

FISH 120

The stock equation for a single yearclass and year is:

$$N_{a+1} = e^{-Z_t} N_a$$

and yield is defined as:

$$Y_a = w_a C_a$$

where w_a is the mean weight at age a .

Yield per Recruit - simple

Using the above equations:

- If $N = 1000$ at age 3, the mean weight at age 3 $w = 1.25\text{kg}$, catch is 7% followed by natural mortality of $M = 0.2$: A) what is the yield from fishing age 3? and B) how many survive to age 4?
- If the mean weight at age 4 is 1.9 kg and the catch at age 4 is 25% followed by $M = 0.2$: A) what is the yield from fishing age 4? and B) how many survive to age 5?

Yield per Recruit - cohort

Simulate a stock with the following parameters:

ages: 1 to 12

von Bertalanffy growth parameters: $L_\infty = 160, \kappa = 0.1, t_0 = 0$

length weight parameters: $a = 0.02, b = 3.1$

age 50% catchable: $s_{50} = 5$

age 50% mature: $p_{50} = 5.5$

Natural mortality: $M = 0.2$

The function defining maturation and selection is:

$$p = \frac{\delta}{(1 + e^{-\alpha*(a-a_{50})})}$$

where α is the rate of change.

The pattern of F_a for a given year/cohort is defined as:

$$F_a = F \cdot s_a$$

where F is a multiplier of the selection pattern s_a .

- Calculate the mean length at age.
- Calculate the mean weight at age.
- Calculate the selection pattern:

```
s50 <- 5      # age at 50% catchable
sa <- round(1.15/(1+exp(-1.1*(ages-s50))),2)
```

The selection pattern should be scaled with the mean over the range used to calculate \bar{F} equal to 1 e.g. 5–10. (This is the age range considered most important in the catch.) To scale sa:

```
ages.F <- 5:10
smult <- 1/mean(sa[ages.F])
sas <- sa*smult
```

- Calculate the maturation ogive:

```
p50 <- 5.5    # age at 50% mature
pa <- round(1/(1+exp(-2*(ages-p50))),2)
```

- Combine in a data frame the data on selection, natural mortality, proportion mature at age and mean weight at age.
- Plot weight, selection and maturity against age.

The catch equation is:

$$C_y = \frac{F_y}{Z_y}(1 - e^{-Z_y})N_y \quad \text{or} \quad C_y = \frac{F_y}{F_y + M}(1 - e^{-(F_y+M)})N_y$$

Using the information in the data.frame and the equations for catch, yield and stock:

- If the F multiplier $F = 0.9$ and $N_1 = R = 1000$
 - A) What is the fishing mortality on age 1?
 - B) What is the biomass of age 1 before fishing?
 - C) What is the catch from age 1?
 - D) What is the yield from age 1?
 - E) How many 2 year olds are there at the start of the next year?

You might find it easier if you add columns to the data frame for scaled selection and Z .
- Using the stock size for age 2 at the start of the year redo the process for age 2.

If

$$C_1 = \frac{F_1}{Z_1}(1 - e^{-Z_1})N_1$$

then using the stock equation C_2 can be written as:

$$\begin{aligned} C_2 &= \frac{F_2}{Z_2}(1 - e^{-Z_2})N_2 \\ &= \frac{F_2}{Z_2}(1 - e^{-Z_2})e^{-Z_1}R \end{aligned}$$

- Recalculate Y_2 and N_3 directly from $N_1 = R = 1000$.

The catch equation can be expanded to:

$$C_a = \frac{F_a}{Z_a}(1 - e^{-Z_a})e^{\sum_{\alpha < a} -Z_\alpha} R$$

and yield per recruit can be written as:

$$Y/R = \sum_a \frac{F_a}{Z_a}(1 - e^{-Z_a})w_a e^{\sum_{\alpha < a} -Z_\alpha}$$

To calculate yield per recruit from the data.frame `data` with $R = 1$ you need to use a new R function `cumsum` which calculates the cumulative sum \sum e.g.

```
x <- c(1,2,3)
cumsum(x)
```

Y/R can then be calculated from:

```
Fmort <- Fm * fish.df$sel           # where Fm is the F multiplier
Z <- Fmort + M                     # total mortality
prop <- (Fmort/Z)*(1-exp(-Z))      # prop at age
Ztemp <- c(0,Z[1:length(Z)-1])
cumZ <- exp(-cumsum(Ztemp))        #
C <- prop*cumZ                     # total catch where R = 1
Y <- sum(fish.df$wgt*C)            # total yield where R = 1
```

- If the F multiplier $Fm = 1.2$ what is the Y/R ?
- Do a barplot of catch in numbers. Which ages are the most common in the catch?
- With $Fm = 0.5$ what happens to the distribution of the catch in numbers? And what is the Y/R ?
- Using the commands you have used to calculate Y/R write a function to calculate Y/R given the F multiplier as an input value.

`sapply` can be used to return the results of a function for a range of values e.g. if your function is called `yperr`:

```
F.vec <- seq(0.01,1.5, 0.01)
ypr.out <- sapply(F.vec,yperr)
yl <- c(0, max(ypr.out)*1.02)
plot(F.vec, ypr.out, xlab="F", ylab="Y/R (kg)", type="l", ylim=yl)
```

Spawning stock biomass per recruit

Spawning stock biomass and spawning stock biomass per recruit can be calculated in a similar way to yield and yield per recruit.

$$SSB_a = w_a p_a N_a$$

where p_a is the proportion mature at age.

- Write a function to calculate spawning stock biomass per recruit.
- Calculate SSB/R for the same values you calculated Y/R for.
- To plot both curves on the same plot:

```

par(mar=c(rep(4.5,3),5.5))      # more space around the plot
yl <- c(0, max(ypr.out)*1.02)
plot(F.vec, ypr.out, xlab="F", ylab="Y/R (kg)", type="l", ylim= yl)
par(new=T)
plot(F.vec, spr.out, xlab="", ylab="", axes=F, type="l", ylim=yl)
yl <- c(0,max(spr.out)*1.02)
axis(4)                          # text marks on 4th axis
mtext("S/R (kg)", side=4, line=3.2) # text on 4th axis
                                   # line = 3.2 is the distance from the axis

```

Reference points

F_{max} the maximum of the Y/R curve (which may not exist).

$F_{0.1}$ the level of F at which the increase in Y/R is 10% of the increase at the origin.

For any of the the Y/R curves you have calculated:

- Does F_{max} exist? And if so, what is it?
- Calculate $F_{0.1}$ – there is a description in your lecture notes.
- Try different selection patterns. How does this affect Y/R , S/R and the reference points.
- Compare Y/R , S/R and the reference points for different biological parameters. eg for a fast growth short lived species and a slower growing species with a longer life span.