

# Sensitivity Testing

## Set Up (following course)

We follow the same protocol and code to set our parameters as outlined in Part 2 Tutorial 1, 2, and 3 of the mizer course.

### Setting/Collecting the Parameters

First we load in the required libraries:

```
library(mizer)
library(mizerExperimental)
library(tidyverse)
library(rfishbase)
```

Load in the the selection of model species and their parameters from Spence et al. (2021)

```
download.file("https://github.com/gustavdelius/mizerCourse/raw/master/build/species_params_spence_et_al.rds",
              destfile = "species_params_spence_et_al.rds")
```

```
sp_spence <- readRDS("species_params_spence_et_al.rds")
names(sp_spence)
```

```
[1] "species" "beta"    "sigma"   "F0"      "w_inf"   "w_mat"   "h"
[8] "ks"      "k_vb"    "Rmax"
```

Then use Spence et al. (2021) list of species to attach the species parameters to

```
sp_spence$species
```

```
[1] Herring      Sprat      Cod      Haddock    Whiting
[6] Blue whiting Norway Pout Poor Cod   European Hake Monkfish
[11] Horse Mackerel Mackerel   Common Dab Plaice     Megrim
[16] Sole         Boarfish
17 Levels: Blue whiting Boarfish Cod Common Dab European Hake ... Whiting
```

```
sp <- select(sp_spence, species)
comment(sp$species) <- "We follow the choice of species made by Spence et.al (2021) https://
```

Find and attach the latin names of the species

```
herring_latin <- common_to_sci("Herring")
```

```
Joining with `by` = join_by(Subfamily, GenCode, FamCode)`
Joining with `by` = join_by(FamCode)`
Joining with `by` = join_by(Order, Ordnum, Class, ClassNum)`
Joining with `by` = join_by(Class, ClassNum)`
```

```
herring_latin
```

```
# A tibble: 331 x 4
  Species                ComName                Language SpecCode
  <chr>                  <chr>                  <chr>      <int>
1 Pristigaster cayana    Amazon hatchet herring English     1657
2 Sauvagella robusta    Amboaboa round herring English    58936
3 Pleuragramma antarcticum Antarctic herring    English      472
4 Strangomera bentincki Araucanian herring    English    1530
5 Clupea harengus        Atlantic herring       English      24
6 Etrumeus sadina        Atlantic round herring English    1455
7 Opisthonema oglinum    Atlantic thread herring English    1486
8 Opisthonema oglinum    Atlantic Thread Herring English    1486
9 Potamalosa richmondia Australian freshwater herring English    1571
10 Elops machnata         Australian giant herring English    5512
# i 321 more rows
```

```
arrange(herring_latin, SpecCode)
```

```
# A tibble: 331 x 4
```

	Species <chr>	ComName <chr>	Language <chr>	SpecCode <int>
1	Clupea harengus	Atlantic herring	English	24
2	Clupea harengus	Baltic herring	English	24
3	Clupea harengus	Bank herring	English	24
4	Clupea harengus	Bismark herring	English	24
5	Clupea harengus	Cleanplate herring	English	24
6	Clupea harengus	Cut spiced herring	English	24
7	Clupea harengus	Fall herring	English	24
8	Clupea harengus	Herring	English	24
9	Clupea harengus	Kipper herring	English	24
10	Clupea harengus	Klondyked herring	English	24

```
# i 321 more rows
```

```
sp$latin_name <- c("Clupea harengus", # Herring  
  "Sprattus sprattus", # Sprat  
  "Gadus morhua", # Cod  
  "Melanogrammus aeglefinus", # Haddock  
  "Merlangius merlangus", # Whiting  
  "Micromesistius poutassou", # Blue whiting  
  "Trisopterus esmarkii", # Norway Pout  
  "Trisopterus minutus", # Poor Cod  
  "Merluccius merluccius", # European Hake  
  "Lophius piscatorius", # Monkfish  
  "Trachurus trachurus", # Horse Mackerel  
  "Scomber scombrus", # Mackerel  
  "Limanda limanda", # Common Dab  
  "Pleuronectes platessa", # Plaice  
  "Lepidorhombus whiffiagonis", # Megrim  
  "Solea solea", # Sole  
  "Capros aper") # Boarfish
```

Now we find and add the asymptotic slope (max weight and max length) parameter to our species parameter data frame. We do this by looking at catch data and applying the asymptotic size for those that have one listed. For those without we use the FishBase data. We convert length to weight using the allometric length-weight relationship.

```

download.file("https://github.com/gustavdelius/mizerCourse/raw/master/build/catch.csv",
              destfile = "catch.csv")
catch <- read.csv("catch.csv")
max_size <- catch |>
  group_by(species) |>
  summarise(l_max = max(length))
missing <- !(sp$species %in% max_size$species)
sp$species[missing]
max_size_fishbase <- rfishbase::species(sp$latin_name[missing]) |>
  select(latin_name = Species, l_max = Length)
max_size_fishbase
max_size_fishbase <- max_size_fishbase |>
  left_join(select(sp, species, latin_name),
            by = "latin_name")
max_size <- bind_rows(max_size, max_size_fishbase) |>
  select(species, l_max)
max_size
length_weight <- estimate(sp$latin_name, fields = c("Species", "a", "b"))
length_weight
sp <- sp |>
  left_join(length_weight, by = c("latin_name" = "Species")) |>
  left_join(max_size) |>
  mutate(w_max = a * l_max ^ b)
comment(sp$a) <- "Taken from the `a` column in the 'estimates' table on FishBase on 07/12/20"
comment(sp$b) <- "Taken from the `b` column in the 'estimates' table on FishBase on 07/12/20"
comment(sp$l_max) <- "See https://mizer.course.sizespectrum.org/build/collect-parameters.html"
comment(sp$w_max) <- "Calculated from `l_max` using weight-length parameters `a` and `b`."

```

Now we add the growth parameters by first getting median of the estimates of the maturity size and age from FishBase and add it to the species parameter data frame.

```
maturity_tbl <- rfishbase::maturity(sp$latin_name)
```

Joining with `by = join\_by(SpecCode)`

```
maturity_tbl
```

```

# A tibble: 575 x 39
  Species   SpecCode autoctr StockCode MaturityRefNo Sex AgeMatMin AgeMatMin2
  <chr>       <int>   <int>   <int>         <int> <chr>   <dbl>   <dbl>

```

```

1 Capros a~      54    9097      64      96852 mixed      NA      NA
2 Capros a~      54    8519      64      97057 mixed      NA      NA
3 Capros a~      54    8648      64      97057 unse~      NA      NA
4 Capros a~      54    8649      64      97057 unse~      NA      NA
5 Clupea h~      24      63      32        796 unse~      NA      NA
6 Clupea h~      24      78      32      2809 unse~      NA      NA
7 Clupea h~      24      79      32      2809 unse~      NA      NA
8 Clupea h~      24      80      32      3561 unse~        2        4
9 Clupea h~      24      99      32     12186 fema~      NA      NA
10 Clupea h~     24     100      32     12186 male      NA      NA
# i 565 more rows
# i 31 more variables: AgeMatRef <int>, tm <dbl>, Number <int>, r2 <dbl>,
#   SE_tm <dbl>, SD_tm <dbl>, LCL_tm <dbl>, UCL_tm <dbl>, LengthMatMin <dbl>,
#   LengthMatMin2 <dbl>, Type1 <chr>, LengthMatRef <int>, Lm <dbl>,
#   LCL_Lm <dbl>, SD_Lm <dbl>, LmaxLm <dbl>, LmaxLmType <chr>, LmaxLmRef <int>,
#   UCL_Lm <dbl>, SE_Lm <dbl>, Locality <chr>, C_Code <chr>, E_CODE <int>,
#   Comment <chr>, Entered <int>, DateEntered <dtm>, Modified <int>, ...

```

```

median_maturity <- maturity_tbl |>
  group_by(Species) |>
  filter(!is.na(tm), !is.na(Lm)) |>
  summarise(age_mat = median(tm),
            l_mat = median(Lm))
median_maturity

```

```

# A tibble: 17 x 3
  Species          age_mat l_mat
  <chr>          <dbl> <dbl>
1 Capros aper          3.40  8.05
2 Clupea harengus       3    25.3
3 Gadus morhua         6.18 66.5
4 Lepidorhombus whiffiagonis 2.75 24.5
5 Limanda limanda       2.75 24.8
6 Lophius piscatorius    4.5  61
7 Melanogrammus aeglefinus 2.80 35
8 Merlangius merlangus   1.5  24.3
9 Merluccius merluccius  3.25 33.2
10 Micromesistius poutassou 2.15 22.1
11 Pleuronectes platessa   3    27.8
12 Scomber scombrus       1.80 26.2
13 Solea solea           3    26.5
14 Sprattus sprattus      2     9.95

```

15	Trachurus trachurus	2.5	23.6
16	Trisopterus esmarkii	2.15	16.6
17	Trisopterus minutus	1	13.3

```
sp <- sp |>
  left_join(median_maturity, by = c("latin_name" = "Species")) |>
  mutate(w_mat = a * l_mat ^ b)

comment(sp$l_mat) <- "Median of `Lm` over all observations on the 'maturity' table on FishBase"
comment(sp$age_mat) <- "Median of `tm` over all observations on the 'maturity' table on FishBase"
comment(sp$w_mat) <- "Calculated from `l_mat` using weight-length parameters `a` and `b`."
```

Now we add the predator preference curve, we get sigma and beta values from Spence et al. (2021)

```
sp <- left_join(sp, select(sp_spence, species, beta, sigma))
```

Joining with `by = join\_by(species)`

```
comment(sp$beta) <- comment(sp$sigma) <- "Taken from Spence et.al (2021) https://doi.org/10.1111/j.1365-3113.2021.00711.x"
```

Now we calculate abundances by averaging the spawning stock biomass of the ICES stock assessment reports over a 10-year period (2012-2021). Then convert to grams per sq meter.

```
download.file("https://github.com/gustavdelius/mizerCourse/raw/master/build/celtic_sea_ssb.rds",
  destfile = "celtic_sea_ssb.rds")
sp$biomass_observed <- readRDS("celtic_sea_ssb.rds")
comment(sp$biomass_observed) <- "Average of spawning stock biomass over the years 2012--2021"
sp$biomass_cutoff <- sp$w_mat
comment(sp$biomass_cutoff) <- "Set to `w_mat` because `biomass_observed` represents spawning stock"
sp |> select(species, biomass_observed, biomass_cutoff)
```

	species	biomass_observed	biomass_cutoff
1	Herring	0.300000000	121.798516
2	Sprat	0.295749801	6.970650
3	Cod	0.008179382	2780.285169
4	Haddock	0.067381049	376.468948
5	Whiting	0.070079361	107.140861
6	Blue whiting	1.188248745	64.779008
7	Norway Pout	0.172520253	32.323777

8	Poor Cod	NA	23.075213
9	European Hake	0.164362236	266.655482
10	Monkfish	0.048720611	2662.619199
11	Horse Mackerel	NA	91.220035
12	Mackerel	NA	145.943498
13	Common Dab	NA	157.089509
14	Plaice	0.022404698	211.647510
15	Megrim	0.074079322	96.920277
16	Sole	0.063519261	169.576150
17	Boarfish	NA	6.687845

Finally save the species parameters with

```
saveRDS(sp, "celtic_species_params.rds")
```

Now we set the species interaction matrix based on the spatial and temporal overlap of species within the ecosystem using the matrix in Spence et al. (2021)

```
download.file("https://raw.githubusercontent.com/gustavdelius/mizerCourse/master/build/celtic_interaction.csv",
              destfile = "celtic_interaction.csv")
celtic_interaction <- read.csv("celtic_interaction.csv", row.names = 1)
```

Now we set the gear parameters based on Spence et al. (2021)

```
download.file("https://raw.githubusercontent.com/gustavdelius/mizerCourse/master/build/celtic_gear_params.csv",
              destfile = "celtic_gear_params.csv")
celtic_gear_params <- read.csv("celtic_gear_params.csv")
```

## Creating the Model

Load in your species parameters

```
celtic_species_params <- readRDS("celtic_species_params.rds")
celtic_gear_params <- read.csv("celtic_gear_params.csv")
celtic_interaction <- read.csv("celtic_interaction.csv", row.names = 1)
```

Create a MizerParams object

```
cel_model <- newMultispeciesParams(species_params = celtic_species_params,
                                   gear_params = celtic_gear_params,
                                   interaction = celtic_interaction,
                                   initial_effort = 1,
                                   lambda = 2.05, n = 3/4, p = 3/4)
```

No h provided for some species, so using age at maturity to calculate it.  
 No ks column so calculating from critical feeding level.  
 Using  $z_0 = z_{0pre} * w_{max} \sim z_{0exp}$  for missing  $z_0$  values.  
 Using  $f_0$ , h, lambda, kappa and the predation kernel to calculate gamma.

```
cel_model <-
  setMetadata(cel_model,
              title = "Celtic Sea model from mizer course in Nov 2022",
              description = "See https://mizer.course.sizespectrum.org/build")
```

Project to steady state, calibrate, match, repeat

```
cel_model2 <- steady(cel_model)
```

Convergence was achieved in 70.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

```
cel_model3 <- calibrateBiomass(cel_model2)
cel_model4 <- matchBiomasses(cel_model3)
```

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

```
cel_model5 <- steady(cel_model4)
```

Convergence was achieved in 19.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

```
age_mat_model = age_mat(cel_model5)
age_mat_observed = celtic_species_params$age_mat
data.frame(age_mat_model, age_mat_observed)
```



	age_mat_model	age_mat_observed
Herring	3.437276	3.00
Sprat	2.160305	2.00
Cod	5.585913	6.18
Haddock	2.775843	2.80
Whiting	1.387149	1.50
Blue whiting	2.154558	2.15
Norway Pout	2.050345	2.15
Poor Cod	1.025128	1.00
European Hake	2.969979	3.25
Monkfish	4.019366	4.50
Horse Mackerel	2.553231	2.50
Mackerel	1.777960	1.80
Common Dab	2.664111	2.75
Plaice	2.932653	3.00
Megrim	2.687203	2.75
Sole	3.031098	3.00
Boarfish	3.711588	3.40

```
cel_model6 <- matchGrowth(cel_model5)
```

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

```
age_mat_model = age_mat(cel_model6)
data.frame(age_mat_model, age_mat_observed)
```

	age_mat_model	age_mat_observed
Herring	2.9981657	3.00
Sprat	2.0000000	2.00
Cod	5.9218530	6.18
Haddock	2.7677011	2.80
Whiting	1.4693113	1.50
Blue whiting	2.1330711	2.15
Norway Pout	2.1228515	2.15
Poor Cod	0.9955497	1.00
European Hake	3.1470023	3.25
Monkfish	4.2707784	4.50
Horse Mackerel	2.4828743	2.50
Mackerel	1.7767834	1.80
Common Dab	2.7110600	2.75
Plaice	2.9519182	3.00

Megrim	2.7256628	2.75
Sole	2.9763381	3.00
Boarfish	3.3999975	3.40

```
cel_model7 <- steady(cel_model6)
```

Convergence was achieved in 16.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

```
age_mat_model = age_mat(cel_model7)
data.frame(age_mat_model, age_mat_observed)
```

	age_mat_model	age_mat_observed
Herring	2.9986616	3.00
Sprat	2.0000000	2.00
Cod	6.0713975	6.18
Haddock	2.7728577	2.80
Whiting	1.4753253	1.50
Blue whiting	2.1335776	2.15
Norway Pout	2.1245329	2.15
Poor Cod	0.9961611	1.00
European Hake	3.2138668	3.25
Monkfish	4.4173217	4.50
Horse Mackerel	2.4838542	2.50
Mackerel	1.7788891	1.80
Common Dab	2.7159953	2.75
Plaice	2.9582446	3.00
Megrim	2.7262428	2.75
Sole	2.9789671	3.00
Boarfish	3.4000035	3.40

```
cel_model8 <- cel_model7 |>
  calibrateBiomass() |> matchBiomasses() |> matchGrowth() |> steady() |>
  calibrateBiomass() |> matchBiomasses() |> matchGrowth() |> steady()
```

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Convergence was achieved in 16.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Convergence was achieved in 12 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

```
age_mat_model = age_mat(cel_model8)
data.frame(age_mat_model, age_mat_observed)
```

	age_mat_model	age_mat_observed
Herring	3.000216	3.00
Sprat	2.000000	2.00
Cod	6.201415	6.18
Haddock	2.805160	2.80
Whiting	1.504011	1.50
Blue whiting	2.153464	2.15
Norway Pout	2.154250	2.15
Poor Cod	1.000787	1.00
European Hake	3.260240	3.25
Monkfish	4.522441	4.50
Horse Mackerel	2.503170	2.50
Mackerel	1.803831	1.80
Common Dab	2.755010	2.75
Plaice	3.006327	3.00
Megrim	2.755029	2.75
Sole	3.003247	3.00
Boarfish	3.400000	3.40

```
saveParams(cel_model8, "cel_model.rds")
```

## Refining the Model

Load in the model we created

```
cel_model <- readParams("cel_model.rds")
```

Increasing the resource down by a factor of 1/2 as instructed in the course and matching biomasses after the fact.

```
cel_model <- scaleDownBackground(cel_model, factor = 1/2)
```

Warning in setBevertonHolt(params, reproduction\_level = 1/4): The following species require a

```
cel_model <- cel_model |> matchGrowth() |> steady()
```

Convergence was achieved in 24 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

```
cel_model <- cel_model |> matchGrowth() |> steady()
```

Convergence was achieved in 13.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

TuneParams function

```
cel_model_trial <- tuneParams(cel_model)
```

Loading required package: shiny

Listening on http://127.0.0.1:4527

Warning in setBevertonHolt(params, reproduction\_level = 1/4): The following species require a

Convergence was achieved in 15 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

Warning: Removed 5 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning: Removed 17 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning: Removed 5 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning: Removed 17 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Warning: Removed 5 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning: Removed 17 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Convergence was achieved in 13.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The followin

Warning: Removed 5 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning: Removed 17 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Warning in setBevertonHolt(params): For the following species `erepro` has been increased to

Convergence was achieved in 6 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The followin

Warning: Removed 5 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 17 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 5 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 17 rows containing missing values or values outside the scale range (``geom_segment()``).

In tuneParams we:

- 1)Scale the background down by a factor of 0.5
- 2)Click steady
- 3)Click match biomass under the abundance tab
- 4)Click steady
- 5)Click steady (with match growth and biomass checked)
- 6)Click return

Now save the model

```
saveParams(cel_model_trial, "cel_model_trial.rds")
```

## Matching Gear Parameters and Maturity Weight

### Trying to match the current model to the one made previously on the course

Load in catch and yield data for our current model (cel\_model\_trial)

```
download.file("https://github.com/gustavdelius/mizerCourse/raw/master/build/catch.csv",
              destfile = "catch.csv")
catch_lengths <- read.csv("catch.csv")
download.file("https://github.com/gustavdelius/mizerCourse/raw/master/build/celtic_yields.rds",
              destfile = "celtic_yields.rds")
gear_params(cel_model_trial)$yield_observed <- readRDS("celtic_yields.rds")
```

Load in the model from the final tutorial in the course (cel\_model\_course), and add the yield data from the previous section to it

```
download.file("https://github.com/gustavdelius/mizerCourse/raw/master/build/cel_model_landings.rds",
              destfile = "cel_model_landings.rds")
cel_model_course <- readParams("cel_model_landings.rds")
gear_params(cel_model_course)$yield_observed <- readRDS("celtic_yields.rds")
```

Match gear params, w\_mat25, and w\_mat of both models

```
gear_params(cel_model_trial) <- gear_params(cel_model_course)

cel_model_trial@species_params[cel_model_trial@species_params$species, c("w_mat25", "w_mat")] <-
cel_model_course@species_params[cel_model_course@species_params$species, c("w_mat25", "w_mat")]
```

After changing the parameters of our model to match the parameters of the final course model. Run our model (cel\_model\_trial) to a steady state matching growth and biomass before hand

```
cel_model_trial <- tuneParams(cel_model_trial)
```

Listening on http://127.0.0.1:4527

Convergence was achieved in 9 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

Warning: Removed 5 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 17 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 5 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 17 rows containing missing values or values outside the scale range (``geom_segment()``).

Warning: Removed 2 rows containing missing values or values outside the scale range  
(`geom\_segment()`).  
Removed 2 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

```
#set to steady state matching growth and biomass  
saveParams(cel_model_trial, "cel_model_trial.rds")
```

Now lets look at the similarity between the params of the final mizer course model and the trial model which we have made similar to the course model

First look at w\_mat25 (values are the same because we set this)

```
species_params(cel_model_trial) |> select(w_mat25)
```

	w_mat25
Herring	98.400000
Sprat	6.240000
Cod	2286.400000
Haddock	402.400000
Whiting	95.145161
Blue whiting	58.039300
Norway Pout	42.364047
Poor Cod	20.240803
European Hake	231.300000
Monkfish	2222.750000
Horse Mackerel	74.400000
Mackerel	126.558007
Common Dab	157.560000
Plaice	229.600000
Megrim	78.891021
Sole	121.721039
Boarfish	5.992032

```
species_params(cel_model_course) |> select(w_mat25)
```

	w_mat25
Herring	98.400000
Sprat	6.240000
Cod	2286.400000
Haddock	402.400000



Whiting	95.145161
Blue whiting	58.039300
Norway Pout	42.364047
Poor Cod	20.240803
European Hake	231.300000
Monkfish	2222.750000
Horse Mackerel	74.400000
Mackerel	126.558007
Common Dab	157.560000
Plaice	229.600000
Megrim	78.891021
Sole	121.721039
Boarfish	5.992032

Then look at w\_mat (values are the same because we set this)

```
species_params(cel_model_trial) |> select(w_mat)
```

	w_mat
Herring	123.000000
Sprat	7.800000
Cod	2858.000000
Haddock	503.000000
Whiting	106.193719
Blue whiting	64.779008
Norway Pout	47.283495
Poor Cod	22.591229
European Hake	257.000000
Monkfish	2615.000000
Horse Mackerel	93.000000
Mackerel	141.254325
Common Dab	202.000000
Plaice	287.000000
Megrim	88.052097
Sole	135.855672
Boarfish	6.687845

```
species_params(cel_model_course) |> select(w_mat)
```

	w_mat
Herring	123.000000

Sprat	7.800000
Cod	2858.000000
Haddock	503.000000
Whiting	106.193719
Blue whiting	64.779008
Norway Pout	47.283495
Poor Cod	22.591229
European Hake	257.000000
Monkfish	2615.000000
Horse Mackerel	93.000000
Mackerel	141.254325
Common Dab	202.000000
Plaice	287.000000
Megrim	88.052097
Sole	135.855672
Boarfish	6.687845

Then look at 150 (values are the same because we set this)

```
gear_params(cel_model_trial) |> select(150)
```

	150
Herring, Commercial	19.6
Sprat, Commercial	9.8
Cod, Commercial	44.0
Haddock, Commercial	31.1
Whiting, Commercial	33.7
Blue whiting, Commercial	21.6
Norway Pout, Commercial	13.2
Poor Cod, Commercial	14.0
European Hake, Commercial	56.7
Monkfish, Commercial	32.1
Horse Mackerel, Commercial	20.0
Mackerel, Commercial	26.8
Common Dab, Commercial	20.7
Plaice, Commercial	28.9
Megrim, Commercial	25.9
Sole, Commercial	18.1
Boarfish, Commercial	8.3

```
gear_params(cel_model_course) |> select(150)
```

	150
Herring, Commercial	19.6
Sprat, Commercial	9.8
Cod, Commercial	44.0
Haddock, Commercial	31.1
Whiting, Commercial	33.7
Blue whiting, Commercial	21.6
Norway Pout, Commercial	13.2
Poor Cod, Commercial	14.0
European Hake, Commercial	56.7
Monkfish, Commercial	32.1
Horse Mackerel, Commercial	20.0
Mackerel, Commercial	26.8
Common Dab, Commercial	20.7
Plaice, Commercial	28.9
Megrim, Commercial	25.9
Sole, Commercial	18.1
Boarfish, Commercial	8.3

Then look at l25 (values are the same because we set this)

```
gear_params(cel_model_trial) |> select(125)
```

	125
Herring, Commercial	18.2
Sprat, Commercial	8.4
Cod, Commercial	39.5
Haddock, Commercial	29.4
Whiting, Commercial	29.2
Blue whiting, Commercial	19.4
Norway Pout, Commercial	11.2
Poor Cod, Commercial	11.9
European Hake, Commercial	49.5
Monkfish, Commercial	27.3
Horse Mackerel, Commercial	18.8
Mackerel, Commercial	22.8
Common Dab, Commercial	19.5
Plaice, Commercial	26.0
Megrim, Commercial	22.0

Sole, Commercial	15.4
Boarfish, Commercial	7.6

```
gear_params(cel_model_course) |> select(125)
```

	125
Herring, Commercial	18.2
Sprat, Commercial	8.4
Cod, Commercial	39.5
Haddock, Commercial	29.4
Whiting, Commercial	29.2
Blue whiting, Commercial	19.4
Norway Pout, Commercial	11.2
Poor Cod, Commercial	11.9
European Hake, Commercial	49.5
Monkfish, Commercial	27.3
Horse Mackerel, Commercial	18.8
Mackerel, Commercial	22.8
Common Dab, Commercial	19.5
Plaice, Commercial	26.0
Megrim, Commercial	22.0
Sole, Commercial	15.4
Boarfish, Commercial	7.6

Then look at catchability (values are the same because we set this)

```
gear_params(cel_model_trial) |> select(catchability)
```

	catchability
Herring, Commercial	0.690
Sprat, Commercial	0.590
Cod, Commercial	0.466
Haddock, Commercial	0.360
Whiting, Commercial	0.450
Blue whiting, Commercial	0.260
Norway Pout, Commercial	0.510
Poor Cod, Commercial	0.011
European Hake, Commercial	0.500
Monkfish, Commercial	0.360
Horse Mackerel, Commercial	0.350
Mackerel, Commercial	0.564

Common Dab, Commercial	0.680
Plaice, Commercial	0.630
Megrim, Commercial	0.240
Sole, Commercial	0.220
Boarfish, Commercial	0.130

```
gear_params(cel_model_course) |> select(catchability)
```

	catchability
Herring, Commercial	0.690
Sprat, Commercial	0.590
Cod, Commercial	0.466
Haddock, Commercial	0.360
Whiting, Commercial	0.450
Blue whiting, Commercial	0.260
Norway Pout, Commercial	0.510
Poor Cod, Commercial	0.011
European Hake, Commercial	0.500
Monkfish, Commercial	0.360
Horse Mackerel, Commercial	0.350
Mackerel, Commercial	0.564
Common Dab, Commercial	0.680
Plaice, Commercial	0.630
Megrim, Commercial	0.240
Sole, Commercial	0.220
Boarfish, Commercial	0.130

Then look at interaction matrix (values are the same because we followed the instructions in the course)

```
interaction_matrix(cel_model_trial)
```

predator	prey					
	Herring	Sprat	Cod	Haddock	Whiting	Blue whiting
Herring	1.0000000	0.8195604	0.6154876	0.5772874	0.6967521	0.4815089
Sprat	0.8195604	1.0000000	0.5804143	0.5840113	0.6776021	0.4733540
Cod	0.6154876	0.5804143	1.0000000	0.7255170	0.7063008	0.6780023
Haddock	0.5772874	0.5840113	0.7255170	1.0000000	0.7875288	0.8354539
Whiting	0.6967521	0.6776021	0.7063008	0.7875288	1.0000000	0.6935270
Blue whiting	0.4815089	0.4733540	0.6780023	0.8354539	0.6935270	1.0000000
Norway Pout	0.6555975	0.6273923	0.6657803	0.6700391	0.6784104	0.5866525

Poor Cod	0.5519318	0.5620791	0.7180307	0.8479253	0.7963420	0.7741834
European Hake	0.5363234	0.5413184	0.7314981	0.8890550	0.7822410	0.8899857
Monkfish	0.5598664	0.5620258	0.7208944	0.7669478	0.6929262	0.7690768
Horse Mackerel	0.5201465	0.5294615	0.6693650	0.8328589	0.7704500	0.8038219
Mackerel	0.6051923	0.5686300	0.6614548	0.8251678	0.8308310	0.7928538
Common Dab	0.8315201	0.8007295	0.6282193	0.6159224	0.7380539	0.5140536
Plaice	0.6591178	0.6058303	0.5745085	0.5327162	0.5920184	0.4555095
Megrim	0.4101717	0.4162067	0.6380550	0.7924981	0.6392792	0.8076951
Sole	0.4345879	0.4082967	0.3738797	0.3111294	0.3539678	0.3014402
Boarfish	0.3947280	0.3977859	0.6108425	0.7465867	0.6090304	0.7544306
prey						
predator	Norway Pout	Poor Cod	European Hake	Monkfish	Horse Mackerel	
Herring	0.6555975	0.5519318	0.5363234	0.5598664	0.5201465	
Sprat	0.6273923	0.5620791	0.5413184	0.5620258	0.5294615	
Cod	0.6657803	0.7180307	0.7314981	0.7208944	0.6693650	
Haddock	0.6700391	0.8479253	0.8890550	0.7669478	0.8328589	
Whiting	0.6784104	0.7963420	0.7822410	0.6929262	0.7704500	
Blue whiting	0.5866525	0.7741834	0.8899857	0.7690768	0.8038219	
Norway Pout	1.0000000	0.6416201	0.6355645	0.6119148	0.5902888	
Poor Cod	0.6416201	1.0000000	0.8639957	0.7494732	0.9293886	
European Hake	0.6355645	0.8639957	1.0000000	0.7974926	0.8628706	
Monkfish	0.6119148	0.7494732	0.7974926	1.0000000	0.7227249	
Horse Mackerel	0.5902888	0.9293886	0.8628706	0.7227249	1.0000000	
Mackerel	0.6363645	0.8084587	0.8573150	0.7218213	0.8324479	
Common Dab	0.6557529	0.5875043	0.5692862	0.5836906	0.5494641	
Plaice	0.6755342	0.4947914	0.4859067	0.5200352	0.4508132	
Megrim	0.6012862	0.7249423	0.8255616	0.6993049	0.7415118	
Sole	0.3577289	0.2803623	0.3053603	0.3375805	0.2729110	
Boarfish	0.5264544	0.7190578	0.7998537	0.6848543	0.7392673	
prey						
predator	Mackerel	Common Dab	Plaice	Megrim	Sole	Boarfish
Herring	0.6051923	0.8315201	0.6591178	0.4101717	0.4345879	0.3947280
Sprat	0.5686300	0.8007295	0.6058303	0.4162067	0.4082967	0.3977859
Cod	0.6614548	0.6282193	0.5745085	0.6380550	0.3738797	0.6108425
Haddock	0.8251678	0.6159224	0.5327162	0.7924981	0.3111294	0.7465867
Whiting	0.8308310	0.7380539	0.5920184	0.6392792	0.3539678	0.6090304
Blue whiting	0.7928538	0.5140536	0.4555095	0.8076951	0.3014402	0.7544306
Norway Pout	0.6363645	0.6557529	0.6755342	0.6012862	0.3577289	0.5264544
Poor Cod	0.8084587	0.5875043	0.4947914	0.7249423	0.2803623	0.7190578
European Hake	0.8573150	0.5692862	0.4859067	0.8255616	0.3053603	0.7998537
Monkfish	0.7218213	0.5836906	0.5200352	0.6993049	0.3375805	0.6848543
Horse Mackerel	0.8324479	0.5494641	0.4508132	0.7415118	0.2729110	0.7392673
Mackerel	1.0000000	0.6436431	0.5341460	0.7324215	0.3242855	0.7229826

Common Dab	0.6436431	1.0000000	0.6309041	0.4489038	0.4089560	0.4321064
Plaice	0.5341460	0.6309041	1.0000000	0.4245130	0.4206197	0.3452631
Megrim	0.7324215	0.4489038	0.4245130	1.0000000	0.2417441	0.8103316
Sole	0.3242855	0.4089560	0.4206197	0.2417441	1.0000000	0.2183369
Boarfish	0.7229826	0.4321064	0.3452631	0.8103316	0.2183369	1.0000000

```
interaction_matrix(cel_model_course)
```

	prey					
predator	Herring	Sprat	Cod	Haddock	Whiting	Blue whiting
Herring	1.0000000	0.8195604	0.6154876	0.5772874	0.6967521	0.4800000
Sprat	0.8200000	1.0000000	0.5804143	0.5840113	0.6776021	0.4733540
Cod	0.6154876	0.5804143	1.0000000	0.7255170	0.7063008	0.6780023
Haddock	0.5772874	0.5840113	0.7255170	1.0000000	0.7875288	0.8354539
Whiting	0.6967521	0.6776021	0.7063008	0.7875288	1.0000000	0.6935270
Blue whiting	0.4815089	0.2600000	0.6780023	0.8354539	0.6935270	1.0000000
Norway Pout	0.6555975	0.6273923	0.6657803	0.6700391	0.6784104	0.5866525
Poor Cod	0.5519318	0.5620791	0.7180307	0.8479253	0.7963420	0.7741834
European Hake	0.5363234	0.5413184	0.7314981	0.8890550	0.7822410	0.8899857
Monkfish	0.5598664	0.5620258	0.7208944	0.7669478	0.6929262	0.7690768
Horse Mackerel	0.5201465	0.5294615	0.6693650	0.8328589	0.7704500	0.8038219
Mackerel	0.6051923	0.3400000	0.6614548	0.8251678	0.8308310	0.7928538
Common Dab	0.8315201	0.8007295	0.6282193	0.6159224	0.7380539	0.5140536
Plaice	0.6591178	0.6058303	0.5745085	0.5327162	0.5920184	0.4555095
Megrim	0.4101717	0.4162067	0.6380550	0.7924981	0.6392792	0.8076951
Sole	0.4345879	0.4082967	0.3738797	0.3111294	0.3539678	0.3014402
Boarfish	0.3900000	0.3977859	0.6108425	0.7465867	0.6090304	0.7544306

	prey					
predator	Norway Pout	Poor Cod	European Hake	Monkfish	Horse Mackerel	
Herring	0.6555975	0.5519318	0.5363234	0.5598664	0.5201465	
Sprat	0.6273923	0.5620791	0.5413184	0.5620258	0.5294615	
Cod	0.6657803	0.7180307	0.7314981	0.7208944	0.6693650	
Haddock	0.6700391	0.8479253	0.8890550	0.7669478	0.8328589	
Whiting	0.6784104	0.7963420	0.7822410	0.6929262	0.7704500	
Blue whiting	0.5866525	0.7741834	0.8899857	0.7690768	0.8038219	
Norway Pout	1.0000000	0.6416201	0.6355645	0.6119148	0.5902888	
Poor Cod	0.6416201	1.0000000	0.8639957	0.7494732	0.9293886	
European Hake	0.6355645	0.8639957	1.0000000	0.7974926	0.8628706	
Monkfish	0.6119148	0.7494732	0.7974926	1.0000000	0.7227249	
Horse Mackerel	0.5902888	0.9293886	0.8628706	0.7227249	1.0000000	
Mackerel	0.6363645	0.8084587	0.8573150	0.7218213	0.8324479	
Common Dab	0.6557529	0.5875043	0.5692862	0.5836906	0.5494641	

Plaice	0.6755342	0.4947914	0.4859067	0.5200352	0.4508132
Megrim	0.6012862	0.7249423	0.8255616	0.6993049	0.7415118
Sole	0.3577289	0.2803623	0.3053603	0.3375805	0.2729110
Boarfish	0.5264544	0.7190578	0.7998537	0.6848543	0.7392673
prey					
predator	Mackerel	Common Dab	Plaice	Megrim	Sole Boarfish
Herring	0.6051923	0.8315201	0.6591178	0.4101717	0.4345879 0.3947280
Sprat	0.5686300	0.8007295	0.6058303	0.4162067	0.4082967 0.3977859
Cod	0.6614548	0.6282193	0.5745085	0.6380550	0.3738797 0.6108425
Haddock	0.8251678	0.6159224	0.5327162	0.7924981	0.3111294 0.7465867
Whiting	0.8308310	0.7380539	0.5920184	0.6392792	0.3539678 0.6090304
Blue whiting	0.7928538	0.5140536	0.4555095	0.8076951	0.3014402 0.1600000
Norway Pout	0.6363645	0.6557529	0.6755342	0.6012862	0.3577289 0.5264544
Poor Cod	0.8084587	0.5875043	0.4947914	0.7249423	0.2803623 0.7190578
European Hake	0.8573150	0.5692862	0.4859067	0.8255616	0.3053603 0.7998537
Monkfish	0.7218213	0.5836906	0.5200352	0.6993049	0.3375805 0.6848543
Horse Mackerel	0.8324479	0.5494641	0.4508132	0.7415118	0.2729110 0.7392673
Mackerel	1.0000000	0.6436431	0.5341460	0.7324215	0.3242855 0.1500000
Common Dab	0.6436431	1.0000000	0.6309041	0.4489038	0.4089560 0.4321064
Plaice	0.5341460	0.6309041	1.0000000	0.4245130	0.4206197 0.3452631
Megrim	0.7324215	0.4489038	0.4245130	1.0000000	0.2417441 0.8103316
Sole	0.3242855	0.4089560	0.4206197	0.2417441	1.0000000 0.2183369
Boarfish	0.7229826	0.4321064	0.3452631	0.8103316	0.2183369 1.0000000

Now look at reproduction levels (they are similar)

```
getReproductionLevel(cel_model_trial)
```

Herring	Sprat	Cod	Haddock	Whiting
0.9373389	0.9731868	0.9885410	0.9662559	0.9530479
Blue whiting	Norway Pout	Poor Cod	European Hake	Monkfish
0.9816480	0.9841776	0.9416135	0.9985964	0.9739586
Horse Mackerel	Mackerel	Common Dab	Plaice	Megrim
0.9865159	0.9345661	0.9862037	0.9750709	0.9958216
Sole	Boarfish			
0.8170719	0.9973818			

```
getReproductionLevel(cel_model_course)
```

Herring	Sprat	Cod	Haddock	Whiting
0.9734878	0.9966888	0.9971724	0.7569318	0.9538825



Blue whiting	Norway Pout	Poor Cod	European Hake	Monkfish
0.9892638	0.9798886	0.9950881	0.9990410	0.9883076
Horse Mackerel	Mackerel	Common Dab	Plaice	Megrim
0.9944085	0.9681944	0.9952773	0.9913926	0.9983078
Sole	Boarfish			
0.8862835	0.9999991			

Then look at Biomass (similar for most species, but different for Sprat, Poor cod, Horse Mackerel, Mackerel, and Boarfish)

```
getBiomass(cel_model_trial)
```

Herring	Sprat	Cod	Haddock	Whiting
0.623053004	1.603242543	0.014512837	0.070970347	0.078451208
Blue whiting	Norway Pout	Poor Cod	European Hake	Monkfish
1.608097542	0.332199064	4.043710283	0.264979226	0.060502641
Horse Mackerel	Mackerel	Common Dab	Plaice	Megrim
0.103241623	1.097235790	0.216677784	0.031744842	0.147979589
Sole	Boarfish			
0.068726133	0.008443328			

```
getBiomass(cel_model_course)
```

Herring	Sprat	Cod	Haddock	Whiting
0.691426141	0.404418530	0.012949244	0.073112963	0.072815033
Blue whiting	Norway Pout	Poor Cod	European Hake	Monkfish
1.430257688	0.258530677	0.007968153	0.170047601	0.060597682
Horse Mackerel	Mackerel	Common Dab	Plaice	Megrim
0.532999576	0.552924607	0.021766977	0.025020510	0.085101948
Sole	Boarfish			
0.068376003	0.151676286			

But when we look at the how low we can set the erepro get even more dissimilar values:

```
cel_model_trial_res_tuning <- setBevertonHolt(cel_model_trial, erepro = 0.001)
```

Warning in setBevertonHolt(cel\_model\_trial, erepro = 0.001): For the following species `erepro`

```
species_params(cel_model_trial_res_tuning) |> select(erepro, R_max)
```

	erepro	R_max
Herring	0.001313705	Inf
Sprat	0.017671321	Inf
Cod	0.001000000	0.0002962099
Haddock	0.001000000	0.0014027078
Whiting	0.001000000	0.0018689631
Blue whiting	0.001245182	Inf
Norway Pout	0.001902600	Inf
Poor Cod	0.001000000	0.2296244918
European Hake	0.001000000	0.0151330895
Monkfish	0.001000000	0.0002172201
Horse Mackerel	0.003300616	Inf
Mackerel	0.001000000	0.1016570148
Common Dab	0.001000000	0.0491921294
Plaice	0.001000000	0.0011675057
Megrim	0.001222652	Inf
Sole	0.001000000	0.0007011753
Boarfish	1.590643390	Inf

```
cel_model_course_res_tuning <- setBevertonHolt(cel_model_course, erepro = 0.001)
species_params(cel_model_course_res_tuning) |> select(erepro, R_max)
```

	erepro	R_max
Herring	0.001 0.3369135240	
Sprat	0.001 0.9592472746	
Cod	0.001 0.0000653820	
Haddock	0.001 0.0003347841	
Whiting	0.001 0.0005564558	
Blue whiting	0.001 0.2309752956	
Norway Pout	0.001 0.2055672725	
Poor Cod	0.001 0.0017380261	
European Hake	0.001 0.0016200795	
Monkfish	0.001 0.0001134333	
Horse Mackerel	0.001 0.0898418890	
Mackerel	0.001 0.0139503716	
Common Dab	0.001 0.0013293500	
Plaice	0.001 0.0002653793	
Megrim	0.001 0.0075371245	
Sole	0.001 0.0002506685	
Boarfish	0.001 0.1340020866	

## Matching Biomasses

### Set Observed Biomasses of the Unknown Biomass Species in Our Model to the Modelled Biomasses of the Course Model

Load the modelled biomasses of the final course model

```
getBiomass(cel_model_course)
```

Herring	Sprat	Cod	Haddock	Whiting
0.691426141	0.404418530	0.012949244	0.073112963	0.072815033
Blue whiting	Norway Pout	Poor Cod	European Hake	Monkfish
1.430257688	0.258530677	0.007968153	0.170047601	0.060597682
Horse Mackerel	Mackerel	Common Dab	Plaice	Megrim
0.532999576	0.552924607	0.021766977	0.025020510	0.085101948
Sole	Boarfish			
0.068376003	0.151676286			

Identify which species we are missing biomasses for in our trial model

```
missing_biomass_species <- cel_model_trial@species_params[is.na(cel_model_trial@species_params$biomass_observed),]  
missing_biomass_species
```

```
[1] "Poor Cod"      "Horse Mackerel" "Mackerel"      "Common Dab"  
[5] "Boarfish"
```

Now we need to set the observed biomass for these species in our trial model to the modelled biomass in the final course model

```
species_to_update <- c("Poor Cod", "Horse Mackerel", "Mackerel", "Common Dab", "Boarfish")  
biomass_course_model <- c(0.007968153, 0.532999576, 0.552924607, 0.021766977, 0.151676286)  
  
# Update biomass_observed for matching species  
cel_model_trial@species_params[cel_model_trial@species_params$species %in% species_to_update, "biomass_observed"] <- biomass_course_model
```

Set the model to steady

```
cel_model_trial <- tuneParams(cel_model_trial)
```

Listening on http://127.0.0.1:4527

Warning: Removed 17 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Removed 17 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Warning: Removed 2 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Removed 2 rows containing missing values or values outside the scale range  
(`geom\_segment()`).

Convergence was achieved in 13.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

Convergence was achieved in 7.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

Convergence was achieved in 1.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

Convergence was achieved in 1.5 years.

Warning in setBevertonHolt(params, reproduction\_level = old\_reproduction\_level): The following

```
#set to steady state matching growth and biomass x3  
saveParams(cel_model_trial, "cel_model_trial_matched_biomass.rds")
```

Now we compare the minimum erepro values

```
cel_model_trial_res_tuning <- setBevertonHolt(cel_model_trial, erepro = 0.001)
```

Warning in setBevertonHolt(cel\_model\_trial, erepro = 0.001): For the following species `erepro`

```
species_params(cel_model_trial_res_tuning) |> select(erepro, R_max)
```

	erepro	R_max
Herring	0.001000000	1.970865e-02
Sprat	0.001000000	5.305406e+01
Cod	0.001000000	1.850268e-05
Haddock	0.001000000	1.316575e-04
Whiting	0.001000000	2.532111e-04
Blue whiting	0.001000000	3.764184e-02
Norway Pout	0.001000000	1.411461e-02
Poor Cod	0.001000000	2.671049e-05
European Hake	0.001000000	4.282419e-04
Monkfish	0.001000000	3.571449e-05
Horse Mackerel	0.001000000	2.414043e-02
Mackerel	0.001000000	5.223251e-03
Common Dab	0.001000000	5.199881e-04
Plaice	0.001000000	1.397637e-04
Megrim	0.001000000	1.175544e-03
Sole	0.001000000	1.801388e-04
Boarfish	0.008257518	Inf

```
cel_model_course_res_tuning <- setBevertonHolt(cel_model_course, erepro = 0.001)
```

```
species_params(cel_model_course_res_tuning) |> select(erepro, R_max)
```

	erepro	R_max
Herring	0.001	0.3369135240
Sprat	0.001	0.9592472746
Cod	0.001	0.0000653820
Haddock	0.001	0.0003347841
Whiting	0.001	0.0005564558
Blue whiting	0.001	0.2309752956
Norway Pout	0.001	0.2055672725
Poor Cod	0.001	0.0017380261
European Hake	0.001	0.0016200795
Monkfish	0.001	0.0001134333
Horse Mackerel	0.001	0.0898418890
Mackerel	0.001	0.0139503716
Common Dab	0.001	0.0013293500
Plaice	0.001	0.0002653793
Megrim	0.001	0.0075371245

Sole	0.001	0.0002506685
Boarfish	0.001	0.1340020866

While the minimum erepro values are more similar now, R\_\_max values for each species at this erepro are sometimes different (ie: Herring, sprat, Norway Pout)