

Adjusting max size of the Final Course Model

Load in Libraries

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

Load in Course Model

```
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")
```

Making a data frame with the new w_max and l_max values

```
cel_model_course <- readParams("cel_model_landings.rds")
params<-species_params(cel_model_course)
saveRDS(params, file = "species_params.rds")
params <- readRDS("species_params.rds")

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")
sp <- select(sp_spence, species)
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
max_size_fishbase <- rfishbase::species(sp$latin_name) |>
  select(latin_name = Species, w_max = Weight, l_max = Length)

```

Joining with `by = join_by(SpecCode)`

```

max_size_fishbase <- left_join(sp, max_size_fishbase, by = "latin_name")
length_weight <- estimate(max_size_fishbase$latin_name, fields = c("Species", "a", "b"))

```

Joining with `by = join_by(SpecCode)`

```

max_size <- max_size_fishbase |>
  left_join(length_weight, by = c("latin_name" = "Species"))
max_size <- max_size |>
  mutate(w_max_calc = a * l_max ^ b)
max_size$w_max[is.na(max_size$w_max)] <- max_size$w_max_calc[is.na(max_size$w_max)]
max_size <- max_size[c("species", "w_max", "l_max")]

```

```

#new species parameters
max_size

```

	species	w_max	l_max
1	Herring	1050.00000	45.0
2	Sprat	30.25037	16.0
3	Cod	96000.00000	200.0
4	Haddock	16800.00000	112.0
5	Whiting	3110.00000	91.5

6	Blue whiting	830.00000	55.5
7	Norway Pout	319.77787	35.0
8	Poor Cod	711.87913	40.0
9	European Hake	15000.00000	140.0
10	Monkfish	57700.00000	200.0
11	Horse Mackerel	2000.00000	70.0
12	Mackerel	3400.00000	60.0
13	Common Dab	1000.00000	40.0
14	Plaice	7000.00000	100.0
15	Megrim	1556.92834	60.0
16	Sole	3000.00000	70.0
17	Boarfish	269.59415	30.0

```
# Merge new w_max and l_max values
cel_model_course@species_params <- merge(
  cel_model_course@species_params,
  max_size,
  by = "species",
  suffixes = c("", ".new")
)

# Overwrite old values
cel_model_course@species_params$w_max <- cel_model_course@species_params$w_max.new
cel_model_course@species_params$l_max <- cel_model_course@species_params$l_max.new

# Clean up the merged columns
cel_model_course@species_params <- cel_model_course@species_params[, !grepl(".new$", names(cel_model_course@species_params))]

#validate
#cel_model_course <- validParams(cel_model_course)
```

Find an error, due to the changing of `w_max`, which occurred due to the fact the `w_max` now exceeds the model's maximum grid weight and that now `w_max` is internally inconsistent with other various slots such as `psi`, `intake_max`, etc.

To fix this we first need to do some diagnosis of the problem and check if the new `w_max` value extends past the weight grid

```
max(cel_model_course@species_params$w_max)
```

```
[1] 96000
```

```
max(ce1_model_course@w)
```

```
[1] 42529.41
```

Yes it does extend past the weight grid: `w_max` is $>$ than `w`, therefore we need to adjust the weight grid.

```
# Save updated species_params before rebuilding
updated_species_params <- ce1_model_course@species_params

# Rebuild MizerParams with updated species_params and same other settings
ce1_model_course <- newMultispeciesParams(
  species_params = updated_species_params,
  interaction = ce1_model_course@interaction,
  gear_params = ce1_model_course@gear_params,
  no_w = 100, # Or adjust for finer resolution
  min_w = min(ce1_model_course@w),
  max_w = max(updated_species_params$w_max) * 1.1 # 10% buffer
)
```

Note: Dimnames of interaction matrix do not match the order of species names in the species c

For the following species I will ignore your value for `l_mat` because it is not consistent wi
For the following species I will ignore your value for `l_max` because it is not consistent wi

```
#validObject(ce1_model_course)
saveRDS(ce1_model_course, "ce1_model_course_updated.rds")
```

Lets check the new model and run to a steady state in `tuneParams`

```
ce1_model_course_updated<-readParams("ce1_model_course_updated.rds")
ce1_model_course_updated<-tuneParams(ce1_model_course_updated)
```

Loading required package: shiny

Warning: package 'shiny' was built under R version 4.4.1

Listening on <http://127.0.0.1:7404>

Simulation run did not converge after 99 years. Value returned by the distance function was:

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

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

After clicking steady twice the model does not converge after 99 years and requires an unrealistic erepro greater than 1 for Blue whiting, Boarfish, Cod, Common Dab, European Hake, Haddock, Herring etc... additionally the feeding level is at 1 for all species.