

# CINAR 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-estimated) 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.

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

**first load packages**

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

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

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

**Setting up the Operating Model** load data

```
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, NA, 935, NA, 1057, NA, 678, NA,
          420, NA, 554, NA, 458, NA, 474, NA, 280)
```

Load the conditioned OM

```
schaefer_fit <- readRDS("schaefer_om.rds")
pars.iter <- schaefer_fit$pars
biomass.iter <- schaefer_fit$bio
```

**Applying the Management Strategy** Define the years for the projection:

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

conduct the evaluation with the model-based estimation method

```
project.emhcr <- em_evaluate(pars.iter, biomass.iter, control.pars,
                             data.years, proj.years, iterations=3, true.m = 2, est.m = 2)
```

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Plot the trajectories:
projection.plot(project.emhcr)
```

