ASMFC MSE Workshop: Model-based Estimation Model

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Replacing our assessment with an estimation model

In the previous examples we used our survey index as the estimate of abundance.

Here we will instead use a model-based estimator, and fit a Schaefer model to the data from the OM to estimate MSY reference points for use in the control rule. (hint we can reuse the code we developed to condition the OM)

1. Build a function for fitting an estimation model to the index.i time series (don't fit to the future time steps that haven't happened yet)
2. Calculate the TAC based on the last year's (model-estiamted) biomass and the estimate of FMSY (r/2) from the fitted model.
3. run a FMSY based control rule

Stretch-goal

4. Compare the performance of the EM-based strategy when the OM is the Pella-Tomlinson model.

```r
#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)

```r
source("first-mse-functions.R")
```

First task is to create a function for the estimation moodel that will use the index data and call the 'assess()' function.

load data

```r
data.years <- 1991:2013
harvest <- c(0.1,3,15,52,76,139,95,93,84,93,86,103,104,
             92,46,67,59,30,54,59,47,33,44)
index <- c(NA,NA,NA,NA,NA,NA,NA,NA,935,NA,1057,NA,678,NA,
           420,NA,554,NA,458,NA,474,NA,280)
```

Condition the OM

```r
set.seed(8675309)
ini.parms <- c(log(1200), log(0.1), log(0.3))
redfish <- assess(harvest,index,calc.vcov=TRUE,ini.parms)
```

```r
biomass.mle <- redfish$biomass
print(biomass.mle)
```

```
##  [1] 1420.2310 1420.1310 1417.1376 1402.3407 1351.5032 1279.8069 1149.1339
##  [8] 1068.5681  992.9793  928.6366  856.7886  793.1563  713.2013  632.5654
## [15]  563.6513  540.0219  495.0459  457.2673  447.6696  413.8427  374.1402
## [22]  345.2745  329.4716  302.1228
```

```r
pars.mle <- redfish$pars
#define the number of iterations for the MSE
niter <- 500
#set up a storage matrix for our alternative parameter sets
pars.iter <- matrix(NA,nrow = niter, ncol=3)
colnames(pars.iter) <- c("logK","r","sigma")

# generate the sets of parameter values
for (i in 1:niter) {
  pars.iter[i,] <- mvtnorm::rmvnorm(1, mean = redfish$pars,
                     sigma = redfish$vcov)
}

# Now generate replicate model outputs
biomass.iter <- data.frame()
for (i in 1:niter) {
  #here we calculate the biomass trajectory for each of the above sampled parameter vectors
  biomass.iter <- rbind(biomass.iter,
                        data.frame(year = seq(min(data.years),
                                              max(data.years)+1),
                                   biomass = dynamics(pars.iter[i,], harvest),
                                   iter = i))
}
```

Applying the Management Strategy Define the years for the projection:

```r
proj.years <- 2014:2034
```

conduct the evaluation with the model-based estimation method

```r
project.emhcr <- em_evaluate(pars.iter, biomass.iter, control.pars,
                        data.years, proj.years, 100)
```

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Plot the trajectories:

```r
projection.plot(project.emhcr)
```

```
## Warning: Removed 200 rows containing non-finite values (stat_summary).

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```

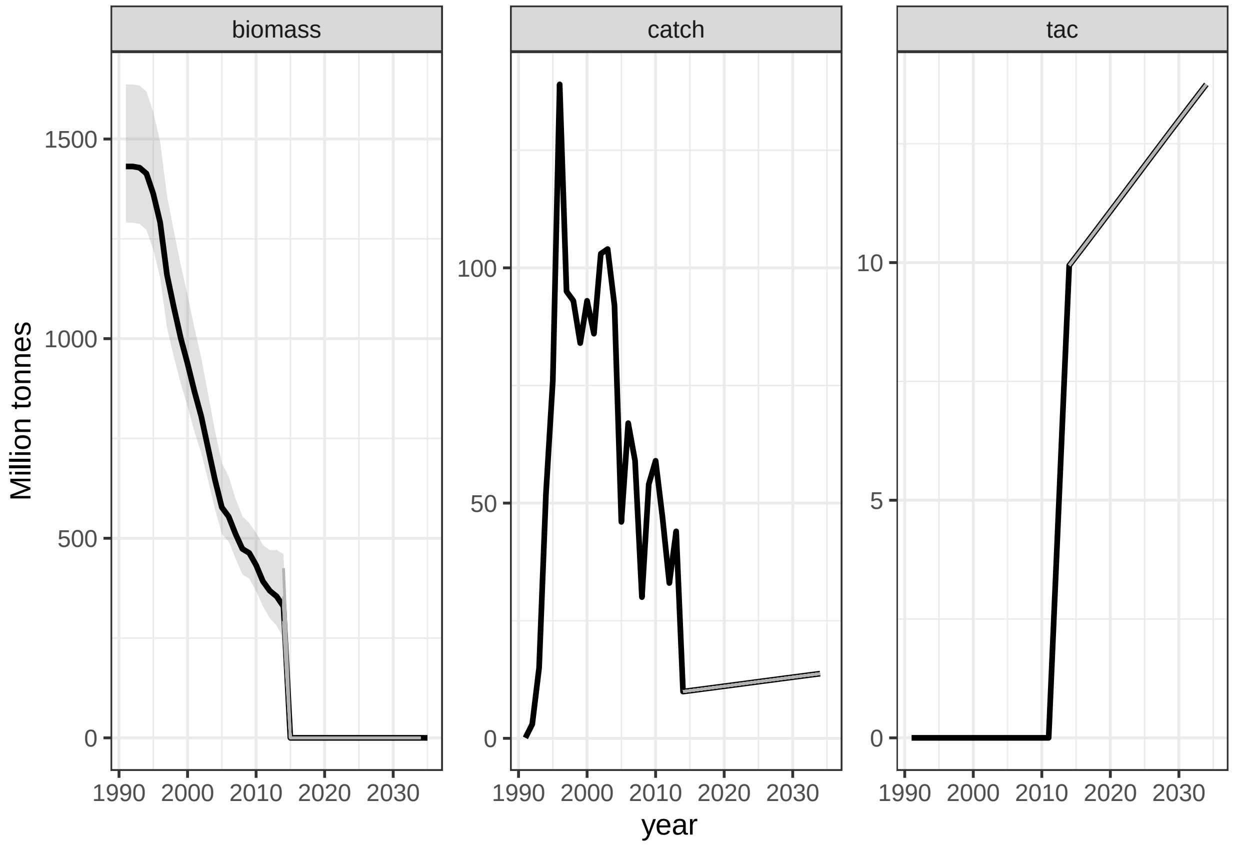

biomass
catch
tac
Million tonnes
year
1500
1000
500
0
100
50
10
5
1990
2000
2010
2020
2030