

Estimates of Escapement and an Evaluation of Abundance Methods for North Fork Lewis River Fall-run Chinook Salmon, 2013 – 2017



Washington
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**FISH and
WILDLIFE**

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Fork Lewis River Fall-run Chinook Salmon, 2013 – 2017**

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Executive Summary

The Washington Department of Fish and Wildlife (WDFW) has estimated the abundance of fall-run Chinook salmon spawners in the North Fork (NF) Lewis River for more than five decades. Over this time period, the methods used to collect spawner data and generate estimates of abundance have varied. Specifically, estimates from 1964 – 1999 were calculated using a peak count expansion (PCE) factor of 5.27 that was derived using the relationship between the peak count (797) and total abundance (4,199) in a single year (1976). In the early-2000s, WDFW re-evaluated the PCE estimator and from this work developed a new expansion estimator known as the Bright-eye method (BEM). The BEM estimates annual abundance for NF Lewis River Chinook salmon using weekly carcass counts and average age-specific recovery rates observed during two years of data collection (2001 and 2002). Although the BEM was thought to be an improved estimator relative to the historical PCE factor, the main assumptions of the BEM (i.e., constant within and among year age-specific carcass recovery rates) have never been evaluated and thus it is unknown if estimates derived using the BEM are unbiased. Additionally, the BEM does not generate an estimate of uncertainty around the point estimate. Therefore, the current BEM estimator does not meet the monitoring recommendations for ESA-listed salmon and steelhead populations that have been outlined by NOAA Fisheries and local watershed management plans.

In an effort to evaluate the BEM and gather additional years of the PCE ratios, WDFW conducted mark-recapture spawning ground surveys for five years (2013 – 2017). The objectives of the mark-recapture carcass tagging surveys were to (1) generate independent and unbiased estimates of spawner abundance and composition with estimates of uncertainty, (2) evaluate whether or not the BEM and PCE can generate unbiased estimates of abundance, and (3) provide recommendations for future surveys and analyses based on the results. Using a mark-recapture Jolly-Seber (JS) model, we generated estimates of abundance for NF Lewis River Chinook by stock (tule, bright), origin (hatchery, wild), sex (jack, female, male), and total age (2 – 6). Across the five years of surveys, estimates of total fall-run Chinook salmon abundance (i.e., tules and brights combined) generated with the JS estimator ranged from approximately 10,000 to 27,000 spawners per year (CV of 2 – 13%) of which approximately 66 – 85% were late-run (“bright” stock) Chinook salmon.

Using the JS estimates, which were assumed to be unbiased, we evaluated the accuracy and precision of abundance estimates derived with the BEM and three different PCE estimators. Among years, the absolute percent error for estimates of abundance derived with the BEM estimator ranged from 3 – 55% (mean absolute percent error: 13 – 24%) while the absolute percent error for estimates of abundance derived with the PCE estimators ranged from <1 – 65% (mean absolute percent error: 7 – 28%). Therefore, in general, the accuracy of abundance estimates derived with the BEM and PCE estimators were quite similar. However, one advantage of the PCE estimators is that abundance estimates are derived with uncertainty, albeit relatively imprecise (CV 28 – 49%). Overall, the main assumptions of the BEM and PCE estimators were not consistently met, which led to inaccurate estimates of abundance in some years. Based on these results, we recommend the continuation of annual mark-recapture surveys (JS method) to estimate the abundance of NF Lewis Chinook salmon until a more cost-effective, alternative method has been developed that can generate abundance estimates by stock, origin, sex, and age with comparable uncertainty and robustness to model assumptions.

Introduction

The Lower Columbia River (LCR) Chinook salmon (*Oncorhynchus tshawytscha*) Evolutionarily Significant Unit (ESU) consists of 32 historical independent populations that are distributed from the mouth of the Columbia River upstream to Hood River in Oregon (NMFS 2013). LCR Chinook salmon exhibit two dominant adult migration patterns based on when individuals return to freshwater to spawn. These two dominant life-history strategies have been used to categorize populations as either spring-run or fall-run Chinook (Myers et al. 2006). Fall-run Chinook populations have been further separated into two groups (i.e., stocks) based on run-timing– “fall-run” and “late fall-run” – and are referred to as “tule” and “bright” Chinook salmon, respectively. Hereafter, the term “fall-run” Chinook will be used in reference to the combination of these two stocks while the terms tule and bright will be used to identify the specific fall-run stock.

In 1999, Chinook salmon in the LCR ESU were listed for protection under the Endangered Species Act (ESA) and have been designated as Threatened ever since. Following listing, the Washington Department of Fish and Wildlife (WDFW) initiated an extensive monitoring program for Chinook salmon (hereafter referred to as just Chinook) throughout Washington’s portion of the LCR ESU. This monitoring program focused on estimating Viable Salmonid Population (VSP) parameters (McElhany et al. 2000) and other specific indicators (Rawding and Rodgers 2013, Rawding et al. 2014) with the purpose of assessing the status, trend, and long-term viability of LCR Chinook. While this relatively recent monitoring program marked the beginning of data collection for many LCR Chinook populations, Chinook in the Lewis River have a much longer monitoring history.

WDFW, formerly the Washington Department of Fisheries, has been conducting spawning ground surveys for Chinook in the Lewis River since the mid-1950s. In the early years, surveys were focused on fall-run Chinook in the North Fork (NF) Lewis River and consisted of live and dead counts in index sections during peak spawning for the purpose of estimating relative abundance. In the mid-1970s, managers commenced several studies to better understand why the numbers of Lewis River Chinook had remained relatively abundant while numbers of most other LCR populations had dwindled. One of the studies was a mark-recapture carcass tagging evaluation. The goal of the study was to estimate the total spawning population of fall-run Chinook in the NF Lewis River for a single year that would allow the generation of a peak count expansion (PCE) factor (McIssac 1976). For the following two and a half decades, WDFW continued to conduct peak count surveys and generated estimates of total Chinook abundance using the PCE factor established in 1976.

In the early 2000s, WDFW revisited the methods that were being used to estimate the abundance of Lewis River Chinook due to several management changes that had occurred over the previous decades. First, the fall Chinook hatchery program on the Lewis River had been discontinued in the mid-1980s and there was evidence that the peak spawning timing had shifted later in the season thereby questioning the accuracy of the 1976 PCE factor. This change in peak spawning also corresponds with environmental conditions (i.e., increased flows, decreased visibility) that make counts of fish much more difficult and in some years impossible. Second, mass-marking (i.e., adipose fin-clipping) of hatchery-origin Chinook had been implemented in the mid-2000s, which now allowed hatchery- and wild-origin stocks to be monitored independently. Third, monitoring standards and guidelines had been refined and specifically, the Chinook Technical Committee

recommended that escapement estimates derived from index expansion factors be regularly evaluated (Hawkins et al. 2003a). Therefore, WDFW conducted a mark-recapture carcass tagging study in three consecutive years (2000 – 2002) to estimate total escapement and establish updated expansion factors for Lewis River fall-run Chinook.

From this work, WDFW developed a new expansion method to estimate total fall-run Chinook abundance in the Lewis River. This new abundance estimator was termed the “Bright-eye method” (BEM) and has been used as the primary estimator since 2000 (e.g., Hawkins 2013; see methods section below for further description). Although the BEM was likely an improvement from the earlier PCE factor, it is not known if BEM estimates of Chinook abundance are accurate (i.e., unbiased). Additionally, the current form of the estimator does not derive estimates of uncertainty (i.e., precision) which means that we are unable to evaluate confidence in the resulting estimate. Therefore, the BEM does not meet the monitoring recommendations for ESA-listed salmon and steelhead populations (Crawford and Rumsey 2011) and monitoring guidelines established by the Lewis River Hatchery and Supplementation Annual Operating Plan (H&S Subgroup 2015). These limitations of the BEM are the impetus for the work contained in this report.

In 2013, WDFW reinitiated mark-recapture carcass surveys of Lewis River Chinook and has continued to use these methods in all subsequent years. The objectives of these mark-recapture carcass tagging surveys were three-fold:

- (1) Generate independent and unbiased estimates of spawner abundance (i.e., escapement) for NF Lewis fall-run Chinook salmon**
 - Describe and evaluate the Jolly-Seber (JS) open population mark-recapture abundance estimator and its corresponding assumptions
 - Estimate abundance using the JS estimator for populations of fall-run Chinook downstream of Merwin Dam from return years 2013 - 2017
 - Report estimates in a manner that is consistent with Chinook populations listed in the Recovery Plan for the Lower Columbia River Evolutionary Significant Unit (NMFS 2013)
- (2) Evaluate the Bright-eye method (BEM) and peak count expansion (PCE) estimators**
 - Describe and evaluate the BEM estimator and its corresponding assumptions
 - Report the estimates of abundance that have been generated using the BEM from 2013 - 2017
 - Develop updated PCE factors, evaluate model assumptions, and derive estimates of abundance
 - Calculate the absolute difference and absolute percent error in abundance estimates derived with the BEM and PCE estimators relative to the JS estimator
- (3) Provide recommendations for future fall-run Chinook monitoring methods and analyses in the Lewis River Basin**

Methods

Study System

The Lewis River is located in southwest Washington and enters the Columbia River approximately 85 miles upstream from the Pacific Ocean (Figure 1). The Lewis River drains a basin of approximately 730 square miles and receives water from snowmelt from Mt. St. Helens and Mt. Adams, spring water, and rainfall. Historically, the diversity of habitats and associated hydrology and water temperatures in the watershed supported a great deal of run timing diversity in Chinook salmon, with earlier returning (e.g., spring and summer) Chinook salmon generally spawning higher in the watershed, and later returning fall spawners using the lower reaches of the watershed. In 1931, Merwin (Ariel) Dam was built at river mile (RM) 19.5 and has blocked natural upstream migration of Chinook and other fishes thereby forcing all Chinook, regardless of run timing to spawn in approximately nine miles of river. Three hatcheries (Lewis River, Merwin, and Speelyai) have been constructed and currently raise coho salmon, spring-run Chinook, kokanee, and steelhead. Hatchery fall-run Chinook were historically released into the Lewis River, but this program was discontinued after 1984 and the last of hatchery releases returned in 1991. However, many other LCR basins still receive releases of hatchery tule juveniles and some of these hatchery tule Chinook return (i.e., stray) to the Lewis River.

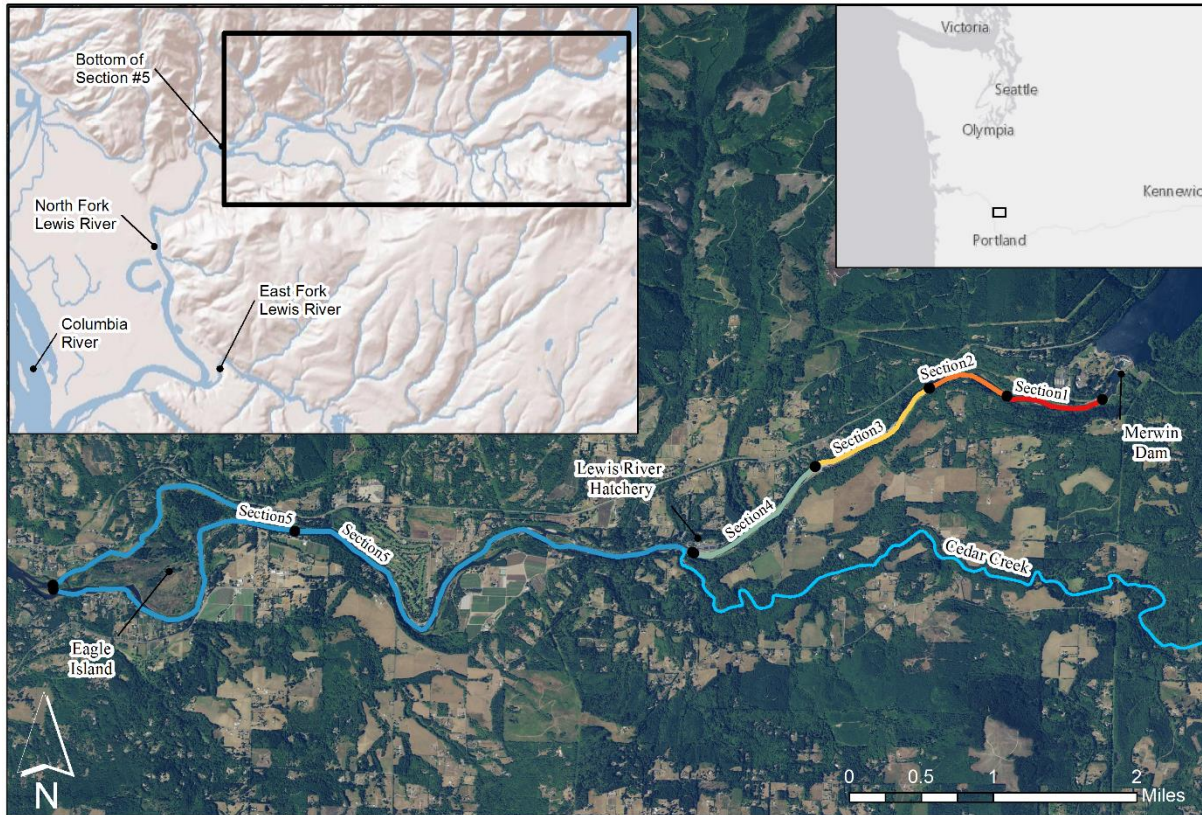


Figure 1. Map of fall-run Chinook salmon carcass survey sections on the NF Lewis River.

The Lewis River watershed contains three of the 32 LCR Chinook populations and together display each of the three unique run-types (spring, fall, and late-fall). The majority of Lewis River fall-run Chinook spawning occurs between the Lewis River Salmon Hatchery (RM 15.7) and the base of Merwin Dam (RM19.5). Additional spawning occurs in the mainstem Lewis River between the bottom of Eagle Island (RM10.0) and Lewis River Salmon Hatchery as well as in two major tributaries: Cedar Creek and the East Fork (EF) Lewis River, which enter the Lewis River at RM 15.7 and 3.5, respectively (Figure 1). The section of the Lewis River upstream from the mouth of the EF Lewis River is often referred to as the North Fork (NF) Lewis River.

The mark-recapture carcass tagging surveys completed in 2000 – 2002 and 2013 – 2017 were conducted in the NF Lewis River from the bottom of Eagle Island upstream to just below Merwin Dam. This total survey area has been delineated into five survey sections (Table 1, Figure 1). These survey sections have remained constant since the original 1976 carcass tagging study. Sections 1 – 4 are each approximately one mile in length and together make up the index count section dating back to the mid-1950s. Section 5 consists of a split channel surrounding Eagle Island. Historically, the 1976 PCE factor included Cedar Creek escapement, but for this evaluation, Cedar Creek and East Fork Lewis River Chinook data were analyzed separately. Therefore, these two data sets were not incorporated into this current evaluation. However, in the future, WDFW will make an effort to generate “total” Lewis River tule and bright abundance estimates that incorporate all major spawning areas (see “Recommendations”).

Table 1 – Description of fall-run Chinook carcass survey sections on the NF Lewis River, 2013 – 2017.

Reach Code	Length (miles)	Description
NFL-1	0.7	Top: Pool Below Merwin Dam (RM 19.1) Bottom: Rocky bluff/Bottom of Sec #1 (RM 18.4)
NFL-2	0.8	Top: Rocky bluff/Bottom of Sec #1 (RM 18.4) Bottom: Waterfall below Hagedorns (RM 17.8)
NFL-3	1.0	Top: Waterfall below Hagedorns (RM 17.8) Bottom: Top of Big Bar (RM 16.8)
NFL-4	1.1	Top: Top of Big Bar (RM 16.8) Bottom: Lewis R. Hatchery Boat Ramp (RM 15.7)
NFL-5	7.7*	Top: Lewis R. Hatchery Boat Ramp (RM 15.7) Bottom: Bottom of Eagle Island (RM 10)

*Length includes both north and south channel around Eagle Island

Data Collection – Mark-recapture carcass surveys

From 2000 – 2002 and 2013 – 2017, mark-recapture carcass surveys were conducted on the NF Lewis River. Each year, surveys began in mid- to late-September and continued through mid-January to mid-February. This time period encompassed the large majority of fall-run Chinook spawn timing in the NF Lewis River. Surveys were conducted weekly given that river conditions were conducive to staff safety and fish visibility. Carcass surveys typically occurred on a single day per week and were aligned with when river flows were the lowest. One to four jet boats were

used to navigate the river and sample Chinook carcasses. During the peak fall-run Chinook spawning timeframe (November through early December), PacifiCorp normally provided five “drawdowns” where river discharge at Merwin Dam was reduced in an effort to facilitate increased carcass recovery rates and improve observer efficiency for live and redd counts. Occasionally, a second survey day in a week was required due to large numbers of carcasses. When multiple surveys occurred in a single week, the data sets were pooled and treated as a single sampling period for mark-recapture analyses. Additionally, when a second survey day occurred in a single week, surveys proceeded upstream starting with the lowest reach first in order to prevent carcasses from being sampled more than once in a single week (e.g., by drifting into a current survey reach from a previously surveyed reach on consecutive days).

During each survey, recovered carcasses were sorted and processed in a sequential manner (Figure 2). First, carcasses were sorted based on their recovery status (i.e., recovered vs. not recovered) and several external features of the carcass. Carcasses that could not be recovered (e.g., too deep, pinned in a log jam) were enumerated and recorded as a Carcass Category 5 (Figure 3; Appendix A). If the carcass could be recovered (i.e., handled), it was initially examined for the presence of a tail. A carcass with a severed (i.e., missing) tail was indicative of a previously sampled fish and was subsequently ignored. Carcasses with intact tails were then sorted based on whether or not a surveyor could determine if the carcass had been previously tagged. Previously tagged carcasses would have a tag on the inside of one or both opercula (see below). Therefore, if a carcass was missing its head and/or opercula its previous tag status could not be determined. These carcasses were enumerated, denoted as either a Carcass Category 1 or 2 and had their tail severed. Carcasses recovered with a slit belly were assumed to not have died naturally (e.g., harvest mortalities) and were enumerated and denoted as a Carcass Category 6.

Second, carcasses with intact heads and/or opercula were sorted as either taggable or untaggable based on its qualitative Carcass Condition (CC) score (Table 2). The purpose of the CC score was to describe the carcass’ state of decomposition. In 2001 – 2002, taggable carcasses typically had a numeric carcass condition score of 2 while untaggable carcasses were classified as either 3 – 6. The exception to this general rule was that early in the survey season when carcass recovery numbers were generally low and carcass persistence was short, carcasses with a score of 3 and sometimes 4 were also tagged. In 2013 – 2017, taggable carcasses had a numeric score of 2, 3, or 4 while untaggable carcasses were classified as either 5 or 6. Carcasses that were in a degraded condition (i.e., CC 5 or 6) were not tagged to reduce the dissimilarity in “survival” (i.e., persistence as a recoverable carcass) among tagged carcasses as older, more decomposed carcasses typically have lower probabilities of surviving to subsequent periods relative to newer carcasses (Sykes and Botsford 1986). Therefore, in all years, untaggable carcasses were designated as “mark sample only”, classified as either a “jack” or an “adult” group carcass (see below), had their adipose-fin status recorded (see below) and Carcass Category recorded, examined for a coded-wire tag (CWT), had their tail severed to signify the carcass had been sampled (i.e., denoted as a “loss on capture” in Jolly-Seber model), and returned to the river.

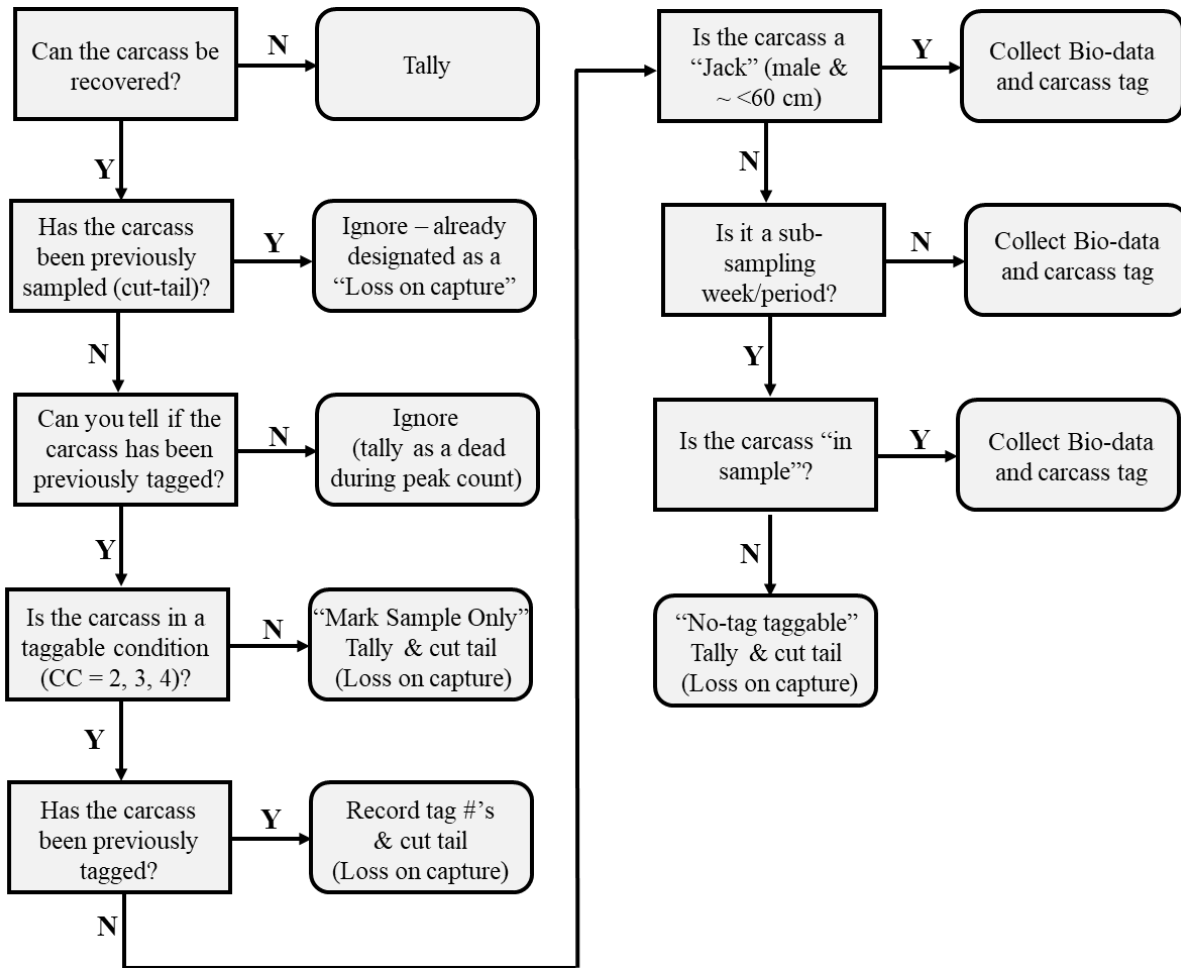


Figure 2. Sampling procedure for Fall Chinook carcass surveys on the NF Lewis River, 2013 – 2017.

Third, carcasses that were in taggable condition were then processed based on their capture history and size/age. Carcasses were sorted into maiden and recapture recoveries. A recaptured carcass would have had a uniquely numbered plastic tag stapled to the inside of one or both opercula while a carcass with no opercal tags was classified as a maiden. Recaptured carcasses had their tag number(s) recorded, tag(s) removed, tail severed to denote the carcass was sampled, and returned to the river. Maiden captures were sorted into two groups based on their sex and fork length. The first group were classified as “jacks/group 1” fish and consisted of small(er) males whose fork length was approximately < 60 cm. The second group were classified as “adults/group 2” fish and consisted of females and large(r) males whose fork length was approximately ≥ 60 cm. It should be noted that these group classifications were largely based on visual assessment of fish length upon collection. Therefore, a portion of the “jack” group carcasses consisted of small “adult” males and vice versa due to both inaccuracies in visually classifying carcasses by length (e.g., a 62 cm carcass placed into the <60 cm “jack” group) and variability in length-at-age (e.g., a 62 cm carcass classified as an “adult” was, in fact, a true, age-2 jack) based on scale analysis. Regardless, this slight variation in the group classification of each carcass (i.e., “jacks” vs. “adults”) did not

have any impact on the accuracy of abundance estimates as age-distribution was apportioned using weekly scale samples (see below).

Fourth, carcasses were then processed based on the weekly sampling rate. Specifically, carcasses were sorted into two groups (“in-sample” or “out-of-sample”) based on the sampling rate for a particular week. In all weeks, “jack” group carcasses were sampled at a 1:1 rate due to the low overall recoveries of carcasses in this category. In most weeks, “adult” group carcasses were sampled at a 1:1 rate. However, sub-sampling occurred in most years during peak weeks when the number of recovered carcasses was too high to sample at a 1:1 rate. Sub-sampling rates were predetermined based on the anticipated number of recoveries for a particular week and varied from 1:2 to 1:10 among weeks and years. Out-of-sample carcasses were enumerated, had their tail severed to denote the carcass was sampled, and returned to the river. All carcasses (in and out of sample) with a missing adipose fin were scanned for a CWT (see below).

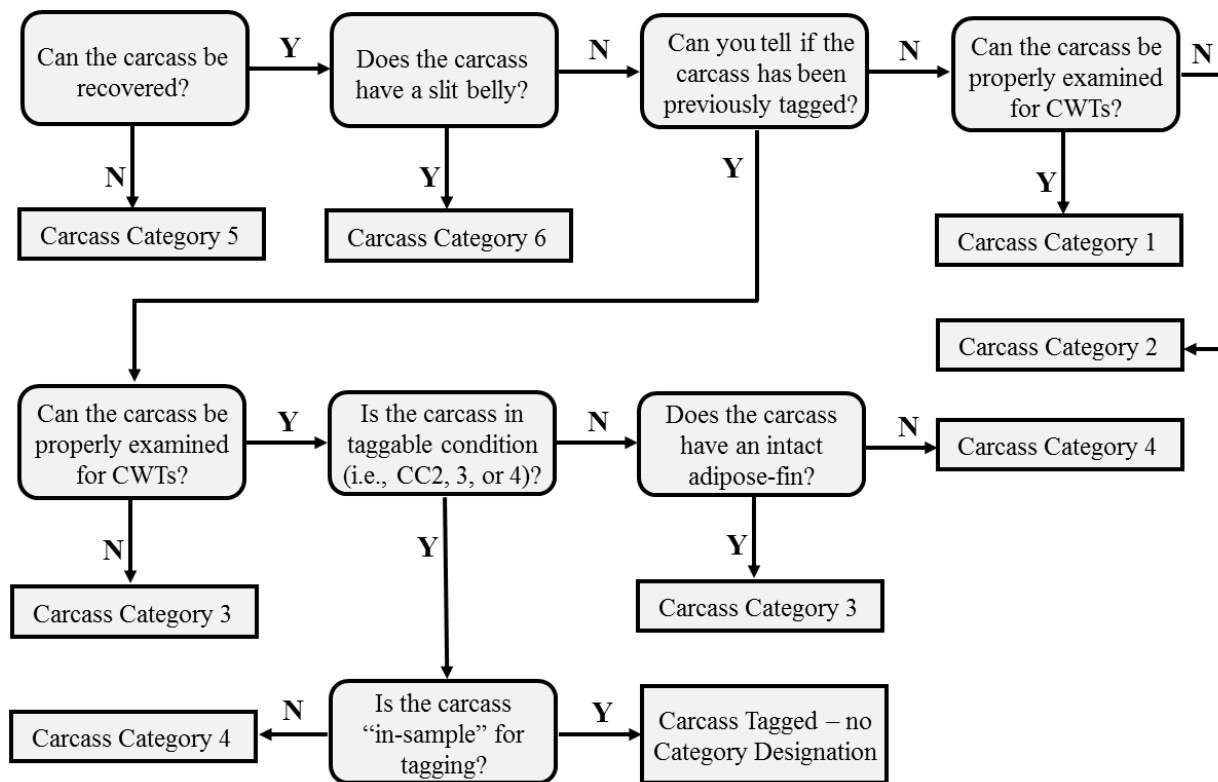


Figure 3. Diagram of Carcass Category designation for carcass surveys conducted on the NF Lewis River. Carcass Categories were only assigned to maiden (i.e., previously unsampled) carcasses that were not carcass tagged.

Lastly, in-sample (taggable, maiden) carcasses were bio-sampled and tagged. Carcasses were examined for the presence or absence of an adipose fin and CWTs. Prior to mid-November, all maiden recovered carcasses were scanned for a CWT using a handheld wand regardless of adipose status due to the possible presence of double-index tagged (DIT) spring run Chinook. After mid-November, only carcasses with missing adipose fins were scanned for CWTs. Carcasses that

wanded positive for a CWT had their snouts removed and collected. All carcasses then had their sex, fork length (FL), and CC score (Table 2) recorded, scales collected for aging, and were tagged. Carcasses were tagged by stapling a uniquely numbered plastic tag on the inside of both opercles. Tagged carcasses were then returned to moving water in the river section they were collected from (Table 1) to facilitate mixing with untagged carcasses.

Table 2. Carcass condition (CC) categories codes and the associated description of a carcass. Categories and definitions are based on criteria developed by Sykes and Botsford (1986).

Category (Numeric)	Category (Alpha)	Description of Carcass Condition
1	L	Live, still gilling or moving*
2	F	Fresh, both eyes clear, firm flesh, gills bright red
3	D-	Slightly decayed, eyes cloudy, firm flesh
4	D	Decayed, eyes cloudy, soft flesh
5	D+	More decayed, eyes cloudy, very soft flesh
6	S	Skeleton, losing flesh

*Note: live fish were not tagged

Data Collection – Bright-eye method (BEM)

“Bright-eye” data collection methods were identical to the mark-recapture methods described above in years when mark-recapture tagging surveys were conducted. In years when mark-recapture carcass surveys were not conducted (i.e., years 2003 – 2012), “bright-eye” data collection methods were similar to the mark-recapture methods with a few exceptions. The major exceptions during these years were that (1) there were only two CC score designations (“fresh” or “mark-sample only”), and (2) the definition of a “fresh” carcass for the BEM is slightly different than the term for mark-recapture surveys (Table 2). Specifically, the term fresh for the BEM is meant to characterize a fish that had died in the same week of the survey (based on professional opinion) as opposed to just the external characteristics of the fish. This slight difference in the definition of a “fresh” carcass mainly impacts how carcasses are categorized during earlier survey periods (i.e., September and October) when water temperatures are higher and thus carcasses degrade faster. Therefore, a CC2 carcass would be classified as a “fresh” fish for both methods regardless of the survey time period. However, under the “bright eye” method a carcass with a CC of 3 or 4 may have been considered fresh depending on when it was recovered. In general, “bright eye” data collection methods considered carcasses to be fresh in September if they had a CC score of 2 – 4, in October if they had a CC score of 2 or 3, and in November to February if they had a CC score of 2. Also, jacks recovered with a CC score of 2 or 3 from October to February were considered fresh due to low sample sizes. Similar to “taggable carcasses” during mark-recapture data collection methods, biological data (i.e., FLs, scales) were only collected from “fresh” carcasses during Bright-eye surveys.

Data Collection – Peak count surveys

In addition to carcass surveys, visual surveys were conducted to count the number of live spawning Chinook in the NF Lewis. Counts coincided with the presumed peak spawn time period for both

tule and bright fall-run Chinook. From 2013 - 2017, two to three counts were conducted for tules in October (generally the 2nd, 3rd, and 4th week of October) and brights in late November to early December (generally 3rd and 4th week of November and 1st week of December) for a total of four to six counts annually. Counts were performed by surveyors in boats and all five sections were surveyed during each count (Table 1). During the early (tule) counts when abundance was low, live fish were typically enumerated at the same time carcasses were being recovered and both live counts and carcass sampling was completed with one boat. During the late (bright) counts when abundance was high, live fish were enumerated separately from carcass surveys. For the bright counts, surveys began in the morning at the top of section #1 and two boats simultaneously counted live Chinook and redds while slowly motoring downstream to the bottom of section #5 (Figure 1). Counts of live fish were separated into jacks and adults by section based on a visual approximation of lengths greater or less than ~60 cm FL. Crews also collected waypoints of spawning aggregations to document spawning distribution. During the bright surveys, counts and carcass surveys were generally conducted on the same day. Therefore, the live count surveys corresponded with the drawdown from Merwin Dam that reduced flows in the lower river and increased visibility.

Data Management

Field data were recorded on a combination of scale cards and a whiteboard. Individual carcasses that were bio-sampled and/or tagged had their corresponding data (collection area, tag number, fork length, carcass condition, scales, etc.) recorded on the front of a scale card. Each column represented one carcass and each card held approximately 20 samples. Information regarding survey date, section number, sample rate, and the number of carcasses sampled was recorded on the back of the scale card. Tag numbers from carcass recoveries and the number of non-taggable (“mark sample only”) carcasses were recorded on the whiteboard. Specific details on field data recording methods and terminology can be found in the WDFW’s “Stream Survey Manual” (WDFW 2018). At the end of each survey day, the number of non-taggable carcasses was tallied and recorded by survey reach in the “plus count” field on the back of a single scale card. Field data were entered into WDFW’s Traps, Weirs, and Surveys (TWS) Access database as well as a separate Excel spreadsheet throughout the survey season. Entered data were QA/QC at the end of the season and any errors or missing information were corrected. Fish scales and CWT samples/recoveries are processed by WDFW laboratories in Olympia, WA. Specific details describing how scales and CWTs are processed can be found in Rawding et al. (2014: page 12).

Data Analysis – Mark-recapture Jolly-Seber (JS) abundance estimates

The abundance of fall-run Chinook adult spawners (i.e., escapement) in 2013 – 2017 was estimated using a Jolly-Seber (JS) open population estimator (Seber 1982, Pollock et al. 1990) using a Bayesian modeling approach. Specifically, we used the “super-population” JS model that was developed by Schwarz et al. (1993) for estimating salmon spawning escapement using mark-capture methods. The super-population JS model built upon previous mark-recapture modeling work by Crosbie & Manly (1985) and Sykes & Botsford (1986). A conceptual diagram of the super-population model and its main components is shown in Figure 4 and detailed summary statistics and equations for the JS model can be found in Appendix B.

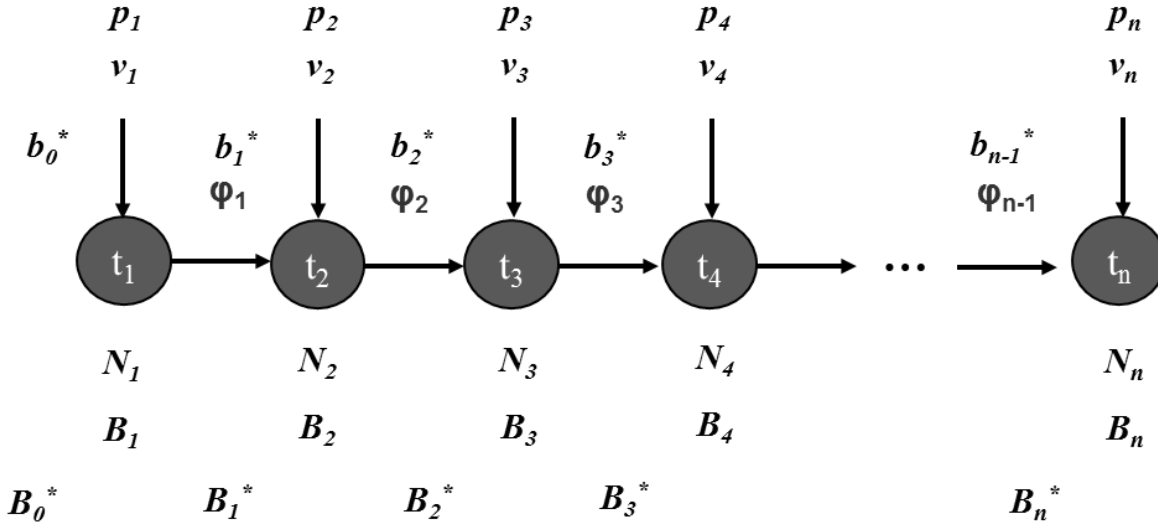


Figure 4. Conceptual diagram of "super population" Jolly-Seber abundance model developed by Schwarz et al. (1993) – diagram adapted from Schwarz and Arnason (2006). Fundamental parameters of the model include: sample period i (t_i), probability of capture at sample period i (p_i), probability that a carcass captured at time i will be released, opposite of a loss-on-capture (v_i), probability that a carcass enters the population between sample periods i and $i+1$, which is referred to as probability of entry (b_i^*), and the probability of a carcass persisting between sample periods i and $i+1$ (φ_i). Derived parameters of the model include: population size at sample period i (N_i), number of fish that enter after sample period i and survive to sample period $i+1$ (B_i), and number of fish that enter between sampling period $i-1$ and i , these are referred to as gross births (B_i^*). Total abundance is calculated as the sum of B^* over all sample periods.

The super-population JS model has been previously implemented by Rawding et al. (2014) to estimate the abundance of fall-run Chinook in the lower Columbia River. Rawding et al. (2014) provide a comprehensive description of the super population JS model, including summary statistics, fundamental parameters, derived parameters, and likelihoods is provided in Rawding et al. (2014). Overall, our analytical methods mirrored those used by Rawding et al. (2014) except in how we estimated the composition of the run (i.e., total abundance stratified by stock, origin, sex, and age) – see below. Briefly, the super-population JS model estimates total spawner escapement by summing “newly arrived” carcasses (i.e., gross births – B^*) that enter the study system over the entire survey period. This estimate of new carcasses includes both the number of carcasses that were present (i.e., available to sample) during each sampling period as well as the number of carcasses that arrived after a particular sampling period but were lost/removed (e.g., washed out) before the subsequent sample period.

The number of new carcasses (B^*) is a derived parameter from the JS model, which is based on a three-part likelihood equation:

$$Likelihood = Pr(\text{first capture}) \times Pr(\text{loss on capture}) \times Pr(\text{subsequent recaptures})$$

where (1) the first component is the probability of first capture based on a super population (N) that enter the population (b_i^*) following a multinomial distribution, (2) the second component is the probability of release on capture (v_i) from a binomial distribution using total fish sampled (n_i)

and the number of n_i that are released (R_i) versus removed (i.e., loss-on-capture), and (3) the last component is the probability of recapture which is the product two binomial distributions to estimate the probability of survival (i.e., carcass remains available to sample) and probability of capture (i.e., catchability based on sampling conditions and characteristics of carcass).

Each year, we summarized the carcass survey data, tested model assumptions, and generated estimates of abundance following a serial approach. First, carcass data for an individual survey year were queried from the TWS Access database and ran through a standardized set of summarizations based on field sampled biological data. These summarizations first classified each sampled carcass by stock (tule, bright) using CWT recoveries, origin (hatchery, wild) using adipose-fin status and CWT recovery, and age (ages 2 – 6) using scale-pattern analysis. These bio-data were then summarized by sample period and these summaries were subsequently used to apportion the JS abundance estimates (see below). Second, we evaluated annual recapture probabilities by sex and size using logistic regression (Link and Barker 2006). The results of these tests influenced how carcass data were stratified (i.e., grouped; see below). Third, capture histories were generated for each individual carcass and JS summary statistics were generated by survey period using the *RMark* package (Laake 2013) implemented through the program R (R Development Core Team 2011). Only tagged individuals or carcasses with a Carcass Category of 3 or 4 were used in the analysis. Fourth, we evaluated the fit of four potential abundance models using Bayesian Goodness-of-Fit (GOF) tests using posterior predictive checks (Gelman et al. 1996). The four JS models that were evaluated included a combination of static (s) or time-varying (t) probabilities of capture (p), persistence/survival (ϕ), and entry (b^*) among survey periods/weeks (i.e., ttt , stt , tst , sst). Note that the third “t” is for the probability of entry, which was always modeled as a time-varying parameter due to intra-annual variation in spawn timing among individuals. Inputs for the JS models are listed in Appendix C.

Based on the results of the logistic regression and GOF tests within and among years, we chose to standardize our modeling procedure across years. First, we stratified the carcass data into three groups – jacks (i.e., small males), females, and males (i.e., larger males) – and generated period-specific estimates of abundance (B^*) for each of the three groupings using the completely time-varying JS estimator (i.e., ttt model). Second, we partitioned the period-specific B^* estimates by stock (tule, bright), origin (wild, hatchery), sex (jack, female, male), and age using period-specific summarized bio-data. Specifically, we partitioned stock using the ratio of CWT recoveries from out-of-basin hatchery tules to Lewis River wild brights, origin using adipose-fin status (clipped, unclipped) from all sampled carcasses, and age using scale-age reads from sampled carcasses. Combinations of stock, origin, and sex were estimated by multiplying probabilities based on binomial distributions while age was estimated with a multinomial distribution. Third, total estimates for a specific compositional grouping (e.g., hatchery tules) were generated by summing all of the period-specific estimates across the three groups.

Again, our overall modeling approach was the same as in Rawding et al. (2014) except in how we partitioned the B^* estimates. Specifically, Rawding et al. (2014) would have summed the all of the B^* estimates for each group and then partitioned the total estimate (N) using the “pooled” bio-data (i.e., bio-data summed across the entire run) for that group. The approach used by Rawding et al. (2014) assumes there is no run-timing variation in the composition of the overall population

whereas our approach allows for run-timing variation and essentially weights the bio-data by the relative proportion of the run. If there is no variability in the composition of the population based on run-timing and/or variability in capture probabilities among sample periods, the two approaches will produce the same results. However, if there is variability in the composition of the population based on run-timing and/or variability in capture probabilities then the “pooled” bio-data partitioning approach may produce biased estimates. Ultimately, the appropriate approach will depend on partially on bio-data sample sizes. Because the NF Lewis bio-data sets were generally large, we were able to partition the bio-data by individual sample periods. This may not be the case for other (smaller) populations.

The Jolly-Seber (JS) models were parameterized using a Bayesian framework. Parameters were estimated from the posterior distribution, which was calculated as the product of the prior distribution and the probability of the data given the model or likelihood (Gelman et al. 2004). A vague “Bayes-LaPlace” uniform prior was used for the probability of capture (ρ), the probability of persistence (ϕ), the probability that a carcass was released (v), and the JS abundance calculations. A Dirichlet prior, with values of 1, was used for the probability of entry (b^*). The weekly proportions of race and origin were estimated based on a Binomial distribution with a Haldane prior (Beta[0.01,0.01]). The weekly age proportions were estimated based on a Multinomial distribution with a Dirichlet prior set to 0.01. The Haldane prior places most of its weight near 0 or 1 and provides a more robust estimate when proportions are near 0 or 1, which occurred for race, origin, and age in our analysis. Samples from the posterior distribution were obtained using Markov chain Monte Carlo (MCMC) simulations (Gilks 2005) in WinBUGS (Lunn et al. 2000) using the *R2WinBUGS* package (Sturtz et al. 2005). WinBUGS implements MCMC simulations using a Metropolis Gibbs sampling algorithm (Spiegelhalter et al. 2003). We ran two chains with the Gibbs sampler with an appropriate number of iterations and burn-in period so that the number of independent samples, as measured by effective sample size (ESS), was approximately 4,000 for each parameter of interest. An ESS of 4,000 provides a 95% credible interval (CI) that has posterior probabilities between 0.94 and 0.96 (Lunn et al. 2012). Initial values for each chain were automatically generated within the WinBUGS package. Modeled converged was based on visual assessment of traceplots for chain mixing and evaluation of the Brook-Gelman-Rubin (BGR) statistic (Su et al. 2001; $Rhat < 1.05$). For each of our reported estimates, we ensured that convergence was achieved and therefore assumed that our reported posterior distributions were accurate and represent the underlying stationary distributions of the estimated parameters.

When the assumptions of a super-population JS model are met, this estimator produces unbiased estimates of escapement with known levels of precision and is robust to minor assumption violations (Schwarz et al. 1993). Within the JS model, there are specific assumptions as to how recruitment (i.e., newly arrived carcasses) is modeled, but overall there are a total of four critical assumptions for open population models that must be met to obtain unbiased estimates (Seber 1982):

1. *Equal Catchability*: Each carcass that is present in the study system during a specific sample event, whether tagged or untagged, has the same probability of being sampled

2. *Equal Persistence*: Each carcass that is present in the study system during a specific sample event, whether tagged or untagged, has the same probability of survival (i.e., persisting in the study area to following sample period)
3. *Tag Loss and Recovery*: Tagged carcasses do not lose their marks and all marks are recognized and read properly on recovery
4. *Instantaneous Sampling*: All samples are instantaneous, i.e., the sampling time is negligible and each release is made immediately after the sample

Data Analysis – Bright-eye method (BEM) abundance estimates

Since 2002, the Bright-eye method (BEM) has been used to estimate the annual abundance of fall-run Chinook spawners. The BEM is similar in concept to the “sequential” estimator that was developed and implemented in Hawkins et al. (2003a, 2003b, 2004) in that abundance estimates are based on weekly carcass recoveries and a pooled expansion factor. However, the BEM is an age-stratified estimator that estimates annual abundance using (1) an adjusted count of weekly carcass recoveries from each survey year, and (2) a constant set of recovery and sample rates that were derived from the mark-recapture carcass tagging surveys conducted in 2001 and 2002 (Table 3).

Estimates of total abundance and composition for NF Lewis River fall-run Chinook were generated using the BEM in four sequential steps. First, the total number of recovered carcasses were summarized by survey week based on the presumed spawn week of each individual fish. This process was done separately for carcasses based on their carcass condition (fresh vs. mark sample - “MS” - only). Because “MS only” carcasses are recovered in a more deteriorated condition, these fish were presumed to have been recovered more than one week after spawning. Therefore, MS only carcasses were adjusted (i.e., assigned back) back to their presumed spawn week based on an average recovery rate of carcasses post-death. For example, during September and October surveys, approximately 80% of fresh carcasses are recovered one-week post tagging and 20% are recovered after two weeks post tagging. Therefore, if 100 MS only carcasses were recovered in survey period #3, 80 carcasses were assigned back to survey period #2 and 20 were assigned back to survey period #1. Based on their definition, fresh carcasses were assumed to have spawned and died in the same week they were recovered and therefore no adjustment was needed. Additionally, if sub-sampling occurred in a particular survey week, the number of fresh carcasses sampled was expanded by the weekly sub-sampling rate.

Second, carcass recoveries were apportioned by age class based on a weekly derived age-distribution separated by sex using scale samples collected from fresh carcasses. This process was done separately for carcasses based on their carcass condition (fresh vs. MS only). Fresh carcasses were directly apportioned based on the weekly sampled age-distribution. For example, if 100 fresh carcasses recovered in a week and age-distribution based on scale-age read from fresh carcasses was 10% age-2, 20% age-3, 40% age-4, and 30% age-5 then the estimated number of age-specific recoveries would have been 10, 20, 40, and 30, respectively. The MS only carcasses were also apportioned based on the weekly age-distribution from fresh carcasses. However, because MS only carcasses were older and thus had been subject to age-specific selectivity longer, the number of MS only recoveries were also “adjusted” by the age-specific recovery rate (Table 3). For

example, if 100 MS only carcasses were recovered in a week and the estimated age-distribution of fresh carcasses was 10% age-2, 20% age-3, 40% age-4, and 30% age-5 then the “adjusted” age-specific MS only recoveries would have been approximately 4, 19, 40, and 37, respectively. Specifically, the number of age-2 MS only carcasses was calculated by: 100 (sampled MS carcasses) \times 10% (age-distribution of age-2s) \times 13% (recovery rate of age-2s) \times 100 (sampled MS carcasses) \div 31.8 (total number of relative carcass recoveries across all ages). Weekly carcass recoveries for each group (fresh, MS only) were summed to get a total number of recovered carcasses by age across the entire survey year.

Table 3. Average age-stratified carcass tag recovery and sample rates used for the Bright-eye method (BEM) that were derived from mark-recapture carcass tagging surveys conducted in 2001 and 2002 (see Hawkins 2012).

Parameter	Age-2	Age-3	Age-4	Age-5	Age-6
Recovery Rate	0.13	0.30	0.32	0.39	0.54
Sample Rate	0.2290	0.5037	0.5837	0.7083	0.8263

Third, total escapement estimates were derived by age for each survey year. The total number of recovered carcasses were expanded to an escapement estimate using a constant set of age-specific sample rates that were derived from the carcass tagging surveys in 2001 and 2002 (Table 3). The age-specific sample rates are based on the age-specific recovery rates, but in essence account for the open population characteristics of the carcasses in the NF Lewis River (i.e., carcass immigration, persist/survive, and then emigrate). For instance, if the estimated recovery rate for age-2 Chinook was 0.13 then the estimated sample rate would have been approximately 0.24. This can be illustrated by the following example: across the entire survey season, a total of 100 carcasses were tagged and 13 were recovered, the calculated recovery rate would be estimated to be 0.13. Therefore, the total estimated number of carcasses (in the NF Lewis) would have been approximately 769 ($100 \div 0.13$) and over the entire survey season a total of 87 untagged carcasses would have been sampled ($769 - 100$ tagged = 669 untagged \times 0.13 = 87 sampled). Thus, over the entire survey season, a total of 187 carcasses would have been sampled or rather 0.24 of the true total of 769. Age-specific sample rates can be calculated for any given recovery rate using this same logic. The age-specific sample rates were slightly modified when the BEM estimator was originally “calibrated”. For example, this slight calibration is why the sample rate for age-2 carcasses was 0.229 as opposed to 0.24 for a recovery rate of 0.13 (Table 3).

Lastly, total estimates of abundance were stratified by stock (tule, bright) and origin (wild, hatchery). Estimates of abundance by stock were based on the general timing of wild CWTs recoveries (i.e., wild Chinook that were tagged with a CWT as a juvenile, assumed to be bright-run Chinook, and subsequently recoveries on the spawning ground 2 – 6 years later). In general, carcasses recovered before the second week of November were assigned as tules while carcasses recovered after the second week of November were assigned as brights. Origin was based on both the timing (i.e., survey week) of recovery and the adipose fin-clip status (AD intact = wild, AD removed = hatchery) of recovered carcasses. Carcasses recovered prior to the second week of

November were assigned an origin based on their adipose fin-clip status while carcasses recovered after the second week of November were assumed to be all wild.

Abundance estimates derived using the BEM require two stringent set of assumptions:

1. *Equal Catchability*: Each carcass has a constant probability of capture (i.e., probability that a carcass is sampled given that it is present in the study system) for a given age-class across all survey periods within a year AND that probability is equal to the average capture probability estimated from mark-recapture data collected in 2001 and 2002.
2. *Equal Persistence*: Each carcass has a constant probability of survival (i.e., persisting in the study area to following sample periods) for a given age-class across all survey periods within a year AND that probability is equal to the average survival probability estimated from mark-recapture data collected in 2001 and 2002.

Data Analysis – Peak count expansion (PCE) estimates

We developed a hierarchical Bayesian model to derive peak count expansion (PCE) factors by stock (tule, bright) using our JS estimates of abundance and peak count (PC) carcass survey data collected from 2013 – 2017. These PCE factors were then used to subsequently generate PCE estimates of abundance for NF Lewis River tule-, bright-, and total fall-run Chinook.

Since 2000, carcass surveys have been completed almost every single week from early Sept through late December each year while the collection of live spawner count data has been more sporadic. In general, from 2000 – 2012, live counts have only been conducted for bright-run Chinook and the counts were typically conducted in early November. From 2013 – 2017, live counts were generally conducted 2 – 3 times per year for both tules and brights for a total of 4 – 6 surveys per years. However, live count surveys were not always completed due to adverse sampling conditions. For example, in 2015, live count surveys were not completed for brights and, in 2016, live counts did not correspond with the anticipated peak for tules.

Therefore, based on the historical live and dead count data, we decided to summarize PC data, and thus calculate PCE factors and estimates of abundance, three separate ways. First, we calculated the “peak lives + deads”, which corresponded to the highest weekly count of carcasses and live spawners combined (i.e., the summation of lives and deads in the same week). Second, we calculated the “peak deads”, which corresponded to the maximum weekly count of carcasses. Third, we calculated the “top 3 deads”, which corresponded to the summation of the three highest weekly counts of carcasses across the sample periods of interest. Across all years, we only used peak count data that were collected during the same anticipated 5 – 6 week peak spawning time period, which corresponded from the first week in October through the first week in November for tules and from the second week in November through the second week in December for brights. We chose to use the “top 3” counts instead of summation of counts across all 5 – 6 periods (per stock) in order to facilitate computation in years when counts were not conducted across all weeks (e.g., missed survey due to poor conditions). Inputs for the PCE estimators are listed in Appendix D.

To fit our PCE model, we started by visually examining the posterior distribution of the JS abundance estimates and fitting a normal, log-normal, and gamma distributions to the draws of the posteriors. Based on these plots and the fits of each distribution, the log-normal distribution provided the best fit. Therefore, before fitting the PCE model, we converted the mean and standard deviation of the posterior of each observed JS abundance estimate into a log-normal mean and standard deviation using:

$$\mu_{\log n_{i,j}} = \log(\mu_{n_{i,j}}) - \frac{1}{2} \log\left(\frac{\mu_{n^2_{i,j}} - \sigma_{n^2_{i,j}}}{\mu_{n^2_{i,j}}}\right) \quad (1)$$

$$\sigma_{\log n_{i,j}} = \sqrt{\log\left(\frac{\mu_{n^2_{i,j}} - \sigma_{n^2_{i,j}}}{\mu_{n^2_{i,j}}}\right)} \quad (2)$$

where μ_n was the mean and σ_n was the standard deviation of the posterior draws of JS abundance estimate n for stock i and year j (Hobbs and Hooten 2015). The observed JS abundance estimates were then used in the following observation model (likelihood):

$$\mu_{\log n_{i,j}} \sim \text{Normal}\left(\log(N_{i,j}), \sigma_{\log n_{i,j}}\right) \quad (3)$$

where the log-normal posterior mean of the JS abundance estimate $\mu_{\log n_{i,j}}$ was normally distributed around the log of the predicted abundance N based on a hierarchical peak count expansion. The predicted abundance based on a hierarchical peak count expansion that was defined by:

$$N_{i,j} = PCE_{i,j} * PC_{i,j} \quad (4)$$

where PCE was the estimated peak count expansion factor and the PC was the peak count of carcasses. The PCE expansion factors were estimated by:

$$PCE_{i,j} = \frac{1}{PCP_{i,j}} \quad (5)$$

Where PCP was the proportion of the total abundance that was counted as part of the peak count. Each peak count expansion factor was estimated based on a hierarchical prior:

$$\text{logit}(PCP_{i,j}) \sim \text{Normal}\left(\mu_{\text{logit}PCP_i}, \sigma_{\text{logit}PCP_i}\right) \quad (6)$$

where the logit of each PCP was modeled as a random variable that was normally distributed around a hierarchical mean $\mu_{\text{logit}PCP}$ with standard deviation $\sigma_{\text{logit}PCP}$. The parameters of the hierarchical prior were then given hyper priors:

$$\mu_{\text{logit}PCP_i} \sim \text{Normal}(-0.75, 0.75) \quad (7)$$

$$\sigma_{\text{logit}PCP_i} \sim \text{Normal}(0, 0.5) \text{ Truncated}[0,] \quad (8)$$

Finally, we generated predictive distributions for the PCE and PCP factors in an unknown year using equations (5) and (6), respectively, and abundances estimates for each year peak counts were available based on these predictive PCEs using equation (4).

The peak count expansion (PCE) model was estimated using a Bayesian framework. Samples from the posterior distribution were obtained using Markov chain Monte Carlo (MCMC) simulations (Gilks 2005) in JAGS (Plummer 2003) using the *R2jags* package (Su and Yajima 2009). We ran four chains with 500,000 iterations, a burn-in period of 250,000, and a thinning rate of 250 so that the number of independent samples, as measured by effective sample size (ESS), was approximately 4,000 for each parameter of interest. Initial values for each chain were automatically generated within the JAGS package. Modeled convergence was assessed in the same manner as the JS models (i.e., assessment of ESS and BGR statistics).

The following is a list of the critical assumptions for the PCE method (Rawding and Rodgers 2013):

1. The entire spawning distribution is surveyed, or if the entire spawning distribution is not surveyed, the proportion of fish using the index area is the same as it was in the years used to develop the peak count expansion factor
2. The proportion of spawners available for counting as lives or carcasses on the peak survey date(s) is the same as it was in the years used to develop the peak count expansion factor
3. Observer efficiency is similar in all years

Comparison of abundance estimators

We evaluated the estimates of tule, bright, and total fall-run (tule and bright combined) Chinook abundance generated from the Bright-eye method (BEM) and peak count expansion (PCE) estimators by calculating the absolute difference, absolute percent (%) error, mean absolute percent error (MAPE) relative to the Jolly-Seber (JS) estimates using the following formulas:

$$\text{Absolute Difference} = X - JS \quad (9)$$

$$\text{Absolute \% Error} = \frac{|X - JS|}{JS} \times 100 \quad (10)$$

$$\text{Mean Absolute \% Error} = \left(\frac{1}{n} \sum \frac{|X - JS|}{JS} \right) \times 100 \quad (11)$$

Where X is an abundance estimate derived using either the BEM or PCE estimator, $| |$ denotes that absolute difference between the BEM or PCE abundance estimate and the JS estimate, and n is the total number of paired estimates.

Results

Mark-recapture Jolly-Seber (JS) abundance estimates

Mark-recapture carcass tagging surveys were conducted for fall-run Chinook in the North Fork (NF) Lewis River for return years 2013 – 2017. Among years, fall-run Chinook surveys began in mid- to late September and continued for 15 to 21 weeks through mid-January to early February. Within a survey year, approximately 7,000 to 15,000 carcasses were recovered (i.e., sampled) of which approximately 2,000 to 3,000, or rather 20 – 40%, were tagged to evaluate seasonal recovery rates (Table 4). Across all years, the total (i.e., pooled) recovery rate of carcasses was estimated to be 41%, but recovery rates varied among years (Table 5). For instance, recovery rates in 2015 were approximately half of those in all other years. Recovery rates also varied among carcass grouping (Table 5). Specifically, the recovery rate of the jack-group carcasses (males <60 cm), which included a mixture of age-2 and age-3 males, was approximately half of that for females and males (≥ 60 cm).

Table 4. Summary of fall-run Chinook mark-recapture carcass surveys conducted in the NF Lewis River, 2013 - 2017. The survey start date reflects the week when the first fall-run Chinook was sampled.

Year	Start Date	End Date	Number of Survey Weeks	# of Carcasses Tagged	# of Carcasses Sampled	% of Sampled Carcasses Tagged
2013	9/12/2013	2/4/2014	21	3,417	11,984	29%
2014	9/11/2014	1/13/2015	19	2,954	14,680	20%
2015	9/23/2015	1/7/2016	15	2,060	9,957	21%
2016	9/22/2016	1/10/2017	17	2,839	7,170	40%
2017	9/27/2017	1/10/2018	16	2,109	4,712	45%

Mark-recapture data were analyzed using a Jolly-Seber (JS) open population mark-recapture estimator. Assumptions of this model were tested prior to generating abundance estimates to ensure unbiased results. The first two (of four) assumptions regarding equal catchability and survival of carcasses were evaluated using logistic regression and Bayesian Goodness-of-Fit (GOF) tests within and among years. Logistic regression tests generally concluded that jacks (males <60 cm), females, and males (≥ 60 cm) carcasses had statistically different recapture rates among years due to differences in body size. The Bayesian GOF tests concluded that while simpler JS models (*tst*, *stt*, *sst*) sometimes provided adequate fit for a particular carcass group (jacks, females, males) within a year, the completely time-varying (*ttt*) model always provided an adequate fit (i.e., $0.025 < \text{Bayesian } p\text{-value} < 0.975$) for all groups among all years. Therefore, we standardized our modeling approach by generating separate estimates of abundance for the three carcass groups (jack, female, and male) within the same model using a JS estimator with a time-varying probability of capture (p), survival (ϕ), and entry (b^*) among survey periods/weeks. The third assumption regarding tag loss was assessed through double tagging of carcasses. Across all years, >97% of carcasses were recaptured with both tags meaning that <0.1% of carcasses would have lost both tags assuming individual tag loss is independent. Therefore, tag loss had a negligible effect on the final estimates and was not adjusted for. Proper reporting of recovered tags was not

directly measured in the field, but careful training, use of experienced staff, development of data collection protocols, and standardized datasheets minimized concern that this assumption was violated. The final assumption, regarding instantaneous sampling, was met by sampling almost every week throughout the survey season and by minimizing the survey duration (1-2 days) relative to the duration between surveys (5-6 days).

Across the five survey years, total mean estimates of fall-run Chinook salmon abundance in the NF Lewis River ranged approximately from 10,000 to 27,000 with tule- and bright-run estimates ranging approximately from 2,700 to 6,300 and 7,600 to 22,000, respectively (Table 6 – Table 10; Figure 5). The total fall-run and bright-run Chinook estimates of abundance had derived coefficient of variations (CV) ranging from 2 – 6% among years. Abundance estimates for tule-run Chinook had CVs ranging from 10 – 24%. Among years, the tule portion of the overall fall-run comprised on average 23% (range 18 – 31%) of the total abundance. In general, tule carcasses were recovered on the spawning grounds from late September through the first week in November with a peak in abundance in mid-October while bright carcasses were recovered from late October through January with the main peak in mid-November to early December and a second, smaller peak in mid- to late December (Appendix E). The second peak during the bright run-timing period corresponds to a sub-stock of brights referred to as “late-bright” by WDFW biologists but is not a formally recognized as a distinct stock of fall-run Chinook. Although there are no fall-run Chinook hatchery plants in the Lewis River, 30 – 64% of recovered tules were of hatchery-origin that had strayed from other lower Columbia River watersheds (Table 11).

Fall-run Chinook return back to the NF Lewis River to spawn between the age of 2 and 6, but the majority of the run in any given year is made up of age 3, 5, and 5-year-olds. The distribution of jacks (age-2 males), females, and males (age-3 to age-6) was relatively similar among tules and brights and across years with typically 1 – 4% of the run comprised of jacks, 40 – 50% males, and 50 – 60% females. The relative age-distribution of tules versus brights was similar among years, but the absolute age-composition was quite variable (Figure 6). Specifically, tules typically had higher proportions of age-3s, similar proportions of age-4s, and lower proportions of age-5s relative to brights for a particular return year. However, Chinook from brood-year 2010 returned at high rates resulting in higher proportions of age-3s in 2013, age-4s in 2014, and age-5s in 2015 relative to most other years for both tules and brights. For instance, approximately 80% of the 2014 run was comprised of age-4s while in all other years age-4s made up approximately 40 – 60%.

Table 5. Summary of mark-recapture recovery data for fall-run Chinook carcass surveys conducted in the NF Lewis River in years 2013 - 2017.

Year	Group	# of Carcasses Tagged	# of Tagged Carcasses Recovered	Average Recovery Rate
2013	Jack	667	206	31%
	Female	1,410	691	49%
	Male	1,339	611	46%
	Total	3,416	1,508	44%
2014	Jack	435	120	28%
	Female	1,610	763	47%
	Male	909	397	44%
	Total	2,954	1,280	43%
2015	Jack	156	13	8%
	Female	1,135	270	24%
	Male	769	220	29%
	Total	2,060	503	24%
2016	Jack	136	26	19%
	Female	1,650	762	46%
	Male	1,053	479	45%
	Total	2,839	1,267	45%
2017	Jack	53	10	19%
	Female	1,444	705	49%
	Male	612	268	44%
	Total	2,109	983	47%
Total	-	13,378	5,541	41%

Table 6. Estimates of abundance (i.e., escapement) and composition for return-year **2013** fall-run Chinook in the NF Lewis River by stock (tule, bright), origin (hatchery, wild), and age.

Stock	Origin	Age	Mean	SD	L.95%	Median	U.95%	CV
Tule			3,511	462	2,642	3,495	4,533	13%
	Hatchery		1,156	171	898	1,133	1,553	15%
		2	47	35	13	36	141	76%
		3	323	67	227	312	484	21%
		4	680	100	525	667	918	15%
		5	100	27	62	95	167	27%
		6	7	5	2	6	20	70%
	Wild		2,355	348	1,665	2,355	3,066	15%
		2	124	65	47	108	290	53%
		3	711	130	485	702	1,007	18%
		4	1,314	200	910	1,321	1,704	15%
		5	193	45	119	188	292	23%
		6	12	7	4	11	29	54%
	Prop. Hatchery		0.33	0.03	0.28	0.33	0.40	
	Prop. Wild		0.67	0.03	0.60	0.67	0.73	
	Prop. Jack		0.05	0.03	0.02	0.04	0.11	
	Prop. Female		0.43	0.05	0.34	0.43	0.51	
	Prop. Male		0.52	0.04	0.44	0.52	0.62	
Bright			17,351	450	16,500	17,340	18,300	3%
	Hatchery [†]		328	49	255	322	435	15%
		2	15	4	10	15	24	25%
		3	105	16	81	104	137	15%
		4	158	29	117	154	222	18%
		5	47	7	35	46	63	16%
		6	3	1	1	2	5	42%
	Wild		17,022	428	16,220	17,010	17,910	3%
		2	697	94	540	687	909	14%
		3	5,205	259	4,716	5,197	5,740	5%
		4	7,993	315	7,374	7,986	8,619	4%
		5	2,953	187	2,601	2,950	3,337	6%
		6	172	46	100	166	277	27%
	Prop. Hatchery [†]		0.02	0.00	0.02	0.02	0.02	
	Prop. Wild		0.98	0.00	0.98	0.98	0.99	
	Prop. Jack		0.04	0.01	0.03	0.04	0.05	
	Prop. Female		0.42	0.01	0.40	0.42	0.44	
	Prop. Male		0.54	0.01	0.52	0.54	0.56	
Total			20,862	496	19,990	20,830	21,940	2%

[†] There are no hatchery brights in NF Lewis River. This result is a minor side effect of apportioning JS abundance estimates with raw biological data collected from carcasses (see methods and discussion).

Table 7. Estimates of abundance (i.e., escapement) and composition for return-year **2014** fall-run Chinook in the NF Lewis River by stock (tule, bright), origin (hatchery, wild), and age.

Stock	Origin	Age	Mean	SD	L.95%	Median	U.95%	CV
Tule			4,055	409	3,326	4,027	4,902	10%
	Hatchery		2,051	173	1,757	2,034	2,438	8%
		2	72	47	22	60	196	65%
		3	241	37	177	237	322	15%
		4	1,557	141	1,320	1,541	1,873	9%
		5	178	29	125	175	242	17%
		6	0	2	-	0	4	361%
	Wild		2,005	320	1,449	1,978	2,674	16%
		2	102	55	36	89	241	54%
		3	189	35	130	186	266	18%
		4	1,570	271	1,105	1,547	2,145	17%
		5	143	29	94	141	206	20%
		6	0	1	-	0	3	335%
	Prop. Hatchery		0.51	0.04	0.43	0.51	0.58	
	Prop. Wild		0.49	0.04	0.42	0.49	0.57	
	Prop. Jack		0.04	0.02	0.02	0.04	0.10	
	Prop. Female		0.55	0.05	0.46	0.56	0.65	
	Prop. Male		0.40	0.05	0.32	0.40	0.50	
Bright			20,803	620	19,670	20,780	22,050	3%
	Hatchery [†]		314	58	215	310	438	18%
		2	14	7	7	13	32	47%
		3	27	6	17	26	43	24%
		4	249	48	168	246	352	19%
		5	24	6	13	23	37	27%
		6	0	0	0	0	0	146%
	Wild		20,489	604	19,380	20,460	21,690	3%
		2	837	101	677	824	1,079	12%
		3	1,832	197	1,479	1,821	2,261	11%
		4	16,321	580	15,230	16,300	17,520	4%
		5	1,481	163	1,186	1,473	1,825	11%
		6	12	11	1	9	38	95%
	Prop. Hatchery [†]		0.01	0.00	0.01	0.02	0.02	
	Prop. Wild		0.99	0.00	0.98	0.99	0.99	
	Prop. Jack		0.04	0.01	0.03	0.04	0.05	
	Prop. Female		0.59	0.02	0.56	0.59	0.62	
	Prop. Male		0.37	0.01	0.34	0.37	0.40	
Total			24,859	588	23,790	24,830	26,100	2%

[†] There are no hatchery brights in NF Lewis River. This result is a minor side effect of apportioning JS abundance estimates with raw biological data collected from carcasses (see methods and discussion).

Table 8. Estimates of abundance (i.e., escapement) and composition for return-year **2015** fall-run Chinook in the NF Lewis River by stock (tule, bright), origin (hatchery, wild), and age.

Stock	Origin	Age	Mean	SD	L.95%	Median	U.95%	CV
Tule			5,449	381	4,759	5,440	6,265	7%
	Hatchery		3,437	228	3,031	3,428	3,917	7%
		2	103	48	46	92	224	47%
		3	998	83	845	996	1,179	8%
		4	1,619	133	1,389	1,609	1,898	8%
		5	716	74	581	712	873	10%
		6	1	2	-	0	5	291%
	Wild		2,012	235	1,636	1,985	2,535	12%
		2	61	28	27	54	135	46%
		3	520	63	415	515	659	12%
		4	927	113	745	915	1,184	12%
		5	503	100	361	487	743	20%
		6	1	7	-	0	6	700%
Prop. Hatchery			0.63	0.03	0.58	0.63	0.68	
Prop. Wild			0.37	0.03	0.33	0.37	0.43	
Prop. Jack			0.03	0.01	0.01	0.03	0.06	
Prop. Female			0.56	0.03	0.49	0.56	0.62	
Prop. Male			0.41	0.03	0.35	0.41	0.48	
Bright			18,915	992	17,120	18,850	21,080	5%
	Hatchery [†]		280	74	206	264	481	26%
		2	7	5	3	6	19	68%
		3	39	22	23	34	96	57%
		4	118	37	83	110	209	32%
		5	116	23	85	112	165	19%
		6	0	0	-	0	2	229%
	Wild		18,635	979	16,850	18,580	20,740	5%
		2	347	126	185	320	659	36%
		3	1,869	309	1,388	1,825	2,597	17%
		4	7,888	639	6,741	7,842	9,287	8%
		5	8,440	618	7,291	8,420	9,726	7%
		6	88	91	6	55	335	104%
Prop. Hatchery [†]			0.01	0.00	0.01	0.01	0.03	
Prop. Wild			0.99	0.00	0.98	0.99	0.99	
Prop. Jack			0.02	0.01	0.01	0.02	0.04	
Prop. Female			0.60	0.03	0.54	0.60	0.65	
Prop. Male			0.38	0.03	0.33	0.38	0.45	
Total			24,364	981	22,550	24,310	26,431	4%

[†] There are no hatchery brights in NF Lewis River. This result is a minor side effect of apportioning JS abundance estimates with raw biological data collected from carcasses (see methods and discussion).

Table 9. Estimates of abundance (i.e., escapement) and composition for return-year **2016** fall-run Chinook in the NF Lewis River by stock (tule, bright), origin (hatchery, wild), and age.

Stock	Origin	Age	Mean	SD	L.95%	Median	U.95%	CV
Tule			4,127	482	3,329	4,073	5,225	12%
	Hatchery		2,469	310	1,952	2,435	3,178	13%
		2	49	30	13	41	122	62%
		3	484	84	348	473	675	17%
		4	1,595	208	1,248	1,570	2,067	13%
		5	325	93	193	309	557	29%
		6	12	20	0	5	67	166%
	Wild		1,658	231	1,284	1,627	2,183	14%
		2	33	20	9	28	82	61%
		3	386	87	256	372	601	23%
		4	1,009	140	785	993	1,326	14%
		5	221	66	132	208	381	30%
		6	7	11	0	3	33	160%
Prop. Hatchery			0.60	0.03	0.53	0.60	0.65	
Prop. Wild			0.40	0.03	0.35	0.40	0.47	
Prop. Jack			0.02	0.01	0.01	0.02	0.05	
Prop. Female			0.60	0.05	0.49	0.60	0.70	
Prop. Male			0.38	0.05	0.28	0.38	0.49	
Bright			9,360	243	8,912	9,357	9,863	3%
	Hatchery [†]		48	51	23	35	181	106%
		2	2	1	1	2	6	55%
		3	8	12	3	5	38	163%
		4	29	32	13	21	117	111%
		5	9	11	4	6	29	128%
		6	0	1	0	0	1	250%
	Wild		9,311	229	8,873	9,313	9,763	2%
		2	232	61	135	223	382	26%
		3	1,073	75	931	1,070	1,227	7%
		4	5,481	170	5,146	5,477	5,834	3%
		5	2,320	110	2,112	2,319	2,543	5%
		6	203	37	139	200	282	18%
Prop. Hatchery [†]			0.00	0.01	0.00	0.00	0.02	
Prop. Wild			1.00	0.01	0.98	1.00	1.00	
Prop. Jack			0.03	0.01	0.02	0.02	0.04	
Prop. Female			0.59	0.01	0.57	0.59	0.62	
Prop. Male			0.38	0.01	0.36	0.38	0.41	
Total			13,487	496	12,660	13,440	14,600	4%

[†] There are no hatchery brights in NF Lewis River. This result is a minor side effect of apportioning JS abundance estimates with raw biological data collected from carcasses (see methods and discussion).

Table 10. Estimates of abundance (i.e., escapement) and composition for return-year **2017** fall-run Chinook in the NF Lewis River by stock (tule, bright), origin (hatchery, wild), and age.

Stock	Origin	Age	Mean	SD	L.95%	Median	U.95%	CV
Tule			2,255	450	1,560	2,203	3,258	20%
	Hatchery		1,310	266	910	1,273	1,944	20%
		2	7	5	2	6	21	74%
		3	628	139	414	608	955	22%
		4	466	114	293	450	739	24%
		5	209	59	121	200	349	28%
		6	1	2	-	0	6	396%
	Wild		944	231	603	908	1,508	24%
		2	17	12	4	13	50	73%
		3	410	102	257	395	651	25%
		4	356	112	198	337	635	31%
		5	160	57	78	151	302	36%
		6	1	3	-	0	6	429%
	Prop. Hatchery		0.58	0.04	0.48	0.59	0.66	
	Prop. Wild		0.42	0.04	0.35	0.41	0.52	
	Prop. Jack		0.01	0.01	0.00	0.01	0.03	
	Prop. Female		0.53	0.09	0.36	0.53	0.71	
	Prop. Male		0.46	0.09	0.28	0.46	0.63	
Bright			7,268	355	6,664	7,240	8,084	5%
	Hatchery [†]		118	62	56	106	250	52%
		2	4	3	1	3	14	80%
		3	29	26	10	23	79	90%
		4	57	27	26	50	116	48%
		5	29	13	15	26	58	44%
		6	0	0	0	0	0	-
	Wild		7,149	323	6,579	7,130	7,869	5%
		2	94	28	55	89	163	30%
		3	825	99	646	818	1,041	12%
		4	3,461	196	3,127	3,446	3,889	6%
		5	2,743	135	2,491	2,739	3,022	5%
		6	25	13	8	23	59	52%
	Prop. Hatchery [†]		0.02	0.01	0.01	0.02	0.03	
	Prop. Wild		0.98	0.01	0.97	0.99	0.99	
	Prop. Jack		0.01	0.00	0.01	0.01	0.02	
	Prop. Female		0.68	0.03	0.63	0.68	0.73	
	Prop. Male		0.31	0.03	0.26	0.31	0.36	
Total			9,523	536	8,632	9,470	10,720	6%

[†] There are no hatchery brights in NF Lewis River. This result is a minor side effect of apportioning JS abundance estimates with raw biological data collected from carcasses (see methods and discussion).

Table 11. Summary of unexpanded coded-wire tag (CWT) recoveries in the NF Lewis River by origin (hatchery, wild), release location, and return year along with the percent composition of hatchery recoveries by release location.

Origin	Release Location	2013	2014	2015	2016	2017	% Comp. Average	% Comp. Range
Hatchery	Cowlitz	1	2	3	1	0	11%	0 - 25%
	Kalama	4	13	6	5	1	42%	20 - 48%
	Fallert (Kalama)	3	9	3	1	3	32%	9 - 60%
	Toutle	0	1	0	0	0	1%	0 - 3%
	Washougal	1	1	0	1	0	5%	0 - 11%
	Big Creek (Oregon)	0	0	0	0	1	4%	0 - 20%
	Upper Columbia	0	1	0	1	0	3%	0 - 10%
	California	0	0	0	2	0	4%	0 - 18%
	Total – Low.Colum.	9	26	12	8	5	-	-
Total - Hatchery	9	27	12	11	5	-	-	
Wild	Lewis River	52	84	69	37	29	-	-
Total		61	111	81	48	34	-	-

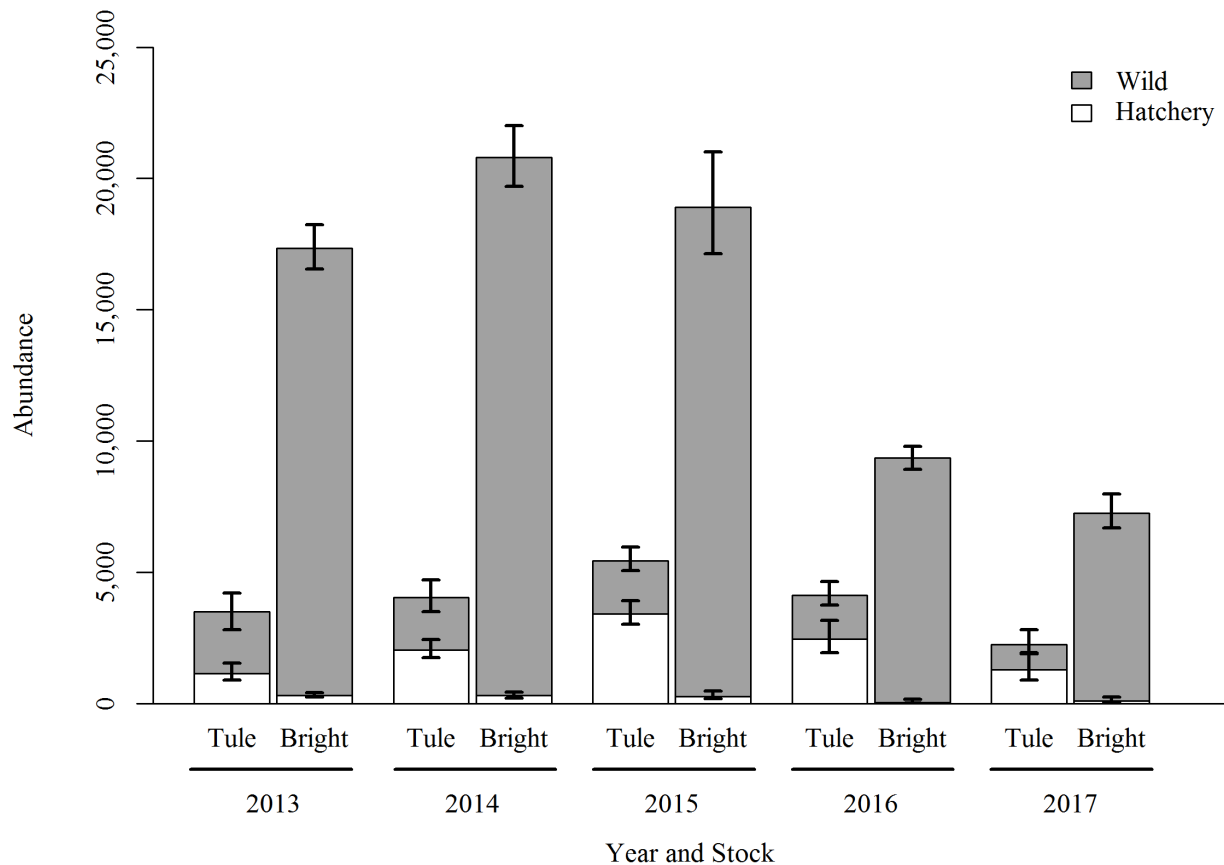


Figure 5. Abundance estimates of NF Lewis River fall-run Chinook salmon by stock (tule, bright) and origin (hatchery, wild) for survey years 2013 – 2017. Bar height is the mean of the posterior distribution from the JS analysis and error bars represent the 95% credible intervals for each stock.

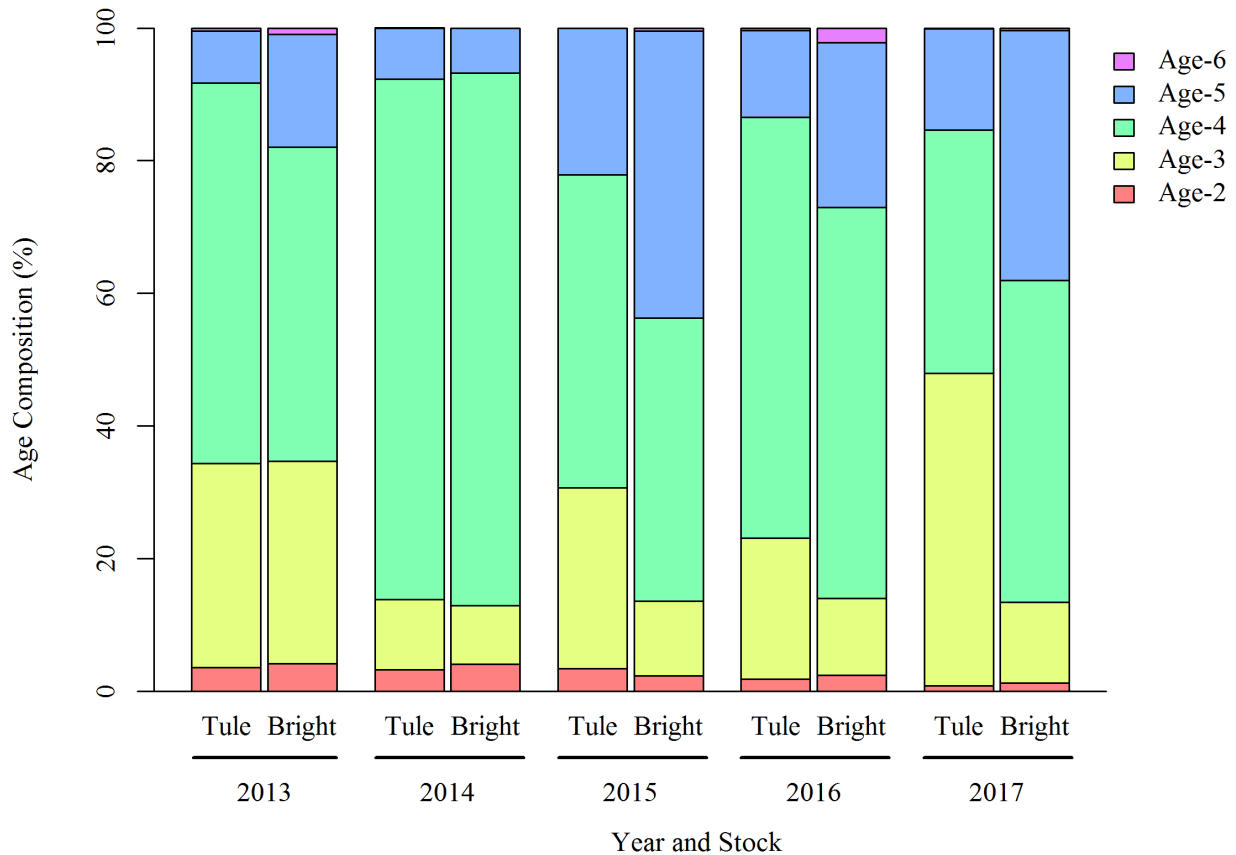


Figure 6. Relative age composition of NF Lewis River fall-run Chinook by stock (tule, bright) and return year.

Evaluation of the Bright-eye method (BEM) estimator

The Bright-eye method (BEM) estimator was developed to estimate annual fall-run Chinook abundance in the NF Lewis River. Estimate of abundance have been derived with the BEM since 2000 and reported in annual reports (e.g., Hawkins 2012). The BEM estimator expands “raw” carcass recoveries to estimates of total abundance using constant age-specific carcass recovery rates (of “fresh” carcasses) that were estimated from a mark-recapture carcass study conducted in the early 2000s. In order for the BEM estimator to generate unbiased estimates of abundance, each recovered carcasses must have the same (i.e., constant) probability of recovery within and among years by age-class. Put another way, the BEM estimator assumes that the recovery rate of carcasses in each weekly survey across all years is always exactly equal to the recovery rates that were estimated in 2001 and 2002 despite potential differences in survey conditions. This assumption was tested by estimating recovery rates within and among years using mark-recapture carcass survey data collected from 2013 – 2017 and comparing these rates with the set of constant BEM recovery rates that were developed with carcass survey data collected in the early 2000s.

First, we calculated the average annual recovery rate by age-class across all years when carcass mark-recapture surveys were conducted (Table 12). Here, the average annual recovery rate was simply the total number of carcass recaptures divided by the total number of carcasses tagged. Overall, the average annual recovery rates by age-class from 2013 – 2017 were relatively similar

to the averaged recovery rates used for the BEM estimator. Specifically, approximately half (13 out of 23) of the age-specific recovery rates from 2013 – 2017 were within ~1 – 5% of the absolute difference in BEM recovery rates. However, there were substantial differences in average annual recovery rates in some years. For example, in 2015, there was a 9 – 18% difference in the absolute recovery rates for the three most dominate age-classes (age-3, 4, and 5). Because recovery rates serve as expansions, the relative difference in recovery rates matter more than absolute recovery rates for the final results. Similar to absolute differences, approximately half (12 out of 23) of the age-specific recovery rates were within 0 – 15% of the relative difference in BEM recovery rates. However, again in 2015, the relative recovery rates were approximately 20 – 90% lower compared to the BEM rates. Therefore, the assumption that recovery rates were constant among years was not meet.

Table 12. Age-stratified carcass recovery rates for “fresh” (i.e., bio-sampled) carcasses in 2001, 2002, and 2013 - 2017. The "Bright-eye" row of data represents the carcass tag recovery rates used for the Bright-eye method (BEM), which was based on data from 2001 and 2002. The “Average” row of data represents “the averaged of the average” recovery rates from 2013 - 2017. Recovery rates were omitted when <10 carcasses were recovered across the entire survey season for a particular age-class.

Year	Age-2	Age-3	Age-4	Age-5	Age-6
2001	0.16	0.34	0.36	0.38	-
2002	0.12	0.25	0.39	0.41	0.75
2013	0.18	0.28	0.32	0.31	0.30
2014	0.19	0.30	0.31	0.29	-
2015	0.11	0.18	0.23	0.21	-
2016	0.11	0.29	0.30	0.34	0.28
2017	0.15	0.23	0.32	0.34	-
Bright-Eye	0.13	0.30	0.32	0.39	0.54
Average ('13 – '17)	0.15	0.26	0.30	0.30	0.29

Second, recovery rates were estimated for each survey period using the estimates of capture and survival probability that were generated from the timing varying (*ttt*) JS model. Specifically, recovery rates were calculated as the product of capture (p) and survival probability (ϕ) for each survey period. Across all five survey years, recovery rates varied throughout the survey season for each of the three estimate groupings (jacks, females, and males). For example, the absolute recovery rates for the male abundance group ranged from 0.07 – 0.31 in 2015 compared to 0.07 – 0.57 in 2016 (Figure 7a). In general, recovery rates within a given year were lower in September, October, and January and were higher in November and December. This seasonal pattern in recovery rates is important given that carcass tags were not deployed uniformly throughout the season (Figure 7b). Rather, the majority of carcass tags were released in November and December, which would result in the overall average recovery rate being weighted towards recovery rates during this time period. Therefore, the BEM assumption that recovery rates are constant within a given survey year was not met.

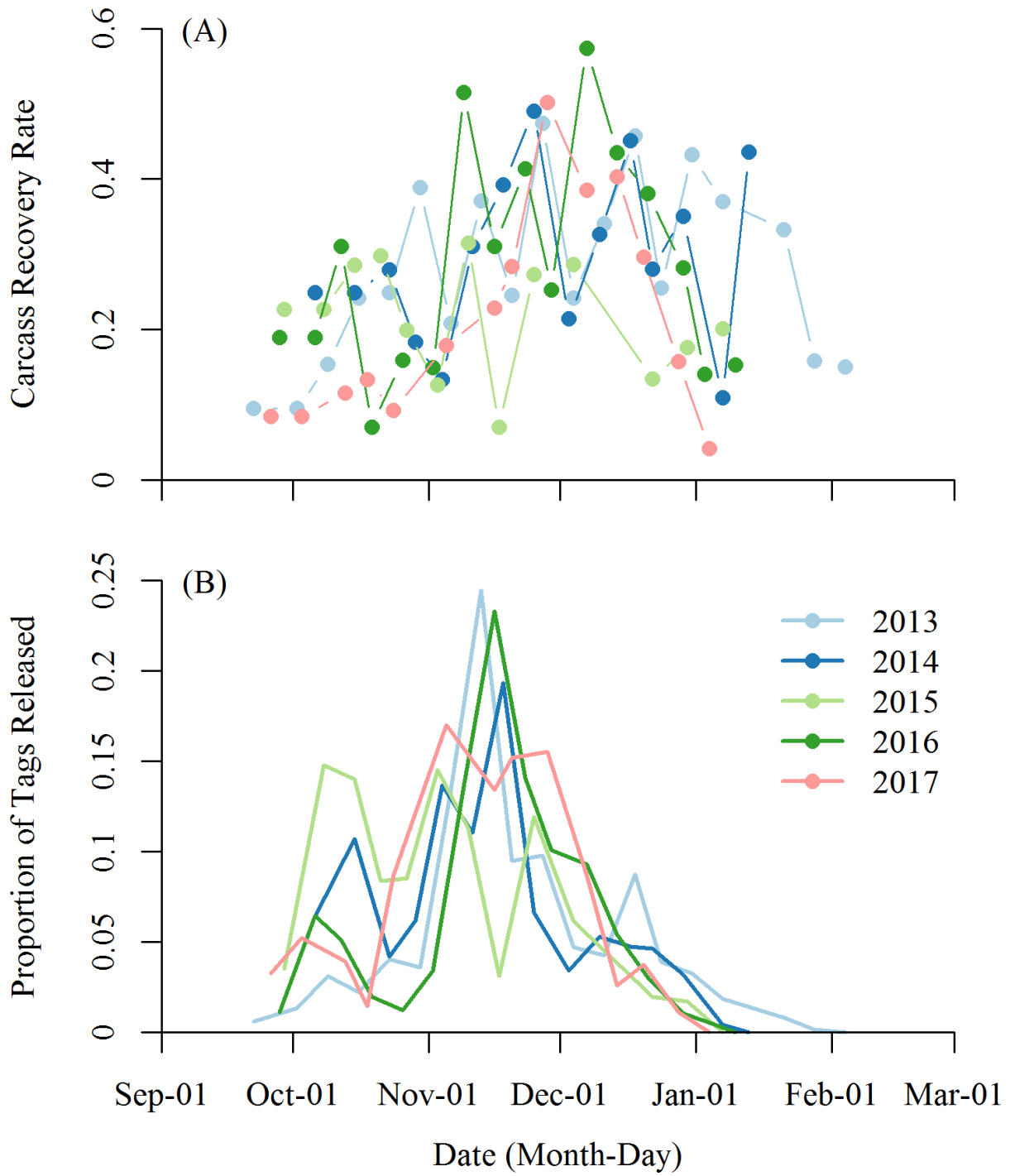


Figure 7. Estimated (A) mean recovery rates and (B) proportion of carcass tags for NF Lewis River fall-run Chinook salmon released by week for males (≥ 60 cm) among years 2013 – 2017.

Evaluation of the peak count expansion (PCE) estimator

Three critical assumptions must be met in order for the peak count expansion (PCE) estimator to generate unbiased abundance estimates. The first assumption was that the spatial distribution of spawners among years was similar to the years used to develop the PCE. This assumption was met given that all five sections (Table 1) were surveyed each year and almost all fall-run Chinook spawning occurs in these five sections.

The second assumption of a PCE estimator was that the proportion of spawners available to sample as either lives or carcasses on the peak survey date(s) was the same as it was in the years used to develop the PCE factor. This assumption was met for the “peak dead” and “top 3 dead” PCE estimators because carcass surveys were completed every week throughout the entire spawn time period and thus all five years of carcass data were used to calculate the PCE factor and derived estimates of abundance. However, this was not always the case with live count data. Specifically, in 2015 and 2016, live counts were not completed during the known peak spawn time period for bright- and tule-run Chinook, respectively. Knowing that the count data from these years did not correspond to the same peak time period in the other years, and thus would knowingly bias our hierarchical PCE factor, we calculated the “live + dead peak” PCE factor excluding these two years of data. Therefore, our “live + dead peak” PCE factor was unbiased but this assumption was violated in 2015 and 2016 for brights and tules, respectively

The third assumption of a PCE estimator was that observer efficiency during carcass and live counts was similar across all surveys. As discussed above, we know that recovery rates of carcasses (i.e., observer efficiency) were not constant within and among years. Although we did not measure observer efficiencies for live counts, we would expect that weekly live count observer efficiencies would track carcass recovery rates due to similar impacts of environmental conditions. Therefore, the third assumption of similar recovery rates within and among years was not met.

Comparison of abundance estimators

In addition to evaluating assumptions of the BEM and PCE estimators, we were ultimately interested in knowing whether or not the two estimators were capable of generating unbiased estimates of fall-run Chinook abundance. Therefore, we calculated the absolute difference, absolute percent (%) error, and mean absolute percent error (MAPE) of the abundance estimates generated with the BEM and PCE estimators relative to the Jolly-Seber (JS) for tule-, bright-, and total fall-run Chinook (Figure 8, Figure 9, Appendix F).

In three of the five survey years (2013, 2014, 2016), the BEM estimator generated a total fall-run Chinook abundance estimate that was within 1,500 fish, or 1 – 7%, of the JS estimates. In the two other years (2015 and 2017), the BEM estimator generated estimates that were approximately 1,500 (16%) and 7,900 (32%) less fish than the JS estimates. Across all years, estimates of tule abundance generated from the two estimators varied by approximately 100 (3%) to 1,900 (55%) fish while estimates of bright abundance varied by approximately 300 (4%) to 8,000 (42%) fish. Overall, the mean absolute percent error (MAPE) was 24% for tules, 14% for brights, and 13% for

total fall-run Chinook (Figure 9). In total, 47% (7 of the 15) of the abundance estimates generated with the BEM estimator did not fall within the 95% credible intervals for the corresponding JS estimate (Figure 8). Therefore, almost half of the abundance estimates generated over the past five years using the BEM estimator were potentially biased due to a violation of the estimator’s main assumption of constant recovery rates within and among years. Based on our comparison with the JS estimates, BEM estimates were more likely to be biased low than high.

Updated peak count expansion (PCE) estimators were developed for tule- and bright-run Chinook using three different peak count (PC) groupings: “peak live + dead”, “peak dead”, and “top 3 dead” (Table 13). Using the PCE factors and PC data, we derived estimates of abundance by stock for 2013 - 2017 (Figure 8, Appendix F). Similar to estimates generated with the BEM estimator, the PCE factors generated some abundance estimates that were relatively accurate in some years while in other years the estimates were highly inaccurate. In general, the accuracy of the estimates derived with the three PCE estimators were relatively similar to one another with mean absolute percentage errors (MAPE) ranging from 26 – 28% for tules, 13 – 18% for brights, and 7 – 10% for total fall-run Chinook (Figure 9), which was similar to the MAPE for BEM estimates. In total, 42% (19 of the 45) of the abundance estimates generated with the BEM estimator did not fall within the 95% credible intervals for the corresponding JS estimate (Figure 8). However, out of the total 45 PCE generated abundance estimates, only two were technically biased (i.e., their 95% prediction interval did not include the “true” JS mean estimate) and these two estimates corresponded to the two years (2015, 2016) when the peak live count did not occur during the anticipated peak time frame. Overall, the PCE derived abundance estimates were mostly unbiased but this was in large part due to the estimates being relatively imprecise. Specifically, the coefficient of variation (CV) of the PCE estimators ranged from 28 – 49% (Table 13).

Table 13. Hierarchical peak count expansion (PCE) factor estimates for tule- and bright-run NF Lewis River Chinook salmon. PCEs were generated using the three peak count data summarizations: the peak lives + deads count, the peak dead only, and the summation of the three largest dead counts per year.

Stock	PCE	Mean	SD	L.95%	Median	U.95%	CV
Tule	Lives + Deads	3.15	1.09	1.91	2.94	5.65	35%
	Deads only	8.86	4.33	3.42	8.15	19.24	49%
	Top 3 Deads	3.81	1.84	1.85	3.44	8.01	48%
Bright	Lives + Deads	4.11	1.22	2.28	3.94	7.21	30%
	Deads only	6.49	2.27	3.33	6.17	11.60	35%
	Top 3 Deads	2.78	0.77	1.82	2.64	4.54	28%

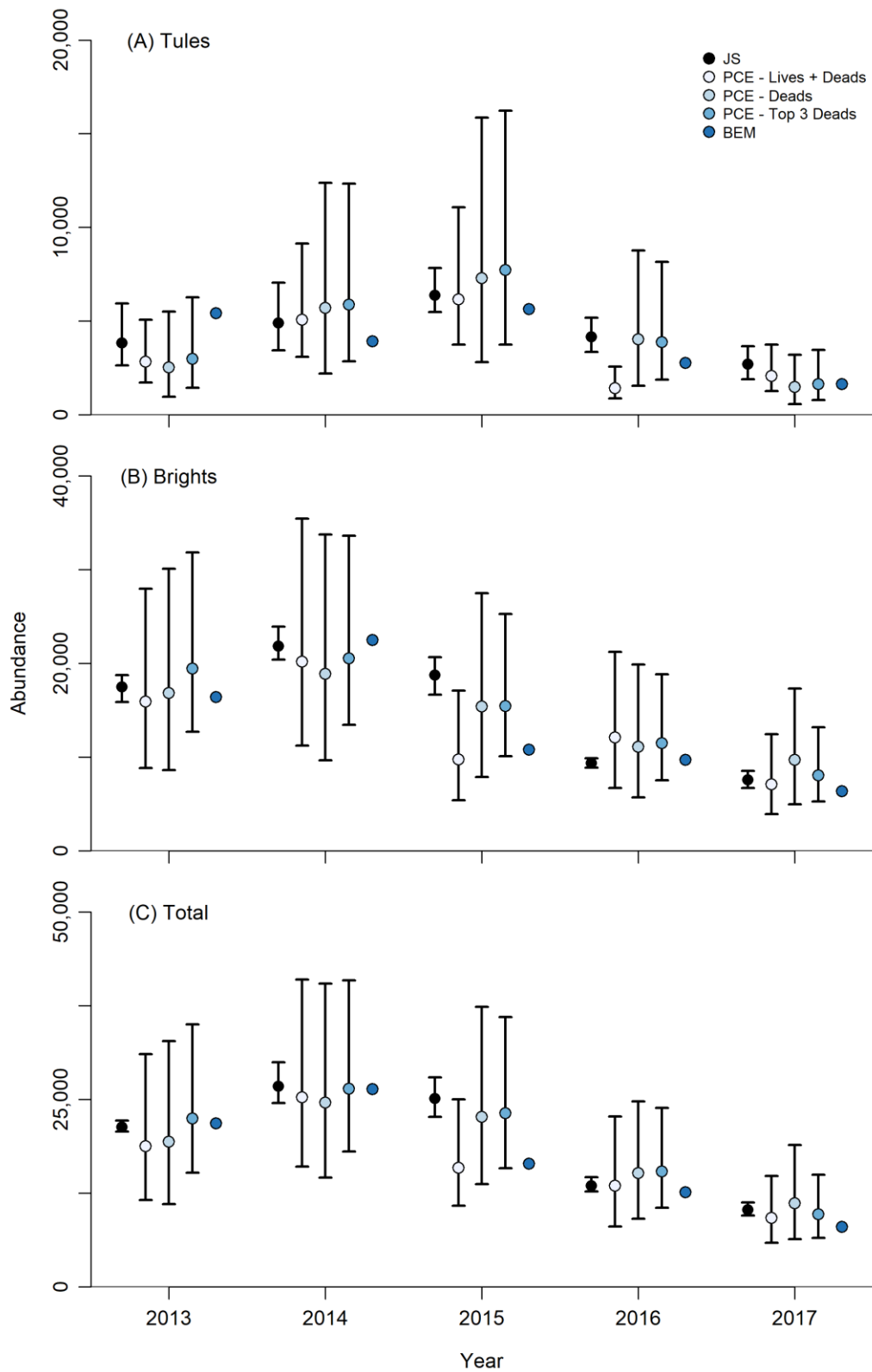


Figure 8. Comparison of estimates of spawner abundance for (A) tules, (B) brights, and (C) the total fall-run Chinook (i.e., tules and bright combined) in the NF Lewis River from 2013 - 2017 using the Jolly-Seber (JS), Bright-eye method (BEM), and the peak count expansion (PCE) estimators. Points are the mean of the posterior distribution (for JS and PCE) and error bars on the estimates represent the 95% prediction interval.

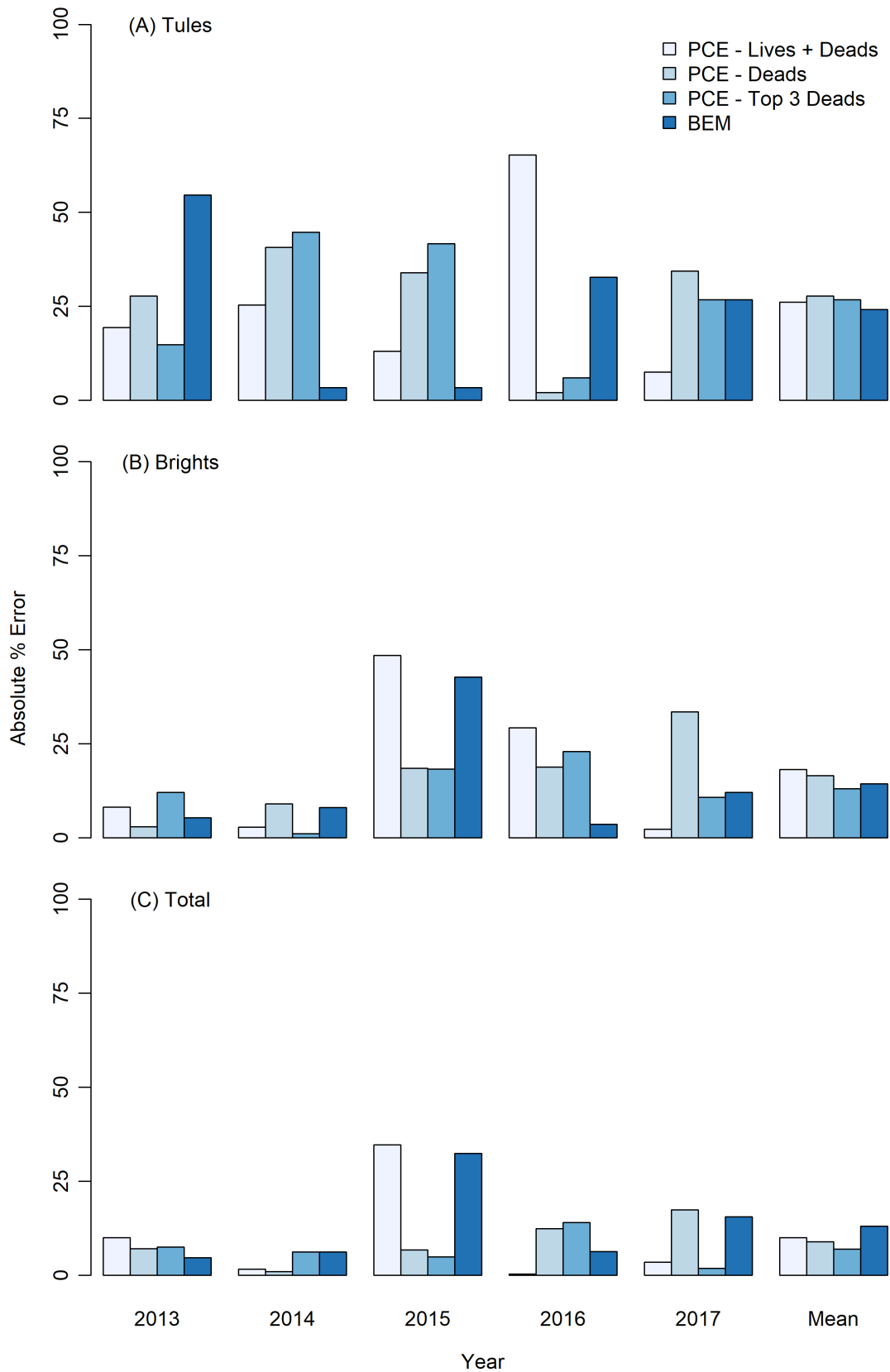


Figure 9. Absolute percent (%) error of spawner abundance estimates generated using the Bright-eye method (BEM) and the peak count expansion (PCE) estimators relative to Jolly-Seber (JS) estimates for (A) tules, (B) brights, and (C) the total fall-run Chinook (i.e., tules and bright combined) in the NF Lewis River from 2013 – 2017.

Discussion

Mark-recapture Jolly-Seber (JS) abundance estimates

The primary goal of our mark-recapture analysis was to derive unbiased estimates of adult spawner abundance and composition along with estimates of uncertainty for North Fork (NF) Lewis River fall-run Chinook for return years 2013 – 2017. We used a Jolly-Seber (JS) open population estimator applied to carcass recovery data with a Bayesian modeling approach. Our analytical methods were developed specifically for estimating salmon spawning escapement using mark-recapture data (Schwarz et al. 1993) and has been successfully implemented to estimate spawner escapement for salmon populations throughout the Lower Columbia River (Rawding et al. 2014). A thorough discussion of our analytical methods can be found in Rawding et al. (2014; pg. 62-63, 66-68) but in short the JS estimator will produce unbiased estimates when the assumptions of the model are met. Although the JS estimator requires multiple assumptions, the assumption that is of greatest importance, and thus requires thorough evaluation, is that every surviving carcass in the population whether tagged or untagged must have the same probability of recovery during each sampling event (Seber 1982). Therefore, prior to generating estimates of abundance each year, we evaluated the variation in recovery rates among carcasses using logistic regression and Bayesian GOF tests.

Previous studies have shown that recovery rates of Chinook salmon carcasses on spawning grounds can be influenced by size and sex (Zhou 2002, Murdoch et al. 2010). The logic is that smaller carcasses are likely easier for scavengers to remove, more difficult for surveyors to detect, and perhaps more readily washed away (Zhou 2002). Therefore, we used a logistic regression analysis to test if carcass recoveries were sex and/or length dependent. Across years, there were slight variations in the regression results, but overall there was always strong support for models with size- and sex-based recovery rates. Depending on the observed recovery rates and the number of carcasses sampled, the regression results typically suggested that a total of 2 – 6 strata were necessary to obtain “apparent” homogeneous groupings that would satisfy the equal probability of capture and persistence assumptions for a given year. However, it was important to consider that the regression tests were evaluating the overall recovery rates (i.e., survey season average) while our JS estimator modeled recovery rates by period. For instance, while there may be a statistically significant difference in overall recovery rates among two groups, stratifying the estimates can result in a low number (<5 – 10) of carcass recoveries per sample period which can lead to biased estimates (Seber 1982). Additionally, stratifying a single group (e.g., “jacks”) into two (e.g., jacks 40 – 50 cm and jacks 50 – 60 cm) can decrease the precision of each individual estimate resulting in the cumulative sum of the two estimates being statistically similar to the single estimate. Based on these results and previous literature, we chose to standardize our carcass stratifications into three groups (jacks, females, males) across all years. Although this standardization may have resulted in fewer or a greater number of groupings for a given year as opposed to those based solely on the regression results, these groupings provide a parsimonious approach for generating unbiased estimates of abundance and composition.

Recovery rates of carcasses can also vary throughout a survey season. This variation can be due to several independent or correlated variables such as flow, weather, visibility, survey effort, and

surveyor experience. Regardless of the mechanism, the JS open population estimator estimates the probability of recovery as a function (i.e., joint likelihood) of the probability of capture (p) and the probability of persistence/survival (ϕ). These two probabilities can be modeled as either timing varying (t) or constant (s) parameters for each survey period throughout a survey season resulting in four candidate JS models (ttt , stt , tst , sst). Prior to running the JS estimates, we tested the fit of each of the four models to the three groups of carcass data (jacks, females, males) using Bayesian GOF tests. Across years, generally all four JS models provided an adequate fit for the “jack” data set (i.e., $0.025 < \text{Bayesian } p\text{-value} < 0.975$) while only the completely time-varying (ttt) model provided an adequate fit for the female and male groupings. Put another way, the GOF tests suggested that JS estimators that assumed either constant or varying probabilities of recovery and survival were adequate models for jacks, but only the JS estimator that assumed varying probabilities of recovery and survival across all sample periods was an adequate model for females and males. Based on these results, we chose to standardize our JS modeling approach and use the completely timing-varying JS model for each carcass grouping across all years. However, prior to running the final estimates as a single model, we would run independent estimates for each carcass group with each of the JS models that provided an adequate fit based on the GOF tests. Across all years and groups, the “ ttt ” JS model provided either the best or a “similarly” good fit based on deviance information criterion (DIC) and all abundance estimates were within a couple hundred fish of one another. Therefore, while it is possible that the “ ttt ” model may have overfit the mark-recapture dataset for a couple of the jack groupings among all years, it likely had little to no influence on our final estimates.

After abundance estimates were generated for the three carcass groupings, we estimated spawner composition by stock (tule, bright), origin (hatchery, wild), sex, and age using biological data collected from recovered carcasses. Specifically, in regards to estimating stock composition, we chose to use the weekly ratio of “raw” (i.e., unadjusted) CWT recoveries to partition the overall abundance estimates as either tules or brights. Although the CWT recoveries allow for a direct estimate of race composition, their use requires several assumptions. First, it assumes that the total “pool” of CWTs that were available to sample was equal among tule- and bright-run Chinook. For example, if two tule and two bright CWTs were recovered in a given week, we would have estimated approximately a 50:50 composition. However, there may have actually been twice as many bright CWTs available to sample, which means the actual ratio was 66:33 tule vs. bright. While we were aware of the potential violation of this assumption, it is difficult to actually calculate the relative sample pools given that all tule recoveries were hatchery strays from multiple basins that (likely) had varying tag rates, release sizes, stray rates, marine survival, harvest rates, and run-timing. Regardless, there was little to no overlap in CWT recoveries for tules and brights across years, which alleviates the concern over violation of this assumption. Second, using CWTs to assign race composition assumes that the actual CWT origin is accurate. Wild fall-run Chinook are CWT tagged as juveniles and the assumption is that all of these juveniles are bright-run Chinook based on their capture location, size, and timing. However, this assumption has not been thoroughly evaluated and there is evidence that there may be a group of fall-run Chinook that are tagged as juveniles but ultimately display phenotypic characteristics of both tules and brights. Third, the use of CWTs assumes that the run-timing of stray hatchery tules is the same as wild tules. For example, if NF Lewis wild tules have a later run-timing than stray hatchery tules, then

at least a portion of the wild tules, which have no CWTs, would have been classified as wild brights. In general, wild tules exhibit a later run-timing relative to hatchery tules in the LCR but these patterns are variable among watersheds (*Jeremy Wilson, personal communication, WDFW*). Lastly, the use of CWTs assumes that the timing of carcass recoveries is representative of the relative run-timing of each stock. Because a carcass is recovered after the fish has died it is possible to recover a CWT carcass weeks after death. This phenomenon is not unique to CWT recoveries and applies to all composition data based on carcass recoveries. For instance, this characteristic of carcass data may explain why a portion (0-2%) of the bright-run fish were also classified as hatchery-origin (i.e., a handful of clipped, non-CWT tules were recovered during the bright-run time period).

An alternative method that could be used for stock assignment with available data would be to use adipose-clip status. Here, we would have to assume that all clipped carcasses without a bright CWT were a tule. This assumption is likely true aside from the relatively small number of bright juveniles that were adipose fin-clipped but too small to CWT or that were clipped and lost their CWT tag. Based on our results, there were unclipped (i.e., wild) fall-run Chinook sampled during the tule time-frame and these individuals are either mis-clipped strays, a naturally occurring population of tules in the mainstem Lewis, stray (out-of-basin) tules, or in-basin tules that originated from Cedar Creek or EF Lewis. Nonetheless, if any portion of the tule-run were indeed wild, then using adipose-clip status would require the same run-timing assumption that is required for CWTs. Overall, the use of CWT recoveries and/or adipose fin-clip status allows us to generate an estimate of stock composition but both rely on some untested assumptions. Therefore, it may be worth exploring alternative methods (e.g., genetic-based analysis) to assign stock composition in future years.

We apportioned the estimates of abundance by origin (hatchery, wild) using the weekly ratio of carcass recoveries and their corresponding adipose fin-clip status. Specifically, we assumed that any carcass with a missing adipose-fin without a Lewis bright CWT was of hatchery-origin while any carcass with an intact adipose-fin was wild. These assumptions meant that our assignment of origin did not account for any possible “mis-clips” whether those were hatchery-origin Chinook that accidentally did not have their adipose fin removed prior to release or wild-origin Chinook that were clipped but were either too small to CWT or lost their CWT. The effect of unclipped hatchery Chinook would impact our tule estimates and potentially result in an underestimate of pHOS for tules while the effect of clipped wild Chinook would impact our bright estimates and potentially result in an overestimate of pHOS for brights. In general, mis-clip rates for LCR hatchery Chinook vary between 1 – 3% (*WDFW unpublished data*). Therefore, while ignoring mis-clip rates may bias our run-specific estimates of abundance, because mis-clip rates are so low, accounting for them here would have had a negligible effect on our estimates. Nonetheless, mis-clip rates could be incorporated into future estimates.

Lastly, we apportioned the estimates of abundance by age using the weekly ratio of carcass recoveries based on scale-age reads. As mentioned earlier, recovery rates of Chinook salmon carcasses on spawning grounds can be influenced by size and sex (Zhou 2002, Murdoch et al. 2010) and therefore apportioning estimates by “raw” ratios of carcasses can lead to biased estimates. However, this potential effect was alleviated by stratifying our estimates into groupings

that had relatively homogeneous recovery rates. In regards to the accuracy of age assignment, a previous analysis has noted that the age-distribution of Chinook can be biased low when using scales to assign ages. Specifically, Wilson (2016) compared Chinook ages based on read scale ages and CWTs collected from the same fish and found that older fish (age 5 and 6) were regularly misread as younger fish. This disparity impacted bright-run Chinook more so than tule-run Chinook due to their generally older age-distributions. Claiborne et al. (2016) attributed the misidentifications to scale resorption, which occurs in all species of Pacific salmon during the anadromous migration and can reduce the number of winter annuli visible on the scale. Currently, our analysis does not account for any potential bias due to scale age mis-reads but should be evaluated in the future to better understand the possible impact on the age distribution.

Evaluation of the Bright-eye method (BEM) estimator

Estimates of fall-run Chinook abundance in the NF Lewis River have been generated using the Bright-eye method (BEM) since the early 2000s. The BEM was developed as an alternative to the peak count expansion (PCE) estimator, which was developed in the mid-1970s and had been used as the sole estimator of Chinook abundance for approximately three decades. Despite the limitations of the BEM (see below), it has several advantages over the PCE estimator. First, the BEM accounts for some sampling variation (i.e., variable age composition and recovery rates) while the PCE estimator relies on a single, constant expansion factor that is also dependent on the peak spawn date being known. Second, the BEM requires carcasses to be bio-sampled, which allows the total estimate to be stratified by stock, origin, sex, and age while the PCE estimator can only generate estimates by stock. Third, the BEM implements weekly surveys throughout the entire spawning time-frame, which allows for a representative estimate of run-timing. Based on this information, it was assumed that estimates derived using the BEM were more robust than the PCE estimator, and thus, has been the preferred estimator over the past 15 years. However, the robustness of BEM estimates was never formally evaluated prior to our analysis.

The BEM generates estimates of abundance for NF Lewis Chinook by expanding “raw” carcass recoveries by age-specific recovery rates. This method is essentially the same as the Jolly-Seber (JS) estimator except that the BEM assumes that the recovery rates for a given age-class of carcasses are constant both within and among years. Based on our analysis, the assumptions of the BEM estimator (i.e., constant recovery rates, see pg. 17) was often violated (see Figure 7) and led to biased estimates of abundance (Figure 8, Figure 9). Interestingly, BEM abundance estimates were not always biased and in some cases were very similar to JS derived estimates. Congruence in some of the abundance estimates can be attributed to relatively consistent overall (i.e., pooled) recovery rates among years (Table 12). This among year consistency in recovery rates is likely a result of some consistency in both sampling effort and environmental conditions. Over the past 15 years, carcass surveys have largely been conducted by the same WDFW crew of individuals resulting in relatively consistent sampling effort within and among years. Environmental conditions on the NF Lewis are heavily influenced by the management of flow through the series of three upriver dams, which are operated by PacifiCorp but mitigated as a part of a Federal Energy Regulatory Commission (FERC) licensing agreement. Specifically, minimum flows are maintained early in the survey season and drawdowns are provided during peak surveys to

facilitate carcass recovery and improve conditions for live and redd counts. The peak survey drawdowns also provide flow ramping which redistribute tagged and untagged carcasses and help to satisfy the assumptions of equal mixing and equal catchability. Despite these efforts to standardize survey effort, recovery rates were still quite variable within and among years leading to biased abundance estimates.

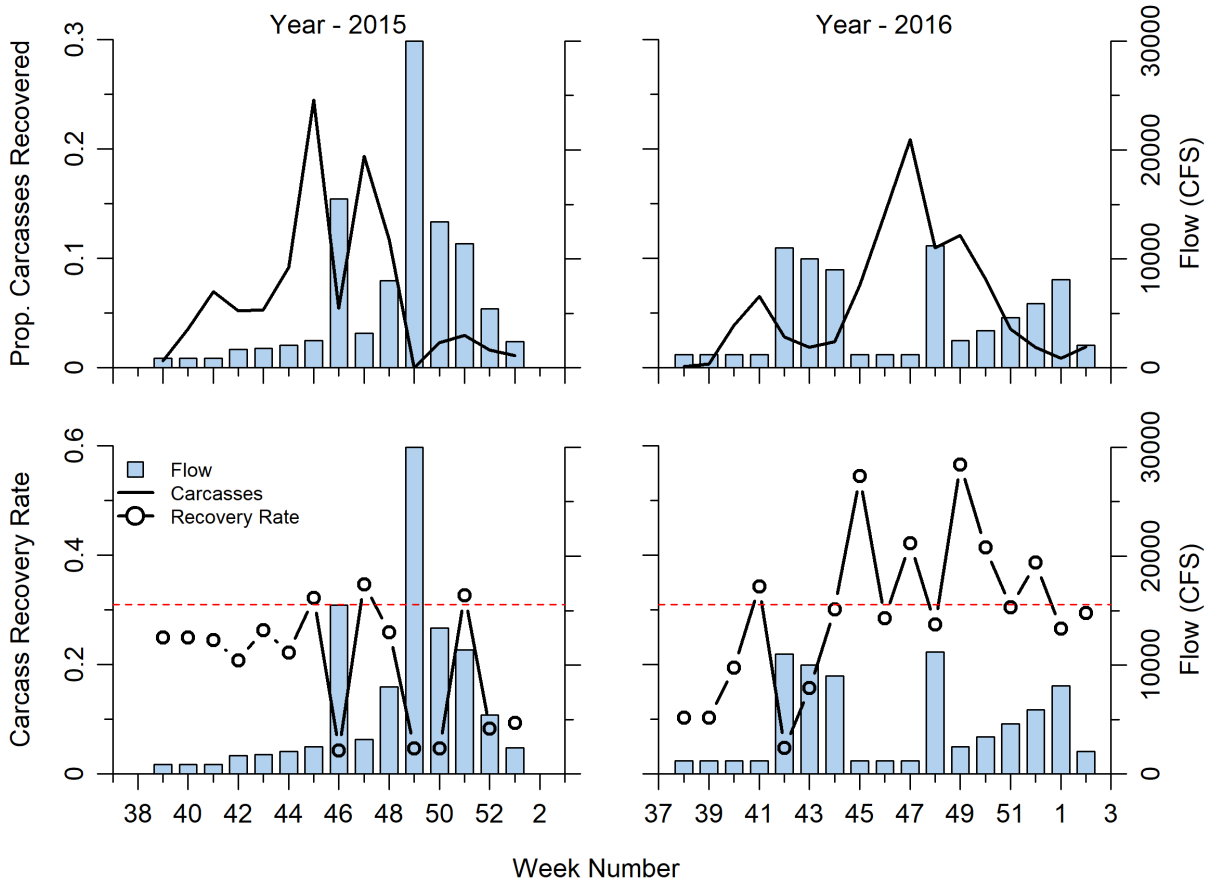


Figure 10. Relative recoveries (top panes – solid lines) and estimated recovery rates (bottom panes – dotted line) of female fall-run Chinook salmon carcasses and peak discharge of the NF Lewis River (blue bars) on the survey date by week for the year 2013 (left) and 2015 (right). The horizontal dashed red line represents the approximate average recovery rate of female carcasses used in the Bright-eye method (BEM) estimator.

Although recovery rates can again be influenced by a suite of factors, it is likely that flow rates in the NF Lewis, which can be correlated with turbidity and visibility, have a large impact on relative recovery rates. This can clearly be seen in two years of mark-recapture data. For instance, in 2016, the average year-specific recovery rates were almost exactly the same as the BEM recovery rates that were calculated from 2001 and 2002 data (Table 12), which lead to similar estimates of total fall-run Chinook between the two estimators (Figure 8). However, upon closer examination of within-year recovery rates and flows, we can see that JS derived recovery rate estimates early in the survey season (weeks 37 – 44) were below the average BEM recovery rates and this corresponded with three weeks when flows were ~10,000 CFS while JS recovery rates later in the

season (weeks 45 – 50) were above the BEM average and this corresponded to relatively low flows (Figure 10). This seasonal shift from below-average recovery rates early in the season to above-average recovery rates later in the season lead to a substantial underestimate in tule abundance and a slight overestimate of bright abundance.

On the other hand, in 2015, almost every weekly calculated recovery rate was lower than the overall average BEM recovery rate leading to underestimates of abundance for tules, brights, and total fall-run Chinook. Specifically, substantially high flows in week 46 lead to extremely low recovery rates and flows were so high in week 49 that the carcass surveys were canceled. In theory, a lower than average or even zero percent capture probability in one week can be offset by higher than average capture probability in subsequent weeks if the persistence (i.e., survival) of carcasses is not affected by the high flow event. However, it appears as though the high flow events affected both capture probability and persistence of carcasses meaning that BEM estimates of abundance will likely be biased low if any carcass surveys are missed throughout the survey period. It should be noted, however, that even though flow clearly influences recovery rates, it is not the only influential variable. For example, recovery rates in early 2015 were lower than average despite flows being at or below the typical minimum allowable rate for that time period (Figure 10).

Evaluation of the peak count expansion (PCE) estimator

Estimates of abundance for fall-run Chinook in NF Lewis River were generated for over 25 years with a peak count expansion (PCE) estimator that was developed back in the 1970s (McIssac 1976). In the early 2000s, multiple years of mark-recapture surveys were conducted that would have allowed the development of an updated PCE estimator. However, the PCE model update was never completed. Instead, the Bright-eye method (BEM) was developed and has been used to generate estimates of fall-run Chinook abundance since 2000. Regardless, there was never a formal evaluation of the PCE (or the BEM) model and whether or not this estimator could generate unbiased estimates of abundance.

Typically, the peak count (PC) refers to an enumeration of fish that corresponds to the largest count of either live spawners, carcasses, or a combination of the two. A peak count expansion (PCE) factor is then calculated as the ratio of the peak count relative to the (estimated) total abundance of spawners (Parsons and Skalski 2009). However, the PCE factor is just one specific form of an expansion factor and a countless number of expansion factors could hypothetically be developed to derive an abundance estimator given the existing data. Hence, we chose to evaluate three different PCE estimators: “peak lives + deads”, “peak deads only”, and “top 3 deads” (see methods). In theory, a PCE estimator that incorporates more data should be more accurate and precise. Therefore, all other things being equal, we hypothesized that the “peak lives + deads” and the “top 3 deads” PCE estimates of abundance should have been better. However, the underlying assumptions of the estimator (see pg. 19) are still of utmost importance. For instance, if incorporating more data leads to greater variability in detection rates of spawners and/or carcasses then the PCE estimator may not be improved. Ultimately, we were interested in the performance of all three estimators based on past data collection efforts and consideration for future surveys. Specifically, peak live counts for tule-run Chinook were not consistently conducted prior to 2013 but carcass (i.e., dead) surveys were completed almost every week. Thus, we would need a PCE

estimator that used exclusively carcass data to generate estimates prior to 2013 but we still wanted to know if incorporating live count data (when available) improved the accuracy and precision of the abundance estimates.

Using the five years of paired Jolly-Seber and PCE estimates of abundance, we evaluated the accuracy and precision of our three different PCE estimators. Based on our analysis, estimates of abundance that were generated with the PCE estimators had mean absolute percent errors (MAPEs) of 7 – 28% but were statistically similar to the JS estimates (i.e., unbiased) for 43 out of the 45 (95%) generated estimates. The uncertainty associated with the abundance estimates as measured with the coefficient of variation (CV) was estimated to be between 28 – 49%, which is well above the recommended precision goal of 15% that have been developed for ESA-listed salmon and steelhead populations by NOAA Fisheries (Crawford and Rumsey 2011) and the Lewis River Hatchery and Supplementation Annual Operating Plan (H&S Subgroup 2015). Still, it is important to highlight that the estimates of uncertainty we generated are underestimated because uncertainty in live and dead counts was not incorporated in the estimate of PCE (see Parsons and Skalski 2009). Hypothetically, we could have potentially incorporated uncertainty in the dead (carcass) counts into our PCE model, which would have increased the estimates of CV. However, this could not have been done for live count data as observer efficiencies have never been measured. Nonetheless, estimates of precision for the PCE estimator were substantially higher than those generated with the JS model.

It should be noted that we used “weakly” informative priors in the development of the PCE estimators. Specifically, the mean and median PCE estimates were not sensitive to the hyper-prior we used for μ_{\logitPCP_i} and σ_{\logitPCP_i} , but the estimate of uncertainty in our PCE estimators was semi-sensitive. We ended up choosing a prior for μ_{\logitPCP_i} of *Normal* (-0.75, 0.75), which corresponds to a prior on PCE that has its 95% distribution between approximately 1.5 and 10, which based on the existing data made biological sense. One thing to remember is that we generated a hierarchical estimate with only 4 – 5 data points. Therefore, the estimate is going to naturally be somewhat uncertain due to low sample size. However, the estimates of uncertainty for our PCE estimators may potentially become more precise as additional years of data are added.

It is important to highlight a detail in how we calculated our PCE estimators. We used carcass recovery data and calibrated those recoveries relative to estimates derived with a mark-recapture model. During the mark-recapture surveys, carcasses that were either recaptured or sampled but not tagged were chopped in half and denoted as “loss-on-capture. Assuming chopped carcass had lower recovery rates, which they almost certainly would, the total number of carcasses surveyed during the following week(s) would be less than if carcasses were not chopped. Therefore, in future years, if we were to only conduct peak carcass counts (i.e., not chop carcasses throughout the entire spawn time period), we would overestimate abundance using the PCE factors that were derived in this study. This bias would likely be relatively small given that the large majority of carcasses are recovered in the first several weeks post-death, but nonetheless the estimate would still be biased. A few solutions to this potential issue would be to (1) develop a PCE estimator that only used counts of live spawners, (2) only enumerate “fresh” carcasses, (3) enumerate and

include the recovery of chopped carcasses in the dead count, or (4) develop a weekly estimate of chopped carcasses that would have survived and been recovered as part of the JS model. This issue does not affect any historical data and derived estimates as recovered carcasses have always been chopped. Nonetheless, this would be an important consideration if there was ever a shift to only conducting peak carcass surveys.

Overall, the assumptions of the PCE model were not consistently met. Although the violation of assumptions did not lead to biased estimates in most years, all of the estimates were highly imprecise and in some years the mean of the estimate was inaccurate (Figure 8, Figure 9, Appendix E). The main issue with the PCE estimator in the NF Lewis was that in several years the peak count survey was not conducted during the peak time frame. When this occurred, the peak count was underestimated and thus the estimate of abundance was biased low or incomputable. In general, though, the main issue with the PCE estimator is that the observer efficiencies for live counts and recovery rates for carcasses must remain constant among surveys. If this assumption is not met, the PCE will not reflect the actual relationship between the count and total abundance, the peak date can be misidentified, and ultimately the abundance estimate will be biased. This issue is similar to the main issue with the BEM. Despite these limitations, our PCE estimators generated estimates of abundance that were unbiased in most years, albeit relatively imprecise, so long as the peak count data were collected during the peak spawn time period.

Recommendations

Based on the results of our analysis and the goals of the North Fork (NF) Lewis River fall-run Chinook surveys salmon, we have developed a list of recommended actions. The list is prioritized in the order that items should be addressed to improve the accuracy and precision of spawner abundance estimates for fall-run Chinook salmon in the NF Lewis River.

- (1) **Continue implementation of mark-recapture surveys for abundance estimation.** One of the main objectives of the NF Lewis River fall-run Chinook salmon surveys is to generate unbiased estimates of spawner abundance with specified uncertainty by stock (tule, bright), origin (hatchery, wild), sex (male, female), and age. Therefore, it is necessary to use an abundance estimator that generates unbiased estimates when the assumptions of the model are met. The Jolly-Seber (JS) open population mark-recapture model we used to estimate Chinook abundance was developed specifically for salmon, has been thoroughly evaluated over the past several decades, and successfully used for other lower Columbia River salmon populations. Our JS modeling approach not only allowed us to directly test the assumptions of the model but also account for heterogeneity in the data and structure it so that unbiased estimates could be generated. Hence, the abundance estimates generated using the JS mark-recapture estimator should be viewed as unbiased.

Conversely, the use of the Bright-eye method (BEM) and peak count expansion (PCE) estimators can lead to biased estimates due to a violation of the model assumptions. Specifically, for the BEM and PCE estimators to generate an unbiased estimate, recovery rates, which are a function of both environmental conditions and sampling effort, have to be constant within and among years. Although averaged age-specific recovery rates of

Chinook in the NF Lewis were relatively constant among the five years of data we analyzed, they are quite variable within a year, which can lead to biased estimates of abundance by stock (tule, bright) and can vary substantially from the averaged recovery rates (e.g., 2015 estimates). In theory, the BEM and PCE estimators could be modified in a manner that allows recovery rates to be estimated as a function of multiple variables and thus vary within and among years (see recommendation #5). However, the feasibility of this model has not been explored and may or may not produce a better estimator.

Therefore, given the limitations of the BEM and PCE estimators, we recommend conducting mark-recapture surveys throughout the entire spawning time frame to estimate the abundance of Chinook salmon in the NF Lewis River until an alternative, more cost-effective method has been developed that can generate an unbiased estimate with a specified level of uncertainty. We want to emphasize that our recommendation for weekly mark-recapture surveys is to meet NOAA viable salmon population (VSP) monitoring guidelines for accuracy and precision of abundance estimates as well as diversity metrics such as spawning time and age structure (Crawford and Rumsey 2011). Unbiased estimates of spawning time (Appendix E: Figures E1 – E5) and age structure (Figure 6) can only be accomplished by weekly surveys.

- (2) **Continue implementation of peak count surveys.** Despite the current limitation of the PCE estimators, we recommend the continuation of peak counts, which include counts of live spawners. Peak live counts are attempted annually for almost all lower Columbia River fall-run Chinook populations in Washington State. Peak counts not only provide VSP data on the spatial structure of a population, they can also be used to generate PCE factors, and thus estimates of abundance with uncertainty. Specifically regarding NF Lewis fall-run Chinook data collection, future peak count data can be used to update the current PCE models, which may provide improved estimates with additional years of data.

Moving forward, we recommend a minimum of three peak count surveys per stock (tule, bright) for a total of at least six counts per year. Counts should be conducted during the peak spawning time frame for each stock, which corresponds to generally the 2nd, 3rd, and 4th week of October for tule-run Chinook and generally the 3rd and 4th week of November and 1st week of December for bright-run Chinook. During each survey, both live and dead (i.e., carcasses) Chinook should be enumerated. However, live counts and carcass surveys should not be conducted simultaneously by the same crew/boat. If possible, peak live counts should be separated by holders (i.e., fish sighted in areas where spawnable habitat is not present and spawning does not occur) and spawners (fish sighted in an area with spawnable habitat). Peak dead counts should be separated by maiden carcasses, recaptured carcasses, previously sampled carcasses (i.e., chopped), and non-sampled carcasses (i.e., Carcass Category 5 and 6 – see Figure 3 and Appendix A).

- (3) **Improve understanding and estimates of population structure.** The NF Lewis River consists of two ESA-listed distinct independent populations (DIPs; a.k.a., stocks) of fall-run Chinook salmon (i.e., tules and brights). Currently, population-specific estimates of abundance are generated using recoveries of CWTs collected on the spawning grounds

during weekly carcass surveys. Although there is coherence between the population-specific estimates of abundance and run-timing distributions (Appendix E), these CWT-based estimations are based on several untested assumptions. Therefore, it may be worth exploring alternative methods to assign stock composition in future years.

Genetic methods have proven useful in distinguishing populations/stocks; however, existing genetic marker panels (i.e., the GAPS microsatellite baseline and the Columbia Basin SNP panels) are limited in scope regarding tules and brights and may not be powerful enough to distinguish them. Therefore, we propose an additional exploration of genetic techniques to better partition the fall-run Chinook abundance estimate by stock. First, a more detailed investigation of existing SNP panels may be useful (e.g., Meek et al. 2016). Second, new distinguishing SNP markers may be discovered using genomic methods. The first step for either of these methods will require tissue collections from groups of known tules and known brights. Therefore, we recommend (1) identifying sample time frames and locations in the NF Lewis River that minimize spawning overlap between tules, brights, and spring-run Chinook, (2) determining necessary tissue collection sample sizes, and (3) collecting genetic samples during the fall of 2018.

- (4) **Generate basin-wide estimates of abundance.** Historically, estimates of abundance for Lewis River fall-run Chinook salmon have been generated independently for four individual “sub-populations”: tules in the NF Lewis River, Cedar Creek, and EF Lewis River and brights in the NF Lewis. However, these individual sub-populations of tules and brights each correspond to a larger geographic DIP that encompasses the entire Lewis River basin. Specifically, the Willamette-Lower Columbia Technical Recovery Team (WLC-TRT) identifies early-run (tules) and late-run (brights) Chinook consisting of fish from both the NF Lewis River (including Cedar Creek) and EF Lewis River (Myers et al. 2006). Currently, WDFW does not generate an estimate of bright-run Chinook in the EF Lewis and, interestingly, LCR Recovery Plan does not list the EF Lewis as a bright-run sub-population (LCFRB 2010). Nonetheless, we recommend the development of analytical methods that would allow the generation of annual abundance estimates for tule- and bright-run Chinook salmon at the Lewis River basin-wide geographic scale, which would correspond to the how Lewis River Chinook are listed under ESA.
- (5) **Explore the development of a model-assisted abundance estimator.** WDFW has used other methods to estimate abundance for other Lower Columbia River Chinook populations (Rawding et al. 2014). Specifically, closed population models based on the tagging of live adults and recovery of carcasses have been effective for some populations but not for the Chinook salmon spawners in the Lewis due to violations of key assumptions (Hawkins et al. 2003a). Genetic methods have been successful on the Coweeman River but depend on the assumption of equal catchability of fish in the first sample with respect to their reproductive success (Rawding et al. 2013). This is likely difficult to achieve especially given the variability in adult capture probabilities discussed above and the prolonged outmigration of juvenile Chinook in the Lewis River. Redd based estimates are also likely problematic due to the challenge of obtaining individual redd counts due to mass spawning and superimposition because of high Chinook salmon densities (i.e., over 1,000 fish per

kilometer). If alternate methods are to be considered, we believe that AUC methods based on counts of “spawners” have the highest chance for success (Parken et al. 2011, Rawding et al. 2014). This approach would require the development of observer efficiency models based on environmental and surveyor experience covariates as well as estimates of apparent residence time. However, development of the additional parameters needed for the AUC approach may not be more cost-effective than the JS approach based on carcass tagging.

The results from the 2013-17 JS model assessment indicated that survival and capture probabilities varied by time. Graphical inspection of Figure 10 suggests that recovery probabilities may be related to flow. In addition, logistic regression also indicated that annual recovery probabilities were related to size. A complementary approach to recommendations #1 and #3 would be to explore a model-assisted JS estimator, which is likely to be a more successful approach than other approaches described in the above paragraph. For example, covariates such as flow, temperature, visibility, survey effort, surveyor experience, sex, and size could be incorporated into weekly estimates of capture and survival probabilities (Kery and Schaub 2012). In addition, the probability of entry parameter could be modeled as a parametric curve (Sethi and Bradley 2015). If this hypothetical model can be shown to consistently generate unbiased estimates, it may be possible to reduce the frequency and/or intensity of mark-recapture surveys or modify the current BEM method.

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Appendix A – Carcass category definitions

Table A1. Carcass categories codes and their associated definitions.

Carcass Category	Definition
-	Any carcass that you <u>can CWT sample</u> and <u>can tell</u> if it had been previously carcass tagged (both opercules intact). No carcass tags present and in condition to be tagged.
1	Any carcass that you <u>can CWT sample</u> but you <u>cannot tell</u> if it had been previously carcass tagged (i.e., missing portions of the head, missing one or both opercules).
2	Any carcass that you <u>cannot CWT sample</u> and you <u>cannot tell</u> if it had been previously carcass tagged (missing portions of the head, missing one or both opercules).
3	Any carcass that you <u>cannot CWT sample</u> but you <u>can tell</u> if it had been previously carcass tagged (both opercules present).
4	Any carcass that you <u>can CWT sample</u> and <u>can tell</u> if it had been previously carcass tagged (both opercules intact) <u>BUT you do not want to tag it</u> (e.g., carcass too old, sub-sampling).
5	Any carcass you are unable to examine but can ID species (e.g., too deep to recover)
6	Any carcass with a slit belly

Appendix B – Jolly-Seber Mark-Recapture Open Population Model Notation

Table B1. Summary statistics used in the Jolly-Seber model

Statistic	Definition/Equation
m_i	Number of fish captured at sample time i that were previously marked.
u_i	Number of fish captured at sample time i that were unmarked.
n_i	Number of fish captured at sample time i . $n_i = m_i + u_i$.
l_i	Number of fish lost on capture at time i .
R_i	Number of fish that were released after the i th sample. R_i need not equal n_i if there were losses on capture or injections of new fish at sample time i .
r_i	Number of R_i fish released at sample time i that were recaptured at one or more future sample times.
z_i	Number of fish captured before time i , not captured at time i , and captured after time i .
T_i	Number of fish captured at before time i and captured at or after time i . $T_i = m_i + z_i$.

Table B2. Fundamental parameters for the Jolly-Seber model under the salmon escapement super population model (Schwarz et al. 1993).

Parameter	Definition/Equation
s, tm	Number of sample times and length of interval between samples
p_i	Probability of capture at sample time i , $i = 1, \dots, s$.
ϕ_i	Probability of a fish surviving and remaining in the population between sample time i and sample time $i + 1$, given it was alive and in the population at sample time i , $i = 1, \dots, s-1$.
b^*_i	Probability that a fish enters the population between sample times i and $i + 1$, $i = 0, \dots, s-1$ under the constrain that $\sum b^*_i = 1$. These are referred to as entry probabilities.
v_i	Probability that a fish captured at time i will be released, $i = 1, \dots, s-1$.
N	Total number of fish that enter the system before the last sample time or the escapement. This is referred to as the super population.

Table B3. Derived parameters for the Jolly-Seber model under the salmon escapement super population model (Schwarz et al. 1993).

Parameter	Definition/Equation
λ_i	Probability that a fish is seen again after sample time i , $i = 1, \dots, s$. $\lambda_i = \phi_i p_{i+1} + \phi_i (1 - p_{i+1}) \lambda_{i+1}$, $i = 1, \dots, s-1$; $\lambda_s = 0$.
τ_i	Conditional probability that a fish is seen at sample time i given that it was seen at or after sample time i , $i = 1, \dots, s$. $\tau_i = p_i / (p_i + (1-p_{i+1}) \lambda_i)$.
ψ_i	Probability that a fish enters the population between sample time $i-1$ and i and survives to the next sampling occasion. $\psi_i = b^*_i$, $\psi_{i+1} = \psi_i (1 - p_i) \phi_i + b^*_i (\phi_i - 1) / \log(\phi_i)$
B^*_i	Number of fish that enter between sampling occasion $i-1$ and i , $i = 0, \dots, s-1$. These are referred to as gross births. $B^*_i = N (b^*_i)$

Table B4. The likelihoods for the Schwarz et al. (1993) model

Description	Likelihood
Pr(first capture part a)	$u_i \sim \text{Binomial}(\sum \psi_i p_i, N), i = 0, \dots, s-1. u. = \sum u_i$
Pr(first capture part b)	$u_i \sim \text{Multinomial}(\psi_i p_i / \sum \psi_i p_i, u.), i = 0, \dots, s-1.$
Pr(release on capture)	$R_i \sim \text{Binomial}(v_i, n_i), i = 1, \dots, s-1.$
Pr(recapture part a)	$m_i \sim \text{Binomial}(\tau_i, T_i), i = 2, \dots, s-1.$
Pr(recapture part b)	$r_i \sim \text{Binomial}(\lambda_i, R_i), i = 1, \dots, s-1.$

Appendix C – Jolly-Seber Mark-Recapture Model Inputs, 2013 – 2017

Table C1. 2013 mark-recapture summary statistics used to estimate the abundance of mainstem North Fork Lewis River fall-run Chinook spawners using a Jolly-Seber open population model. Estimates were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm). "j.date" was formatted as the day of year. Periods "-1" and "+1" only apply to "j.date" data where an additional date was needed before the first period and after the last period to run the model.

Statistic	Group	Period																				
		-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	+1
j.date	Jack	273	280	297	310	317	324	331	338	345	352	358	365	372	393	400	-	-	-	-	-	-
	Female	261	268	275	282	289	296	303	310	317	324	331	338	345	352	358	365	372	386	393	400	407
	Male	258	265	275	282	289	296	303	310	317	324	331	338	345	352	358	365	372	386	393	400	407
n	Jack		4	21	57	115	135	335	110	116	89	26	23	14	1	NA	NA	NA	NA	NA	NA	
	Female		15	39	129	84	103	140	377	837	1005	1126	711	542	421	170	227	165	85	30	15	
	Male		11	26	84	89	129	116	343	1031	1209	1196	577	585	370	147	127	109	39	11	10	
R	Jack		4	20	54	104	119	202	55	53	34	8	11	3	0	NA	NA	NA	NA	NA	NA	
	Female		13	26	66	26	40	67	191	256	105	126	79	52	139	56	96	39	21	5	0	
	Male		8	18	42	30	54	48	180	327	127	131	63	57	117	52	44	25	11	2	0	
u	Jack		4	20	55	104	126	290	73	72	58	16	18	4	0	NA	NA	NA	NA	NA	NA	
	Female		15	36	124	65	88	124	346	750	923	1041	656	485	382	123	171	118	57	20	10	
	Male		11	25	81	78	118	90	326	955	1124	1080	533	540	325	115	80	75	30	8	5	
z	Jack		0	0	0	2	10	9	33	15	8	9	6	0	0	NA	NA	NA	NA	NA	NA	
	Female		0	0	3	4	3	4	8	14	37	11	24	25	15	49	26	17	7	4	0	
	Male		0	0	0	5	3	3	3	15	69	23	31	19	10	33	19	2	5	5	0	
r	Jack		1	2	13	17	44	61	26	24	11	2	4	1	0	NA	NA	NA	NA	NA	NA	
	Female		3	8	20	14	17	35	93	105	59	68	58	29	81	33	38	18	7	1	0	
	Male		1	3	16	9	26	17	88	139	70	52	33	36	55	33	17	12	3	0	0	
m	Jack		0	1	2	11	9	45	37	44	31	10	5	10	1	NA	NA	NA	NA	NA	NA	
	Female		0	3	5	19	15	16	31	87	82	85	55	57	39	47	56	47	28	10	5	
	Male		0	1	3	11	11	26	17	76	85	116	44	45	45	32	47	34	9	3	5	

Table C2. 2013 biological data summary data used to apportion the abundance estimates of mainstem North Fork Lewis River fall-run Chinook spawners that were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm) – into reporting groups by stock (tule, brights), origin (hatchery, wild), sex, and age.

Group	Variable	Parameter	Period																		
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Jack	Stock	Tule	1	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
		Total	1	4	4	10	12	14	5	6	3	1	1	1	1						
	Origin	Hatchery	169	207	61	41	31	14	7	7	1	0	2	2	0						
		Total	299	590	727	1809	1247	1383	694	661	764	254	269	197	130						
	Age	Age-2	2	13	21	47	56	60	13	12	6	1	1	1	0						
		Age-3	2	7	32	57	60	129	35	38	24	6	10	2	0						
		Age-4	0	0	0	0	0	0	0	1	0	0	0	0	0						
		Age-5	0	0	0	0	0	0	0	0	0	0	0	0	0						
Age-6		0	0	0	0	0	0	0	0	0	0	0	0	0							
Female	Stock	Tule	1	1	1	1	2	1	3	0	0	0	0	0	0	0	0	0	0	0	
		Total	1	1	1	1	2	1	4	10	12	14	5	6	3	1	1	1	1	1	1
	Origin	Hatchery	16	29	124	89	69	49	61	41	31	14	7	7	1	0	2	2	0	0	0
		Total	29	62	208	149	210	231	727	1809	1247	1383	694	661	764	254	269	197	87	28	15
	Age	Age-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Age-3	0	1	7	2	3	9	21	20	8	9	4	3	5	1	1	0	0	0	0
		Age-4	11	19	64	21	32	44	138	183	63	80	54	27	78	21	38	17	7	1	0
		Age-5	3	6	15	0	4	5	24	44	25	26	16	17	47	26	43	14	10	2	4
Age-6		1	0	0	2	0	1	1	3	1	1	1	0	0	1	5	4	2	0	2	
Male	Stock	Tule	1	1	1	1	2	1	3	0	0	0	0	0	0	0	0	0	0	0	
		Total	1	1	1	1	2	1	4	10	12	14	5	6	3	1	1	1	1	1	1
	Origin	Hatchery	16	29	124	89	69	49	61	41	31	14	7	7	1	0	2	2	0	0	0
		Total	29	62	208	149	210	231	727	1809	1247	1383	694	661	764	254	269	197	87	28	15
	Age	Age-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Age-3	2	7	23	13	29	13	79	146	54	63	32	17	43	10	5	3	1	1	0
		Age-4	6	8	31	15	21	27	88	140	50	50	21	22	41	22	13	9	1	1	1
		Age-5	1	1	3	0	0	4	10	34	14	5	5	13	28	17	21	11	6	0	1
Age-6		0	0	0	0	0	1	0	1	1	1	0	1	0	0	2	1	2	0	0	

Table C3. 2014 mark-recapture summary statistics used to estimate the abundance of mainstem North Fork Lewis River fall-run Chinook spawners using a Jolly-Seber open population model. Estimates were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm). "j.date" was formatted as the day of year. Periods "-1" and "+1" only apply to "j.date" data where an additional date was needed before the first period and after the last period to run the model.

Statistic	Group	Period																		
		-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	+1
j.date	Jack	281	288	300	308	315	322	329	337	344	351	356	363	370	NA	NA	NA	NA	NA	NA
	Female	260	267	276	281	288	296	302	308	315	322	329	337	344	351	356	363	372	378	385
	Male	272	279	288	296	302	308	315	322	329	337	344	351	356	363	372	378	385	NA	NA
n	Jack		7	15	15	48	184	187	65	31	21	3	3	NA	NA	NA	NA	NA	NA	
	Female		16	54	109	237	414	272	404	884	1396	1833	934	990	1195	360	438	92	118	
	Male		95	193	278	115	275	623	1265	1051	531	404	543	108	116	17	19	NA	NA	
R	Jack		7	14	14	47	166	122	38	17	8	2	0	NA	NA	NA	NA	NA		
	Female		5	25	73	118	63	131	175	136	182	111	54	127	100	147	103	30	0	
	Male		58	97	38	56	124	100	175	60	31	48	43	42	29	4	0	NA	NA	
u	Jack		7	14	14	47	167	126	52	21	8	2	1	NA	NA	NA	NA	NA		
	Female		16	53	99	215	360	246	371	814	1294	1738	905	967	1090	329	330	73	84	
	Male		95	177	244	105	261	583	1194	956	518	384	508	95	93	12	11	NA	NA	
z	Jack		0	0	0	1	1	3	4	7	2	2	0	NA	NA	NA	NA	NA		
	Female		0	0	3	6	1	1	6	28	17	16	22	30	13	32	8	16	0	
	Male		0	3	3	2	1	24	8	13	17	13	4	10	4	4	0	NA	NA	
r	Jack		1	1	2	17	63	14	13	8	1	0	0	NA	NA	NA	NA	NA		
	Female		1	13	25	49	26	38	92	91	94	35	31	88	50	84	27	18	0	
	Male		19	34	9	13	63	55	100	17	16	26	19	17	5	4	0	NA	NA	
m	Jack		0	1	1	1	17	61	13	10	13	1	2	NA	NA	NA	NA	NA		
	Female		0	1	10	22	54	26	33	70	102	95	29	23	105	31	108	19	34	
	Male		0	16	34	10	14	40	71	95	13	20	35	13	23	5	8	NA	NA	

Table C4. 2014 biological data summary data used to apportion the abundance estimates of mainstem North Fork Lewis River fall-run Chinook spawners that were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm) – into reporting groups by stock (tule, brights), origin (hatchery, wild), sex, and age.

Group	Variable	Parameter	Period																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Jack	Stock	Tule	12	9	4	1	0	0	0	0	0	0	0						
		Total	12	10	8	9	17	19	6	13	12	3	1						
	Origin	Hatchery	540	492	39	10	14	8	1	5	5	3	0						
		Total	660	969	646	500	1227	1290	712	674	1037	426	604						
	Age	Age-2	5	14	13	35	143	103	26	13	6	2	1						
		Age-3	2	0	1	12	19	16	10	4	2	0	0						
		Age-4	0	0	0	0	1	0	0	0	0	0	0						
		Age-5	0	0	0	0	0	0	0	0	0	0	0						
Age-6		0	0	0	0	0	0	0	0	0	0	0							
Female	Stock	Tule	2	1	2	8	8	1	4	1	0	0	0	0	0	0	0	0	0
		Total	2	1	2	8	8	2	8	9	17	19	6	13	12	3	1	1	1
	Origin	Hatchery	14	58	153	315	387	105	39	10	14	8	1	5	5	3	0	0	0
		Total	21	75	167	397	609	360	646	500	1227	1290	712	674	1037	426	424	85	95
	Age	Age-2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Age-3	1	1	2	2	3	4	10	2	7	6	0	3	4	2	0	2	0
		Age-4	11	36	61	101	47	105	152	117	156	89	50	102	82	120	74	17	22
		Age-5	2	3	6	12	11	17	9	13	11	10	3	18	8	18	24	8	8
Age-6		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Male	Stock	Tule	4	8	8	1	4	1	0	0	0	0	0	0	0	0	0	0	
		Total	4	8	8	2	8	9	17	19	6	13	12	3	1	1	1		
	Origin	Hatchery	225	315	387	105	39	10	14	8	1	5	5	3	0	0	0		
		Total	263	397	609	360	646	500	1227	1290	712	674	1037	426	424	85	95		
	Age	Age-2	2	0	0	0	0	0	0	1	0	0	0	0	2	0	0		
		Age-3	16	20	12	8	13	10	37	16	4	8	8	5	1	1	0		
		Age-4	45	71	27	44	100	81	122	35	27	37	32	30	21	3	3		
		Age-5	5	4	2	2	4	4	7	3	0	3	3	5	4	1	1		
Age-6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			

Table C5. 2015 mark-recapture summary statistics used to estimate the abundance of mainstem North Fork Lewis River fall-run Chinook spawners using a Jolly-Seber open population model. Estimates were derived for three groups – jacks (males <60 cm), females, and males (≥ 60 cm). "j.date" was formatted as day of year. Periods "-1" and "+1" only apply to "j.date" data where an additional date was needed before the first period and after the last period to run the model.

Statistic	Group	Period															
		-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	+1
j.date	Jack	274	281	288	294	300	307	315	329	336	361	368	NA	NA	NA	NA	NA
	Female	266	273	281	288	294	300	307	314	321	329	336	350	356	364	372	379
	Male	265	272	281	288	294	300	307	314	321	329	338	356	364	372	379	NA
n	Jack		4	13	8	8	14	49	39	31	3	NA	NA	NA	NA	NA	
	Female		39	216	443	340	337	568	1520	325	1160	726	138	188	100	71	
	Male		34	204	360	323	215	293	902	259	930	394	77	65	62	NA	
R	Jack		4	12	7	7	13	48	34	29	0	NA	NA	NA	NA	NA	
	Female		30	121	136	70	103	213	142	29	115	85	22	37	20	0	
	Male		27	113	107	64	65	111	86	24	91	47	15	13	0	NA	
u	Jack		4	12	7	7	13	48	34	29	2	NA	NA	NA	NA	NA	
	Female		39	208	412	309	313	543	1446	321	1142	694	136	175	96	67	
	Male		34	195	323	287	198	281	859	254	917	363	69	63	57	NA	
z	Jack		0	0	0	0	0	0	0	0	0	NA	NA	NA	NA	NA	
	Female		0	1	3	6	3	7	1	11	3	0	6	3	2	0	
	Male		0	0	0	4	4	4	0	9	2	1	1	2	0	NA	
r	Jack		1	1	1	1	1	5	2	1	0	NA	NA	NA	NA	NA	
	Female		9	33	34	21	29	68	14	10	29	8	10	3	2	0	
	Male		9	37	40	17	12	39	14	6	30	8	3	3	0	NA	
m	Jack		0	1	1	1	1	1	5	2	1	NA	NA	NA	NA	NA	
	Female		0	8	31	31	24	25	74	4	18	32	2	13	4	4	
	Male		0	9	37	36	17	12	43	5	13	31	8	2	5	NA	

Table C6. 2015 biological data summary data used to apportion the abundance estimates of mainstem North Fork Lewis River fall-run Chinook spawners that were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm) – into reporting groups by stock (tule, brights), origin (hatchery, wild), sex, and age.

Group	Variable	Parameter	Period													
			1	2	3	4	5	6	7	8	9	10	11	12	13	14
Jack	Stock	Tule	3	1	3	4	0	1	0	0	0					
		Total	3	1	3	4	7	23	21	16	3					
	Origin	Hatchery	413	567	398	193	63	24	2	4	0					
		Total	480	747	603	518	837	1813	1275	745	529					
	Age	Age-2	4	11	6	6	10	36	29	0	2					
		Age-3	0	1	1	1	3	12	3	0	0					
		Age-4	0	0	0	0	0	0	0	0	0					
		Age-5	0	0	0	0	0	0	0	0	0					
Age-6		0	0	0	0	0	0	0	0	0						
Female	Stock	Tule	1	2	1	3	4	0	1	0	0	0	0	0	0	0
		Total	1	2	1	3	4	7	16	7	21	14	2	2	1	1
	Origin	Hatchery	62	351	567	398	193	63	24	0	2	4	0	0	0	0
		Total	73	407	747	603	518	837	1440	373	1275	547	198	245	159	125
	Age	Age-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Age-3	2	17	23	10	13	14	10	0	8	6	0	2	0	0
		Age-4	17	62	69	39	51	78	55	9	47	31	6	17	10	8
		Age-5	4	34	34	16	31	113	64	18	51	42	12	15	9	3
Age-6		0	0	0	0	0	0	0	0	0	0	0	0	0	1	
Male	Stock	Tule	1	2	1	3	4	0	1	0	0	0	0	0	0	
		Total	1	2	1	3	4	7	16	7	21	16	2	1	1	
	Origin	Hatchery	62	351	567	398	193	63	24	0	2	4	0	0	0	
		Total	73	407	747	603	518	837	1440	373	1275	745	245	159	125	
	Age	Age-2	0	0	0	2	0	1	0	0	0	0	0	0	0	
		Age-3	9	51	59	29	23	20	24	5	10	7	1	1	0	
		Age-4	12	44	28	25	25	52	40	12	40	21	7	6	4	
		Age-5	4	10	11	8	14	32	18	7	33	15	5	4	6	
Age-6		0	0	0	0	0	0	0	0	0	0	0	1	0		

Table C7. 2016 mark-recapture summary statistics used to estimate the abundance of mainstem North Fork Lewis River fall-run Chinook spawners using a Jolly-Seber open population model. Estimates were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm). "j.date" was formatted as the number of day of year. Periods "-1" and "+1" only apply to "j.date" data where an additional date was needed before the first period and after the last period to run the model.

Statistic	Group	Period																		
		-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	+1
j.date	Jack	281	288	313	320	327	333	341	353	360	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female	259	266	271	279	285	292	299	306	313	320	327	333	341	348	355	363	369	376	383
	Male	264	271	279	285	292	299	306	313	320	327	333	341	348	355	363	369	376	383	NA
n	Jack		18	28	47	35	13	18	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		5	16	170	313	126	89	115	363	655	1027	549	685	452	208	123	60	116	
	Male		14	131	179	75	43	64	318	582	719	287	413	203	98	38	20	18	NA	
R	Jack		18	27	41	28	11	10	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		5	15	88	96	36	27	61	158	279	220	213	163	139	71	50	15	0	
	Male		12	68	54	21	13	36	143	245	148	106	98	57	32	11	7	0	NA	
u	Jack		18	27	41	28	11	10	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		5	15	167	283	122	82	104	325	607	899	474	522	349	153	81	38	84	
	Male		14	129	158	71	39	61	295	537	607	238	318	142	68	20	17	10	NA	
z	Jack		0	1	1	0	6	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		0	0	1	1	2	3	4	3	12	24	52	41	17	23	26	26	0	
	Male		0	1	1	1	3	4	1	13	21	41	21	12	11	8	7	0	NA	
r	Jack		2	6	6	8	3	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		1	4	30	5	8	12	37	57	140	103	152	79	61	45	22	6	0	
	Male		3	21	4	6	4	20	57	120	69	75	52	29	15	2	1	0	NA	
m	Jack		0	1	6	7	2	8	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		0	1	3	30	4	7	11	38	48	128	75	163	103	55	42	22	32	
	Male		0	2	21	4	4	3	23	45	112	49	95	61	30	18	3	8	NA	

Table C8. 2016 biological data summary data used to apportion the abundance estimates of mainstem North Fork Lewis River fall-run Chinook spawners that were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm) – into reporting groups by stock (tule, brights), origin (hatchery, wild), sex, and age.

Group	Variable	Parameter	Period																	
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	
Jack	Stock	Tule	8	0	0	0	0	0	0											
		Total	8	4	6	12	8	3	4											
	Origin	Hatchery	762	12	4	1	0	2	3											
		Total	1268	647	1185	1167	723	850	963											
	Age	Age-2	17	22	30	11	3	6	1											
		Age-3	1	4	8	17	6	2	0											
		Age-4	0	0	1	0	1	0	0											
		Age-5	0	0	0	0	0	0	0											
Age-6		0	0	0	0	0	0	0												
Female	Stock	Tule	1	1	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0	
		Total	1	1	3	3	1	1	1	4	6	12	8	3	1	3	1	1	1	
	Origin	Hatchery	2	19	222	323	129	51	16	12	4	1	0	2	3	0	0	0	0	
		Total	6	28	304	446	193	121	170	647	1185	1167	723	850	492	221	101	55	94	
	Age	Age-2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
		Age-3	0	0	6	10	7	7	6	14	12	11	11	6	7	1	0	0	0	
		Age-4	3	7	61	75	21	15	41	113	193	139	116	91	63	40	29	9	4	
		Age-5	2	5	13	7	7	4	11	23	54	57	71	47	56	21	16	5	9	
Age-6		0	1	0	0	0	0	0	1	2	5	7	2	3	4	3	0	2		
Male	Stock	Tule	1	3	3	1	1	1	0	0	0	0	0	0	0	0	0	0		
		Total	1	3	3	1	1	1	4	6	12	8	3	1	3	1	1	1		
	Origin	Hatchery	21	222	323	129	51	16	12	4	1	0	2	3	0	0	0	0		
		Total	34	304	446	193	121	170	647	1185	1167	723	850	492	221	101	55	94		
	Age	Age-2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0		
		Age-3	2	21	15	6	5	17	35	43	34	20	23	8	5	2	0	0		
		Age-4	5	40	35	13	6	17	79	151	77	58	45	25	21	5	2	1		
		Age-5	1	3	3	1	1	1	21	41	31	20	23	17	4	4	3	1		
Age-6		0	0	0	0	0	0	2	4	2	2	0	0	0	1	1	0			

Table C9. 2017 mark-recapture summary statistics used to estimate the abundance of mainstem North Fork Lewis River fall-run Chinook spawners using a Jolly-Seber open population model. Estimates were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm). "j.date" was formatted the day of year. Periods "-1" and "+1" only apply to "j.date" data where an additional date was needed before the first period and after the last period to run the model.

Statistic	Group	Period																
		-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	+1
j.date	Jack	309	316	324	332	343	357	375	382	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female	271	278	286	291	297	304	311	320	324	332	341	348	354	362	369	375	382
	Male	269	276	286	291	297	309	320	324	332	341	348	354	362	369	375	382	NA
n	Jack		19	11	15	9	8	1	3	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		41	84	100	57	21	89	274	293	481	1118	577	454	234	126	51	
	Male		36	70	65	55	127	202	148	210	329	143	130	75	36	6	NA	
R	Jack		19	10	13	7	4	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		29	38	36	9	3	46	140	168	220	363	231	57	64	26	0	
	Male		20	32	24	9	53	104	82	93	95	53	16	23	7	0	NA	
u	Jack		19	10	13	7	4	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		41	83	93	51	19	88	261	248	428	961	415	301	169	99	38	
	Male		36	68	60	51	126	192	121	179	254	99	83	61	29	5	NA	
z	Jack		0	0	1	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		0	0	0	1	0	1	0	24	43	37	81	56	17	9	0	
	Male		0	0	2	1	0	3	16	32	12	35	12	5	1	0	NA	
r	Jack		1	3	2	3	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		1	7	7	1	2	12	69	72	151	206	128	26	19	4	0	
	Male		2	7	3	0	13	40	47	55	67	24	7	3	0	0	NA	
m	Jack		0	1	2	2	4	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Female		0	1	7	6	2	1	13	45	53	157	162	153	65	27	13	
	Male		0	2	5	4	1	10	27	31	75	44	47	14	7	1	NA	

Table C10. 2017 biological data summary data used to apportion the abundance estimates of mainstem North Fork Lewis River fall-run Chinook spawners that were derived for three groups – jacks (males <60 cm), females, and males (≥60 cm) – into reporting groups by stock (tule, brights), origin (hatchery, wild), sex, and age.

Group	Variable	Parameter	Period														
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Jack	Stock	Tule	5	0	0	0	0	0									
		Total	8	6	4	11	5	1									
	Origin	Hatchery	348	0	3	5	1	0									
		Total	1188	379	620	1736	746	43									
	Age	Age-2	16	8	12	6	2	0									
		Age-3	2	2	1	1	0	0									
		Age-4	1	0	0	0	0	0									
		Age-5	0	0	0	0	0	0									
	Age-6	0	0	0	0	0	0										
Female	Stock	Tule	2	1	2	1	1	0	0	0	0	0	0	0	0	0	0
		Total	2	1	2	1	1	2	1	6	4	7	4	1	2	2	1
	Origin	Hatchery	48	108	109	45	17	14	7	0	3	4	1	0	1	0	0
		Total	77	153	153	102	51	184	468	379	620	1220	516	386	231	129	43
	Age	Age-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Age-3	9	17	11	4	1	7	11	17	16	5	9	2	1	2	0
		Age-4	17	14	13	2	2	27	76	96	103	162	96	18	28	7	6
		Age-5	12	6	7	2	0	11	42	46	87	163	93	23	29	16	5
	Age-6	0	0	0	0	0	0	0	0	1	1	2	0	0	1	0	
Male	Stock	Tule	2	1	2	1	1	0	0	0	0	0	0	0	0	0	
		Total	2	1	2	1	3	1	6	4	7	4	1	2	2	1	
	Origin	Hatchery	48	108	109	45	31	7	0	3	4	1	0	1	0	0	
		Total	77	153	153	102	235	468	379	620	1220	516	386	231	129	43	
	Age	Age-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
		Age-3	17	21	12	5	16	38	20	16	9	3	1	1	1	0	
		Age-4	12	8	8	3	25	37	42	37	43	21	1	11	3	2	
		Age-5	3	2	4	1	12	21	16	32	31	22	3	9	3	0	
	Age-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

Appendix D – Peak Count Expansion (PCE) Model Inputs, 2013 – 2017

Table D1. Summary of NF Lewis fall-run Chinook data used to develop the peak count expansion (PCE) estimators, 2013 - 2017. The estimated mean and standard deviation (SD) of NF Lewis River fall-run Chinook abundance was generated using a Jolly-Seber (JS) open population mark-recapture model. Peak count (PC) data were summarized three ways: (1) “peak lives + deads” = maximum weekly count of carcasses and live spawners combined, (2) “peak deads” = maximum weekly count of carcasses, and (3) “top 3 deads” = summation of the three highest weekly counts of carcasses. Note: we did not use the “peak lives + dead” count data for brights in 2015 and tules in 2016 to develop the hierarchical PCE as the live count in those two years was not conducted during the known peak time period based on all other years of data.

Stock	Parameter	Year				
		2013	2014	2015	2016	2017
Tule	JS Abundance - mean	3511	4055	5449	4127	2225
	JS Abundance - SD	462	409	381	482	450
	PC – Peak Live + Dead	900	1616	2190	939	663
	PC – Peak Dead	286	644	824	456	167
	PC – Top 3 Dead	784	1540	2026	1018	433
Bright	JS Abundance - mean	17351	20803	18915	9360	7268
	JS Abundance - SD	450	620	992	243	355
	PC – Peak Live + Dead	3878	4945	2372	3209	1832
	PC – Peak Dead	2594	2912	2372	1714	1495
	PC – Top 3 Dead	7010	7406	5564	4147	2901

Appendix E – Plots of Run-Timing by Stock and Origin

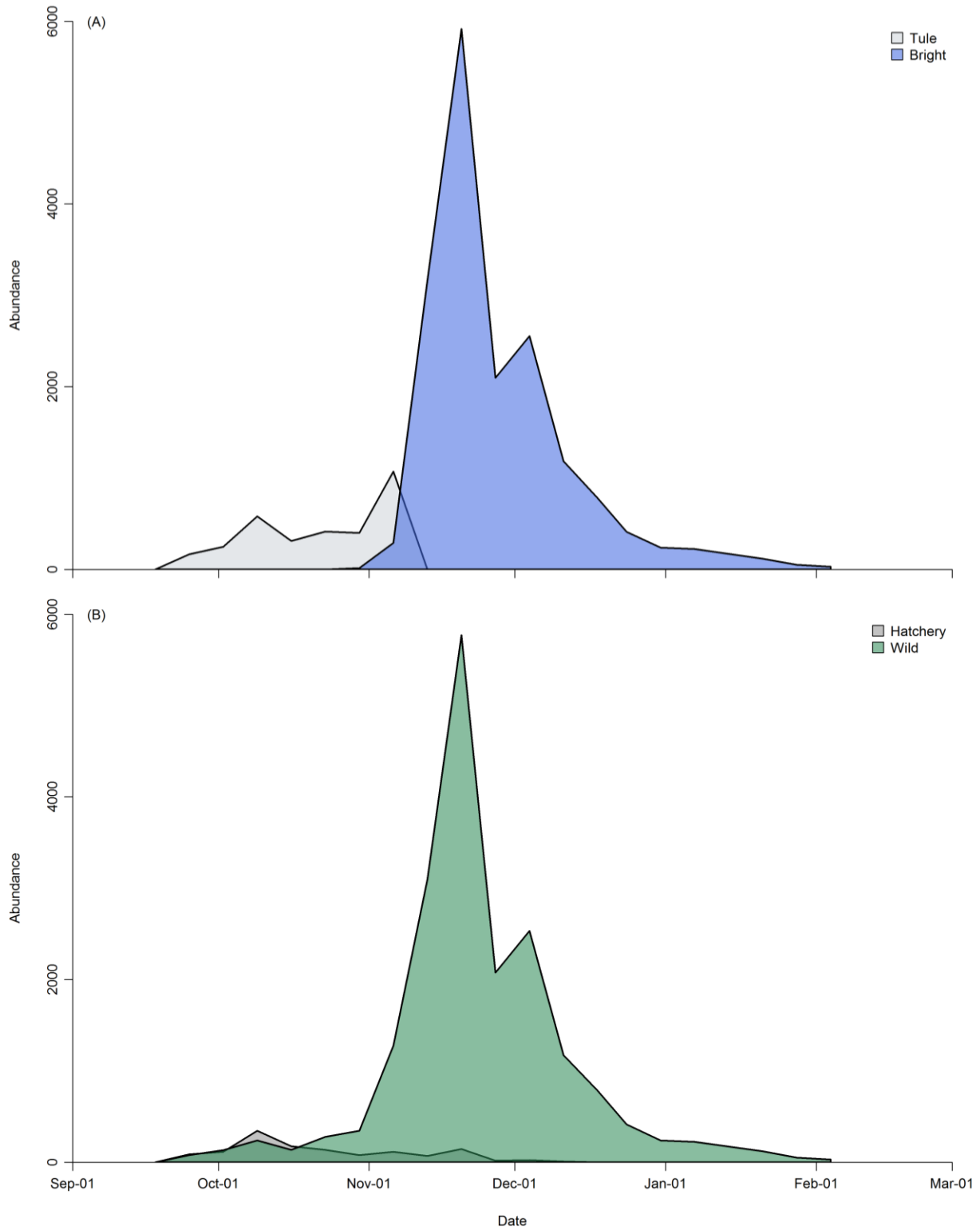


Figure E1. 2013 weekly abundance of fall-run Chinook by (A) stock (tule, bright) and (B) origin (hatchery, wild) in the NF Lewis. Estimates of abundance were derived using an open Jolly-Seber estimator applied to mark-recapture carcasses recovery data.

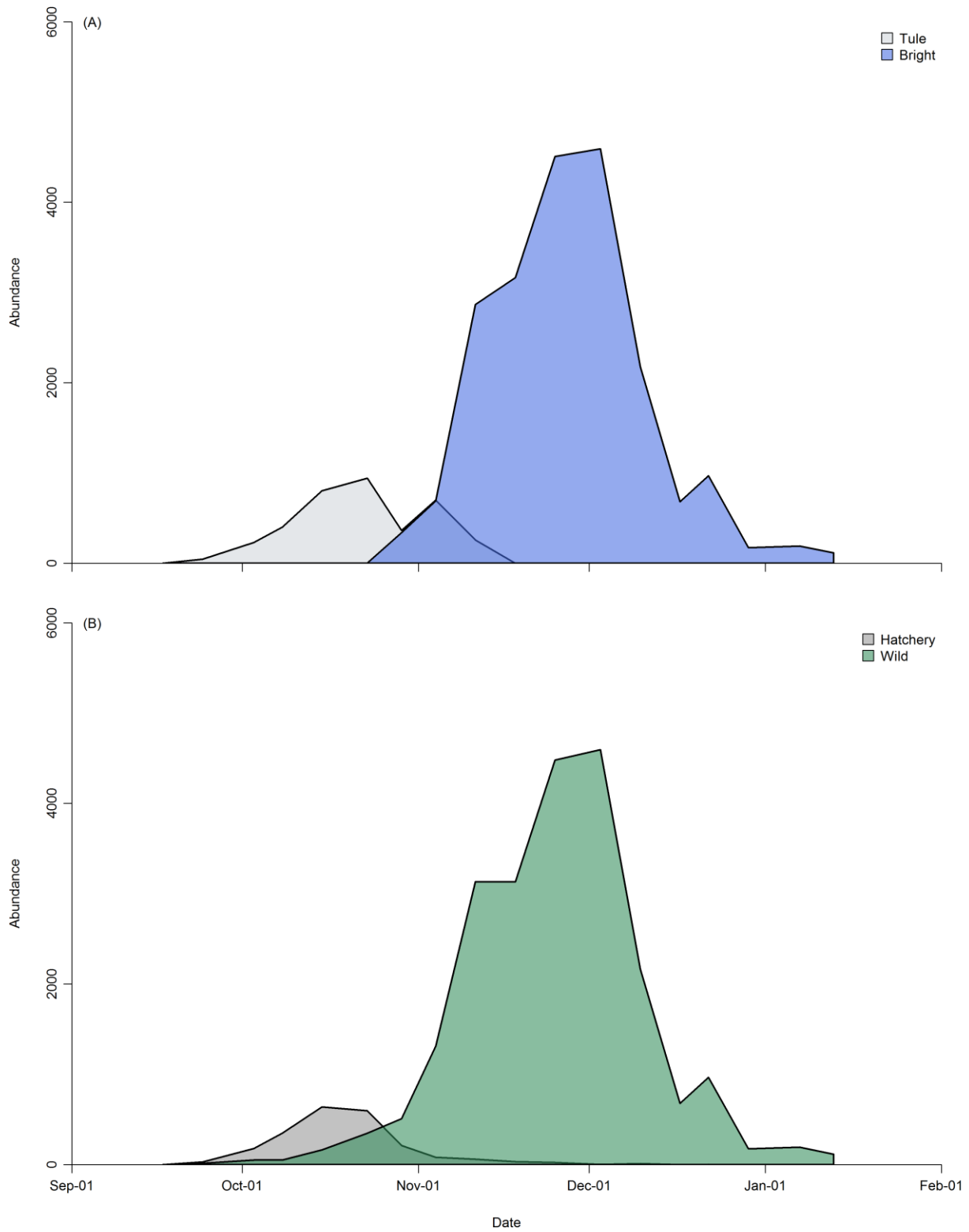


Figure E2. 2014 weekly abundance of fall-run Chinook by (A) stock (tule, bright) and (B) origin (hatchery, wild) in the NF Lewis. Estimates of abundance were derived using an open Jolly-Seber estimator applied to mark-recapture carcasses recovery data.

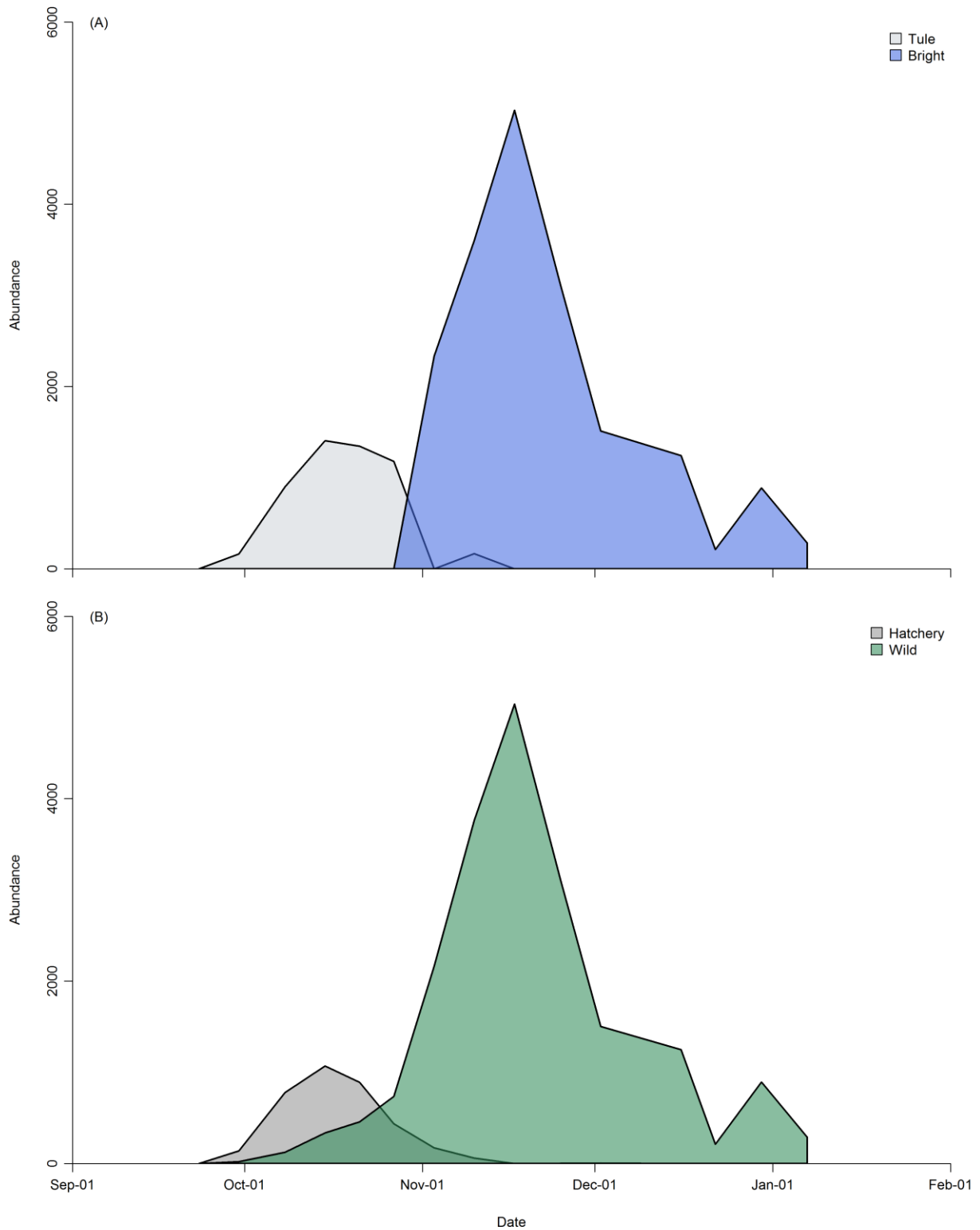


Figure E3. 2015 weekly abundance of fall-run Chinook by (A) stock (tule, bright) and (B) origin (hatchery, wild) in the NF Lewis. Estimates of abundance were derived using an open Jolly-Seber estimator applied to mark-recapture carcasses recovery data.

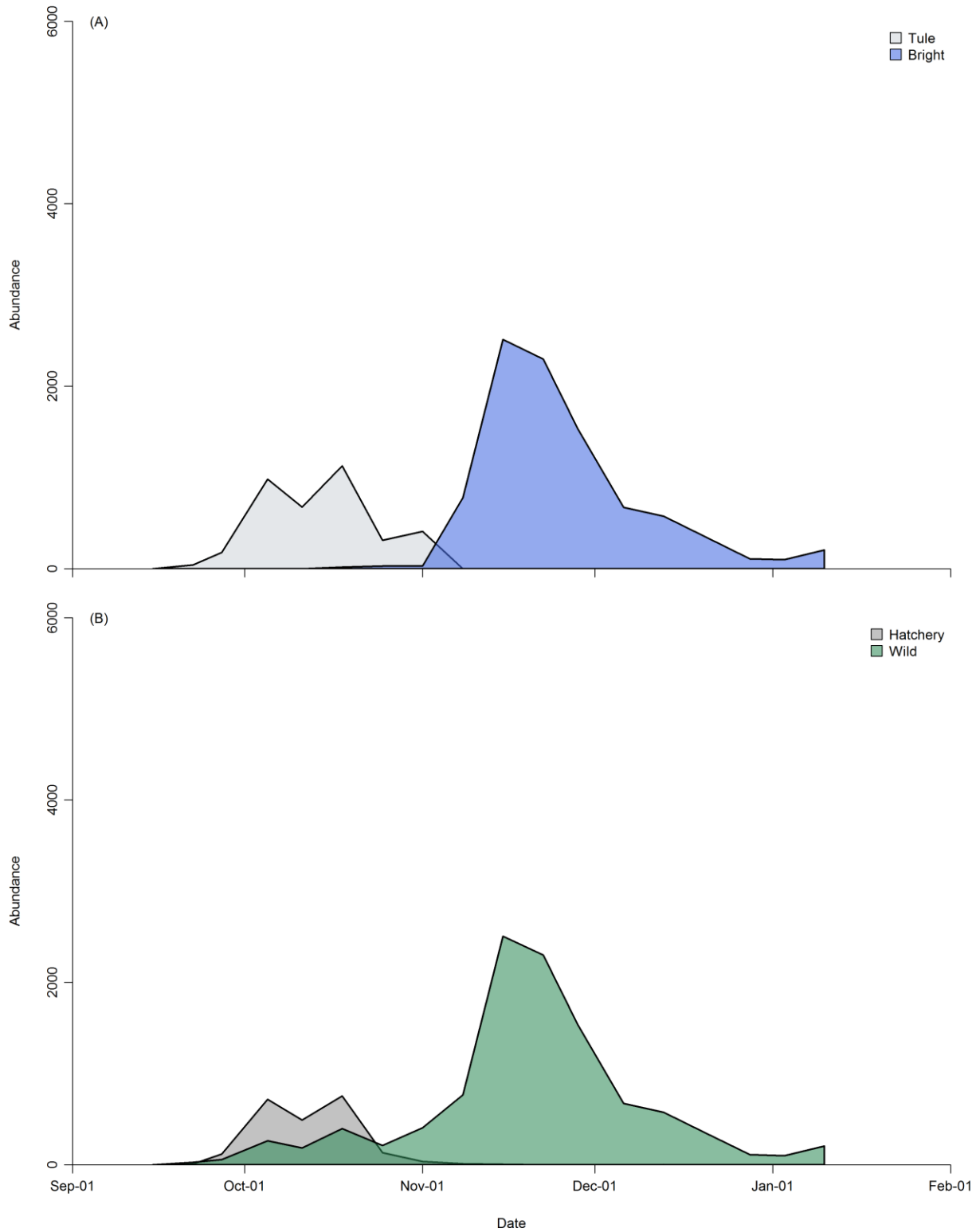


Figure E4. 2016 weekly abundance of fall-run Chinook by (A) stock (tule, bright) and (B) origin (hatchery, wild) in the NF Lewis. Estimates of abundance were derived using an open Jolly-Seber estimator applied to mark-recapture carcasses recovery data.

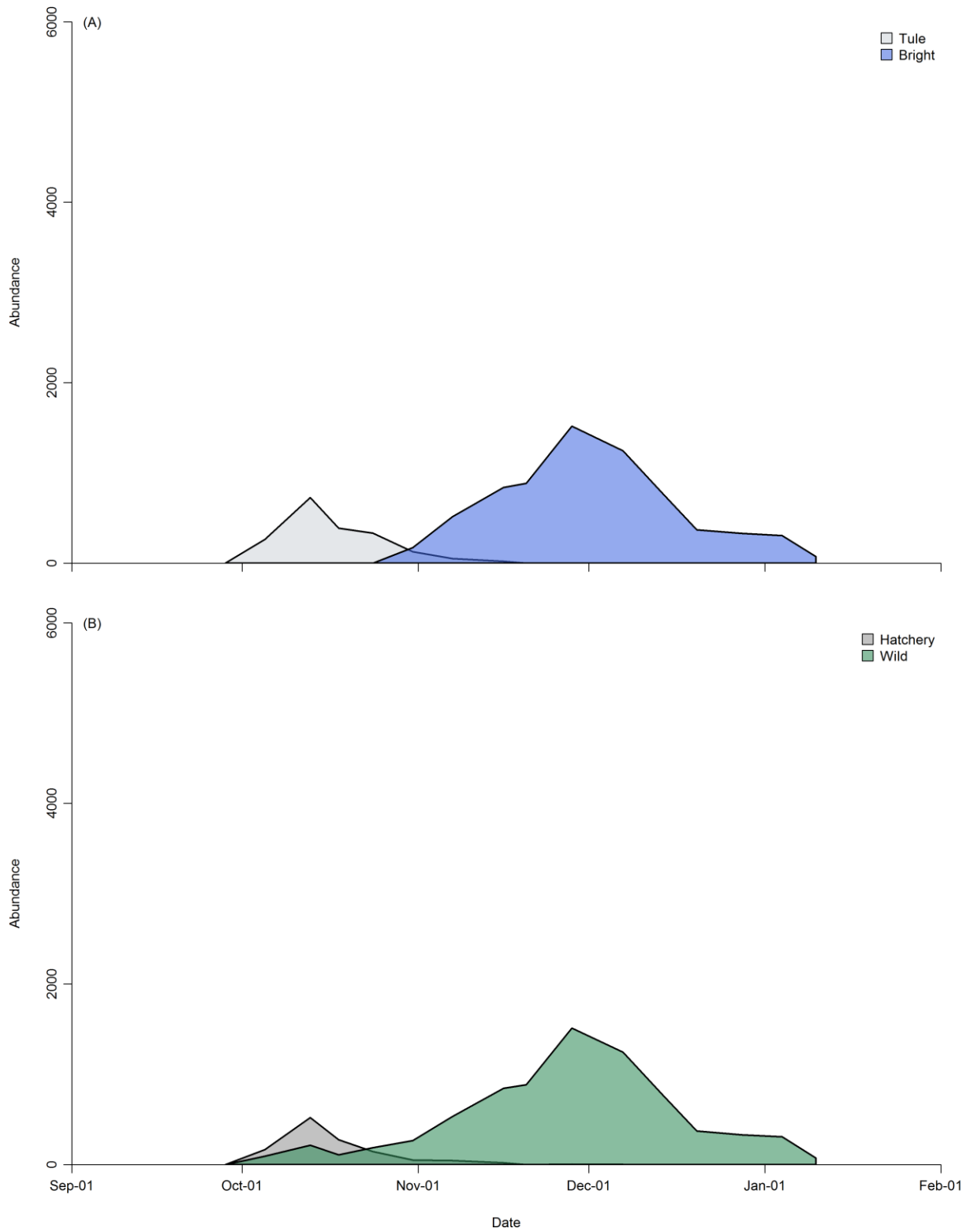


Figure E5. 2017 weekly abundance of fall-run Chinook by (A) stock (tule, bright) and (B) origin (hatchery, wild) in the NF Lewis. Estimates of abundance were derived using an open Jolly-Seber estimator applied to mark-recapture carcasses recovery data.

Appendix F – Comparison of abundance estimates

Table F1. Comparison of abundance estimates derived for North Fork Lewis River fall-run Chinook salmon, 2013 - 2017, using the Jolly-Seber (JS), Bright-eye method (BEM), and peak count expansion (PCE) estimators. Absolute difference and absolute percent (%) error in abundance were calculated for the BEM and PCE estimates relative to the JS estimates.

		Abundance Estimator												
Year	Group	J-S	BEM		PCE - Peak Live + Dead			PCE - Peak Dead			PCE - Top 3 Dead			
		Estimate (mean)	Estimate (mean)	Abs. Diff.	Abs. % Error	Estimate (mean)	Abs. Diff.	Abs. % Error	Estimate (mean)	Abs. Diff.	Abs. % Error	Estimate (mean)	Abs. Diff.	Abs. % Error
2013	Tules	3,511	5,427	1,916	55%	2,831	680	19%	2,535	976	28%	2,988	523	15%
	Brights	17,351	16,421	930	5%	15,925	1,426	8%	16,842	509	3%	19,457	2,106	12%
	Total	20,862	21,847	985	5%	18,756	2,106	10%	19,376	1,486	7%	22,446	1,584	8%
2014	Tules	4,055	3,917	138	3%	5,083	1,028	25%	5,708	1,653	41%	5,870	1,815	45%
	Brights	20,803	22,493	1,690	8%	20,204	599	3%	18,906	1,897	9%	20,556	247	1%
	Total	24,859	26,410	1,551	6%	25,287	428	2%	24,614	245	1%	26,426	1,567	6%
2015	Tules	5,449	5,633	184	3%	6,162	713	13%	7,303	1,854	34%	7,722	2,273	42%
	Brights	18,915	10,826	8,089	43%	9,741	9,174	49%	15,400	3,515	19%	15,444	3,471	18%
	Total	24,364	16,459	7,905	32%	15,903	8,461	35%	22,703	1,661	7%	23,166	1,198	5%
2016	Tules	4,127	2,776	1,351	33%	1,434	2,693	65%	4,041	86	2%	3,880	247	6%
	Brights	9,360	9,699	339	4%	12,098	2,738	29%	11,128	1,768	19%	11,511	2,151	23%
	Total	13,487	12,631	856	6%	13,532	45	0%	15,170	1,683	12%	15,391	1,904	14%
2017	Tules	2,255	1,651	604	27%	2,085	170	8%	1,480	775	34%	1,650	605	27%
	Brights	7,268	6,387	881	12%	7,100	168	2%	9,706	2,438	34%	8,052	784	11%
	Total	9,523	8,038	1,485	16%	9,186	337	4%	11,186	1,663	17%	9,703	180	2%

