FISH 558 Final Project: A decision analysis for Chiwawa River spring Chinook conservation hatchery control rules

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# Introduction

Pacific salmon (*Oncorhynchus spp.*) and steelhead (*O. mykiss*) are iconic species with tremendous ecological, cultural, and economic value. The Columbia River has one of the largest runs of Chinook salmon; however, much of the historical abundance and diversity has been lost due to habitat reduction and modification. Declining abundances led to the listing of five Evolutionarily Significant Units (ESUs) of Chinook salmon in the Columbia River Basin under the Endangered Species Act between 1992 and 1999. However, despite substantial investment, recovery has proven challenging and slow due to the wide range of habitats upon which salmon depend and the numerous threats that they face at different life stages.

Given the multiple life stages and threats affecting salmon, population modeling is a critical tool for projecting population trajectories to assess outcomes of management actions and environmental variability. Life-cycle models, which simulate population dynamics based on demographic processes across all life stages, are increasingly being used to evaluate and plan salmon conservation in the Columbia River Basin. Although there are many opportunities for integrated life-cycle models to inform management, there are also many challenges associated with developing them in a robust manner. Population projection models have traditionally been developed through separate analyses of individual data sets to estimate demographic rates for different life stages. Outputs from individual models are then combined. However, this is often done in an ad hoc manner that does not fully integrate demographic processes and uncertainty. Statistical power can be improved, and more complete models can be constructed by analyzing disparate data sets with integrated population models (IPMs).

My dissertation work is to develop an IPM for Endangered wild Wenatchee River spring Chinook salmon and to use the model to assess management strategies for their conservation, while also providing a template for IPMs of other salmon populations. As a step toward this goal, I developed an IPM for the subpopulation in the Chiwawa River, a tributary of the Chiwawa river that supports the most adult spawners of any of the subpopulations in the basin. The Chiwawa subpopulation is supplemented by a conservation hatchery program, which incorporates wild fish in its broodstock. I used the parameters from the IPM to project population dynamics under different hatchery management control rules and evaluated performance metrics.

Juveniles of this population rear in freshwater for an entire year before migrating to sea. However, they exhibit life-history diversity, with some individuals emigrating from their natal streams as sub-yearlings (parr) to overwinter downstream and others emigrating as yearlings (smolts) and moving directly to the ocean. Among the subyearling migrants, there are three modes of outmigration (life histories). Estimates of the abundance juveniles in each of these life histories are available from data collected at a downstream migrant trap at the mouth of the Chiwawa River. I incorporated these data in the IPM to better understand how juvenile production and survival to maturity affect population dynamics.

# Methods

## Population model

Because juveniles emigrate from their natal stream at different times of year, and therefore survive at different rates to spawning, I modeled four different juvenile life histories representing different modes in the average outmigration. The first three life histories, fry, summer parr, and fall parr, all emigrate from the natal stream at age . These juveniles continue to rear in the lower Wenatchee River until their second spring, at which time they migrate to the marine environment. The number of juveniles in each of these three life histories is best represented as a sigmoidal function of the number of spawners in the previous year. The sigmoid relationship is likely due to a combination of density dependent emigration and survival, where density dependent emigration is the dominant factor at lower spawner densities and density dependent survival becomes more important at higher spawner densities. I chose to represent this relationship with the cumulative density function of a Weibull distribution scaled by a parameter that represents the upper capacity for a given lifestage. The final juvenile life history is fish that remain in the natal stream until , when they go to sea (smolts). Their abundance is represented by a Beverton-Holt function of the number of spawners two years previous.

Instead of estimating annual survival and maturation rates between juvenile emigration and adult return, I modeled a single survival rate to adult ruturn for each juvenile life history and an adult age distribution that was conditional on survival. My thinking was that this would be the maximum number of identifiable parameters given that survival and maturation probabilities would be confounded (Buhle et al. 2018). Adults return at ages 3-5. Some number of the returning adults are removed to be used in the conservation hatchery broodstock. Some number of hatchery-origin adults spawn naturally with the natural-origin spawners. Therefore, the population model is,

(1)

The process error for the juvenile abundances corresponding to a given brood year was assumed to be multivariate lognormal with covariance matrix ,

, (2)

allowing for correlation to reflect shared environmental conditions or competition among life histories from a given brood year.

### Survival

The average survival of each juvenile life history was modeled on the logit scale as a function of the average length at emigration. The effect of length, z-scored across life histories, on logit(*s*) was set to 0.18 based on a previous analysis, so the odds of survival increased by 20% with each standard deviation increase in length. The annual process error was shared among all life histories from a brood year and followed an AR1 process,

(3)

(4)

(5)

where was the autocorrelation coefficient. The average lengths(mm) were as follows: fry = 36, summer parr = 64, fall parr = 80, and yearling smolts = 92.

### Adult age proportions

The vector of adult age proportions was shared by the three juvenile life histories that emigrate at age 1, while the smolt juvenile life history was allowed a unique adult age distribution. The additive log ratio (alr) transformed vectors of age proportions for each year were drawn from a multivariate normal AR1 process with autocorrelation coefficient , mean vector and covariance matrix. The multivariate AR1 process included the alr age proportions for subyearling and yearling migrants from a given brood year *b* to allow for covariance between them.

(6)

(7)

(8)

### Hatchery origin spawners

The number of hatchery-origin spawners was parameterized as a function of the number of natural-origin spawners and the proportion of hatchery origin spawners

(9)

## Likelihood

### Juvenile abundances

The data on the number of juvenile emigrants in each life history come in the form of a vector of outputs of a Monte-Carlo simulation from an model that predicts the number of daily emigrants with a Lincoln-Peterson style estimator and then adds emigrants across days (Sorel 559 final project 2018). The data are assumed to be lognormally distributed around the true number of juvenile emigrants, with a unique variance for each year and life history that reflects uncertainty in the estimating model during that period.

(10)

### Spawner age proportions

Two sources of data on adult age proportions were used. The first was from fish that were PIT-tagged as juveniles emigrating from the natal stream and were later detected as adults returning to the river. The numbers of fish that emigrated from the natal stream at a given age and returned at each adult age 3, 4 or 5 were assumed to be multinomially distributed.

(11)

The second source of data came from the aging of carcasses recovered on the spawning grounds. The brood year and juvenile life history of each carcass is unknown but can inform the age proportions of all adult spawners in a given year , which can be derived from the population model.

(12)

### Spawner abundances and origins

The index of total number of spawners based on redd surveys is assumed to be an unbiased estimate of the true number of spawners with lognormally distributed error. The CV of the spawner abundance survey is assumed to remain constant among years.

(13)

The carcasses that are recovered on the spawning grounds are identified as being of hatchery or natural origin, and therefore inform the proportion of hatchery origin spawners,

. (14)

### Model fitting

The model was developed in Template Model Builder (Kristensen et al. 2016) which uses Laplace approximation of the negative log of the marginal distribution across random variables. The number of wild spawners in the first 5 years cannot be calculated based on previous years, so they were estimated as parameters in the model. The following parameters were treated as random effects: *log*(), *log*(), *logit*(), and *alr*(), which were marginalized out of the likelihood using the Laplace approximation.

## Projection and decision analysis

To inform hatchery management, we projected the population 25 years into the future with different control rules and evaluated performance metrics. The two hatchery management decisions are the number of hatchery-origin adults to allowed onto the spawning grounds and the number of natural-origin adults to remove for use in broodstock. A rough control rule was developed in 2013 that designated the minimum acceptable proportionate natural influence (*pNI*) at different levels of adult return, where , *pHOS* is the proportion of hatchery-origin spawners on the spawning grounds and pNOB is the proportion of natural-origin adults in the broodstock.

For forward simulation, we assumed that the total number of fish in the broodstock was 74 in all years. A constant fraction of the return of wild adults *pREM* was taken for broodstock up to the point where that equaled 74 fish, above which only 74 fish were taken. The remainder of the broodstock was filled with hatchery fish if necessary. There was a maximum number of hatchery-origin adults allowed to spawn naturally *Hmax* when 0 natural-origin adults returned. As the number of returning natural-origin adult returns increased, the number of hatchery-origin spawners declined linearly up to a point above which no hatchery-origin adults were allowed to spawn naturally, *NORcutoff*.

We considered three different control rules. The first was to eliminate the hatchery program. The second was designed to produce a pNI just above the minimum prescribed by the 2013 guidance, and had *Hmax* = 200, *NORcutoff* = 500, and *pREM* = 0.33. Lastly, we simulated a rule with *Hmax* = 600, *NORcutoff* = 300, and *pREM* = 0.4. This rule involved allowing more hatchery-origin spawners at low natural-origin abundance but with a lower *NORcutoff* − the number of natural-orgin spawners above which *pHOS* = 0. It also removed of a slightly higher-proportion of natural-origin spawners for broodstock. We assumed that there was always a sufficient return of hatchery-origin adults to implement the control rule and did not model the dynamics of the hatchery population.

1,000 simulations were conducted for each scenario and 5 performance metrics were calculated. The probability of quasi extinction was calculated as the proportion of simulations in which the 4-year running mean number of spawners fell below a QET of 50 adults. We also calculated the geometric mean number of spawners across simulation years and took the arithmetic mean across simulations. Finally, we report *pHOS*, *pNOB*, and *pNI*.

# Results

## Model

All juvenile life histories showed strong evidence of density dependent survival (Figure 1). There was substantially more process error for fry and summer parr migrants than fall parr and smolts.

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Figure 1. Spawner to juvenile relationships for each juvenile life history. Shaded area represents 95% confidence interval of process error. Points are model predictions of the latent true number of juvenile emigrants.

There were positive correlations in the process errors for juvenile abundances among life histories, indicating that they were responding to common environmental conditions (Table 1). The greatest correlation was between fry migrants and summer migrants (0.56).

Table 1. Correlation between the annual process errors of the number of juveniles in each life history.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | fry | summer | fall | smolt |
| fry | 1.00 | 0.56 | -0.01 | -0.02 |
| summer | 0.56 | 1.00 | 0.34 | 0.44 |
| fall | -0.01 | 0.34 | 1.00 | 0.29 |
| smolt | -0.02 | 0.44 | 0.29 | 1.00 |

Average survival from emigration to adult return was 0.32% (0.18,0.66) and had an autocorrelation coefficient of 0.24 (-.32,0.67) (Figure 2).

A close up of a map

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Figure 2. Survival to adulthood by brood year for each juvenile life history.

Juveniles the emigrated from the natal stream as subyearlings returned at slightly earlier ages than those that emigrated as smolts (Figure 3). The predominant adult age was 4, followed by 5, and then 3 (jacks). The alr age proportions were highly correlated (Table 2) but there was essentially no autocorrelation, = -0.02 (.51, -.55).

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Figure 3. Adult age proportion by brood year for juveniles emigrating at age 1 or 2. In the legend, the freshwater emigration year precedes the adult age, so 2-4 is a yearling smolt that returned at age 4.

Table 2. Correlation of additive log ratio transformed adult age proportions. In the column and row labels, the freshwater emigration year proceeds the adult age, so 2-4 is a yearling smolt that returned at age 4.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1-3 | 1-4 | 2-3 | 2-4 |
| 1-3 | 1.00 | 0.92 | 0.50 | 0.81 |
| 1-4 | 0.92 | 1.00 | 0.60 | 0.97 |
| 2-3 | 0.50 | 0.60 | 1.00 | 0.67 |
| 2-4 | 0.81 | 0.97 | 0.67 | 1.00 |

## Decision analysis

The scenario with no conservation hatchery program resulted in a 19% quasi-extinction probability and the lowest average number of wild adult spawners (274), but had the lowest pHOS (0.0) and highest pNI (1.0) (Table 3, Figure 4). The two other control rules had similar pQET and pHOS. The rule with lower Hmax and higher NORcut resulted in a slightly higher average wild adult spawner abundance, whereas the other control rule resulted in a slightly lower pNOB and higher pNI.

Table 3. Decision table with three different control rules on the columns and five performance metrics on the rows. *pQET* is the probability of falling below a quasi-extinction threshold in the 25 year projection; geomean Sw is the geometric mean number of wild spawners; *pHOS* is the proportion of hatchery origin spawners; *pNOB* is the proportion of natural origin broodstock; and *pNI* is the proportionate natural influence.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| control rules | Hmax | 0 | 200 | 600 |
| NORcutoff | 0 | 500 | 300 |
| pREM | 0 | 0.33 | 0.4 |
| Performance metrics | pQET | 0.19 | 0.03 | 0.03 |
| Geomean Sw | 274.48 | 343.80 | 333.89 |
| pHOS | 0.00 | 0.31 | 0.29 |
| pNOB | NA | 0.83 | 0.87 |
| pNI | 1.00 | 0.74 | 0.78 |

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Figure 4. Top row: Proportionate natural influence (pNI) versus wild adult return numbers based on the control rule in the scenario outlined at the top of the column of panels. The thick black like is the pNI given the control rule in the scenario, and the thin black line is the minimum pNI allowed given the 2013 control rule. Middle and bottow rows: spawners fit to data and 25 year projection, with 50% and 95% confidence intervals.

# Discussion

This population model shows promise as a tool for informing hatchery management. I was able to present two control rules that fit within the current guidance and their associated population performance metrics. The population has a substantial risk of quasi-extinction within the next 25 years if the hatchery were to be eliminated. Allowing more hatchery fish to spawn in the wild when natural-spawner abundance is low reduces pQET but increases pHOS. Reducing the number of hatchery-origin spawners as the number of natural-origin spawners increases leads to a lower pHOS without much effect on pQET. However, there may be a limit to the number of hatchery-origin spawners available in years when the natural-origin return is very low, which I did not account for.

Within the performance metrics used in this analysis, the offspring of a hatchery-origin spawner and the offspring of a natural-origin spawner are treated the same, as natural-origin spawners. However, the genetic composition of the natural-origin population could be tracked in the model, and would seem to be a valuable performance metric. Additionally, previous studies have found that hatchery-origin spawners produce fewer offspring than natural-offspring spawners, which could be reflected in future iteration of this model (Williamson et al. 2010).

This study assumed that the hatchery managers had perfect knowledge of the number of natural origin returns, and perfect control of the number of hatchery origin adults; neither of which is remotely realistic. Developing this study into an operating model for management strategy evaluation would be large improvement in realism and for informing hatchery management.

I chose not to model the hatchery population dynamics for simplicity, but could do so if there was concern about not having enough hatchery-origin adult returns, or what the opimal broodstock size was. Information could be shared between the natural and hatchery populations, and optimizing the hatchery broodstock size could result in removing fewer natural-origin adults over time. For a management strategy evaluation of the conservation hatchery program, a simpler operating model, which does not include the juvenile life stage might be preferable, because the management only acts on the adult lifestage.

Aside from the decision analysis, however, this population model reveals insights into factors governing population dynamics at different lifestages. As has been observed for several populations of spring Chinook in the Interior Columbia River, juvenile production is strongly density dependent despite the population being at low abundance (Walters et al. 2013). There is no consensus about the reason for this phenomenon, but it could be a result of allee effects. Another possibility is that survival from juvenile emigration to adult return has been substantially reduced from historic levels as could result of changing ocean conditions, dams, and predators.

The positive correlation between abundances of the different juvenile life histories suggests that they are responding to common environmental conditions. The strongest correlation was between fry and summer parr, which also had the highest process variance. Testing for effects of freshwater factors like stream discharge, temperature, and redd distribution might explain some of the covariance and could reveal insights into factors governing juvenile production. Information on environmental factors governing juvenile production is highly valuable for informing habitat restoration and projecting climate impacts on population dynamics.

Mortality between juvenile emigration from the natal stream and adult return was highly variable and had a strong effect on adult population dynamics. A next step in developing the stage-structured population model is to incorporate detections of PIT-tagged fish at dams on the mainstem Columbia River to further inform survival. Most fish >50 mm captured when emigrating from the natal stream have been PIT-tagged since 2005. Adding this data may allow for separation of survival and maturation probability between when juveniles emigrate from the natal stream and when they return as adults.

## Acknowledgements

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