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Coded-Wire Tag Expansion Factors for Chinook Salmon Carcass Surveys in California: Estimating the Numbers and Proportions of Hatchery-Origin Fish

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ABSTRACT

Recovery of fish with adipose fin clips (adc) and coded-wire tags (cwt) in escapement surveys allows calculation of expansion factors used in estimation of the total number of fish from each adc,cwt release group, allowing escapement to be resolved by age and stock of origin. Expanded recoveries are used to derive important estimates such as the total number and proportion of hatchery-origin fish present. The standard estimation scheme assumes accurate visual classification of adc status, which can be problematic for decomposing carcasses. Failure to account for this potential misclassification can lead to significant estimation bias. We reviewed sample expansion factors used for the California Central Valley Chinook salmon 2010 carcass surveys in this context. For upper Sacramento River fall-run and late fall-run carcass surveys, the estimated proportions of adc,cwt fish for fresh and non-fresh carcasses differed substantially, likely from the under-recognition of adc fish in non-fresh carcasses. The resulting estimated proportions of hatchery-origin fish in the upper Sacramento River

fall-run and late fall-run carcass surveys were 2.33 to 2.89 times higher if only fresh carcasses are considered. Similar biases can be avoided by consideration of only fresh carcasses for which determination of adc status is relatively straightforward; however, restricting the analysis entirely to fresh carcasses may limit precision because of reduced sample size, and is only possible if protocols for sampling and recording data ensure that the sample data and results for fresh carcasses can be extracted. Thus we recommend sampling protocols that are clearly documented and separately track fresh versus non-fresh carcasses, either collecting only definitively adc fish or that carefully track non-fresh carcasses that are definitively adc versus those that are possibly adc. This would allow judicious use of non-fresh carcass data when sample sizes are otherwise inadequate.

KEY WORDS

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INTRODUCTION

Quality estimates of Chinook salmon (*Oncorhynchus tshawytscha*) escapement to California's Central Valley are needed for several purposes. The Pacific Fishery Management Council relies on estimates of Sacramento River fall-run escapement to evaluate the ocean fishery's consistency with harvest and conservation objectives (PFMC 2012a). The state's "Salmon, Steelhead Trout, and Anadromous Fisheries Program Act" and the federal "Central Valley Project Improvement Act" both establish goals related to spawner numbers and production (Bergman et al. 2012). Escapement metrics also underlie several viability criteria (Lindley et al. 2007) applied to Central Valley salmonid populations, which include the threatened spring run and the endangered winter run.

While there is much focus on total escapement, there is an increasing appreciation of the importance of age structure (PFMC 2008, p. 23; PFMC 2012b, p. 3), understanding the relative contribution of fish spawned in hatcheries versus in natural areas (Lindley et al. 2007; CA HSRG 2012), and documenting and controlling straying rates of hatchery-produced fish (CA HSRG 2012). Although a variety of techniques can provide small-scale information on some of these metrics (e.g. scales for aging, otolith microchemistiy for natal origin), the largest potential data source relevant to age and stock of origin comes from the marking and tagging program used by all Chinook salmon hatcheries in California. The mark used is an adipose fin clip (adc), and the tag used is a coded-wire tag (cwt), which is a short length of metal wire inserted into the nasal cartilage of fish, bearing an inscribed tag code that is unique to each release group (Johnson 1990; Nandor et al. 2010). In California, all Chinook salmon that receive a cwt also receive an adc, and vice-versa, making them adc,cwt. The adc thus provides a visual means of identifying coded-wire tagged fish. In practice some fish may receive adc but not cwt or vice versa because of the inherent challenges in processing thousands or millions of fish, but typically this occurs at rates below 1%.

With the recovery of fish that are marked and tagged in sample surveys designed for the estimation of harvest and escapement, it is possible to assess hatchery-origin vs. natural-origin contribution, release group recovery rates, and stray proportions (Kormos et al. 2012; Hinrichsen et al. 2012). It is also possible to assess early-life survival rates, pre-fishery recruitment, ocean and river harvest rates, and maturation rates with these same data collected across years using cohort-reconstruction methods (Mohr 2006; Hankin and Logan 2010; O'Farrell et al. 2012).

Coded-wire tag recovery depends on adequate sampling of ocean harvest, river harvest, and river and hatchery escapement. The sampling of ocean harvest for cwt recovery is summarized by Nandor et al. (2010), the sampling of river harvest is summarized in Bergman et al. (2012, Appendix C) and in Titus et al. (2010), and escapement sampling is described in Bergman et al. (2012) and in Kormos et al. (2012, Table 1). Survey estimates for ocean harvest are stratified by time, area, sector (i.e., commercial versus recreational), and species. Survey estimates for river harvest are stratified by time, area, species, and run. Survey estimates for natural area spawning escapement are stratified by area, species, and run.

Previously, marking and tagging rates on Sacramento River fall-run Chinook salmon releases were low and variable, limiting the ability to make age- and stock-specific inferences. With the recent initiation of constant fractional marking in Central Valley hatcheries (Buttars 2010), at least 25% of fish from each hatchery release group of Chinook salmon in California are currently marked and tagged. Some release groups are marked and tagged at higher rates, including nearly 100% marking and tagging of "experimental releases" of Central Valley fall-run Chinook salmon as well as late fall run, winter run, and Feather River Hatchery spring run (CA HSRG 2012). Combined with the recent focus on obtaining the best possible estimates of salmon escapement in the Central Valley (Bergman et al. 2012), there exists a great potential for marked and tagged salmon to make increased contributions to Central Valley salmon management,

and it is crucial that these data be collected and analyzed appropriately.

If all release groups of Chinook salmon were 100% adc,cwt, and all adc,cwt fish in the harvest and escapement were recovered, estimating age- and stock-specific escapement would be straightforward. This is not generally the case in California, and thus to obtain estimates of these quantities one must first estimate what fraction of the adc,cwt fish in the harvest or escapement survey stratum were recovered and decoded, and what fraction of the fish in each of the represented release groups were adc,cwt. Each decoded recovery is then expanded by the inverse of these fractions, the so-called "sample" and "production" expansion factors, respectively, so that the recovery data across release groups with different adc,cwt fractions and across sampling strata with different sampling fractions can be appropriately aggregated for assessment. Thus proper estimation of these proportions of fish with adc,cwt is critical to determining the correct value of these expansion factors, and therefore critical to all subsequent calculations and analyses which depend on expanded recovery estimates.

In the sections that follow we present general formulas for the sample and production expansion factors and explain how they influence estimates of release group-specific escapement ($\hat{N}_i$), total escapement of hatchery-origin fish ($\hat{N}_H$), and the proportion of hatchery-origin fish ($\hat{p}_H$). Calculation and interpretation of production expansion factors are relatively straightforward, but sample expansion factors can present difficulties. For harvest and hatchery return surveys, where only fresh fish are encountered and the adc status of an individual fish is effectively certain, estimation of the proportion of fish in the survey stratum that are adc,cwt ($p_{adc,cwt}$) is relatively straightforward and thus so is calculation of the sample expansion factor. But for carcass surveys, which encounter both fresh and non-fresh carcasses, adc status for a non-fresh carcass can be uncertain (eventually it becomes impossible to ascertain once they decay to the point of becoming a "skeleton").

Killam (2009) defines a "fresh" carcass as one having at least one clear eye, relatively firm body texture, or pink gills. For these surveys, estimation of $p_{adc,cwt}$ is less straightforward. We present efficient and unbiased estimators of this component under four alternative assumptions regarding the potential misclassification in non-fresh carcasses: no misclassification, false negatives, false positives, and false negatives/positives. We then explain why, depending on the nature of the potential misclassification, portions of the non-fresh carcass data should or should not be included in the estimation. This is followed by a review of the expansion factors used for the California Central Valley Chinook salmon 2010 carcass surveys (Kormos et al. 2012), which assume no misclassification of adc status. We provide an example of the potential bias this assumption can introduce through an assessment of adc status misclassification in the upper Sacramento River fall-run and late fall-run Chinook salmon 2010 carcass surveys and its effects on derived estimates. We conclude with a summary of appropriate calculations under different scenarios, and then offer practical advice on survey design and when to include non-fresh data in various estimates.

METHODS

Estimating the Number of Hatchery-Origin Fish

For Chinook salmon carcass surveys in California, the total number of release group i fish in the natural area escapement (N_i) is estimated as

$$\hat{N}_i = n_{\text{cwt-decoded},i} \cdot \hat{F}_{\text{samp}} \cdot \hat{F}_{\text{prod},i}, \tag{1}$$

where $n_{\text{cwt-decoded},i}$ denotes the number of release group i decoded cwt recoveries, and the $\hat{F}$ expansion factors scale the number of recoveries to account for the partial sampling of the escapement ($\hat{F}_{\text{samp}}$) and the partial marking and tagging of release group i ($\hat{F}_{\text{prod},i}$). Note that the sampling rate is survey stratum-specific but not code-specific (Kormos et al. 2012), whereas marking and tagging rates are code-specific. Because all California hatchery Chinook

salmon release groups are marked and tagged at some level, total hatchery-origin natural area spawning escapement (N_H) is estimated as

$$\hat{N}_H = \sum_i^m \hat{N}_i , \qquad (2)$$

with the sum taken over the m unique cwt codes observed in the survey that were applied to hatchery-origin fish (potentially, some natural-origin fish may also be adc,cwt). The proportion of the overall escapement composed of hatchery-origin fish (p_H) is then estimated as

$$\hat{p}_H = \hat{N}_H / \hat{N} , \qquad (3)$$

where $\hat{N}$ is the estimated overall natural area escapement (hatchery- and natural-origin fish). Table 1 defines all of the notation used in this paper.

Release group i recovery rate and stray proportion estimates similarly depend on $\hat{F}_{samp}$, but not on $\hat{F}_{prod,i}$ because recovery and straying rates are defined at the release group adc,cwt level (Kormos et al. 2012) and thus are independent of the number of release group i fish that are unmarked or untagged, other release group fish, and natural-origin fish.

Given the form of equations (1), (2) and (3), it is clear that the results of an assessment may be sensitive to the values of $\hat{F}_{samp}$ and $\hat{F}_{prod,i}$. In the sections that follow we present general formulas for the sample and production expansion factors, and show that $\hat{F}_{samp}$ (and hence $\hat{N}_i$, $\hat{N}_H$, and $\hat{p}_H$) depends on an estimate of $p_{adc,cwt}$, the proportion of fish in the stratum that are adc,cwt. We provide efficient and unbiased estimators of this component under four alternative assumptions regarding the potential misclassification in non-fresh carcasses: no misclassification, false negatives, false positives, and false negatives/positives.

Sample Expansion Factor

The sample expansion factor is, by definition, the inverse of the fraction sampled. Specifically, the fraction of the survey stratum adc,cwt fish that were recovered and decoded, and thus

$$F_{samp} = \frac{N_{adc,cwt}}{n_{cwt\text{-}decoded}} . \qquad (4)$$

Noting that $N_{adc,cwt} = N \cdot p_{adc,cwt}$ leads to the following estimator for the sample expansion factor

$$\hat{F}_{samp,c} = \frac{\hat{N} \cdot \hat{p}_{adc,cwt,c}}{n_{cwt\text{-}decoded}} , \qquad (5)$$

where $\hat{p}_{adc,cwt,c}$ depends on the case (c) of potential adc status misclassification involved (described below).

The sample expansion factor is used to scale the observed number of adc,cwt decoded recoveries from release group i in a sample into an estimate of the total number of adc,cwt fish of release group i in the survey stratum. This number includes both adc,cwt for which tags were recovered and decoded as well as adc,cwt present in the survey stratum but for which tags were not decoded. Non-decoding of an adc,cwt fish in the stratum may result from it not being in the sample. Or, it may be in the sample but (a) not recognized as an adc fish, (b) recognized, but the head not processed, (c) recognized, processed, but the cwt not detected, (d) recognized, processed, detected, but the cwt not decoded:

$$\hat{N}_{i,adc,cwt} = n_{cwt\text{-}decoded,i} \cdot \hat{F}_{samp} . \qquad (6)$$

Thus, for each decoded recovery for adc,cwt release group i in a sample, it is estimated that there are ($\hat{F}_{samp} - 1$) non-decoded adc,cwt release group i fish in the survey stratum. The sample expansion factor is survey stratum-specific, not release group-specific, and thus assumes that adc classification and cwt detection probabilities in adc,cwt fish, and successful decoding of a detected cwt, are independent of release group.

For fresh carcasses, we assumed that adc classification is certain. For non-fresh carcasses four cases ($c = 1, 2, 3, 4$) are considered in this paper: (1) *certain* — adc status is correctly classified; (2) *false negatives* — some adc fish are misclassified; (3) *false positives* — some non-adc fish are misclassified; (4) *false negatives/positives* — some adc and non-adc

Table 1 Definition of notation used in this paper

Level	Notation	Definition
General	^	overscript denoting "estimate of" (i.e., $\hat{x}$ is an estimate of x)
	c	case, $c = \{1,2,3,4\}$ (classification scenario for non-fresh carcasses)
	adc	adipose fin clip
	non-adc	no adc
	cwt	coded-wire tag
	adc,cwt	adc and cwt
	non-adc,cwt	not adc,cwt
	fresh	fresh carcass condition
	non-fresh	non-fresh carcass condition
Stratum	N	total number of fish in survey stratum
	N_{adc}	number of adc fish
	$N_{adc,cwt}$	number of adc fish with cwt
	N_i	number of release group i fish
	$N_{i,adc,cwt}$	number of release group i fish with adc and cwt
	p_{adc}	proportion of N with adc
	$p_{adc,cwt}$	proportion of N with adc and cwt
	$p_{cwt|adc}$	proportion of N_{adc} with cwt
	$p_{i|adc,cwt}$	proportion of $N_{adc,cwt}$ that are release group i
	$p_{adc,cwt|i}$	proportion of N_i with adc and cwt
Sample	i	particular release group (common cwt code)
	m	number of unique hatchery-origin cwt codes observed in sample
	n	sample size: number of fish examined for adc status (fresh and non-fresh)
	n_{adc}	number of adc fish
	$n_{head-processed}$	number of heads processed
	$n_{cwt-detected}$	number of cwts detected
	$n_{cwt-decoded}$	number of cwts decoded
	$n_{cwt-decoded,i}$	number of cwts decoded from release group i
	n_{fresh}	number of fresh fish
	$n_{fresh,adc}$	number of fresh fish with adc
	$n_{fresh,head-processed}$	number of fresh fish heads processed
	$n_{fresh,cwt-detected}$	number of fresh fish cwts detected
	$\hat{p}_{adc}$	proportion of n with adc
	$\hat{p}_{adc,cwt,c}$	proportion of n with adc and cwt, case c estimator
	$\hat{p}_{cwt|adc}$	proportion of $n_{head-processed}$ with cwt
	$\hat{p}_{adc|fresh}$	proportion of n_{fresh} with adc
	$\hat{p}_{cwt|fresh,adc}$	proportion of $n_{fresh,head-processed}$ with cwt
	$\hat{p}_{i|adc,cwt}$	proportion of $n_{cwt-decoded}$ from release group i
	$\hat{F}_{prod,i}$	production expansion factor for release group i
	$\bar{F}_{prod}$	average production expansion factor for $n_{cwt-decoded}$ recoveries
	f_e	fraction of $\hat{N}$ sampled (examined for adc status)
	f_a	fraction of n_{adc} with head processed
	f_d	fraction of $n_{cwt-detected}$ successfully decoded
	$\hat{F}_{samp,c}$	sample expansion factor based on $\hat{p}_{adc,cwt,c}$
	$\hat{N}_{H,c}$	estimated number of hatchery-origin fish in survey stratum based on $\hat{F}_{samp,c}$
	$\hat{p}_{H,c}$	estimated proportion of hatchery-origin fish in survey stratum based on $\hat{F}_{samp,c}$
	r_c	ratio, $r_c = \hat{p}_{adc,cwt,c} / \hat{p}_{adc,cwt,1}$

fish are misclassified (Table 2). For all carcasses it is assumed that a cwt is detected in a processed head if present, which implies that failure to detect a cwt in an adc fish means the fish was not tagged or it shed its tag prior to sampling, both of which are accounted for by F_{prod}. Following Mohr (2002) and O'Farrell et al. (2012), because the cwt status (present or not present) will not necessarily be known for all carcasses classified as adc (e.g., head not collected, lost, or not processed), the $p_{\mathrm{adc,cwt}}$ estimators are based on the factorization

$$p_{\mathrm{adc,cwt}} = p_{\mathrm{adc}} \cdot p_{\mathrm{cwt|adc}},\qquad(7)$$

both components of which are estimable from data collected during carcass surveys. For Chinook salmon carcass surveys in California, the latter component will typically be near 1 and thus $p_{\mathrm{adc,cwt}}$ is largely determined by the value of p_{adc}.

Production Expansion Factor

The production expansion factor for release group i is, by definition, the inverse of the fraction marked and tagged or specifically, the fraction of the survey stratum release group i fish that are adc,cwt, and thus

$$F_{\mathrm{prod},i} = \frac{N_i}{N_{i,\mathrm{adc,cwt}}}\ .\qquad(8)$$

Noting that $N_{i,\mathrm{adc,cwt}} = N_i \cdot p_{\mathrm{adc,cwt|}i}$ leads to the following estimator for the production expansion factor

$$\hat{F}_{\mathrm{prod},i} = \hat{p}^{-1}_{\mathrm{adc,cwt|}i},\qquad(9)$$

where $\hat{p}_{\mathrm{adc,cwt|}i}$ is taken to be the estimated proportion of release group i that were adc,cwt at the time of release. This adc,cwt estimated proportion includes only fish that received an adc and retained a cwt; it does not include adc fish without cwt, or cwt fish without adc (Kormos et al. 2012).

Table 2 Qualitative summary of non-fresh carcass classification accuracy under Cases 1 through 4. For a given case/truth-state, a dot (•) indicates some or all sampled carcasses are correctly classified, and an "X" indicates some sampled carcasses are incorrectly classified. The top row legend defines the nature of correct/incorrect classification, with "positive" referring to adc classification, and "negative" referring to non-adc classification. The appropriate estimator $\hat{p}_{\mathrm{adc,cwt},c}$ for each case is noted.

			Classification		
Case (c)	**Description**	**Truth**	**adc**	**non-adc**	$\hat{p}_{\mathrm{adc,cwt},c}$
		adc	true positive	false negative	
		non-adc	false positive	true negative	
1	certain	adc	•		$\hat{p}_{\mathrm{adc}} \cdot \hat{p}_{\mathrm{cwt|adc}}$
		non-adc		•	
2	false negatives	adc	•	X	$\hat{p}_{\mathrm{adc|fresh}} \cdot \hat{p}_{\mathrm{cwt|adc}}$
		non-adc		•	
3	false positives	adc	•		$\hat{p}_{\mathrm{adc|fresh}} \cdot \hat{p}_{\mathrm{cwt|fresh,adc}}$
		non-adc	X	•	
4	false negatives/positives	adc	•	X	$\hat{p}_{\mathrm{adc|fresh}} \cdot \hat{p}_{\mathrm{cwt|fresh,adc}}$
		non-adc	X	•	

The production expansion factor is used to scale the estimated total number of adc,cwt fish from release group i in a survey stratum into an estimate of the total number of fish of release group i in that stratum (adc,cwt fish and non-adc,cwt fish):

$$\hat{N}_i = \hat{N}_{i,\text{adc,cwt}} \cdot \hat{F}_{\text{prod},i} \quad . \tag{10}$$

Thus, for each adc,cwt fish of release group i in a stratum, it is estimated that there are ($\hat{F}_{\text{prod},i} - 1$) non-adc,cwt fish of release group i in that stratum.

Currently, the target marking and tagging proportion for California Chinook salmon fall-run production release groups is 0.25, which if achieved would yield a production expansion factor of $1/0.25 = 4$. For fall-run experimental release groups, and late fall-run, spring-run, and winter-run release groups, the target marking and tagging proportion is 1, which if achieved would yield a production expansion factor of 1. The marking and tagging proportion actually achieved for any particular release group deviates somewhat from these targets because of the inherent challenges involved in the marking and tagging of thousands or millions of fish, but it is assumed to be relatively well estimated at the time of release.

RESULTS

Unbiased Estimators

In the four subsections below, we present unbiased estimators of p_{adc} and $p_{\text{cwt|adc}}$ under the four cases of misclassification considered. The component estimators are statistically independent of each other in each case, and thus their product as an estimator for $p_{\text{adc,cwt}}$ is also unbiased.

Case 1—Certain

In this case, all adc fish are correctly classified. This characterizes most harvest and hatchery return surveys, or carcass surveys that consider only fresh carcasses. When there is no misclassification, all sampled fish can be used to estimate $p_{\text{adc,cwt}}$ as

$$\hat{p}_{\text{adc,cwt,1}} = \hat{p}_{\text{adc}} \cdot \hat{p}_{\text{cwt|adc}}, \tag{11}$$

with

$$\hat{p}_{\text{adc}} = \frac{n_{\text{adc}}}{n}, \tag{12}$$

the observed fraction of adc fish in the sample (of those examined for adc status), and

$$\hat{p}_{\text{cwt|adc}} = \frac{n_{\text{cwt-detected}}}{n_{\text{head-processed}}}, \tag{13}$$

the observed fraction of processed heads of adc fish in the sample for which a cwt was detected. Substituting equation (11) into equation (5) gives

$$\hat{F}_{\text{samp,1}} = \frac{\hat{N} \cdot \hat{p}_{\text{adc}} \cdot \hat{p}_{\text{cwt|adc}}}{n_{\text{cwt-decoded}}}, \tag{14}$$

and substituting equations (12) and (13) into equation (14) and rearranging terms yields the sample expansion factor equation used by Kormos et al. (2012),

$$\hat{F}_{\text{samp,1}} = \left[\frac{n}{\hat{N}} \cdot \frac{n_{\text{head-processed}}}{n_{\text{adc}}} \cdot \frac{n_{\text{cwt-decoded}}}{n_{\text{cwt-detected}}} \right]^{-1} = \left[f_e \cdot f_a \cdot f_d \right]^{-1}. \tag{15}$$

Thus, $\hat{F}_{\text{samp,1}}^{-1}$ may be thought of as the estimated sampling fraction (f_e) as reduced by the "subsampling" of observed adc fish heads that were processed (f_a), and of detected cwts that were decoded (f_d).

Case 2—False Negatives

In this case, some adc fish are misclassified as non-adc in non-fresh carcasses. For example, with a non-fresh carcass, a sampler might classify the status as adc "only when fairly certain of it," or, as one reviewer of this manuscript suggested, some samplers may deliberately under-sample and under-report marked carcasses. When there are false negatives, the overall fraction of adc-classified fish is biased low for p_{adc}, and p_{adc} should be estimated based on the fresh carcass data only. However, since the non-fresh fish classified as adc are in fact adc, the entire sample (fresh and non-fresh carcasses) can be used to unbiasedly estimate $p_{cwt|adc}$. Therefore,

$$\hat{p}_{adc,cwt,2} = \hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|adc} , \qquad (16)$$

with

$$\hat{p}_{adc|fresh} = \frac{n_{fresh,adc}}{n_{fresh}} , \qquad (17)$$

the observed fraction of adc fish among the fresh carcasses sampled. Substituting equation (16) into equation (5) gives

$$\hat{F}_{samp,2} = \frac{\hat{N} \cdot \hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|adc}}{n_{cwt-decoded}} . \qquad (18)$$

Case 3—False Positives

In this case, some non-adc fish are misclassified as adc in non-fresh carcasses. For example, with a non-fresh carcass, a sampler may not be certain about the adc status for some non-adc fish, but classify them as adc fish "just in case they are," or the adipose fin may have been lost to decomposition while the remainder of the fish remained reasonably intact. When there are false positives, the overall fraction of adc-classified fish is biased high for p_{adc}, and the overall fraction of adc-classified heads for which a cwt was detected is biased low for $p_{cwt|adc}$. Because the degree to which these biases would offset one another in the taking of their product is unknown, estimation of both components should be based on the fresh carcass data only. Therefore,

$$\hat{p}_{adc,cwt,3} = \hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|fresh,adc} , \qquad (19)$$

with

$$\hat{p}_{adc|fresh,adc} = \frac{n_{fresh,cwt-detected}}{n_{fresh,head-processed}} , \qquad (20)$$

the observed fraction of adc fresh processed heads for which a cwt was detected. Substituting equation (19) into equation (5) gives

$$\hat{F}_{samp,3} = \frac{\hat{N} \cdot \hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|fresh,adc}}{n_{cwt-decoded}} . \qquad (21)$$

Case 4—False Negatives/Positives

In this case, some adc and non-adc fish are misclassified in non-fresh carcasses. For example, with a non-fresh carcass, a sampler might attribute the missing adipose fin of an adc fish to decomposition, or attribute the decomposed adipose fin of a non-adc fish to adc. When there are both false negatives and false positives, the overall fraction of adc-classified fish is a biased estimator for p_{adc}, but whether it is biased low or biased high would depend on the relative probabilities of misclassification for a false negative versus a false positive, and on the relative numbers of adc versus non-adc carcasses. As in Case 3, the overall fraction of adc-classified heads for which a cwt was detected is biased low for $p_{cwt|adc}$. Thus, as in Case 3, estimation of both components should be based on the fresh carcass data only. Therefore,

$$\hat{p}_{adc,cwt,4} = \hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|fresh,adc} , \qquad (22)$$

and substituting equation (22) into equation (5) gives

$$\hat{F}_{samp,4} = \frac{\hat{N} \cdot \hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|fresh,adc}}{n_{cwt-decoded}} , \qquad (23)$$

noting that $\hat{F}_{samp,4} = \hat{F}_{samp,3}$.

Estimator Interpretation and Sampling Variance

Let us now revisit the estimators for N_i, N_H, and p_H in light of the general formula for $\hat{F}_{samp,c}$.

Substitution of equation (5) into equations (1), (2), and (3) gives

$$\hat{N}_{i,c} = \left[\hat{N} \cdot \hat{p}_{\text{adc,cwt},c} \right] \cdot \hat{p}_{i|\text{adc,cwt}} \cdot \hat{F}_{\text{prod},i} \qquad (24)$$

$$\hat{N}_{H,c} = \left[\hat{N} \cdot \hat{p}_{\text{adc,cwt},c} \right] \cdot \sum_{i=1}^{m} \hat{p}_{i|\text{adc,cwt}} \cdot \hat{F}_{\text{prod},i} = \left[\hat{N} \cdot \hat{p}_{\text{adc,cwt},c} \right] \cdot \bar{F}_{\text{prod}} \qquad (25)$$

$$\hat{p}_{H,c} = \hat{p}_{\text{adc,cwt},c} \cdot \bar{F}_{\text{prod}}, \qquad (26)$$

where $\hat{p}_{i|\text{adc,cwt}} = n_{\text{cwt-decoded},i} / n_{\text{cwt-decoded}}$ is the proportion of decoded cwt recoveries that were release group i, and $\bar{F}_{\text{prod}} = \sum \hat{p}_{i|\text{adc,cwt}} \cdot \hat{F}_{\text{prod},i}$ is the average production expansion factor for the sample's decoded cwt recoveries. Thus, the estimated total number of release group i fish in the stratum, $\hat{N}_{i,c}$, is equal to the estimated total number of adc,cwt fish in the stratum, $\hat{N} \cdot \hat{p}_{\text{adc,cwt},c}$, multiplied by the estimated proportion of them that are release group i, $\hat{p}_{i|\text{adc,cwt}}$, scaled up by $\hat{F}_{\text{prod},i}$ to account for the non-adc,cwt fish in release group i. The estimated total number of hatchery-origin fish in the stratum, $\hat{N}_{H,c}$, is equal to the estimated total number of adc,cwt fish in the stratum, $\hat{N} \cdot \hat{p}_{\text{adc,cwt},c}$, scaled up by the average production expansion factor to account for the non-adc,cwt hatchery-origin fish in the stratum. The estimated proportion of hatchery-origin fish in the stratum, $\hat{p}_{H,c}$, is equal to the estimated proportion of adc,cwt fish for the stratum, $\hat{p}_{\text{adc,cwt},c}$, scaled up by the average production expansion factor to account for the non-adc,cwt hatchery-origin fish in the stratum. Note that because the summation used to calculate $\bar{F}_{\text{prod}}$ occurs only over the m hatchery release groups, $\sum_{i=1}^{m} p_{i|\text{adc,cwt}}$ will be less than 1 if there are marked natural-origin fish in the sampled escapement, so this weighted average will appropriately discount natural-origin cwt,adc fish assuming the $\hat{p}_{i|\text{adc,cwt}}$ are estimated accurately.

Also note that while $\hat{p}_{\text{adc,cwt},c}$ may or may not include the non-fresh carcass data depending on the nature

of misclassification involved, the estimated set of tag code proportions for the adc,cwt fish in the stratum $\{ \hat{p}_{i|\text{adc,cwt}} , \; i = 1,2,...\}$, is based on all cwt-decoded recoveries, whether from fresh or non-fresh carcasses. While one could restrict estimation of $\{ p_{i|\text{adc,cwt}} \}$ to fresh carcasses only, unless there is reason to believe the code composition is different between the fresh and non-fresh carcasses (after all, non-fresh carcasses were once fresh), doing so will reduce the precision of the estimated code composition and average production factor. Now, it is possible that some of the cwt-decoded recoveries came from misclassified non-adc,cwt fish, and if their code composition is notably different than that of the adc,cwt fish, this would introduce bias into $\{ p_{i|\text{adc,cwt}} \}$. For example, the adipose fin clipping "error rate" that generates the non-adc,cwt fish in the first place might vary substantially across release groups. However, the fraction of decoded-cwt recoveries deriving from non-adc fish is expected to be small given that the proportion of cwt fish released without an adc is on the order of 0.002 (estimated based on an unpublished analysis of 2006 through 2008 California hatchery Chinook salmon release data by A. Grover, NOAA).

Note also that, despite the appearance of equation (3), $\hat{p}_{H,c}$ is statistically independent of $\hat{N}$, whereas $\hat{N}_{i,c}$ and $\hat{N}_{H,c}$ are not. If all adc,cwt fish are hatchery-origin and the $\{ \hat{F}_{\text{prod},i} \}$ are relatively constant for the cwt release groups observed in the survey (e.g., for fall-run Chinook salmon production release groups, $\hat{F}_{\text{prod},i} \approx 4$), $\hat{p}_{H,c}$ and $\hat{N}_{H,c}$ will be nearly independent of the estimated code composition $\{ \hat{p}_{i|\text{adc,cwt}} \}$. In this case, the sampling variance of $\hat{p}_{H,c}$ will depend primarily on the variance of $\hat{p}_{\text{adc,cwt},c}$, whereas the sampling variance of $\hat{N}_{H,c}$ will also depend on the variance of $\hat{N}$. The sampling variance of $\hat{N}_{i,c}$ will depend on the variances of $\hat{N}$, $\hat{p}_{\text{adc,cwt},c}$, $\hat{p}_{i|\text{adc,cwt}}$, and $\hat{F}_{\text{prod},i}$.

Review of Expansion Factors Used for the Central Valley Chinook Salmon 2010 Carcass Surveys

Kormos et al. (2012) report the sample and production expansion factors used for the 2010 Central Valley escapement surveys, including the three component elements of $\hat{F}_{\text{samp},1}$: the fraction of carcasses sampled (f_e), the fraction of adc-classified fish whose head was processed (f_a), and the fraction of detected cwts that were decoded (f_d). Below we review the reported values, to the extent possible, for whether they are: (1) consistent with general expectation, (2) notably high or low considering other surveys, and (3) a valid characterization of the underlying sampling process. In the case of the Mokelumne River fall-run Chinook salmon survey, our review focuses on whether the alternative method of estimation used for that survey can be justified using the results presented in this paper. We recognize the logistical challenges inherent in conducting the individual surveys, and in collating information from multiple sources collected through a variety of methods. We chose the Kormos et al. (2012) report for review solely because it provides a published valley-wide example (2010) summary data set, and do not intend this paper to be in any way a criticism of specific agencies, surveys, or studies.

Sample Expansion Factor

As shown in equation (15), the sample expansion factor formulation used by Kormos et al. (2012), $\hat{F}_{\text{samp}} = [f_e \cdot f_a \cdot f_d]^{-1}$, is equivalent to $\hat{F}_{\text{samp},1}$. The Kormos et al. (2012, Table 4) reported values of f_a and f_d are nearly 1 for all ocean and river harvest surveys, and for all hatchery return and natural area escapement surveys. As a result, $\hat{F}_{\text{samp},1} \approx f_e^{-1}$.

Sampled Fraction: f_e

The fraction of fish observed (examined for adc status) in the survey, f_e, was relatively high for the ocean harvest surveys, ranging from 0.23 to 0.79, and quite low for the river harvest surveys, ranging from 0.06 to 0.13. These sampling fractions are con-

sistent with expectations for these survey programs in 2010.

For hatchery returns, the f_e were essentially 1, consistent with the general practice in hatcheries of examining every fish that enters the hatchery for its adc status. For escapement to natural spawning areas, f_e ranged from 0.06 to 0.22 for ten of the sample surveys, 0.56 for Butte Creek spring run, and 1.00 for the remaining five surveys: Mokelumne River fall run, Mill Creek spring run and fall run, Deer Creek fall run, and American River late fall run. The sampling fraction of 0.56 for Butte Creek spring-run spawning escapement is high, but apparently is not unusual for this survey (e.g., in 2008, f_e = 5,238/10,082 = 0.52 [Garman and McReynolds 2009, p.13]).

The f_e value of 1 for Mokelumne River fall run is surprising. Certainly not all natural area spawners were examined for adc status, and the heads from all adc fish collected and processed. As explained by Kormos et al. (2012), the video monitoring system on this river can estimate the total number of adc fish that enter the river. Subtracting the number of adc fish that enter the hatchery and are collected at the hatchery weir provides an estimate of the total number of adc fish that remain in natural areas, $\hat{N}_{\text{adc}}$. This has led to a very different approach being used for the expansion of cwt recoveries in the Mokelumne River, which at least initially appears to be ad hoc. However, the approach can be justified using the results presented earlier in this paper. The N_i estimator described by Kormos et al. (2012), for example, can be obtained by (a) assuming certain classification, (b) substituting equation (11) into equation (24), and (c) replacing $\hat{N} \cdot \hat{p}_{\text{adc}}$ with the video-based $\hat{N}_{\text{adc}}$:

$$\hat{N}_i = \hat{N}_{\text{adc}} \cdot \hat{p}_{\text{cwt|adc}} \cdot \hat{p}_{i|\text{adc,cwt}} \cdot \hat{F}_{\text{prod},i}. \qquad (27)$$

Note that this formula covers the entire expansion; not just the portion due to f_e. For Mokelumne River fall run in 2010, $\hat{N}_{\text{adc}}$ = 820. Because only a small number of adc carcass heads were collected in natural areas during "sporadic surveys," apparently $p_{\text{cwt|adc}}$ and $\{p_{i|\text{adc,cwt}}\}$ were estimated using the hatchery cwt recovery data alone. If so, there is an error in

the reported percent composition results by release-type (Kormos et al. 2012, p. 9) because they are not the same for the hatchery and natural areas, although they appear to be the same in the respective pie charts (Kormos et al. 2012, Figure 8). It is unclear whether the production expansion factor, $\hat{F}_{\text{prod},i}$ was applied as in equation (27), although we suspect it was. The reported value of $f_e = 1$ for this survey is somewhat misleading, and it should not be inferred that there is no uncertainty in the derived estimates, which clearly is not the case. The general estimation approach applied in this system is appropriate, but given the significant numbers of fish released off-site by the fall-run Chinook salmon program at the Mokelumne River Hatchery, the potential clearly exists for a difference in $\{\hat{p}_{i|\text{adc,cwt}}\}$ between natural areas and hatchery returns.

For the other four surveys (Mill Creek spring run and fall run, Deer Creek fall run, and American River late fall run), no information was provided on how many fish in the escapement were not sampled. The value of f_e was thus unknown, but set equal to 1 to allow the $\hat{N}_H$ calculations to proceed. In other words, the sample results were not expanded to the stratum level and pertain only to the fish sampled—not to the total spawning escapement. The results for these surveys are thus biased low for the number of hatchery-origin fish, but not for the proportion of hatchery-origin fish (recall that $\hat{p}_H$ is statistically independent of $\hat{N}$).

Processed Fraction: f_a

The fraction of sampled adc fish whose head was processed, f_a, was effectively 1 for ocean and river harvest surveys, and for hatchery returns. This is reasonable, given that the heads of all adc fish encountered are supposed to be taken in these surveys, and given that the adc status of all encountered fish is readily discernable given their fresh condition. For the natural area escapement surveys, three of the reported f_a values ranged from 0.96 to 0.99 (Feather River fall run, upper Sacramento River fall run and late fall run), and the other 13 reported f_a values were equal to 1. For these surveys, values of f_a near 1 are questionable

given that most derive from carcass surveys, which encounter both fresh and non-fresh carcasses (mostly non-fresh), and it is known that adc status determination can be difficult with non-fresh carcasses. These carcass survey programs have been advised,

> *for a carcass that is too decayed to determine its adc status, its head should not be collected and it should not be counted toward the number of carcasses examined for adc status* (Bergman et al. 2012, p. 34–35).

This would not bias the survey results and f_a near 1 would be appropriate as long as the value reported for n was the number of carcasses examined for which a definitive adc status determination was made, and the value reported for n_{adc} was the number of those carcasses determined to be adc. But if, for example, the value reported for n was the total number of carcasses encountered (whether or not adc status determination was made), and the value reported for n_{adc} was the number of carcasses classified as adc (as opposed to the number that actually were adc), f_a, $\hat{F}_{\text{samp}}$, $\hat{N}_i$, $\hat{N}_H$, and $\hat{p}_H$ would all be biased. In the next section, we examine the direction and magnitude of this potential bias for upper Sacramento River fall-run and late fall-run Chinook salmon 2010 carcass surveys. Similar biases may exist in other surveys, but sufficient data were not available to test for them.

Decoded Fraction: f_d

The fraction of detected cwts that were decoded, f_d, was at least 0.97 for all surveys, and often equal to 1, as would be expected.

Production Expansion Factor

Reported $\hat{F}_{\text{prod},i}^{-1} = \hat{p}_{\text{adc,cwt}|i}$ varied for fall-run production releases from 0.24 to 0.30, for fall-run experimental releases from 0.95 to 1.00, for late fall-run releases from 0.97 to 0.98, and for spring-run releases from 0.96 to 1.00 (Kormos et al. 2012, Table 3),

which is consistent with expectations given the target adc,cwt rates for these release types in California.

Assessment of adc Status in Carcass Surveys

In this section, we evaluate the potential for adc mis-classification in non-fresh carcasses and its effect on $\hat{p}_{adc,cwt,c}$, $\hat{F}_{samp,c}$, $\hat{N}_{i,c}$, $\hat{N}_{H,c}$, and $\hat{p}_{H,c}$ using the 2010 carcass surveys for fall-run and late fall-run Chinook salmon in the upper Sacramento River as case studies. The two survey data sets we chose for this assessment were the only survey data sets analyzed by Kormos et al. (2012) for which we had access to the source data (Killam 2011) at the time this paper was written. The presentation and analysis of these data that follows is based on Killam (2011). Table 3 summarizes the car-cass survey data stratified by carcass condition, which pertains to the classification issue.

The estimated p_{adc} and $p_{cwt|adc}$ for fresh and non-fresh carcasses are fairly consistent between the two surveys. The estimated p_{adc} for fresh carcasses was 3.3 and 5.5 times higher than for non-fresh carcasses in the fall-run and late fall-run surveys, respectively ($p < 0.0001$, one-tailed Fisher's exact tests for both cases). Given that all non-fresh carcasses were once fresh, this suggests substantial under-recognition (or misreporting) of adc fish among the non-fresh car-casses (high false negative rate). The estimated $p_{cwt|adc}$

for fresh carcasses was near 1, but was 1.1 and 1.2 times higher than for non-fresh carcasses in the fall-run and late fall-run surveys, respectively ($p = 0.118$ and $p = 0.053$, respectively, one-tailed Fisher's exact tests, $p = 0.0156$ for fall and late fall combined). This suggests that non-fresh carcasses were classified as adc only when the sampler was fairly certain about the designation, otherwise the estimated $p_{cwt|adc}$ for non-fresh carcasses would have been notably lower. However, the non-fresh carcass $p_{cwt|adc}$ estimates are less than the fresh carcass estimates and this sug-gests that some non-adc fish were misclassified as adc fish among the non-fresh carcasses (low, but non-zero, false positive rate). Thus, of the misclas-sification scenarios described in Sections 3.1 through 3.4, it appears that Case 4, *false negatives/positives*, best characterizes the misclassification in non-fresh carcasses for these surveys in 2010. Note also that, because the non-fresh carcasses comprise 79% and 77% of the total number of carcasses examined for adc status in the fall-run and late fall-run surveys, respectively, $\hat{p}_{adc}$ and $\hat{p}_{cwt|adc}$ over all carcasses (fresh and non-fresh) are much closer to the correspond-ing estimates for non-fresh carcasses than for fresh carcasses. A similar bias may exist in other surveys, such that the hatchery contribution may be underes-timated in other river systems as well.

Table 3 Data from 2010 carcass survey of fall-run and late fall-run Chinook salmon in the upper Sacramento River (Source: Killam 2011, worksheets 10-Sac, CWT Fall-10, CWT Late Fall-10). Table does not include fish of unknown adc status, or skeletons (highly decomposed carcasses). Estimates are survey-condition specific: $\hat{p}_{adc} = n_{adc} / n$ and $\hat{p}_{cwt|adc} = n_{cwt\text{-}detected} / n_{head\text{-}processed}$.

Survey	Condition	n	n_{adc}	$n_{head\text{-}processed}$	$n_{cwt\text{-}detected}$	$\hat{p}_{adc}$	$\hat{p}_{cwt|adc}$
Fall run	Fresh	290	59	58	55	0.20	0.95
	Non-fresh	1124	70	70	61	0.06	0.87
	All	1414	129	128	116	0.09	0.91
Late fall run	Fresh	187	28	27	27	0.15	1.00
	Non-fresh	622	17	17	14	0.03	0.82
	All	809	45	44	41	0.06	0.93

To evaluate the sensitivity of $\hat{p}_{adc,cwt,c}$, $\hat{F}_{samp,c}$, $\hat{N}_{i,c}$, $\hat{N}_{H,c}$, and $\hat{p}_{H,c}$ to the case (c) of potential misclassification for these data (c = 1,2,3,4), note that for a given data set, $\hat{F}_{samp,c}$, $\hat{N}_{i,c}$, $\hat{N}_{H,c}$, and $\hat{p}_{H,c}$ are all a scalar multiple of their c = 1 values:

$$\hat{F}_{samp,c} = \hat{F}_{samp,1} \cdot r_c, \; \hat{N}_{i,c} = \hat{N}_{i,1} \cdot r_c, \; \hat{N}_{H,c} = \hat{N}_{H,1c} \cdot r_c, \; \hat{p}_{H,c} = \hat{p}_{H,1} \cdot r_c \tag{28}$$

where

$$r_c = \frac{\hat{p}_{adc,cwt,c}}{\hat{p}_{adc,cwt,1}} \tag{29}$$

[see equations (5), (24), (25), (26)]. Table 4 lists $\{\hat{p}_{adc,cwt,c}; c = 1,2,3,4\}$ for these data obtained by applying equations (11), (16), (19), and (22) to the p_{adc} and $p_{cwt|adc}$ estimates derived in Table 3, along with the resulting ratios $\{r_c; c = 1,2,3,4\}$. Applying these ratios to the reported values of $\hat{F}_{samp,1}$ (Kormos et al. 2012, Table 4) and $\hat{p}_{H,1}$ (Kormos et al. 2012, Figure 4) yields the $\{\hat{F}_{samp,c}; c = 2,3,4\}$ and $\{\hat{p}_{H,c}; c = 2,3,4\}$ values listed in Table 4. From the reported $\hat{N}$ (Kormos et al. 2012, Table 4), $\hat{N}_{H,1} = \hat{N} \cdot \hat{p}_{H,1}$ was derived and the ratios $\{r_c; c = 2,3,4\}$ applied to obtain the $\{\hat{N}_{H,c}; c = 2,3,4\}$ values listed in Table 4. Values of $\{\hat{N}_{i,1}\}$ are not reported in Kormos et al. (2012).

The resulting estimates for these data sets are clearly sensitive to the choice of the p_{adc} estimator. Since the sample expansion factor, the estimated number of hatchery-origin fish, and the estimated proportion of hatchery-origin fish all scale up with the p_{adc} estimate, all three quantities are 2.23 to 2.69 times higher if $\hat{p}_{adc|fresh}$ rather than $\hat{p}_{adc}$ is used as an estimate of p_{adc} (i.e., c = 2 versus c = 1). The estimates are much less sensitive to the $p_{cwt|adc}$ estimator (c = 3,4 versus c = 2, which differ imperceptibly for fall run and by a factor of 1.07 for late fall run), as would be expected given that the difference between $\hat{p}_{cwt|adc}$ and $\hat{p}_{cwt|fresh,adc}$ was not large. Combining both sources of bias, the sample expansion factor, estimated number of hatchery-origin fish, and estimated proportion of hatchery-origin fish is 2.33 to 2.89 times higher if $\hat{p}_{adc|fresh} \cdot \hat{p}_{cwt|fresh,adc}$ is used as an estimator of $p_{adc,cwt}$ rather than $\hat{p}_{adc} \cdot \hat{p}_{cwt|adc}$.

Table 4 Sensitivity of estimators to the case (c) of potential adc status misclassification with the data from 2010 carcass survey of fall-run and late fall-run Chinook salmon in the upper Sacramento River. Case 1 assumes adc status is determined without error and includes both fresh and non-fresh carcass data in estimating the proportion of fish with cwt and adc ($\hat{p}_{adc,cwt,c}$). Case 2 assumes false negatives only (some fish non-fresh carcasses with adc are classified as non-adc) and excludes non-fresh carcass data from the calculation of p_{adc} but not $p_{cwt|adc}$. Case 3 assumes false positives only, while Case 4 assumes both false negatives and false positives, in both cases only fresh carcass data are used. The ratio of $\hat{p}_{adc,cwt,c}$ to $\hat{p}_{adc,cwt,1}$ is given by r_c. Note that the sample expansion factor ($\hat{F}_{samp,c}$), proportion of hatchery-origin fish ($\hat{p}_{H,c}$), and number of fish of hatchery origin ($\hat{N}_{H,c}$) all have this same ratio with respect to their Case 1 value.

Survey	Case (c)	$\hat{p}_{adc,cwt,c}$	r_c	$\hat{F}_{samp,c}$	$\hat{p}_{H,c}$	$\hat{N}_{H,c}$
Fall run	1	0.08	1	11.66	0.20	3,274
	2	0.18	2.23	26.00	0.45	7,302
	3	0.19	2.33	27.21	0.47	7,641
	4	0.19	2.33	27.21	0.47	7,641
Late fall run	1	0.05	1	5.52	0.06	257
	2	0.14	2.69	14.86	0.16	692
	3	0.15	2.89	15.95	0.17	742
	4	0.15	2.89	15.95	0.17	742

DISCUSSION

The potential for serious estimation bias in salmon carcass surveys arising from misclassification (or mis-reporting) of adc status in non-fresh carcasses does not appear to be fully appreciated. Hinrichsen et al. (2012) and Kormos et al. (2012), for example, do not mention this issue. Also, some of the Chinook salmon carcass surveys in California appear not to be sepa-rately tracking the fresh/non-fresh carcass data for cwt expansion purposes (Kormos et al. 2012, Table 1), although this is certainly not true of all surveys. The Sacramento River winter-run Chinook salmon carcass survey, for example, has for many years used $\hat{p}_{\mathrm{adc|fresh}}$ as an estimator of p_{adc} in developing that survey's cwt sample expansion factor (USFWS 2011, Appendix A-1).

The importance of obtaining quality estimates $\hat{F}_{\mathrm{prod},i}$ and $\hat{F}_{\mathrm{samp}}$ is hard to overstate given the multiplica-tive form of the estimators $\hat{N}_i$, $\hat{N}_H$, and $\hat{p}_H$. For $\hat{F}_{\mathrm{prod},i}$ this requires a good estimate of the proportion of release group i fish that are adc,cwt at the time of release, especially for production releases of fall-run Chinook salmon given their target adc,cwt fraction of 0.25 (expansion factor of 4). For $\hat{F}_{\mathrm{samp}}$ this requires a detailed adc and cwt sampling plan at a minimum, as described in the final section of this paper.

For Chinook salmon carcass surveys in California, $\hat{F}_{\mathrm{samp}}$ is equal to the estimated number of adc,cwt fish in the escapement divided by the number of adc,cwt decoded recoveries, with the numerator in turn being equal to the estimated total escapement multiplied by an estimate of the proportion of the escapement that is adc,cwt. This latter estimate can be seriously biased if adc status misclassification in non-fresh carcasses is not properly accounted for. The $\{\hat{N}_i\}$ from a car-cass survey are used to generate a variety of other estimates besides $\hat{N}_H$ and $\hat{p}_H$, and any attendant bias in the $\{\hat{N}_i\}$ will propagate through these other estimates as well. For example, negatively biased $\{\hat{N}_i\}$ would result in positively biased estimates of ocean and river harvest rates and negatively biased estimates of early life survival rates, pre-fishery recruitment, maturation rates, and recovery rates, all

of which are essential quantities for assessment pur-poses. Estimates of stray proportions would be biased as well, with the direction of bias depending on which survey estimates were biased and the underly-ing distribution of straying. Thus, bias in $\{\hat{N}_i\}$ has significant consequences beyond $\{\hat{N}_i\}$ itself.

Although this paper is primarily concerned with esti-mator bias, estimator variance is also an important topic and worthy of further development. The section "Estimator Interpretation and Sampling Variance" (pg. 8) identifies the principal quantities that affect the sampling variances of $\hat{N}_i$, $\hat{N}_H$, and $\hat{p}_H$, but the sampling variance formulas themselves and associ-ated estimators remain to be derived. Goodman's (1962) results concerning the variance of a product of random variables could be used directly for this purpose. Sampling variance (and coefficient of varia-tion) formulas would be useful to develop sample size targets that would achieve a desired level of estima-tor precision, and variance estimators would allow for the reporting of precision estimates alongside of point estimates. Without the latter, all point estimates are typically treated in assessments as "equally infor-mative observed values." This is clearly not the case given that the variance of $\hat{N}_i$ increases with $\hat{F}_{\mathrm{samp}}$, and the reported $\hat{F}_{\mathrm{samp}}$ vary widely in magnitude (Kormos et al. 2012, Table 4): approximately 1 for hatchery returns, 1 to 5 for ocean harvest surveys, and 5 to 18 for most river harvest and carcass surveys.

RECOMMENDATIONS

While detailed advice on coded-wire tag sampling protocols is beyond the scope of this paper, some general advice may be offered. False negatives (clas-sifying non-fresh carcasses as non-adc when in fact they are adc) will generate estimates of p_{adc} that are biased low, but generally will not bias estimates of $p_{\mathrm{cwt|adc}}$. False positives (classifying non-fresh carcass-es as adc when they are not) will generate estimates of p_{adc} that are biased high and estimates of $p_{\mathrm{cwt|adc}}$ that are biased low. When both false negatives and false positives occur, the direction of bias in p_{adc}

depends on the relative rates of each misclassification type while estimates of $p_{\text{cwt|adc}}$ will be biased low.

There is a simple recommendation for avoiding bias: never use non-fresh carcass data for either of these estimates. The downside to this approach is a reduction in precision owing to the reduction in sample size. Recall that for the data from the 2010 carcass survey of fall- and late fall-run Chinook salmon in the upper Sacramento River, for example, the non-fresh carcasses outnumbered the fresh carcasses 4 to 1. Thus it may be worth considering the use of non-fresh carcass data, particularly in the estimation of $p_{\text{cwt|adc}}$, so long as data from fresh and non-fresh carcasses are tracked separately such that every step of the analysis can be restricted to fresh carcass data only, if need be.

Unbiased estimators for four idealized cases of misclassification were considered: (1) no misclassification, (2) false negatives, (3) false positives, and (4) false negatives/positives. To estimate the p_{adc} component, we showed that the non-fresh carcass data can be included only if classification is accurate (Case 1) using equation (12), otherwise only the fresh carcass data should be included using equation (17). Thus, we generally recommend restricting estimation of p_{adc} to fresh carcasses only. To estimate the $p_{\text{cwt|adc}}$ component, we showed that the non-fresh carcass data can be included if classification is accurate for the non-adc fish (i.e., either there is no misclassification or the only misclassifications are false negatives; Cases 1 and 2) using equation (13), otherwise only the fresh carcass data should be included using equation (20).

Because of the potential for adc misclassification or misreporting to introduce bias, the survey protocol should explicitly address the collection of adc and cwt data from fresh and non-fresh carcasses, along with its associated reporting. The protocol should explicitly define how subsampling is to be performed should that become necessary (e.g., "too many adc carcass heads to handle") in order to guard against sampling bias and to discourage under-reporting. The protocol should provide clear guidance on what a sampler should do if the adc status is unclear.

Since false positives will bias estimates of both p_{adc} and $p_{\text{cwt|adc}}$, while false negatives should only bias estimates of p_{adc}, we recommend protocols that err on the side of false negatives (e.g., for non-fresh carcasses, only collect heads and treat as adc when certain of it) while minimizing false positives, unless the circumstances of a particular case argue against this. Alternatively, samplers could collect heads from all carcasses that might be adc, as long as the sample data and results could be stratified into the following classes: 1) fresh, adc; 2) non-fresh, definitively adc; and 3) non-fresh, possibly adc. Specific guidance and information are important, both at the data collection stage and at the estimation stage, and this should be well documented. Survey protocols should provide detailed guidance on adc carcass head collection, the avoidance of bias, sample size targets, and the importance of documenting deviations from established protocols.

There has been a serious effort of late to produce quality estimates of Chinook salmon escapement in the Central Valley (Bergman et al. 2012), and this is an opportune time to undertake a similar effort for the cwt recovery portion of these surveys (and also for river harvest surveys given their $\hat{F}_{\text{samp}}$ double-digit magnitude). Survey leaders should know what is actually involved in the $\hat{F}_{\text{samp}}$ formulation and calculation, and how it can be affected by adc status misclassification. Survey leaders should also be aware of the variety of other estimates that are generated from the $\{\hat{N}_i\}$, and of their use and importance. Survey leaders need to know that cwt recoveries are not just for "determining stock composition" or for "ocean fishery purposes." In short, the priority level for adc and cwt sampling, collection, documentation, and estimation needs to be elevated. The estimates that derive from these data are too important for it to be relegated to secondary status (Bergman et al. 2012, p. ix–x).

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REFERENCES

Bergman JM, Nielson RM, Low A. 2012. Central Valley Chinook salmon in-river escapement monitoring plan. Sacramento (CA): California Department of Fish and Game, Fisheries Branch. Administrative Report Number: 2012-1. [cited 2013 May 17]. Available from: *https://nrm.dfg.ca.gov/FileHandler.ashx?DocumentID=42213*

Buttars B. 2010. Constant fractional marking/tagging program for Central Valley fall-run Chinook salmon, 2010 marking season. Red Bluff (CA): Pacific States Marine Fisheries Commission. [cited 2013 May 17]. Available from: *http://www.fws.gov/sacramento/Fisheries/CAMP-Program/Documents-Reports/Documents/2010%20Constant%20Fractional%20Marking%20Report.pdf*

[CA HSRG] California Hatchery Scientific Review Group. 2012. California Hatchery Review Report. Prepared for the U.S. Fish and Wildlife Service and Pacific States Marine Fisheries Commission. June 2012. 100 p. [cited 2013 May 17]. Available from: *http://cahatcheryreview.com/wp-content/uploads/2012/08/CA%20Hatchery%20Review%20Report%20Final%207-31-12.pdf*

Garman CE, McReynolds TR. 2009. Butte and Big Chico creeks spring-run Chinook salmon, *Oncoryhnchus* [sic] *tshawytscha* life history investigation 2007-2008. Rancho Cordova (CA): California Department of Fish and Game, Inland Fisheries Administrative Report No. 2009-1. [cited 2013 May 17]. Available from: *https://nrm.dfg.ca.gov/FileHandler.ashx?DocumentVersionID=56853*

Goodman LA. 1962. The variance of the product of K random variables. J Am Stat Assoc 57:54–60.

Hankin DG, Logan E. 2010. A preliminary analysis of Chinook salmon coded-wire tag recovery data from Iron Gate, Trinity River and Cole Rivers hatcheries, brood years 1978–2004. Arcata (CA): Contract report prepared for the Hoopa Valley Tribal Council. 65 p. [cited 2013 May 17]. Available from: *http://www.fws.gov/arcata/fisheries/reports/technical/IGHTRH.CWTanalysis2009%20Hankin%20Rpt.pdf*

Hinrichsen RA, Sharma R, Fisher TR. 2012. Precision and accuracy of estimators of the proportion of hatchery-origin spawners. Trans Am Fish Soc 141(2):437–454.

Johnson JK. 1990. Regional overview of coded-wire tagging of anadromous salmon and steelhead in northwest America. Am Fish Soc Symp 7:782–816.

Killam D. 2009. Chinook salmon populations for the Upper Sacramento River Basin in 2008. Red Bluff (CA): California Department of Fish and Game, Sacramento River Salmon and Steelhead Assessment Project, SRSSAP Technical Report No. 09-1 (as revised 1-11-2010). [cited 2013 May 17]. Available from: *https://nrm.dfg.ca.gov/FileHandler.ashx?DocumentVersionID=56849*

Killam D. 2011. 2010 CWT results report. [Excel spreadsheet]. California Department of Fish and Game, Red Bluff, CA.

Kormos BM, Palmer-Zwahlen M, Low A. 2012. Recovery of coded-wire tags from Chinook salmon in California's Central Valley escapement and ocean harvest in 2010. Santa Rosa (CA): California Department of Fish and Game, Fisheries Branch Administrative Report 2012-02. [cited 2013 May 17]. Available from: *https://nrm.dfg.ca.gov/FileHandler. ashx?DocumentID=44306*

Lindley ST, Schick RS, Mora E, Adams PB, Anderson JJ, Greene S, Hanson C, May BP, McEwan DR, MacFarlane RB, Swanson C, Williams JG. 2007. Framework for assessing viability of threatened and endangered Chinook salmon and steelhead in the Sacramento–San Joaquin Basin. San Fran Estuar Water Sci [Internet]. [cited 2013 May 17]; 5(1):4. Available from: *http://repositories.cdlib.org/ jmie/sfews/vol5/iss1/art4*

Mohr MS. 2002. CWT expansion for cohort analyses in Central Valley carcass surveys. Santa Cruz (CA): Fisheries Ecology Division, Southwest Fisheries Science Center, National Marine Fisheries Service, NOAA. Unpublished report.

Mohr MS. 2006. The cohort reconstruction model for Klamath River fall Chinook salmon. Santa Cruz (CA): Fisheries Ecology Division, Southwest Fisheries Science Center, National Marine Fisheries Service, NOAA. Unpublished report.

Nandor GF, Longwill JR, Webb DL. 2010. Overview of the coded-wire tag program in the greater Pacific region of North America. In: Wolf KS, O'Neal JS, editors. PNAMP Special Publication: Tagging, telemetry and marking measures for monitoring fish populations—a compendium of new and recent science for use in informing technique and decision modalities. Portland (OR): Pacific Northwest Aquatic Monitoring Partnership Special Publication 2010-002. p. 5–46. [cited 2013 May 17]. Available from: *http:// www.pnamp.org/sites/default/files/ttmchap02.pdf*

O'Farrell MR, Mohr MS, Grover AM, Satterthwaite WH. 2012. Sacramento River winter Chinook cohort reconstruction: analysis of ocean fishery impacts. Santa Cruz (CA): U.S. Department of Commerce, NOAA Technical Memorandum NMFS, NOAA-TM-NMFS-SWFSC-491. [cited 2013 May 17]. Available from: *http://swfsc.noaa.gov/publications/ TM/SWFSC/NOAA-TM-NMFS-SWFSC-491.pdf*

[PFMC] Pacific Fishery Management Council. 2008. Research and data needs. Portland (OR): Pacific Fishery Management Council. [cited 2013 May 17]. Available from: *http://www.pcouncil.org/wp-content/ uploads/Res_Data_Needs_2008_Final_OCT08.pdf*

[PFMC] Pacific Fishery Management Council. 2012a. Pacific Coast salmon fishery management plan for commercial and recreational salmon fisheries off the coasts of Washington, Oregon, and California as revised through Amendment 17. Portland (OR): Pacific Fishery Management Council. [cited 2013 May 17]. Available from: *http://www.pcouncil.org/ wp-content/uploads/FMP_through_A-17_Final.pdf*

[PFMC] Pacific Fishery Management Council. 2012b. Preseason report I: stock abundance analysis and environmental assessment part 1 for 2012 ocean salmon fishery regulations. Portland (OR): Pacific Fishery Management Council. [cited 2013 May 17]. Available from: *http://www.pcouncil.org/wp-content/ uploads/Preseason_Report_I_2012.pdf*

Titus R, Brown M, Lyons J, Collins E, Koerber L. 2010. Annual project performance report: Central Valley angler survey July 1, 2009 to June 30, 2010 [SFRA F-119-R]. Sacramento (CA): California Department of Fish and Game. [cited 2013 May 17]. Available from: *http://nrm.dfg.ca.gov/FileHandler. ashx?DocumentID=33186*

[USFWS] U.S. Fish and Wildlife Service. 2011. Upper Sacramento River winter Chinook salmon carcass survey, 2010 annual report. Red Bluff (CA): U.S. Fish and Wildlife Service. [cited 2013 May 17]. Available from: *http://www.fws.gov/redbluff/getReport. aspx?id=115*