

Developing Rebuilding Exploitation Rates for Puget Sound Chinook Salmon

The Viability and Risk Assessment Procedure (VRAP) Including the use of the Dynamic Model (DM) for computing Rebuilding Exploitation Rates (RERs)

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INTRODUCTION

The Puget Sound Chinook salmon Evolutionarily Significant Unit (ESU) is listed as threatened under the Endangered Species Act (ESA). The ESU includes 22 independent populations in 14 watersheds. The Viability Risk Assessment Procedure (VRAP) provides a framework and methodology to assess risk through estimation of rebuilding exploitation rates (RERs) for individual populations within the ESU. The RERs are projected to result in a low risk to survival and a moderately high to high probability of rebuilding *of the population* over a pre-defined period of time. NOAA Fisheries uses this framework to assess risk of proposed fishery actions on listed Puget Sound Chinook salmon to determine whether the proposed action is likely to jeopardize the species.

The RER is the highest allowable exploitation rate for a salmon population that satisfies specified risk criteria related to survival and recovery. The rate is designed to both minimize the risk of natural origin (NOR) spawning escapement falling below some Critical Escapement Threshold (CET) and ensure, at a given level of probability, that the escapement would reach a Rebuilding Escapement Threshold (RET) if the RER was maintained over 25 years. The RER is inclusive of all harvest mortalities on the population, direct and indirect. The derivation of the CET, RET and RER are explained below. Additional detail on the approach is found in NMFS 2000.

It is important to note that although component populations contribute fundamentally to the structure and diversity of the Evolutionarily Significant Unit (ESU), it is the ESU, not an individual population, which is the listed species under the ESA. NOAA Fisheries uses the RERs, and the CETs in addition to other relevant information to assist it in evaluating the effects of the proposed actions on survival and recovery of the populations within the ESU. The rates that result from the proposed fisheries are compared to the relevant RERs. Generally speaking, if estimated impacts of proposed fisheries are less than or equal to the RERs, NOAA Fisheries considers the fisheries to present a low risk to that population (NMFS 2004b). However, the RERs for individual populations are not jeopardy standards.

There are five analytical stages to developing an RER: (1) population-specific data collection, (2) fitting the population dynamics model to the data, (3) determination of criteria against which to assess risk (i.e., Critical and Rebuilding Escapement Thresholds), (4) the risk assessment using with the Viability and Risk Assessment Procedure (VRAP) to identify the appropriate RER, and (5) converting the A&P-RER to an equivalent FRAM-RER. These steps are implemented in the R libraries RER and RERconvert and which are described in a companion document, the RER tutorial (NWFSC 2018).

DATA

Data are housed in MS Excel spreadsheets (NWFSC A&P Tables) and account for all categories of fish that contribute to adult returns, both hatchery and natural origin for a specific population. This information provides the basis for cohort analyses and derivation of spawner-recruit parameters. A&P Tables summarize:

1. **Escapement data** for both natural-origin (NOR) and hatchery-origin (HOR) fish that stray and spawn naturally;
2. **Age composition data** for the NOR-only spawners, i.e., numbers of fish (carcasses) from each age category (freshwater – fingerling and yearling, and ocean – 2, 3, 4, 5 year olds) collected on spawning grounds;
3. **Hatchery return data**, including NOR spawners removed and used for broodstock, NOR and HOR spawners that return to the hatchery rather than to the river to spawn;
4. **Fishing rate estimates** for Puget Sound Chinook Salmon from coded wire tag (CWT) recoveries from indicator stocks, calculated by the Pacific Salmon Commission Chinook Technical Committee (PSC CTC) used in their exploitation rate analysis and the PSC model calibration.

THE POPULATION DYNAMICS MODEL (DM)

The population dynamics model describes the population over time. Fitting this model to the historical data allows us to estimate parameters necessary to project forward in time in the VRAP step. We use a state-space model that can be broken down into two components, a process model which describes the underlying population dynamics, and the observation model which compares the predictions made by the process model to the available escapement and age composition data.

The process model starts with the number of age 3 to 5 natural spawners, E_{BY} . A spawner recruit relationship, f , with log normal process error models the relationship between these spawners and age 2 ocean fish, $P_{2,BY}$.

$$(1) P_{2,BY} \sim \text{lognormal}(f(E_{BY}, \text{prod}, \text{cap}, \text{msCoef}, \text{flowCoef})/Q, \sigma_{\text{proc}})$$

Here the term Q is introduced to allow the recruitment parameters (e.g. prod =productivity and cap =capacity) to be expressed in terms of adult equivalents (Q is defined below).

The spawner-recruit relationship is assumed to follow one of three forms, the Beverton Holt,

$$(2) SRmodel(E_{BY}, \text{prod}, \text{cap}) = \frac{E_{BY}}{\frac{1}{\text{prod}} + \frac{E_{BY}}{\text{cap}}}$$

the Hockey stick,

$$(3) SRmodel(E_{BY}, \text{prod}, \text{cap}) = \min(\text{prod} \cdot E_{BY}, \text{cap})$$

or the Ricker,

$$(4) SRmodel(E_{BY}, \text{prod}, \text{cap}) = \text{prod} \cdot E_{BY} \cdot \exp\left(-\frac{E_{BY}}{\text{cap}}\right)$$

For each successive year the fish in the ocean are exposed to natural mortality, m , and an ocean harvest, f . Of those, a certain proportion mature and return to the river,

$$(5) M_{age,BY} = P_{age-1,BY} \cdot (1 - m_i) \cdot (1 - f_{i,BY}) \cdot r_{age,BY}$$

The remaining fish stay in the ocean:

$$(6) P_{age,BY} = P_{age-1,BY} \cdot (1 - m_i) \cdot (1 - f_{i,BY}) \cdot (1 - r_{age,BY})$$

The fish that mature are then exposed to terminal (i.e. mature) fisheries, $t_{age,Y}$ ¹, as they near natal river mouths, and pre-spawn mortality, $s_{age,Y}$, after they enter the river. The total natural origin escapement, N_Y , is then the sum of these fish from the different brood years that return in the same year.

$$(7) N_Y = \sum_{i=3}^5 M_{i,Y-i} (1 - t_{i,Y})(1 - s_{i,Y})$$

Total escapement, E_Y , is then calculated by adjusting the natural origin escapement for natural origin fish, NOR_Y , that return to the hatchery and hatchery origin, HOR_Y , fish that return to the spawning grounds²:

$$(8) E_Y = N_Y + HOR_Y - NOR_Y$$

The fishing rates and natural mortality are assumed known. The parameters that are estimated are, productivity (*prod*), capacity (*cap*), , process error and observation error standard deviation ($\sigma_{proc}, \sigma_{obs}$), and maturation rates ($r_{age,Y}$). Maturation rates are allowed to vary by year and age but are assumed to follow a hierarchical structure across years.

$$(9) \text{logit}(r_{age,Y}) \sim \text{normal}(y_{age,Y}, \sigma_r)$$

Where:

$$(10) \quad y_{age,Y} \sim \text{normal}(\mu_{age}, \sigma_{age})$$

The observation model then compares the predictions made by the process model to the observed escapement and age data. The observed escapement data, $obsE_Y$, is assumed to have log normal error where the true (un-observed) escapement, E_Y , is the median and the standard deviation, σ_{obs} , is unknown:

$$(11) \quad obsE_Y = \text{lognormal}(E_Y, \sigma_{obs})$$

For years when fish age composition data are available, the number of fish of each age within the sample, $obsAge_Y$, are assumed to come from a multinomial distribution

$$(12) \quad obsAge_Y \sim \text{multinomial}(pAge_Y, totObs_Y),$$

where the probability of selecting a fish from the different ages, $pAge_Y$, is based on the age composition of the natural origin spawners.

$$(13) \quad pAge_{Y,age} = M_{age,Y} / \sum M_{age,Y}$$

¹ This harvest rate may include some ocean fisheries that only the mature fish are exposed to.

² In most cases, error estimates are not available for these numbers so they are simply included as a multiplicative adjustment to natural origin escapement. However, these values could be modeled as unknown values with binomial observation models.

For Chinook salmon, spawners typically return to spawn after residing in the ocean for 2, 3 or 4 years. Chinook salmon that return after only 1 year in the ocean (age 2) are considered ‘precocious’ and are typically males (aka. ‘jacks’). Every population has a percentage of precocious age 2 jacks that return, but because they are smaller and weigh less, carcasses are often lost or overlooked during spawner surveys. They are more easily captured/consumed by predators, and they are more easily washed downstream particularly during high flow events. Thus age 2 Chinook salmon are less likely to be sampled and are typically under-represented in survey data. We allow for the model to accommodate this by multiplying the mature age two fish, $M_{2,Y}$, by a value between 0 and 1, adj . So the equation becomes:

$$(14) \quad pAge_{Y,age} = \widehat{M}_{age,Y} / \sum \widehat{M}_{age,Y} \text{ where } \widehat{M}_{2,Y} = adj \cdot M_{2,Y} \text{ and } \widehat{M}_{age \neq 2,Y} = M_{2,Y}$$

Because age 2 fish comprise a relatively small proportion of the returns and are assumed to not contribute to the spawners, errors in the adjustment are unlikely to have a large effect on the results. The factor Q , used to adjust recruits to age 2 ocean fish, is a product of natural mortality and maturation terms.

$$(15) \quad Q = Q_1(1 - m_2) \text{ where } Q_6 = 1 \text{ and } Q_i = r_i + (1 - r_i) \cdot (1 - m_{i+1}) \cdot Q_{i+1}$$

The parameter r_i is the average maturation rate for age i and is defined as the inverse logit of μ_{age} from equation 11. The recurrence relation (16) can also be expressed as:

$$(16) \quad Q = \sum_{a=2}^5 [r_i(1 - m_a) \prod_{i=1}^{a-1} [(1 - r_i)(1 - m_i)]]$$

As with all Bayesian models, prior distributions are necessary for the model parameters. Because, spawner-recruit data is often very noisy and has little information to constrain model parameters (like productivity and capacity), these priors can form an important part of the model. While inclusion of the priors introduces subjectivity into the analysis, this subjectivity was also implicit in the maximum likelihood analysis that was previously used. There are a number of approaches for developing priors. Information from the literature on basic biology can be used. For example, a combination of estimates of fecundity and age specific survivals. Basin specific information can also be used. For example, estimates of capacity based on habitat analysis can be used to constrain the capacity parameter.

CRITERIA FOR ASSESSING RISK

As described earlier, an RER is the highest allowable (“ceiling”) exploitation rate that satisfies specified risk criteria related to survival and recovery for an individual population. Calculation of RERs depends on the selection of two abundance-related reference points (referred to as Critical and Rebuilding Escapement Thresholds) assessed against defined levels of risk that

define the probability that a population will fall below the CET and exceed the RET. Both thresholds represent natural-origin spawners.

Critical Escapement Threshold: The critical escapement threshold (CET) represents a boundary below which uncertainties about population dynamics increase substantially. If sufficient stock-specific information is available, we can use the population dynamics relationship to define this point. Otherwise, we use alternative population-specific data, or general literature-based guidance provided by NOAA Fisheries on a range of critical thresholds in its document, *Viable Salmonid Populations* (McElhane et al. 2000). Guidance from the VSP paper suggests that population sizes of 167-1,667 per generation ($N_b = 50-500$) are at high to very high risk. The population size range per generation represents an annual spawner abundance range of 42-417 when divided by four, the approximate generation length for Chinook salmon. Factors associated with demographic risks include environmental variability and depensation. Environmental variation presents risks to small populations when conditions reduce survival or reproduction to chronically low levels. The VSP paper suggests that abundance levels of 1,000-10,000 spawners per generation, represent a low risk of extinction, i.e., a viable threshold. Assuming the same four year generation length, this converts to a range of 250 - 2,500 spawners per year. Since escapement within this range is considered to be at low risk, the critical escapement level with regard to environmental variation must be somewhat lower. Because most of the populations that were subject to the RER analysis were relatively small, an escapement level of 200 fish was selected from these ranges to represent a generic critical threshold related to genetic and environmental risk factors (method 1).

Where population-specific data are sufficient we used two other methods to define the CET. Method 2 was derived from an analysis of the Ricker population-recruit relationship based on Peterman's work (1977, 1987). He provided a rationale for depensation and suggested relating the escapement level at which depensation occurs to the size of the population in the absence of fishing (equilibrium escapement level). Based on Peterman's work, NOAA Fisheries set this measure of the critical threshold equal to 5% of the equilibrium escapement level. Method 3 defines the CET as the lowest escapement with a greater than one return per spawner ratio.

Rebuilding Escapement Threshold: The Rebuilding Escapement Threshold (RET) represents a higher abundance level that would generally indicate recovery or a point beyond which ESA protections are no longer required. Because we are isolating the effects of harvest, the RET in this context represents an escapement level consistent with estimates of maximum sustainable yield (MSY) under the current productivity and capacity of the available habitat. The RET varies with the assumed freshwater covariate and also with the particular form of the spawner-recruit relationship.

In the absence of sufficient population-specific data to define MSY, a similar method was used to establish the viable population or recovery level. In this case, the criteria were 1,250 spawners (the VSP genetic guideline range of 1,670 -16,700 spawners per generation or the VSP environmental variance guideline range of 1,000-10,000 spawners per generation, divided by the average generation length of approximately 4 years).

There is often some confusion about the relationship between RET used in the VRAP analysis, and abundance related recovery goals. The RET are generally significantly less than recovery goals that are specified in recovery plans. VRAP seeks to analyze a population in its existing habitat given current conditions. As the productivity and capacity of the habitat improves, the VRAP analysis will be adjusted to reflect those changes. Thus the RET serves as a step in the progression to recovery, which will occur as the contributions from recovery action across all sectors are realized.

VIABILITY AND RISK ASSESSMENT PROCEDURE (VRAP) FOR COMPUTING REBUILDING EXPLOITATION RATES (RER)

The Viability and Risk Assessment Procedure (VRAP) model uses parameter estimates from the Dynamic Model to simulate spawning escapement into the future for a range of exploitation rates. The simulation model mirrors the process model portion of the Dynamic Model. The simulation starts with an initial age-specific population size, applies an age-specific natural mortality, and then ocean fishing mortality. Using maturation rates, the terminal run size is computed from the remaining fish at age and the terminal fishing mortality is applied. The result is an escapement by age. Fish that do not mature and return to their natal streams to spawn, remain in the ocean for another year, are aged one year, and constitute the “ocean standing stock” in the next year.

Adult equivalent recruits are calculated by applying the spawner recruit function to the total age 3 to 5 annual escapement. Adult equivalent recruits are then divided by an age 1 factor to get the age 1 cohort size (Q in equation 15). The escapement data are saved, the remainder of the cohort is run through the fisheries, and escapement determinations made again as described above. Each simulation is run for 25 years by default with 1,000 iterations (these values can be changed as needed).

Uncertainty is introduced into the simulations using process error (estimated from the population dynamics model, DM) and management error (deviation of actual exploitation rates to target exploitation rates: see appendix B).

The main VRAP output is the fraction of simulations that exceed RET or fall below CET for a specified exploitation rate. This information is used to determine the rebuilding exploitation rate (RER). The fraction that exceed RET are based on the number of simulations for which the average of the spawning escapements in years 21-25 exceed the RET. The fraction that fall below the CET are based on the number of years that the spawning escapement fell below the CET. These fractions are then compared to risk criteria that reflect the context of the ESA determination (see discussion in following sections).

CONVERSION TO FRAM EQUIVALENTS

To make the RER compatible with modeled exploitation rates used in fishery planning (the FRAM model), the RERs derived from data in the A&P tables were converted to FRAM equivalent RERs. We convert because the RERs are based on exploitation rates derived from the ERA analysis and these values are substantially different from the FRAM exploitation rates used in domestic management. We converted these values to FRAM equivalents using a logit-logit model fit to historic values of both exploitation rates.

IMPLEMENTATION

Population dynamics model (DM) fitting and the population projections (VRAP) are implemented using the R library, RER. The conversion to FRAM equivalent RERs is accomplished using the R library, Rconvert. Both libraries include functions to read and prepare the data, run the models, and provide many different tabular and graphical views of the results. See the RER_tutorial for instructions on how to use these libraries.

LITERATURE CITED

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APPENDIX A:

MANAGEMENT ERROR

Management error is included in the VRAP simulations using a rate parameter that describes the ratio between the desired harvest rate and the actual harvest rate. This parameter (management error) is assumed to follow a gamma distribution which is based on the Fisheries Resource Assessment Model (FRAM) pre- and post-season harvest rates for 13 populations from 2004 through 2014. Here we estimate the population specific gamma parameters by calculating the year specific ratios of pre- and post-season FRAM exploitation rates, calculating the mean and standard deviations of the ratios for each population, and then transforming the means and standard deviations into the gamma A and gamma B parameters ($\text{gammaA} = \text{mean}^2/\text{sd}^2$, $\text{gammaB} = \text{sd}^2/\text{mean}$) (Table 1).

Table 1. The mean, standard deviation and gammaA and gammaB parameters describing the distributions of ratios of pre- and post-season FRAM exploitation rates.

population	mean	st_dev	gammaA	gammaB
Nooksack.Spring	1.3606	0.3137	18.8112	0.0723
Skagit.Spring	0.8478	0.1846	21.0950	0.0402
White	0.8175	0.2409	11.5195	0.0710
Skagit.S.F	1.0977	0.1629	45.3884	0.0242
Stillaguamish	0.7998	0.2709	8.7182	0.0917
Snohomish	0.7783	0.2306	11.3958	0.0683
Lake.WA	1.0688	0.2066	26.7718	0.0399
Green	1.0747	0.2775	14.9929	0.0717
Puyallup	1.2443	0.1162	114.6761	0.0109
Nisqually	1.0350	0.1053	96.6096	0.0107
Hoko	1.1588	0.2062	31.5684	0.0367
Mid.Hood.Canal	1.0094	0.1643	37.7320	0.0268
Skokomish	1.0983	0.0917	143.4785	0.0077

