `erepro` or `R_max`. Instead of `R_max` you can alternatively specify the `reproduction_level` which is the ratio between the density-dependent reproduction rate  $R_{dd}$  and the maximal reproduction rate  $R_{max}$ .

If you do not provide a value for any of the reproduction parameter arguments, then `erepro` will be set to the value it has in the current species parameter data frame. If you do provide one of the reproduction parameters, this can be either a vector with one value for each species, or a named vector where the names determine which species are affected, or a single unnamed value that is then used for all species. Any species for which the given value is NA will remain unaffected.

The values for `R_max` must be larger than  $R_{dd}$  and can range up to Inf. If a smaller value is requested a warning is issued and the value is increased to the value required for a reproduction level of 0.99.

The values for the `reproduction_level` must be positive and less than 1. The values for `erepro` must be large enough to allow the required reproduction rate. If a smaller value is requested a warning is issued and the value is increased to the smallest possible value. The values for `erepro` should also be smaller than 1 to be physiologically sensible, but this is not enforced by the function.

As can be seen in the graph above, choosing a lower value for `R_max` or a higher value for `erepro` means that near the steady state the reproduction will be less sensitive to a change in the energy

invested into reproduction and hence less sensitive to changes in the spawning stock biomass or its energy income. As a result the species will also be less sensitive to fishing, leading to a higher  $F_{MSY}$ .

### Value

A MizerParams object

### Examples

```
params <- NS_params
species_params(params)$erepro
# Attempting to set the same erepro for all species
params <- setBevertonHolt(params, erepro = 0.1)
t(species_params(params)[, c("erepro", "R_max")])
# Setting erepro for some species
params <- setBevertonHolt(params, erepro = c("Gurnard" = 0.6, "Plaice" = 0.95))
t(species_params(params)[, c("erepro", "R_max")])
# Setting R_max
R_max <- 1e17 * species_params(params)$w_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")])
```

---

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.

Do not use this for setting the colours or linetypes of species, because those are determined by setting the `linecolour` and `linetype` variables in the species parameter data frame.

You can use the same colours in your own `ggplot2` plots by adding `scale_colour_manual(values = getColours(params))` to your plot. Similarly you can use the linetypes with `scale_linetype_manual(values = getLinetypes(params))`.

**Value**

`setColours`: The `MizerParams` object with updated line colours

`getColours()`: A named vector of colours

`setLinetypes`: The `MizerParams` object with updated linetypes

`getLinetypes()`: A named vector of linetypes

**Examples**

```
params <- setColours(NS_params, list("Resource" = "red", "Total" = "#0000ff"))
params <- setLinetypes(NS_params, list("Total" = "dotted"))
# Set colours and linetypes for species
species_params(params)["Cod", "linecolour"] <- "black"
species_params(params)["Cod", "linetype"] <- "dashed"
plotSpectra(params, total = TRUE)
getColours(params)
getLinetypes(params)
```

---

setComponent

*Add a dynamical ecosystem component*

---

**Description**

By default, mizer models any number of size-resolved consumer species and a single size-resolved resource spectrum. Your model may require additional components, like for example detritus or carrion or multiple resources or .... This function allows you to set up such components.

**Usage**

```
setComponent(
  params,
  component,
  initial_value,
  dynamics_fun,
  encounter_fun,
  mort_fun,
  component_params
```



```
)
removeComponent(params, component)
```

### Arguments

params	A MizerParams object
component	Name of the component
initial_value	Initial value of the component
dynamics_fun	Name of function to calculate value at the next time step
encounter_fun	Name of function to calculate contribution to encounter rate. Optional.
mort_fun	Name of function to calculate contribution to the mortality rate. Optional.
component_params	Object holding the parameters needed by the component functions. This could for example be a named list of parameters. Optional.

### Details

The component can be a number, a vector, an array, a list, or any other data structure you like.

If you set a component with a new name, the new component will be added to the existing components. If you set a component with an existing name, that component will be overwritten. You can remove a component with `removeComponent()`.

### Value

The updated MizerParams object

---

setExtEncounter	<i>Set external encounter rate</i>
-----------------	------------------------------------

---

### Description

Set external encounter rate

### Usage

```
setExtEncounter(params, ext_encounter = NULL, ...)
getExtEncounter(params)
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, the external encounter rate is left unchanged. Initially is set to 0.
...	Unused
value	ext_encounter

**Value**

setExtEncounter(): A MizerParams object with updated external encounter rate.

getExtEncounter() or equivalently ext\_encounter(): An array (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\(\)](#).

**See Also**

Other functions for setting parameters: [gear\\_params\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

**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	<i>Set external mortality rate</i>
------------	------------------------------------

---

### Description

Set external mortality rate

### Usage

```
setExtMort(
  params,
  ext_mort = NULL,
  z0pre = 0.6,
  z0exp = -1/4,
  reset = FALSE,
  z0 = deprecated(),
  ...
)
```

```
getExtMort(params)
```

```
ext_mort(params)
```

```
ext_mort(params) <- value
```

### Arguments

params	MizerParams
ext_mort	Optional. An array (species x size) holding the external mortality rate. 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 a column in the species data frame, it is calculated as $z0pre * w\_max ^ z0exp$ . Default value is 0.6.
z0exp	If z0, the mortality from other sources, is not a column in the species data frame, it is calculated as $z0pre * w\_max ^ z0exp$ . Default value is n-1.
reset	<b>[Experimental]</b> If set to TRUE, then the external mortality rate will be reset to the value calculated from the z0 parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
z0	<b>[Deprecated]</b> Use ext_mort instead. Not to be confused with the species_parameter z0.
...	Unused
value	ext_mort

**Value**

setExtMort(): A MizerParams object with updated external mortality rate.

getExtMort() or equivalently ext\_mort(): An array (species x size) with the external mortality.

**Setting external mortality rate**

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

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

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

$$z_{0,i} = z_{0pre,i} w_{inf}^{z_{0exp}}$$

**See Also**

Other functions for setting parameters: [gear\\_params\(\)](#), [setExtEncounter\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

**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,
  ...
)

getCatchability(params)

catchability(params)

catchability(params) <- value

getSelectivity(params)

selectivity(params)

selectivity(params) <- value

getInitialEffort(params)

```

**Arguments**

params	A MizerParams object
selectivity	Optional. An array (gear x species x size) that holds the selectivity of each gear for species and size, $S_{g,i,w}$ .
catchability	Optional. An array (gear x species) that holds the catchability of each species by each gear, $Q_{g,i}$ .
reset	<b>[Experimental]</b> If set to TRUE, then both catchability and selectivity will be reset to the values calculated from the gear parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the gear parameters will take place only if no custom value has been set.
initial_effort	Optional. A number or a named numeric vector specifying the fishing effort. If a number, the same effort is used for all gears. If a vector, must be named by gear.
...	Unused
value	.

**Value**

setFishing(): A MizerParams object with updated fishing parameters.

getCatchability() or equivalently catchability(): An array (gear x species) that holds the catchability of each species by each gear,  $Q_{g,i}$ . The names of the dimensions are "gear, "sp".

`getSelectivity()` or equivalently `selectivity()`: An array (gear x species x size) that holds the selectivity of each gear for species and size,  $S_{g,i,w}$ . The names of the dimensions are "gear", "sp", "w".

`getInitialEffort()` or equivalently `initial_effort()`: A named vector with the initial fishing effort for each gear.

## Setting fishing

### Gears

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

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

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

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

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

### Selectivity

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

To allow the calculation of the selectivity array, the `gear_params` slot must be a data frame with one row for each gear-species combination. So if for example a gear can select three species, then that gear contributes three rows to the `gear_params` data frame, one for each species it can select. The data frame must have columns `gear`, holding the name of the gear, `species`, holding the name of the species, and `sel_func`, holding the name of the function that calculates the selectivity curve. Some selectivity functions are included in the package: `knife_edge()`, `sigmoid_length()`, `double_sigmoid_length()`, and `sigmoid_weight()`. Users are able to write their own size-based selectivity function. The first argument to the function must be `w` and the function must return a vector of the selectivity (between 0 and 1) at size.

Each selectivity function may have parameters. Values for these parameters must be included as columns in the gear parameters data.frame. The names of the columns must exactly match the names of the corresponding arguments of the selectivity function. For example, the default selectivity function is `knife_edge()` that 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 150 and 125

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 150 and 125 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\(\)](#), [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

### Examples

```
str(getCatchability(NS_params))
str(getSelectivity(NS_params))
str(getInitialEffort(NS_params))
```

---

setInitialValues

*Set initial values to values from a simulation*

---

### Description

This is used to use the results from one simulation as the starting values for another 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	<b>[Experimental]</b> 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.

**Details**

The initial abundances (for both species and resource) in the params object are set to the abundances in a MizerSim object, averaged over a range of times. Similarly, the initial effort in the params object is set to the effort in the MizerSim object, again averaged over that range of times. When no time range is specified, the initial values are taken from the final time step of the simulation.

If the model described by sim and params has additional components created with [setComponent\(\)](#) then the values of these components are also averaged and copied to params.

The MizerSim object must come from a model with the same set of species and gears and other components and the same size bins as the MizerParams object. Otherwise an error is raised.

**Value**

The params object with updated initial values and initial effort. Because of the way the R language works, setInitialValues() does not make the changes to the params object that you pass to it but instead returns a new params object. So to affect the change you call the function in the form `params <- setInitialValues(params, sim)`.

**See Also**

Other functions for setting parameters: [gear\\_params\(\)](#), [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

**Examples**

```
params <- NS_params
sim <- project(params, t_max = 20, effort = 0.5)
params <- setInitialValues(params, sim)
```



---

setInteraction	<i>Set species interaction matrix</i>
----------------	---------------------------------------

---

**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.
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  $\theta_{ij}$  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 warn if it is different. One way of creating your own interaction matrix is to enter the data using a spreadsheet program and saving it as a .csv file. The data can 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()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setReproduction()`, `setSearchVolume()`, `species_params()`

### Examples

```
params <- newTraitParams(no_sp = 3)
inter <- getInteraction(params)
inter[1, 2:3] <- 0
params <- setInteraction(params, interaction = inter)
getInteraction(params)
```

---

<code>setMaxIntakeRate</code>	<i>Set maximum intake rate</i>
-------------------------------	--------------------------------

---

### Description

Set maximum intake rate

### Usage

```
setMaxIntakeRate(params, intake_max = NULL, reset = FALSE, ...)
```

```
getMaxIntakeRate(params)
```

```
intake_max(params)
```

```
intake_max(params) <- value
```

### Arguments

<code>params</code>	MizerParams
<code>intake_max</code>	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".
<code>reset</code>	<b>[Experimental]</b> 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.
<code>...</code>	Unused
<code>value</code>	<code>intake_max</code>

**Value**

setReproduction(): A MizerParams object with updated maximum intake rate.

getMaxIntakeRate() or equivalently intake\_max(): An array (species x size) with the maximum intake rate.

**Setting maximum intake rate**

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

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

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

The values of  $h_i$  (the maximum intake rate of an individual of size 1 gram) and  $n_i$  (the allometric exponent for the intake rate) are taken from the h and n columns in the species parameter dataframe. If the h column is not supplied in the species parameter dataframe, it is calculated by the [get\\_h\\_default\(\)](#) function.

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

**See Also**

Other functions for setting parameters: [gear\\_params\(\)](#), [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

---

setMetabolicRate	<i>Set metabolic rate</i>
------------------	---------------------------

---

**Description**

Sets the rate at which energy is used for metabolism and activity

**Usage**

```
setMetabolicRate(params, metab = NULL, p = NULL, reset = FALSE, ...)
```

```
getMetabolicRate(params)
```

```
metab(params)
```

```
metab(params) <- value
```

**Arguments**

params	MizerParams
metab	Optional. An array (species x size) holding the metabolic rate for each species at size. If not supplied, a default is set as described in the section "Setting metabolic rate".
p	The allometric metabolic exponent. This is only used if metab is not given explicitly and if the exponent is not specified in a p column in the species_params.
reset	<b>[Experimental]</b> If set to TRUE, then the metabolic rate will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
...	Unused
value	metab

**Value**

setMetabolicRate(): A MizerParams object with updated metabolic rate.

getMetabolicRate() or equivalently metab(): An array (species x size) with the metabolic rate.

**Setting metabolic rate**

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

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

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

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

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

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

**See Also**

Other functions for setting parameters: [gear\\_params\(\)](#), [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

---

setMetadata	<i>Set metadata for a model</i>
-------------	---------------------------------

---

### Description

**[Experimental]** Setting metadata is particularly important for sharing your model with others. All metadata fields are optional and you can also add other fields of your own choosing. If you set a value for a field that already existed, the old value will be overwritten.

### Usage

```
setMetadata(params, title, description, authors, url, doi, ...)

getMetadata(params)
```

### Arguments

params	The MizerParams object for the model
title	A string with the title for the model
description	A string with a description of the model. This could for example contain information about any publications using the model.
authors	An author entry or a list of author entries, where each author entry could either be just a name or could itself be a list with fields like name, orcid, possibly email.
url	A URL where more information about the model can be found. This could be a blog post on the mizer blog, for example.
doi	The digital object identifier for your model. To create a doi you can use online services like <a href="https://zenodo.org/">https://zenodo.org/</a> or <a href="https://figshare.com">https://figshare.com</a> .
...	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 vector of strings where each name is the name of an extension package needed to run the model and each value is a string giving the information that the remotes package needs to install the correct version of the extension package, see <https://remotes.r-lib.org/>. This field is set by the extension packages.
- `time_created` A POSIXct date-time object with the creation time.
- `time_modified` A POSIXct date-time object with the last modified time.

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`.

---

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\(\)](#)
- [setReproduction\(\)](#)
- [setFishing\(\)](#)
- [setResource\(\)](#)

See the Details section below for a discussion of how to use this function.

### Usage

```
setParams(params, interaction = NULL, ...)
```

### Arguments

- |             |  |
|-------------|--|
| params      | A <a href="#">MizerParams</a> 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.  |
| ...         | Arguments passed on to <a href="#">setPredKernel</a> , <a href="#">setSearchVolume</a> , <a href="#">setMaxIntakeRate</a> , <a href="#">setMetabolicRate</a> , <a href="#">setExtMort</a> , <a href="#">setReproduction</a> , <a href="#">setFishing</a> |
| pred_kernel | Optional. An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If not supplied, a default is set as described in section "Setting predation kernel".                          |

- `search_vol` Optional. An array (species x size) holding the search volume for each species at size. If not supplied, a default is set as described in the section "Setting search volume".
- `intake_max` Optional. An array (species x size) holding the maximum intake rate for each species at size. If not supplied, a default is set as described in the section "Setting maximum intake rate".
- `metab` Optional. An array (species x size) holding the metabolic rate for each species at size. If not supplied, a default is set as described in the section "Setting metabolic rate".
- `p` The allometric metabolic exponent. This is only used if `metab` is not given explicitly and if the exponent is not specified in a `p` column in the `species_params`.
- `ext_mort` Optional. An array (species x size) holding the external mortality rate. 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 a column in the species data frame, it is calculated as  $z0pre * w\_max ^ z0exp$ . Default value is 0.6.
- `z0exp` If `z0`, the mortality from other sources, is not a column in the species data frame, it is calculated as  $z0pre * w\_max ^ z0exp$ . Default value is  $n-1$ .
- `z0` **[Deprecated]** Use `ext_mort` instead. Not to be confused with the `species_parameter` `z0`.
- `maturity` Optional. An array (species x size) that holds the proportion of individuals of each species at size that are mature. If not supplied, a default is set as described in the section "Setting reproduction".
- `repro_prop` Optional. An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. If not supplied, a default is set as described in the section "Setting reproduction".
- `RDD` The name of the function calculating the density-dependent reproduction rate from the density-independent rate. Defaults to "`BevertonHoltRDD()`".
- `selectivity` Optional. An array (gear x species x size) that holds the selectivity of each gear for species and size,  $S_{g,i,w}$ .
- `catchability` Optional. An array (gear x species) that holds the catchability of each species by each gear,  $Q_{g,i}$ .
- `initial_effort` Optional. A number or a named numeric vector specifying the fishing effort. If a number, the same effort is used for all gears. If a vector, must be named by gear.

## Details

If you are not happy with the assumptions that `mizer` makes by default about the shape of the model functions, for example if you want to change one of the allometric scaling assumptions, you can do this by providing your choice as an array in the appropriate argument to `setParams()`. The sections below discuss all the model functions that you can change this way.

Because of the way the R language works, `setParams` does not make the changes to the `params` object that you pass to it but instead returns a new `params` object. So to affect the change you call the function in the form `params <- setParams(params, ...)`.

Usually, if you are happy with the way mizer calculates its model functions from the species parameters and only want to change the values of some species parameters, you would make those changes in the `species_params` data frame contained in the `params` object using `species_params<-()`. Here is an example which assumes that you have a `MizerParams` object `params` in which you just want to change the `gamma` parameter of the third species:

```
species_params(params)$gamma[[3]] <- 1000
```

Internally that will actually call `setParams()` to recalculate any of the other parameters that are affected by the change in the species parameter.

`setParams()` will use the species parameters in the `params` object to recalculate the values of all the model functions except those for which you have set custom values.

### Value

A `MizerParams` object

### Units in mizer

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

Mizer is agnostic about whether abundances are given as

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

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

Your choice will also affect the units of the quantities you may want to calculate with the model. For example, the yield will be in `grams/year/m2` in case 1 if you choose `m2` as your measure of area, in `grams/year/m3` in case 2 if you choose `m3` 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  $\theta_{ij}$  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 warn if it is different. One way of creating your own interaction matrix is to enter the data using a spreadsheet program and saving it as a `.csv` file. The data can 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. An alternative `pred_kernel` type is "box", implemented by the function `box_pred_kernel()`, and "power\_law", implemented by the function `power_law_pred_kernel()`. These functions require certain species parameters in the `species_params` data frame. For the lognormal kernel these are `beta` and `sigma`, for the box kernel they are `ppmr_min` and `ppmr_max`. They are explained in the help pages for the kernel functions. Except for `beta` and `sigma`, no defaults are set for these parameters. If they are missing from the `species_params` data frame then `mizer` will issue an error message.

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

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

### Kernel dependent on both predator and prey size

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

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

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

### Setting search volume

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

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

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

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

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

### Setting maximum intake rate

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

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

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

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

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

### Setting metabolic rate

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

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

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

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

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

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

### Setting external mortality rate

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

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

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

$$z_{0,i} = z_{0pre,i} w_{inf}^{z_{0exp}}.$$

### 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\(\)](#).

### Setting reproduction

For each species and at each size, the proportion  $\psi$  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 all the energy is invested into reproduction and therefore all growth stops. There can be no fish larger than `w_repro_max`. If you have not specified the `w_repro_max` column in the species parameter data frame, then the maximum size `w_max` 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:

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

(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 maximum weight in the `w_max` 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 1 only asymptotically. Mizer instead sets the function equal to 1 already at a size taken from the `w_repro_max` column in the species parameter data frame, if it exists, or otherwise from the `w_max` column. Also, for computational simplicity, any proportion smaller than  $1e-8$  is set to  $\emptyset$ .

**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

$$\text{repro\_prop}(w) = \left( \frac{w}{w_{mat\_max}} \right)^{m-n}.$$

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

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

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

**Reproductive efficiency:** The reproductive efficiency  $\epsilon$ , 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 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 150 and 125 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 150 and 125 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\(\)](#), [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [setSearchVolume\(\)](#), [species\\_params\(\)](#)

---

setPredKernel

*Set predation kernel*

---

### Description

The predation kernel determines the distribution of prey sizes that a predator feeds on. It is used in [getEncounter\(\)](#) when calculating the rate at which food is encountered and in [getPredRate\(\)](#) when calculating the rate at which a prey is predated upon. The predation kernel can be a function of the predator/prey size ratio or it can be a function of the predator size and the prey size separately. Both types can be set up with this function.

**Usage**

```

setPredKernel(params, pred_kernel = NULL, reset = FALSE, ...)

getPredKernel(params)

pred_kernel(params)

pred_kernel(params) <- value

```

**Arguments**

params	A MizerParams object
pred_kernel	Optional. An array (species x predator size x prey size) that holds the predation coefficient of each predator at size on each prey size. If not supplied, a default is set as described in section "Setting predation kernel".
reset	<b>[Experimental]</b> If set to TRUE, then the predation kernel will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
...	Unused
value	pred_kernel

**Value**

setPredKernel(): A MizerParams object with updated predation kernel.

getPredKernel() or equivalently pred\_kernel(): An array (predator species x predator\_size x prey\_size)

**Setting predation kernel****Kernel dependent on predator to prey size ratio**

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

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

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

When using a kernel that depends on the predator/prey size ratio only, `mizer` does not need to store the entire three dimensional array in the `MizerParams` object. Such an array can be very big when

there is a large number of size bins. Instead, mizer only needs to store two two-dimensional arrays that hold Fourier transforms of the feeding kernel function that allow the encounter rate and the predation rate to be calculated very efficiently. However, if you need the full three-dimensional array you can calculate it with the `getPredKernel()` function.

### Kernel dependent on both predator and prey size

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

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

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

### See Also

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

### 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), getPredKernel(params)["Cod", 100, ], type="l", log="x")

## If you need a kernel that depends also on prey size you need to define
# it yourself.
pred_kernel <- getPredKernel(params)
pred_kernel["Herring", , ] <- sweep(pred_kernel["Herring", , ], 2,
                                   params@w_full, "*")
params<- setPredKernel(params, pred_kernel = pred_kernel)
```



## Description

If the way mizer calculates a fundamental rate entering the model is not flexible enough for you (for example if you need to introduce time dependence) then you can write your own functions for calculating that rate and use `setRateFunction()` to register it with mizer.

## Usage

```
setRateFunction(params, rate, fun)
```

```
getRateFunction(params, rate)
```

```
other_params(params)
```

```
other_params(params) <- value
```

## Arguments

params	A MizerParams object
rate	Name of the rate for which a new function is to be set.
fun	Name of the function to use to calculate the rate.
value	Values for other parameters

## Details

At each time step during a simulation with the `project()` function, mizer needs to calculate the instantaneous values of the various rates. By default it calls the `mizerRates()` function which creates a list with the following components:

- encounter from `mizerEncounter()`
- feeding\_level from `mizerFeedingLevel()`
- pred\_rate from `mizerPredRate()`
- pred\_mort from `mizerPredMort()`
- f\_mort from `mizerFMort()`
- mort from `mizerMort()`
- resource\_mort from `mizerResourceMort()`
- e from `mizerEReproAndGrowth()`
- e\_repro from `mizerERepro()`
- e\_growth from `mizerEGrowth()`
- rdi from `mizerRDI()`
- rdd from `BevertonHoltRDD()`

For each of these you can substitute your own function. So for example if you have written your own function for calculating the total mortality rate and have called it `myMort` and have a mizer model stored in a MizerParams object called `params` that you want to run with your new mortality rate, then you would call

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

In general if you want to replace a function `mizerSomeRateFunc()` with a function `myVersionOfThis()` you would call

```
params <- setRateFunction(params, "SomeRateFunc", "myVersionOfThis")
```

In some extreme cases you may need to swap out the entire `mizerRates()` function for your own function called `myRates()`. That you can do with

```
params <- setRateFunction(params, "Rates", "myRates")
```

Your new rate functions may need their own model parameters. These you can store in `other_params(params)`. For example

```
other_params(params)$my_param <- 42
```

Note that your own rate functions need to be defined in the global environment or in a package. If they are defined within a function then `mizer` will not find them.

### Value

For `setRateFunction()`: An updated `MizerParams` object

For `getRateFunction()`: The name of the registered rate function for the requested rate, or the list of all rate functions if called without rate argument.

For `other_params()`: A named list with all the parameters for which you have set values.

---

<code>setReproduction</code>	<i>Set reproduction parameters</i>
------------------------------	------------------------------------

---

### Description

Sets the proportion of the total energy available for reproduction and growth that is invested into reproduction as a function of the size of the individual and sets additional density dependence.

### Usage

```
setReproduction(
  params,
  maturity = NULL,
  repro_prop = NULL,
  reset = FALSE,
  RDD = NULL,
  ...
)
```

```

getMaturityProportion(params)

maturity(params)

maturity(params) <- value

getReproductionProportion(params)

repro_prop(params)

repro_prop(params) <- value

```

### Arguments

params	A MizerParams object
maturity	Optional. An array (species x size) that holds the proportion of individuals of each species at size that are mature. If not supplied, a default is set as described in the section "Setting reproduction".
repro_prop	Optional. An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. If not supplied, a default is set as described in the section "Setting reproduction".
reset	<b>[Experimental]</b> 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 " <a href="#">BevertonHoltRDD()</a> ".
...	Unused
value	.

### Value

setReproduction(): A MizerParams object with updated reproduction parameters.

getMaturityProportion() or equivalently maturity(): An array (species x size) that holds the proportion of individuals of each species at size that are mature.

getReproductionProportion() or equivalently repro\_prop(): An array (species x size) that holds the proportion of consumed energy that a mature individual allocates to reproduction for each species at size. For sizes where the maturity proportion is zero, also the reproduction proportion is returned as zero.

### Setting reproduction

For each species and at each size, the proportion  $\psi$  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 all the energy is invested into reproduction and

therefore all growth stops. There can be no fish larger than `w_repro_max`. If you have not specified the `w_repro_max` column in the species parameter data frame, then the maximum size `w_max` 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:

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

(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 maximum weight in the `w_max` 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 1 only asymptotically. Mizer instead sets the function equal to 1 already at a size taken from the `w_repro_max` column in the species parameter data frame, if it exists, or otherwise from the `w_max` column. Also, for computational simplicity, any proportion smaller than  $1e-8$  is set to  $\emptyset$ .

**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

$$\text{repro\_prop}(w) = \left( \frac{w}{w_{mat,max}} \right)^{m-n}.$$

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

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

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

**Reproductive efficiency:** The reproductive efficiency  $\epsilon$ , 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()`, `setExtEncounter()`, `setExtMort()`, `setFishing()`, `setInitialValues()`, `setInteraction()`, `setMaxIntakeRate()`, `setMetabolicRate()`, `setParams()`, `setPredKernel()`, `setSearchVolume()`, `species_params()`

### Examples

```
# Plot maturity and reproduction ogives for Cod in North Sea model
maturity <- getMaturityProportion(NS_params)["Cod", ]
repro_prop <- getReproductionProportion(NS_params)["Cod", ]
df <- data.frame(Size = w(NS_params),
                 Reproduction = repro_prop,
                 Maturity = maturity,
                 Total = maturity * repro_prop)
dff <- melt(df, id.vars = "Size",
           variable.name = "Type",
           value.name = "Proportion")
library(ggplot2)
ggplot(dff) + geom_line(aes(x = Size, y = Proportion, colour = Type))
```

---

setResource

*Set resource dynamics*

---

### Description

Sets the intrinsic resource growth rate and the intrinsic resource carrying capacity as well as the name of the function used to simulate the resource dynamics. By default this function changes both the rate and the capacity together in such a way 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,
balance = NULL,
lambda = resource_params(params)[["lambda"]],
n = resource_params(params)[["n"]],
w_pp_cutoff = resource_params(params)[["w_pp_cutoff"]],
r_pp = deprecated(),
kappa = deprecated(),
...
)

resource_rate(params)

resource_rate(params) <- value

resource_capacity(params)

resource_capacity(params) <- value

resource_level(params)

resource_level(params) <- value

resource_dynamics(params)

resource_dynamics(params) <- value

```

### Arguments

<code>params</code>	A MizerParams object
<code>resource_rate</code>	Optional. Vector of resource intrinsic birth rates or coefficient in the power-law for the birth rate, see Details. Must be strictly positive.
<code>resource_capacity</code>	Optional. Vector of resource intrinsic carrying capacities or coefficient in the power-law for the capacity, see Details. The resource capacity must be larger than the resource abundance.
<code>resource_level</code>	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 strictly between 0 and 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 <code>resource_capacity</code> .
<code>resource_dynamics</code>	Optional. Name of the function that determines the resource dynamics by calculating the resource spectrum at the next time step from the current state.
<code>balance</code>	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.
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 only if resource_capacity is given as a single number.
r_pp	<b>[Deprecated]</b> . Use resource_rate argument instead.
kappa	<b>[Deprecated]</b> . Use resource_capacity argument instead.
...	Unused
value	The desired new value for the respective parameter.

### Value

setResource: A MizerParams object with updated resource parameters

### Setting resource dynamics

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.

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 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 growth rate for each size class. Alternatively it can be a single number, which is then used as the coefficient in a power law: then the intrinsic growth 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, which is then used as the coefficient in a truncated power law: then the intrinsic growth rate  $c_R(w)$  at size  $w$  is set to

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

for all  $w$  less than `w_pp_cutoff` and zero for larger sizes. The power-law exponent  $\lambda$  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. That list can be accessed with `resource_params()`. It also holds the coefficient `kappa` that describes the steady-state resource abundance.

## Examples

```
params <- NS_params
resource_dynamics(params)
resource_dynamics(params) <- "resource_constant"
```

---

setRmax	<i>Alias for setBevertonHolt()</i>
---------	------------------------------------

---

## Description

### [Deprecated]

An alias provided for backward compatibility with `mizer` version  $\leq 2.0.4$

## Usage

```
setRmax(params, R_factor = deprecated(), erepro, R_max, reproduction_level)
```

## Arguments

<code>params</code>	A <code>MizerParams</code> object
<code>R_factor</code>	<b>[Deprecated]</b> Use <code>reproduction_level = 1 / R_factor</code> instead.
<code>erepro</code>	Reproductive efficiency for each species. See details.
<code>R_max</code>	Maximum reproduction rate. See details.
<code>reproduction_level</code>	Sets <code>R_max</code> so that the reproduction rate at the initial state is <code>R_max * reproduction_level</code> .

## 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,

$$R_{di} = \frac{erepro}{2w_{min}} E_R,$$

where the proportionality factor is given by the reproductive efficiency `erepro` divided by the egg size `w_min` to convert energy to egg number and divided by 2 to account for the two sexes.

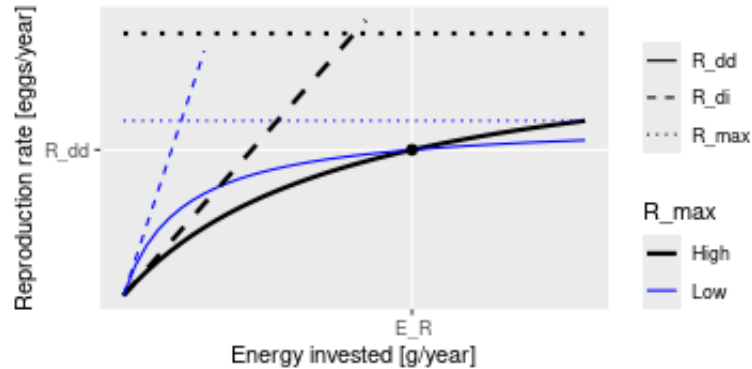


Imposing a finite maximum reproduction rate  $R_{max}$  leads to a non-linear relationship between energy invested and eggs hatched. This density-dependent reproduction rate  $R_{dd}$  is given as

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

(All quantities in the above equations are species-specific but we dropped the species index for simplicity.)

The following plot illustrates the Beverton-Holt density dependence in the reproduction rate for two



different choices of parameters.

This plot shows that a given energy  $E_R$  invested into reproduction can lead to the same reproduction rate  $R_{dd}$  with different choices of the parameters  $R_{max}$  and  $erepro$ .  $R_{max}$  determines the asymptote of the curve and  $erepro$  its initial slope. A higher  $R_{max}$  coupled with a lower  $erepro$  (black curves) can give the same value as a lower  $R_{max}$  coupled with a higher  $erepro$  (blue curves).

For the given initial state in the MizerParams object `params` one can calculate the energy  $E_R$  that is invested into reproduction by the mature individuals and the reproduction rate  $R_{dd}$  that is required to keep the egg abundance constant. These two values determine the location of the black dot in the above graph. You then only need one parameter to select one curve from the family of Beverton-Holt curves going through that point. This parameter can be `erepro` or `R_max`. Instead of `R_max` you can alternatively specify the `reproduction_level` which is the ratio between the density-dependent reproduction rate  $R_{dd}$  and the maximal reproduction rate  $R_{max}$ .

If you do not provide a value for any of the reproduction parameter arguments, then `erepro` will be set to the value it has in the current species parameter data frame. If you do provide one of the reproduction parameters, this can be either a vector with one value for each species, or a named vector where the names determine which species are affected, or a single unnamed value that is then used for all species. Any species for which the given value is NA will remain unaffected.

The values for `R_max` must be larger than  $R_{dd}$  and can range up to Inf. If a smaller value is requested a warning is issued and the value is increased to the value required for a reproduction level of 0.99.

The values for the `reproduction_level` must be positive and less than 1. The values for `erepro` must be large enough to allow the required reproduction rate. If a smaller value is requested a warning is issued and the value is increased to the smallest possible value. The values for `erepro` should also be smaller than 1 to be physiologically sensible, but this is not enforced by the function.

As can be seen in the graph above, choosing a lower value for `R_max` or a higher value for `erepro` means that near the steady state the reproduction will be less sensitive to a change in the energy

invested into reproduction and hence less sensitive to changes in the spawning stock biomass or its energy income. As a result the species will also be less sensitive to fishing, leading to a higher  $F_{MSY}$ .

### Value

A MizerParams object

### Examples

```
params <- NS_params
species_params(params)$erepro
# Attempting to set the same erepro for all species
params <- setBevertonHolt(params, erepro = 0.1)
t(species_params(params)[, c("erepro", "R_max")])
# Setting erepro for some species
params <- setBevertonHolt(params, erepro = c("Gurnard" = 0.6, "Plaice" = 0.95))
t(species_params(params)[, c("erepro", "R_max")])
# Setting R_max
R_max <- 1e17 * species_params(params)$w_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")])
```

---

setSearchVolume	<i>Set search volume</i>
-----------------	--------------------------

---

### Description

Set search volume

### Usage

```
setSearchVolume(params, search_vol = NULL, reset = FALSE, ...)
```

```
getSearchVolume(params)
```

```
search_vol(params)
```

```
search_vol(params) <- value
```

### Arguments

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

reset	<b>[Experimental]</b> If set to TRUE, then the search volume will be reset to the value calculated from the species parameters, even if it was previously overwritten with a custom value. If set to FALSE (default) then a recalculation from the species parameters will take place only if no custom value has been set.
...	Unused
value	search_vol

### Value

setSearchVolume(): A MizerParams object with updated search volume.

getSearchVolume() or equivalently search\_vol(): An array (species x size) holding the search volume

### Setting search volume

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

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

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

$$\gamma_i(w) = \gamma_i w_i^{q_i}.$$

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

### See Also

Other functions for setting parameters: [gear\\_params\(\)](#), [setExtEncounter\(\)](#), [setExtMort\(\)](#), [setFishing\(\)](#), [setInitialValues\(\)](#), [setInteraction\(\)](#), [setMaxIntakeRate\(\)](#), [setMetabolicRate\(\)](#), [setParams\(\)](#), [setPredKernel\(\)](#), [setReproduction\(\)](#), [species\\_params\(\)](#)

---

set\_community\_model     *Deprecated function for setting up parameters for a community-type model*

---

### Description

#### **[Deprecated]**

This function has been deprecated in favour of the function [newCommunityParams\(\)](#) that sets better default values.

**Usage**

```

set_community_model(
  max_w = 1e+06,
  min_w = 0.001,
  min_w_pp = 1e-10,
  z0 = 0.1,
  alpha = 0.2,
  h = 10,
  beta = 100,
  sigma = 2,
  q = 0.8,
  n = 2/3,
  kappa = 1000,
  lambda = 2 + q - n,
  f0 = 0.7,
  r_pp = 10,
  gamma = NA,
  knife_edge_size = 1000,
  knife_is_min = TRUE,
  recruitment = kappa * min_w^-lambda,
  rec_mult = 1,
  ...
)

```

**Arguments**

max_w	The maximum size of the community. The $w_{inf}$ of the species used to represent the community is set to this value. The default value is 1e6.
min_w	The minimum size of the community. Default value is 1e-3.
min_w_pp	The smallest size of the resource spectrum.
z0	The background mortality of the community. Default value is 0.1.
alpha	The assimilation efficiency of the community. Default value 0.2
h	The maximum food intake rate. Default value is 10.
beta	The preferred predator prey mass ratio. Default value is 100.
sigma	The width of the prey preference. Default value is 2.0.
q	The search volume exponent. Default value is 0.8.
n	The scaling of the intake. Default value is 2/3.
kappa	The carrying capacity of the resource spectrum. Default value is 1000.
lambda	The exponent of the resource spectrum. Default value is $2 + q - n$ .
f0	The average feeding level of individuals who feed on a power-law spectrum. This value is used to calculate the search rate parameter gamma (see the package vignette). Default value is 0.7.
r_pp	Growth rate parameter for the resource spectrum. Default value is 10.
gamma	Volumetric search rate. Estimated using h, f0 and kappa if not supplied.

knife_edge_size	The size at the edge of the knife-selectivity function. Default value is 1000.
knife_is_min	Is the knife-edge selectivity function selecting above (TRUE) or below (FALSE) the edge. Default is TRUE.
recruitment	The constant recruitment in the smallest size class of the community spectrum. This should be set so that the community spectrum continues the resource spectrum. Default value = $\kappa * \min_w^{-\lambda}$ .
rec_mult	Additional multiplier for the constant recruitment. Default value is 1.
...	Other arguments to pass to the MizerParams constructor.

### Details

This function 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.

## 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

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

f0	Expected average feeding level. Used to set gamma, the coefficient in the search rate. Ignored if gamma is given explicitly.
kappa	The coefficient of the initial resource abundance power-law.
lambda	Used to set power-law exponent for resource capacity if the resource_capacity argument is given as a single number.
r_pp	<b>[Deprecated]</b> . Use resource_rate argument instead.
...	Unused

**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.

**Usage**

```
set_species_param_default(object, parname, default, message = NULL)
```

**Arguments**

object	Either a MizerParams object or a species parameter data frame
parname	A string with the name of the species parameter to set
default	A single default value or a vector with one default value for each species
message	A string with a message to be issued when the parameter did not already exist

**Value**

The object with an updated column in the species params data frame.

---

set\_trait\_model      *Deprecated function for setting up parameters for a trait-based model*

---

## Description

### [Deprecated]

This function has been deprecated in favour of the function `newTraitParams()` that sets better default values.

## Usage

```
set_trait_model(
  no_sp = 10,
  min_w_inf = 10,
  max_w_inf = 1e+05,
  no_w = 100,
  min_w = 0.001,
  max_w = max_w_inf * 1.1,
  min_w_pp = 1e-10,
  w_pp_cutoff = 1,
  k0 = 50,
  n = 2/3,
  p = 0.75,
  q = 0.9,
  eta = 0.25,
  r_pp = 4,
  kappa = 0.005,
  lambda = 2 + q - n,
  alpha = 0.6,
  ks = 4,
  z0pre = 0.6,
  h = 30,
  beta = 100,
  sigma = 1.3,
  f0 = 0.5,
  gamma = NA,
  knife_edge_size = 1000,
  gear_names = "knife_edge_gear",
  ...
)
```

## Arguments

no_sp	The number of species in the model. The default value is 10. The more species, the longer takes to run.
min_w_inf	The asymptotic size of the smallest species in the community.



max_w_inf	The asymptotic size of the largest species in the community.
no_w	The number of size bins in the community spectrum.
min_w	The smallest size of the community spectrum.
max_w	Obsolete argument because the maximum size of the consumer spectrum is set to max_w_inf.
min_w_pp	Obsolete argument because the smallest resource size is set to the smallest size at which the consumers feed.
w_pp_cutoff	The cut off size of the resource spectrum. Default value is 1.
k0	Multiplier for the maximum recruitment. Default value is 50.
n	Scaling of the intake. Default value is 2/3.
p	Scaling of the standard metabolism. Default value is 0.75.
q	Exponent of the search volume. Default value is 0.9.
eta	Factor to calculate w_mat from asymptotic size.
r_pp	Growth rate parameter for the resource spectrum. Default value is 4.
kappa	Coefficient in abundance power law. Default value is 0.005.
lambda	Exponent of the abundance power law. Default value is (2+q-n).
alpha	The assimilation efficiency of the community. The default value is 0.6
ks	Standard metabolism coefficient. Default value is 4.
z0pre	The coefficient of the background mortality of the community. $z0 = z0pre * w\_inf^{(n-1)}$ . The default value is 0.6.
h	Maximum food intake rate. Default value is 30.
beta	Preferred predator prey mass ratio. Default value is 100.
sigma	Width of prey size preference. Default value is 1.3.
f0	Expected average feeding level. Used to set gamma, the factor for the search volume. The default value is 0.5.
gamma	Volumetric search rate. Estimated using h, f0 and kappa if not supplied.
knife_edge_size	The minimum size at which the gear or gears select species. Must be of length 1 or no_sp.
gear_names	The names of the fishing gears. A character vector, the same length as the number of species. Default is 1 - no_sp.
...	Other arguments to pass to the MizerParams constructor.

## Details

This function 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,  $k\theta$ . Users should adjust  $k\theta$  to get the spectra they want.

The factor for the search volume,  $\gamma$ , is calculated using the expected feeding level,  $f\theta$ .

Fishing selectivity is modelled as a knife-edge function with one parameter, `knife_edge_size`, which is the size at which species are selected. Each species can either be fished by the same gear (`knife_edge_size` has a length of 1) or by a different gear (the length of `knife_edge_size` has the same length as the number of species and the order of selectivity size is that of the asymptotic size).

The resulting `MizerParams` object can be projected forward using `project` like any other `MizerParams` object. When projecting the community model it may be necessary to reduce `dt` to 0.1 to avoid any instabilities with the solver. You can check this by plotting the biomass or abundance through time after the projection.

## Value

An object of type `MizerParams`

## References

K. H. Andersen and M. Pedersen, 2010, Damped trophic cascades driven by fishing in model marine ecosystems. *Proceedings of the Royal Society V, Biological Sciences*, 1682, 795-802.

---

SheperdRDD

*Sheperd function to calculate density-dependent reproduction rate*

---

## Description

**[Experimental]** Takes the density-independent rates  $R_{di}$  of egg production and returns reduced, density-dependent rates  $R_{dd}$  given as

$$R_{dd} = \frac{R_{di}}{1 + (b R_{di})^c}$$

## Usage

`SheperdRDD(rdi, species_params, ...)`

**Arguments**

rdi	Vector of density-independent reproduction rates $R_{di}$ for all species.
species_params	A species parameter dataframe. Must contain columns sheperd_b and sheperd_c with the parameters b and c.
...	Unused

**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	<i>Length based sigmoid selectivity function</i>
----------------	--

---

**Description**

A sigmoid shaped selectivity function. Based on two parameters 125 and 150 which determine the length at which 25% and 50% of the stock is selected respectively.

**Usage**

```
sigmoid_length(w, 125, 150, species_params, ...)
```

**Arguments**

w	Vector of sizes.
125	the length which gives a selectivity of 25%.
150	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**

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\(\)](#), [sigmoid\\_weight\(\)](#)

---

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 the knife-edge operates.
sigmoidal_sigma	The width of the selection function.
...	Unused

**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\(\)](#), [sigmoid\\_length\(\)](#)

---

species_params	<i>Species parameters</i>
----------------	---------------------------

---

**Description**

These functions allow you to get or set the species-specific parameters stored in a MizerParams object.

**Usage**

```
species_params(params)
```

```
species_params(params) <- value
```

```
given_species_params(params)
```

```
given_species_params(params) <- value
```

```
calculated_species_params(params)
```

**Arguments**

params            A MizerParams object

value            A data frame with the species parameters

**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_max` for its maximum size. However if you have information about the values of other parameters then you should provide them.

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()`.

If you change given species parameters with `given_species_params<-()` this will trigger a recalculation of the calculated species parameters, where necessary. However if you change species parameters with `species_params<-()` no recalculation will take place and furthermore your values

could be overwritten by a future recalculation triggered by a call to `given_species_params<-()` . So in most use cases you will only want to use `given_species_params<-()`.

There are some species parameters that are used to set up the size-dependent parameters that are used in the mizer model:

- `gamma` and `q` are used to set the search volume, see [setSearchVolume\(\)](#).
- `h` and `n` are used to set the maximum intake rate, see [setMaxIntakeRate\(\)](#).
- `k`, `ks` and `p` are used to set activity and basic metabolic rate, see [setMetabolicRate\(\)](#).
- `z0` is used to set the external mortality rate, see [setExtMort\(\)](#).
- `w_mat`, `w_mat25`, `w_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\(\)](#). There will be other parameters if you are using other predation kernel functions.

When you change one of the above species parameters using `given_species_params<-()` or `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.

There are some species parameters that are used directly in the model rather than being used for setting up size-dependent parameters:

- `alpha` is the assimilation efficiency, the proportion of the consumed biomass that can be used for growth, metabolism and reproduction, see the help for [getEReproAndGrowth\(\)](#).
- `w_min` is the egg size.
- `interaction_resource` sets the interaction strength with the resource, see "Predation encounter" section in the help for [getEncounter\(\)](#).
- `erepro` is the reproductive efficiency, the proportion of the energy invested into reproduction that is converted to egg biomass, see [getRDI\(\)](#).
- `Rmax` is the parameter in the Beverton-Holt density dependence added to the reproduction, see [setBevertonHolt\(\)](#). There will be other such parameters if you use other density dependence functions, see the "Density dependence" section in the help for [setReproduction\(\)](#).

Two parameters are used only by functions that need to convert between weight and length:

- `a` and `b` are the parameters in the allometric weight-length relationship  $w = ab^b$ .

If you have supplied the `a` and `b` parameters, then you can replace weight parameters like `w_max`, `w_mat`, `w_mat25`, `w_repro_max` and `w_min` by their corresponding length parameters `l_max`, `l_mat`, `l_mat25`, `l_repro_max` and `l_min`.

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()`.

Note that setting these parameters with `species_params<-()` will have no effect. You need to set them with `given_species_params<-()` in order to trigger a re-calculation of the other species parameters.

In the past, `mizer` also used the von Bertalanffy parameters `k_vb`, `w_inf` and `t0` to determine a default for  $h$ . This is unreliable and is therefore now deprecated.

There are other species parameters that are used in tuning the model to observations:

- `biomass_observed` and `biomass_cutoff` allow you to specify for each species the total observed biomass above some cutoff size. This is used by `calibrateBiomass()` and `matchBiomasses()`.
- `yield_observed` allows you to specify for each species the total annual fisheries yield. This is used by `calibrateYield()` and `matchYields()`.

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

Data frame of species parameters

## See Also

`validSpeciesParams()`, `setParams()`

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

---

steady	<i>Set initial values to a steady state for the model</i>
--------	---

---

### Description

The steady state is found by running the dynamics while keeping reproduction, resource and other components constant until the size spectra no longer change much (or until time `t_max` is reached, if earlier).

### Usage

```
steady(
  params,
  t_max = 100,
  t_per = 1.5,
  dt = 0.1,
  tol = 0.1 * dt,
  return_sim = FALSE,
  preserve = c("reproduction_level", "erepro", "R_max"),
  progress_bar = TRUE
)
```

### Arguments

params	A <a href="#">MizerParams</a> object
t_max	The maximum number of years to run the simulation. Default is 100.
t_per	The simulation is broken up into shorter runs of <code>t_per</code> years, after each of which we check for convergence. Default value is 1.5. This should be chosen as an odd multiple of the timestep <code>dt</code> in order to be able to detect period 2 cycles.
dt	The time step to use in <code>project()</code> .
tol	The simulation stops when the relative change in the egg production RDI over <code>t_per</code> years is less than <code>tol</code> for every species.
return_sim	If TRUE, the function returns the <code>MizerSim</code> object holding the result of the simulation run, saved at intervals of <code>t_per</code> . If FALSE (default) the function returns a <code>MizerParams</code> object with the "initial" slots set to the steady state.
preserve	<b>[Experimental]</b> Specifies whether the <code>reproduction_level</code> should be preserved (default) or the maximum reproduction rate <code>R_max</code> or the reproductive efficiency <code>erepro</code> . See <a href="#">setBevertonHolt()</a> for an explanation of the <code>reproduction_level</code> .
progress_bar	A shiny progress object to implement a progress bar in a shiny app. Default FALSE.

### Details

If the model use Beverton-Holt reproduction then the reproduction parameters are set to values that give the level of reproduction observed in that steady state. The `preserve` argument can be used to specify which of the reproduction parameters should be preserved.



**Value**

A MizerParams or a MizerSim object

**Examples**

```
params <- newTraitParams()
species_params(params)$gamma[5] <- 3000
params <- steady(params)
plotSpectra(params)
```

---

steadySingleSpecies    *Set initial abundances to single-species steady state abundances*

---

**Description**

**[Experimental]** This first calculates growth and death rates that arise from the current initial abundances. Then it uses these growth and death rates to determine the steady-state abundances of the selected species.

**Usage**

```
steadySingleSpecies(
  params,
  species = NULL,
  keep = c("egg", "biomass", "number")
)
```

**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.

**Details**

The result of applying this function is of course not a multi-species steady state, because after changing the abundances of the selected species the growth and death rates will have changed.

**Value**

A MizerParams object in which the initial abundances of the selected species are changed to their single-species steady state abundances.

---

summary,MizerParams-method

*Summarize MizerParams object*

---

**Description**

Outputs a general summary of the structure and content of the object

**Usage**

```
## S4 method for signature 'MizerParams'
summary(object, ...)
```

**Arguments**

object	A MizerParams object.
...	Other arguments (currently not used).

**Value**

The MizerParams object, invisibly

**Examples**

```
summary(NS_params)
```

---

summary,MizerSim-method

*Summarize MizerSim object*

---

**Description**

Outputs a general summary of the structure and content of the object

**Usage**

```
## S4 method for signature 'MizerSim'
summary(object, ...)
```

**Arguments**

object            A MizerSim object.  
 ...              Other arguments (currently not used).

**Value**

The MizerSim object, invisibly

**Examples**

```
summary(NS_sim)
```

---

summary_functions	<i>Description of summary functions</i>
-------------------	---

---

**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
<a href="#">getDiet()</a>	Three dimensional array (predator x size x prey)	Diet of predator at size, resolved by prey species
<a href="#">getSSB()</a>	Two dimensional array (time x species)	Total Spawning Stock Biomass (SSB) of each species
<a href="#">getBiomass()</a>	Two dimensional array (time x species)	Total biomass of each species through time.
<a href="#">getN()</a>	Two dimensional array (time x species)	Total abundance of each species through time.
<a href="#">getFeedingLevel()</a>	Three dimensional array (time x species x size)	Feeding level of each species by size through time.
<a href="#">getM2</a>	Three dimensional array (time x species x size)	The predation mortality imposed on each species
<a href="#">getFMort()</a>	Three dimensional array (time x species x size)	Total fishing mortality on each species by size
<a href="#">getFMortGear()</a>	Four dimensional array (time x gear x species x size)	Fishing mortality on each species by each gear
<a href="#">getYieldGear()</a>	Three dimensional array (time x gear x species)	Total yield by gear and species through time.
<a href="#">getYield()</a>	Two dimensional array (time x species)	Total yield of each species across all gears through time.

**See Also**

[indicator\\_functions](#), [plotting\\_functions](#)

---

truncated\_lognormal\_pred\_kernel

*Truncated lognormal predation kernel*


---

### Description

This is like the `lognormal_pred_kernel()` but with an imposed maximum predator/prey mass ratio

### Usage

```
truncated_lognormal_pred_kernel(ppmr, beta, sigma)
```

### Arguments

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

### Details

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

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

if  $w/w_p$  is between 1 and  $\beta_i \exp(3\sigma_i)$  and zero otherwise. Here  $\beta_i$  is the preferred predator-prey mass ratio and  $\sigma_i$  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()`, `lognormal_pred_kernel()`, `power_law_pred_kernel()`

### Examples

```
params <- NS_params
species_params(params)$pred_kernel_type <- "truncated_lognormal"
plot(w_full(params), getPredKernel(params)["Cod", 10, ], type="l", log="x")
```

---

validGearParams	<i>Check validity of gear parameters and set defaults</i>
-----------------	---

---

### 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 `knife_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)
```

**Arguments**

`params`            The MizerParams object to validate

**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).

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.

Besides upgrading, if necessary, the only changes that may be made to the given MizerParams object is that the `w_min_idx` and `ft_mask` slots are recalculated.

**Value**

A valid 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. Checks whether any abundances are non-finite and if any are found, a warning is issued and the simulation is truncated at the last time step where all results are 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)
```

```
validGivenSpeciesParams(species_params)
```

### Arguments

`species_params` The user-supplied species parameter data frame

### Details

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

- the species column does not exist or contains duplicates
- the maximum size is not specified for all species



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 a warning is issued if the two are inconsistent.

If a *w\_inf* column is given but no *w\_max* then the value from *w\_inf* is used. This is for backwards compatibility. But note that the von Bertalanffy parameter *w\_inf* is not the maximum size of the largest individual, but the asymptotic size of an average individual.

Some inconsistencies in the size parameters are resolved as follows:

- Any *w\_mat* that is not smaller than *w\_max* is set to  $w_{max} / 4$ .
- Any *w\_mat25* that is not smaller than *w\_mat* is set to NA.
- 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.

`validSpeciesParams()` first calls `validateGivenSpeciesParams()` but then goes further by adding default values for species parameters that were not provided. The function sets default values if any of the following species parameters are missing or NA:

- *w\_repro\_max* is set to *w\_max*
- *w\_mat* is set to  $w_{max}/4$
- *w\_min* is set to 0.001
- *alpha* is set to 0.6
- *interaction\_resource* is set to 1
- *n* is set to 3/4

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).

## 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\(\)](#)

---

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.

---

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.

---

w	<i>Size bins</i>
---	------------------

---

**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)
```

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