

Week 9: Review of the fisheries stock assessment course

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1 Review

This course was designed to give students in the Bren School an introduction to fisheries stock assessment. The course focused on the basic principles of fisheries population biology and not necessarily the gritty details associated with fitting the models to data; however, we did fit all of the models to data using sums-of-squares. All of the associated labs were done in Excel. While programs like **R** and **S-Plus** are convenient for fitting models that do not allow the novice to really understand what is taking place behind the scenes.

There were some major limitations to the course. First, this was my first time teaching a course. Second, this was the first time students had taken a fisheries course. Naturally this led to a lot of blank stares and interesting dialogue. Third, was the fact that this class only met for 2 hours a week for ten weeks. And since two weeks were devoted solely to the mid-term and final, this left only eight weeks, or sixteen hours, to discuss and implement five major fisheries topics.

A few suggestions would be to first, make the class three hours a week, one hour of lecture and two hours of lab. Second, would be to make the class earlier in the morning. Third, would be to make this class part of a fisheries series. Fisheries are where the money's at. Students should be encouraged to be more knowledgeable of them.

Finally, while you are now well versed in how to conduct basic stock assessments you should use considerable caution when you move forward with your work. And, while I mentioned that you would be able to understand 95% of fisheries stocks assessment, the remaining 5% is where the devil lies. For instance, many stock assessments assume that catch is removed halfway through time-step. There can also be different ways of accounting for discards, natural mortality, and selectivity, that were different than what we did in class. You could even be asked to estimate the selectivity curve based on the data.

But perhaps the most glaring omission in this course was the fact that we never went beyond sums of squares. Most stock assessments these days are *statistical* catch at age, or catch at length models. And by statistical, I mean you have to actually use statistics, either in the form of likelihoods or Bayesian analysis. While this was beyond the scope of the class it is something that you should keep in the back of your mind if you are confronted with a stock assessment. Like my old advisor said, you can teach anyone the biology in a day (or eight days in our case), you can't teach the statistics in

a day.

If you are interested in quantitative population modeling I would encourage you to take as many math classes as possible. Even if you suck at them, you will still be far ahead of 95% of the competition.

2 Growth models

We began the course with simply learning how to model the growth of a fish. In particular, we used the Von Bertalanffy growth equation to model the length-at-age. Using a simple power function we transformed the length-at-age into the weight-at-age. Below are the descriptions of the length- and weight-at-age.

2.1 Von Bertalanffy length at age

Von Bertalanffy used the following differential equation to describe the growth of a fish

$$\frac{\Delta l}{\Delta t} = K * (L_{\infty} - L(t)). \quad (1)$$

The equation simply says that the growth of an *average* individual changes as a function of how big the individual is. When we solved the differential equation to get a function that describes the length of an individual with respect to how old it is we got the following

$$L(t) = L_{\infty}(1 - e^{-K(t-t_0)}) \quad (2)$$

where K , L_{∞} and t_0 are all parameters that we can *guesstimate* if we were presented a graph of length versus age data. Do it for figure 1 if you don't remember how. You can guess that the average maximum length (L_{∞} is 400 mm. You can assume that t_0 is 0 to start with. K is the only tricky one, but if you use equation (1) it's actually pretty simple. The only question part is the left-hand side of the equation. Start with the average lengths at ages 2 and 4, 250 and 330, respectively. Then Δl is 80, which is $330 - 250$. Δt is simply 2, since $4 - 2 = 2$. Then using equation (1), $K = (80/2)/(400 - 250)$.

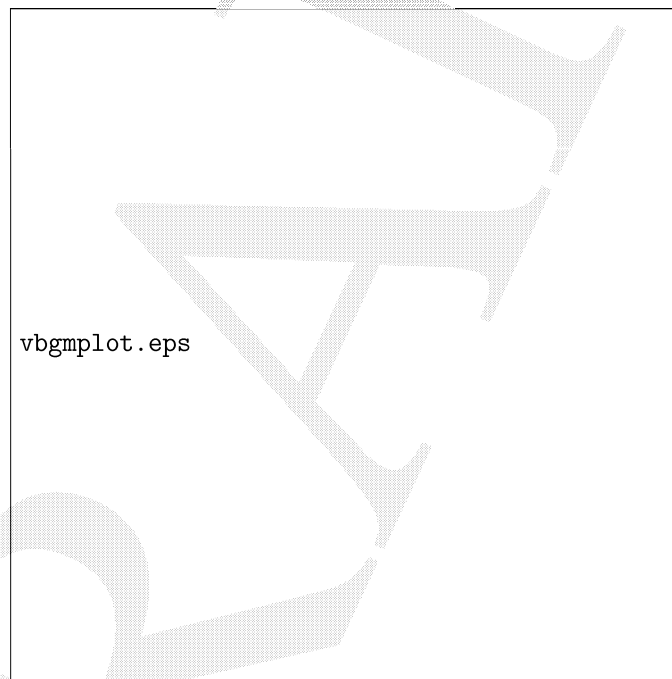
2.2 Weight at age

Weight-at-age is most typically modeled as a power function based on length.

$$w(t) = al(t)^b \quad (3)$$

a and b are parameters of the model, and b is almost always 3.0, or some value very close to it. If length is measured in millimeters a is probably close to $5.0e-6$, and if it is measured in centimeters it is probably close to $5.0e-4$.

Figure 1: Length at age relationship for species XX (data taken from Derek Ogle's R vignette).



2.3 Exercise

We used data from an R vignette, and shown in figure (1) to understand how to get initial guesses for the parameters but also how to use solver, and sums-of-squares, to estimate the parameters that best fit the data. Next we named the parameters: t_0 , K , L_{inf} . You can name the cells that correspond to the values in the upper naming box on the Excel worksheet. In this case if you select the box "B3" where the value for L_{inf} will be put, and the you look in the upper left hand corner of the screen you will see "B3" in a box.

To predict the average length of different aged individuals we needed to get our best estimates of the parameters based on the data. t_0 we set to zero - the age at which the fish has length zero, L_{inf} was the average maximum value, 400, from the graph or the pivot table. K was the only thing we had to *guesstimate*, $K = (80/2)/(400 - 250)$. For every row of data we calculated $L(a) = L_{inf} * (1 - \exp(-K(t_0 - a)))$. Where a is the age of the fish in each row, and $L(a)$ becomes our prediction.

3 Spawner-recruit relationships

Over their life span animals tend to produce more offspring than is needed to replace themselves. For instance, in any given year a bird will lay several eggs, a fish will produce thousands or millions of eggs, and over its life span it can produce many orders of magnitude more offspring than is needed to replace itself. This is necessary because of predation, disease, harvest, and natural catastrophes.

These models describe the relationship between the number, or weight, of spawners in the population at time t , and the number of recruits (i.e. juveniles, young-of-the-year, age-1) at some time in the future.

3.1 Ricker

The Ricker (4) curve bends over to account over-compensation in the population where things like cannibalism or spawning habitat limitations are likely to occur.

$$R = \alpha S e^{-\beta S} \quad (4)$$

α is the slope of the model at the origin, and β is the inversely proportional to the average number of spawners that produce the maximum number of recruits.

You should know what the parameters of the Ricker model mean, if not how we determined them. The derivative of the model describes the slope of the line - steeper slope, higher production. To determine the slope we take the derivative.

$$\frac{dR}{dS} = \frac{d}{dS} \alpha S e^{-\beta S} \quad (5)$$

$$\frac{dR}{dS} = \alpha e^{-\beta S} + (-\beta \alpha S e^{-\beta S}) \quad (6)$$

$$\frac{dR}{dS} = \alpha e^{-\beta S} (1 - \beta S) \quad (7)$$

The slope of the model at $S = 0$ is α . Then setting the derivative equal to zero

$$\frac{dR}{dS} = 0 \quad (8)$$

$$\alpha e^{-\beta S}(1 - \beta S) = 0 \quad (9)$$

$$(1 - \beta S) = 0 \quad (10)$$

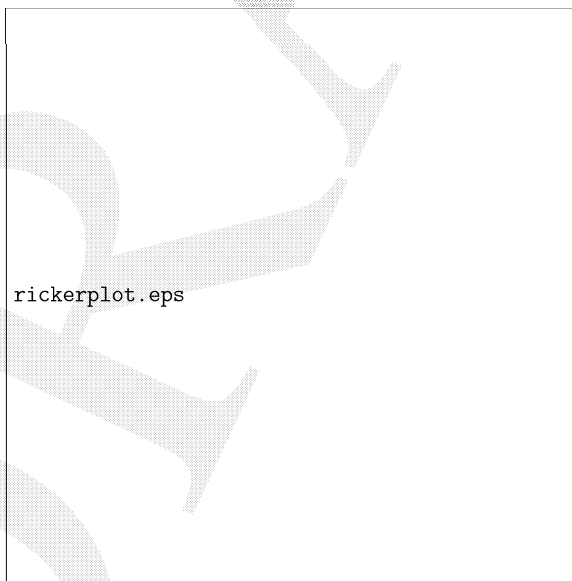
$$S_{max} = \frac{1}{\beta} \quad (11)$$

β is equal to the inverse of the number of spawners, that on average produce the largest number of recruits (12).

$$\beta = \frac{1}{S_{max}} \quad (12)$$

The blue line, which is an estimate of the Ricker model describing the the Chignik data (figure 2), is made based on an *guesstimate* of $\alpha = 5$. This is based on looking at the dots near the origin – 1,000,000 recruits on the y-axis divided by 200,000 spawners on the x-axis. $\beta = 1/800,000$ because, on average, 800,000 spawners produced the highest number of recruits.

Figure 2: Ricker spawner-recruit relationship. The dots are the observed recruits verses spawners. The black line is the one-to-one (i.e. replacement) line. The blue line in the model of the spawner recruit relationship based on our *guesstimates* of $\alpha = 5$ and $\beta = 1/800,000$.



3.2 Beverton-Holt

Similar to the Ricker model, we want to know what the parameters of the B-H model mean. In the case of the B-H model (13) the α parameter is inversely proportional to the slope at the origin. So instead of $\alpha = R/S$ at the origin, as in the case of the Ricker, α is S/R at the origin. β is not inversely proportion to the spawners that produce the maximum recruitment in the case of the Ricker, instead β is inversely proportion to the maximum of the average number of recruits produced.

$$R = \frac{S}{\alpha + \beta S} \quad (13)$$

We repeat the process with the Ricker model and take the derivative of the Beverton-Holt model.

$$\frac{dR}{dS} = \frac{d}{ds} \frac{S}{\alpha + \beta S} \quad (14)$$

$$\frac{dR}{dS} = \frac{(\alpha + \beta S) - S\beta}{(\alpha + \beta S)^2} \quad (15)$$

$$\frac{dR}{dS} = \frac{\alpha}{(\alpha + \beta S)^2} \quad (16)$$

Similar to the Ricker model, we want to see what happens to the slope of the B-H as spawners approach zero.

$$\lim_{s \rightarrow 0} \frac{dR}{dS} = \lim_{s \rightarrow 0} \frac{\alpha}{(\alpha + \beta S)^2} \quad (17)$$

$$\Rightarrow \lim_{s \rightarrow 0} \frac{dR}{dS} = \frac{\alpha}{(\alpha + 0)^2} \quad (18)$$

$$\Rightarrow \lim_{s \rightarrow 0} \frac{dR}{dS} = \frac{\alpha}{\alpha^2} \quad (19)$$

$$\Rightarrow \lim_{s \rightarrow 0} \frac{dR}{dS} = \frac{1}{\alpha} \quad (20)$$

However, unlike the Ricker model, the B-H model does not have an obvious maximum in the model where the slope would be equal to zero. Instead, we take the limit of the actual equation and ask what happens to $R(S)$ as

$S \rightarrow \infty$, that is as S gets really large (21) what happens to R .

$$\lim_{S \rightarrow \infty} R(S) = \frac{\lim_{S \rightarrow \infty} S}{\lim_{S \rightarrow \infty} (\alpha + \beta S)} \quad (21)$$

l'Hospital

$$\lim_{S \rightarrow \infty} R(S) = \frac{1}{\beta} \quad (22)$$

$R = 1/\beta$ as S gets really large. Conversely, a good approximation of β is $1/R_{max}$, where R_{max} is the maximum number of recruits.

If we look at the data in figure 3 we see that the inverse of the slope at the origin is 200 spawners divided by 400 recruits (red lines), and the average maximum recruits is 2,500, resulting in initial *guesstimates* of $\alpha = 0.5$ and $\beta = 1/2,500$. It's not a perfect *fit* to the data, but it's close, and you should be able to judge why other people's guesses may or may not be appropriate.

Figure 3: Beverton-Holt spawner recruit relationship.



3.3 Beverton-Holt with steepness

This re-parameterization of the Beverton-Holt equation which is more widely used and has more biologically meaningful parameters. It relates the parameter h (**steepness**) to virgin recruit and virgin spawning biomass. h is a

dimensionless parameter between 0 and 1. In this way, populations can be more easily compared.

Begin with B-H model (this is slightly different than our previous B-H model (13))

$$R_0 = \frac{aB_0}{b + B_0}. \quad (23)$$

where, R_0 is the virgin recruitment, B_0 is the virgin spawning biomass, and a and b are parameters of the B-H model.

Steepness is the fraction of virgin recruitment achieved by a biomass that is 20% of virgin spawning biomass.

$$hR_0 = \frac{a0.2B_0}{b + 0.2B_0}. \quad (24)$$

where $0.2B_0$ is 20% of the virgin spawning biomass, and hR_0 is the number of recruits produced by $0.2B_0$. If you solve the equation for h by substituting 23 into 24 you get

$$\begin{aligned} h \frac{aB_0}{b + B_0} &= \frac{a0.2B_0}{b + 0.2B_0} \\ h &= \frac{b + B_0}{aB_0} \frac{a0.2B_0}{b + 0.2B_0} \\ h &= \frac{b + B_0}{aB_0} \frac{a0.2B_0}{b + 0.2B_0} \\ h &= \frac{0.2(b + B_0)}{b + 0.2B_0}. \end{aligned} \quad (25)$$

Right now you should be thinking this is pretty cool. Now solve that 25 for b

$$\begin{aligned} h &= \frac{0.2(b + B_0)}{b + 0.2B_0} \\ h(b + 0.2B_0) &= 0.2b + 0.2B_0 \\ hb + 0.2hB_0 &= 0.2b + 0.2B_0 \\ hb - 0.2b &= 0.2B_0 - 0.2hB_0 \\ b(5h - 1) &= B_0(1 - h) \\ b &= \frac{B_0(1 - h)}{5h - 1} \end{aligned} \quad (26)$$

Now put 26 into equation 23 and solve for a .

$$a = \frac{4hR_0}{5h - 1} \quad (27)$$


However, we want to put the a and b in terms of the parameters in our original B-H parameterization (13). To do that $\alpha = b/a$ and $\beta = 1/a$. So α and β for the B-H model in equation 13 in terms of steepness and virgin recruitment are 28 and 29, respectively.

$$\alpha = \frac{S_0(1 - h)}{4hR_0} \quad (28)$$

$$\beta = \frac{5h - 1}{4hR_0} \quad (29)$$

Take a population where you set the virgin spawning biomass to 1,000 tonnes, and the virgin recruitment in numbers is 1,000, and the steepness is 0.8: $B_0 = 1,000$, $R_0 = 1,000$ and $h = 0.95$. Then you know that you can expect 950 recruits when the biomass is 200 tonnes. If $h = 0.6$ then you would expect 600 recruits from a biomass of 200 tonnes (figure 4)

Figure 4: Spanwer-recruit relationship for the Beverton-Holt model parameterized for steepness. For a population with an R_0 and B_0 of 1,000, the green line is based on a steepness of 0.6 and the blue line is based on steepness of 0.95.



steepnessplot.eps

3.4 Exercise

You will see what is known as a brood table for salmon, in this case the Chignik sockeye salmon population in Chignik, Alaska. The rows are known as brood years - the year in which the salmon spawned and buried eggs in the gravel of their natal streams. There is column labeled "Escapement." What is escapement? The other columns are the number of fish that returned from the escapement in a particular brood year. What is a brood year? There are several different columns because sockeye salmon born in one year do not all return in the same subsequent year. The sum of the numbers separated by a period, plus 1 for the year that the eggs spend in the gravel, is the age of the fish when it returned to spawn or be caught in the fishery. The first number is the number of years the fish spent in freshwater, and the second number is the number of years that the fish spent in saltwater.

The purpose of this lab is to:

1. Familiarize you with spawner-recruit functions
2. Be able to "guess" the best parameter estimates
3. Estimate the best parameter with solver
4. Determine MSY, the escapement that produces maximum sustainable yield, and U_{msy} the harvest rate that produces maximum sustainable yield.
5. Estimate the lost yield of alternatives to MSY.

4 Age aggregation: Surplus production / Graham-Schaeffer model

Rather than assuming that population growth forever, a more realistic model of population growth is the logistic model. Any population that is interesting must individuals that are killed. So from the logistic equation arises what is known as the Schaefer model in fisheries; it looks identical to the logistic model (equation 30) but it has a term for catch. In fisheries these models are called surplus production models and they have several derivations: Schaefer, Pella-Tomlinson, Fox, and Schnute models to name a few. The logistic growth has the form

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right). \quad (30)$$

Simply put, when the population N is below a certain level, K , the rate of change in the populations, $\frac{dN}{dt}$, is positive because the part of the equation, $(1 - \frac{N}{K})$ is positive. Conversely, when $N > K$, $(1 - \frac{N}{K})$ is negative and the rate of change in the population is negative. Unfortunately, the solving the differential equation in equation 30 would be taught in the second week rather than the second day of a class in differential equations. Rather than describing elementary Diff Eq's, partial fractions, and u substitutions we will simply ignore the instantaneous growth of the population using the logistic model, and solve for the discrete model similar to equation xx.

$$\begin{aligned} \frac{dN}{dt} &= rN\left(1 - \frac{N}{K}\right) \\ \frac{N_{t+1} - N_t}{t + 1 - t} &= rN_t\left(1 - \frac{N_t}{K}\right) \\ N_{t+1} &= N_t + rN_t\left(1 - \frac{N_t}{K}\right) \\ N_{t+1} &= N_t\left(1 + r\left(1 - \frac{N_t}{K}\right)\right) \end{aligned} \quad (31)$$

Surplus production models (30) are age-aggregate models. There is no difference between recruits or spawners, young or old, big or small individuals in these models. Additionally, births and deaths are included in a single parameter of the model, r . r is the population growth rate. An $r = 0.1$ mean the population grows at 10% a year under ideal conditions, and no

density dependence. K is the carrying capacity of the system - the point at which births and deaths are equal and the population is at equilibrium. C_t is the catch during time step t , or the model can include a harvest rate h instead (equation 32).

$$\begin{aligned} N_{t+1} &= N_t \left(1 + r \left(1 - \frac{N_t}{K}\right)\right) - C_t \\ N_{t+1} &= N_t + rN_t \left(1 - \frac{N_t}{K}\right) - C_t \\ N_{t+1} &= N_t + rN_t \left(1 - \frac{N_t}{K}\right) - hN_t \end{aligned} \quad (32)$$

Yet another way to think about the model is

$$N_{t+1} = N_t + S_t - C_t. \quad (33)$$

Here N_t is the population size at time t , S_t is the surplus production (thus these are commonly referred to as surplus production models), and C_t is the catch or harvest. Figure 5 shows the relationship between surplus production and population size (upper panel), and total population growth and time (lower panel), for r and K values of 0.2 and 1,000, respectively.

Obviously, for this example, catch (C_t) will have the same units as N (i.e. number or biomass), and the harvest fraction, h , needs to be between 0 and 1.

It's worth noting some of the more interesting characteristics of the Schaefer model such as the population size a MSY. If we start with the just $S(t)$, the surplus production part of the equation, take the derivative, and set it equal to zero, we can solve for the population size, N , that produces the maximum surplus production, or MSY.

$$\begin{aligned} S &= rN \left(1 - \frac{N}{K}\right) \\ \frac{dS}{dN} &= r \left(1 - \frac{N}{K}\right) + rN \left(-\frac{1}{K}\right) \\ 0 &= r - \frac{rN}{K} - \frac{rN}{K} \\ \frac{K}{2} &= N \end{aligned} \quad (34)$$

The population size that produces MSY is $\frac{K}{2}$. If you know the population size that produces MSY, you can find the Y_{MSY} or the yield at MSY, by again taking the surplus part of the model and plus in the $\frac{K}{2}$ for N .

$$\begin{aligned}
 Y_{MSY} &= \frac{rK}{2} \left(1 - \frac{K}{2}\right) \\
 Y_{MSY} &= \frac{rK}{2} - \frac{rK^2}{4} \\
 Y_{MSY} &= \frac{rK}{2} - \frac{rK}{4} \\
 Y_{MSY} &= \frac{rK}{4}
 \end{aligned} \tag{35}$$

Now that you know the yield and N at MSY, it is pretty easy to calculate U_{MSY}

$$\begin{aligned}
 U_{MSY} &= Y_{MSY}/N_{MSY} \\
 U_{MSY} &= \frac{\frac{rK}{4}}{\frac{K}{2}} \\
 U_{MSY} &= 2r
 \end{aligned} \tag{36}$$

4.1 Catchability coefficients: relating estimates biomass to index data

Because we never know what the number of fish in the ocean is, we have find a way of comparing our estimates population size to some data that is reflective of the population size. For the purposes of this course we will be comparing our population estimates to catch per unit effort (CPUE) or fishery independent surveys. This requires that we estimate two additional parameters, q_{CPUE} and q_{surv} .

The idea is simple: if you divide the catch by a constant unit of effort, then as the biomass declines you would expect the CPUE effort to decline. Similarly, if you conducted a transect survey, either visual or with some type of fishing gear, then as the population changes you would expect the survey numbers to reflect the change in the population.

4.2 Exercise

The exercise dealt with pepino data from the Galapagos. We modeled the *number* of pepino as opposed to the biomass. We also introduce the idea that population size, biomass or numbers, should be proportional the indices of abundance whether it is catch-per-unit-effort or fishery independent surveys. Because we never know what the number of fish in the ocean is, we have find a way of comparing our populations estimates to some data that is reflective of the population size. In the case of the pepino we compared our estimate of population size based on the parameters r and K , and the catch data, to the observed CPUE and independent survey data. This required that we estimate two additional parameters, q_{CPUE} and q_{surv} .

1. Fit the surplus production model to the pepino data
 - (a) CPUE only
 - (b) Survey only
 - (c) Both CPUE and survey
2. Find MSY , N_{msy} , and U_{msy} .

Figure 5: The following figures show the surplus production of a population with an $r = 0.2$ and a $K = 1000$. The upper panel shows how the production changes according to the size of the population, and the lower panel shows how the population changes over time starting from an initial population of 1. The blue lines show the relationship between surplus production and population size when the population size is at 500, and the red lines show the relationship when the population size is at 100.



5 Mid-term: (1) fitting spawner-recruit relationships in a mixed-stock fishery, (2) modeling the population dynamics of North Atlantic Minke whales

The assignment is due by mid-night February 15th, 2012. You are expected to complete the spreadsheet analysis of the data using the spawner-recruit and surplus production models, as well as answer the associated management questions. You will be analyzing spawner recruit data from the Nushagak district in Bristol Bay, Alaska. This is a "mixed-stock" fishery, which means salmon from two distinct spawning populations are harvested in the same commercial fishery. The second set of data you will be analyzing is minke whale catch (numbers) and catch-per-unit-effort (whales captured per unit of time fished) data from official Norwegian whaling statistics.

Note: Your job is to be a scientist not an advocate. This is your opportunity to show that in a crowd of advocates, scientists, and industry groups, your analysis is objective and unbiased. Always start by asking what does the data tell us.

5.1 Mixed-stock spawner-recruit data

The purpose of this exercise is to use evaluate the productivity of two stocks of salmon in mixed-stock salmon fishery. Treat each river (Wood vs. Igushik) as if it were a separate stock. This means you will need to determine two sets of spawner-recruit parameters. The recruit data are in the spreadsheet labeled "Recruits", and the spawner data are in the spreadsheet labeled "Spawners". This is a very really world situation. The State of California is spending \$10's of millions on salmon issues in the San Joaquin and Sacramento valleys, and the State of Alaska confronts the issue optimal spawn population size bi-annually at its Board of Fish meetings.

1. Plot the data.
2. Estimate the parameters of the model for both stocks.
3. Find the reference points MSY , S_{msy} (spawning size that produces msy), and U_{msy} for both stocks.

4. Use the table function to discuss the sensitivity of the reference points.
5. Write-up your results. I want plots of the data and fits to the data. I want a table of the model parameters, as well as plots of alternative hypotheses. I want your recommendation for the sustainable levels of harvest. I also want you discuss the problems of a mixed stock fishery in terms of optimal harvest rates.

Hint: Use a pivot table to determine the sum of the number of recruits for each year, for each stock

5.2 Norwegian minke whale data

The purpose of this exercise is to determine the status and productivity of Norwegian minke whales. This has very real world implications. There has been a call for ending the whaling moratorium and you may be asked by an organization whether or not harvests are sustainable.

1. Plot the data.
2. Estimate the parameters of the model.
3. Find MSY , N_{msy} , and U_{msy} .
4. Sensitivity analysis using table functions
5. Write-up your results. I want plots of the data and fits to the data. I want table of the model parameters, as well as plots of alternative hypotheses. I want your recommendation for the sustainable levels of harvest. I would encourage you to add a discussion section describing the advantages and disadvantages of the type of model you chose.

Hint: You will need to be a little creative - think pepino model solver issues - to keep you predicted population size from going negative.

6 Separating recruits from adults: the delay difference model

Last week talked about delay difference models in terms of numbers. This week we are going to talk about delay difference models in terms of biomass. The delay difference equation for biomass is

$$B_t = s_{t-1}B_{t-1} + \rho s_{t-1}B_{t-1} - \rho s_{t-1}s_{t-2}B_{t-2} - \rho s_{t-1}w_{t-1}R_{t-1} + w_t R_t \quad (37)$$

The equation is very messy looking but if you look at the components it actually makes intuitive sense. For now, assume that ρ is a measure of allometric growth between ages. Then $s_{t-1}B_{t-1}$ represents the survival of the biomass from the previous time step, and $\rho s_{t-1}B_{t-1} - \rho s_{t-1}s_{t-2}B_{t-2} - \rho s_{t-1}w_{t-1}R_{t-1}$ represents the growth of the biomass from the previous time step, and $w_t R_t$ represents the new recruitment to the population. Getting to that equation is an exercise in first principles.

6.1 Principle equations

There are some background equations that we need to discuss. These principle equations deal with weight, numbers, recruitment and survival. A lot of this is algebra, but learning how to manipulate these principle equations will lead us to equation (37).

6.1.1 Modeling weight at age

Start with the following relationship between weight and age (38). It says that growth between ages is proportional. The ρ parameter is similar to the K parameter of the Von bertalanffy growth function ($K = (dL/dt)/(L_\infty - L)$), where K describes the change in L as a function of age t relative to L_∞ . ρ is a constant ratio that describes the change in weight between *successive* ages.

$$\begin{aligned} w_{a+1} - w_a &= \rho(w_a - w_{a-1}) \\ w_{a+1} &= \rho(w_a - w_{a-1}) + w_a \\ w_{a+1} &= (1 + \rho)w_a - \rho w_{a-1} \end{aligned} \quad (38)$$

6.1.2 Numbers at age and survival

Consider the following model of the number of fish that are age a .

$$N_{t+1,a+1} = N_{t,a} s_t \quad (39)$$

It says the number of fish age $a + 1$ in time $t + 1$ is equal to the number of fish in the previous age category and time step, times the survival rate in the previous time step. The number of people in a population that are age 20 next year, is equal 19 year olds this year times the fraction that survive. The total population is

$$N_t = \sum_{a=L}^{\max(a)} N_{t,a} \quad (40)$$

where L is the age when the fish first recruit to the fishery. The total population in the next time step ($t + 1$) is little trickier. It is

$$\begin{aligned} N_{t+1} &= \sum_{a=L}^{\max(a)} N_{t+1,a} \\ \Rightarrow N_{t+1} &= \sum_{a=L}^{\max(a)} N_{t+1,a+1} + R_{t+1} \end{aligned} \quad (41)$$

where R_t is the recruitment to the fishery in time t .

Finally, a slightly more obscure situation, but one we will need to consider, the numbers at age in the previous year ($t - 1$) is

$$\begin{aligned} N_{t-1} &= \sum_{a=L}^{\max(a)} N_{t-1,a} \\ N_{t-1} &= \sum_{a=L}^{\max(a)} N_{t-1,a-1} - N_{t-1,a-1} \\ \Rightarrow N_{t-1} &= \sum_{a=L}^{\max(a)} N_{t-1,a-1} - N_{t-1,L-1} \end{aligned} \quad (42)$$

Notice that the subscripts now includes the age class ($L - 1$), but the $N_{t-1,L-1}$ will not have recruited to the fishery since age $L - 1$ is less than age L . So, we need to subtract where $N_{t-1,L-1}$ from the population. The only remaining question is what is $N_{t-1,a-1}$. Our model only keeps track of the recruits and

the biomass (see equation 37), we need to change $N_{t-1,L-1}$ into a recruits. Remember, the $R_t = N_{t-1,L-1}s_{t-1}$, so

$$\begin{aligned} N_{t-1,L-1} &= \frac{N_{t,L}}{s_{t-1}} \\ \Rightarrow N_{t-1,L-1} &= \frac{R_t}{s_{t-1}} \end{aligned} \quad (43)$$

6.1.3 Changing numbers to biomass

Now consider the following, the biomass of the population that is age a at time t . It is the product of the weight at age (w_a) and the numbers at age ($N_{t,a}$)

$$B_{t,a} = N_{t,a}w_a \quad (44)$$

To calculate the total biomass at any time we simply sum over all of the ages

$$B_t = \sum_{a=L}^{\max(a)} N_{t,a}w_a \quad (45)$$

where, L is the age at recruitment, and $\max(a)$ in the maximum age of fish capture in the fishery. The key is that the age subscript for both the weight and numbers have the same a subscript.

To calculate the biomass of the population at $t + 1$ we have to use what we learned from equation (41).

$$B_{t+1} = \sum_{a=L}^{\max(a)} N_{t+1,a+1}w_{a+1} + w_{a=L}R_{t+1} \quad (46)$$

Finally, to calculate the biomass of the population at $t - 1$ we have to use what we learned from equation (41).

$$B_{t-1} = \sum_{a=L}^{\max(a)} N_{t-1,a-1}w_{a-1} - w_{a=L-1}\frac{R_t}{s_{t-1}} \quad (47)$$

6.2 Combining parts 6.1.1, 6.1.2, & 6.1.3

To calculate the biomass we need to begin by weight t age and numbers at age, thus using equation (44) and multiplying by $N_{t+1,a+1}$. We get

$$N_{t+1,a+1}w_{a+1} = (1 + \rho)w_a N_{t+1,a+1} - \rho w_{a-1} N_{t+1,a+1} \quad (48)$$

And if we want to turn equation 48 into biomass total we need to sum across all ages (see equation 45)

$$\begin{aligned} \sum_{a=L} N_{t+1,a+1}w_{a+1} &= \sum_{a=L} [(1 + \rho)w_a N_{t+1,a+1} - \sum_{a=L} \rho w_{a-1} N_{t+1,a+1}] \\ \Rightarrow \sum_{a=L} N_{t+1,a+1}w_{a+1} &= \sum_{a=L} [(1 + \rho)w_a N_{t,a} S_t - \sum_{a=L} \rho w_{a-1} N_{t-1,a-1} s_t s_{t-1}] \end{aligned} \quad (49)$$

Based on equation (46) we change the right side of the equation (48) to look like

$$B_{t+1} + w_{a=L} R_{t+1} = \sum_{a=L} [(1 + \rho)w_a N_{t,a} S_t - \sum_{a=L} \rho w_{a-1} N_{t-1,a-1} s_t s_{t-1}] \quad (50)$$

On the right side of the equation (50) we can use equation (44) and (47) to get

$$B_{t+1} + w_{a=L} R_{t+1} = (1 + \rho)B_t s_t - \rho [B_{t-1} - w_{a=L-1} \frac{R_t}{s_{t-1}}] s_t s_{t-1} \quad (51)$$

When you multiply every, and cancel things out, you end up with

$$B_{t+1} = (1 + \rho)B_t s_t - \rho s_t s_{t-1} B_{t-1} + w_{a=L-1} s_t R_t - w_{a=L} R_{t+1} \quad (52)$$

At this point you are done. However, equation (52) predicts the biomass in year $t + 1$. Personally, my mind works better if the equation looks more like the original equation (37). To do this simply subtract 1 from everywhere you see a $t + 1$ and you will end up with equation (37).

6.3 Adding a recruitment function

Besides changing numbers to biomass, one of the keys to this model is that we are modeling recruitment explicitly. To do this we could choose from a number of spawner recruit functions, but I will you the Beverton-Holt with steepness.

$$R(t) = f(B_{t-L}) = \frac{0.8R_0hB_{t-L}}{0.2\Theta R_0(1-h) + (h-0.2)B_{t-L}} \quad (53)$$

One of the caveats of the delay difference model is that the year a fish recruits to the fisheries they are vulnerable to fishery and they contribute directly to the spawning biomass. In many cases, however, the fish do not recruit to the fishery the year following spawning. This is why we include a lag in the biomass that results in the recruitment in year t . For instance the recruitment in 2012 would be based on the spawners in 2009 if there was a three year lag between spawning and recruitment.

It turns out that the R_0 can be determine directly from equation (37) if we assume the population is at equilibrium. The biomass at equilibrium is

$$B_0 = sB_0 + \rho sB_0 - \rho s^2B_0 - \rho sw_{t-1}R_0 + w_tR_0 \quad (54)$$

The reason is because by definition if the population is at *equilibrium* the survival will be *equal* every year, the biomass will be *equal* every year, and recruitment will be *equal* every year. If B_0 is an estimable parameter of the model, then R_0 is as follows,

$$\begin{aligned} B_0 &= sB_0 + \rho sB_0 - \rho s^2B_0 - \rho sw_{t-1}R_0 + w_tR_0 \\ \Rightarrow B_0 &= sB_0(1 + \rho - \rho s^2) - R_0(\rho sw_{t-1} + w_t) \\ \Rightarrow R_0(\rho sw_{t-1} - w_t) &= B_0(s + \rho - \rho s^2) - B_0 \\ \Rightarrow R_0(\rho sw_{t-1} - w_t) &= B_0(s + \rho - \rho s^2 - 1) \\ \Rightarrow R_0 &= B_0 \frac{(s + \rho - \rho s^2 - 1)}{(\rho sw_{t-1} - w_t)} \end{aligned} \quad (55)$$

6.4 Exercise

You will be fitting a delay-difference model to the South African Cape hake data. Additionally, you fit a surplus production model to the same data and

compare the results. The data are the catches from 1917 to 1992, and *cpue* from 1955 to 1992. The parameters of the model you will be estimating are B_0 , h , s , and q_{cpue} . Additional parameters of the model include Θ , R_0 , ρ , w_L , w_{L-1} .

6.4.1 Step 1: Create you columns

In this instance we will need to keep track of the biomass at time t ($B(t)$), the recruits ($R(t)$), the spawners ($S(t)$), and the survival s_t . If you are interested in comparing the results to the surplus production model, you should create an additional biomass prediction for the surplus production model. Since we will be fitting the model the *cpue* data, you will need to create a column for the predicted *cpue*.

6.4.2 Step 2: Name your cells

There are a lot more parameter to keep track of this model than there were in previous models. All of the following parameters will figure into our model: B_0 , h , and q_{cpue} , and Θ , R_0 , ρ , s , w_L , w_{L-1} . Only B_0 , h , and q_{cpue} will be estimated. Although we could estimate ρ and s , this introduces a lot of instability to the model.

6.4.3 Step 3: Build your model

We will divide the modeling into several steps. The first is the preliminary calculations - particularly calculations for parameters that we do not need to estimate. Second, we will break down the model into components - recruits, spawners, and survival - so the we minimize the errors that might be introduced by putting the entire biomass calculation into one cell. Third, we will calculate the predicted *cpue*. Finally, we will calculate the sums-of-squares and at minimize it using solver to find the best fit to the data.

6.4.4 Preliminary calculations

Although it is not necessarily a calculation I always start by guessing what B_0 is. I have found the best way to do this is to assume that the maximum catch is 10% of B_0 . The maximum catch occurred in 1973 at 243, so my first guess of B_0 is 2430.

Next, we will be using the Beverton-Holt stock recruitment function parameterized for steepness, h (74).

$$R(t) = f(B_{t-L+1}) = \frac{0.8R_0hB_{t-L+1}}{0.2\Theta R_0(1-h) + (h-0.2)B_{t-L+1}} \quad (56)$$

It turns out that the R_0 can be determine directly from equation (??) if we assume the population is at equilibrium. The biomass at equilibrium is

$$B_0 = sB_0 + \rho sB_0 - \rho s^2B_0 - \rho sw_{t-1}R_0 + w_tR_0 \quad (57)$$

The reason is because by definition if the population is at *equilibrium* the survival will be *equal* every year, the biomass will be *equal* every year, and recruitment will be *equal* every year. If B_0 is an estimable parameter of the model, then R_0 is as follows,

$$\begin{aligned} B_0 &= sB_0 + \rho sB_0 - \rho s^2B_0 - \rho sw_{t-1}R_0 + w_tR_0 \\ \Rightarrow B_0 &= sB_0(1 + \rho - \rho s^2) - R_0(\rho sw_{t-1} + w_t) \\ \Rightarrow R_0(\rho sw_{t-1} - w_t) &= B_0(s + \rho - \rho s^2) - B_0 \\ \Rightarrow R_0(\rho sw_{t-1} - w_t) &= B_0(s + \rho - \rho s^2 - 1) \\ \Rightarrow R_0 &= B_0 \frac{(s + \rho - \rho s^2 - 1)}{(\rho sw_{t-1} - w_t)} \end{aligned} \quad (58)$$

based on the s , ρ , and B_0 using the following equation

$$R_0 = B_0 \frac{(1 - s - \rho s + \rho s^2)}{(w_0 - \rho sw_1)} \quad (59)$$

This is equation is actually derived from first principles, but we will not take the time to do that here. Another parameter of the spawner-recruit function is Θ , the ratio of virgin biomass to the virgin recruitment.

$$\Theta = \frac{B_0}{R_0} \quad (60)$$

Part of the delay difference model is growing the recruits up to the size when they first enter the fishery. If you look at the worksheet labeled "Brody"

you will see the average weight of observed hake in grams. There are a couple of things to note about this data. First, hake do not "recruit" to the fishery until age 3 therefore the weight at recruitment (W_L) is 382 grams. The weight of the hake one year prior to recruitment (W_{L-1}) is 161 grams. You should enter both of these values where you have labeled these parameters on the *Model* spreadsheet.

The last thing we need to do is calculate the Brody parameter ρ . Remember that the Brody parameter describes the proportional relationship between the weight at age $a + 1$ and a , and a and $a - 1$. Such that

$$w_{a+1} = (1 + \rho)w_a - \rho w_{a-1} \quad (61)$$

Based on the data in the Brody worksheet you have observations of the weight at age, and based on equation 61 you can predict the weight at age. By minimizing the square difference between the observed and predicted weight at age you can calculate the Brody coefficient.

You have now completed the preliminary calculations. Now things get tricky.

6.4.5 Building the components

You will start to that the a lot the math associated with fisheries model is pretty straight forward. Where most people run into problems is the accounting, and delay difference models have a lot of accounting. This is the first model where you are being asked to keep track of more than just a single life history stage.

If you look at the model you will see that there are different life history stages, as well as different time steps in the same equation. There are both adult and juveniles on the right side of the equation and those adults and juveniles arise from different periods. Keep track of these things by adding as many columns as you need in order to make sense of the equations. I have added the following columns: "recruits", "spawners", and "survival".

The first thing you will need to do is add a couple of years prior to the first year there is data. This is important because fish are 3 years old when they first recruit to the fishery, and as a result we need to go back a couple of years in the past to "seed" the model. From 1914 to 1917 you can assume that the population is at B_0 because either fishing just started or hasn't

begun. Similarly the recruitment in those years is equal to R_0 the virgin recruitment.

Begin with the easiest one, survival. Survival in 1914 is

$$s_{1914} = s(1 - C_{1914}/B_{1914}) \quad (62)$$

Since there was no catch in 1914, the survival in 1914 you simply be equal to the average survival s . Copy this equation down.

Simplicity sake we will simply assume that the spawning biomass is equal to the biomass in the biomass column.

Now the tricky part, calculating the recruitment. First, look at the delay difference model. We are predicting the biomass at time $t + 1$, but we know that the recruits at $t+1$ (R_{t+1}) are actually based on the spawners three years ago. Therefore, starting in 1918 the first real year of predictions, the recruits in 1918 will be a function of the spawners in 1915 - three years earlier.

Now all we have to do is simply calculate the biomass in year 1918 using the delay difference equation and copy it down.

At this point you should be well aware of how to calculate the predicted *cpue* and the square difference between the observed and predicted *cpue*. You should do this respective columns and copy the equations down. Only calculate the square difference for those years that actually have *cpue* data.

7 Cohort analysis: fully age structured model

Until now we have dealt with models that aggregate the age-structure of populations into totals numbers or biomass, and estimate aggregate population parameters - intrinsic growth rate, steepness, carrying capacity. The problem is that populations do have age structure and it can be very informative about a population's trend. We are going to learn to build age-structured models of populations that are more realistic and flexible than the age-aggregated models we have built thus far. The real disadvantages of these models is that they are model complex (I think they are actually less complex than delay-difference models), and they these models still assume closed populations without any predation, spatial complexity, or competition.

Table 1: Table of variables, forcing functions, and parameters for an age-structured model.

$N_{t,a}$	Number of fish that are age a during time t
SB_t	spawning biomass during time t
TB_t	total biomass during time t
CB_t	commercial biomass during time t
ν_a	vulnerability of age a
l_a	length of age a
w_a	weight of age a
m_a	maturity of age a
M_a	natural mortality of age a
h	steepness
R_0	initial recruitment
Θ	stock recruitment parameter
L_∞	maximum length of average individual
K	Von Bertalanffy growth parameter
t_0	length at age zero
l_{50}	length at 50% vulnerability
l_{95}	length at 95% vulnerability
m_{50}	maturity at 50%
m_{95}	maturity at 95%

7.1 Natural mortality

There are two ways to describe natural mortality: instantaneous versus discrete mortality. The discrete model simply says that the natural mortality, or survival, in a given year is simply a fraction of the total population. For instance, if survival is 0.8, then 80% of the population survives to the next time step. If we consider that the natural mortality occurs instantaneously throughout the year we can use the following differential equation

$$\frac{dN}{dt} = MN. \quad (63)$$

Solving the equation in terms of N and t we get

$$N_t = N_0 e^{-Mt}. \quad (64)$$

Since we are only considering yearly time steps, you can determine the population size at any time t based on the following equation

$$N_t = N_{t-1} e^{-M}. \quad (65)$$

Similarly, the survival half way through the year would be $N_t = N_{t-1} e^{-0.5M}$. And extending the model to an age-specific model.

$$N_{t,a} = N_{t-1,a} e^{-M_a}. \quad (66)$$

This formulation is slightly more useful if you want to consider situations where spawning or natural mortality occur at specific times in the year.

7.2 Growth: von Bertalanffy growth equation, length-weight relationship

We use the von Bertalanffy growth model to describe the length of a fish that is age a

$$l_a = L_\infty (1 - e^{-K(a-a_0)}) \quad (67)$$

The weight at age is simply

$$w_a = \gamma l_a^b \quad (68)$$

7.3 Biomass: total, commercial, spawning

The following are the equations for spawning biomass (69), commercial biomass (70), and total biomass (71) of a population of fish at time t that are age a .

$$SB_{t,a} = N_{t,a}w_a m_a \quad (69)$$

$$CB_{t,a} = N_{t,a}w_a \nu_a \quad (70)$$

$$TB_{t,a} = N_{t,a}w_a \quad (71)$$

To determine the biomass in a particular year, we would sum across ages, \sum_a .

7.4 Vulnerability/selectivity and maturity ogives

All fishing gear is selective. One of the biggest advantages of age structured models is that they allows us to account for the vulnerability/selectivity (72) of fishing gear on different age classes.

$$\nu_a = \frac{1}{1 + e^{-\ln(19)\left[\frac{(l_a - s_{50})}{(s_{95} - s_{50})}\right]}} \quad (72)$$

Additionally, we can assume that there is differential maturity (73) for each age class.

$$m_a = \frac{1}{1 + e^{-\ln(19)\left[\frac{(l_a - m_{50})}{(m_{95} - m_{50})}\right]}} \quad (73)$$

The curves are logistic curves, whose rates are symmetric about the s_{50} or m_{50} inflection points. s_{50} is the length at which 50% of the fish would be captured if the harvest was 100%. Similarly, the s_{95} is the at which 95% of the fish would be captured if the harvest fraction was 100%. The closer the two parameters are to one another the more *knife-edge* the selectivity is. A similar analogy applies for the maturity at age ogive.

7.5 Population dynamics

7.5.1 Numbers at age

There may be many age classes within a given year, but there are only three equations you need to remember. You need to calculate the recruits, the intermediate ages, and the plus group (7.5.1).

$$N_{t,a} = \begin{cases} f(SB_{t-1}) & a = 1 \\ N_{t-1,a-1}(1 - u_{t-1}\nu_{a-1})e^{-M} & 1 < a \leq a_x \\ N_{t-1,a-1}(1 - u_{t-1}\nu_{a-1})e^{-M} + N_{t-1,x}(1 - u_{t-1}\nu_x)e^{-M} & a = x \end{cases}$$

The recruits are a function of the spawning biomass in the previous year. The number of fish the next that are age a is simply the number of fish one age younger from the previous year, multiplied by the natural and fishing mortality. The *plus group*, the oldest age individuals in the model, are equal to the sum of those individuals one year younger the previous year, and the numbers in the plus group from the previous year, times the survival of both.

7.5.2 Recruitment

This is easy, you have already done it numerous times. We will use the B-H with steepness, and the recruits this year are a function of the spawning biomass last year.

$$R(t) = f(SB_{t-1}) = \frac{0.8R_0hSB_{t-1}}{0.2\Theta R_0(1-h) + (h-0.2)SB_{t-1}} \quad (74)$$

where SB_{t-1} is found by equation (69).

7.5.3 Initial population size

The population has to start somewhere; we call this the initial population size, or virgin population. We begin with the recruits in the first year being the *virgin* recruitment, R_0 . The number of two year old fish in the first year ($N_{1,2}$) is simply $R_0e^{(-M)}$. The number of three old fish in the first year ($N_{1,3}$) is simply $R_0e^{(-2M)}$, or $N_{1,2}e^{(-M)}$. When you get to the last age group, the *plus group*, you need to do something a little tricky. You need to account for all those fish that live past the maximum age of the model. For instance, if your species lives to be 40 but your model only goes out to age 10, because age 10 are the old fish in the catch, then you plus group should be age 10 or 11.

$$N(1,x) = \frac{N_{1,x-1}e^{-M}}{1 - e^{-M}} \quad (75)$$

8 Sums-of-squares

You may have conducted experiments in the lab, where you control for a bunch of conditions and tweak one thing. You measure the response and then you test the null hypothesis that the thing you tweaked has no effect on the response variable.

In our case, fishing is the experiment and the population is response variable. This means that the parameters of our models are actually hypotheses; however, instead of testing a null hypothesis we use a tool to find the parameters (i.e. hypothesis) of the model that best explain the data. The tool we are using is sums-of-squares. Sums-of-squares is the first step toward the more formal process of using likelihoods to test hypotheses.

$$SSQ = \sum_i (observation_i - predicted_i)^2 \quad (76)$$

What is sums-of-squares really asking?

The "squares" part of sums-of-squares refers to the square difference between the observed and predicted values, where $(observation_i - predicted_i)$ is the difference for the i th observation. $(observation_i - predicted_i)$ is also known as the error for the model. Because our model is not perfect it does not pass through every data point and there is a difference between the model and every data point.

The "sum-of", \sum_i , refers to taking the sum of all the square differences between the observed and predicted values. The model that best explains the data is the one that minimizes that **SSQ**.

Take the Chignik spawner-recruit data as an example again, and look at the difference between the predicted number of recruits from the model and the observed number of recruits from the 1943 brood year (figure 6). The model predicts 1,493,852, but the observed returns were 4,592,190. Therefore the square-difference for the 1943 observation is $(1,493,852 - 4,592,190)^2$. If you sum up the square-differences for all years you get the *SSQ*.

But that is only one square difference for a single set of parameters. The square difference would change for another set of parameters. Since the square-difference is a measure of the error in our model's ability to describe the relationship between spawners and recruits using a Ricker model, we want to know which parameter set (α and β) results in the smallest square-difference. It is possible you tweak your *guesstimates* of α and β a little bit

and eventually find the best parameter set, but that would probably take a very long time.

This is why we use solver. Solver uses an algorithm to find the set of parameters that minimizes the difference you have calculated. But solver isn't perfect. As you saw in lab it is possible for solver to find a number of solutions that it *thinks* is the minimum square difference. The geeky answer as to why this occurs is there are several local minima, and solvers algorithm may not smart enough to escape the local minima on its way to finding the global minima. One solution to this problem is to set your initial parameter values to a couple of different values and see if your model converges to the same parameters estimates.

Another problem that we ran into, and this is more of a model specification problem, is the our model would predict negative values for population size. Rather using the rule, $(observation_i - predicted_i)^2$, we would use the rule $(\ln(observation_i) - \ln(predicted_i))^2$, where \ln is the natural logarithm with base e . When the model predictions become less than or equal to 0 (i.e. ≤ 0) the value of the square difference blows up because you can't take the log of a number that is less than or equal to 0.

Figure 6: Ricker spawner-recruit relationship for the Chignik sockeye salmon run, and the error (dashed line) between the observed recruits and the model (blue line) estimate.



9 Final project: Complete a stock assessment of Bacaccio rockfish (*Sebastes paucispinis*) using a Graham-Schaeffer, delay-difference, and age-structured model

For your final project you will complete a stock assessment of the Bacaccio rockfish (*Sebastes paucispinis*) off the California coast. Like the yelloweye rockfish, the Bacaccio has seen dramatic reductions in the total allowable catch (TAC) based on perceived biomass declines from fishery dependent and independent survey data.

Using the models you have learned in this class you can now assess for yourself whether the Bacaccio are in fact over-harvested and by how much. I would encourage you to fit each population model: surplus production, delay-difference, and age structured model to the data. You will see that each model has its benefits and limitations, and the biological conclusions that one can draw from the models very dramatically.

I have provided Excel workbooks for each model. The worksheets have been formatted so that all you need to do is begin building the model. The surplus production model will be the easiest - it has the fewest *moving parts*. The delay difference and age structured models will be a little more difficult because the equations are larger and more involved.

Finally, there are a number of ways to check your results as you build the models. First, you will assume that the populations start out at equilibrium, make sure the population stays at equilibrium if the catch time series is zero. Second

9.1 Description of biological parameters

In your models you will be estimating a number of biological parameters: either r and B_0 , or R_0 and h - for the delay difference model you will also be estimating the Brody (ρ) coefficient, but this is exogenous to the rest of the model. For the delay difference model and the age structured model there are several other parameters that must be included to complete the models; they are listed below.

Model	parameter	calculation	value
Delay difference			
	s (average survival)	$e^{(-0.15)}$	0.81
Age structured			
	M (natural mortality)		0.15
	L_{∞}		91
	t_0		-1.81
	K		0.15
	a		6.00e-6
	b		3.01
	m_{50} (len. 50% mature)		46.00
	m_{95} (len. 95% mature)		51.00
	ν_{50} (len. 50% vulnerable)		40.00
	ν_{95} (len. 95% vulnerable)	$\nu_{50} + 5$	45.00

9.2 Description of catch

Each spreadsheet has a time series of commercial (trawl, hook and line, and set net) and recreational (RecSouth and RecNorth) catch data. You can choose to fit to one or all (summed across all fisheries) data. The catches include discards and are record in metric tonnes (MT).

9.3 Description of indices

There are a number of indices of stock status that are available for the Bacaccio. The fishery independent surveys include a triennial (Triennial) survey conducted by NOAA, the California Cooperative Oceanic Fisheries Investigations (CalCOFI) index of spawning abundance, recruitment indices (Rec Index and Juv Survey). While fishery dependent surveys for the commercial fleet include an area weighed catch per unit effort (Area weighted CPUE) and the Vandenberg CPUE (Vandenberg CPUE), and for the recreational fishery there is northern California (MRF north) and southern California (MRF soCal) index.