

ASMFC MSE Workshop: Alternative Operating Models

Gavin Fay

August 2021

Operating Model uncertainty

In the previous example we characterized OM uncertainty using parameter uncertainty in the fit to the original data.

Here we will compare the performance of our simple HCRs given operating model structure uncertainty.

1. Build a function for when the operating model dynamics are governed by the Pella-Tomlinson model (i.e. yield function is not symmetric)
2. Compare the performance of our HCRs from day 1 to both OMs

Stretch-goal

3. Develop an OM that includes process error (recruitment variability?) in the population dynamics

```
#install.packages('ggplot2')
library(ggplot2)
library(Hmisc)
library(mvtnorm)
```

first load packages

load the functions we used yesterday (sourced from a script to make things easy and reduce clutter in this document)

```
source("first-mse-functions.R")
#e.g
schaefer
```

```
## function(B,C,K,r) {
##   #function schaefer takes the current biomass, a catch,
##   #and the model parameters to compute next year's biomass
##   res <- B + B * r * (1 - B/K) - C
##   return(max(0.001,res)) # we add a constraint to prevent negative biomass
## }
```

The Operating Model The population dynamics for the operating model (the ‘real’ dynamics) are governed by the Pella-Tomlinson equation:

$$B_{y+1} = B_y + B_y * r * \left(1 - \left(\frac{B_y}{K}\right)^{m-1}\right) - C_y$$

where B_y is the biomass in year y , C_y is the catch in year y , r is the population intrinsic growth rate, K is the population carrying capacity, and m is a shape parameter that determines the location of BMSY.

First task is to create a function for the P-T dynamics (hint modify the schaefer function that we used yesterday. Remember there is an extra parameter)

```
schaefer <- function(B,C,K,r) {  
  #function schaefer takes the current biomass, a catch,  
  #and the model parameters to compute next year's biomass  
  res <- B + B * r * (1 - B/K) - C  
  return(max(0.001,res)) # we add a constraint to prevent negative biomass  
}
```

Once you have this, condition your OM as yesterday but with a fixed value for the shape parameter of 1.2 (Hint, you will want to adjust the biomass projection to use your new function)

Then perform the MSE evaluation given the new OM. For this morning, use just one HCR, e.g.

```
control.pars <- list()  
control.pars$H1 <- 0.05  
control.pars$H2 <- 0  
control.pars$Bmax <- max(index, na.rm =TRUE)  
control.pars$B2 <- 0.2*control.pars$Bmax  
control.pars$B1 <- 0.5*control.pars$Bmax  
  
# you will want to make sure you are using your revised functions  
proj.hcr1.noerror <- evaluate(pars.iter, biomass.iter,  
                             control.pars, data.years,  
                             proj.years, niter,  
                             overshoot = 0)
```

Compare output with the Schaefer model runs done yesterday/this morning.