Hatchery Tagging to Estimate pHOS Using IPTDS Detections

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January 15, 2020

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Introduction

The Dam Adult Branch Occupancy Model (DABOM) is currently used to estimate adult escapement of natural origin spring/summer Chinook salmon *Onchorhynchus tshawytscha* and steelhead *O. mykiss* into watersheds and populations of the Snake River Basin (SRB). Escapement estimates are made based on the tagging of a random sample of adults at Lower Granite Dam (LGR) and the subsequent detection of those adults at instream PIT tag detection systems (IPTDS) throughout the SRB. DABOM could also be used to generate estimates of hatchery escapement to various locations as well, which would be useful for estimating hatchery abundance in natural areas and the proportion of hatchery origin spawners (*pHOS*). Doing so, with reasonable precision, may require a random sample (or similar) of adult hatchery fish also be PIT tagged at LGR. Here, we wish to determine expected levels of precision for *pHOS* given current levels of PIT tagging in the SRB, and further, determine the additional tagging, expressed as a tagging rate or number of tags, required in hatchery adults at LGR to achieve unbiased estimates of hatchery escapement and *pHOS* with reasonable levels of precision (e.g., coefficient of variaion [CV] of $\leq 15\%$).

Simultaneously estimating escapement of hatchery origin (HOR) and natural origin (NOR) adults to IPTDS locations throughout the SRB based on PIT tagging at LGR is a trivial extension of the DABOM model. Factually, the previous and existing instance of the DABOM model was developed for the upper Columbia River (upstream of Priest Rapids Dam), which capitalized on the same sampling assumptions applied to natural origin escapement past LGR. However, for multiple reasons (ergonomic limitations at LGR, political considerations, ethical concerns), the random sampling and PIT tagging of HOR adults (specifically ad-clipped adults) at LGR has been precluded. Notably, given trap operations at LGR, HOR adults are trapped, anesthetized, weighed, and measured at the same rate as NOR - a function of "trap rate" constituting a fraction of every hour wherein adults in the ladder are bypassed to the trap. Thus, it is arguable that implantation of a PIT tag constitutes a significantly greater offense to captured hatchery adults.

Importantly, NOR and HOR refer to the origin of Chinook salmon or steelhead born in the natural or hatchery environment, respectively. Related, three phenotypic origins of adult Chinook salmon and steelhead are identified at LGR and include wild (W), hatchery ad-intact (HNC), and hatchery ad-clipped (H). NOR includes only W adults whereas HOR includes both the HNC and H groups despite HNC individuals often being phenotypically W. Currently, all ad-intact fish are systematically PIT tagged at LGR which includes both the W and HNC origins i.e., some HOR adults are currently tagged at LGR, but we need to consider differential tagging rates between HNC and H adults when evaluating the precision of *pHOS* given current levels of PIT tagging.

Unbeknownst to the proposal for this evaluation, a condition of the Hatchery and Genetics Management Plan (HGMP) required the operation of IDFG HOR steelhead production to conduct a study on HOR contributions to NOR populations. Thusly, IDFG and NOAA Fisheries endeavored to compile and estimate straying of HOR steelhead upstream of LGR.

This document seeks to begin collaboration between IDFG, NOAA Fisheries, and Biomark, Inc. to:

- Capitalize on existing progress on stray rates, and
- Advance statistical modeling to determine whether *pHOS* estimates can be reliablly prosecuted by adult HOR PIT tagging at LGR.

In its developed form, the DABOM model includes escapement for NOR and HOR adult salmonids. Demonstrably, the DABOM is fully functional for multiple populations of spring/summer Chinook salmon and steelhead upstream of LGR. The performance of DABOM in the upper Columbia River (above Priest Rapids Dam) strongly suggests that the model can be reliably extended to HOR adults in the Snake River. Contents of this document, including findings, will be reported as part of a Final (Annual) Progress Report for Bonneville Power Administration (BPA) project 2019-006-00.

Objectives

This assessment aims to determine the number or tagging rate of HOR adults at LGR necessary to determine *pHOS* across watersheds or populations of SRB steelhead estimated by the DABOM model (and supported by the operation of IPTDS maintained and operated under BPA project 2018-002-00) and with "reasonable" uncertainty (e.g., CV $\leq$ 15%). As a natural extension, we may also explore additional effort necessary to estimate *pHOS* in watersheds or populations of interest for Chinook salmon. Our objectives are as follows:

1. Determined expected CVs for current estimates of *pHOS* that could be generated for locations or populations in the SRB given current levels of PIT tagging. Current tagging includes:

- 1A. Individuals tagged within hatchery smolt releases, and
- 1B. Ad-intact hatchery (HNC) adults that are systematically PIT tagged at LGR to evaluate abundance and composition at LGR (e.g., Camacho et al. (2017)) and at IPTDS (e.g., Orme and Kinzer (2018)).

2. Determine additional tagging at LGR of ad-clipped adult HOR fish that would allow reasonable estimates of *pHOS*.

We will define reasonable as an estimate with a CV of 15% or less. Our simulation will focus on desired or critical populations/locations.

Methods

Section 1A. Expected precision of *pHOS* given current PIT tagging of hatchery smolt releases

Here, our aim is to evaluate the expected precision (CV) of *pHOS* using observations of individuals tagged within hatchery smolt releases and expansion values (inverse of tagging fraction) for those releases.

$$\hat{N}_h = \sum_{r=1}^{n} n_r * \psi_r$$

where $\hat{N}_h$ is the HOR abundance, n_r is the number of observations of HOR individuals from release r and ψ_r is the expansion value for release r. HOR escapement to a given location can then be combined with estimates for NOR escapement from DABOM to estimate *pHOS* with uncertainty.

$$p_{HOS} = \frac{\hat{N}_h}{\hat{N}_h + \hat{N}_n}$$

where $\hat{N}_n$ is the NOR abundance. Importantly, DABOM requires a random sample of tagged individuals (e.g., at the adult trap), and thus, we cannot generate abundance estimates in the DABOM model using juvenile tagging; hence, the tag expansion approach. In other words, we need to expand the number of hatchery observations from each release group by the tagging fraction for that release groups and then sum across groups, and further, account for the detection probability of IPTDS sites within a location. Note that in this scenario we don't need to account for differential survival among groups; we are only interested in tagging fractions within groups as long as we are willing to assume equal survival between tagged and untagged smolts.

Approach

The IDFG provided us with tagging fraction (i.e., expansion factor) information by brood year (BY), rearing hatchery, and mark type (H vs. HNC) for steelhead hatchery releases within Idaho from BY2013-2018. In addition, we have interrogation data and abundance estimates for wild steelhead populations available through spawn year (SY) 2019. Hatchery steelhead in Idaho are always released and emigrate to the ocean as 1 year olds. Using SY2019 hatchery adults as an example, those adults would have entered the Columbia River to initiate their spawning run during summer 2018; and thus 1-ocean adults would have emigrated to the ocen in 2017 (hence BY2016) and 2-ocean adults would have emigrated in 2016 (BY2015). Following this logic, we can consider the following BY smolt releases for each adult SY:

- SY2019: 1-ocean = BY2016, 2-ocean = BY2015
- SY2018: 1-ocean = BY2015, 2-ocean = BY2014
- SY2017: 1-ocean = BY2014, 2-ocean = BY2013

And thus, the earliest SY we can consider is 2017 as their 2-ocean adults originate from BY2013.

Locations

A recent assessment by See et al. (2019) identified steelhead TRT populations or locations containing IPTDS that can be used to estimate wild population abundance. We then performed a PTAGIS query for locations evaluated there, and in addition, queried for hatchery adult observations in the Lochsa, Selway, and North Fork Salmon rivers (areas with particular management interest where IPTDS have recently been installed) from smolt releases. Table 1 summarizes TRT populations and iterrogation sites for which we queried observations of hatchery adults during SY2017-2019. The following constraints were placed on our PTAGIS query:

- Species: Steelhead
- Rear: Hatchery
- Last Obs Date/Time: 07/01/2017 - 06/30/2019

- Obs Site: In Table 1

Table 1: Steelhead TRT populations and interrogation sites for which we queried interrogation of hatchery adults during spawn years 2017-2019.

TRT	Name	SiteID
CRLMA-s	Clearwater River lower mainstem	CLC, HLM, JUL, KHS, LAP, MIS, PCM, SWT, WEB
CRLOC-s	Lochsa River	LRL, LRU
CRLOL-s	Lolo Creek	LC1, LC2
CRSEL-s	Selway River	SW1, SW2
CRSFC-s	South Fork Clearwater River	CRT, RRT, SC1, SC2
GRJOS-s	Joseph Creek	JOC
GRLMT-s	Grande Ronde River lower mainstem tributaries	WEN
GRUMA-s	Grande Ronde River upper mainstem	CCW, UGR, UGS
GRWAL-s	Wallowa River	WR1, WR2
IRMAI-s	Imnaha River	BSC, CMP, COC, CZY, IML, IR1, IR2, IR3, IR4, IR5
MFBIG-s	Big, Camas, and Loon Creek	TAY
SFMAI-s	South Fork Salmon River	ESS, KRS, STR, YPP
SFSEC-s	Secesh River	ZEN
SNASO-s	Asotin Creek	ACB, ACM, AFC, CCA
SRLEM-s	Lemhi River	18M, AGC, BHC, BTL, BTM, BTU, CAC, CRC, HEC, HYC, KEN, LB8, LBS, LCL, LLR, LLS, LRW, WPC
SRNFS-s	North Fork Salmon River	NFS
SRUMA-s	Salmon River upper mainstem	RFL, STL, VC1, VC2, YFK

Next, we filtered the above results from the PTAGIS query to only include the following observations:

- Mark Site Code Value: From Snake River hatcheries for which we have tagging fraction data for BY2013-2018 (i.e., CLWH, DWOR, HAGE, MAVA, NISP).
- Mark Year: Excluded marks that occurred prior to 2013. This includes filtering "orphan" tags.
- Last Obs Time - Mark Year < 1: In many cases, the mark year was less than 1 year prior to the final IPTDS observation. These observations are presumably from hatchery smolt releases and were removed.
- Spawn Year - Brood Year = 3 or 4: Returning adult hatchery steelhead should be 3 ('A-run') or 4 ('B-run') years old. We excluded any observations where this was not the case.

And finally, for each observation, personnel from the IDFG identified whether each tag was from an RAL or RTR release, and for RAL fish, the appropriate expansion value. RTR observations were ignored. Descriptions of RTR vs. RAL are as follows:

- RTR ("Return-to-River"): A sort-by-code designation for smolts that will automatically be returned to the river when detected at a dam, when other fish may be getting transported. They do not represent the release group at-large, therefore represent only themselves with an expansion value of "1".
- RAL ("Run-at-Large"): A sort-by-code designation for smolts that will be transported or returned to the river in accordance with the protocol at the dam when they are detected. They represent the release group with a tagging rate that excludes any smolts that have an RTR tag in them. The expansion value of RAL tagged fish is the inverse of the tag rate.

Table 2 shows the number of RTR observations from hatchery smolt releases by TRT population, spawn year, and rearing hatchery in our final dataset. Observations were then expanded and compared to wild spawner abundance in those locations.

Table 2: The number of observations of adult hatchery steelhead by location, spawn year, and mark site.

TRT	Spawn Year	CLWH	DWOR	HAGE	MAVA	NISP	Total
CRLMA-s	2017	1	-	-	-	-	1
CRLOL-s	2017	-	14	-	-	-	14
CRLOL-s	2018	-	6	-	-	-	6
CRLOL-s	2019	-	2	-	-	-	2
CRSFC-s	2017	103	11	-	-	-	114
CRSFC-s	2018	25	7	-	-	-	32
CRSFC-s	2019	66	16	-	-	-	82
IRMAI-s	2018	-	-	-	2	-	2
MFBIG-s	2018	-	-	1	-	-	1
MFBIG-s	2019	-	-	1	-	-	1
SRLEM-s	2017	-	-	-	2	-	2
SRLEM-s	2018	-	1	-	6	1	8
SRNFS-s	2018	-	-	-	2	-	2
SRUMA-s	2017	-	-	3	8	-	11
SRUMA-s	2018	-	-	17	1	-	18
SRUMA-s	2019	-	-	2	2	-	4

Section 1B. Expected precision of *pHOS* given current systematic PIT tagging of HNC adults at LGR

Next, we evaluated the expected precision (CV) of *pHOS* estimates given current PIT tagging rates of ad-intact adults, both wild (W) and hatchery (HNC) at LGR. This leverages the fact that all ad-intact adults trapped at LGR are already implanted with a PIT tag. Estimates of wild adult abundance across select TRT populations and locations in the SRB are already available from DABOM. Here, we will re-run DABOM for HNC individuals for SY 2017 through 2019 to get HNC abundance estimates for locations and populations where we already report W abundance using DABOM. The HNC and W abundance estimates, at the same spatial scales, can then easily be combined to estimate *pHOS* with uncertainty.

This evaluation ignores ad-clipped H adults, but is effective for estimating *pHOS* among ad-intact individuals and may be of particular interest for supplementation locations (e.g., South Fork Clearwater steelhead). Unfortunately, it seems there is no easy way to combine juvenile smolt release tagging (tag expansion approach) and adult tagging information at LGR (DABOM model, transition probability approach) to estimate hatchery abundance and *pHOS* using IPTDS observations.

Section 2. Expected precision of *pHOS* by adding tagging of ad-clipped hatchery (H) adults at LGR

Finally, we evaluated the expected precision (CV) of *pHOS* estimates given additional (theoretical) tagging of ad-clipped hatchery (H) adults at LGR using a simulation approach. Here, again, we must ignore PIT tagged hatchery smolt releases and the tag expansion approach as the DABOM model is reliant on systematic tagging of the adult return. First, we demonstrate how an estimate of *pHOS* can be generated under the DABOM framework.

Mathematical Reasoning

The estimate of *pHOS* at any branch i in the DABOM model can be written as

$$pH\hat{O}S_i = \frac{\mu_{h,i}}{\mu_{h,i} + \mu_{w,i}}$$

where $\mu_{h,i}$ and $\mu_{w,i}$ are the estimates of hatchery and wild fish who have escaped to spawn in branch i. Ignoring the subscript i, let σ_h^2 and σ_w^2 represent the variance of those estimates. Then we can re-write our

equation for $pHOS$ as a function of hatchery and wild escapement estimates, assuming they are independent of one another (and assuming multivariate normality):

$$p\hat{H}OS = \frac{h}{h+w} = g\left(\begin{array}{c} h \\ w \end{array}\right)$$

$$g\left(\begin{array}{c} h \\ w \end{array}\right) \sim N\left(\begin{array}{c} \mu_h \\ \mu_w \end{array}, \left(\begin{array}{cc} \sigma_h^2 & 0 \\ 0 & \sigma_w^2 \end{array}\right)\right)$$

$$\equiv N(\boldsymbol{\mu}, \Sigma)$$

Then, via the delta method (or Taylor approximation) (Doob 1935), we can derive the variance of our estimates of $pHOS$:

$$Var(g) = \left(\frac{\partial g}{\partial h}, \frac{\partial g}{\partial w}\right) \Sigma \left(\begin{array}{c} \frac{\partial g}{\partial h} \\ \frac{\partial g}{\partial w} \end{array}\right)$$

$$= \left(\frac{w}{(h+w)^2}, \frac{h}{(h+w)^2}\right) \left(\begin{array}{cc} \sigma_h^2 & 0 \\ 0 & \sigma_w^2 \end{array}\right) \left(\begin{array}{c} \frac{w}{(h+w)^2} \\ \frac{h}{(h+w)^2} \end{array}\right)$$

$$= \left(\frac{w\sigma_h^2}{(h+w)^2}, \frac{h\sigma_w^2}{(h+w)^2}\right) \left(\begin{array}{c} \frac{w}{(h+w)^2} \\ \frac{h}{(h+w)^2} \end{array}\right)$$

$$= \frac{w^2\sigma_h^2 + h^2\sigma_w^2}{(h+w)^4},$$

so the standard error of $pHOS$ is

$$SE(g) = \frac{w\sigma_h + h\sigma_w}{(h+w)^2},$$

which implies that the CV of $pHOS$ can be derived as

$$CV(g) = \frac{SE(g)}{g}$$

$$= \frac{w\sigma_h + h\sigma_w}{(h+w)^2} * \frac{(h+w)}{h}$$

$$= \frac{w\sigma_h + h\sigma_w}{h(h+w)}$$

$$= \frac{h\sigma_w}{h(h+w)} + \frac{w\sigma_h}{h(h+w)}$$

$$= \frac{\sigma_w}{(h+w)} + \frac{w}{(h+w)} * \frac{\sigma_h}{h}$$

$$= \frac{w}{(h+w)} \left(\frac{\sigma_w}{w} + \frac{\sigma_h}{h} \right),$$

which is a combination of the proportion of wild fish, the CV of the estimate of wild fish and the CV of the estimate of hatchery fish. In other words, we can predict the CV of *pHOS* for a variety of situations for a given branch i by varying the percent wild fish in a stream, and the precision (or CV) of our escapement estimates of wild and hatchery fish in branch i. We selected several levels of precision in our estimates of wild fish, with CVs from 0.01 to 0.5, and a range of precision in our hatchery estimates, with CVs from 0 to 1.5, and then calculated the predicted CV of *pHOS* on those values.

Simulation

From the DABOM estimates of wild escapement for spawn years 2013-2019, we will first calculate the average CV of the wild abundance estimate for each population where IPTDS infrastructure is in place for population monitoring. We chose 2013 as the first year as IPTDS infrastructure in the SRB has been relatively stable since then (See et al. 2019). The average CVs of the wild estimates for each population will then show us where we fall on the x-axis in Figure 2. We will then use the average estimate of *pHOS* from Table 4 for each population to determine where on the y-axis we are for each population. If we know where on Figure 2 most CVs of wild escapement and percentage of wild spawners we observe among Snake River populations, this will tell us what CV is required for an estimate of hatchery abundance for each population. Finally, we can then translate that into a number of tags we'd like to detect in each population. Here, we will focus on steelhead TRT populations with a proposed status of "Viable" or "Highly Viable" which includes the following: South Fork Salmon R, Lower Middle Fork Salmon R, Upper Middle Fork Salmon R, Chamberlain Cr, North Fork Salmon R, Lemhi R, Lower Mainstem Clearwater, Selway R, Lochsa R, Imnah R., Lower Grande Ronde, Joseph Cr, Wallowa River, Upper Grande Ronde R., Asotin Cr, Tucannon R.

We also have information showing the percentage of hatchery adults, tagged as juveniles, that are detected within 'recipient populations' out of all the hatchery tags that are detected at LGR (and summarized by release groups; Brian Leth, IDFG, personal communication). We will divide the number of detections we require for each population by these percentages (Table 5) to determine how many tags we would expect to need to put out at Lower Granite in order to achieve determined precision goals.

Table 5: The percentage of hatchery steelhead adults, tagged as juveniles, observed straying into recipient populations from all those tags passing Lower Granite Dam, summarized by release groups. Note all values in table are expressed as a percentage.

Release Group	Upper Salmon	Pahsimeroi	Lemhi	North Fork Salmon	Middle Fork Salmon	South Fork Salmon	Imnaha River	Grande Ronde River	Lower Clearwater	Lolo	S.F. Clearwater	Selway	Lochsa	Lower Snake R.	Total
Upper Salmon-SAW	0.693	0.185	0.37	-	0.277	-	-	-	-	-	-	-	-	-	1.526
Upper Salmon-Pah	-	0.2	0.2	0.1	-	-	0.05	-	-	-	-	-	-	0.1	0.651
Upper Salmon-EF	-	0.234	0.234	0.234	-	-	-	-	-	-	-	-	-	-	0.703
Upper Salmon-DWOR/USR	-	-	1.218	-	-	-	-	-	-	-	-	-	-	0.152	1.37
Little Salmon-SAW/PAH	0.163	-	-	-	-	-	0.081	-	-	-	-	-	-	0.163	0.407
Little Salmon-DWOR/USR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0
Hells Canyon	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0
DNFH/Clearwater FH-SF Clearwater	-	-	-	-	-	-	-	-	0.069	-	-	-	-	-	0.069
DNFH-NF	-	-	-	-	-	-	-	-	0.157	0.157	0.079	-	-	-	0.394
DNFH/CLWH-Lolo/Clear Cr	-	-	-	-	-	-	-	-	-	0.274	3.288	-	-	-	3.562
Weighted Average	0.162	0.086	0.2	0.029	0.057	0	0.019	0	0.029	0.029	0.124	0	0	0.048	0.779

Results

Section 1A. Expected precision of *pHOS* given current PIT tagging of hatchery smolt releases

Table 3 summarizes hatchery, wild, and total abundance estimates and the corresponding *pHOS* estimates for locations and spawn years in which there were IPTDS observations of hatchery adults from RTR smolt releases. Wild abundance estimates are from the DABOM model whereas hatchery abundance estimates are using the expansion approach outlined above. Table 3 also includes the number of hatchery and wild tags observed and the CV of the wild abundance estimates for context. Unfortunately, we are currently unable to estimate uncertainty in hatchery abundance, and thus, unable to estimate uncertainty in *pHOS* using this approach. To do so, we would have to identify and estimate sources of uncertainty in the hatchery abundance estimates; uncertainty in the tagging fraction (i.e., expansion value) would be one such example.

Table 3: Hatchery, wild, and total abundance estimates and associated pHOS estimates for location x spawn year combinations with hatchery observations from smolt releases in the Snake River Basin.

TRT	Spawn Year	n. Tags Hatchery	CLWH	DWOR	RAGE	MAVA	NISP	Hatchery Abundance	n. Tags Wild	Wild Abundance	CV (%)	Total Abundance	pHOS
CRLMA-s	2017	1	77	-	-	-	-	77	52	272	7.5	349	0.221
CRLOI-s	2017	14	-	992	-	-	-	992	23	125	10.6	1,117	0.888
CRLOI-s	2018	6	-	592	-	-	-	592	30	134	11.3	726	0.815
CRLOI-s	2019	2	-	197	-	-	-	197	16	2,050	38.3	2,247	0.088
CRSFC-s	2017	114	7,454	1,372	-	-	-	8,826	81	499	8.1	9,325	0.946
CRSFC-s	2018	32	1,558	568	-	-	-	2,126	20	122	13.7	2,248	0.946
CRSFC-s	2019	82	3,912	1,298	-	-	-	5,210	26	151	15.7	5,361	0.972
IRMAI-s	2018	2	-	-	-	141	-	141	155	672	6.2	813	0.173
MFBIG-s	2018	1	-	-	72	-	-	72	32	140	10.8	212	0.34
MFBIG-s	2019	1	-	-	83	-	-	83	17	80	16.8	163	0.509
SRLEM-s	2017	2	-	-	-	79	-	79	34	169	9.5	248	0.319
SRLEM-s	2018	8	-	119	-	383	133	635	25	108	10.5	743	0.855
SRNFS-s	2018	2	-	-	-	136	-	136	12	205	71.8	341	0.399
SRUMA-s	2017	11	-	-	496	460	-	956	12	73	30.6	1,029	0.929
SRUMA-s	2018	18	-	-	1,235	40	-	1,275	11	50	30.7	1,325	0.962
SRUMA-s	2019	4	-	-	166	108	-	274	8	38	37.5	312	0.878

Section 1B. Expected precision of *pHOS* given current PIT tagging of W and HNC adults at LGR

We estimated the abundance of ad-intact adults using the systematic tagging of those adults at LGR, detection at IPTDS throughout the SRB, and using the DABOM model for steelhead, SY2017-2019 (Table 4). Abundances were then combined to estimate *pHOS* with SE and CV which accounts for uncertainty in both the wild and HNC abundance estimates.

Table 4: Estimates of adundance for ad-intact steelhead including wild and hatchery (HNC), spawn years 2017-2019 and estimates of the proportion of hatchery origin spawners (pHOS) with standard error (SE) and coefficient of variation (CV) that takes into account uncertainty in the abundance estimates.

TRT	Year	HNC	Wild	pHOS	pHOS_se	pHOS_cv
CRLMA-s	2017	27	273	0.090	0.039	0.433
CRLMA-s	2018	22	273	0.075	0.030	0.401
CRLMA-s	2019	NA	NA	NA	NA	NA
CRLOC-s	2017	744	1386	0.349	0.221	0.634

TRT	Year	HNC	Wild	pHOS	pHOS_se	pHOS_cv
CRLOC-s	2018	20	356	0.053	0.044	0.827
CRLOC-s	2019	87	455	0.161	0.174	1.086
CRLOL-s	2017	565	126	0.818	0.024	0.029
CRLOL-s	2018	129	135	0.489	0.056	0.114
CRLOL-s	2019	141	2214	0.060	0.038	0.642
CRSEL-s	2017	NA	NA	NA	NA	NA
CRSEL-s	2018	16	306	0.050	0.030	0.612
CRSEL-s	2019	123	272	0.311	0.274	0.880
CRSFC-s	2017	3824	500	0.884	0.011	0.012
CRSFC-s	2018	976	123	0.888	0.016	0.018
CRSFC-s	2019	1567	154	0.911	0.015	0.017
GRJOS-s	2017	NA	NA	NA	NA	NA
GRJOS-s	2018	14	753	0.018	0.011	0.600
GRJOS-s	2019	20	487	0.039	0.033	0.843
GRWAL-s	2017	72	457	0.136	0.035	0.260
GRWAL-s	2018	74	289	0.204	0.044	0.217
GRWAL-s	2019	38	660	0.054	0.022	0.413
IRMAI-s	2017	28	922	0.029	0.014	0.464
IRMAI-s	2018	17	672	0.025	0.012	0.480
IRMAI-s	2019	18	725	0.024	0.013	0.532
MFBIG-s	2017	NA	NA	NA	NA	NA
MFBIG-s	2018	11	140	0.073	0.065	0.891
MFBIG-s	2019	NA	NA	NA	NA	NA
SFMAI-s	2017	11	487	0.022	0.014	0.644
SFMAI-s	2018	9	148	0.057	0.034	0.602
SFMAI-s	2019	NA	NA	NA	NA	NA
SNASO-s	2017	28	315	0.082	0.035	0.428
SNASO-s	2018	27	308	0.081	0.030	0.369
SNASO-s	2019	10	326	0.030	0.024	0.810
SNTUC-s	2017	91	302	0.232	0.058	0.251
SNTUC-s	2018	125	481	0.206	0.041	0.200
SNTUC-s	2019	67	294	0.186	0.057	0.304
SREFS-s	2017	132	0	1.000	0.000	0.000
SREFS-s	2018	51	0	1.000	0.000	0.000
SREFS-s	2019	51	29	0.638	0.117	0.183
SRLEM-s	2017	33	170	0.163	0.059	0.362
SRLEM-s	2018	13	108	0.107	0.058	0.537
SRLEM-s	2019	NA	NA	NA	NA	NA
SRPAH-s	2017	134	13	0.912	0.049	0.053
SRPAH-s	2018	107	33	0.764	0.074	0.096
SRPAH-s	2019	235	37	0.864	0.046	0.053
SRUMA-s	2017	181	75	0.707	0.074	0.105
SRUMA-s	2018	54	52	0.509	0.104	0.205
SRUMA-s	2019	26	41	0.388	0.136	0.351

Section 2. Expected precision of *pHOS* by adding tagging of ad-clipped hatchery (H) adults at LGR

Mathematical Reasoning

We predicted the CV of *pHOS* across a range of values for both hatchery escapement CV (0 - 1.5) and proportion wild (i.e., inverse of *pHOS*). The results are shown in Figure 1.

The general patterns show that as the proportion of wild fish in the stream descreases, the precision of *pHOS* improves for a given precision level of wild and hatchery escapement estimates. Also, as the precision of the wild estimates improves (i.e. smaller CV), there are more scenarios under which the precision of the *pHOS* estimate is reasonable. As a reference, the CVs of the estimates for spring/summer Chinook escapement to the Lemhi range from 0.1 to 0.25 for years 2010 - 2018.

Another way to look at it would be to examine the maximum CV of hatchery estimates that would provide a reasonable estimate of *pHOS* for a given proportion of wild fish and precision of wild escapement. One way to visualize these results in in the plot below.
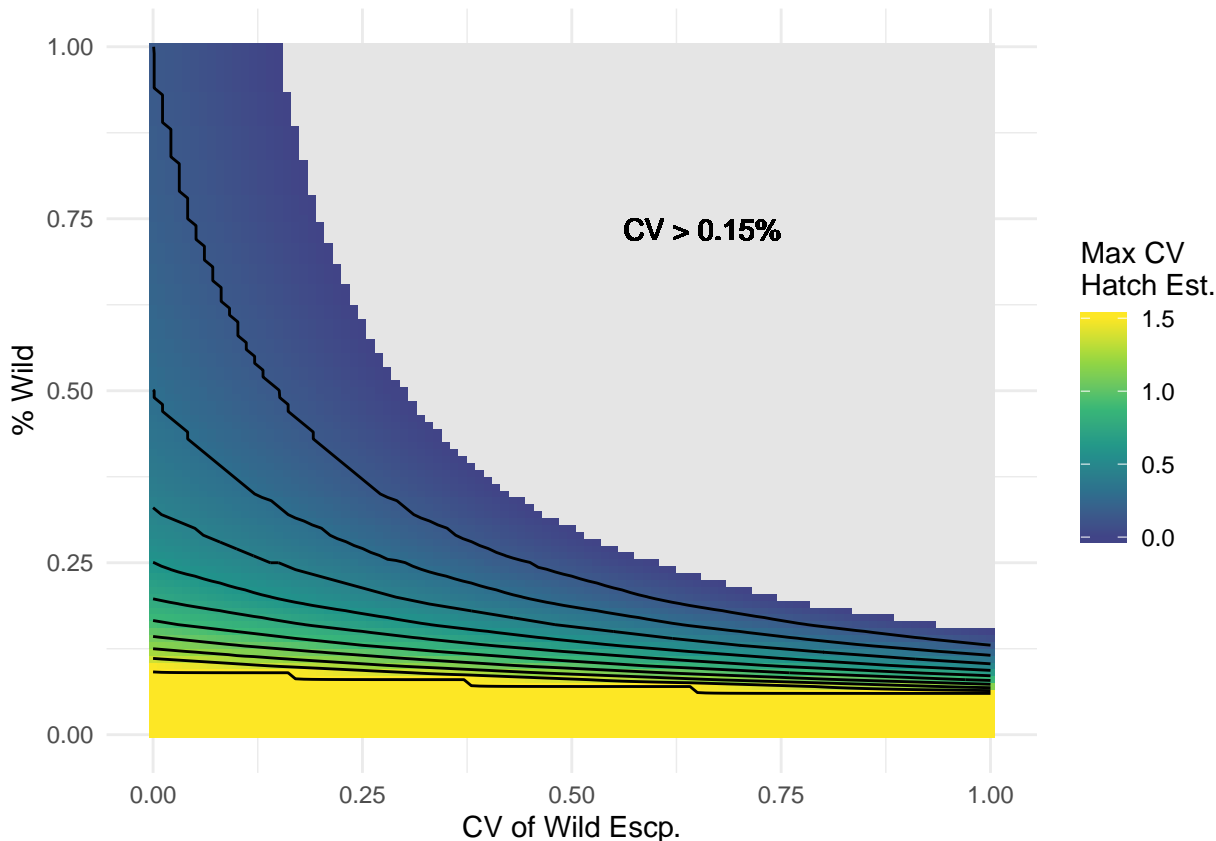

Figure 1: Figure 2: The maximum CV of hatchery abundance estimates that would provide an estimate of pHOS with reasonable precision for a given proportion of wild fish (inverse pHOS) and precision of wild escapement.

From this plot, it is clear that as long as the proportion of wild fish in a stream is below a certain threshold (around 10%), then regardless of the CV of wild or hatchery escapement, reasonable precision of *pHOS* will be obtained.

Simulation

Results from simulation here...

MPG_DPS	Name	TRT	cvW	propWild	maxHcv	n_tags	conv_rate	LGR_
Imnaha	Imnaha River	IRMAI-s	0.08	0.97	0.07	82	0.00019	431
Clearwater	Lower Clearwater River	CRLMA-s	0.08	0.92	0.08	75	0.00029	258
Salmon	Lower Middle Fork Salmon River	MFBIG-s	0.13	0.93	0.03	127	0.00057	222
Clearwater	Lolo Creek	CRLOL-s	0.14	0.54	0.13	50	0.00029	172

MPG_DPS	Name	TRT	cvW	propWild	maxHcv	n_tags	conv_rate	LGR_
Lower Snake	Tucannon River	SNTUC-s	0.11	0.79	0.07	82	0.00048	170
Salmon	Upper Mainstem Salmon River	SRUMA-s	0.26	0.47	0.05	100	0.00162	61
Salmon	Lemhi River	SRLEM-s	0.12	0.86	0.05	100	0.00200	50
Salmon	Pahsimeroi River	SRPAH-s	0.37	0.15	0.63	1	0.00086	1
Clearwater	South Fork Clearwater River	CRSFC-s	0.10	0.11	1.26	1	0.00124	

Discussion

Next Steps

- Incorporate results and implications from Craig Busack's script located in ../R/idahopit.R
    - from Lance Hebdon, August 5, 2019: I would contact Busack directly, we never saw any specific analysis only Craig's description of how low a confidence we would have given the low tag rates and detection rates at a single array in a single year basis. Also some of the issues we had with Craig's analysis was his assumption that straying was equal across the landscape, as opposed to straying being more likely near the release points, the effect of transportation on straying, the ability to aggregate information from multiple years to further understand patterns in straying, and a few other things that I don't have on the top of my head.
- Identify 2-3 locations of interest for each Chinook salmon and steelhead to perform evaluations
- Do we need to perform a PTAGIS query for particular locations to identify HOR observations; and can we track down release 'groups' for each observation?

Assumptions and Considerations

- What are the appropriate transition probabilities for hatchery fish along model branches? Need to consider harvest of hatchery fish. Presumably transition probabilities are lower for hatchery fish (relative to natural origin fish) due to harvest.
- Do hatchery fish mimic movement of wild fish? Probably not, due to the location of origin hatcheries and releases.
- Do some branches contain 0 hatchery fish?
- Should branches further upstream of LGR automatically include lower transition probabilities due to fishing on the mainstem?
- Do we need to accomodate time-varying movement probabilities in the simulation?
- Appropriate detection probabilities for each detection node in the simulation model.
- We must assume a fraction of hatchery fish will be harvested prior to reaching tributary habitats.
- How many total hatchery fish escape past LGR? We can run STADEM to determine range of values over the last several years.
- Is 15% CV for pHOS an appropriate, or even achievable, goal?

References

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