

Framework to Estimate Snake Basin Steelhead and Chinook Population Abundance and Productivity

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Background

PIT-tagging and biological sampling at Lower Granite Dam provides a simple, scientifically defensible, and cost efficient approach to estimating and understanding status and trends of fish populations returning to key spawning locations. The approach also provides a consistent methodology, placing population estimates on equal footing, for conducting trend comparisons across Snake River basin populations. Previously developed PIT-tag based models adhere to the principal of parsimony (i.e., use the simplest approach that requires the fewest assumptions for meeting the objective), which, is generally recognized as the best approach (Coelho et al. 2018) for ecological modeling applications with a specific and known target (i.e., estimating population indicators). Together, the developed PIT-tag based abundance models, STADEM and DABOM, inform fisheries managers of the abundance of fish returning to the Snake River (Lower Granite Dam) and of those escaping in basin fisheries and surviving to spawning locations. Abundance is estimated from direct observations of tagged fish returning to known spawnings locations without making unnecessary assumptions; examples of unnecessary assumptions include migration corridor conditions or fish straying behavior. The developed models only require basic mark-recapture assumptions (See et al. 2016) that are widely accepted and common place in animal marking studies and two other main assumptions; 1) all fish returning to the same population have similar run-timing past Lower Granite Dam, and 2) the most upstream tag detection location represents the location or area of spawning. These same PIT-tag observations used in the DABOM model, combined with biological sampling information collected at Lower Granite Dam, can also provide fisheries managers with valuable life history metrics for each population (Powell et al. 2018). Thus, eliminating the need for additional data collection and the required funds, data processing and QA/QC, and further modeling assumptions regarding life history group survival differences during migration. Additionally, by simply combining the two metrics estimated from the same PIT-tag observation dataset (i.e., abundance and life history proportions) biologists can develop run-reconstruction brood tables and estimate productivity efficiently.

In addition to being the simplest, most cost effective, regionally consistent and statistically robust approach for estimating population status and trends, the previously developed PIT-tag based approaches yield unbiased estimates of uncertainty. The level of uncertainty surrounding status and trend metrics is absolutely necessary for fisheries managers and provide a gauge to the true state of the population in question. Without uncertainty surrounding status and trend estimates, an unknown amount of risk is tied to each management decision regarding the population. The STADEM/DABOM approach estimates uncertainty in population indicators by including all available sources of error in Lower Granite abundance estimates and tag observations using a state-space modeling approach (See et al. 2016). Kinzer et al. (2017) showed the estimated uncertainty around population abundance was unbiased with coverage probabilities matching desired alpha levels. And although Powell et al. (2018) did not report uncertainty around estimated life history metrics, variance calculations for proportions are well known (Agresti 2002; Casella and Berger 2002) and have reliable statistical properties. Once variances are calculated for life history metrics we can use common variance properties to produce uncertainty around brood table components and adult-to-adult productivity values thus giving fisheries managers the tools necessary for sound and confident decision making.

This document serves as a draft outline of the methods necessary to estimate Snake River basin steelhead and Chinook salmon population abundance and productivity with uncertainty by integrating available models.

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Model integration is explicitly defined in this document and provide fisheries managers with a framework and path forward to estimate the abundance of various life history groups (e.g., females, age classes) within populations with sufficient PIT-tag monitoring, and for developing population productivity estimates with uncertainty. We propose using a regionally consistent framework that takes full advantage of the existing sampling and tagging effort at Lower Granite Dam and the current PIT tag detection infrastructure to estimate and report fish population indicators and metrics for the purpose of ESA status assessments by adapting the STADEM and DABOM models to integrate with life history information.

Methodology

Population Abundance

Weekly main tributary branch abundance is estimated by combining the posterior distributions of wild escapement (w) past Lower Granite Dam for each weekly (t) time period, $(X_{w,t})$, from STADEM with weekly movement probabilities, $(\psi_{j,t})$, into each main tributary branch (j) from DABOM. Total tributary branch abundance is then estimated by summing across the product for all n weeks.

$$\hat{N}_j = \sum_{t=1}^n X_{w,t} \psi_{j,t}$$

Population spawner abundance is obtained by summing across all main branch estimates that belong to population Pop .

$$\hat{N}_{Pop} = \sum_{j \in Pop} \hat{N}_j$$

The above methodology for population abundance estimates assumes 100% spatial coverage of population areas. In many populations, we know this assumption is violated to some degree. In most populations with instream PIT-tag arrays, 14 out of 21, greater than 80% of all spawning areas identified by TRT intrinsic potential maps are covered with current infrastructure. Arrys in ten of the populations cover greater than 95% of the available spawning habitat and only 3 populations have less than 50% coverage (Lower Clearwater and Lower and Upper Middle Fork). Acknowledging full coverage is desired, population abundance estimates from the above equations can be expanded with the proportion of intrinsic potential area covered, thus yielding an unbiased estimate of population abundance.

Life History Proportions

Female proportions in each population (ϕ_{Pop}) can be estimated using a hierarchical model and the sum of individuals observed with a known sex (n_j) in each branch (j). A hierarchical model was developed to allow for borrowing of information from larger branches to smaller branches, to avoid skewing the sex ratio due solely to small sample sizes in some branches.

$$f_j \sim Bin(\phi_{Pop}, n_j)$$

$$\text{logit}(\phi_{Pop}) \sim N(\mu, \sigma^2)$$

Where f_j is the number of females observed in a branch, n_j is the total number of sexed tags observed in that branch, and ϕ_{Pop} is the proportion of females for the population containing model branch j (the main quantity of interest). We imposed hierarchy by assuming that the logit of ϕ_{Pop} comes from a normal distribution centered around a common value, μ , that represents the mean female proportion for the entire ESU/DPS. The variation between populations is captured by σ^2 .

A hierarchical model is also used to estimate the proportion of adults belonging to each returning age class within the population (π_{Pop}). The hierarchical approach allows the sharing of information between larger and smaller branches; allowing age proportions to represent all returning age classes regardless of each class being observed in smaller populations. Age proportions are estimated from the vector of individuals belonging to each age classes (A_j) returning to branch j and the sum of all individuals observed of known age (n_j), and the multinomial distribution.

$$A_j \sim Mn(\pi_{Pop}, n_j)$$

Where π_{Pop} is the vector of age proportions for each return age class. Hierarchy is imposed by assuming the vector of age proportions for each population is drawn from a multivariate logistic normal distribution, with a mean vector μ and the covariance matrix Σ .

$$alr(\pi_{Pop}) \sim MVN(\mu, \Sigma)$$

Where $alr(\pi_{Pop})$ is the additive log ratio transformation, $alr(\pi_{Pop}) = (\log \frac{(n_{Pop,a3})}{(n_{Pop,a2})}, \dots, \log \frac{(n_{Pop,aMAX})}{(n_{Pop,a2})})$. The formulation requires a choice of reference age so that the length of μ is one less than the total number of ages observed. We chose to use the smallest age, age 2 (a_2), as the reference age.

Productivity

After branch proportions are estimated for each life history group, abundance is estimated for each group by multiplying posterior distributions of population metrics; abundance (\hat{N}_{Pop}), female proportion (ϕ_{Pop}) and age class proportions (π_{Pop}).

$$\begin{aligned}\hat{N}_{Females,Pop} &= \hat{N}_{Pop} \phi_{Pop} \\ \hat{N}_{Age,Pop} &= \hat{N}_{Pop} \pi_{Pop}\end{aligned}$$

Brood tables and adult to adult productivity (λ_{Pop}) estimates for each population are then formed by summing age classes of returning fish (i.e., recruits; R) belonging to similar brood years (BY) and dividing by the estimated population spawner abundance ($\hat{N}_{BY,Pop}$) for the same year.

$$\begin{aligned}\hat{R}_{BY,Pop} &= \sum_{a \in BY} \hat{N}_{Pop,a} \\ \hat{\lambda}_{BY,Pop} &= \frac{\hat{R}_{BY,Pop}}{\hat{N}_{BY,Pop}}\end{aligned}$$

Proportion of Hatchery Origin Spawners

The proportion of hatchery origin spawner abundance ($pHOS$) contributing to natural spawning is often needed for status assessments and other management needs. Using only fish PIT-tag as juveniles for each hatchery stock observed at tributary in-stream PIT-tag antennas (n_{Stock}^{Trib}), and hatchery stock abundance at Lower Granite Dam from parent-based tagging (\hat{N}_{Stock}^{LGD}) we can estimate $pHOS$ assuming a consistent PIT-tagged to un-tagged ratio. The estimate of population level $pHOS_{Pop}$ is derived by first calculating the abundance of each hatchery stock ($\hat{N}_{Pop,Stock}^{Trib}$) returning to population tributaries.

$$\hat{N}_{Pop,Stock}^{Trib} = \frac{n_{POP,Stock}^{Trib} \hat{N}_{Stock}^{LGD}}{n_{Stock}^{LGD}}$$

Then, total hatchery returns to a population is the sum across hatchery stocks in a population.

$$\hat{N}_{Pop,Hat} = \sum_{Stock \in Pop} \hat{N}_{POP,Stock}^{Trib}$$

And, $p\hat{HOS}_{Pop}$ becomes ratio of all hatchery fish returning to the population, minus brood stock removals and tributary harvest, divided by total (i.e., hatchery and natural) fish returning.

$$p\hat{HOS}_{Pop} = \frac{\hat{N}_{Pop,Hat}^{Trib} - (BroodStock + Harvest)}{\hat{N}_{Pop,Hat}^{Trib} + \hat{N}_{POP,Nat}^{Trib}}$$