

FISH 480

Stock–recruit relationships

The Ricker stock recruit relationship is:

$$R = \alpha S e^{-S/K} \quad (1)$$

and the Beverton Holt stock recruit relationship is:

$$R = \frac{\alpha S}{1 + S/K}$$

In both cases α is a multiplier for prospective recruitment.

In the Beverton–Holt αK is a limit on recruitment as $S \rightarrow \infty$ and represents maximum recruitment in the Ricker model. In the Beverton–Holt model, K is the size of spawning stock biomass corresponding to half the maximum recruitment. Whereas, in the Ricker model, maximum recruitment is when spawning stock biomass equals K .

- Plot some stock–recruit curves, both with the Beverton–Holt and Ricker equations and compare different parameter values.
- You can write a function (as you did for the von Bertalanffy growth function) and read in the parameter values α and K . You will need a range of values for S eg `S <- seq(0,1000,1)` to predict R .
- Vary the parameters systematically, e.g. for $\alpha = 1$ compare several values of K and for fixed K compare several values of α . Plot the curves to compare them using `plot` and `lines`.

Alternative linearised formulations

The Ricker stock recruit relationship can be rewritten as:

$$\ln\left(\frac{R}{S}\right) = \ln(\alpha) - (1/K)S \quad (2)$$

The Beverton–Holt function can be rewritten as:

$$\ln\left(\frac{R}{S}\right) = \ln(\alpha) - \ln(1 + S/K)$$

where α is the maximum number of recruits (asymptote) and $1/K$ the spawning stock required to produce recruitment equal to half the maximum.

The residual errors, *ie* the difference between the observed and fitted values, are lognormal for both models.

Estimation

The data are in www.hafro.is/~lorna/srdata. Year corresponds to the birth year of the cohort, even though recruitment is the number at age 2.

- Plot the data – the axes for the spawning stock biomass and recruitment should start at 0. e.g. `plot(ssb, rec, xlim=c(0, max(ssb)), ylim=c(0, max(rec)))`
- Estimate the parameter values for the Ricker function using the second formulation of the function (equation 2). This means you can fit a linear regression using `lm`. e.g.

```
ydat <- log(rec/ssb)
fit <- lm(ydat ~ ssb)
alpha <- exp(fit$coef[1])
K <- -1/fit$coef[2]
```

- Add the estimated curve to the plot of the data. You need to create a vector of SSB values, then compute the corresponding predicted R. e.g.

```
Sp <- seq(0, max(SSB), 100)
Rp <- alpha*Sp*exp(-(1/K)*Sp)

plot(ssb, rec, xlim=c(0, max(ssb)), ylim=c(0, max(r)), xlab="SSB",
      ylab="R")
lines(Sp, Rp)
```

- Now fit equation 1 to the data. The function could look like:

```
SSB <- ssb
R <- rec

ric <- function(input){
  a <- input[1]
  K <- input[2]
  Rhat <- a*SSB*exp(-(1/K)*SSB)
  sse <- sum((log(R) - log(Rhat))^2)
  return(sse)
}

# minimise with e.g.
est <- nlm(ric, c(4,20000), typsize=c(4,20000))
```

- Add this curve to the plot as before.
- How would the function be modified to print the estimated values of a and K at each iteration? Or to plot the fitted curves?
- Write a function to fit the Beverton–Holt equation to the data and add it to the plot.
- Do the B–H and Ricker give different interpretations of the data?

Reference points from SSB and R data

These reference points are based on the ratio of R to SSB for each year.

F_{med} median
 F_{high} only 10% of ratios are higher (ie 90% quantile of R/SSB)
 F_{low} only 10% of ratios are lower (ie 10% quantile of R/SSB)

- Calculate F_{med} , F_{high} and F_{low} from the R and SSB data.

To calculate the median `median(SSB/R)`

To calculate quantiles `quantile(SSB/R, probs=x)` with x your required value. Median can also be calculated using the `quantile` command.

- Add the lines corresponding to these reference points to the plot. How do they relate to the stock recruit curves?

```
abline(0, 1/median(SSB/R))    #Fmed  
abline(0,1/quantile(SSB/R, probs=0.1), col=2)    #Fhigh  
abline(0,1/quantile(SSB/R, probs=0.9), col=4)    #Flow
```

Production and replacement

The stock–recruit relationship (production) can be used with data on spawning stock biomass per recruit derived from observations on mean weight at age, natural mortality, selection and the maturity ogive.

To generate an appropriate dataset use the von Bertalanffy function to generate mean weight at age data, the equation for selection and maturation used in the spawning stock biomass per recruit calculations and the function to calculate spawning stock biomass per recruit.

```
# mean weight at age (kg) from von Bertalanffy

Linf <- 160
k <- 0.1
beta <- 3
cond <- 0.02
ages <- 1:14
t0 <- 0

lage <- Linf*(1-exp(-k*(ages-t0)))
wage <- round((cond*lage^beta)/1000, 2)

# selection pattern
s50 <- 5          # age at 50% selection
sage <- round(1/(1+exp(-1.1*(ages-s50))), 2)

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

# natural mortality
M <- 0.5

# spawning stock biomass per recruit function
srfun <- function(Fmult){
  Fmort <- Fmult*sage
  Z <- Fmort+M
  Ztemp <- c(0, Z[1:length(Z)-1])
  cumZ <- exp(-cumsum(Ztemp))
  S <- sum(wage*page*cumZ)
  return(S)
}

# the parameters of the stock--recruit curve will be
alpha <- 2.5
K <- 2000
```

- Plot mean length at age, mean weight at age, selection at age, maturation at age.
- Plot the production curve (stock–recruit relationship, use Beverton–Holt).
- Add the replacement curves to the plot for several values of fishing mortality F .

To add the replacement curves:

```
# values of F
sF1 <- 0
sF2 <- 0.25
sF3 <- 0.35
sF4 <- 1.1

# spawning stock biomass per recruit at these levels of F
sr1 <- srfun(sF1)
sr2 <- srfun(sF2)
sr3 <- srfun(sF3)
sr4 <- srfun(sF4)

# add to the plot -- you can change the colour if you wish
Sp <- seq(0, 200000, 100)
lines(Sp, Sp/sr1)
lines(Sp, Sp/sr2)
lines(Sp, Sp/sr3)
lines(Sp, Sp/sr4)
```

Yield potential

This is an extension of Y/R and SSB/R analysis which incorporates information from the stock–recruit relationship and assumes equilibrium conditions. Equilibrium values of SSB , R and Y are calculated for each value of F .

Ricker equation

Equation 1 can be written as:

$$\alpha \frac{S}{R} = e^{S/K}$$

taking the natural log

$$\ln \left(\alpha \frac{S}{R} \right) = S/K$$

which can be written as

$$S_e = \ln \left(\alpha \frac{SSB}{R} \right) K \quad (3)$$

where $\frac{SSB}{R}$ is from the spawning stock biomass per recruit analysis.

The corresponding equilibrium recruitment and yield are:

$$R_e = \frac{S_e}{SSB/R} \quad Y_e = R_e(Y/R) \quad (4)$$

where Y/R is from the yield per recruit analysis.

Use the population you generated for the production analysis. There are further commands on this in your class notes. The yield per recruit and spawning stock biomass per recruit functions are those in FISH 120.

- Go through the following sequence. It can be useful to check that everything is working by initially considering a single point estimate, then calculate for a vector of F .
- Calculate S_e (eqn 3) using the α and K provided – or other values if you prefer.
- Using S_e compute R_e and Y_e (eqns 4). Use the yield per recruit function from FISH 120 along with the spawning stock biomass per recruit function above.
- Plot Y_e against F .
- At which value of F is the equilibrium yield the highest? (F_{MSY})
- At which value of F is Y_e zero? (F_{crash})
- Plot yield per recruit, ssb per recruit, equilibrium yield, equilibrium ssb.
- The following R code calculates the equilibrium values assuming the yield per recruit function is called `srfun` and the yield per recruit function `yrfun`.

```
# generate vectors for F, SSB/R and Y/R
F.vec <- seq(0, 2.5, 0.05)
spr <- sapply(F.vec, srfun)
ypr <- sapply(F.vec, yrfun)

# equilibrium values
Se.vec <- log(alpha*spr)*K
Se.vec[Se.vec<0] <- 0      # when <0 change to 0
Re.vec <- Se.vec/spr
Ye.vec <- Re.vec*ypr

# plotting - add appropriate labels
par(mfrow=c(2,2))
plot(F.vec, ypr, type="l")
plot(F.vec, Se.vec, type="l")
plot(F.vec, Re.vec, type="l")
plot(F.vec, Ye.vec, type="l")

# Fmsy
Fmsy <- F.vec[Ye.vec==max(Ye.vec)]
# Fcrash
Fcr <- min(F.vec[Ye.vec==0&&F.vec!=0])

# add the Fmsy line
abline(v=Fmsy, lty=2)
```

- What are the corresponding equilibrium equations for the Beverton Holt model? (look at your class notes)
- Repeat the calculations for the Beverton Holt model.