# Models with internal age structure fish5108statass Statistical stock assessment methods

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#### Introduction

Internal age structure Incorporate growth information Link to any available data

- Length measurements
- Age data
- Survey indices

#### Biomass or numbers

Choose whether population model is in biomass or numbers

#### Forwards or backwards

Should computations be forwards or backwards in time?

#### Models of catches

Want to include errors in catches Unlike many bulk biomass and VPA models Can use  $F_{ay} = F_y s_a$  to reduce parameters

# The plus group

Traditional biomass model

$$B_{y+1} = B_y + rB_y(1 - B_y/K) - Y_y$$

Numbers model with true ages  $1, \ldots, A$ :

$$N_{A+1,y+1} = (N_{A,y} + N_{A+1,y}) e^{-Z_A}$$

#### Recruitment

Numbers model: Recruitment is the number of individuals in an incoming yearclass. Growth of older individuals, natural mortality and weight of recruits is separate. Typical model:  $R = \alpha S/(1+S/K)$ .

Production model: Recruitment is a growth in biomass or surplus production. Incorporates growth of individuals, natural mortality and recruiting yearclass in weight. Use e.g. rB(1 - B/K).

## Initial population size

In a forward projection: Need to set initial population (all ages, in first year)

Can use equilibrium assumption  $\Rightarrow$  only one parameter:

$$N_{0,a} = N_{0,0} e^{-M \cdot a}$$

(where we start the ages and years from 0 so  $N_{y,0} = R_y$ ) Can try to estimate all ages  $\Rightarrow$  more parameters but also more potential to fit data for initial year (if available).

### Initialising an estimation procedure

Example: R code setting initial values in a statistical age-based population model. Nephrops in Icelandic waters from 1980.

```
# aspminit.r
# Set up initial values for age-structured dynamic stock-production models
# Set up data-nephrops specific
vrs<-1980:1998
# Annual catch data
Y<-c(2398,2520,2603,2672,2459,2385,2564,
     2712,2240,1866,1692,2157,2230,2381,
     2238.1027.1633.1228.1411)
# Annual abundance index
I \leftarrow c(45.5, 51.8, 51.5, 47.8, 45.6, 56.4, 61.3,
     52.6.39.9.36.0.40.0.42.1.51.3.
     51.4.38.0.27.0.35.2.31.3.38.9)
wts<-c(8,14,23,34,46,60,75,89,104,119,131,145,159,175) # Wt ages 3-16, MRI 2011 report
# Number of ages and years
g<-4
                                # Number of true age groups
totyrs <-length (Y)
                                # Number of years
# Initialize values of all parameters
# Some will later be estimated - others simply fixed at assumed values
                                # Natural mortality
M \leftarrow rep(0.3, (g+1))
aveRecr<-100
selpat<-c(0.1,0.333,0.667,1,1) # Selection pattern-Might estimate
                                # Initial value of catchability
q < -1
Fvec<-rep(0.5,totyrs)
                                # Annual fishing mortality
# now set up an appropriate mean weight at age for age grps 1:g and plus grp 🚚 🔭 📜
\frac{7}{2}
                                # cum7 values in the plus group
```

# Projecting a stock in numbers forward in time

See http://vr3pc109.rhi.hi.is/fish/fish5108 statass/lecture 60/sl60/aspm.r or

http://vr3x113.rhi.hi.is:8080/tutor-web/fish/fish5108statass/lecture60/sl60/

- append the file name to the number of this slide

**Example:** R code to project stock forward. Stock-numbers model with true ages and plus group. Only estimation of R and F. Initial stock size=equilibrium stock from constant recruitment.

```
# aspm.r
# aspm: Performs forward simulation of populations, given values of parameters
aspm<-function(Fvec,Rvec,totyrs,M,w){
  Yhat<-NULL
 Bhat<-NULL
 Rtemp<-Rvec[1]
 #NO<-Ninit
                                   # First start-of-year stock size - fixed
  #NO<-Rtemp*exp(-cumsum(c(0,M[1:(length(M)-1)]))) # initial start-of-year stock
  NO<-aveRecr*exp(-cumsum(c(0,M))[1:g]) # better: first only true ages
  NO<-c(NO,aveRecr*exp(-g*M[g+1])/(1-exp(-M[g+1])))# then append the plus group
  for(year in 1:totyrs){
   baseF<-Fvec[year]
                                   # Base fishing mortality
   F0<-baseF*selpat
                                   # Fishing mortality during the year
   C < -(F0/(F0+M))*(1-exp(-(F0+M)))*N0
```

# Evaluating a model fit

Usually an evaluation of a fit is coded as a function, which return a fit measure for a given set of parameters.

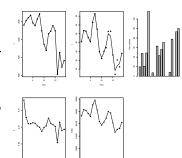
A typical fit-evaluation function in R.

```
#ssefcn.r
 ssefcn<-function(parameters,Y,I,M,w){
   totyrs < -length (Y)
   Fvec<-exp(parameters[1:totyrs])</pre>
   Rvec<-exp(parameters[(totyrs+1):(2*totyrs)])</pre>
   q<-exp(parameters[2*totyrs+1])
   #alpha<-parameters[2*totyrs+2]
   #K<-parameters[2*totyrs+3]
   proj <- aspm(Fvec, Rvec, totyrs, M, w)
   Yhat <-proj$Yhat
   Bhat <-proj$Bhat
   Ihat < - q * Bhat
   SSEY <- sum((log(Y)-log(Yhat))^2)
   SSEI <- sum((log(I)-log(Ihat))^2)
   SSE<-SSET+SSEY
   return(SSE)
```

## A complete run

Need more data, e.g. on recruitment in order to reduce the number of parameters compared to number of data points.

Would prefer production to be linked to stock size.



**Example:** When fitting a model to the nephrops data and plotting the results the following R commands can be used.

Models with internal age structure

```
#filename="aspmrun.r"
# Download this file from http://vr3pc109.rhi.hi.is/fish/fish5108statass/lecture60
```

Download the other files below from the same directory

# To do a complete assessment give the command:

# source("aspmrun.r")

#### References ISBN:

ISBN: