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_sp
              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

```r
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
```

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

Find and attach the latin names of the species

```r
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)`
```

```r
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
```

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

```
# A tibble: 331 x 4
   Species         ComName              Language SpecCode
   <chr>           <chr>                <chr>       <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
```

```r
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.

```r
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 07/12/202
comment(sp$b) <- "Taken from the `b` column in the 'estimates' table on FishBase on 07/12/202
comment(sp$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 paramter data frame.

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

```
Joining with `by = join_by(SpecCode)`
```

```r
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 <dttm>, 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$l_mat) <- "Median of `Lm` over all observations on the 'maturity' table on FishBas
comment(sp$age_mat) <- "Median of `tm` over all observations on the 'maturity' table on FishB
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.
```

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.rd
              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
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/celti
              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/celti
              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

```r
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 z0 = z0pre * w_max ^ z0exp for missing z0 values.
Using f0, h, lambda, kappa and the predation kernel to calculate gamma.
```

```r
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

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

```
Convergence was achieved in 70.5 years.

Warning in setBevertonHolt(params, reproduction_level = old_reproduction_level): The followi
```

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

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

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

```
Convergence was achieved in 19.5 years.

Warning in setBevertonHolt(params, reproduction_level = old_reproduction_level): The followi
```

```r
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
```

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

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

```r
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
```

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

```
Convergence was achieved in 16.5 years.
```

```
Warning in setBevertonHolt(params, reproduction_level = old_reproduction_level): The followi
```

```r
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
```

```r
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 followi

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 followi
```

```
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

```r
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.

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

```
Warning in setBevertonHolt(params, reproduction_level = 1/4): The following species require a
```

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

```
Convergence was achieved in 24 years.
```

```
Warning in setBevertonHolt(params, reproduction_level = old_reproduction_level): The followin
```

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

```
Convergence was achieved in 13.5 years.
```

```
Warning in setBevertonHolt(params, reproduction_level = old_reproduction_level): The followin
```

TuneParams function

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

```
Loading required package: shiny
```

```
Listening on http://127.0.0.1:6554
```

```
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 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()`).

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 followi

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 followi
```

```
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 and Testing

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_landing
              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_ma
```

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://127.0.0.1:6554
```

```
Convergence was achieved in 9 years.
```

```
Warning in setBevertonHolt(params, reproduction_level = old_reproduction_level): The followi
```

```
#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
```

```r
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)

```r
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
```

```r
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 l50 (values are the same because we set this)

```
gear_params(cel_model_trial) |> select(l50)
```

```
                              l50
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(l50)
```

```
                              l50
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)

```r
gear_params(cel_model_trial) |> select(l25)
```

```
                            l25
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
```

```r
gear_params(cel_model_course) |> select(l25)
```

```
                            l25
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)
```

```
                prey
predator           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
```

```r
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
```

```r
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:

```r
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 `erep
```

```r
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
```

```r
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
```