Compositional forecasting of Chinook Salmon Evolutionarily Significant Units in bycatch for Pacific Hake fisheries

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ABSTRACT: Bycatch impacts on non-target species present significant management problems in diverse fisheries throughout the world. Despite successful efforts to minimize bycatch in US West Coast Pacific Hake fisheries, these impacts remain a concern, particularly for sensitive populations of Chinook Salmon. NOAA Fisheries needed predictive models to estimate proportions of Chinook Salmon Evolutionarily Significant Units (ESUs) expected in bycatch. We used genetic mixture analysis to estimate ESU proportions from at-sea bycatch between 2008 and 2015. Using latitude as a predictor and applying jackknife cross validation, we found Dirichlet regression more accurately estimated abundant ESUs, whereas multinomial logistic regression performed better with rare ESUs. This targeted, ESU-specific approach showed the spatial distribution of sensitive stocks in bycatch and supported NOAA's obligations to forecast impacts on listed ESUs. The overarching goal of this continuing work is to maximize sustainable harvest while protecting threatened and endangered Chinook Salmon ESUs.

INTRODUCTION

Pacific Hake¹ (*Merluccius productus*) are distributed from the Gulf of Alaska to the Gulf of California (Quirollo et al. 2001). This abundant marine resource supports a large-scale trawl fishery off the US West Coast. Trawling in this region began slowly in the 1870s but increased in the 1920s with implementation of diesel engines and other technological advances (Easley 2001). By 1966 harvest reached 137 kMT and now represents an important economic resource to the region and to the nation (Hamel et al. 2015). In 2016, commercial landings of Pacific Hake totaled more than 260.8 kMT valued at over US\$42 million (NOAA 2019).

Incidental Take Statement for the US West Coast groundfish fisheries

Despite much effort and management action to reduce impacts on non-target species, bycatch remains a concern in this commercially important fishery (Somers et al. 2015). There is special concern for bycatch of Chinook Salmon (*Oncorhynchus tshawytscha*) protected under the US Endangered Species Act (ESA). By international treaty (PSC 2020), management of coastal Pacific hake fisheries is shared among Canadian Department of Fisheries and Oceans, NOAA Fisheries, and the Joint Management Committee. In cooperation with the Pacific Fishery Management Council (PFMC), NOAA manages the Pacific Hake fishery on the US West Coast in Federal waters (3 to 200 miles offshore). Federal agencies must consult with NOAA on activities that might jeopardize the continued existence of protected marine species (essentially any action that involves “take”). As part of the 2017 ESA Consultation for the West Coast Groundfish Fishery Management Plan salmon biological opinion (BiOp),

¹ Also referred to by the industry name “Pacific whiting”

the PFMC and NOAA faced a series of questions related to alternative fishery regulation scenarios. For example: What would be the actual number of Chinook Salmon individuals in bycatch from each Evolutionarily Significant Unit (ESU), if the current restriction were rescinded on processing Pacific Hake south of latitude 42? What if there was a resumption of the tribal mothership fishery off the north coast of Washington State? Ultimately, NOAA's Incidental Take Statement needed to forecast the actual number of Chinook Salmon from each ESU taken in bycatch, given predicted spatial distribution of fishing effort (Matson and Erickson 2018) and under different management scenarios (NMFS—WCR 2017).

Limited CWT recoveries in bycatch

Tiny coded-wire tags (CWTs) are implanted in the snouts of juvenile hatchery fish, and much has been learned about Chinook Salmon migration patterns and ocean distribution from CWT recoveries (Weitkamp 2010; Riddell et al. 2018; Shelton et al 2019). We know that particular stocks have characteristic patterns of tag recovery, primarily in commercial salmon harvest. Importantly, these patterns of migration were shown to be surprisingly stable across years, despite high interannual variation in ocean conditions and relative abundance (Weitkamp 2010). In spite of broad utility in harvest management and basic research, coded-wire-tag recoveries in bycatch have generally been inadequate to estimate relative abundance and distribution of 17 ESUs (identified in Appendix 1). In parallel with tissue sampling, only 687 CWTs were recovered from among 9,862 Chinook Salmon sampled by NOAA At-Sea Observers over the 8 years of this study (2008 – 2015). Therefore, genetic analysis, where every fish, hatchery and wild,

is effectively “tagged,” presented an opportunity to significantly augment what was known from sparse CWT recoveries (NMFS—WCR 2017).

In the current study, we used genetic mixture analysis to characterize stock composition of Chinook Salmon ESUs in the US West Coast, at-sea, Pacific Hake fishery. We also tested accuracy and precision of different predictive regression models used to forecast ESU impacts in a management context; the goal being to provide the most powerful forecasting tool requiring the simplest possible inputs. Beyond specific interest to salmon conservation and Pacific hake harvest, our results are relevant to broader studies of more general statistical challenges of multinomial regression modeling and measures of forecasting accuracy—both common problems in ecology and natural resource management.

MATERIALS AND METHODS

NOAA’s At-Sea Hake Observer Program (A-SHOP) collected Chinook Salmon tissue samples from the catcher/processor, mothership, and at-sea tribal sectors (NWFSC 2021). Rayed fin-clip samples were folded in Whatman 3MM chromatography paper, dried immediately, and stored in barcoded coin envelopes at ambient temperature. Samples were deposited in the Northwest Fisheries Science Center (NWFSC) Conservation Biology Division’s Genetic Tissue Archive (accession numbers in Table 1). All samples were collected during the normal fishing season beginning 15 May and ending 31 December. Tissue samples selected for genotyping (4,498) were drawn randomly each year between 2008 and 2015. Annual sample sizes were dictated by project resources available in a given year, not total bycatch. Table 1 illustrates the

filtering process and identifies the following: total estimated bycatch, samples collected by observers, random sub-sample for genotyping, and filtered for genotyping quality and filtered for ≥ 0.8 assignment probability. The latter two sample sets provided the primary input data for this study and reflect two distinctly different statistical approaches; 1) modeled genetic stock composition estimates based on all individuals for all ESUs simultaneously, and 2) discrete individual assignment of each fish to population of origin. Our sample was intended to accurately reflect ESU-specific, spatial and temporal bycatch impacts over the course of each year in the fishery. That was the essential focus of NOAA's BiOp as related to Chinook salmon impacts (NMFS—WCR 2017).

[Table 1 near here]

Genotyping, genetic mixture modeling, and individual assignment

DNA was extracted and purified by using Qiagen® DNeasy™ membrane capture. Purified DNA was amplified and genotyped for 13 internationally standardized microsatellite loci (see below). Microsatellite products were sized using an Applied Biosystems Incorporated (ABI) 3100 Genetic Analyzer. Genotypes were inferred from electropherograms by using ABI Genescan and Genotyper software. We used conditional maximum likelihood mixture modeling (CMLMM) to simultaneously estimate stock compositions and make individual assignments to population of origin (Rannala and Mountain 1997; ONCOR, Kalinowski et al. 2007), with bias correction (Anderson et al. 2008). Population-level allocation was then aggregated by ESU reporting group. Genetic mixture analysis using ONCOR was replicated and confirmed with the R package 'rubias' (Moran and Anderson 2019). The two sets of genetic results from ONCOR, 1) modeled

proportions and 2) individual assignments, were used for the two different classes of statistical analysis, 1) Dirichlet regression (DR; Maier 2014) and 2) multinomial logistic regression (MLR; Hilbe 2009). CMLMM is taken to be the best possible estimate of ESU proportions in a given year. We use the term “observed” in reference to observed genotypes and observed latitudes that are compared to “predicted” ESU proportions from the regression models. We calculated credibility intervals for CMLMM proportions, however, we relied principally on cross validation of predictions and evaluation of accuracy with scale-dependent and -independent metrics (see below).

CMLMM depends on a baseline dataset of known-origin reference samples that is assumed to represent all potentially contributing populations. In this study, we used the most comprehensive Chinook Salmon baseline available, the internationally standardized, microsatellite dataset (i.e., common loci and consistent allele designations, Moran et al. 2006) that was developed by the Genetic Analysis of Pacific Salmonids consortium (GAPS; Moran et al. 2005; Seeb et al. 2007). The GAPS baseline was designed for eastern Pacific fishery mixtures, primarily harvest, but the geographic coverage of potential source populations is complete from Southeast Alaska to Central Valley, California. The version of the baseline we used included more than 20,000 known-origin fish from 163 populations representing all ESUs and major Canadian and Alaskan stocks that contribute to these fisheries (Appendix 1). The GAPS baseline is thoroughly vetted by the salmon genetics community and has been widely used in studies of harvest impacts (Bellinger et al. 2015; Satterthwaite et al. 2015; Moran et al. 2018).

Predictive regression models and cross validation

Input data for our preliminary exploration included the ESU to which each fish assigned, collection year, ordinal day of the year, latitude (decimal degrees), fork length (cm), and fishing depth (m). Akaike information criterion (AIC) was used to evaluate different predictive models. Focusing on mean latitude of an annual bycatch sample, we compared two multinomial regression methods for predictive forecasting. DR was used to relate observed proportions for an annual sample of individuals relative to the mean latitudes over which those individuals were taken. MLR was also used to estimate an expected proportion for each ESU as a function of latitude but was based on individual fish rather than annual means. Compositional proportions are bounded by zero and one, and not normally distributed or homoscedastic. This class of proportions violates assumptions of linear regression and common parametric analyses such as t-tests and ANOVA, when used as a dependent variable. To evaluate the absolute and relative accuracy and precision of the two regression methods, we conducted sequential, independent, cross-validation analyses holding out each of 8 individual years, one at a time, as test datasets and using all remaining years as training data. We used a similar jackknife approach for both regression methods. In each case, we evaluated the accuracy of the prediction (based on the training data set) against the independent, cross-validation, test set (the “actual” or “observed” ESU proportions derived from observed genotypes). Central Valley Spring ESU only occurred in one test set (annual sample), so that ESU was omitted from the jackknife. To the extent possible, the jackknife is a sequential test of forecasting accuracy, “predicting” the composition of each annual sample as if it were a new observation.

To quantify accuracy and precision of our forecast predictions compared to observed genotypes, we used scale-dependent and scale-independent error metrics. For a scale-dependent metric we selected the widely used and easily understood mean squared error (MSE),

$$\text{MSE} = 1/N \sum (y_t - f_t)^2.$$

Where N = number of tests, y_t = observed composition in the t^{th} test, and f_t = the t^{th} forecast.

For a scale-independent metric we chose the less widely known mean arctangent absolute percentage error (MAAPE),

$$\text{MAAPE} = 1/N \sum (\arctan(|y_t - f_t| / f_t)).$$

MAAPE can be interpreted intuitively as an absolute percentage error like the commonly used mean absolute percentage error (MAPE). However, MAAPE is less biased in greater penalties for positive errors than negative (Makridakis 1993). Moreover, the bounded range of the arctangent function ($\lim_{x \rightarrow \infty} \tan^{-1} x = \pi / 2$) overcomes the MAPE's limitation of going to infinity as the observed value approaches zero (Kim and Kim 2016).

For context, we compared the accuracy of our modeled estimates with interannual variability between members of paired samples (observed data) that had similar mean latitudes. We selected pairs of annual samples that differed by less than 0.25 degrees in

mean latitude (2013 and 2014 at latitudes 43.8 and 43.5, respectively; and 2013 and 2015 at latitudes 43.8 and 43.9). This interannual variability should represent the minimum error possible in a forecast estimate. We used the R statistical package (R Core Team 2017) for most of our analyses and figures.

RESULTS

NOAA fishery observers from the A-SHOP collected 9,862 individual tissue samples, which represented 41% of the total estimated Chinook Salmon bycatch between 2008 and 2015 (Table 1). Samples were stratified by year, and a total of 4,498 fish were randomly subsampled for DNA extraction and analysis (19% of total bycatch). Geographic distribution of individual tissue samples extended from Shelter Cove (41.43°), north to the Canadian border (48.48°); fishing depth 46 - 507 m (mean 246, SD 90.4); bottom depth 66 - 2,743 m (mean 427, SD 217.4), and fork length 24 - 113 cm (mean 58.7, SD 11.9). A slight female bias was observed (0.54). Mean latitude values for each annual bycatch sample ranged over 4.4 degrees (43.5° - 47.9°). A general shift to the south was observed in fishing effort and bycatch beginning in 2011 (Table 1). Clearly, similar values for mean latitude might produce very different stock compositions if they have different distribution, e.g., non-normal. Through practical application and cross validation, our results demonstrate the sensitivity of our models to those violations of normality.

Genotyping and genetic mixture modeling

Of 4,498 fish subsampled for genotyping, 96% met genotyping quality criteria. In addition to high genotyping success, high individual fish assignment probabilities were

also observed. About 78% of fish successfully genotyped met the assignment probability criterion of ≥ 0.8 ($N = 3,360$, 14% of total bycatch; see Moran et al. 2014 for sensitivity analysis). Modeled genetic estimates of overall proportions derived from all fish successfully genotyped (“observed”) showed that most of the Chinook Salmon bycatch in this period came from Upper Klamath-Trinity River and S. Oregon and N. California Coastal ESUs (Fig. 1). Those two ESUs accounted for more than 50% of all bycatch in the study period. Secondary contributors included the Oregon Coast and Puget Sound ESUs and Southern British Columbia (lower Fraser River, data not shown).

[Fig. 1 near here]

Managers often focus on fishery management areas. Differences in ESU composition between fishery management areas north and south of Cape Falcon (45.77°) showed the effect of latitude (See figs. 2 and 3 for area boundaries). The two southern ESUs—Upper Klamath-Trinity Rivers and S. Oregon/N. California—dominated bycatch south of Cape Falcon but dropped to only ~5% each to the north of Cape Falcon. The opposite was true of the northern ESU, Puget Sound, and Southern BC populations. Spatial variation was also reflected when comparing the annual samples, which were each taken at different mean latitudes and showed different ESU proportions (see Jackknife cross validation below).

[Fig. 2 near here]

Individual assignment

Again, our analysis included two fundamentally different approaches, modeled proportions versus individual assignment. The ESU stock composition results above

describe fitted genetic models to all observed genotypic data simultaneously (Koljonen et al. 2005). At this point we shift to analyses based on individual fish assignment. First, we simply created a scatter plot of individually georeferenced fish, color coded by ESU, and overlaid on a map of the US West Coast (Fig. 3). That heuristic presentation also showed strong effects of latitude on ESU composition. No fish assigned to Sacramento Winter ESU, preventing inclusion of that ESU in the exploratory regression analysis described below.

[Fig. 3 near here]

Individual assignment was used to explore the ESU-specific predictive power of multiple sample attributes (e.g., latitude, depth, fork length, etc.). Previous simulations using the GAPS baseline showed that individual assignment with a threshold of ≥ 0.8 for inclusion, and regressing traits on ESUs is a robust and generally unbiased approach to inferring ESU-specific phenotypes (Moran et al. 2014). However, we recognize that individual assignment for compositional prediction raises issues of potential bias that go beyond the scope of this article. Nevertheless, our cross-validation approach subsumes those errors, allowing meaningful comparisons between disparate statistical methods. According to AIC evaluation of MLR models in particular, latitude was by far the most powerful single predictor of ESU origin (similar GAM results not shown). Other factors, most notably year, clearly explained additional variation, but Burnham and Anderson's (2004) ΔAIC values for individual factors, relative to latitude alone, were compelling: year 1505, depth 1574, ordinal day 2271, and fork length 2544. More complex models gave lower AIC values, but were less suitable as predictors and as practical fishery management regulatory elements.

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274 Plotting DR and MLR curves further illustrated the importance of latitude for
275 most ESUs (Fig. 4). Consistent with the plot of fishery management areas (Fig. 2),
276 northern ESUs were encountered primarily in the north, whereas southern ESUs were
277 concentrated in southern and central coastal areas. Cape Falcon marked an abrupt
278 transition in ESU composition of Chinook salmon bycatch.

279

280 [Fig. 4 near here]

281

Jackknife cross validation

282 The estimated regression curves in Figure 4 can be compared with observed
283 proportions in each annual sample (points in Fig. 4). However, the regression estimates
284 include all data and are therefore not independent from the point observations in Figure 4
285 (i.e., potentially presenting an overly optimistic interpretation of predictive power). By
286 contrast, the jackknife, cross-validation analysis provided an independent observation for
287 every ESU proportion in every year. Figure 5 compares observed ESU proportions for
288 each year with independently derived estimates from the two regression methods and
289 latitude alone. Figure 6 almost perfectly summarizes all individual years (Fig. 4) by
290 averaging over jackknife iterations. Despite a major difference in the MLR estimate for
291 Upper Klamath/Trinity Rivers, estimates for both regression models were close to one
292 another and close to observation for most ESUs.

293

294 [Fig. 5 and Fig. 6 near here]

295

Annual replicates at similar latitude

By chance, some annual samples had very similar mean latitudes. Consistent with latitude being more important than year in the AIC, similar ESU proportions were observed in those annual samples that had similar mean latitudes (i.e., 2013, 2014, and 2015; Fig. 5). Comparison of variation between years with the accuracy of our forecast was mixed. Forecast predictions for large contributors showed substantially greater errors than variation observed between years at similar latitude (MSE = 0.0005 for DR and 0.0008 for MLR compared with only 0.0001 for the annual replicates). However, the scale-independent metric suggested that prediction errors were quite similar to interannual variation (MAAPE = 0.670 and 0.564 for DR and MLR versus 0.572 for interannual replicates).

Accuracy of DR vs MLR, overall and by ESU

In predicting the ESU composition obtained from CMLMM in a given year, DR outperformed MLR for most ESUs that contributed more than 2.5%; however, the distribution of errors was complicated. For all contributors, MSE (most sensitive to large contributors) was 38% lower for DR than for MLR. Yet DR errors were more than three times as variable across years (CV = 56% for DR versus 21% for MLR). By contrast MAAPE (sensitive to small contributors) was 16% lower for MLR but nearly twice as variable (CV = 27% for MLR versus 14% for DR). So in each case, the more accurate regression method was less precise. A few patterns were evident in the accuracy and precision of individual ESU estimates. DR underpredicted Upper Klamath-Trinity Rivers ESU, in contrast to MLR that substantially overpredicted that ESU in nearly all years. Large MSE values for MLR were driven largely—but not entirely—by the extreme overprediction of Upper Klamath-Trinity Rivers ESU (Fig. 6; omitting Klamath/Trinity

only reduced MSE from 0.0008 to 0.0007, still greater than 0.0005 for DR, and much greater than 0.0001 observed between years at the same latitude). With the notable exception of S. Oregon and N. California Coastal ESU, which MLR estimated almost exactly, southern ESUs were overestimated by MLR, whereas northern ESUs were underestimated. DR underestimated all larger contributors (>5%), but consistently overestimated smaller contributors, e.g., Washington Coast, Upper Willamette River, Mid-Columbia River Spring, Upper Columbia River Spring Snake River Spring/Summer, Snake River Fall ESUs [all years except 2009], and Central British Columbia and Alaska). Extensive additional analyses did not show an obvious effect of omitting fish that failed to meet the 0.8 probability criterion for MLR.

Discussion

We succeeded in developing useful predictive models for Chinook Salmon ESU stock composition estimates in a fishery management context. Latitudinal clines and stock-specific distributions observed here were generally consistent with distribution of CWT recoveries in harvest fisheries (Weitkamp 2010; Shelton et al. 2019; Shelton et al. 2021). However, the current study, is the first we know of to describe pre-season prediction of ESU-specific impacts based simply on anticipated latitude of a proposed fishery. Given estimated bycatch numbers and latitudes (Matson and Erickson 2018), NOAA needed to parse total numbers by ESU to give predictions of actual fish counts, based on forecast proportions. These models were used previously in support of the 2017 Chinook salmon ITS and BiOp for the West Coast Groundfish Fishery Management Plan (NMFS—WCR 2017). This paper is an extension of the ground truthing that went into the BiOp. Because management needed to estimate ESU-specific impacts at various

levels of take, our application required estimating proportions. Our approach was dictated by specific management needs, but the challenges of compositional forecasting and characterization of errors are ubiquitous in fields as disparate as ecological genetics and economic market research (Aitchison 1986). Even more broadly, the analysis of individuals versus aggregates is a fundamental statistical dichotomy.

Broadly similar results between methods

We evaluated the performance of two accepted multinomial regression models representing two different analytical approaches, one based on genetic mixture modeling and DR, and the other based on individual assignment and MLR. We observed broadly similar results, despite differences in both the treatment of genetic data and in the regression. Independent cross validation showed that both analysis methods gave surprisingly accurate estimates despite a range of potential challenges. Not least, that different distributions of bycatch, with different stock compositions, might have similar means, thus confounding our prediction.

On initial inspection, Dirichlet regression appeared more accurate than MLR, but neither method provided a clear advantage across both rare and abundant ESUs. For example, MLR consistently overestimated the abundant Upper Klamath-Trinity Rivers ESU, especially in 2008 and 2011, whereas DR was much more accurate. DR was clearly more accurate than MLR in estimating large contributors; however, DR consistently overestimated small contributors, such as Upper Willamette River, Snake River Spring/Summer, and Snake River Fall—all listed as Threatened under the US Endangered Species Act. MLR was much more accurate than DR in estimating those

small contributors at all latitudes and in nearly all years. Essentially all prediction errors for large contributors were greater than observed between members of paired annual samples at similar mean latitude—clearly room for improvement. However, for small contributors, prediction accuracy was extremely good. For example, 8 of 17 ESUs showed less variation between MLR prediction and observed ESU proportions in a given year than between years at similar latitude (6 of 17 for DR). In other words, prediction error with MLR was no larger than interannual variation for these small contributors.

Prediction accuracy is often critical for small contributors to mixed fisheries. Overprediction of sensitive or ESA-listed ESUs can lead to elevated concern, fishery restrictions, and needless forgone harvest. Moreover, a scale-independent metric like MAAPE could be considered a more appropriate measure of general forecasting accuracy than MSE. So, the recommended method depends on specific application and relative concern for abundant versus rare stocks. Harvest allocation might call for DR, whereas conservation might be better served by MLR. Managers are advised to examine both DR- and MLR-based take estimates and weigh the implications of specific inconsistencies.

Comparison of Chinook Salmon stocks in bycatch versus directed harvest

We noted interesting differences from stock compositions previously reported for harvest. Direct comparison is difficult, but it appeared anecdotally that the Bellinger et al. (2015) study of commercial troll observed substantially higher proportions of Central Valley Fall ESU and lower proportions of Klamath-Trinity ESU than the current study. Also, Columbia River populations were more abundant in troll than in bycatch (Fig. 5 e, f,

and g in Bellinger et al. 2015 compared to our Fig. 1). Similar results were seen in harvest studies (commercial and recreational fisheries) that sampled areas farther south (Winans et al. 2001; Satterthwaite et al. 2015).

With respect to latitude, the most direct available comparison between harvest and bycatch comes from the Washington commercial troll fishery (Moran et al. 2018). The mean latitude for all samples observed in that study between 2012 and 2015 was 47.4°, which was similar to the annual bycatch sample that we analyzed in 2009 (47.9°). Despite that similarity in latitude, the observed stock compositions were quite different. The relative abundance of Lower Columbia River and Upper Columbia River Summer/Fall was much higher in Washington troll than in bycatch from similar latitude. By contrast, proportions of Puget Sound and Southern British Columbia were much lower in troll than in bycatch. A difference worth noting is that at-sea bycatch tends to be unimodal in latitude within years (either north or south) but bimodal among years, whereas Washington coastal troll is strongly bimodal every year (Moran et al. 2018). There are also differences in depth and distance offshore. These anecdotal stock composition differences among disparate studies are difficult to interpret without broader spatial overlap and temporal replication. Eventually, however, the hope is that meta-analyses among fisheries can help discriminate where fish are caught from exactly where they are and how different populations use the marine environment in time and space.

Fishery-dependent focus: Opportunities and limitations

Satterthwaite et al. (2014:128) pointed out that, for management purposes, “variability in interactions with the fishery is more relevant than ecological distribution.”

The focus of the current study was not stock-specific, ecological distribution. Instead, we measured fishery impacts explicitly, and we limited most of our analysis to high-level spatial and temporal strata (i.e., coast-wide, annual). We chose both the scale and the compositional forecasting approach to provide fishery managers with a tool that required only simple inputs and would help meet obligations for predicting ESU impacts. In the context of depressed populations, it's worth recognizing the inherent challenge in estimating very small bycatch numbers. Some ESUs were rare or absent in our analysis. Fewer than 10 fish were observed for each of six ESUs, and no Sacramento Winter fish were observed. Despite small numbers of observations for some ESUs, the expected proportions for those rare ESUs are not independent and are partially informed by the proportions of all other ESUs, including abundant ESUs for which estimates are much more confident. Despite concerns about interannual variability, non-normal latitudinal distributions, and the utility of mean latitude, our cross validation showed that error in the MLR estimate was essentially indistinguishable from interannual variation between samples taken at the same latitude. Again, we point out that “errors” in our regression estimates are relative to “observation” that is also an estimate but is based on observed genotypes and is our best estimates of ESU proportions in a given year. We use the term observation to emphasize the distinction between estimation and prediction, an observed mixed fishery versus a compositional forecast.

Results of Weitkamp (2010) suggested stable Chinook Salmon stock distributions across years, despite different ocean conditions and relative stock abundance (but see Satterthwaite et al. 2012; Shelton et al. 2019; Shelton et al. 2021). Seasonal variation in bycatch composition is substantially dampened, relative to directed harvest, because of

the broad distribution of age classes in bycatch. For future genetic bycatch data, we will conduct a detailed exploration of stock-specific associations with oceanographic variables (sea-surface temperature, chlorophyll, etc.). Irrespective of spatial changes in fishing activity, if Chinook Salmon change their distribution or relative abundance in response to climate change, will the curves remain the same, shift uniformly north (or south), or will shapes and relative relationships of the curves change fundamentally, as predicted by Shelton et al (2021)? Climate effects on these latitudinal distributions could go beyond Chinook ESU impacts and conservation, to the extent ESA-listed southern resident killer whales target preferred Chinook salmon stocks (Hanson et al. 2010).

These questions are important, as the fishing industry becomes increasingly sophisticated in their requests for data on salmon distribution. Not only do fishing fleets want to avoid Chinook Salmon bycatch, they especially want to avoid protected or sensitive ESUs like Puget Sound, Lower Columbia River, Upper Klamath-Trinity Rivers, California Coast, and Central Valley Fall. Our figures 3 and 4 summarize what we know about where these ESUs are most likely to be caught. An obvious measure to avoid particular ESUs is to avoid nearby latitudes. The trouble is, moving north to avoid the threatened California Coast ESU, for example, would likely shift impacts to Puget Sound and Lower Columbia River, also listed as threatened under the US ESA. Moreover, moving fishing pressure north or south has a big effect on ESUs like Upper Klamath-Trinity Rivers or Puget Sound that have steep latitudinal clines, but less effect on ESUs like California Coast that have broader, flatter distributions. Despite that practical limitation to active avoidance of sensitive stocks, our regression models successfully

address thorny statistical challenges and offer practical tools that are useful in evaluating ESU-specific impacts under different fishery management scenarios.

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REFERENCES

- Aitchison, J. 1986. The statistical analysis of compositional data. Chapman and Hall, London, 416 p. doi.org/10.1007/978-94-009-4109-0
- Anderson, E. C. R. S. Waples, and S. T. Kalinowski. 2008. An improved method for predicting the accuracy of genetic stock identification. *Canadian Journal of Fisheries and Aquatic Sciences* 65:1475-1486.

486 Bellinger, M. R., M. A. Banks, S. J. Bates, E. D. Crandall, J. C. Garza, G. Sylvia, and P.
487 W. Lawson. 2015. Geo-referenced, abundance calibrated ocean distribution of Chinook
488 Salmon (*Oncorhynchus tshawytscha*) stocks across the West Coast of North America.
489 PLOS (Public Library of Science) ONE [online serial] 10(7):e0131276.
490
491 Burnham, K. P. and D. R. Anderson. 2002. Model selection and multimodel inference: A
492 practical information-theoretic approach. New York, NY: Springer.
493
494 Easley, J. 2001. History of trawling off the Pacific Coast. In: Microbehavior and
495 Macroresults: Proceedings of the Tenth Biennial Conference of the International Institute
496 of Fisheries Economics and Trade, July 10-14, 2000, Corvallis, Oregon, USA. Edited by
497 Richard S. Johnston and compiled by Ann L. Shriver. International Institute of Fisheries
498 Economics and Trade (IIFET), Corvallis, OR, 2001. CD ROM. ISBN: 0-9763432-2-3
499
500 Hamel, O. S., P. H. Ressler, R. E. Thomas, D. A. Waldeck, A. C. Hicks, J. A. Holmes, G.
501 W. Fleischer. 2015. Biology, fisheries, assessment and management of Pacific hake
502 (*Merluccius productus*). In Arancibia, H. (Ed.) Hake: Biology, Fisheries and Markets
503 [2nd Edition]. Wiley-Blackwell Science.
504
505 Hanson, M. B., R.W. Baird, J. K. B. Ford, J. Hempelmann-Halos, D. M. Van Doornik, J.
506 R. Candy, C. K. Emmon1, G. S. Schorr, B. Gisborne, K. L. Ayres, S. K. Wasser, K. C.
507 Balcomb, K. Balcomb-Bartok, J. G. Sneva, and M. J. Ford. 2010. Species and stock
508 identification of prey consumed by endangered southern resident killer whales in their
509 summer range. 11:69-82.

510

511 Hilbe, J. M. 2009. Logistic regression models. Chapman and Hall/CRC Press.

512

513 Kalinowski, S. T., K. R. Manlove, and M. L. Taper. 2007. ONCOR A computer program
514 for Genetic Stock Identification. Department of Ecology, Montana State University,
515 Bozeman MT 59717. Available: montana.edu/kalinowski.

516

517 Kim, S. and H. Kim. 2016. A new metric of absolute percentage error for intermittent
518 demand forecasts. *International Journal of Forecasting* 32:669-679.

519

520 Koljonen, M.-L., J. J. Pella, and M. Masuda. 2005. Classical individual assignments
521 versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*)
522 catches from DNA microsatellite data. *Canadian Journal of Fisheries and Aquatic*
523 *Sciences* 62:2143-2158.

524

525 Maier, M. J. 2014. DirichletReg: Dirichlet regression for compositional data in R.
526 Research Report Series/Department of Statistics and Mathematics, 125. WU Vienna
527 University of Economics and Business, Vienna. Available: epub.wu.ac.at/4077/

528

529 Makridakis, S. 1993. Accuracy measures: theoretical and practical concerns. *International*
530 *Journal of Forecasting*. 9:527-529.

531

532 Matson, S. E. and D. Erickson. 2018. Analysis of West Coast Groundfish Fisheries for
533 the 2017 Salmon ESA Biological Opinion, NOAA. NOAA Technical Memorandum
534 NMFS-OSF-X, 113 p.
535

536 Moran, B. M. and E. C. Anderson. 2019. Bayesian inference from the conditional genetic
537 stock identification model. *Canadian Journal of Fisheries and Aquatic Sciences* 76:551-
538 560.
539

540 Moran, P., M. Banks, T. Beacham, C. Garza, S. Narum, M. Powell, M. Campbell, L.
541 Seeb, R. Wilmot, S. Young, B. Ardren, and J. Wenburg. 2005. Interlaboratory
542 standardization of coast-wide Chinook salmon genetic data for international harvest
543 management. Progress report from the Genetic Analysis of Pacific Salmonids (GAPS)
544 consortium to the Chinook Technical Committee of the Pacific Salmon Commission,
545 FY2004, FY2005, 44 p. Available:
546 nwafc.noaa.gov/research/divisions/cb/documents/gaps_year2_final.pdf
547

548 Moran, P., D. J. Teel, E. S. LaHood, J. Drake, and S. Kalinowski. 2006. Standardising
549 multi-laboratory microsatellite data in Pacific salmon: an historical view of the future.
550 *Ecology of Freshwater Fish*. 15:597-605.
551

552 Moran, P., D. J. Teel, M. A. Banks, T. D. Beacham, M. R. Bellinger, S. M. Blankenship,
553 J. R. Candy, J. C. Garza, J. E. Hess, S. R. Narum, L. W. Seeb, W. D. Templin, C. G.
554 Wallace, and C. T. Smith. 2013. Divergent life-history races do not represent Chinook
555 salmon coast-wide: the importance of scale in Quaternary biogeography. *Canadian*

Journal of Fisheries and Aquatic Sciences 70:415–435.

Moran, P., J. B. Bromaghin, and M. Masuda. 2014. Use of genetic data to infer population-specific ecological and phenotypic traits from mixed aggregations. *PLoS ONE* 9(6):e98470.

Moran, P., J. Dazey, L. LaVoy, and S. Young. 2018. Genetic mixture analysis supports re-calibration of the Fishery Regulation Assessment Model. *Fisheries* 43:83-97.

NMFS—WCR (National Marine Fisheries Service, West Coast Region). 2017. Endangered Species Act (ESA) Section 7(a)(2) Biological Opinion. Reinitiation of Section 7 Consultation regarding the Pacific Fisheries Management Council's Groundfish Fishery Management Plan, NMFS Consultation Number: F/WCR-2017-7552. Available [westcoast.fisheries.noaa.gov/publications/fishery_management/groundfish/s7-groundfish-biop-121117.pdf](https://www.westcoast.fisheries.noaa.gov/publications/fishery_management/groundfish/s7-groundfish-biop-121117.pdf)

NOAA (National Oceanic and Atmospheric Administration). 2019. FishWatch U.S. Seafood Facts. Available: fishwatch.gov/profiles/pacific-whiting (accessed 5 June 2019).

NWFSC (Northwest Fisheries Science Center,). 2021. At-Sea Hake Observer Program Sampling Manual. Fishery Resource Analysis and Monitoring Division. Available: <https://media.fisheries.noaa.gov/2021-04/A-SHOP-Manual%202021-508-compliant-updated.pdf?null>.

580

581 PSC (Pacific Salmon Commission). 2020. Treaty between the Government of Canada

582 and the Government of the United States of America concerning Pacific salmon.

583 Prepared by the Pacific Salmon Commission, January 2020. Available:

584 <https://www.psc.org/download/45/miscellaneous/2337/pacific-salmon-treaty.pdf>.

585

586 Quirollo, L. F., V. G. Wespestad, and M. W. Dorn. 2001. Pacific hake, in California's

587 living marine resources: A status report. California Department of Fish and Game. Pages

588 393 – 397. Available: nrm.dfg.ca.gov/FileHandler.ashx?DocumentID=34265&inline.

589

590 R Core Team. 2017. R: A language and environment for statistical computing. R

591 Foundation for Statistical Computing, Vienna, Austria. Available: R-project.org/.

592

593 Rannala, B. and J. L. Mountain. 1997. Detecting immigration by using multilocus

594 genotypes. Proceedings of the National Academy of Sciences USA. 94:9197–9201.

595

596 Riddell, B. E., R. D. Brodeur, A. V. Bugaev, P. Moran, J. M. Murphy, J. A. Orsi, M.

597 Trudel, L. A. Weitkamp, B. K. Wells, and A. C. Wertheimer. 2018. Ocean ecology of

598 Chinook Salmon. Pages 555 – 696 in: R. Beamish (ed.) Ocean ecology of Pacific salmon

599 and trout. American Fisheries Society. 1147 p.

600

601 Satterthwaite, W.H., Michael Steven Mohr, Michael Robert O'Farrell, and Brian Kenneth

602 Wells. 2012. A Bayesian hierarchical model of size-at-age in ocean-harvested stocks —

quantifying effects of climate and temporal variability. Canadian Journal of Fisheries and Aquatic Sciences. 69:942-954.

605

Satterthwaite, W. H., M. S. Mohr, M. R. O'Farrell, E. C. Anderson, M. A. Banks, S. J. Bates, M. R. Bellinger, L. A. Borgerson, E. D. Crandall, J. C. Garza, B. J. Kormos, P. W. Lawson, and M. L. Palmer-Zwahlen. 2014. Use of stock identification data for comparison of the ocean spatial distribution, size at age, and fishery exposure of an untagged stock and its indicator: California coastal versus Klamath River Chinook Salmon. Transactions of the American Fisheries Society 143:117–133.

612

Satterthwaite, W. H., J. Ciancio, E. Crandall, M. L. Palmer-Zwahlen, A. M. Grover, M. R. O'Farrell, E. C. Anderson, M. S. Mohr, J.C. Garza. 2015. Stock composition and ocean spatial distribution inference from California recreational Chinook salmon fisheries using genetic stock identification. Fisheries Research 170:166–178.

617

Seeb, L.W., A. Antonovich, M.A. Banks, T.D. Beacham, M.R. Bellinger, S.M. Blankenship, M. Campbell, N. A. Decovich, J. C. Garza, C. M. Guthrie III, T.A. Lundrigen, P. Moran, S.R. Narum, J.J. Stephenson, K J. Supernault, D.J. Teel, W.D. Templin, J.K. Wenburg, S.F. Young, and C.T. Smith. 2007. Development of a standardized DNA database for Chinook salmon. Fisheries 32:540-552.

623

Shelton, A.O., W.H. Satterthwaite, E.J. Ward, B.E. Feist, and B. Burke. 2019. Using hierarchical models to estimate stock-specific and seasonal variation in ocean distribution, survivorship, and aggregate abundance of fall run Chinook salmon. Canadian Journal of

627 Aquatic Sciences. 76:95-108.

628

629 Shelton, A.O., G.H. Sullaway, E.J. Ward, B.E. Feist, K.A. Somers, V.J. Tuttle, J.T.

630 Watson, and W.H. Satterthwaite. 2021. Redistribution of salmon populations in the

631 northeast Pacific ocean in response to climate. Fish and Fisheries 22:503-517.

632

633 Somers, K. A., M. A. Bellman, J. E. Jannot, Y. W. Lee, J. McVeigh, V. Tuttle. 2015.

634 Observed and estimated total bycatch of salmon in the 2002-2013 U.S. West Coast

635 fisheries. West Coast Groundfish Observer Program. National Marine Fisheries Service,

636 NWFSC, 2725 Montlake Blvd E., Seattle, WA 98112. Available:

637 [nwfsc.noaa.gov/research/divisions/fram/observation/pdf/Salmon_Bycatch_Report_2002-](https://www.nwfsc.noaa.gov/research/divisions/fram/observation/pdf/Salmon_Bycatch_Report_2002-2013.pdf)

638 [2013.pdf](https://www.nwfsc.noaa.gov/research/divisions/fram/observation/pdf/Salmon_Bycatch_Report_2002-2013.pdf)

639

640 Weitkamp, L. A. 2010. Marine distribution of Chinook Salmon (*Oncorhynchus*

641 *tshawytscha*) from the West Coast of North America determined by coded wire tag

642 recoveries. Transactions of the American Fisheries Society 139:147–170.

643

644 Winans, G. A., D. Viele, A. Grover, M. Palmer-Zwahlen, D. Teel, and D. Van Doornik.

645 2001. An update of genetic stock identification of Chinook Salmon in the Pacific

646 Northwest: Test fisheries in California. Reviews in Fisheries Science, 9:213–237.

647 Table 1. Chinook Salmon bycatch in the at-sea sectors of the US West Coast Pacific
 648 Hake fishery (where >0.8 is the number of individual fish that met that assignment
 649 probability threshold, and Mean latitude is derived from all fish genotyped)

Year	Bycatch¹	Collected	Subsampled	Genotyped	>0.8	Mean lat.	Accession #²
2008	875	271	271	258	178	46.32	34801
2009	1,142	403	403	390	326	47.89	34592
2010	1,364	680	680	664	548	46.89	34927
2011	4,360	1,837	1,835 ³	1,693	1,284	44.77	90517
2012	4,209	2,013	288	288	215	44.43	90598
2013	3,739	1,542	288	285	218	43.78	90601
2014	6,695	2,368	384	381	295	43.54	90627
2015	1,806	748	349	345	296	43.91	90654
Total	24,190	9,862	4,498	4,304	3,360	45.21	

¹Estimated total Chinook bycatch

nwfsc.noaa.gov/research/divisions/fram/observation/xls/SalmonBycatch_Expanded_2002-2015.xlsx

²NWFSC Conservation Biology Division Tissue Archive

³Essentially all collected samples were selected for genotyping in 2012

650

651

652 APPENDIX

653 Reference populations and reporting group structure for genetic mixture analysis based
 654 on Evolutionarily Significant Units (J. Myers, pers. comm. January 2016). Populations
 655 modified from Seeb et al. (2007). Status: E = Endangered, T = Threatened, C = Candidate,
 656 NW = Not Warranted, N/A = Not Applicable, stock aggregates that are not ESUs, which
 657 are only defined for the conterminous, US West Coast states. Carson Hatchery is a
 658 mixed-origin broodstock that is not listed under the ESA.

Genetic baseline population	ESU reporting group	Status
Sacramento Hatchery	Sacramento Winter	E
Butte Creek sp	Central Valley Spring	T
Deer Creek sp	Central Valley Spring	T
Mill Creek sp	Central Valley Spring	T
Feather Hatchery sp	Central Valley Fall	C
Feather Hatchery fa	Central Valley Fall	C
Butte Creek fa	Central Valley Fall	C
Stanislaus River	Central Valley Fall	C
Battle Creek	Central Valley Fall	C
Russian River	California Coastal	T
Eel River	California Coastal	T
Trinity Hatchery fa	Upper Klamath-Trinity Rivers	NW
Trinity Hatchery sp	Upper Klamath-Trinity Rivers	NW
Klamath River fa	Upper Klamath-Trinity Rivers	NW
Chetco River	S. Oregon and N. California Coastal	NW
Applegate Creek	S. Oregon and N. California Coastal	NW
Cole Rivers Hatchery	S. Oregon and N. California Coastal	NW

Genetic baseline population	ESU reporting group	Status
Elk Hatchery	Oregon Coast	NW
Sixes River	Oregon Coast	NW
Coquille River	Oregon Coast	NW
Coos Hatchery	Oregon Coast	NW
S Umpqua Hatchery	Oregon Coast	NW
Umpqua Hatchery	Oregon Coast	NW
Siuslaw River	Oregon Coast	NW
Alsea River	Oregon Coast	NW
Yaquina River	Oregon Coast	NW
Siletz River	Oregon Coast	NW
Salmon River fa	Oregon Coast	NW
Nestucca Hatchery	Oregon Coast	NW
Trask River	Oregon Coast	NW
Wilson River	Oregon Coast	NW
Kilchis River	Oregon Coast	NW
Nehalem River	Oregon Coast	NW
Necanicum Hatchery	Oregon Coast	NW
Forks Creek Hatchery	Washington Coast	NW
Humtulpis Hatchery	Washington Coast	NW
Queets River	Washington Coast	NW
Hoh River	Washington Coast	NW
Sol Duc Hatchery	Washington Coast	NW
Makah Hatchery	Washington Coast	NW
Lewis Hatchery sp	Lower Columbia River	T

Genetic baseline population	ESU reporting group	Status
Kalama Hatchery sp	Lower Columbia River	T
Cowlitz Hatchery sp	Lower Columbia River	T
Cowlitz Hatchery fa	Lower Columbia River	T
Sandy River	Lower Columbia River	T
Lewis River fa	Lower Columbia River	T
Spring Creek Hatchery	Lower Columbia River	T
McKenzie Hatchery	Upper Willamette River	T
N Santiam Hatchery	Upper Willamette River	T
Warm Springs Hatchery	Mid-Columbia River Spring	NW
John Day River	Mid-Columbia River Spring	NW
U Yakima Hatchery	Mid-Columbia River Spring	NW
Wenatchee River sp	Upper Columbia River Spring	E
Wenatchee Hatchery sp	Upper Columbia River Spring	E
Carson Hatchery	Upper Columbia River Spring	N/A
U Deschutes River	Deschutes River Summer/Fall	NW
L Deschutes River	Deschutes River Summer/Fall	NW
Hanford Reach	Upper Columbia River Summer/Fall	NW
Wenatchee River su/fa	Upper Columbia River Summer/Fall	NW
Wells Hatchery	Upper Columbia River Summer/Fall	NW
Methow River	Upper Columbia River Summer/Fall	NW
Lyons Ferry Hatchery	Snake River Fall	T
EF Salmon River	Snake River Spring/Summer	T
WF Yankee Fork	Snake River Spring/Summer	T
Secesh River	Snake River Spring/Summer	T

Genetic baseline population	ESU reporting group	Status
Rapid River Hatchery	Snake River Spring/Summer	T
Minam River	Snake River Spring/Summer	T
Imnaha River	Snake River Spring/Summer	T
Newsome Creek	Snake River Spring/Summer	T
Tucannon Hatchery	Snake River Spring/Summer	T
Tucannon River	Snake River Spring/Summer	T
Clear Creek Hatchery	Puget Sound	T
Voights Hatchery	Puget Sound	T
S Prairie Creek	Puget Sound	T
Soos Hatchery	Puget Sound	T
George Adams Hatchery	Puget Sound	T
Hamma Hamma River	Puget Sound	T
Snoqualmie River	Puget Sound	T
Samish Hatchery	Puget Sound	T
Elwha Hatchery	Puget Sound	T
Elwha River	Puget Sound	T
Dungeness River	Puget Sound	T
NF Nooksack Hatchery	Puget Sound	T
White Hatchery	Puget Sound	T
Hatcheryupp Sp Hatchery	Puget Sound	T
Skykomish River	Puget Sound	T
Wallace Hatchery	Puget Sound	T
NF Stillaguam Hatchery	Puget Sound	T
Skagit River	Puget Sound	T

Genetic baseline population	ESU reporting group	Status
U Sauk River	Puget Sound	T
Suiattle River	Puget Sound	T
L Sauk River	Puget Sound	T
Marblemount Hatchery sp	Puget Sound	T
Marblemount Hatchery su	Puget Sound	T
U Cascade River	Puget Sound	T
U Skagit River	Puget Sound	T
W Chilliwack Hatchery	Southern BC	N/A
Maria Slough	Southern BC	N/A
Birkenhead Hatchery	Southern BC	N/A
M Shuswap Hatchery	Southern BC	N/A
L Thomson River	Southern BC	N/A
L Adams Hatchery	Southern BC	N/A
Clearwater River	Southern BC	N/A
Riveraft River	Southern BC	N/A
Spius Hatchery	Southern BC	N/A
Nicola Hatchery	Southern BC	N/A
Louis Creek	Southern BC	N/A
Deadman Hatchery	Southern BC	N/A
U Chilcotin River	Southern BC	N/A
Chilko River	Southern BC	N/A
Quesnel River	Southern BC	N/A
Nechako River	Southern BC	N/A
Stuart River	Southern BC	N/A

Genetic baseline population	ESU reporting group	Status
Swift River	Southern BC	N/A
Morkill River	Southern BC	N/A
Salmon River sp	Southern BC	N/A
Cowichan Hatchery	Southern BC	N/A
Nanaimo Hatchery fa	Southern BC	N/A
Big Qualicum Hatchery	Southern BC	N/A
Puntledge Hatchery fa	Southern BC	N/A
Quinsam Hatchery	Southern BC	N/A
Nitinat Hatchery	Southern BC	N/A
Sarita Hatchery	Southern BC	N/A
Tranquil River	Southern BC	N/A
Robertson Hatchery	Southern BC	N/A
Conuma Hatchery	Southern BC	N/A
Tahsis River	Southern BC	N/A
Marble Hatchery	Southern BC	N/A
Porteau Cove Hatchery	Southern BC	N/A
Klinaklini River	Southern BC	N/A
Wannock Hatchery	Central BC-AK	N/A
Atnarko Hatchery	Central BC-AK	N/A
Kitimat Hatchery	Central BC-AK	N/A
Ecstall River	Central BC-AK	N/A
L Kalum River	Central BC-AK	N/A
Bulkley River	Central BC-AK	N/A
Sustut River	Central BC-AK	N/A

Genetic baseline population	ESU reporting group	Status
Kincolith River	Central BC-AK	N/A
Kwinageese River	Central BC-AK	N/A
Damdochax River	Central BC-AK	N/A
Owegee River	Central BC-AK	N/A
L Tahltan River	Central BC-AK	N/A
Nakina River	Central BC-AK	N/A
Kowatua Creek	Central BC-AK	N/A
Tatsatua Creek	Central BC-AK	N/A
U Nahlin River	Central BC-AK	N/A
Chickamin/White Hatchery	Central BC-AK	N/A
Chickamin Hatchery	Central BC-AK	N/A
Chickamin River	Central BC-AK	N/A
Keta River	Central BC-AK	N/A
King Creek	Central BC-AK	N/A
Clear Creek	Central BC-AK	N/A
Creekipple Creek	Central BC-AK	N/A
Andrew Creek	Central BC-AK	N/A
Andrew/Mac Hatchery	Central BC-AK	N/A
Andrew/Med Hatchery	Central BC-AK	N/A
Andrew/Cry Hatchery	Central BC-AK	N/A
King Salmon River	Central BC-AK	N/A
Big Boulder Creek	Central BC-AK	N/A
Tahini River	Central BC-AK	N/A
Tahini/Mac Hatchery	Central BC-AK	N/A

Genetic baseline population	ESU reporting group	Status
Klukshu River	Central BC-AK	N/A
Situk River	Central BC-AK	N/A

659 ¹Feather River spring run brood stock was extensively hybridized with fall run in that
660 program and the two are now genetically indistinguishable.

661 ²Brood stock from Cole M. Rivers Hatchery on the Rogue River in Southern Oregon is
662 currently propagated and released in Young's Bay at the mouth of the Columbia River.

Figure captions

Figure 1. Overall Chinook Salmon ESU proportions observed in at-sea Pacific Hake trawl fisheries for all years combined 2008 - 2015. ESUs and two stock aggregates are ordered from south to north.

Figure 2. Chinook Salmon ESU proportions, stratified by fishery management area, ordered from south to north. Area 1: North of Cape Falcon, Oregon (45.77°); Area 2: Cape Falcon, Oregon to Cape Blanco, Oregon (42.75° to 45.77°); Area 3: Cape Blanco, Oregon to Cape Mendocino, California (40.16° to 42.75°). See Figure 3 for area boundaries.

Figure 3. Individual Chinook Salmon taken in bycatch, color coded by most likely ESU of origin, from red in the south to blue in the north. Fishery management area boundaries are shown as red lines with associated latitudes (see Fig. 2 for area descriptions).

Figure 4. Dirichlet regression (solid) and multinomial logistic regression (dashed) with observed proportions (summing to one over all four panels) and mean latitudes of annual samples (points). Data ranges differ because DR is based on mean latitudes, whereas MLR is fitted to individual fish, their observed latitude, and the ESU to which they were assigned. Regional divisions simply facilitate interpretation.

Figure 5. Selected realizations of the jackknife analysis are shown in each panel, where one entire annual sample (identified in title) was held out as a cross-validation test set (Obs). The remaining years were used as a training set to estimate ESU proportions given the observed latitude. Those proportions shifted beginning in 2011 and from 2012 to

684 2015 northern ESUs nearly disappeared. Note that observed proportions were similar
685 between 2013 and 2015, when mean latitudes were also similar (~43.8°, Table 1).

686 Figure 6. Model cross validation, summarized from Figure 5, comparing observed ESU
687 proportions (Obs) with values predicted from Dirichlet regression (DR) and multinomial
688 logistic regression (MLR), independent of observation.
689

Northern ESUs

Columbia ESUs

Coastal ESUs

Southern ESUs