

Model Selection in the Stock Assessment

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1 Introduction

For my Sea Grant/NMFS population dynamics graduate fellowship I spent three summers as an intern with Dr. Alec MacCall at the Southwest Fisheries Science Center Santa Cruz Lab. During that time we investigated the problem of model uncertainty in the stock assessment. I was particularly concerned the population biology of the slow growing genus *Sebastes*.

To understand the influence of model uncertainty, I developed a population simulation model. I fit population models to the simulation model and compare parameter estimates to the “true” simulation values [Hilborn and Mangel(1997)]. I also compare goodness of fit measures. The simulation model was parameterized to mimic the biology of widow rockfish (*Sebastes entomelas*).

There are three sources of stochasticity in the simulation model. The model has stochastic recruitment, stochastic natural mortality and stochastic individual growth. Stock assessments routinely estimate stochasticity in the recruitment function [Methot(2005)]. However, it is very rare to estimate uncertainty in the natural mortality rate. And, to the best of my knowledge, no stock assessment has assumed stochasticity in individual growth.

2 The Simulation Model

I developed a simulation model for the dynamics of a rockfish-like species. The simulation model is age-structured, stochastic and parameterized for widow rockfish (*Sebastes entomelas*). There are three potential sources of stochasticity included in the model. There is variability in recruitment, the rate of natural mortality and the rate of individual growth.

2.1 Recruitment

Most rockfish stock assessment use a Beverton-Holt stock recruitment model [Dorn(2002)], including the most recent assessment for widow rockfish [He et al.(2003)He, Ralston, and ...]. In this simulation I made recruitment stochastic by adding a multiplicative error term to a standard Beverton-Holt model.

$$R = \frac{\alpha S}{1 + \beta S} \epsilon_r \quad (1)$$

where R is the number of recruits, S is the spawning stock biomass, α is the maximum rate of growth, and β is the rate of density-dependence. Variability in recruitment comes from a lognormal random variable (ϵ_r) with mean zero and standard deviation σ_r .

$$\epsilon_r \sim \text{lognormal}(0, \sigma_r) \quad (2)$$

2.2 Natural Mortality

A significant portion of natural mortality is due to predation and the predation rate is usually a function of body length [Paradis et al.(1996)Paradis, Pepin, and Brown]. Following Lorenzen [Lorenzen(2000)], I have modeled mortality with a size-dependent and a size-independent component.

$$M = \left(m_0 + \frac{m_1}{L} \right) \epsilon_m \quad (3)$$

Variability in natural mortality comes from a lognormal random variable (ϵ_m) with mean zero and standard deviation σ_m .

$$\epsilon_m \sim \text{lognormal}(0, \sigma_m) \quad (4)$$

2.3 Individual Growth

Individual growth is made to vary according to a simulated environmental index. This introduces cohort wide variation in growth. Body length is a modified version of the traditional von Bertalanffy growth equation [Quinn and Deriso(1999)]

$$\tilde{L} = L_\infty \left(1 - e^{-\kappa(a-t_0)} \right) \quad (5)$$

I have modified the rate of growth so that

$$L(a+1, t+1) = L(a, t) + \left(\tilde{L}(a+1) - \tilde{L}(a) \right) e^{-Z\xi(t)} \quad (6)$$

where ξ is a simulated measure of the environment variability and Z is a tuning parameter that controls the strength of impact of environmental variability on individual growth. Environmental variability is modeled as an oscillation with two wavelengths. The first wavelength is for short term cycles (like the El Niño Southern Oscillation) and the second wavelength is for long term cycles (like the Pacific Decadal Oscillation).

$$\xi(t) = \frac{1}{2} \sin\left(\frac{2\pi t}{\lambda_s}\right) + \frac{1}{2} \sin\left(\frac{2\pi t}{\lambda_l}\right) \quad (7)$$

where λ_s is the wavelength for the short term oscillation and λ_l is the wavelength for the long term oscillation. The wavelengths (λ_i) are modeled as random variables

$$\lambda_i = z_i + \epsilon_i \quad (8)$$

where z_i is the average wavelength and ϵ_i is a lognormal random variable with standard deviation σ_i .

$$\epsilon_i \sim \text{lognormal}(0, \sigma_i) \quad (9)$$

the average period is given by z_i and the standard deviation of values for the random variable is σ_i . In Figure 1 I show an example outcome of this model. In Figure 2, I show several outcomes of the simulation.

3 Proof of Concept

To illustrate the method I fit two very basic population dynamics models to the simulation output: the Schaefer surplus production model,

$$\frac{dN}{dt} = rN \left(1 - \frac{N}{K} \right) \quad (10)$$

and, a very basic modification of the Schaefer model, the Pella-Tomlinson surplus production model,

$$\frac{dN}{dt} = rN \left(1 - \left(\frac{N}{K} \right)^p \right) \quad (11)$$

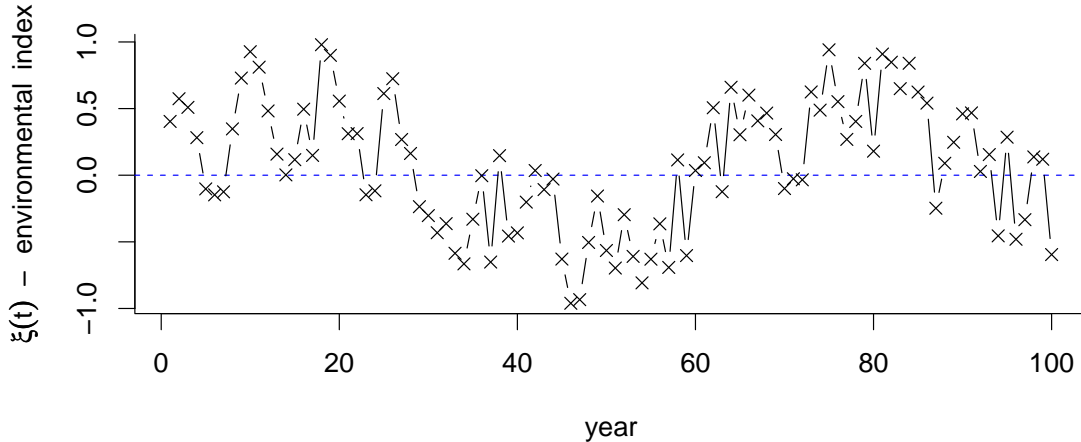


Figure 1: Example outcome of model described in Equations 7–9 where $z_s = 8$, $\sigma_s = 2$, $z_l = 60$ and $\sigma_l = 0.1$.

I fit both models with sum of squares minimization. Fitting the Schaefer model requires the estimation of two parameters: r (the intrinsic rate of population growth) and K (the carrying capacity). Fitting the Pella-Tomlinson model requires the estimation both r and K and one addition parameter, p (a shape parameter).

In Figure 3, I show an example output of the simulation along with the best fit Schaefer and Pella-Tomlinson models. We can see that both models fail to predict much of the population variability in the “true” population trajectory. The two models are more similar to each other than to the population data. The two models perform best at lower population sizes when the population is growing. I measure goodness of fit of the models with three measures: the F -statistic, the related R^2 value and the Bayesian Information Criterion (BIC),

$$BIC = n \log \left(\frac{RSS}{n} \right) + k \log(n) \quad (12)$$

where n is the sample size, k is the number of model parameters to be fit and RSS is the residual sum of squares.

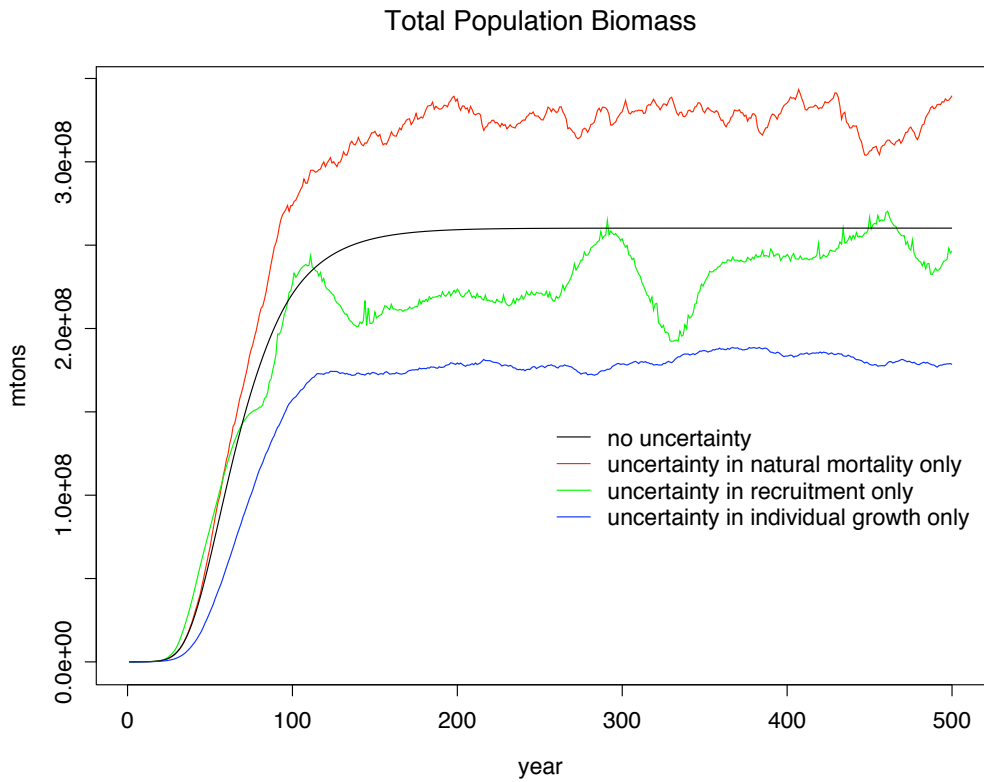


Figure 2: Illustration of simulation model. The black line is the deterministic case ($\sigma_r = \sigma_m = Z = 0$), The red line is the case where there is only variability in natural mortality ($\sigma_m = 1$ and $\sigma_r = Z = 0$). The green line is the case of variability in recruitment only ($\sigma_r = 1$ and $\sigma_m = Z = 0$). The blue line is the case of variability in growth only ($Z = 1$ and $\sigma_r = \sigma_m = 0$).

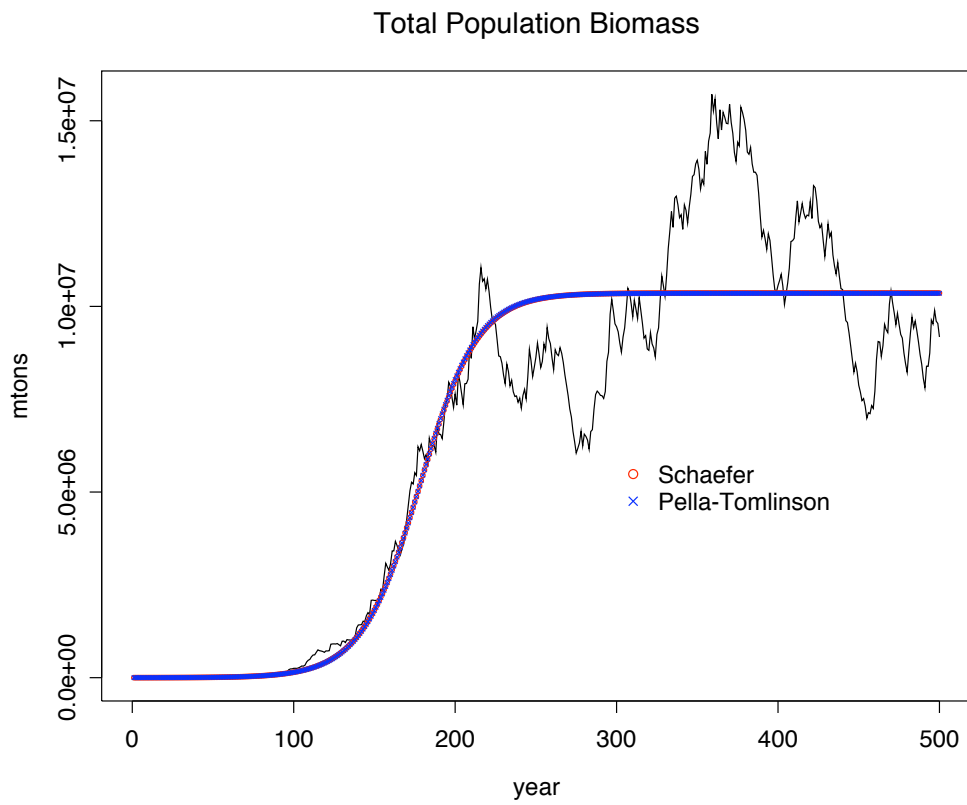


Figure 3: The best fit Schaefer and Pella-Tomlinson models for one example outcome of the simulation model.

4 Results

In Figure 4 I show a comparison of parameter estimates of the two models given varying amounts of stochasticity. Here, B_0 is an estimator of K based on the average biomass of the simulated population after the initial growth period. Therefore, when the model is most correct when $K/B_0 = 1$. We

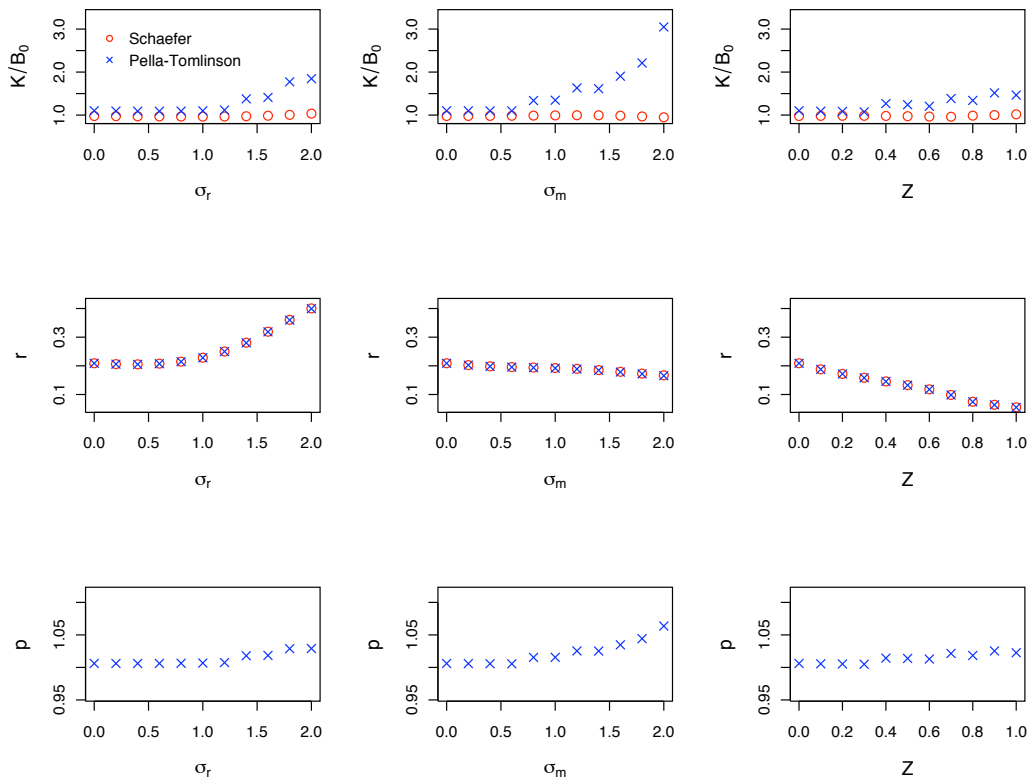


Figure 4: Comparison of parameter estimates between the Schaefer and Pella-Tomlinson models given varying levels of stochasticity.

can see that mostly the two models estimate the same values for r and K . However, when population variability is high, the Pella-Tomlinson model significantly overestimates K . We can see that there is a positive correlation between the estimate of p for the Pella-Tomlinson model and the amount

of stochasticity in the simulation. In this case, the additional parameter, p , allows the model to do a better job of fitting the growth portion of the population time series, but leads to a less correct estimate for K .

In Figure 5, compares goodness of fit measures between the two models given varying levels of stochasticity. Neither model fits well, and there is very little distinction between the models visible in the BIC or R^2 .

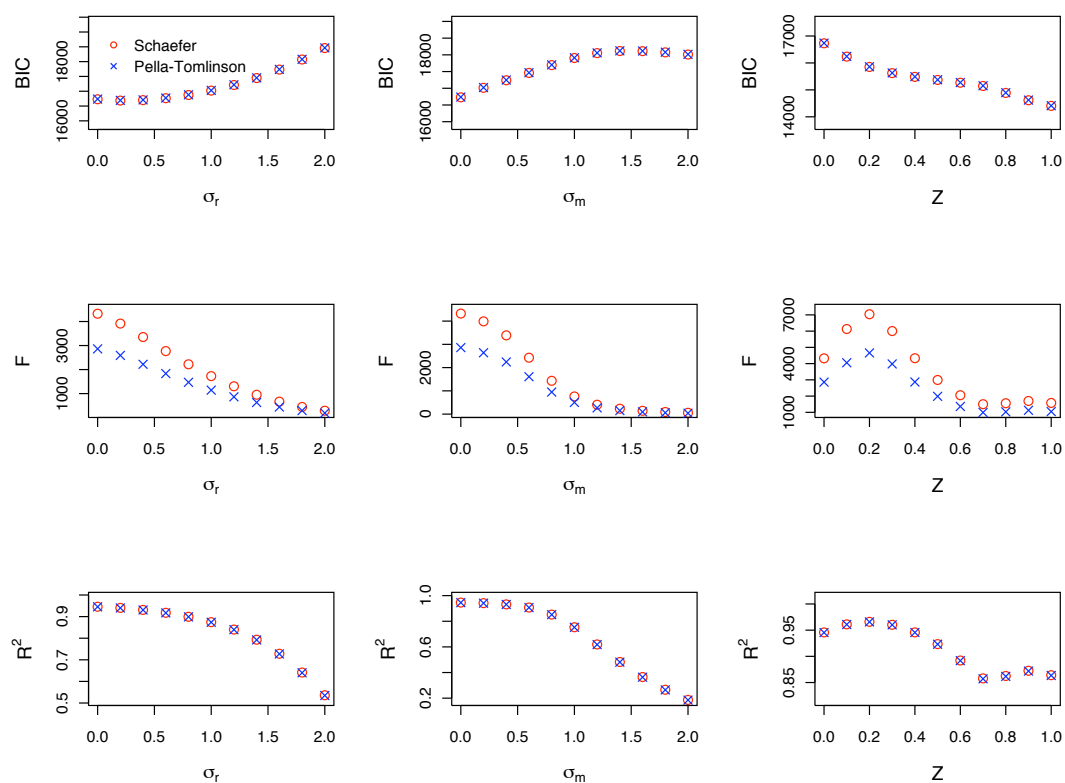


Figure 5: Comparison of goodness of fit measures between the Schaefer and Pella-Tomlinson models given varying levels of stochasticity.

In most cases, the more stochasticity in the system, the worse these two simple models perform. The only exceptions to this rule are in the third column. As we increase the influence of environmental variability we see an initial improvement in the F -statistic. This is essentially because the

increased variability in the simulated dataset serves to lower the bar for goodness of fit.

More unusual is the negative correlation between the BIC and Z . It seems that the more variation there is in individual growth, the better these two models perform. If we examine Figure 3 we see that these two surplus production models are poor at fitting the shape of the population growth part of the time series. It seems that connecting growth and environmental variability makes the population trajectory resemble a Schaefer or Pella-Tomlinson model more closely.

Also, there is usually little distinction between the goodness of fit of the two models. The F -statistic suggests that at low variability the Schaefer model performs better. However, as we raise the stochasticity in the system the two models are again difficult to distinguish.

5 Discussion

The work presented here is a demonstration of the method with a lot of emphasis on the operating model. This work can be expanded to include more sophisticated estimation models and more sophisticated goodness of fit measures. This approach can quantify the consequences of simplifying assumptions in estimation models.

I chose to create an operating model with stochastic natural mortality and stochastic individual growth because these are biologically realistic and estimation models used in stock assessments usually do not reflect them. These models are designed to challenge the usual simplifying assumptions that we rely on to do timely estimation for stock assessments. In particular, variation in individual growth introduces a non-stationary source of stochasticity that significantly violates the assumptions of parametric estimation models.

It is interesting that while the Pella-Tomlinson model has one additional parameter to fit than the Schaefer, this additional parameter does not always improve model estimation. In fact, in some cases the Pella-Tomlinson fit is worse than the Schaefer fit. This is paradoxical because a priori we would assume that the case where the Pella-Tomlinson model cannot improve the fit, the best fit model would be when $p = 1$, i.e., when the two models are equivalent. However, in certain cases where the fit is quite poor, the additional parameter can actually make the fit even poorer.

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