Carter Adamson

FISH 558

Lab 7 HW

3/5/2024

1. **Density dependent, Beverton-Holt, and Ricker stock-recruit models**
   1. **Generate a single graph with all three model fits**

A graph with different colored lines and dots

Description automatically generated

Figure 1: Graph of recruit abundance (tens of thousands of individuals) vs spawner abundance (thousands of individuals) for three models fit to a stock-recruitment dataset. The green, pink, and blue lines correspond to model fits from density-independent, Beverton-Holt, and Ricker models respectively.

* 1. **Diagnostic plots for the three models to evaluate assumptions of normality and HOV**

**A group of graphs showing different values

Description automatically generatedA group of graphs showing different values

Description automatically generatedA group of graphs and diagrams

Description automatically generated**

a

c

b

Figure 2: Four diagnostic plots for each of the models fit in question 1a. Figure 2a comprises diagnostic plots for the density-independent model, 2b for the Beverton-Holt model, and 2c for the Ricker model. Each model has four diagnostic plots: a histogram of residuals, a Q-Q plot, a plot of residuals vs. x (spawners, in thousands of individuals), and a plot for residuals vs. fitted values.

These diagnostic plots are used to evaluate whether assumptions are met: the histogram and Q-Q plots evaluate the assumption of normality, while the residual vs X or fitted plots evaluate homogeneity of variance (HOV).

For the density-independent model (fig. 2a), the histogram and Q-Q plot look slightly off – there appears to be left skew, where the histogram is lopsided rather than bell-shaped, and the Q-Q plot falls off the Q-Q line. Additionally, there seems to be heteroscedasticity since there is not a random spread of residuals. Rather, the residuals are more positive with fewer spawners and more negative with more spawners. This model therefore violates both assumptions.

For the Beverton-Holt model (fig. 2b), the histogram and Q-Q plot also look off – the histogram exhibits a plateau rather than a typical normal shape, and the Q-Q plot falls off the Q-Q line. Both plots of residuals look better than they do in fig. 2a, however, showing a more “random” pattern distributed evenly around the y=0 line. This model therefore violates the assumption of normality but meets the assumption of HOV.

For the Ricker model (fig. 2c), the histogram and Q-Q plot look somewhat better – there still appears to be some right left like in fig. 2a, but it may be less pronounced. The shape of the Q-Q plot also indicates potential left skew, deviating below the line at low values. The plots evaluating HOV look more promising, however. Though the residuals vs. fitted plot is data-poor at low fitted values, there still appears to be a random spread around y=0 in both plots.

* 1. **AIC table**

Table 1: Table summarizing AIC results for the three models fit in Question 1a. The best fitting model (i.e. the model with the lowest AIC and dAIC=0) is highlighted in yellow.

|  |  |  |
| --- | --- | --- |
| **Model** | **AIC** | **dAIC** |
| Density-independent | 72.937 | 59.821 |
| Beverton-Holt | 21.835 | 8.719 |
| Ricker | 13.116 | 0.000 |

1. **Skipped**
2. **In layman’s terms, explain to gramps why stock-recruitment models are important**

Stock-recruitment models are a mathematical way to predict recruitment, or the number of new fish added to a population. These models combines reproduction with survival of eggs and larva. They help describe the relationship between the number of fish that are spawning, and the number of fish that they produce. Understanding how many fish will be recruited is very important for managing a stock; overestimating recruitment can lead to overfishing, while underestimating recruitment can mean that the fishery is not achieving its optimum yield. If we don’t understand how many fish are being added to a fishery, we cannot estimate the future status of the population or set accurate fishing targets.

1. **Extra questions**
   1. **How many hours?**

5 hours

* 1. **Selfie?**

I worked alone this time.

* 1. **What did you struggle with?**

I like to generate my visualizations using ggplot rather than r’s default plots, but in this lab I had difficulty getting many of the plots to come out right in ggplot. Googling and checking out my old ggplot code helped in some cases, but in others I just stuck to the default r plots.

1. **Simulate data for a Ricker model**
   1. Graph effects of changing each parameter, describe the effects

A group of graphs with numbers

Description automatically generated

Figure 3: Graphs of predicted recruitment from simulated spawner populations using a Ricker stock-recruit model. S.sim refers to the simulated number of spawners (thousands of individuals), and R.sim refers to the predicted number of recruits (tens of thousands of individuals). Graph titles list the values of the Ricker model’s parameters used to generate the graph below.

The above graphs show the effects of modifying each of this Ricker model’s three parameters using simulated data. If we think of the top left graph as a “default”, then each of the other graphs increases one of the three parameters by one order of magnitude. The effect of increasing a from 3 to 30 might not initially be obvious, but examining the y-axis shows that the predicted recruits have also increased by an order of magnitude. The effect of increasing a is vertically “stretching” the plot and allowing much more recruits per spawner. The effect of increasing b from 0.0015 to 0.015 can be seen in the bottom left, where the population of recruits only achieves relatively small values before crashing. The effect of increasing e.sd can be seen in the bottom right. Increasing this increases the standard deviation of the normal distribution that defines the error. In other words, there is more random variation and larger residuals.

* 1. How can a fisheries manager use this kind of simulation?

Fisheries managers may be very interested in learning which demographic and environmental factors have the largest positive impact on a fish population, or might want to simulate populations according to predicted parameter values for a future year. These simulations allow for that without having to put an actual population at risk.

* 1. Experience with functions and future applications?

I am quite familiar with functions through my coding experience in R and Java. These are very useful for reproducibility and condensing repeated chunks of code. I used another function in this very same lab to generate the quartet of diagnostic plots for each model.

**Appendix: CODE pasted below**

library(ggplot2)

setwd("/Users/cpadamson/Dropbox/Grad/FISH 558/Lab 07 - Stock-recruitment")

# Question 1 ####

sr.data<-read.csv("SR\_data.csv")

#a - fit three models, graph

mod.ind<-nls(log(Recruits)~log(a\*Spawners),data=sr.data,start=c(a=2.0),trace=T)

summary(mod.ind)

see.ind<-summary(mod.ind)$sigma

pred.ind<-exp(predict(mod.ind))\*exp((see.ind^2)/2)

mod.bh<-nls(log(Recruits)~log(a\*Spawners/(1+b\*Spawners)), data = sr.data, start=c(a=1.0,b=5e-5), trace=T)

summary(mod.bh)

see.bh<-summary(mod.bh)$sigma

pred.bh<-exp(predict(mod.bh))\*exp((see.bh^2)/2)

mod.ric<-nls(log(Recruits)~log(a\*Spawners\*exp(-b\*Spawners)), data=sr.data, start=c(a=1,b=0.00005), trace=T)

summary(mod.ric)

see.ric<-summary(mod.ric)$sigma

pred.ric<-exp(predict(mod.ric))\*exp((see.ric^2)/2)

plot.1<-ggplot(data=sr.data, aes(x=Spawners, y=Recruits))+geom\_point()+theme\_bw()+

geom\_line(aes(y=pred.ind, color = "Density-Independent"))+

geom\_line(aes(y=pred.bh, color = "Beverton-Holt"))+

geom\_line(aes(y=pred.ric, color = "Ricker")) + ylim(0, 1250)

plot.1

#b - diagnostic plots for each

par(mfrow=c(2,2))

res<-resid(mod.ind)

fit<-fitted(mod.ind)

diagnostics = function(mod, xvar, xname){

par(mfrow=c(2,2))

r <- resid(mod)

f <- fitted(mod)

hist(r,xlab='Residual', prob=TRUE)

qqnorm(r)

qqline(r)

plot(r~xvar, ylab="Residuals", xlab=xname)

abline(0,0)

plot(r~f, ylab = "Residuals", xlab = "Fitted Values")

abline(0,0)

par(mfrow=c(1,1))

}

diagnostics(mod.ind, sr.data$Spawners, "Spawners")

diagnostics(mod.bh, sr.data$Spawners, "Spawners")

diagnostics(mod.ric, sr.data$Spawners, "Spawners")

#c - AIC table for each

AICs=c(AIC(mod.ind),AIC(mod.bh),AIC(mod.ric))

dAICs = AICs-min(AICs)

AICs

dAICs

# Question 5 ####

#prep - create a simulation function for Ricker

RicSim=function(a=3, b=0.0015, e.sd=0.1){

S.sim=seq(0,1500, length=45)

R.sim = a\*S.sim\*exp(-b\*S.sim)\*exp(rnorm(n=length(S.sim),mean=0,sd=e.sd))

R.sim.noe= a\*S.sim\*exp(-b\*S.sim)

plot(x=S.sim, y=R.sim, main=paste("a=", a,", b=",b,", e.sd=",e.sd, sep=""))

lines(S.sim, R.sim.noe)

}

#a - Describe/graph effects of modifying parameters

par(mfrow=c(2,2))

RicSim(a=3, b=0.0015, e.sd=0.1)

RicSim(a=30, b=0.0015, e.sd=0.1)

RicSim(a=3, b=0.015, e.sd=0.1)

RicSim(a=3, b=0.0015, e.sd=1)