Preseason Forecasts of Pink Salmon Harvests in Southeast Alaska Using Bayesian Model Averaging

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ABSTRACT: Competing models for generating a forecast of salmon returns may give differing predictions yet have similar credibility. Within a single model, a wide range of alternative parameter values may also have similar credibility. Bayesian methods allow us to incorporate a wide range of models, weighting their forecasts by the posterior probability of each model and parameter combination. I illustrate this procedure by forecasting pink salmon harvests for the year 2002 for northern and southern Southeast Alaska.

INTRODUCTION

Preseason forecasts of Southeast Alaska pink salmon returns are used by Alaska Department of Fish & Game (ADF&G) managers in setting harvest strategies early in the season (Su 2002). However, more accurate inseason assessments (McKinstry 1993; Zheng and Mathisen 1998) supplant preseason indicators fairly early in the fishing season. Nonetheless, the fishing industry relies heavily on preseason forecasts of harvests, particularly for planning purchase of supplies, how many workers to hire, how many tenders to contract, and for arranging short-term financing.

Preseason forecasts of salmon returns are notoriously unreliable (Adkison and Peterman 1999). Among Pacific salmon species pink salmon predictions are more difficult than most, as their rigid two-year life cycle means early indications of the cohort strength (e.g., jacks and other siblings, often the best information for forecasting (Adkison and Peterman 1999) are not available.

In Southeast Alaska, forecast models have included density dependent survival, winter severity, sea and air temperatures, coastal upwelling, and early marine growth of juvenile pink salmon as predictors (Hofmeister 1994; Adkison and Shotwell 2000; T. Zadina, Alaska Department of Fish and Game, Ketchikan, personal communication). Cross-validation studies have shown that environmental variables and growth indices do reduce forecasting error, albeit only modestly (Adkison and Mathisen 1997). Forecasts are generally prepared separately for the northern and southern regions of Southeast Alaska (NSE and SSE, respectively), as tagging studies and other biological evidence suggest their pink salmon stocks have distinct dynamics (Nakatani et al. 1975; Alexandersdottir 1987).

Forecasts of Southeast Alaska pink salmon harvests have always been based on a single model containing one or a few of these predictors. Examination of the relative evidence for competing models suggests that the "best" model is not much favored over competing ones (Adkison and Shotwell 2000). In addition, the parameter values of the chosen model may be highly uncertain.

This uncertainty about which predictors to include lends itself to model averaging (Burnham and Anderson 1998), a technique that has been employed in other applications to natural resource management. Bayesian model averaging allows consideration of both alternative parameter values and model structures (Gelman et al. 1995). Patterson (1999) employed Bayesian model averaging in examining alternative harvest control laws, assigning prior weights to several competing model forms. A simpler approach creates a model

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structure where the competing models are all special cases (e.g., specific parameter combinations) of a broad model for which the posterior probability distribution of the parameters is calculated.

I employ this approach to forecasting harvests of pink salmon in Southeast Alaska. A model containing the commonly-used predictors is constructed and the joint posterior probability distribution of its parameters is computed. A Bayesian posterior predictive distribution of the harvest of pink salmon in 2002 is calculated by sampling from the posterior distribution for model parameters, then drawing a stochastic forecast from each sample.

METHODS

Models considered

A variety of models were constructed using different combinations of four environmental predictors, with and without density-dependent effects. Environmental variables were all calculated as the deviation from their monthly long-term averages. These deviations were then averaged over the 12 month period (September to August) following parental spawning. This period encompasses both incubation in the stream gravel (Hofmeister 1994) and the early marine stage (Mathisen and Van Alen 1995; Courtney 1997), the two periods thought to most affect cohort survival rates. The candidate models were all special cases of the full model (Quinn and Deriso 1999),

$$ R = S \exp\left(\begin{array}{l} \alpha - \beta S + k_1 \text{Air} + k_2 \text{SST} + \\ k_3 \text{Upwelling} + k_4 \text{Scales} + \varepsilon_y \end{array} \right), \quad (1) $$

where

S = number of spawners (parents). This value is calculated as 2.5 times the index of peak escapement aerial survey counts (Van Alen 2000). The index is the sum of multiple streams, identified in discrete geographical units and identified as individual streams that had a long-term escapement data set. The individual escapement counts have recently been adjusted by ADF&G to account for differences among observers (Jones et al. 1998; T. Zadina, Alaska Department of Fish and Game, Ketchikan, personal communication).

R = number of offspring produced (total returns). This value is calculated as the catches plus 2.5 times the peak escapement count two years after the parents spawned.

α, β = the parameters of the Ricker stock-recruitment equation (Ricker 1954)

Air = the average air temperature anomaly in Juneau and Annette Island from September to August over the 12 months following spawning. Data from the National Oceanographic and Atmospheric Administration (NOAA)'s National Climate Data Center (http://lwf.ncdc.noaa.gov/oa/ncdc.html).

SST = the average anomaly of sea surface temperatures in the Gulf of Alaska on a 1x1 degree grid, lat 55°–60° N, long 135°–160° W. Data from NOAA's Pacific Fisheries Environmental Laboratory (http://www.pfeg.noaa.gov/), from the Comprehensive Ocean-Atmosphere Data Set (COADS) and Global Temperature-Salinity (GTS) databases.

Upwelling = average upwelling anomalies from 3 coastal sites [(lat 57°N, long 137°W) (lat 60°N, long 146°W) (lat 60°N, long 149°W)]. Data from NOAA's Pacific Fisheries Environmental Laboratory.

Scales = This index of growth is computed from scales taken from juveniles captured in northern Southeast Alaska in the summer of their first year (Orsi et al. 1999, 2000). The measurement is the average length from the focus to the sixth circulus (Courtney 1997). As this sampling program has only been in place since 1994, I used an adjusted time series of adult scale measurements from Auke Creek (H.W. Jaenicke, National Oceanic and Atmospheric Administration (retired), Juneau, personal communication) to extend the data series back to 1977 (Adkison and Mathisen 1997).

k_1 = the weight assigned to each environmental predictor

ε_y = a normally distributed random value with mean of zero and standard deviation σ.

Maximum likelihood predictions

I calculated the maximum likelihood parameter estimates (MLEs) for Ricker models (S is the only predictor) for both NSE and SSE, and also the MLEs of all four Ricker models with one of the environmental predictors added to the model. I also calculated the mean squared residual (MSE) from each model fit. For each model form, the expected return in 2002 was calculated from Eq. (1) with the MLE using the spawning abundance in 2000 and the value of the environmental predictor, then multiplying this expected return by exp(MSE/2) (Hilborn and Walters 1992). Expected harvest was calculated as the expected return multiplied by the average harvest fraction for the last 5 years (0.44 for NSE, 0.51 for SSE (Adkison and Shotwell 2000)).

Bayesian posterior predictive distributions

I used a Bayesian approach that considered all possible parameter combinations. A Markov chain Monte Carlo algorithm was used to generate random draws from the joint posterior distribution of the model parameters a, b, k_{1-4}, and s (details below). A forecast harvest was generated by drawing a random e from a normal $(0, s^2)$ distribution, using this value and the parameter values drawn to calculate an R using Eq. (1), then multiplying by the appropriate harvest rate.

Prior probabilities and likelihood

I assumed log-normal error in the abundance of returning adults. The likelihood of any parameter combination was calculated by comparing the natural log of observed recruits (R_y) to the natural log of predicted recruits ($\hat{R}_y$) for each cohort from the 1960 to 1999 brood years. Thus,

$$\ln L = -0.5\ln\left(2ps^2\right) - \frac{\sum_y\left[\ln\left(R_y\right) - \ln\left(\hat{R}_y\right)\right]^2}{2s^2} \quad (2)$$

Bayesian posterior probabilities are proportional to the product of the likelihood and a prior probability. The prior probabilities assigned to specific parameter combinations were constant over a broad range (Table 1) for all parameters except s, the standard deviation of e_y. Following conventional practice, the prior distribution of this parameter was assumed proportional to $1/s$ (Gelman et al. 1995).

Markov chain Monte Carlo algorithm

The probability distribution of the forecast was calculated by drawing samples from the posterior distribution using a Markov chain Monte Carlo algorithm. I used the Metropolis algorithm (Gelman et al. 1995), with a jumping distribution that was a uniformly distributed random draw from within a hypercube centered about the current location of the chain. Candidate points outside the boundaries were not considered; this caused only minor irregularities as the chains spent little time near these boundaries.

Five separate chains of length 1,000,000 were generated from differing initial parameter combinations. Based on convergence tests using Gelman's R statistic (Gelman et al. 1995), the first 200,000 iterations of each chain were discarded. At each point in the chain, a single forecast was generated from Eq. (1) using a

Table 1. Bayesian prior distributions of model parameters.

Parameter	Shape of Prior	Range
a	constant	0.01 to infinity
b	constant	0 to infinity
k_i	constant	-infinity to infinity
s	$1/s$	0.0001 to infinity

random e from a N$(0,s)$ distribution and the parameter values from the chain.

Probability distributions were summarized by graphing the cumulative probability of harvests both less than or greater than a fixed amount. An 80% credible interval was calculated as the interval between the 10th and 90th percentile of the probability distribution.

Diagnostics

Efficiency of the Markov chain Monte Carlo algorithm was assessed by monitoring the fraction of time the chain moved to a new location. The width of the hypercube used as the jumping distribution was adjusted by trial and error until this fraction was between 0.23–0.44 (Gelman et al. 1995). Convergence of Markov chain Monte Carlo chains was assessed by comparing the within to between chain variance in the forecast (Gelman et al. 1995). Trace and bivariate plots of sections of each chain were graphed to visually search for convergence problems or attraction to a parameter boundary.

Calibration

Bayesian forecasts, like their classical counterparts, have uncertainties that grow with the range of models considered. To check whether the probability distribution of the forecast contained the appropriate amount of uncertainty, I generated hindcast probability distributions for returns for each year from 1960 to 2001 in exactly the same manner as was done for the 2002 forecast. I then examined the coverage properties of these probability distributions.

For each year, I calculated what fraction of the hindcast probability distribution fell below the actual return. If these hindcast distributions were properly calibrated, this statistic should take on any value from 0 to 1 with equal probability. As a visual check, I ordered these fractions from lowest to highest and plotted them in sequence. If the probabilities of the observed returns ranged from zero to one with equal probability, then this sequence should roughly follow a straight line.

RESULTS

Maximum likelihood predictions

The maximum likelihood parameterizations of different model forms gave quite different predictions of abundance. For example, the Ricker model predicted a harvest of 35.8 million fish but when the best-supported environmental predictor, sea surface temperature, was added the forecast increased to 51.6 million fish (Table 2). None of these models fit the data much better than the others, based on their similar MSE values (Table 2).

Table 2. Predicted harvests and mean squared error values (in parentheses) under maximum likelihood for five competing models.

	NSE	SSE	Total
Ricker	13.6 (0.37)	22.2 (0.40)	35.8
w/ scales	14.4 (0.35)	23.6 (0.38)	38.0
w/ air temperature	13.9 (0.33)	25.7 (0.34)	39.6
w/ sea surface temperature	20.3 (0.30)	31.3 (0.37)	51.6
w/ upwelling	14.3 (0.35)	23.6 (0.36)	37.9

Bayesian probability distributions

The harvest forecasts are given as two probability curves (Figures 1 and 2). The decreasing curve gives the probability that the harvest is larger than the value on the x-axis. For instance, for NSE the probability of a harvest greater than 10 million was about 90% (Fig-

ure 1). The increasing curve gives the probability that the harvest is smaller than the value on the x-axis. For instance, for NSE the probability that the run is less than 40 million was about 86% (Figure 1). Where these two curves cross (21 million for NSE, 30 million for SSE), the odds are even that the harvest will be larger or smaller than this value.

The probability distributions for different levels of harvest tended to be skewed. That is, there were large harvests that had a small but non-negligible probability of occurrence. As a result of the influence of these possible large harvests, the average expected harvest was larger than the values at the 50th percentile. For NSE, the expected harvest was 29 million, and for SSE 36 million.

Diagnostics

Trace plots of parameter values in the latter part of the Markov chain Monte Carlo chains revealed no aberrant behavior. Gelman's R statistic was very close to 1.0, indicating satisfactory convergence of the Markov chain Monte Carlo chains. The jumping distributions used performed fairly efficiently, producing acceptance frequencies of 37% and 46% (Gelman et al. 1995).

Calibration

The 80% credible intervals calculated are the range of plausible harvests. Their interpretation is that there is only a 1 in 5 chance that the harvest in NSE will not be in the range 13.0 - 34.5 million or that of SSE will not
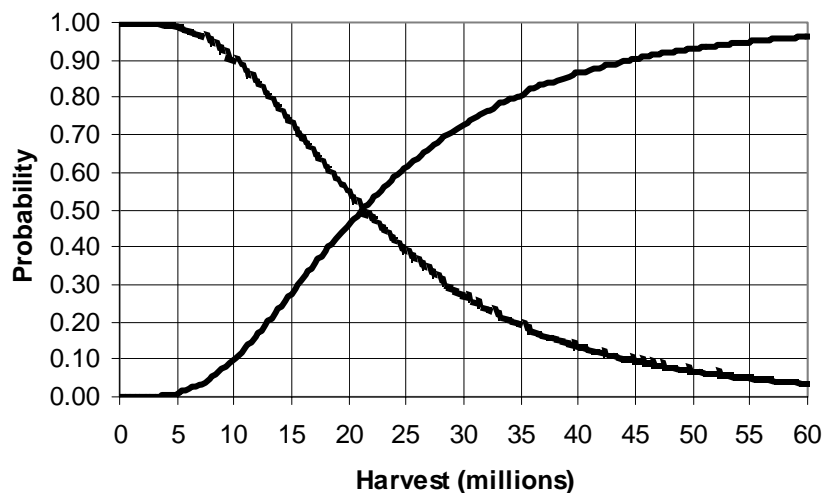

Figure 1. Probabilities of different harvest levels for NSE. The decreasing curve gives the probability that the harvest is larger than the value on the x-axis. The increasing curve gives the probability that the harvest is smaller than the value on the x-axis.
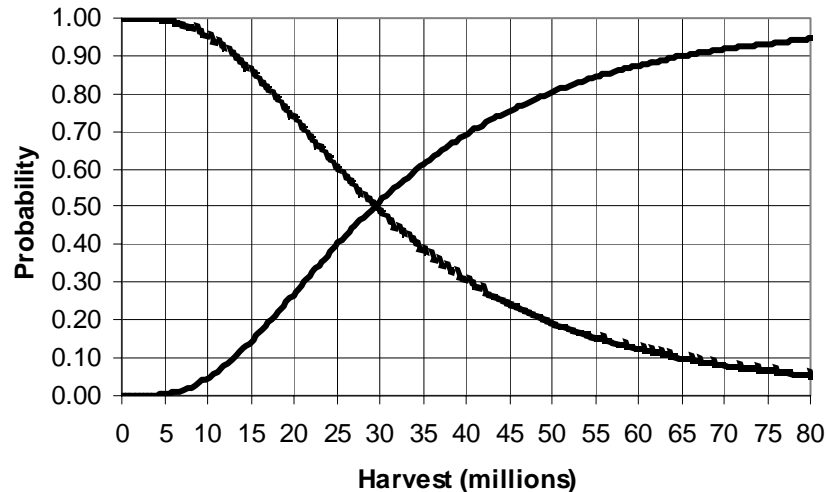
Figure 2. Probabilities of different harvest levels for SSE. The decreasing curve gives the probability that the harvest is larger than the value on the x-axis. The increasing curve gives the probability that the harvest is smaller than the value on the x-axis.

be between 17.3 - 50.0 million pinks. As a check, forecast probability distributions were calculated for all return years from 1962-2001. If the probability distributions were properly calibrated (not too wide or too narrow), then 20% of the returns should have been below the 20th percentile, 50% below the 50th percentile, etc. Figure 3 shows that these probability distributions were well-calibrated, and thus that the 80% intervals calculated for 2002 harvests are reasonable representations of the uncertainty in the forecast.

DISCUSSION

A variety of data sources and statistical techniques have been employed for forecasting salmon harvests (Mundy 1982; Fried and Yuen 1987; McKinstry 1993; Zheng and Mathisen 1998), including some previous Bayesian efforts (Fried and Hilborn 1988). Despite these efforts, forecasts of salmon returns are notoriously imprecise (Adkison and Peterman 1999).

Quite frequently in resource management, the underlying mechanisms controlling the dynamics of the resource are poorly known. The magnitude of various influences on the resource are not well known, resulting in uncertainty about the values of model parameters. In addition, it's often not clear what these influences are, and the functional form of their expression; this results in uncertainty about the basic structure of the management model. Model averaging is a methodology for incorporating this uncertainty about model structure and parameter values into the outputs of an analysis.

Frequentist techniques for model averaging do exist (Burnham and Anderson 1998). Bayesian methodologies have the advantage of weighting competing hypotheses more intuitively, by their relative probabilities. Competing model structures can be assigned prior probabilities that are updated by the model's correspondence to available data (Patterson 1999). The calculations involved in this approach can be somewhat cumbersome, as the Markov chain Monte Carlo sampling algorithm must be able to jump from one model structure to another. If all models can be incorporated as special cases of a broader model (e.g., certain parameters may have a value of zero or infinity for a particular model form), then jumping between model structures is no longer necessary. However, the disadvantage of this approach is that it is necessary to think carefully about the prior probability distribution for the parameters of the broad model, to ensure that implausible biological structures are not accidentally incorporated in a quest for a general model form.

As with classical frequentist approaches to modeling, uncertainty grows the wider the range of models one considers. Using a frequentist approach, this uncertainty would manifest itself as wide confidence intervals for the quantities of interest. In Bayesian approaches, the uncertainty from considering a wider range of models or parameter values manifests itself as a flattening and widening of the posterior probability distribution (Walters and Ludwig 1994; McAllister and Kirkwood 1998), leading to wide credible intervals.

From a practical point of view, it was important to determine whether the probability distribution of the 2002 harvest was too wide or too narrow. That is, did I
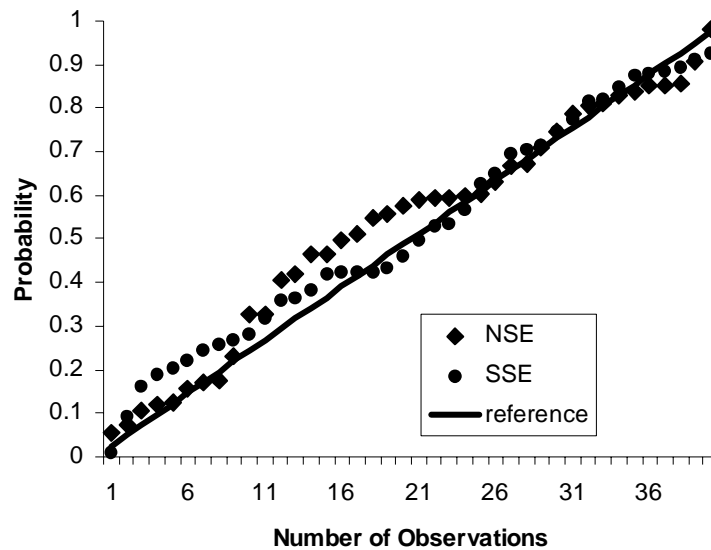
Figure 3. The calibration of probability distributions of forecasts of returns of pink salmon, Southeast Alaska, 1962-2001. For each region, NSE or SSE, I generated a forecast probability distribution for the harvest of pink salmon for each year. I then calculated what fraction of this probability fell below the observed return. These fractions were sorted from lowest to highest and then plotted. If the forecast probability distributions were properly calibrated, these values should follow the reference line.

ignore significant uncertainty, for example by specifying a modified Ricker stock-recruitment relationship while ignoring other possible functional forms? Or did I include too much uncertainty, for example by specifying equal prior probabilities for both parameter combinations that implied strong effects of all environmental factors and parameter combinations that implied no environmental effects at all?

The calibration check involved use of the Bayesian *P*-value (Gelman et al. 1995), and was analogous to calculating coverage probabilities of confidence intervals in frequentist applications. Bayesian *P*-values are somewhat of an oxymoron. The prior and posterior distributions are supposed to be representations of the analyst's degree of belief in alternative hypotheses, and thus the theoretical foundation of checking the calibration of a posterior distribution is weak at best. However, any modeling exercise involves numerous somewhat arbitrary decisions (Punt and Hilborn 1997; Patterson 1999; Schnute et al. 2000); in this example the decisions include whether to include a wider variety of stock-recruitment curves, which environmental parameters to consider, what parameter bounds to set, whether to use log-normal, normal, or even a t-distributed likelihood, etc. Many of these decisions are based on very little pre-existing knowledge. In the face of these many choices, as practical-minded natural resource analysts we should find empirical demonstrations of good performance reassuring.

Although the width of the calculated credible intervals appears justified, they are distressingly large. There are two explanations for this large uncertainty. The first is that alternative modeling efforts could produce more precise forecasts from the existing data. While this is certainly a possibility, it's more probable that the existing data has little to say about the magnitude of returns from a cohort of pink salmon.

Part of the data limitation may reflect inaccuracies in the determination of spawning abundance. The size of the parental spawning stock is estimated from periodic aerial counts (Van Alen 2000). These estimation methods have several known deficiencies, and several suggestions for improvement have been made (Jones et al. 1998; Su et al. 2001; Adkison and Su 2001). Additionally, not all streams are surveyed and total escapement is calculated by a 2.5-fold extrapolation.

While improvements in estimating the abundance of the parental spawning stock might improve forecasts, it must be recognized that survival rates vary tremendously from cohort to cohort (Pyper et al. 2001; Willette et al. 2001). Thus, parental abundance becomes a weak predictor of returns from a cohort. The environmental indices that have been incorporated in forecasts explain very little of this variation (Adkison and Mathisen 1997), although recent intensive studies of factors determining growth and survival in Southeast Alaska (Orsi et al. 1999, 2000; Mortenson et al. 2000) and Prince William Sound (Willette 2001; Willette et al.

2001; Cooney et al. 2001) provide valuable guidance on what factors are most important to measure. Forecasts of returns for other species of salmon rely heavily on sibling returns, a direct index of the realized abundance of the cohort (Adkison and Peterman 1999). Reducing the uncertainty in forecasts of pink salmon harvests will likely require direct measures of a cohort's abundance in coastal or marine waters.

Finally, recent market conditions have substantially changed the processing sector's demand for Southeast Alaskan pink salmon. Several processors are considering reducing purchases or even curtailing operations for the summer of 2002. ADF&G is considering altering its schedule of harvest openings to accommodate proposals by fisheries participants designed to increase the quality of pink salmon that are taken (Phil Doherty, Alaska Department of Fish and Game, Ketchikan, personal communication). These changes have the potential to reduce harvest rates below the historical averages we've assumed here, reducing the 2002 harvest.

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