PACIFIC SALMON FOUNDATION

HATCHERY, PREDATION, AND CLIMATE EFFECTS ON PRODUCTIVITY OF WILD CHINOOK, COHO, AND CHUM SALMON

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Hatchery, predation, and climate effects on productivity of wild Chinook, Coho, and Chum salmon

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Introduction

Survival rates for both wild and hatchery-released Chinook (*Oncorhynchus tshawytscha*) and Coho (*O. kisutch*) salmon have been declining throughout the Strait of Georgia since the 1980s (Cole 2000, Beamish et al. 2010, Zimmerman et al. 2015, PSC 2019, Doherty and Cox 2021). In addition, widespread declines in productivity have also occurred for wild Chum (*O. keta*) stocks in central and northern British Columbia over the last two decades (Malick and Cox 2016). Hypothesized mechanisms underlying declining survival rates for wild salmon in general include changing environmental conditions, increased predation, habitat loss, genetic changes, hydroelectric dams, and large-scale hatchery production (Hilborn et al. 1992, Bradford and Irvine 2000, Mueter et al. 2005, Naish et al. 2007, Schindler et al. 2010, Anderson et al. 2019, Nelson et al. 2019). While most of these hypotheses have been examined in varying levels of detail, few studies evaluate their possible joint effects by simultaneously considering multiple covariate types on survival outcomes (Cunningham et al. 2018, Chilcote et al. 2011, Nelson et al. 2019, Connors et al. 2020). Models that ignore multiple effects on productivity may produce misleading conclusions that over-estimate effect sizes or incorrectly identify the main factors driving changes in productivity. For example, stock-recruitment models for Chinook in the Salish Sea that include covariates for Harbour Seal density and hatchery Chinook releases perform better than models that ignore one or the other covariate, although Harbour Seal density is ultimately responsible for most of the improved performance (Nelson et al. 2019).

This paper presents a Bayesian hierarchical approach for developing and comparing performance of multi-population spawner-recruitment models that estimate potential hatchery, predation, and/or environmental covariates effects on wild productivity for Chinook, Coho, and Chum populations in British Columbia. We investigate wild salmon productivity relationships with multiple covariates using multi-population Ricker models fit with spawner-recruit time series from 1954-2015 for 23 Coho conservations units (CUs), 1986-2013 for 24 Chinook populations (8 stocks, 16 CUs), and 1973-2013 for 28 Chum CUs. Our Bayesian multi-population approach allows for improved statistical power relative to single population models, which can have the dual effect of reducing uncertainty in estimated productivity relationships between covariates and reduce the chance of identifying spurious relationships (Myers and Mertz 1998, Malick et al. 2015). The use of a hierarchical approach allows information sharing across different populations in BC to estimate common hatchery, predation and environmental effects across populations, while allowing for population-specific hatchery effects where data are informative. Our models found that some covariates had the same effects on productivity for all 3 species, including negative effects from seal predation and positive effects from hatchery covariates for density dependence, whereas other covariate effects differed by species (i.e., sea surface temperature) and across populations (i.e., cumulative hatchery effects). We found that a combination of hatchery, predation, and marine conditions better explains changes in wild Salmon productivity over time than models excluding select covariates.

Methods

Data

Spawner-recruit time series for wild populations of Coho, Chinook, and Chum salmon in British Columbia were obtained for their respective conservation units (Holtby and Ciruna 2007, Tables CK.1, CO.1, CM.1) from the Pacific Salmon Explorer (PSE) database (Pacific Salmon Foundation (PSF), www.salmonexplorer.ca, accessed August 2021) and from Inner South Coast Chum run reconstructions (unpublished data, Pieter Van Will, DFO).

A Conservation Unit (CU) is defined as *"a group of wild Pacific salmon sufficiently isolated from other groups that, if extirpated, is very unlikely to recolonize naturally within an acceptable timeframe, such as a human lifetime or a specified number of salmon generations."* (DFO 2005).

We obtained stock-specific spawner recruit datasets for 8 Chinook stocks in the Strait of Georgia (Nelson et al. 2019).

Outliers from log recruits-per-spawner (RPS) estimates that were +/- 3 standard deviations from the mean for each species (16, 14, and 19 observations for Coho, Chinook, and Chum, respectively) were removed prior to model fitting. The rationale for excluding RPS outliers a priori was that some outliers were not considered ecologically realistic (based on consultations with PSF team and stock assessment group) and were likely associated with errors in the escapement or catch estimates. The outliers removed were RPS > 72 and RPS < 0.04 for Chinook, RPS > 39 and RPS < 0.06 for Coho, and RPS > 44 and RPS < 0.04 for Chum.

Note that we identify tables and figures using prefixes CK for Chinook, CO for Coho, and CM for Chum for easier referencing. All CK tables and figures are presented first in Appendix CK, followed by those for CO and then CM in Appendices CO and CM, respectively.

Single-population Ricker models to guide hatchery covariate selection

Hatchery activity can potentially impact wild salmon survival via a variety of mechanisms and spatial scales. For example, hatchery activity could be related to (i) density-dependent mortality (e.g., competition, predator swamping) in juvenile freshwater habitats; (ii) density-dependent mortality in early marine residence; (iii) cumulative effects via increased disease, reduced genetic fitness or diversity;, and (iv) changing predator-prey dynamics to name a few. Unfortunately, there are no data specifically isolating any of these mechanisms or their relationships to hatchery activity. Therefore, we first aimed to select a subset of hatchery activity indicators that could represent these mechanisms to the extent possible. In this section, we used Pearson correlations ρ between residuals from single-stock Ricker models and six hatchery activity covariates to identify covariates that might best explain variating in wild salmon survival.

Single-population Ricker spawner-recruit models for Coho, Chinook, and Chum were of the form,

$$(1)\ R_t = \alpha S_t e^{-\beta + \varepsilon_t}$$

where S_t is the number of spawners in brood year t, R_t is the number of adult recruits from S_t, α is the intrinsic productivity (i.e., productivity at low spawner abundance without density dependence), β is the density-dependence coefficient (Ricker 1954), and $\varepsilon_t \sim N(0, \sigma_\varepsilon^2)$.

Linearizing Eq (1) gives the following form used for model fitting:

$$(2)\ \ln(R_t/S_t) = \ln\alpha - \beta S_t + \varepsilon_t$$

Hatchery activity indicators with numbers in brackets indicating the possible mechanisms given above:
- annual and cumulative intraspecies releases in CUs (i),
- annual ratios of intraspecies hatchery smolts to wild smolts within a CU (i),
- annual ratios of intraspecies hatchery smolts to wild smolts within ocean entry regions (ii),
- annual and cumulative hatcheries operating in a CU (iii,iv), and
- annual and cumulative hatchery release sites in a CU (iii, iv).
- annual percentage of hatchery origin spawners (pHOS, Withler et al. 2018) on spawning grounds (iii)

We selected three hatchery activity covariates H to include in multi-population models described in next section:
  a) species-specific hatchery releases per wild smolt by CU (H^{relCU})
  b) species-specific hatchery releases per wild smolt by ocean entry region (H^{relOE})
  c) cumulative release sites by CU (H^{cSite})

where covariates (i) and (ii) are used to estimate hatchery effects within juvenile freshwater habitats and iii) is for effects in habitats during early marine residency. These hatchery covariates had higher correlations on average for Chinook, Coho, and Chum with the single population Ricker model residuals ($H^{relRatioCU}$:0.04 < ρ < 0.14,

H^{cSite}: -0.34 < ρ < -0.17, $H^{relRatioOE}$: -0.10 < ρ < 0.14) and, therefore, were selected for model inclusion from the larger suite of hatchery indicator activities initially considered. For iii) we identified six ocean entry regions (Figure 1) adapted from Pacific Salmon Marine Adaptive Zones (Holtby and Ciruna 2007):

1. Strait of Georgia (SOG)
2. West Coast Vancouver Island (WCVI)
3. Queen Charlotte Strait, Johnstone Strait, and Discovery Passage (QCSDPASS)
4. Central Coast (CC)
5. North Coast (NC)
6. Haida Gwaii (HG)

Pearson correlations for pHOS with residuals from single population Chinook Ricker models ranged from 0.37 to -0.65 with a mean value of -0.09 (Table 1, Figure 2). Unfortunately, pHOS data is only available for 11 Chinook populations represented by the spawner-recruit timeseries data available for model fitting and therefore it could not be included in multi-population models fit to the full spawner recruit datasets. Therefore we fit two types of models for Chinook: 1) a 24-Chinook population model without a pHOS covariate, and 2) an 11-Chinook population model with an additional hatchery covariate for pHOS.

Multi-population Bayesian hierarchical modelling for estimating hatchery effects on wild salmon productivity

We extended Eq 2 to create a base hierarchical multi-population (we use "population" to represent CU and stock-level data) spawner-recruit model involving only spawners as the single covariate, i.e.,

$$(3)\ \ln\left(R_{i,t}/S_{i,t}\right) = \ln\alpha + \Delta_i^\alpha - \left(\beta + \Delta_i^\beta\right)S_{i,t} + \varepsilon_{i,t}$$

where α is the average productivity over all populations in the absence of density dependence, β is the average density dependence effect for all i populations, Δ_i^α and Δ_i^β are population-specific deviations from the mean effects α and β, respectively. Population-specific deviation terms ($\Delta_i^\alpha, \Delta_i^\beta$) are random effects with assumed normal distributions, i.e., $\Delta_i^\alpha \sim N(0, \sigma_\alpha^2)$ and $\Delta_i^\beta \sim N\left(0, \sigma_\beta^2\right)$ and the residual $\varepsilon_{i,t} \sim N(0, \sigma_\varepsilon^2)$ is population- and year-specific.

The following sections extend Eq (3) with covariates for hatchery activity, predation, and environmental conditions.

Hatchery activity

We modify the base hierarchical model to account for potential hatchery activity effects on wild salmon productivity that occur 1) within juvenile freshwater habitats, and 2) juvenile habitats for early marine residence:

$$(4)\ \ln\left(R_{i,t}/S_{i,t}\right) = \ln\alpha + \Delta_i^\alpha - \left(\beta + \Delta_i^\beta\right)S_{i,t} + \tau H_{i,t}^{relCU} + \phi H_{i,t}^{relOE} + \left(\theta + \Delta_i^\theta\right)H_{i,t}^{cSites} + \varepsilon_{i,t}$$

where H denotes the three hatchery activity covariates selected from single-population models (H^{relCU}, H^{relOE}) H^{cSite}) with average hatchery activity effects τ, ϕ, and θ across all i populations, and Δ_i^θ is a random population-specific deviation from the mean effect ($\Delta_i^\theta \sim N(0, \sigma_\theta^2)$). We use a half t-distribution prior with $\nu = 6$ degrees of freedom to constrain the random effect variance σ_θ^2.

Initial model fitting included population specific deviations for H^{relCU} (i.e., $\tau + \Delta_i^\tau$) and H^{relOE} (i.e., $\phi + \Delta_i^\phi$), but had difficulty estimating non-zero deviations (i.e., there was little information to indicate population-specific differences from the mean effects τ, ϕ) so subsequent model fits excluded deviations for H^{relCU} and H^{pHOS} covariates.

We fit a separate model for the 11 Chinook populations with sufficient pHOS data:

$$(5) \ln(R_{i,t}/S_{i,t}) = \ln\alpha + \Delta_i^\alpha - (\beta + \Delta_i^\beta)S_{i,t} + \tau H_{i,t}^{relCU} + \phi H_{i,t}^{relOE} + H_{i,t}^{cSites} + \lambda H_{i,t}^{pHOS} + \varepsilon_{i,t}$$

where the pHOS covariate is $H_{i,t}^{pHOS}$.

Initial fits for the 11-population model included population specific deviations for H^{relCU} (i.e., $\tau + \Delta_i^\tau$), H^{relOE} (i.e., $\phi + \Delta_i^\phi$), H^{cSites} (i.e., $\theta + \Delta_i^\theta$), and H^{pHOS}(i.e., $\lambda + \Delta_i^\lambda$), but there was little information to indicate population-specific differences from the mean effects $\tau, \phi, \theta, \lambda$; therefore, subsequent model fits only included mean effects for all hatchery covariates.

Predators

We add a predator density covariate to equation 4 to account for possible predation during juvenile salmon outmigration and the period of early marine residence, i.e.,

$$(6) \ \ln(R_{i,t}/S_{i,t}) = \ln\alpha + \Delta_i^\alpha - (\beta + \Delta_i^\beta)S_{i,t} + \tau H_{i,t}^{relCU} + \phi H_{i,t}^{relOE} + (\theta + \Delta_i^\theta)H_{i,t}^{sites} + \rho P_{i,t+1} + \varepsilon_{i,t}$$

where P is regional Harbour Seal (*Phoca vitulina*) density in one of six ocean entry regions (SOG, WCVI, QCSJSDP, CC, NC, HG) for smolts in the ocean entry year (i.e., *t+1)* and ρ is the average seal effect. Harbour Seal densities (Figure 3) were estimated using abundance time series estimated via deterministic generalized logistic growth models and estimates of shoreline lengths for each region (Details in Appendix HS).

Environmental conditions

Wild salmon productivity may also be affected by regional-scale climate indices, such as sea surface temperature (Malick et al. 2017, Connors et al. 2020, Malick 2020), most likely, by changing ecosystem composition of predators and prey. To account for oceanographic trends, we modified equation 6 to include a sea surface temperature (SST) covariate:

$$(7) \ \ln(R_{i,t}/S_{i,t}) = \ln\alpha + \Delta_i^\alpha - (\beta + \Delta_i^\beta)S_{i,t} + \tau H_{i,t}^{relCU} + \phi H_{i,t}^{relOE} + (\theta + \Delta_i^\theta)H_{i,t}^{sites} + \rho P_{i,t+1} + \gamma T_{i,t+1} + \varepsilon_{i,t}$$

where γ is the average effect across all CUs/stocks for SST (*T*) in the ocean entry year. The SST data captures regional variability in ocean temperatures spanning several hundred kilometres (Muerter et al. 2002), using monthly SST for 2° x 2° grid cells from NOAA's National Centre of Environmental Information (NCEI) based on NOAA's extended reconstruction of SST (ERSSTv5, Huang et al. 2017). For each stock, we identified a region of early ocean residence for juvenile salmon that was +/- 40 km in directions perpendicular to the shoreline and +/- 125 km from ocean entry points in directions parallel to the shoreline. We applied the same approach for populations at the CU-level, however extended regions +/- 125 km in directions parallel to the northern and southern most shorelines in CU boundaries (See example in Figure 4). A maximum distance of 40 km off the coast was based on findings that the highest catches of juvenile salmon occurred within 40 km of the shoreline in Southeast Alaska (Orsi et al. 2003).

We used average monthly SST during juvenile outmigration and early marine residence based on the weighted proportion of ERSST grid cells that overlap with the ocean residence polygons. Monthly SST was averaged for May-August for Shuswap Chinook (pers. comm, Dave Scott and Misty MacDuffee, Raincoast Conservation Society) and March-July for all other Chinook populations, April-June for Coho, and March-May for Chum populations based on a review of the available outmigration timing data for BC (Carr-Harris et al. 2015, Chalifour et al. 2021, Muerter et al. 2002, Roias et al. 2021)

We also include predator and temperature covariates in the 11-population Chinook model with a hatchery covariate for pHOS:

$$(8)\ \ln\left(R_{i,t}/S_{i,t}\right) = \ln\alpha + \Delta_i^\alpha - \left(\beta + \Delta_i^\beta\right)S_{i,t} + \tau H_{i,t}^{relCU} + \phi H_{i,t}^{relOE} + H_{i,t}^{sites} + \lambda H_{i,t}^{pHOS} + \rho P_{i,t+1} + \gamma T_{i,t+1} + \varepsilon_{i,t}$$

Model fitting

We fit the full models (eqn. 7, 8) along with models leaving out different covariates and use the Leave-One-Out Cross-validation Information Criterion (LOOIC, Vehtari et al. 2017) to compare predictive performance of Bayesian models and avoid over-fitting. The LOOIC is similar to other information criteria (e.g., AICc, Burnham and Anderson 2002) where low LOOIC indicates better predictive performance.

All hierarchical multi-population Ricker models were developed using the Template Model Builder package (TMB, Kristensen et al. 2016) within R version 4.1.0 (R Core Team 2020). Posterior distributions of parameter estimates were generated using a Hamiltonian Monte Carlo method in the tmbstan package in R (Monnahan and Kristensen 2018) and LOOIC calculations were done using the loo package in R (Vehtari et al. 2017).

Results

In the subsequent sections, we summarize the main findings from hierarchical multi-population Ricker models used to evaluates hatchery, predation, and environmental effects on wild salmon productivity for Chinook, Coho and Chum. Comparisons of the candidate multi-population Ricker models are shown in Tables CK.2,CK.5, CO.2, & CM.2.

Chinook

Hatchery covariates in the full Chinook 24-population model had mixed effects on Chinook productivity. We found significant positive effects from hatchery releases per wild smolt by CU (H^{relCU}, τ=0.002, 95% CI:-0.001, 0.003, Table CK.2) and ocean entry region (H^{relOE}, ϕ=0.01, 95% CI:0.004, 0.02). Increases of 1 SDU for hatchery releases per wild smolts within CUs and ocean entry regions produced mean increases in RPS of 6.4% and 7.5%, respectively (Table CK.3). The effect sizes from a 1SDU increase in H^{relOE} are larger for SOG and QCSDPASS populations since a 1SD increase in SOG (2-26 hatchery releases per wild smolt) is much larger than a 1 SD increase in the other regions (0.2-1 hatchery releases per wild smolt).

We found significant negative effects from cumulative release sites (H^{cSite}, θ=-0.01, 95% CI:-0.03, -0.005) with an average decrease of 12% in RPS for a 1SDU increase in releases sites across all populations. The cumulative release site effect for a 1SDU increase varies by population with changes in RPS ranging -32% to 7% due to variation in the size of a 1SDU increase (2-35 sites) as well as population-specific deviations in the coefficient (Fig. CK.2). The largest declines (20-32%) occurred for 5 populations (CK-50: Kalum-late CU, CK-53: Middle Skeena – Large Lakes CU, CK-54: Middle Skeena – Mainstem Tributaries CU, Quinsam River stock, Cowichan River stock, Table CK.3) with significant negative coefficients (Fig. CK.3). The North & Central Coast – Early Timing CU (CK-42) was the only population with a positive coefficient for H^{cSite}, which produced a 7% increase in RPS for a 1SDU increase.

Seal density has a negative effect (ρ= -0.05 95% CI:-0.11, 0.02) on average on Chinook productivity, with a 1 SDU increase in seal density producing an average 6.3% decrease in RPS (Table CK.3). The seal density effects associated with a 1SDU increase are larger for SOG populations because a 1SD increase in SOG (1.9-3.3 seals/km) is much larger than a 1 SD increase in the other regions (0.2-0.7 seals/km). SST had on average a slight positive (γ= 0.04, 95% CI:-0.06, 0.13) but non-significant effect (i.e. 95% credible intervals overlap with zero) on Chinook productivity whereby a 1 SDU increase (0.5-0.7 degrees across populations) produced an average increase in RPS of 2.3% (Table CK.3).

The 11-population model showed little evidence of a pHOS effect (H^{pHOS}, λ=0.05, 95% CI:-0.44, 0.59, Table CK.5). The modal coefficient estimate indicates a slight positive effect; however only 61% of the posterior distribution is positive, while 39% is negative (Fig. CK.5). Increases of 1 SDU in pHOS produces a 0.9% increase in mean RPS for each population (Table CK.6). Including a pHOS covariate in the 11-population subset had little impact on the estimated effects for temperature, seal density, and other hatchery covariates (Fig. CK.5)

Hatchery covariates in the full Chinook 24-population model had mixed effects on Chinook productivity. We found significant positive effects from hatchery releases per wild smolt by by CU (H^{relCU}, τ=0.002, 95% CI:-0.001, 0.003, Table CK.2) and ocean entry region (H^{relOE}, ϕ=0.01, 95% CI:0.004, 0.02). Increases of 1 SDU for hatchery releases per wild smolts within CUs and ocean entry regions produced mean increases in RPS of 6.4% and 7.5%, respectively (Table CK.3). The effect sizes from a 1SDU increase in H^{relOE} are larger for SOG and QCSDPASS populations since a 1SD increase in SOG (2-26 hatchery releases per wild smolt) is much larger than a 1 SD increase in the other regions (0.2-1 hatchery releases per wild smolt).

We did not find evidence of model-overfitting as the full models were within 2.7 and 10 LOOIC units for the 24-population model and the 11-population model with pHOS data, respectively, of the model with the lowest LOOIC, indicating similar performance (Table CK.2, CK.%). The size of the covariate effects have considerable variation across populations and regions shown in Table CK.3. Ricker spawner-recruit curves and model fits to $\ln(R_t/S_t)$ observations are shown in Figures CK.4-5.

Coho

Hatchery covariates in the full Coho model had mixed effects on Coho productivity. We found positive effects from hatchery releases per wild smolt by by CU (H^{relCU}, τ=0.1, 95% CI:-0.09, 0.26) and by ocean entry region (H^{relOE}, ϕ=0.45, 95% CI:0.13, 0.83) and), but only the latter was significant with 95% credible intervals that do not overlap with zero. Increases of 1 SDU for the hatchery releases per wild smolts within CUs and ocean entry regions produced mean increases of 1.9% and 5.6%, respectively on RPS (Table CO.3). The effect sizes from a 1SDU increase are larger for SOG populations since a 1SD increase in SOG (0.28 hatchery releases per wild smolt) is much larger than a 1 SD increase in the other regions (0.02-0.1 hatchery releases per wild smolt).

We found significant negative effects from cumulative release sites (H^{cSite}, θ=-0.004, 95% CI:-0.007, -0.0004) with an average 6.2% decrease in RPS for a 1SDU increase in releases sites. The cumulative release site effect for a 1SDU increase varies by population with changes in RPS ranging -21% to 15% due to variation in the size of a 1SDU increase (2-60 sites) as well as population-specific deviations in the coefficient (Fig. CO.2). The largest declines (16-21%) occurred for the 4 populations (CO-31: Skeena Estuary, CO-32: Lower Skeena,CO-27:Hecate Strait Mainland, CO-7:Lower Thompson, Table CO.3) with the most negative coefficients (Fig. CO.3). The Middle Skeena CU was the only population with a positive coefficient for H^{cSite}, which produced a 15% increase in RPS for a 1SDU increase in release sites.

Seal density had the largest effect (ρ= -0.12, 95% CI:-0.16,-0.06) on average on Coho productivity, with a 1 SDU increase in seal density producing an average 8.2% decrease on recruits-per-spawner (Table CO.3). The seal density effects associated with a 1 SDU increase are larger for SOG populations because a 1 SDU increase in SOG (2 seals/km) is much larger than a 1 SDU increase in the other regions (0.3-1 seals/km). SST had a significant positive effect (γ= 0.09, 95% CI:0.02, 0.15) on Coho productivity whereby a 1 SDU increase (0.6-0.7 degrees across populations) produced an average increase of 6.0% in RPS (Table CO.3).

We did not find evidence of model-overfitting as the full model was within 2.0 LOOIC units of the model with the lowest LOOIC, indicating similar performance (Table CO.2). The size of the covariate effects have considerable variation across populations and regions shown in Table CO.3. Ricker spawner-recruit curves and model fits to $\ln(R_t/S_t)$ observations are shown in Figures CO.4-5.

Chum

The full Chum model had significant positive effects from hatchery activity covariates for hatchery releases per wild smolt by CU (H^{relCU}, τ=0.02, 95% CI:0.01, 0.04) and by ocean entry region (H^{relOE}, ϕ=0.06, 95% CI:0.004, 0.11). Average effects from the cumulative release sites hatchery covariate (H^{cSite}) were near zero (θ=-0.002, 95% CI:-0.01, 0.004) and not significant, while mode posteriors for population-specific effects ranged from -0.01 to 0.011 (Fig.

CM.3) with significant positive effects for SOG populations (CM-3: Howe Sound-Burrard Inlet, CM-4: Georgia Strait). Increases of 1 SDU for hatchery releases per wild smolts within CUs (0-40 hatchery releases per wild smolt) and ocean entry regions (0.2-1.9 hatchery releases per wild smolt) produced a median increase of 3.2% and 6.4%, respectively on RPS (Table CM.3). We report median values since the mean is skewed by a large % increase in RPS for the Bella Coola River late CU, where a 1 SDU increase (40 hatchery releases per wild smolt) is much larger than the other populations (0-5.7 hatchery releases per wild smolt) due to a shorter time series for Bella Coola (2003-2014, Table CM.1). The effect from a 1 SDU increase in cumulative hatchery release sites is much more variable across populations due to variation in the size of a 1 SDU increase (0.2-210 sites) as well as population-specific deviations in the coefficient (Fig. CM.2) leading to changes in RPS ranging from -17% to 18% for populations outside SOG. The Howe Sound-Burrard Inlet (CM-3) and Georgia Strait (CM-3) populations in SOG have 173% and 119% increases in RPS, respectively, associated with a 1 SDU increases in releases.

Non-hatchery covariates had significant negative effects from seal density (ρ= -0.21, 95% CI:-0.28, -0.12, Fig. CM.2-3, Table CM.2) and SST (γ= -0.08, 95% CI:-0.16,-0.01) on Chum productivity. Seal density had the largest effect on average on Chum productivity, with a 1 SDU increase in seal density producing an average 13.1% decrease in recruits-per-spawner (Table CM.3). The seal density effects associated with a 1 SDU increase are larger for SOG populations because a 1 SDU increase in SOG (3.5 seals/km) is much larger than a 1 SDU increase in the other regions (0.3-1 seals/km). SST also had a negative effect on productivity, with a mean decline in RPS of 5% for a 1SDU increase in SST.

We did not find evidence of model-overfitting as the full model had the lowest LOOIC (Table CM.2) of all models considered. The sizes of covariate effects have considerable variation across populations and regions shown in Table CM.3. Ricker spawner-recruit curves and model fits to $\ln(R_t/S_t)$ observations are shown in Figures CM.4-5.

Discussion

We developed hierarchical multi-population spawner-recruit models for wild Chinook, Coho, and Chum salmon populations in BC that account for multiple covariate types to explain historical trends in wild salmon productivity. Models including the joint effects of hatchery activity indicators, seal predation, and sea surface temperature (SST) had better predictive performance and were not overfit compared to models that excluded multiple effects from different covariate types. Hatchery activity covariates for density dependence and seal predation had similar trends across species, whereas cumulative hatchery effects and SST effects differed by species. Hatchery covariates for density dependence were positively linked with productivity for all three species, while seal predation was negatively associated with RPS for all species. The cumulative hatchery effects negatively affected productivity across most populations but had positive associations with RPS for 1 Chinook, 1 Coho, and 5 Chum populations. SST was positively associated with Coho and Chinook productivity, while it was negatively associated with Chum productivity.

We found that increased hatchery operations over time (i.e., H^{cSite}, cumulative release sites) was negatively associated with RPS for most populations and on average had the largest effect size of the different hatchery covariates considered. Cumulative release sites were the only hatchery covariate for which we could fit models that estimated population-specific effects. While the effect size and significance varied across Chinook, Coho, and Chum populations, increasing release sites had a negative effect on productivity for nearly all populations with a few exceptions (CK-42: North & Central Coast – Early Timing Chinook, CO-33: Middle Skeena Coho, CM-16: Bella Coola – Dean Rivers Chum, CM-11: Northwest Vancouver Island Chum, CM-5: Northeast Vancouver Island Chum, CM-3: Howe Sound - Burrard Inlet Chum, CM-4: Georgia Strait Chum). The negative effect from increasing release sites may be associated with cumulative effects (Miller et al. 2014) in hatchery regions such as increased disease, changing predator-prey dynamics, and reduced genetic diversity or fitness (e.g., inbreeding, Naish et al 2007). Loss of genetic diversity may occur from various hatchery management outcomes such as broodstock collection, fertilization techniques, and differences in sex ratios during spawning (Allendorf 1993, Campton 2004, Naish et al. 2007). In some instances, when population sizes are adequate, it may be possible to maintain or enhance genetic diversity through deliberate management steps such as equalizing sex ratios and family sizes (Allendorf 1993,

Campton 2004, Naish et al 2007). It would be interesting to evaluate whether there are notable differences in spawning practices, predator populations, and disease monitoring at the hatcheries in CUs where positive effects from cumulative release sites were observed, particularly for the SOG Chum CUs where the effects were significant. Alternatively, it is possible the positive cumulative release site effects are spurious given the small number of CUs where we found positive associations between cumulative release sites and productivity. Estimates of hatchery effects on wild salmon productivity can also be influenced by biased recruits-per-spawner data when this bias is due to hatchery activity. For example, overestimates of wild escapement may occur by counting hatchery fish on spawning grounds and can also bias estimates of total adult returns (catch + escapement) derived from exploitation rates and escapement. We identified the potential for a negative bias (i.e., underestimate) in recruits-per-spawner related to hatchery activity for some Chinook and Chum populations (Appendix SR), which could generate a perceived negative effect of hatchery activity on productivity or lead to overestimates of negative hatchery effects.

We investigated the potential effects of changing gene flow on 11 Chinook populations via a model that included the percentage Hatchery Origin Spawners (pHOS) as an indicator of genetic diversity. The fitted models did not show evidence of a pHOS effect on Chinook productivity, nor did they affect estimates of other covariates in the 24-population Chinook model. This is not surprising as only the pHOS time series for Cowichan had a strong negative correlation with Ricker residuals.

In contrast to the hatchery release sites covariate, hatchery covariates related to density-dependent mortality in juvenile freshwater habitats (i.e., H^{relCU}, hatchery releases per wild smolt in CUs) and areas of early marine residence (i.e., H^{relOE}, hatchery releases per wild smolt in ocean entry regions) were positively associated with RPS (i.e., positive-density dependence). Positive density-dependent mortality may occur via predator-swamping (Furey et al. 2016) where an increase in hatchery releases may relieve predation pressure on wild populations, particularly if wild smolts possess any advantages over hatchery fish for avoiding predation (Abrahams and Sutterlin 1999). Another potential mechanism for positive density dependence is cannibalism of conspecifics in cases where hatchery releases are smaller than wild smolts, whereby hatchery releases could provide additional food sources for wild stocks when other food sources are limited (Devlin et al. 2004).

Seal density was negatively associated with Chinook, Coho, and Chum productivity, which is consistent with previous findings for Chinook salmon in Strait of Georgia and Northern Washington (Nelson et al. 2019). This is not surprising given that Harbour Seals are one of the largest sources of predation on out-migrating smolts (Lance et al. 2012, Allegue 2017, Allegue et al. 2017, Chasco et al. 2017). Seal predation had the largest effect on productivity for populations in Strait of Georgia where seal density is estimated at 3-10 times higher than other regions. Most Coho (Interior Fraser, Fraser Canyon, South Thompson, North Thompson) and Chinook (Cowichan, Puntledge, Nanaimo, Qualicum, Chilliwack, Shuswap) salmon populations experienced sharp declines in productivity starting in the 1980s before stabilizing circa 1995 around the same time when Harbour seals reached carrying capacity in SOG. Other sources of predation such as consumption of adult salmon by Stellar Sea Lions (Walters et al.2020) and Killer Whales (Chasco et al. 2017) may also contribute to changes in wild salmon productivity; however, their abundance time series are strongly correlated to Harbour Seals, which may lead to challenges with collinearity when attempting to fit multiple marine mammal covariates in the same model. We focussed on Harbour Seal predation mortality on juvenile salmon because estimates for the Pacific Northwest indicate Harbour seals consume approximately 10 times more juveniles than adults are consumed by Killer Whales or Stellar Sea Lions (Chasco et al. 2017).

Increasing sea surface temperature had a significant positive effect on Coho productivity and a significant negative effect on Chum productivity, while only a small non-significant (i.e., credible intervals overlapped with zero) positive effect was seen for Chinook. Our findings for Chum Salmon are consistent with previous studies for SST associations with Chum productivity (Mueter et al. 2002, Litzow et al. 2019). Litzow et al. 2019 found neutral effects of SST on Chum productivity in BC for the period prior to the 1989 decline in the Aleutian Low variance and negative effects for the period post-1989 (Litzow et al. 2019). It is not thought that SST has a direct effect on salmon productivity, but that is acts as a proxy for other marine conditions affecting salmon productivity such as spring bloom timing and food availability (Mueter et al. 2002, Malick et al. 2015, Malick 2020).

We did not find that a single cause explains historical changes in Salmon productivity but rather that a combination of hatchery, predation, and marine conditions better explain changes in Salmon productivity over time. Our analysis highlights the importance of covariate selection when modelling salmon productivity, as the exclusion of important predictor variables may lead to different findings or misinterpretation of covariate effect sizes. In our multi-population models, we found that interpretation of covariate associations with productivity (i.e., positive or negative effects) did not change for models, although the magnitude of the effects did change, for models fit to subsets of the full suite of covariates. Additional covariates and model hypotheses that were beyond the scope of this project, but could warrant further investigation include: adult competition (e.g., Pink Salmon abundance, Connors et al. 2020), interspecies density dependence from other salmonoid hatchery releases (e.g., competition for food and predation), predation mortality on adult salmon (e.g., Killer Whales, Stellar Sea Lions, Chasco et al. 2017, Walters et al. 2020), and large-scale climate indices (e.g., PDO, NPGO, Malick et al. 2020, Chasco et al. 2021). Our findings identify how hatchery, predation, and sea surface temperature conditions influence historical trends in Chinook, Coho, and Chum productivity, which could be used to predict spawner-recruitment dynamics for future ecosystem and hatchery conditions and inform management decisions for wild Pacific Salmon.

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Table

Table 1. Pearson correlations between different indicators of hatchery activity and residuals from single-population Ricker models for Chinook populations. For CUs, percentage Hatchery Origin Spawner (pHOS) data is from Atnarko River (Bella Coola – Bentinck CU), Kitsumkalum River Summer (Kalum – late timing CU), and Upper Bulkley River Spring (Upper Bulkley River) stocks.

| CU/Stock | Hatchery activity indicators | | | | | | | | |
| | Conspecific hatchery releases | | Ratio of hatchery releases to wild smolts | | Number of hatcheries operating | | Release Sites | | pHOS CWT |
	Annual	Cumulative	CU	Ocean Entry	Annual	Cumulative	Annual	Cumulative	
Bella Coola – Bentinck*	0.24	-0.32	0.19	0.26		-0.32	-0.04	-0.32	-0.07
Kalum - late timing*	-0.43	-0.66	-0.21	-0.26	-0.61	-0.70	-0.42	-0.69	-0.45
Upper Bulkley River*	0.18	-0.18	0.27	0.04	0.19	-0.15	0.14	-0.16	0.22
Cowichan River	-0.35	-0.66	-0.13	0.51	-0.28	-0.66	-0.31	-0.67	-0.65
Puntledge River - fall	-0.28	-0.05	0.16	0.07	-0.29	-0.07	-0.23	-0.06	-0.23
Nanaimo River - fall	-0.57	-0.81	-0.34	0.68		-0.81		-0.81	-0.05
Quinsam River	-0.20	-0.35	0.14	0.07	0.04	-0.35	0.21	-0.35	-0.11
Big Qualicum River	-0.53	-0.34	-0.09	0.51	-0.57	-0.37	-0.57	-0.37	0.37
Harrison River	-0.56	-0.56	-0.45	0.39	-0.44	-0.57	-0.44	-0.57	-0.11
Shuswap River - lower	0.08	-0.10	0.39	0.12	-0.30	-0.09	0.04	-0.08	-0.13
Chilliwack River - fall	0.32	-0.27	0.53	0.37		-0.27		-0.27	0.18
MEAN	**-0.19**	**-0.39**	**0.04**	**0.25**	**-0.28**	**-0.40**	**-0.18**	**-0.40**	**-0.09**
MAX	0.32	-0.05	0.53	0.68	0.19	-0.07	0.21	-0.06	0.37
MIN	-0.57	-0.81	-0.45	-0.26	-0.61	-0.81	-0.57	-0.81	-0.65

* Conservation Units (CUs)

Figures
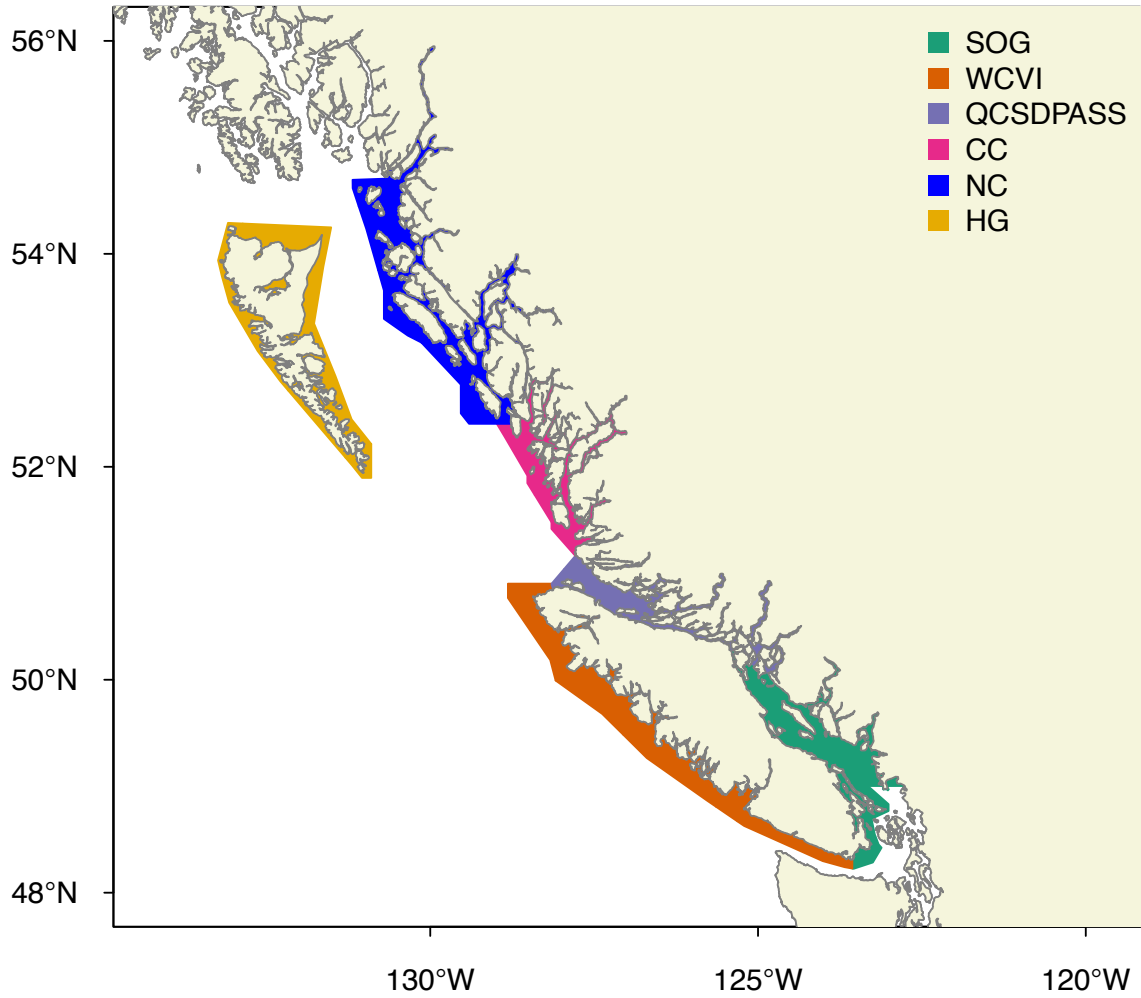
Figure 1. Map of six ocean entry regions (SOG= Strait of Georgia, WCVI=West Coast Vancouver Island, QCSDPASS = Queen Charlotte Strait, Johnstone Strait, and Discovery Passage, CC=Central Coast, NC=North Coast, HG= Haida Gwaii) for Pacific Salmon in British Columbia used for compiling hatchery activity and seal density covariates.
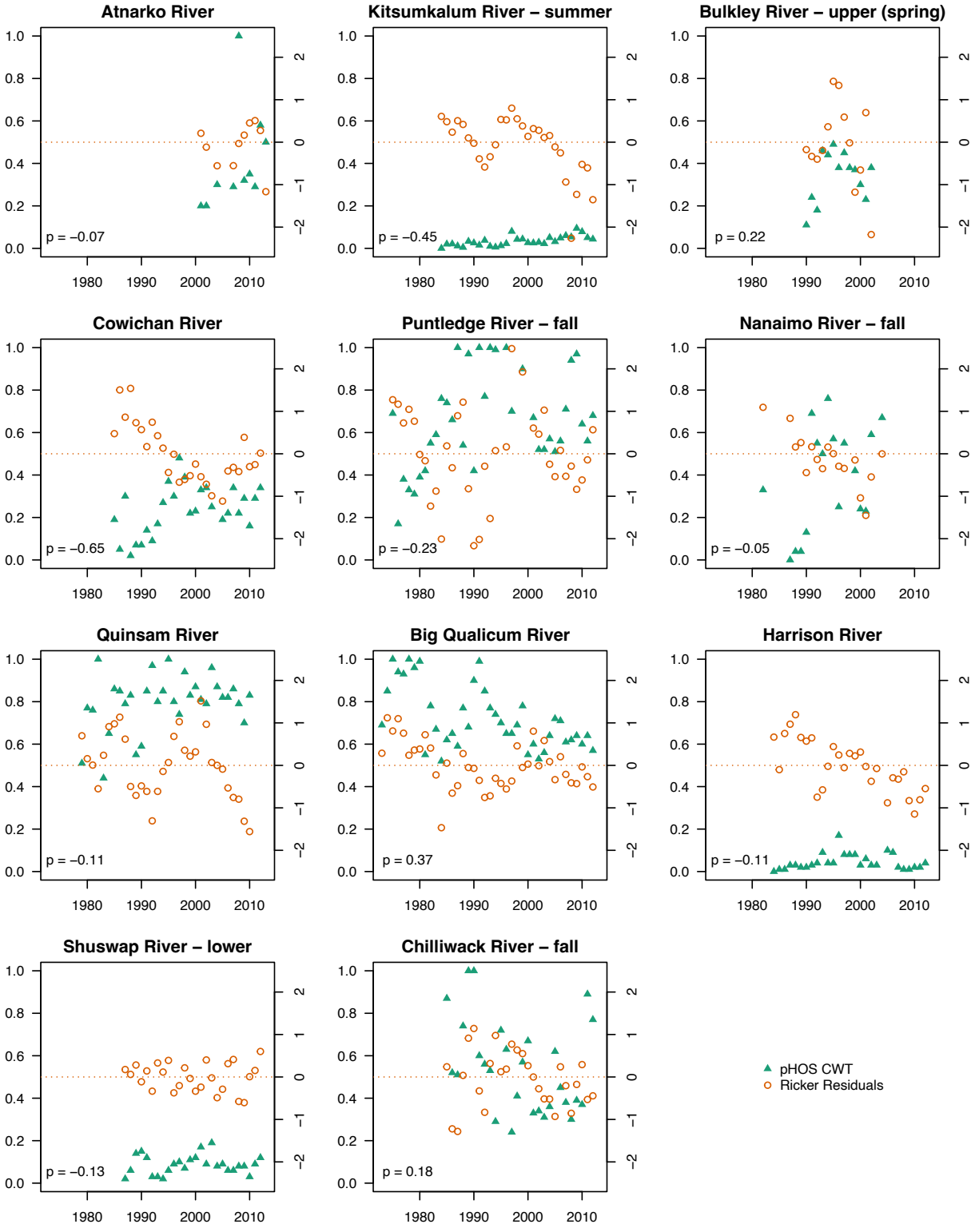
Figure 2. Residuals from single population Ricker models (right y-axes) and pHOS CWT data (left y-axes) for 11 Chinook populations with sufficient pHOS data for inclusion in multi-population models. Pearson correlations ρ for pHOS and residuals are shown in bottom left corners of each plot.
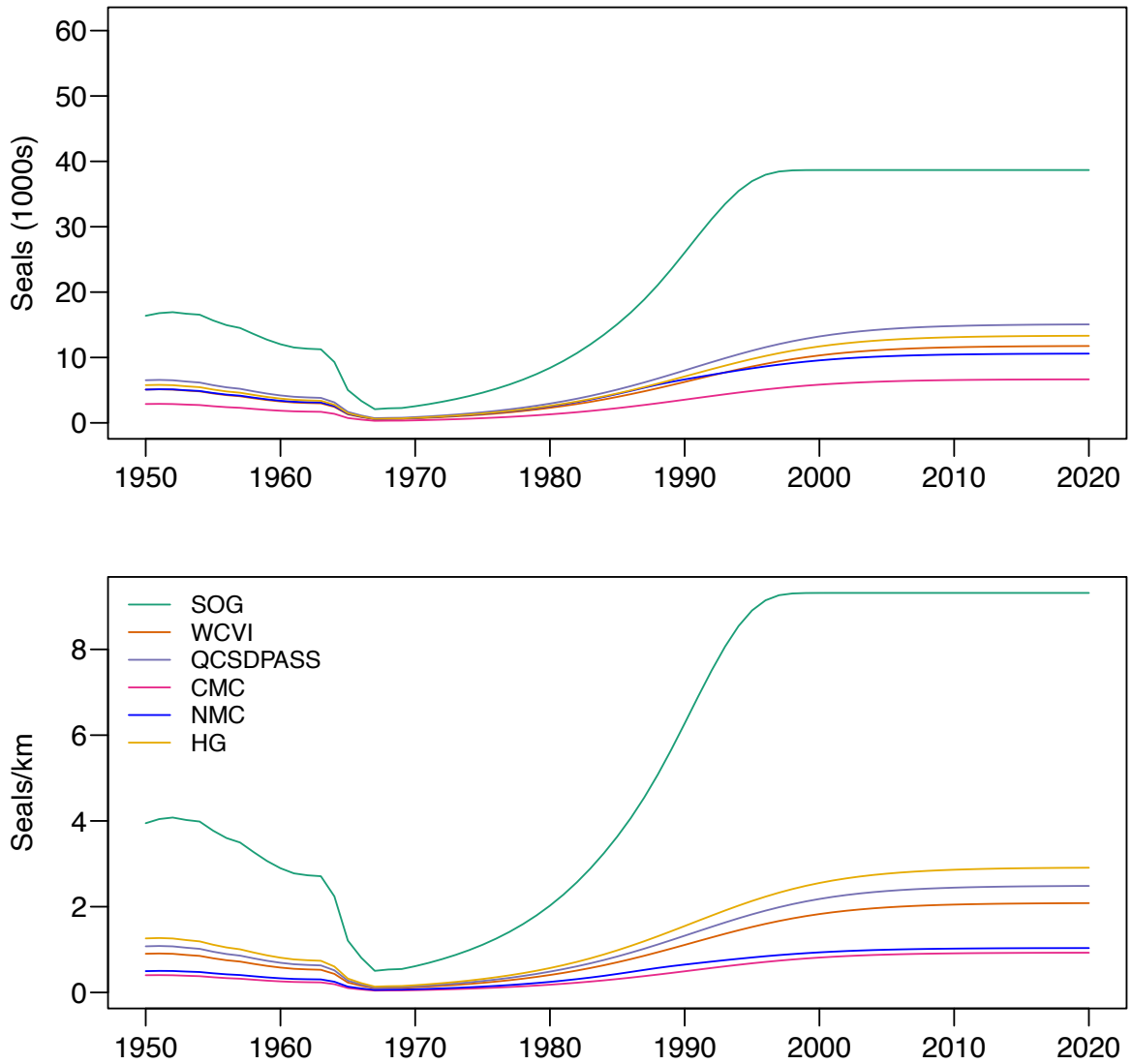
Figure 3. BC seal abundance (a) and seal density estimates for Strait of Georgia (SOG), North Coast (NC), Central Coast (CC), Queen Charlotte Strait, Johnstone Strait, and Discovery Passage (QCSDPASS), West Coast Vancouver Island (WCVI), and Haida Gwaii (HG).
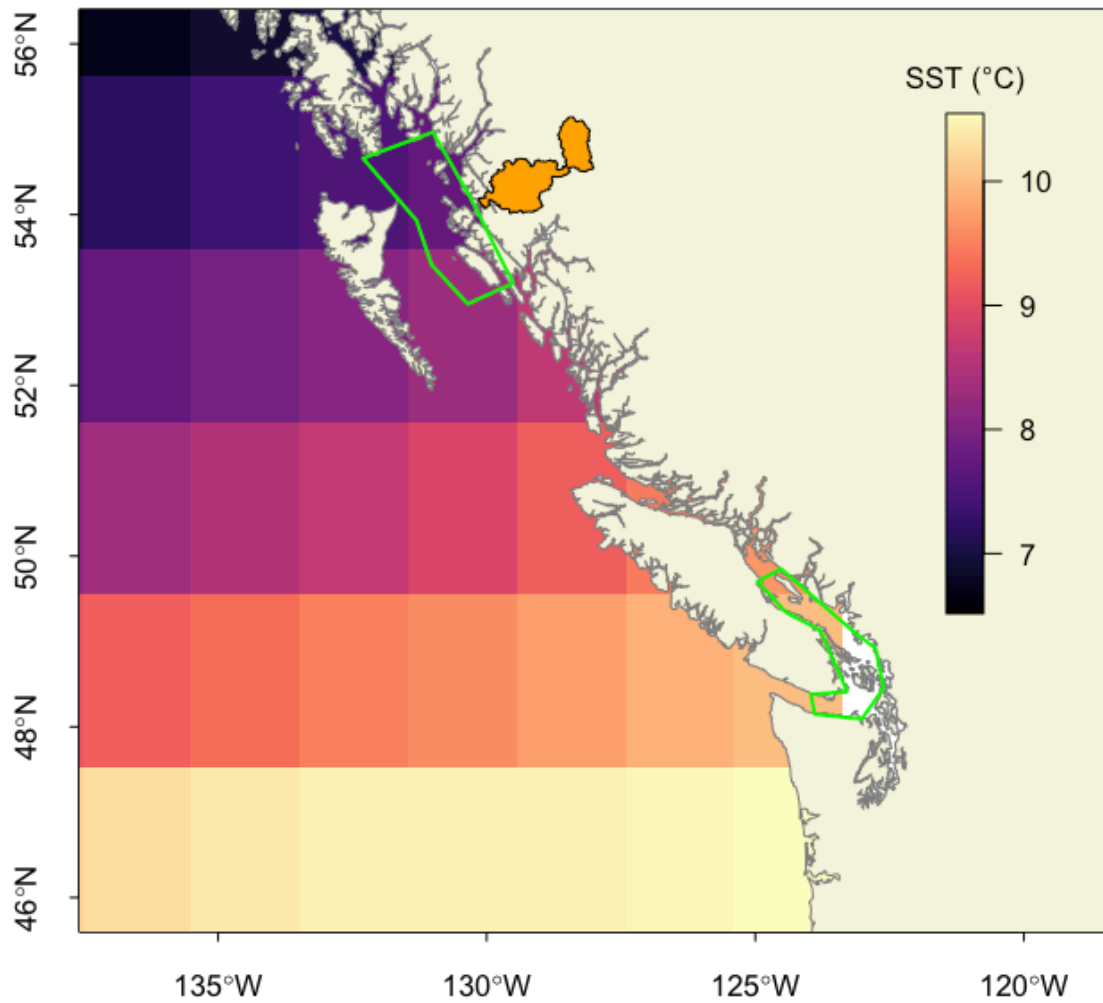
Figure 4. Regions of early marine residence (green polygons) used for extracting sea surface temperature for Lower Skeena Chinook CU (CK-48 shown in orange) and Fraser River Chinook stocks (Harrison, Shuswap, Chilliwack). Mean sea surface temperature shown for 2x2 degree grid cells from April 2014.

Appendix CK – Chinook Tables and Figures

Chinook Tables

Table CK.1. Summary of spawner-recruit datasets for BC Chinook conservation units (CUs) and stocks. All CU data is from the Pacific Salmon Foundation's Pacific Salmon Explorer (PSE, www.salmonexplorer.ca) by region (NC=North Coast, CC=Central Coast, SOG=Strait of Georgia, QCSDPASS= Queen Charlotte Strait, Johnstone Strait, and Discovery Passage).

Regions	CU/Stock ID	CU/Stock Name	Source	Brood year range	n
NC	CK-57	PORTLAND SOUND-OBSERVATORY INLET-LOWER NASS	PSE	1986-2013	28
	CK-58	UPPER NASS	PSE	1986-2013	28
	CK-46	ECSTALL	PSE	1980-1994	14
	CK-48	LOWER SKEENA	PSE	1980-2010	30
	CK-49	KALUM-EARLY TIMING	PSE	1980-2008	29
	CK-50	KALUM-LATE TIMING	PSE	1980-2012	33
	CK-53	MIDDLE SKEENA-LARGE LAKES	PSE	1980-2013	34
	CK-54	MIDDLE SKEENA-MAINSTEM TRIBUTARIES	PSE	1980-2013	33
	CK-55	UPPER BULKLEY RIVER	PSE	1980-2003	24
	CK-41	NORTH & CENTRAL COAST-LATE TIMING	PSE	1984-2013	21
	CK-42	NORTH & CENTRAL COAST-EARLY TIMING	PSE	1985-2013	29
CC	CK-36	DOCEE	PSE	1980-2008	29
	CK-39	BELLA COOLA-BENTINCK	PSE	1985-2013	29
	CK-40	DEAN RIVER	PSE	1985-2013	29
	CK-37	RIVERS INLET	PSE	1980-2013	34
	CK-38	WANNOCK	PSE	1980-2013	34
QCSDPASS	stockCK-4	QUINSAM RIVER	Nelson et al. 2019	1976-2010	34
SOG	stockCK-1	COWICHAN RIVER	Nelson et al. 2019	1985-2012	27
	stockCK-2	PUNTLEDGE RIVER – FALL	Nelson et al. 2019	1975-2012	37
	stockCK-3	NANAIMO RIVER – FALL	Nelson et al. 2019	1979-2004	19
	stockCK-5	QUALICUM RIVER	Nelson et al. 2019	1973-2012	40
	stockCK-6	HARRISON RIVER	Nelson et al. 2019	1984-2012	28
	stockCK-7	SHUSWAP RIVER	Nelson et al. 2019	1984-2012	29
	stockCK-8	CHILLIWACK RIVER - FALL	Nelson et al. 2019	1981-2012	32

Table CK2. Comparison of Chinook 24-population Ricker models with full suite and subset of covariates. The mode posterior coefficient estimates and 95% credible intervals () are shown for hatchery (H), predator (P), and sea surface temperature (T) covariates. Models include three different hatchery covariates (i) aspecies-specific hatchery releases per wild smolt by CU (H^{relCU}), and/or (iii) species-specific hatchery releases per wild smolt by ocean entry region (H^{reloE}), (iii) cumulative release sites by CU (H^{cSite}). The full model and the basic ricker model with only the Spawner abundance covariate are shown in bold. Note that population-specific estimates for α, β and H^{cSite} are not shown.

Coefficient estimates for hierarchical Ricker model and covariates							LOOIC	
α	β	H^{relCU}	H^{reloE}	H^{cSite}	P	T	ΔLOOIC	SE
4.53 (3.46, 6.70)	0.129 (0.078, 0.243)	0.002 (0.001, 0.003)	0.01 (0.00, 0.02)	-0.01 (-0.03, 0.00)	-0.04 (-0.11, 0.02)	-	-	67
5.19 (3.87, 8.06)	0.136 (0.078, 0.251)	0.002 (0.001, 0.003)	-	-0.01 (-0.03, 0.00)	-0.08 (-0.14, -0.02)	-	1	67
2.85 (1.23, 9.74)	**0.133 (0.075, 0.243)**	**0.002 (0.001, 0.003)**	**0.01 (0.00, 0.02)**	**-0.01 (-0.03, 0.00)**	**-0.05 (-0.11, 0.02)**	**0.04 (-0.06, 0.13)**	**3**	**67**
4.47 (3.31, 5.96)	0.132 (0.078, 0.240)	0.002 (0.001, 0.003)	0.01 (0.01, 0.02)	-0.02 (-0.03, -0.01)	-	-	3	66
2.73 (1.43, 10.00)	0.127 (0.077, 0.253)	0.002 (0.001, 0.003)	0.01 (0.01, 0.02)	-0.02 (-0.03, -0.01)	-	0.01 (-0.07, 0.10)	7	66
4.85 (3.68, 6.87)	0.136 (0.080, 0.257)	0.002 (0.001, 0.003)	-	-0.02 (-0.03, -0.01)	-	-	9	66
5.27 (4.00, 8.18)	0.138 (0.084, 0.274)	-	-	-0.01 (-0.03, 0.00)	-0.07 (-0.13, -0.01)	-	9	67
4.77 (3.62, 7.06)	0.138 (0.082, 0.258)	-	0.01 (0.00, 0.01)	-0.01 (-0.03, 0.00)	-0.04 (-0.11, 0.03)	-	11	67
2.89 (1.48, 11.79)	0.137 (0.084, 0.255)	0.002 (0.001, 0.003)	-	-0.02 (-0.03, -0.01)	-	0.01 (-0.08, 0.11)	12	66
2.87 (1.20, 10.04)	0.138 (0.078, 0.255)	-	0.01 (0.00, 0.01)	-0.01 (-0.03, 0.00)	-0.05 (-0.11, 0.02)	0.03 (-0.06, 0.13)	13	67
4.50 (3.43, 6.38)	0.131 (0.079, 0.258)	-	0.01 (0.00, 0.02)	-0.02 (-0.03, -0.01)	-	-	13	67
2.69 (1.22, 10.16)	0.140 (0.079, 0.262)	-	-	-0.01 (-0.03, 0.00)	-0.08 (-0.14, -0.01)	0.04 (-0.05, 0.14)	13	67
4.91 (3.66, 7.04)	0.142 (0.080, 0.252)	-	-	-0.02 (-0.03, -0.01)	-	-	14	66
3.24 (1.37, 10.85)	0.130 (0.082, 0.251)	-	0.01 (0.00, 0.02)	-0.02 (-0.03, -0.01)	-	0.01 (-0.07, 0.11)	16	67
3.11 (1.48, 11.64)	0.138 (0.082, 0.275)	-	-	-0.02 (-0.03, -0.01)	-	0.03 (-0.07, 0.11)	16	66

| | | Coefficient estimates for hierarchical Ricker model and covariates | | | | | LOOIC | |
α	β	H^{relCU}	H^{relOE}	H^{cSite}	P	T	ΔLOOIC	SE
4.82 (3.65, 7.13)	0.124 (0.076, 0.253)	0.002 (0.001, 0.003)	-	-	-0.11 (-0.16, -0.07)	-	32	65
1.81 (0.74, 5.92)	0.129 (0.076, 0.255)	0.002 (0.001, 0.003)	-	-	-0.12 (-0.16, -0.07)	0.07 (-0.01, 0.18)	33	65
1.60 (0.75, 6.31)	0.140 (0.076, 0.254)	0.002 (0.001, 0.003)	0.01 (0.00, 0.01)	-	-0.08 (-0.13, -0.04)	0.08 (-0.03, 0.16)	33	65
4.27 (3.27, 5.93)	0.136 (0.078, 0.259)	0.002 (0.001, 0.003)	0.01 (0.00, 0.02)	-	-0.08 (-0.12, -0.03)	-	34	66
5.12 (3.81, 7.14)	0.145 (0.075, 0.272)	-	-	-	-0.10 (-0.14, -0.06)	-	44	65
1.55 (0.80, 6.62)	0.146 (0.084, 0.288)	-	-	-	-0.11 (-0.15, -0.06)	0.08 (-0.02, 0.17)	45	65
4.32 (3.45, 6.32)	0.141 (0.082, 0.264)	-	0.01 (0.00, 0.01)	-	-0.07 (-0.12, -0.02)	-	47	65
1.75 (0.77, 6.32)	0.140 (0.081, 0.266)	-	0.01 (0.00, 0.01)	-	-0.08 (-0.13, -0.03)	0.08 (-0.03, 0.16)	47	65
3.43 (2.85, 4.28)	0.138 (0.079, 0.258)	0.002 (0.001, 0.003)	0.01 (0.01, 0.02)	-	-	-	49	63
1.97 (0.93, 6.24)	0.134 (0.082, 0.252)	0.002 (0.001, 0.003)	0.01 (0.01, 0.02)	-	-	0.02 (-0.05, 0.12)	50	63
3.66 (3.03, 4.63)	0.142 (0.085, 0.269)	-	0.01 (0.01, 0.02)	-	-	-	62	63
1.83 (0.91, 6.43)	0.152 (0.089, 0.278)	-	0.01 (0.01, 0.02)	-	-	0.04 (-0.05, 0.13)	62	63
3.93 (3.08, 4.91)	0.141 (0.085, 0.269)	0.002 (0.001, 0.003)	-	-	-	-	63	62
1.98 (0.87, 6.48)	0.148 (0.088, 0.274)	0.002 (0.001, 0.003)	-	-	-	0.05 (-0.05, 0.14)	67	61
4.10 (3.21, 5.26)	**0.151 (0.090, 0.283)**	-	-	-	-	-	**72**	**62**
1.90 (0.88, 7.01)	0.145 (0.089, 0.275)	-	-	-	-	0.05 (-0.05, 0.14)	74	62

Table CK.3. Percent change in posterior mode recruits-per-spawner (RPS) for the full 24-population Chinook model for a 1SD increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 1SD increase for each covariate.

Region	Population	Percent change in RPS for 1SD increase in covariates				
		$\overline{H}_i^{relCU} + 1SD$	$\overline{H}_i^{relOE} + 1SD$	$\overline{H}_i^{cSite} + 1SD$	$\overline{P}_i + 1SD$	$\overline{T}_i + 1SD$
NC	PORTLAND SOUND-OBSERVATORY INLET-LOWER NASS	0.3%	0.2%	-9.6%	-0.9%	2.2%
	UPPER NASS		0.2%		-0.9%	2.2%
	ECSTALL		0.3%		-0.9%	1.8%
	LOWER SKEENA	<0.01%	0.3%	-3.1%	-1.4%	2.1%
	KALUM-EARLY TIMING	0.3%	0.3%	-6.6%	-1.3%	2.1%
	KALUM-LATE TIMING	<0.01%	0.3%	-32.0%	-1.4%	2.2%
	MIDDLE SKEENA-LARGE LAKES	<0.01%	0.3%	-20.2%	-1.4%	2.2%
	MIDDLE SKEENA-MAINSTEM TRIBUTARIES	0.1%	0.3%	-21.0%	-1.3%	2.2%
	UPPER BULKLEY RIVER	0.5%	0.3%	-9.3%	-1.3%	2.0%
	NORTH & CENTRAL COAST-LATE TIMING		0.2%		-1.3%	2.4%
	NORTH & CENTRAL COAST-EARLY TIMING	48.4%	0.2%	6.7%	-1.0%	2.3%
CC	BELLA COOLA-BENTINCK	0.3%	0.8%	-10.2%	-1.1%	2.4%
	DEAN RIVER		0.8%		-1.1%	2.4%
	RIVERS INLET	0.5%	1.0%	-9.3%	-1.3%	2.3%
	WANNOCK	0.1%	1.0%	-9.2%	-1.3%	2.3%
	DOCEE		0.7%		-1.3%	2.4%
QCSDPASS	QUINSAM	3.7%	29.6%	-29.0%	-3.7%	2.4%
SOG	COWICHAN	2.0%	1.9%	-26.7%	-9.6%	2.3%
	PUNTLEDGE	24.2%	29.0%	-2.0%	-15.7%	2.3%
	NANAIMO	0.6%	13.5%	-11.3%	-13.2%	2.1%
	QUALICUM	32.3%	29.3%	-10.1%	-16.3%	2.4%
	HARRISON	<0.01%	1.9%	-2.9%	-10.4%	2.3%
	CHILLIWACK	0.8%	11.3%	-9.5%	-10.5%	2.4%
	SHUSWAP	0.2%	1.9%	-1.6%	-10.4%	2.6%
MEAN ALL POPULATIONS		**6.4%**	**7.5%**	**-12.0%**	**-6.3%**	**2.3%**
MEAN NC		**5.8%**	**0.2%**	**-12.9%**	**-1.2%**	**2.2%**
MEAN CC		**0.3%**	**0.9%**	**-9.6%**	**-1.2%**	**2.4%**
MEAN SOG		**8.5%**	**13.1%**	**-10.0%**	**-12.5%**	**2.3%**

Table CK.4. Percent change in posterior mode recruits-per-spawner (RPS) for the full 24-population Chinook model for a 10% increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 10% increase for each covariate.

Region	Population	Percent change in RPS for 10% increase in covariates				
		$\overline{H}_i^{relCU} + 10\%$	$\overline{H}_i^{relOE} + 10\%$	$\overline{H}_i^{cSite} + 10\%$	$\overline{P}_i + 10\%$	$\overline{T}_i + 10\%$
NC	PORTLAND SOUND-OBSERVATORY INLET-LOWER NASS	0.0%	0.1%	-2.3%	-0.5%	3.9%
	UPPER NASS		0.1%		-0.5%	3.9%
	ECSTALL		0.1%		-0.3%	3.9%
	LOWER SKEENA	0.00%	0.1%	-0.5%	-0.4%	3.9%
	KALUM-EARLY TIMING	0.01%	0.1%	-1.2%	-0.4%	3.9%
	KALUM-LATE TIMING	0.01%	0.1%	-5.2%	-0.4%	3.9%
	MIDDLE SKEENA-LARGE LAKES	0.00%	0.1%	-4.8%	-0.4%	3.9%
	MIDDLE SKEENA-MAINSTEM TRIBUTARIES	0.00%	0.1%	-4.5%	-0.4%	3.9%
	UPPER BULKLEY RIVER	0.05%	0.1%	-1.4%	-0.3%	3.9%
	NORTH & CENTRAL COAST-LATE TIMING		0.1%		-0.4%	4.1%
	NORTH & CENTRAL COAST-EARLY TIMING	2.1%	0.1%	1.6%	-0.5%	4.1%
CC	BELLA COOLA-BENTINCK	0.1%	0.2%	-2.1%	-0.4%	4.3%
	DEAN RIVER		0.2%		-0.4%	4.3%
	RIVERS INLET	0.0%	0.2%	-1.3%	-0.3%	4.3%
	WANNOCK	0.0%	0.2%	-1.3%	-0.3%	4.3%
	DOCEE		0.1%		-0.3%	4.3%
QCSDPASS	QUINSAM	0.6%	3.8%	-5.3%	-0.9%	4.6%
SOG	COWICHAN	0.1%	0.4%	-5.3%	-4.2%	4.7%
	PUNTLEDGE	1.2%	1.6%	-0.4%	-3.3%	4.6%
	NANAIMO	0.1%	0.9%	-2.5%	-3.7%	4.7%
	QUALICUM	1.9%	1.7%	-1.9%	-3.3%	4.6%
	HARRISON	0.0%	0.4%	-0.8%	-4.1%	4.7%
	CHILLIWACK	0.0%	0.6%	-2.0%	-4.1%	4.7%
	SHUSWAP	0.0%	0.4%	-0.3%	-4.2%	5.5%
MEAN ALL POPULATIONS		0.4%	0.6%	-2.4%	-1.9%	4.4%
MEAN NC		0.3%	0.1%	-2.6%	-0.4%	3.9%
MEAN CC		0.0%	0.2%	-1.5%	-0.4%	4.3%
MEAN SOG		0.5%	0.9%	-2.1%	-3.8%	4.8%

Table CK5. Comparison of Chinook 11-population Ricker models with full suite and subset of covariates. The median posterior coefficient estimates and 95% credible intervals () are shown for hatchery (H), predator (P), and sea surface temperature (T) covariates. Models include four different hatchery covariates (i) species-specific hatchery releases per wild smolt by CU (H^{relCU}), and/or (iii) species-specific hatchery releases per wild smolt by ocean entry region (H^{reloE}), (iii) cumulative release sites by CU (H^{cSite}), and iv) percent hatchery-origin spawners (H^{pHOS}). The full model and the basic ricker model with only the Spawner abundance covariate are shown in bold. Note that population-specific estimates for α and β are not shown.

Coefficient estimates for hierarchical Ricker model and covariates								LOOIC	
α	β	H^{relCU}	H^{reloE}	H^{cSite}	H^{pHOS}	P	T	ΔLOOIC	SE
7.98 (5.37, 15.94)	0.082 (0.041, 0.233)	-	-	-0.02 (-0.02, -0.01)	-	-	-	-	32
7.21 (4.86, 13.54)	0.075 (0.037, 0.225)	-	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	-	-	-	1	32
7.78 (5.28, 13.99)	0.082 (0.039, 0.228)	0.001 (0.00, 0.002)	-	-0.02 (-0.02, -0.01)	-	-	-	1	31
5.38 (1.96, 48.69)	0.085 (0.037, 0.238)	-	-	-0.02 (-0.02, -0.01)	-	-	-0.03 (-0.14, 0.13)	2	32
7.88 (5.05, 15.15)	0.085 (0.037, 0.238)	-	-	-0.02 (-0.02, -0.01)	0.00 (-0.47, 0.58)	-	-	3	32
8.92 (6.03, 16.23)	0.072 (0.036, 0.246)	0.001 (0.00, 0.002)	-	-0.01 (-0.02, 0.00)	-	-0.05 (-0.11, 0.00)	-	3	34
5.89 (2.17, 52.31)	0.083 (0.040, 0.240)	0.001 (0.00, 0.002)	-	-0.02 (-0.02, -0.01)	-	-	0.00 (-0.16, 0.11)	3	32
7.81 (5.25, 14.46)	0.070 (0.037, 0.211)	-	0.00 (0.00, 0.01)	-0.01 (-0.02, -0.01)	-	-0.03 (-0.09, 0.03)	-	3	34
6.47 (4.61, 11.74)	0.074 (0.032, 0.207)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	-	-	-	3	32
3.68 (1.29, 36.26)	0.072 (0.038, 0.218)	-	-	-0.01 (-0.02, 0.00)	-	-0.06 (-0.11, 0.00)	0.04 (-0.11, 0.17)	3	34
6.69 (4.47, 13.10)	0.074 (0.035, 0.234)	-	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	0.06 (-0.39, 0.60)	-	-	4	32
8.66 (5.66, 16.25)	0.075 (0.035, 0.224)	-	-	-0.01 (-0.02, 0.00)	0.12 (-0.42, 0.59)	-0.05 (-0.10, 0.01)	-	4	34
4.97 (1.65, 37.97)	0.077 (0.036, 0.217)	-	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	-	-	-0.01 (-0.13, 0.12)	4	32
6.40 (4.19, 12.13)	0.072 (0.035, 0.190)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	0.05 (-0.45, 0.55)	-	-	4	32
7.69 (5.09, 15.59)	0.078 (0.036, 0.209)	0.001 (0.00, 0.002)	-	-0.02 (-0.02, -0.01)	0.03 (-0.51, 0.53)	-	-	5	32
8.47 (5.56, 15.96)	0.083 (0.034, 0.219)	0.001 (0.00, 0.002)	-	-0.01 (-0.02, 0.00)	0.11 (-0.44, 0.55)	-0.05 (-0.11, 0.00)	-	5	34
5.18 (1.74, 50.27)	0.088 (0.039, 0.231)	-	-	-0.02 (-0.02, -0.01)	0.12 (-0.42, 0.55)	-	0.00 (-0.14, 0.13)	5	32
7.63 (4.64, 14.89)	0.073 (0.033, 0.219)	-	0.00 (0.00, 0.01)	-0.01 (-0.02, -0.01)	0.14 (-0.36, 0.63)	-0.03 (-0.09, 0.02)	-	5	33
7.69 (5.02, 13.58)	0.076 (0.034, 0.200)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, 0.00)	-	-0.04 (-0.09, 0.02)	-	5	34
5.30 (1.87, 53.61)	0.079 (0.040, 0.226)	0.001 (0.00, 0.002)	-	-0.02 (-0.02, -0.01)	0.04 (-0.46, 0.53)	-	-0.04 (-0.15, 0.12)	6	32
3.69 (1.22, 32.05)	0.076 (0.037, 0.237)	-	-	-0.01 (-0.02, 0.00)	0.12 (-0.37, 0.62)	-0.05 (-0.11, 0.00)	0.03 (-0.09, 0.18)	6	34

3.95 (1.23, 35.78)	0.069 (0.037, 0.198)	0.001 (0.00, 0.002)	-	-0.01 (-0.02, 0.00)	-	-0.06 (-0.11, -0.01)	0.02 (-0.11, 0.17)	6	34
5.08 (1.69, 43.73)	0.080 (0.035, 0.210)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	-	-	-0.02 (-0.16, 0.12)	6	32
4.29 (1.49, 40.14)	0.076 (0.036, 0.221)	-	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	0.09 (-0.40, 0.60)	-	-0.01 (-0.14, 0.13)	6	32
3.56 (1.31, 34.35)	0.071 (0.038, 0.204)	-	0.00 (0.00, 0.01)	-0.01 (-0.02, 0.00)	-	-0.03 (-0.09, 0.03)	0.02 (-0.12, 0.17)	6	33
6.95 (4.50, 13.64)	0.071 (0.036, 0.192)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, 0.00)	0.01 (-0.43, 0.58)	-0.04 (-0.09, 0.02)	-	6	33
4.77 (1.65, 40.27)	0.074 (0.038, 0.211)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, -0.01)	0.05 (-0.44, 0.52)	-	-0.02 (-0.15, 0.12)	7	32
3.55 (1.42, 33.92)	0.078 (0.033, 0.190)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-0.01 (-0.02, 0.00)	-	-0.04 (-0.10, 0.02)	0.01 (-0.12, 0.15)	7	34
3.72 (1.28, 36.03)	0.077 (0.036, 0.204)	0.001 (0.00, 0.002)	-	-0.01 (-0.02, 0.00)	0.11 (-0.45, 0.58)	-0.06 (-0.11, -0.01)	0.04 (-0.11, 0.17)	8	34
3.63 (1.20, 33.63)	0.081 (0.038, 0.206)	-	0.00 (0.00, 0.01)	-0.01 (-0.02, 0.00)	0.08 (-0.40, 0.64)	-0.03 (-0.09, 0.02)	0.03 (-0.12, 0.17)	8	33
3.58 (1.20, 37.85)	**0.065 (0.032, 0.208)**	**0.001 (0.00004, 0.003)**	**0.01 (0.00, 0.01)**	**-0.01 (-0.02, 0.00)**	**0.05 (-0.44, 0.59)**	**-0.04 (-0.10, 0.02)**	**0.01 (-0.13, 0.16)**	**10**	**33**
8.33 (5.49, 14.79)	0.073 (0.034, 0.221)	0.001 (0.00, 0.003)	-	-	-	-0.11 (-0.15, -0.06)	-	14	34
1.60 (0.65, 15.03)	0.081 (0.038, 0.216)	-	-	-	-	-0.11 (-0.15, -0.06)	0.11 (-0.04, 0.23)	14	34
8.42 (5.68, 14.70)	0.074 (0.038, 0.233)	-	-	-	-	-0.10 (-0.14, -0.05)	-	15	35
8.10 (5.20, 15.27)	0.080 (0.036, 0.218)	-	-	-	0.08 (-0.45, 0.60)	-0.10 (-0.15, -0.05)	-	16	34
1.80 (0.69, 15.58)	0.075 (0.037, 0.210)	0.001 (0.00, 0.003)	-	-	-	-0.11 (-0.16, -0.07)	0.11 (-0.05, 0.22)	16	34
8.53 (5.13, 15.05)	0.076 (0.035, 0.193)	0.001 (0.00, 0.003)	-	-	-0.04 (-0.49, 0.52)	-0.11 (-0.15, -0.06)	-	16	34
7.27 (4.72, 12.89)	0.073 (0.036, 0.203)	-	0.00 (0.00, 0.01)	-	-	-0.08 (-0.13, -0.03)	-	17	34
6.98 (4.56, 12.26)	0.071 (0.033, 0.200)	0.001 (0.00, 0.003)	0.00 (0.00, 0.01)	-	-	-0.08 (-0.14, -0.03)	-	17	34
1.76 (0.57, 15.14)	0.071 (0.038, 0.219)	-	0.00 (0.00, 0.01)	-	-	-0.09 (-0.14, -0.04)	0.09 (-0.05, 0.23)	17	34
1.63 (0.62, 14.84)	0.079 (0.031, 0.220)	-	-	-	0.11 (-0.43, 0.59)	-0.11 (-0.15, -0.06)	0.09 (-0.04, 0.23)	17	34
1.73 (0.58, 15.75)	0.078 (0.033, 0.208)	0.001 (0.00, 0.002)	-	-	0.05 (-0.48, 0.53)	-0.11 (-0.16, -0.07)	0.09 (-0.05, 0.24)	18	34
6.93 (4.23, 13.17)	0.068 (0.030, 0.189)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-	-0.03 (-0.49, 0.54)	-0.08 (-0.14, -0.04)	-	18	34
6.79 (4.48, 13.67)	0.076 (0.036, 0.200)	-	0.00 (0.00, 0.01)	-	0.09 (-0.44, 0.58)	-0.08 (-0.13, -0.03)	-	18	34
1.67 (0.61, 14.16)	0.065 (0.031, 0.188)	0.001 (0.00, 0.003)	0.01 (0.00, 0.01)	-	-	-0.09 (-0.14, -0.04)	0.09 (-0.05, 0.22)	19	34
1.54 (0.59, 14.63)	0.079 (0.033, 0.190)	-	0.00 (0.00, 0.01)	-	0.06 (-0.44, 0.59)	-0.09 (-0.14, -0.04)	0.10 (-0.05, 0.23)	20	34
1.71 (0.56, 14.93)	0.075 (0.034, 0.216)	0.001 (0.00, 0.003)	0.00 (0.00, 0.01)	-	0.04 (-0.47, 0.51)	-0.09 (-0.14, -0.04)	0.09 (-0.06, 0.22)	20	34
4.95 (3.56, 6.96)	0.077 (0.037, 0.216)	-	0.01 (0.00, 0.01)	-	-	-	-	28	30

4.34 (3.23, 6.36)	0.076 (0.038, 0.210)	0.001 (0.00, 0.003)	0.01 (0.00, 0.02)	-	-	-	-	29	30
2.39 (0.77, 16.18)	0.074 (0.038, 0.210)	-	0.01 (0.00, 0.01)	-	-	-	0.04 (-0.10, 0.16)	30	30
2.10 (0.74, 16.65)	0.076 (0.037, 0.209)	0.001 (0.00, 0.003)	0.01 (0.00, 0.02)	-	-	-	0.05 (-0.11, 0.16)	31	30
4.76 (3.20, 7.63)	0.082 (0.040, 0.219)	-	0.01 (0.00, 0.01)	-	0.02 (-0.46, 0.52)	-	-	31	30
2.03 (0.73, 16.39)	0.085 (0.038, 0.242)	-	0.01 (0.00, 0.01)	-	0.00 (-0.49, 0.51)	-	0.02 (-0.10, 0.16)	32	30
5.69 (3.93, 8.47)	**0.089 (0.040, 0.241)**	-	-	-	-	-	-	**32**	**29**
4.29 (3.10, 7.15)	0.074 (0.036, 0.212)	0.001 (0.00, 0.003)	0.01 (0.00, 0.02)	-	-0.07 (-0.56, 0.45)	-	-	32	30
1.98 (0.72, 16.41)	0.071 (0.035, 0.201)	0.001 (0.00, 0.003)	0.01 (0.00, 0.02)	-	-0.08 (-0.53, 0.44)	-	0.03 (-0.10, 0.16)	34	30
5.51 (3.84, 9.37)	0.088 (0.043, 0.260)	-	-	-	-0.04 (-0.57, 0.49)	-	-	34	29
2.61 (0.81, 19.39)	0.091 (0.042, 0.245)	-	-	-	-	-	0.02 (-0.10, 0.16)	34	29
5.31 (3.87, 8.01)	0.091 (0.043, 0.236)	0.001 (0.00, 0.002)	-	-	-	-	-	35	29
2.26 (0.82, 23.56)	0.091 (0.042, 0.241)	-	-	-	-0.06 (-0.57, 0.51)	-	0.03 (-0.11, 0.17)	36	29
5.60 (3.70, 8.91)	0.091 (0.042, 0.257)	0.001 (-0.001, 0.002)	-	-	-0.07 (-0.59, 0.48)	-	-	37	29
2.28 (0.83, 21.37)	0.089 (0.041, 0.245)	0.001 (-0.001, 0.002)	-	-	-	-	0.02 (-0.11, 0.16)	38	29
2.38 (0.93, 21.61)	0.087 (0.041, 0.244)	0.001 (-0.001, 0.002)	-	-	-0.04 (-0.59, 0.47)	-	0.03 (-0.12, 0.16)	39	29

Table CK.6. Percent change in posterior mode recruits-per-spawner (RPS) for the full Chinook 11-population model for a 1SD increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 1SD increase for each covariate.

| Region	Population	Percent change in RPS for 1SD increase in covariates					
		$\bar{H}_i^{relCU}$+ 1SD	$\bar{H}_i^{relOE}$+ 1SD	$\bar{H}_i^{cSite}$ + 1SD	$\bar{H}_i^{pHOS}$ + 1SD	$\bar{P}_i$ + 10%	$\bar{T}_i$ + 10%
NC	KALUM-EARLY TIMING	0.0%	0.1%	-15.5%	0.1%	-0.8%	0.6%
	UPPER BULKLEY RIVER	0.3%	0.1%	-4.5%	0.7%	-0.4%	0.6%
CC	BELLA COOLA-BENTINCK	0.3%	1.1%	-17.9%	1.3%	-0.1%	0.6%
QCSDPASS	QUINSAM	2.6%	15.1%	-25.6%	0.7%	-2.7%	0.6%
SOG	COWICHAN	1.4%	1.0%	-22.0%	0.6%	-7.1%	0.6%
	PUNTLEDGE	16.2%	16.1%	-13.5%	1.3%	-11.8%	0.6%
	NANAIMO	0.4%	6.8%	-6.9%	1.4%	-7.8%	0.6%
	QUALICUM	21.3%	16.1%	-23.7%	0.8%	-12.2%	0.6%
	HARRISON	0.0%	1.0%	-2.5%	0.2%	-7.8%	0.6%
	CHILLIWACK	0.4%	1.0%	-9.4%	1.2%	-7.1%	0.6%
	SHUSWAP	0.1%	1.0%	-16.7%	0.2%	-5.6%	0.7%
MEAN ALL POPULATIONS		**4.4%**	**6.2%**	**-14.9%**	**0.9%**	**-6.7%**	**0.6%**
MEAN SOG		5.5%	6.4%	-13.9%	0.9%	-8.5%	0.6%

Chinook Figures
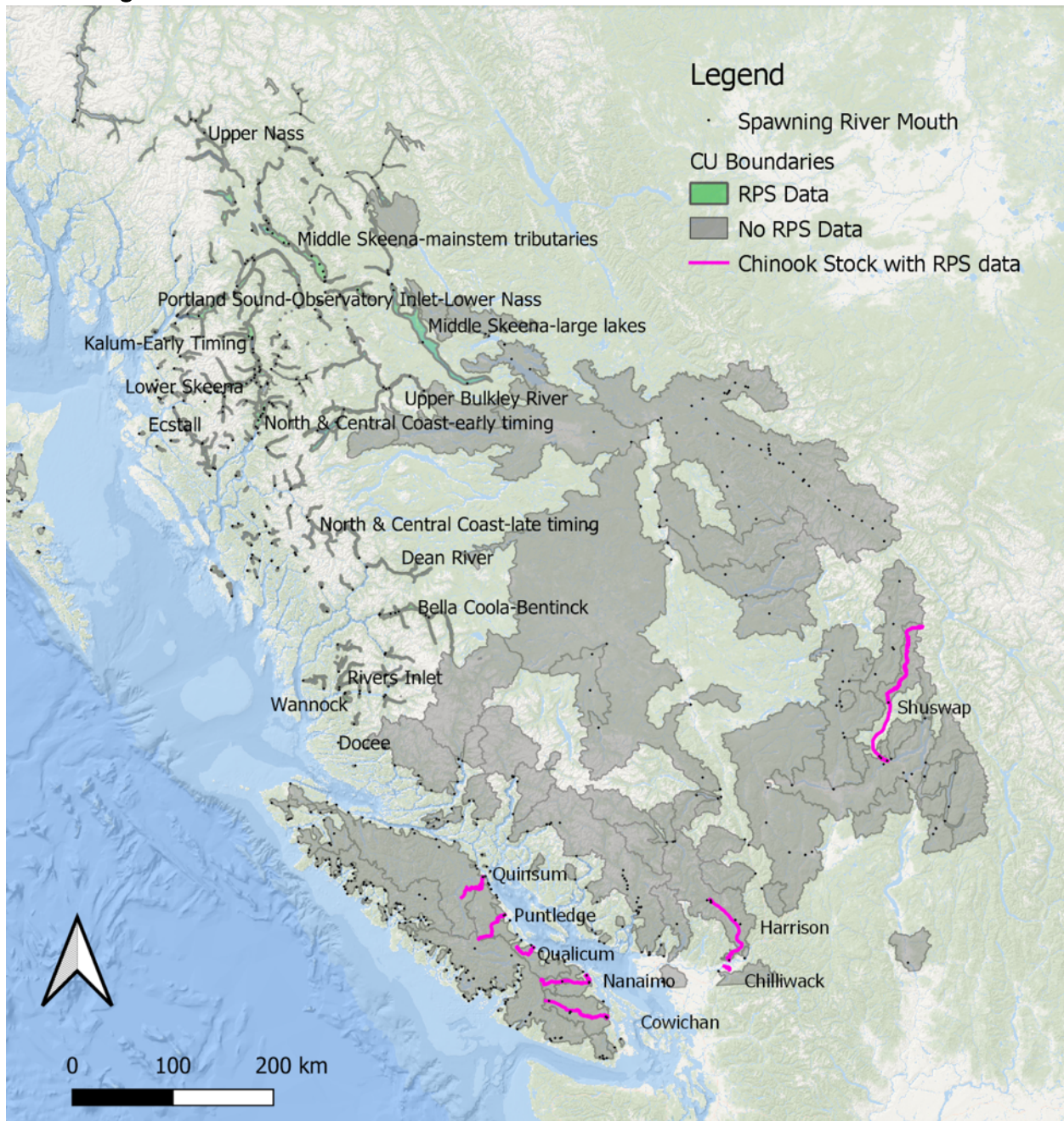
Figure CK.1 Locations of Conservation Units and Stocks with recruits per spawner (RPS) data for Chinook models.
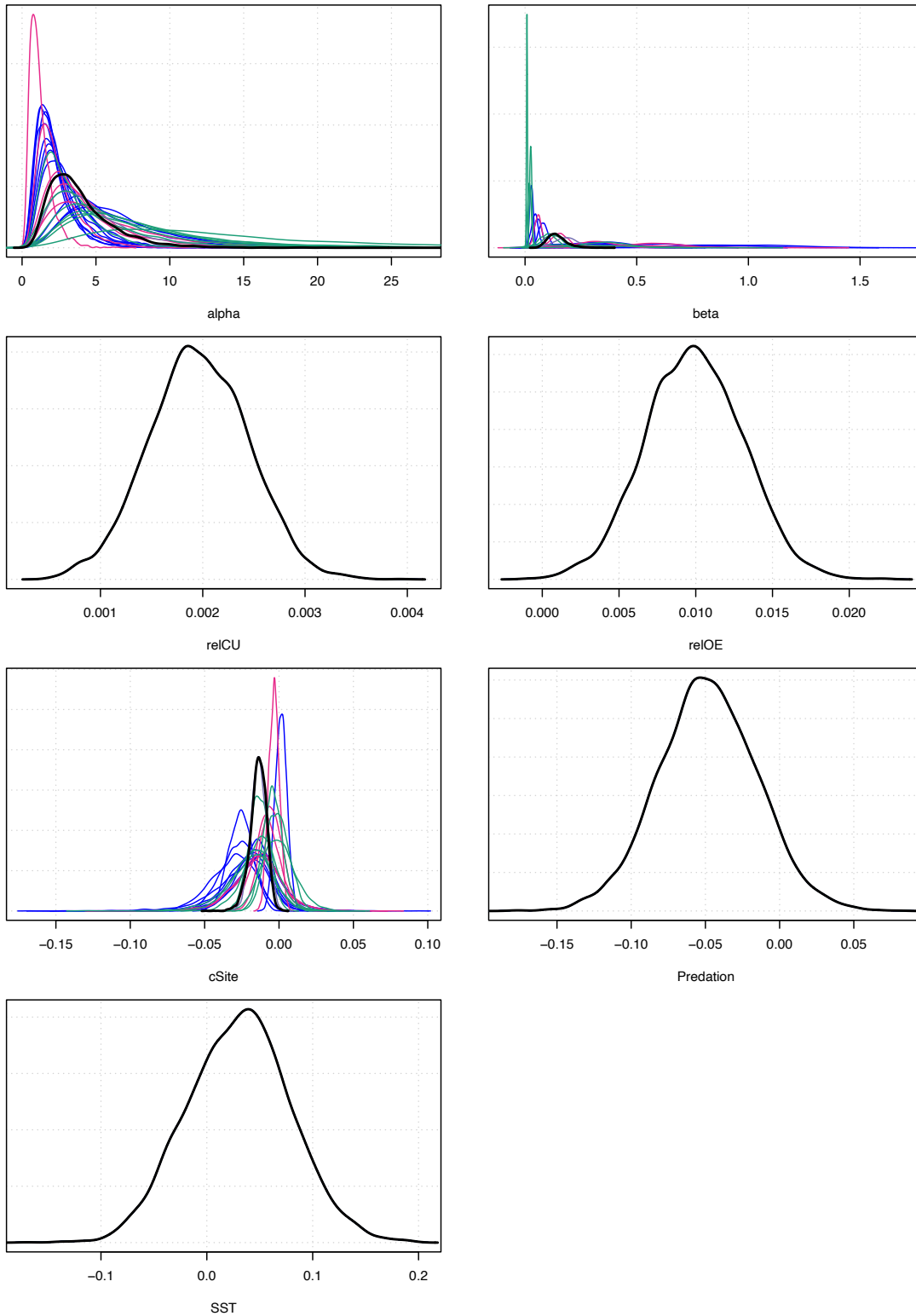
Fig CK.2. Posterior distribution of coefficient estimates for intrinsic productivity (α), density dependence (β), hatchery (H^{relCU}, H^{relOE}, H^{cSite}), predation, and sea surface temperature (SST) for full 24-population Chinook model. Colors indicate different regions for Chinook populations (NC= blue, CC=pink, HG= yellow, SOG=green, WCVI=orange, QCSDPASS=purple)
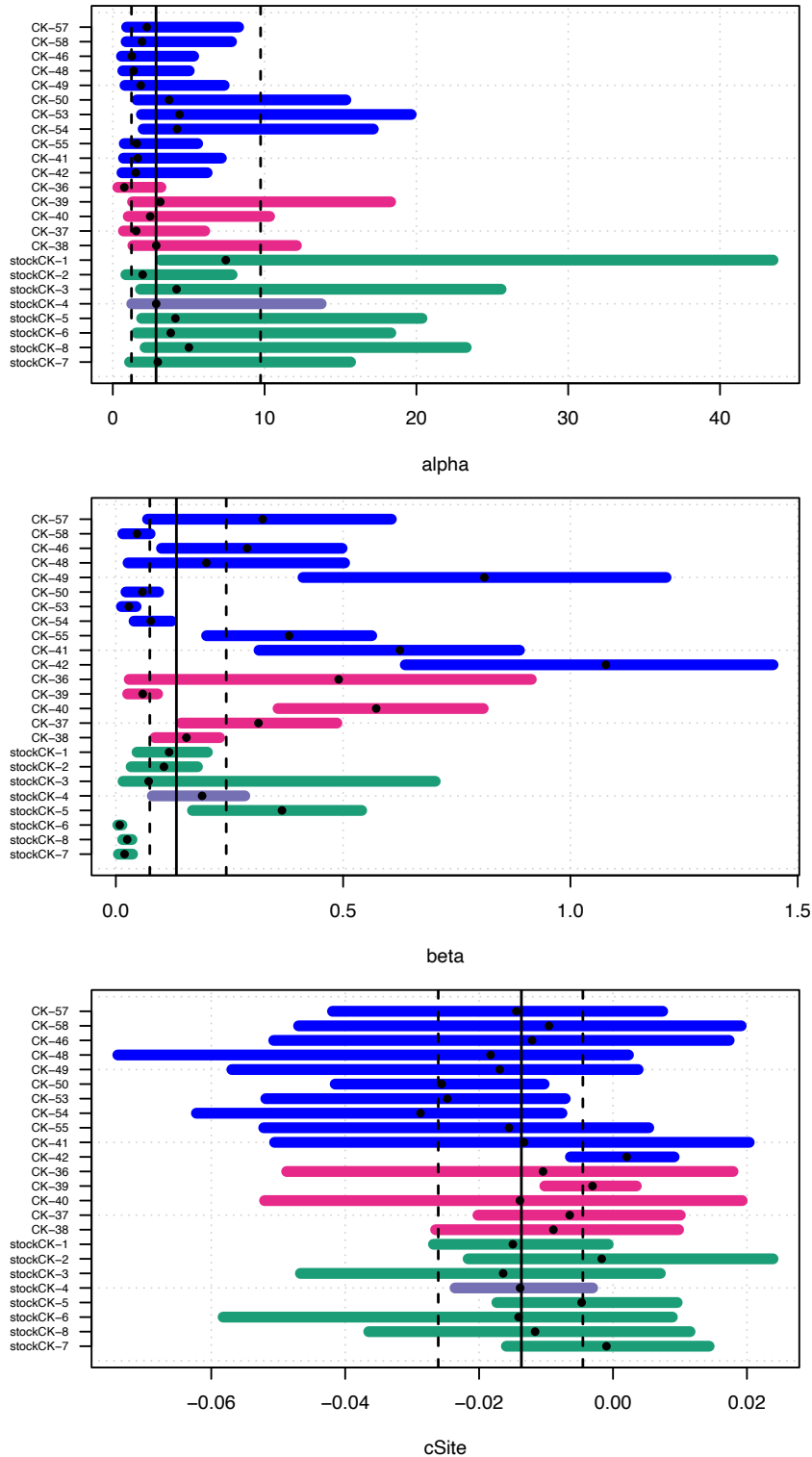
Fig CK.3. Coefficient estimates for α, β, cumulative hatchery release sites (H^{cSite}) from full 24-population Chinook model. The circles indicate population specific mean posterior estimates along with 95% credible intervals, while the vertical lines indicate the mean posterior for the average effect across all populations (vertical solid black line) with 95% credible intervals (vertical dotted black lines). Colors indicate different regions for Chinook populations (NC= blue, CC=pink, SOG=green, QCSDPASS=purple)
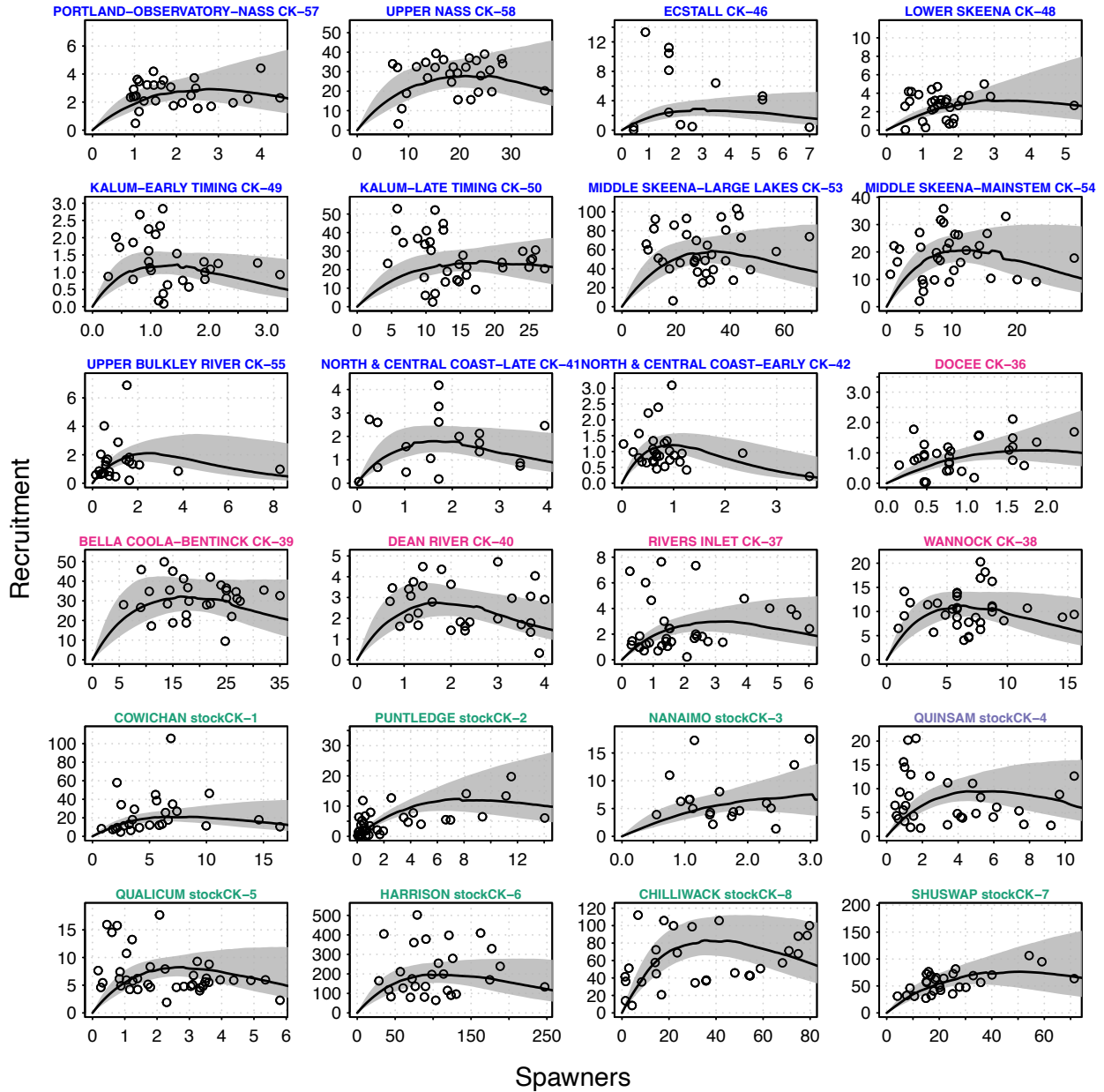
Fig CK.4. Median posterior (black line) and 95% credible intervals (shaded area) spawner-recruit curve from full 24-population Chinook Ricker model with cumulative release sites and seal density covariate. Colors for population names indicate different regions for Chinook populations (NC= blue, CC=pink, SOG=green, QCSDPASS=purple).
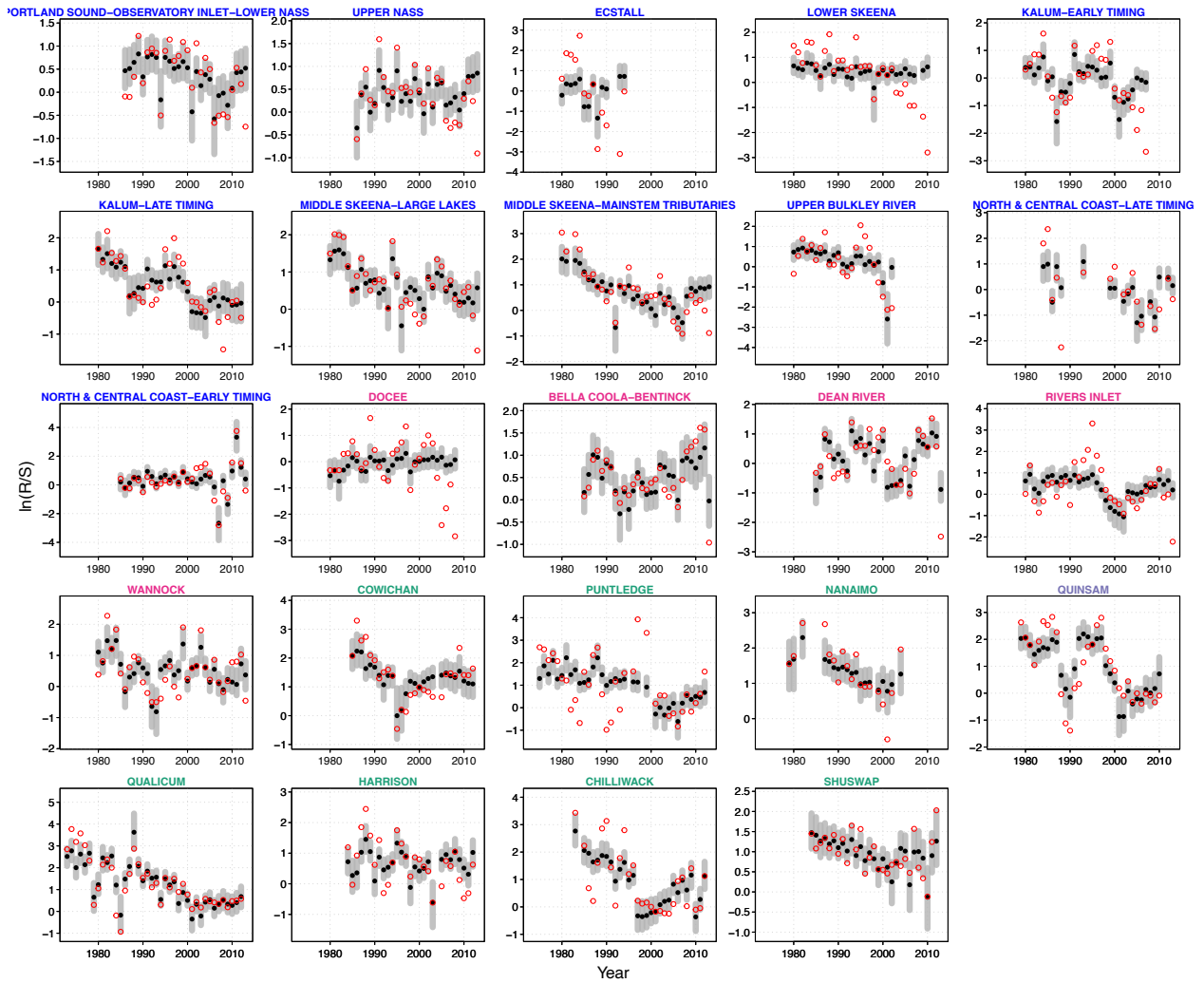
Figure CK.5. Log recruits-per-spawner observations (red circles) by brood year and median estimates (black dots) with 95% credible intervals (grey lines) from full 24-population Chinook Model.

Fig CK.6. Posterior distribution of coefficient estimates for intrinsic productivity (α), density dependence (β), hatchery (H^{relCU}, H^{relOE}, H^{cSite}, H^{pHOS}),), predation, and sea surface temperature (SST) for full 11-population Chinook model. Colors indicate different regions for Chinook populations (NC= blue, CC=pink, HG= yellow, SOG=green, WCVI=orange, QCSDPASS=purple).
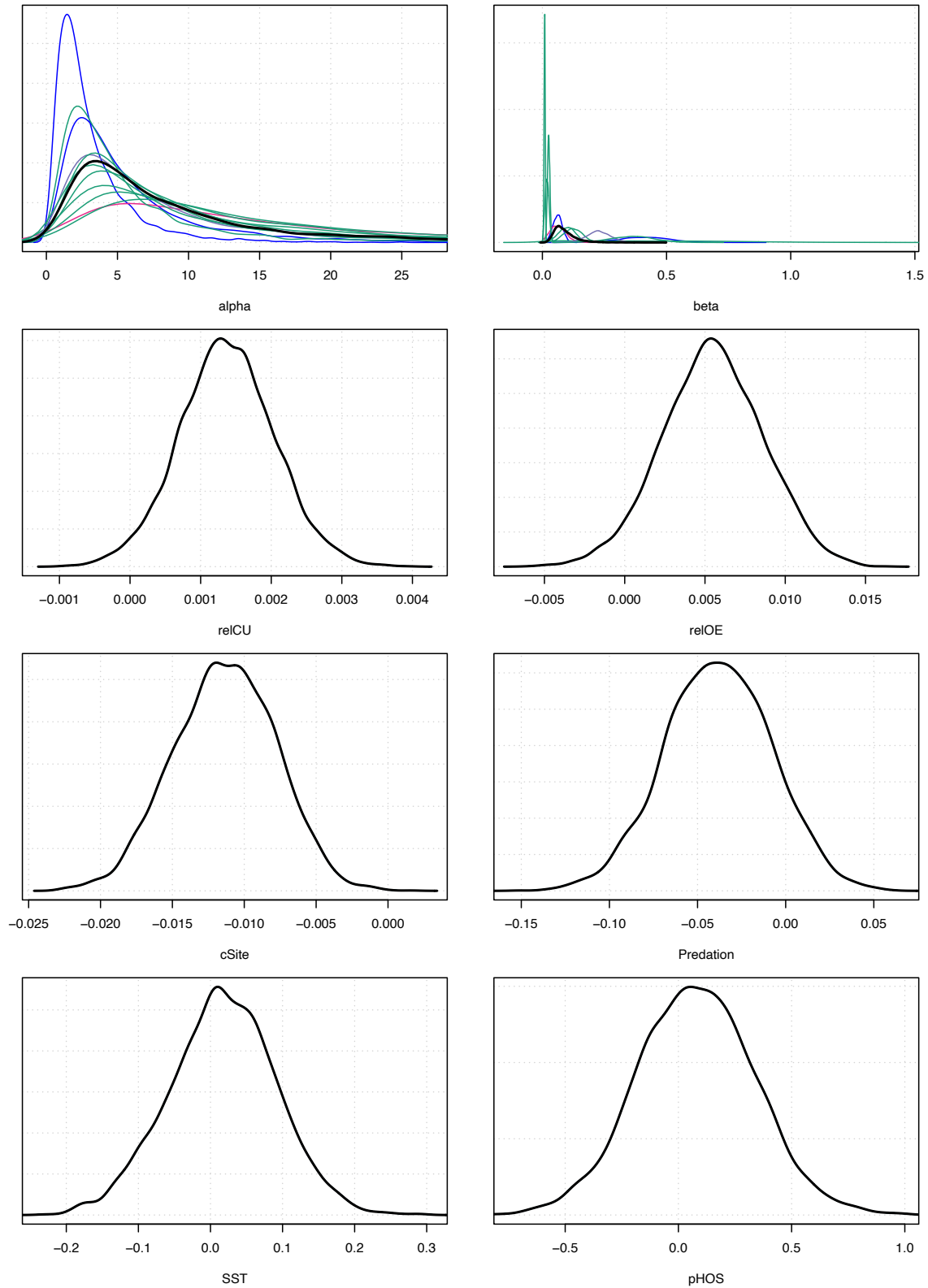
Appendix CO – Coho Tables and Figures

Coho Tables

Table CO.1. Summary of spawner-recruit datasets for BC Coho conservation units (CU) from the Pacific Salmon Foundation's Pacific Salmon Explorer (PSE, www.salmonexplorer.ca) database by region (HG=Haida Gwaii, NC=North Coast, CC=Central Coast, SOG=Strait of Georgia).

Regions	CU/Stock ID	CU Name	Source	Brood year range	n
HG	CO-23	HG-EAST	PSE	1954-2014	61
	CO-24	HG-WEST	PSE	1954-2005	41
	CO-25	HG-GRAHAM ISLAND LOWLANDS	PSE	1954-2012	54
NC	CO-35	LOWER NASS	PSE	1959-2014	55
	CO-36	UPPER NASS	PSE	1969-2014	45
	CO-37	PORTLAND SOUND-OBSERVATORY INLET-PORTLAND CANAL	PSE	1954-2010	45
	CO-31	SKEENA ESTUARY	PSE	1954-2010	49
	CO-32	LOWER SKEENA	PSE	1954-2014	60
	CO-33	MIDDLE SKEENA	PSE	1954-2014	61
	CO-34	UPPER SKEENA	PSE	1954-2014	28
	CO-27	HECATE STRAIT MAINLAND	PSE	1954-2014	61
	CO-29	DOUGLAS CHANNEL-KITIMAT ARM	PSE	1954-2014	51
	CO-30	NORTHERN COASTAL STREAMS	PSE	1954-2014	61
CC	CO-28	BRIM-WAHOO	PSE	1954-2014	54
	CO-20	SMITH INLET	PSE	1954-2011	30
	CO-22	BELLA COOLA-DEAN RIVERS	PSE	1954-2014	61
	CO-26	MUSSEL-KYNOCH	PSE	1954-2013	60
	CO-21	RIVERS INLET	PSE	1954-2010	42
SOG	CO-48	INTERIOR FRASER	PSE	1984-2015	32
	CO-5	FRASER CANYON	PSE	1984-2015	32
	CO-7	LOWER THOMPSON	PSE	1984-2015	32
	CO-8	SOUTH THOMPSON	PSE	1984-2015	32
	CO-9	NORTH THOMPSON	PSE	1984-2015	32

Table CO2. Comparison of Coho multi-population Ricker models with full suite and subset of covariates. The median posterior coefficient estimates and 95% credible intervals () are shown for hatchery (*H*), predator (*P*), and sea surface temperature (T) covariates. Models include three different hatchery covariates (i) species-specific hatchery releases per wild smolt by CU (H^{relCU}), and/or (iii) species-specific hatchery releases per wild smolt by ocean entry region (H^{relOE}), (iii) cumulative release sites by CU (H^{cSite}). The full model and the basic ricker model with only the spawner abundance covariate are shown in bold. Note that population-specific estimates for α, β and H^{cSite} are not shown.

Coefficient estimates for hierarchical Ricker model and covariates							LOOIC	
α	β	H^{relCU}	H^{relOE}	H^{cSite}	P	T	ΔLOOIC	SE
1.22 (0.71, 2.72)	0.010 (0.006, 0.018)	-	0.66 (0.29, 1.01)	-0.003 (-0.007, 0.00)	-0.11 (-0.16, -0.06)	0.08 (0.01, 0.15)	0	61
1.54 (0.87, 3.48)	0.010 (0.006, 0.018)	-	0.41 (0.06, 0.80)	-0.007 (-0.013, -0.003)	-	0.05 (-0.02, 0.12)	1	60
1.51 (0.87, 3.52)	0.011 (0.006, 0.019)	0.08 (-0.10, 0.25)	0.36 (-0.03, 0.76)	-0.007 (-0.013, -0.002)	-	0.04 (-0.02, 0.12)	2	60
1.20 (0.66, 2.78)	**0.010 (0.006, 0.018)**	**0.08 (-0.09, 0.26)**	**0.56 (0.15, 0.96)**	**-0.004 (-0.008, -0.0004)**	**-0.11 (-0.16, -0.06)**	**0.09 (0.01, 0.16)**	**2**	**61**
2.77 (2.31, 3.35)	0.011 (0.006, 0.019)	-	0.48 (0.15, 0.84)	-0.007 (-0.013, -0.002)	-	-	4	61
2.98 (2.56, 3.71)	0.010 (0.006, 0.018)	-	0.68 (0.35, 1.07)	-0.004 (-0.007, 0.00)	-0.09 (-0.14, -0.04)	-	4	61
2.77 (2.34, 3.35)	0.011 (0.006, 0.019)	0.07 (-0.09, 0.26)	0.44 (-0.01, 0.80)	-0.007 (-0.012, -0.002)	-	-	5	61
1.12 (0.62, 2.48)	0.011 (0.007, 0.020)	-	-	-0.004 (-0.009, -0.001)	-0.08 (-0.14, -0.03)	0.10 (0.03, 0.17)	6	61
1.19 (0.64, 2.65)	0.010 (0.006, 0.018)	0.20 (0.04, 0.34)	-	-0.004 (-0.008, 0.00)	-0.09 (-0.14, -0.04)	0.10 (0.02, 0.17)	7	61
1.50 (0.83, 3.32)	0.011 (0.006, 0.019)	0.16 (0.00, 0.31)	-	-0.007 (-0.013, -0.002)	-	0.06 (-0.01, 0.12)	7	60
1.44 (0.77, 3.14)	0.010 (0.006, 0.019)	-	-	-0.007 (-0.013, -0.002)	-	0.07 (0.00, 0.13)	7	60
3.04 (2.59, 3.69)	0.010 (0.006, 0.018)	0.10 (-0.08, 0.27)	0.60 (0.20, 1.00)	-0.003 (-0.008, 0.00)	-0.09 (-0.14, -0.05)	-	8	61
2.85 (2.43, 3.42)	0.010 (0.006, 0.018)	0.17 (0.02, 0.32)	-	-0.007 (-0.012, -0.002)	-	-	8	61
2.96 (2.51, 3.55)	0.010 (0.006, 0.020)	-	-	-0.007 (-0.012, -0.002)	-	-	10	61
3.16 (2.66, 3.85)	0.010 (0.006, 0.018)	0.23 (0.05, 0.37)	-	-0.004 (-0.008, -0.001)	-0.07 (-0.12, -0.02)	-	11	61
3.19 (2.68, 3.92)	0.011 (0.006, 0.019)	-	-	-0.004 (-0.009, -0.001)	-0.06 (-0.11, 0.00)	-	13	61
1.30 (0.66, 2.71)	0.009 (0.006, 0.018)	-	0.78 (0.38, 1.12)	-	-0.14 (-0.19, -0.11)	0.08 (0.01, 0.16)	24	60
1.29 (0.68, 2.72)	0.010 (0.006, 0.018)	0.08 (-0.09, 0.26)	0.68 (0.26, 1.05)	-	-0.15 (-0.19, -0.11)	0.08 (0.01, 0.15)	24	60
2.97 (2.53, 3.58)	0.009 (0.005, 0.017)	-	0.81 (0.45, 1.18)	-	-0.13 (-0.17, -0.09)	-	27	60
2.93 (2.52, 3.57)	0.009 (0.005, 0.017)	0.09 (-0.10, 0.26)	0.72 (0.33, 1.14)	-	-0.13 (-0.17, -0.09)	-	28	60
1.19 (0.62, 2.52)	0.010 (0.005, 0.018)	0.22 (0.06, 0.37)	-	-	-0.14 (-0.18, -0.10)	0.09 (0.03, 0.17)	31	60

Coefficient estimates for hierarchical Ricker model and covariates							LOOIC	
α	β	H^{relCU}	H^{relOE}	H^{cSite}	P	T	ΔLOOIC	SE
3.06 (2.63, 3.79)	0.010 (0.006, 0.018)	0.21 (0.08, 0.38)	-	-	-0.12 (-0.16, -0.08)	-	36	60
0.99 (0.60, 2.37)	0.010 (0.006, 0.019)	-	-	-	-0.13 (-0.18, -0.09)	0.10 (0.03, 0.17)	36	60
3.15 (2.68, 3.96)	0.010 (0.006, 0.019)	-	-	-	-0.11 (-0.15, -0.07)	-	41	60
1.88 (1.05, 4.57)	0.009 (0.005, 0.017)	-	0.54 (0.13, 0.89)	-	-	0.01 (-0.07, 0.07)	64	57
2.28 (1.86, 2.82)	0.009 (0.005, 0.016)	-	0.49 (0.14, 0.87)	-	-	-	65	57
2.28 (1.88, 2.81)	0.008 (0.005, 0.018)	0.09 (-0.11, 0.26)	0.39 (-0.01, 0.84)	-	-	-	67	57
1.97 (1.03, 4.60)	0.009 (0.005, 0.016)	0.07 (-0.10, 0.26)	0.41 (0.00, 0.84)	-	-	0.00 (-0.07, 0.08)	67	57
2.36 (2.02, 2.87)	0.009 (0.005, 0.016)	0.15 (0.00, 0.32)	-	-	-	-	72	57
1.87 (1.06, 4.51)	0.009 (0.005, 0.018)	0.17 (0.00, 0.33)	-	-	-	0.01 (-0.06, 0.08)	74	57
2.43 (2.06, 2.92)	**0.010 (0.006, 0.017)**	**-**	**-**	**-**	**-**	**-**	**76**	**57**
1.80 (1.02, 4.43)	0.009 (0.005, 0.018)	-	-	-	-	0.01 (-0.06, 0.09)	77	57

Table CO.3. Percent change in posterior mode recruits-per-spawner (RPS) for the full Coho model for a 1SD increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 1SD increase for each covariate.

Region	Population	Percent change in RPS for 1SD increase in covariates				
		$\bar{H}_i^{relCU}$ + 1SD	$\bar{H}_i^{relOE}$ + 1SD	$\bar{H}_i^{cSite}$ + 1SD	$\bar{P}_i$ + 1SD	$\bar{T}_i$ + 1SD
HG	HG-EAST	0.9%	3.5%	-9.0%	-10.8%	6.0%
	HG-WEST	0.5%	3.7%	-2.2%	-9.7%	5.6%
	HG-GRAHAM ISLAND LOWLANDS	0.5%	2.8%	-7.3%	-10.0%	6.0%
NC	LOWER NASS	0.1%	1.5%	-1.0%	-4.1%	5.8%
	UPPER NASS		1.5%		-4.0%	5.8%
	PORTLAND SOUND-OBSERVATORY INLET-PORTLAND CANAL	0.2%	1.6%	-4.5%	-3.9%	6.2%
	SKEENA ESTUARY	1.9%	1.4%	-15.9%	-3.8%	6.0%
	LOWER SKEENA	0.3%	1.5%	-20.8%	-4.0%	6.0%
	MIDDLE SKEENA	1.3%	1.5%	15.3%	-3.9%	6.0%
	UPPER SKEENA		0.9%		-4.5%	6.2%
	HECATE STRAIT MAINLAND	0.4%	1.5%	-17.8%	-3.9%	6.1%
	DOUGLAS CHANNEL-KITIMAT ARM	2.0%	1.5%	-3.0%	-4.0%	5.8%
	NORTHERN COASTAL STREAMS	0.1%	1.5%	-1.1%	-3.9%	6.2%
CC	BRIM-WAHOO		4.9%		-3.8%	6.0%
	SMITH INLET		1.1%		-4.2%	6.8%
	BELLA COOLA-DEAN RIVERS	1.3%	5.6%	-11.7%	-3.6%	6.2%
	MUSSEL-KYNOCH		5.6%		-3.6%	6.2%
	RIVERS INLET		1.2%	-0.4%	-3.3%	6.2%
SOG	INTERIOR FRASER	2.4%	17.5%	-3.0%	-20.5%	5.8%
	FRASER CANYON	0.1%	17.5%	-1.5%	-20.5%	5.8%
	LOWER THOMPSON	11.9%	17.5%	-16.8%	-20.5%	5.8%
	SOUTH THOMPSON	10.1%	17.5%	-8.5%	-20.5%	5.8%
	NORTH THOMPSON	1.1%	17.5%	-11.2%	-20.5%	5.8%
MEAN ALL POPULATIONS		1.9%	5.6%	-6.2%	-8.2%	6.0%
MEAN NC		0.7%	1.4%	-5.3%	-4.0%	6.0%
MEAN HG		0.6%	3.3%	-6.2%	-10.2%	5.9%
MEAN CC		0.6%	3.9%	-5.9%	-3.6%	6.2%
MEAN SOG		4.9%	17.5%	-7.9%	-20.5%	5.8%

Table CO.4. Percent change in posterior mode recruits-per-spawner (RPS) for the full Coho model for a 10% increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 10% increase for each covariate.

Region	Population	Percent change in RPS for 1SD increase in covariates				
		$\overline{H}_i^{relCU} + 10\%$	$\overline{H}_i^{relOE} + 10\%$	$\overline{H}_i^{cSite} + 10\%$	$\overline{P}_i + 10\%$	$\overline{T}_i + 10\%$
HG	HG-EAST	0.1%	0.2%	-0.7%	-1.6%	8.4%
	HG-WEST	<0.1%	0.3%	-0.2%	-1.3%	8.0%
	HG-GRAHAM ISLAND LOWLANDS	<0.1%	0.2%	-0.6%	-1.4%	8.1%
NC	LOWER NASS	<0.1%	0.1%	-0.1%	-0.6%	8.2%
	UPPER NASS		0.2%		-0.7%	8.2%
	PORTLAND SOUND-OBSERVATORY INLET-PORTLAND CANAL	<0.1%	0.1%	-0.5%	-0.6%	8.2%
	SKEENA ESTUARY	0.1%	0.1%	-1.2%	-0.5%	8.3%
	LOWER SKEENA	<0.1%	0.1%	-2.4%	-0.6%	8.3%
	MIDDLE SKEENA	<0.1%	0.1%	1.5%	-0.6%	8.3%
	UPPER SKEENA		0.1%		-0.7%	8.4%
	HECATE STRAIT MAINLAND	<0.1%	0.1%	-1.5%	-0.6%	8.8%
	DOUGLAS CHANNEL-KITIMAT ARM	0.1%	0.1%	-0.3%	-0.6%	8.6%
	NORTHERN COASTAL STREAMS	<0.1%	0.1%	-0.1%	-0.6%	8.9%
CC	BRIM-WAHOO		0.2%		-0.5%	8.6%
	SMITH INLET		0.1%		-0.6%	9.2%
	BELLA COOLA-DEAN RIVERS	0.1%	0.3%	-1.0%	-0.5%	9.2%
	MUSSEL-KYNOCH		0.3%		-0.5%	8.9%
	RIVERS INLET	<0.1%	0.1%	0.0%	-0.4%	9.0%
SOG	INTERIOR FRASER	0.1%	2.7%	-0.8%	-8.9%	10.6%
	FRASER CANYON	<0.1%	2.7%	-0.1%	-8.9%	10.6%
	LOWER THOMPSON	1.0%	2.7%	-2.4%	-8.9%	10.6%
	SOUTH THOMPSON	0.8%	2.7%	-2.3%	-8.9%	10.6%
	NORTH THOMPSON	0.1%	2.7%	-2.8%	-8.9%	10.6%
MEAN ALL POPULATIONS		0.1%	0.7%	-0.8%	-2.5%	9.0%
MEAN NC		<0.1%	0.1%	-0.5%	-0.6%	8.4%
MEAN HG		<0.1%	0.2%	-0.5%	-1.4%	8.2%
MEAN CC		<0.1%	0.2%	-0.5%	-0.5%	9.0%
MEAN SOG		0.4%	2.7%	-1.6%	-8.9%	10.6%

Coho Figures

Figure CO.1. Locations of Conservation Units with recruits per spawner (RPS) data for Coho models.
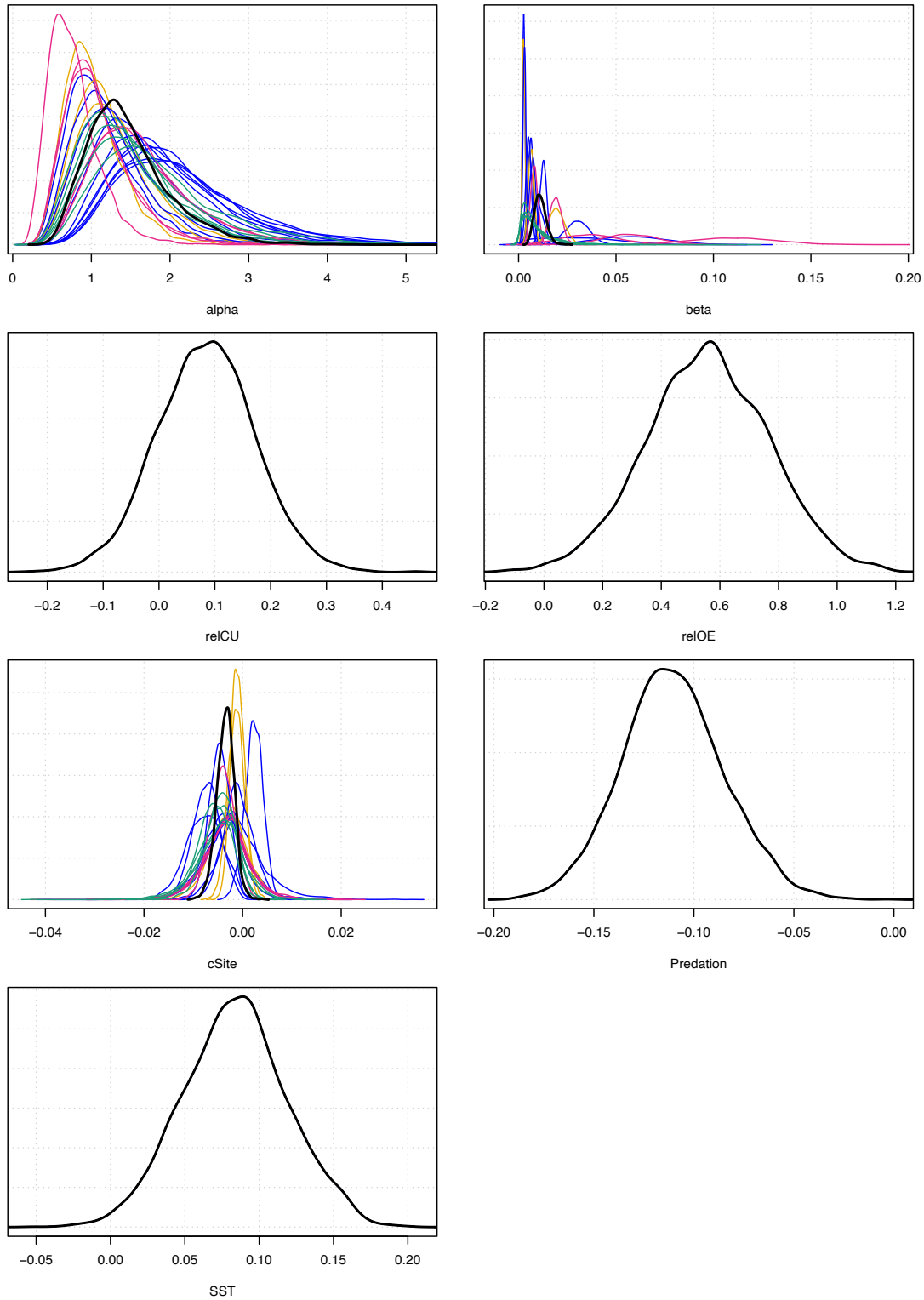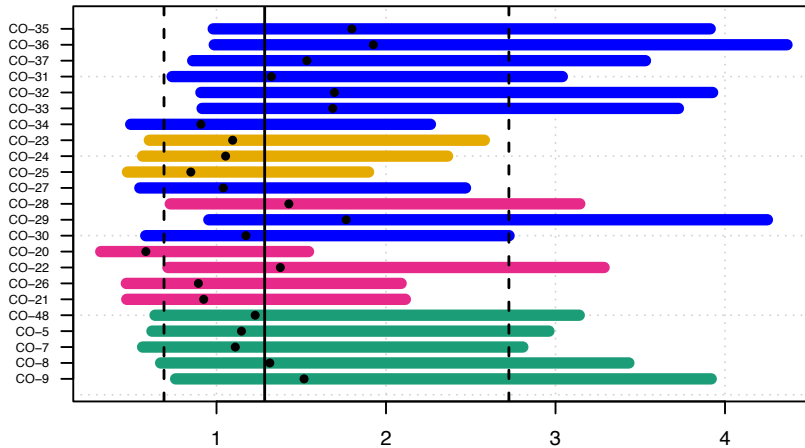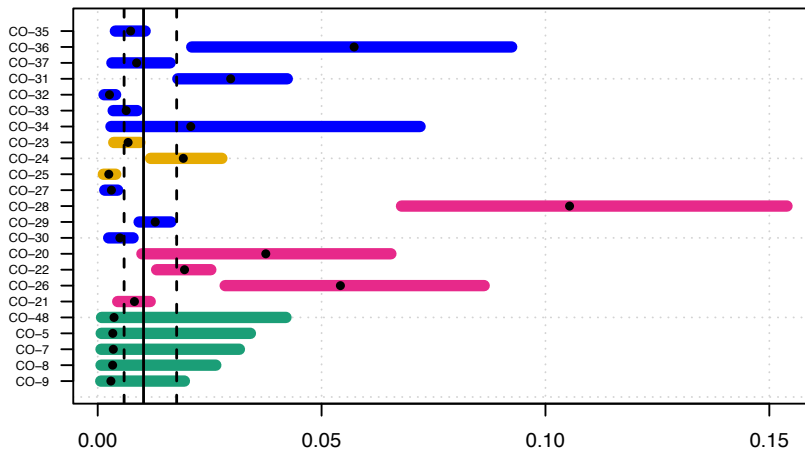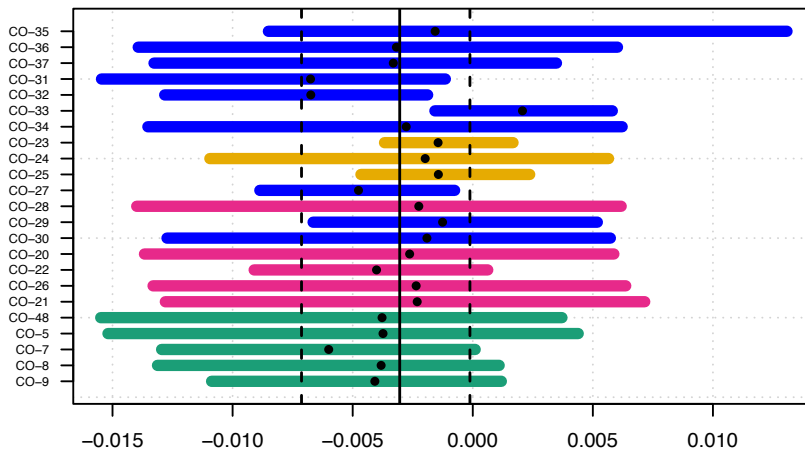
Fig CO.2. Posterior distribution of coefficient estimates for intrinsic productivity (α), density dependence (β), hatchery (H^{relCU}, H^{relOE}, H^{cSite}), predation, and sea surface temperature (SST) for full Coho model. Colors indicate different regions for Coho populations (NC= blue, HG=yellow, CC=pink, SOG=green).

Fig CO.3. Coefficient estimates for α, β, cumulative hatchery release sites (H^{cSite}) for full Coho model. The circles indicate population specific mean posterior estimates along with 95% credible intervals, while the vertical lines indicate the mean posterior for the average effect across all populations (vertical solid black line) with 95% credible intervals (vertical dotted black lines). Colors indicate different regions for Coho populations (NC= blue, HG=yellow, CC=pink, SOG=green)
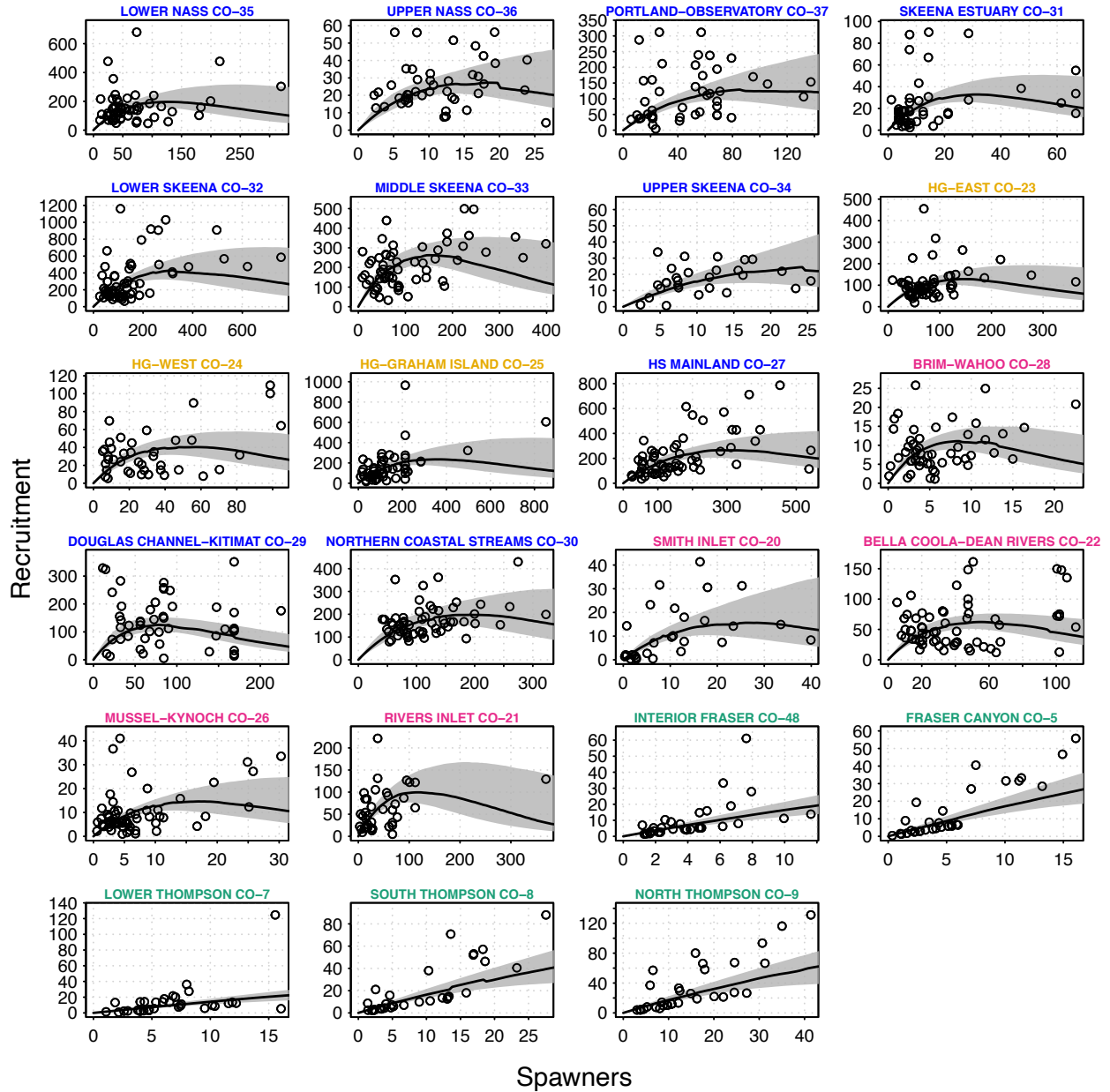
Fig CO.4. Median posterior (black line) and 95% credible intervals (shaded area) spawner-recruit curve from top Coho multi-population Ricker model with cumulative release sites and seal density covariate. Colors for population names indicate different regions for Coho populations (NC= blue, HG=yellow, CC=pink, SOG=green).
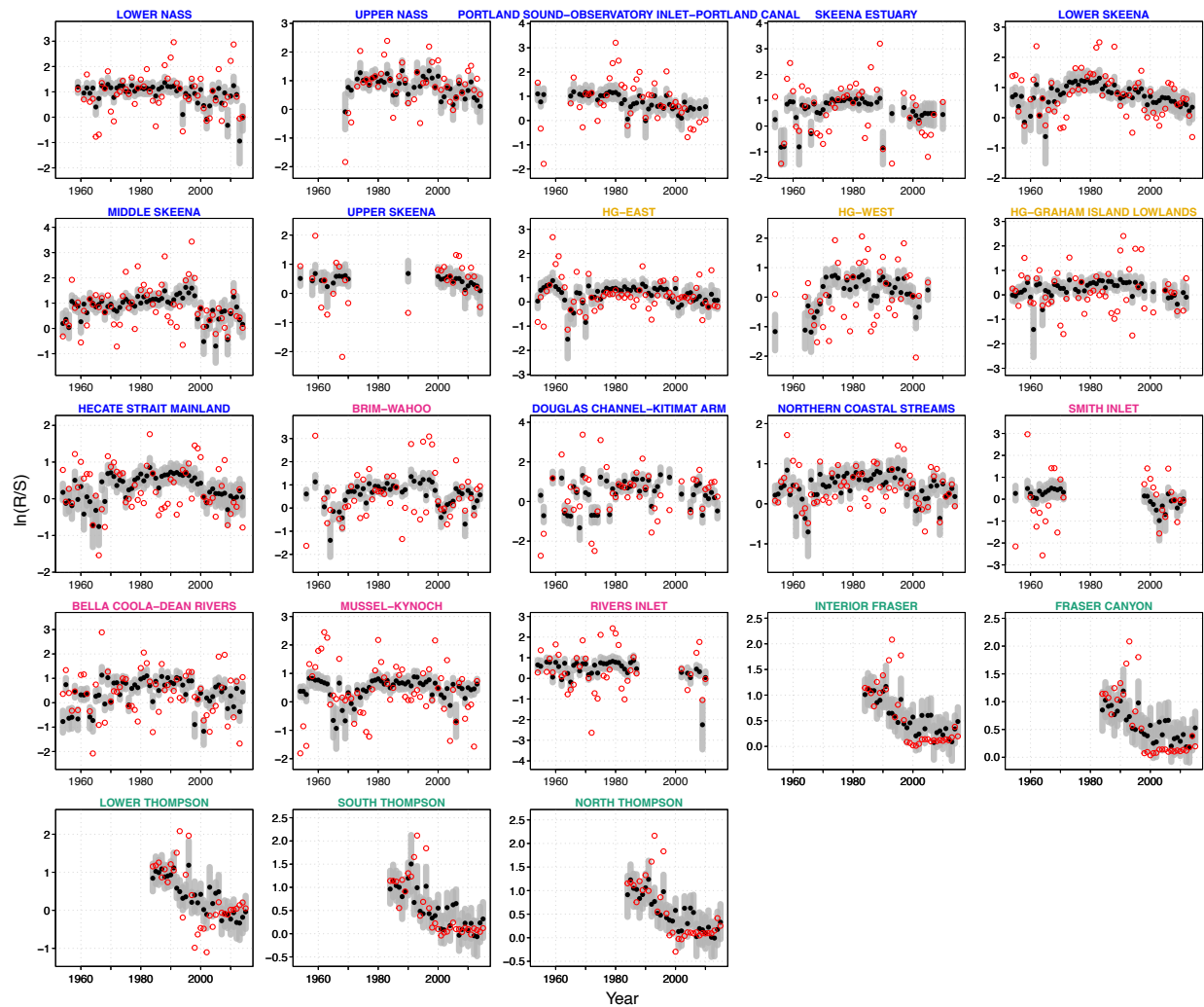
Figure CO.5. Log recruits-per-spawner observations (red circles) by brood year and median estimates (black dots) with 95% credible intervals (grey lines) from top Coho Model with cumulative hatchery release sites and seal density covariates.

Appendix CM – Chum Tables and Figures

Chum Tables

Table CM.1. Summary of spawner-recruit datasets for BC Chum conservation units (CUs) from the Pacific Salmon Foundation's Pacific Salmon Explorer (PSE, www.salmonexplorer.ca) and Inner South Coast Stock Reconstructions unpublished data, Pieter Van Will, DFO) by region (HG=Haida Gwaii, NC=North Coast, CC=Central Coast, QCSDPASS= Queen Charlotte Strait, Johnstone Strait, and Discovery Passage, SOG=Strait of Georgia).

Regions	CU/Stock ID	CU Name	Source	Brood year range	n
HG	CM-21	EAST HG	PSE	1954-2012	59
	CM-22	SKIDEGATE	PSE	1954-2012	59
	CM-23	WEST HAIDA GWAII	PSE	1954-2011	58
	CM-24	NORTH HAIDA GWAII	PSE	1954-2009	55
	CM-25	NORTH HAIDA GWAII-STANLEY CREEK	PSE	1957-2007	40
NC	CM-31	LOWER NASS	PSE	1958-2013	23
	CM-32	PORTLAND CANAL-OBSERVATORY	PSE	1954-2014	61
	CM-26	SKEENA ESTUARY	PSE	1954-2013	38
	CM-27	LOWER SKEENA	PSE	1954-2014	58
	CM-28	MIDDLE SKEENA	PSE	1954-2014	53
	CM-18	HECATE LOWLANDS	PSE	1954-2014	61
	CM-20	DOUGLAS-GARDNER	PSE	1954-2014	61
	CM-30	PORTLAND INLET	PSE	1954-2013	60
CC	CM-12	SMITH INLET	PSE	1954-2013	60
	CM-15	SPILLER-FITZ HUGH-BURKE	PSE	1954-2014	61
	CM-16	BELLA COOLA-DEAN RIVERS	PSE	1954-2014	61
	CM-17	BELLA COOLA RIVER-LATE	PSE	2003-2014	12
	CM-19	MUSSEL-KYNOCH	PSE	1954-2014	61
	CM-13	RIVERS INLET	PSE	1954-2011	58
QCSDPASS	CM-5	NORTHEAST VANCOUVER ISLAND	ISC	1955-2012	58
	CM-6	LOUGHBOROUGH	ISC	1955-2012	58
	CM-7	BUTE INLET	ISC	1955-1998	44
	CM-8	SOUTHERN COASTAL STREAMS	ISC	1955-2012	57
	CM-9	UPPER KNIGHT	ISC	1955-1973	17
WCVI	CM-11	NORTHWEST VANCOUVER ISLAND	PSE	1954-2012	56
	CM-10	SOUTHWEST VANCOUVER ISLAND	PSE	1954-2012	57
SOG	CM-3	HOWE SOUND-BURRARD INLET	ISC	1955-2012	58
	CM-4	GEORGIA STRAIT	ISC	1955-2012	58

Table CM2. Comparison of Chum multi-population Ricker models with full suite and subset of covariates. The median posterior coefficient estimates and 95% credible intervals () are shown for hatchery (H), predator (P), and sea surface temperature (T) covariates. Models include three different hatchery covariates (i) species-specific hatchery releases per wild smolt by CU (H^{relCU}), and/or (iii) species-specific hatchery releases per wild smolt by ocean entry region (H^{relOE}), (iii) cumulative release sites by CU (H^{cSite}). The full model and the basic ricker model with only the spawner abundance covariate are shown in bold. Note that population-specific estimates for α, β and H^{cSite} are not shown.

| Coefficient estimates for hierarchical Ricker model and covariates | | | | | | | LOOIC | |
α	β	H^{relCU}	H^{relOE}	H^{cSite}	P	T	ΔLOOIC	SE
5.00 (2.80, 10.14)	**0.009 (0.006, 0.016)**	**0.022 (0.01, 0.04)**	**0.06 (0.004, 0.11)**	**-0.0003 (-0.011, 0.004)**	**-0.20 (-0.28, -0.12)**	**-0.08 (-0.16, -0.01)**	**0**	**67**
5.00 (2.74, 10.44)	0.010 (0.006, 0.016)	0.024 (0.01, 0.04)	-	-0.002 (-0.012, 0.004)	-0.18 (-0.26, -0.11)	-0.08 (-0.16, 0.00)	2	67
2.74 (2.29, 3.36)	0.010 (0.007, 0.017)	0.023 (0.01, 0.04)	-	-0.001 (-0.011, 0.004)	-0.20 (-0.28, -0.13)	-	5	67
2.67 (2.23, 3.36)	0.009 (0.006, 0.016)	0.022 (0.01, 0.03)	0.05 (0.00, 0.11)	-0.001 (-0.01, 0.004)	-0.23 (-0.31, -0.15)	-	6	67
5.11 (2.76, 10.37)	0.010 (0.006, 0.018)	-	0.08 (0.02, 0.14)	-0.001 (-0.011, 0.004)	-0.20 (-0.29, -0.13)	-0.08 (-0.15, 0.00)	9	67
4.62 (2.68, 9.97)	0.010 (0.007, 0.018)	-	-	0.00 (-0.011, 0.005)	-0.18 (-0.27, -0.11)	-0.08 (-0.15, 0.00)	11	67
2.77 (2.26, 3.39)	0.010 (0.006, 0.017)	-	0.07 (0.02, 0.13)	0.00 (-0.01, 0.005)	-0.24 (-0.31, -0.15)	-	12	67
2.79 (2.32, 3.48)	0.010 (0.007, 0.018)	-	-	0.00 (-0.009, 0.005)	-0.21 (-0.28, -0.14)	-	14	67
6.41 (3.92, 14.05)	0.009 (0.006, 0.015)	0.027 (0.01, 0.04)	-	-0.007 (-0.021, -0.001)	-	-0.13 (-0.21, -0.06)	23	68
6.31 (3.93, 14.17)	0.009 (0.006, 0.016)	-	0.05 (0.00, 0.11)	-0.006 (-0.027, -0.001)	-	-0.14 (-0.21, -0.06)	29	68
6.43 (3.74, 13.96)	0.009 (0.006, 0.016)	-	-	-0.006 (-0.024, 0.00)	-	-0.13 (-0.20, -0.05)	30	68
2.28 (1.93, 2.88)	0.008 (0.006, 0.015)	0.026 (0.01, 0.04)	-	-0.007 (-0.025, -0.001)	-	-	35	67
2.37 (1.90, 2.85)	0.009 (0.006, 0.014)	0.024 (0.01, 0.04)	0.02 (-0.04, 0.07)	-0.007 (-0.027, -0.001)	-	-	37	67
2.36 (1.94, 2.92)	0.009 (0.006, 0.016)	-	0.04 (-0.01, 0.10)	-0.008 (-0.029, -0.001)	-	-	39	68
2.38 (1.97, 2.98)	0.010 (0.006, 0.016)	-	-	-0.007 (-0.028, -0.001)	-	-	40	68
6.39 (3.57, 12.60)	0.008 (0.005, 0.015)	0.023 (0.01, 0.03)	0.03 (-0.03, 0.08)	-	-0.06 (-0.10, -0.01)	-0.13 (-0.20, -0.05)	60	67
6.02 (3.48, 12.52)	0.008 (0.006, 0.015)	0.024 (0.01, 0.04)	-	-	-0.04 (-0.09, 0.00)	-0.12 (-0.20, -0.05)	61	67
6.73 (3.88, 14.08)	0.008 (0.005, 0.014)	0.024 (0.01, 0.04)	-	-	-	-0.14 (-0.21, -0.07)	66	67
7.00 (3.95, 14.51)	0.008 (0.005, 0.015)	0.024 (0.01, 0.04)	0.01 (-0.04, 0.07)	-	-	-0.15 (-0.22, -0.07)	67	67
6.38 (3.44, 13.15)	0.009 (0.006, 0.016)	-	0.05 (-0.01, 0.10)	-	-0.05 (-0.10, -0.01)	-0.12 (-0.20, -0.05)	70	67

| Coefficient estimates for hierarchical Ricker model and covariates | | | | | | | LOOIC | |
α	β	H^{relCU}	H^{relOE}	H^{cSite}	P	T	ΔLOOIC	SE
2.27 (1.94, 2.82)	0.009 (0.005, 0.015)	0.023 (0.01, 0.03)	-	-	-0.07 (-0.11, -0.03)	-	71	66
5.75 (3.35, 12.96)	0.008 (0.006, 0.016)	-	-	-	-0.05 (-0.09, 0.00)	-0.11 (-0.19, -0.04)	72	67
2.31 (1.92, 2.83)	0.008 (0.005, 0.015)	0.023 (0.01, 0.03)	0.02 (-0.04, 0.07)	-	-0.07 (-0.11, -0.03)	-	73	66
6.95 (3.81, 14.01)	0.009 (0.006, 0.015)	-	-	-	-	-0.14 (-0.21, -0.07)	74	67
6.42 (4.01, 14.31)	0.009 (0.006, 0.015)	-	0.04 (-0.02, 0.09)	-	-	-0.15 (-0.22, -0.07)	77	67
2.41 (1.96, 2.87)	0.009 (0.005, 0.015)	-	0.03 (-0.01, 0.09)	-	-0.07 (-0.11, -0.03)	-	83	66
2.17 (1.81, 2.62)	0.008 (0.006, 0.014)	0.022 (0.01, 0.03)	-	-	-	-	84	67
2.17 (1.83, 2.65)	0.009 (0.005, 0.014)	0.023 (0.01, 0.03)	-0.01 (-0.05, 0.05)	-	-	-	85	67
2.22 (1.88, 2.71)	**0.009 (0.006, 0.015)**	-	-	-	-	-	**91**	**67**

Table CM.3. Percent change in posterior mode recruits-per-spawner (RPS) for the full Chum model for a 1SD increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 1SD increase for each covariate.

Region	Population	Percent change in RPS for 1SD increase in covariates				
		$\bar{H}_i^{relCU} + 1SD$	$\bar{H}_i^{relOE} + 1SD$	$\bar{H}_i^{cSite} + 1SD$	$\bar{P}_i + 1SD$	$\bar{T}_i + 1SD$
HG	EAST HG	6.7%	2.6%	-16.9%	-18.2%	-4.8%
	SKIDEGATE	0.0%	2.6%	-13.6%	-18.2%	-4.8%
	WEST HAIDA GWAII	0.0%	2.6%	-0.2%	-18.0%	-4.8%
	NORTH HAIDA GWAII		2.6%		-16.9%	-4.8%
	NORTH HAIDA GWAII-STANLEY CREEK		2.7%		-17.3%	-4.9%
NC	LOWER NASS		1.1%		-7.3%	-5.3%
	PORTLAND CANAL-OBSERVATORY	0.0%	1.3%	-0.7%	-7.0%	-4.7%
	SKEENA ESTUARY		1.0%	0.0%	-6.6%	-5.2%
	LOWER SKEENA	0.2%	1.3%	-2.5%	-7.0%	-4.9%
	MIDDLE SKEENA		1.3%		-7.0%	-5.1%
	HECATE LOWLANDS	0.3%	1.3%	-8.9%	-7.0%	-4.9%
	DOUGLAS-GARDNER	1.6%	1.3%	-3.8%	-7.0%	-4.9%
	PORTLAND INLET		1.3%		-6.9%	-4.8%
CC	SMITH INLET		1.1%		-6.3%	-5.0%
	SPILLER-FITZ HUGH-BURKE	0.2%	1.1%	-9.7%	-6.4%	-5.0%
	BELLA COOLA-DEAN RIVERS	1.0%	1.1%	3.1%	-6.4%	-5.0%
	BELLA COOLA RIVER-LATE	155.0%	1.5%	-0.6%	-0.4%	-5.3%
	MUSSEL-KYNOCH		1.1%		-6.4%	-5.0%
	RIVERS INLET		1.1%		-6.1%	-5.1%
WCVI	NORTHWEST VANCOUVER ISLAND	0.3%	10.7%	17.6%	-13.7%	-5.0%
	SOUTHWEST VANCOUVER ISLAND	5.0%	10.7%	-8.9%	-13.7%	-5.0%
QCSDPASS	NORTHEAST VANCOUVER ISLAND	14.0%	8.1%	7.3%	-15.9%	-5.1%
	LOUGHBOROUGH	0.2%	8.1%	-0.8%	-15.9%	-5.1%
	BUTE INLET	0.1%	1.5%	0.0%	-11.1%	-5.2%
	SOUTHERN COASTAL STREAMS	2.3%	8.0%	-0.7%	-15.7%	-5.1%
	UPPER KNIGHT				-6.1%	-4.8%
SOG	HOWE SOUND-BURRARD INLET	0.1%	11.3%	172.6%	-51.2%	-5.1%
	GEORGIA STRAIT	6.9%	11.3%	118.6%	-51.2%	-5.1%
	MEAN ALL POPULATIONS	**17.4%**	**3.4%**	**14.9%**	**-13.1%**	**-5.0%**
	MEDIAN ALL POPULATIONS	**3.2%**	**6.4%**	**-8.9%**	**-18.5%**	**-5.0%**
	MEAN NC	**0.6%**	**1.2%**	**-3.3%**	**-7.0%**	**-4.9%**
	MEAN HG	**2.5%**	**2.6%**	**-10.7%**	**-17.8%**	**-4.8%**
	MEAN CC	**67.6%**	**1.2%**	**-1.7%**	**-4.8%**	**-5.1%**
	MEAN QCSDPASS	**4.0%**	**6.1%**	**1.4%**	**-13.4%**	**-5.1%**
	MEAN WCVI	**2.8%**	**10.7%**	**3.8%**	**-13.7%**	**-5.0%**
	MEAN SOG	**3.5%**	**11.3%**	**145.8%**	**-51.2%**	**-5.1%**

Table CM.3. Percent change in posterior mode recruits-per-spawner (RPS) for the full Chum model for a 10% increase in covariates. For each population the RPS is calculated with mean values for all covariates and the change in RPS from a 10% increase for each covariate.

| Region	Population	Percent change in RPS for 1SD increase in covariates				
		$\bar{H}_i^{relCU} + 10\%$	$\bar{H}_i^{relOE} + 10\%$	$\bar{H}_i^{cSite} + 10\%$	$\bar{P}_i + 10\%$	$\bar{T}_i + 10\%$
HG	EAST HG	0.2%	0.2%	-1.7%	-2.8%	-6.1%
	SKIDEGATE	<0.1%	0.2%	-1.2%	-2.8%	-6.1%
	WEST HAIDA GWAII	<0.1%	0.2%	<0.1%	-2.7%	-6.0%
	NORTH HAIDA GWAII		0.2%		-2.5%	-6.0%
	NORTH HAIDA GWAII-STANLEY CREEK		0.2%		-2.4%	-5.9%
NC	LOWER NASS		0.1%		-1.0%	-6.1%
	PORTLAND CANAL-OBSERVATORY	<0.1%	0.1%	<0.1%	-1.1%	-6.0%
	SKEENA ESTUARY		0.1%	<0.1%	-1.0%	-6.2%
	LOWER SKEENA	<0.1%	0.1%	-0.2%	-1.1%	-6.1%
	MIDDLE SKEENA		0.1%		-1.0%	-6.1%
	HECATE LOWLANDS	<0.1%	0.1%	-0.7%	-1.1%	-6.4%
	DOUGLAS-GARDNER	0.1%	0.1%	-0.3%	-1.1%	-6.4%
	PORTLAND INLET		0.1%		-1.1%	-6.0%
CC	SMITH INLET		0.1%		-0.9%	-6.9%
	SPILLER-FITZ HUGH-BURKE	<0.1%	0.1%	-0.9%	-0.9%	-6.6%
	BELLA COOLA-DEAN RIVERS	0.1%	0.1%	0.3%	-0.9%	-6.9%
	BELLA COOLA RIVER-LATE	5.6%	0.2%	-0.5%	-1.9%	-6.9%
	MUSSEL-KYNOCH		0.1%		-0.9%	-6.6%
	RIVERS INLET		0.1%		-0.9%	-6.9%
WCVI	NORTHWEST VANCOUVER ISLAND	<0.1%	0.8%	1.5%	-2.1%	-7.0%
	SOUTHWEST VANCOUVER ISLAND	0.4%	0.8%	-0.8%	-2.0%	-7.4%
QCSDPASS	NORTHEAST VANCOUVER ISLAND	0.3%	0.2%	0.6%	-2.4%	-7.2%
	LOUGHBOROUGH	<0.1%	0.2%	-0.1%	-2.4%	-7.3%
	BUTE INLET	<0.1%	0.1%	<0.1%	-1.6%	-7.5%
	SOUTHERN COASTAL STREAMS	<0.1%	0.2%	-0.1%	-2.3%	-7.1%
	UPPER KNIGHT				-1.1%	-7.1%
SOG	HOWE SOUND-BURRARD INLET	<0.1%	1.4%	7.8%	-9.7%	-7.6%
	GEORGIA STRAIT	0.9%	1.4%	7.1%	-9.7%	-7.6%
	MEAN ALL POPULATIONS	0.7%	0.3%	0.6%	-2.3%	-6.7%
	MEAN NC	<0.1%	0.1%	-0.3%	-1.1%	-6.2%
	MEAN HG	0.1%	0.2%	-1.0%	-2.7%	-6.0%
	MEAN CC	2.4%	0.1%	-0.3%	-1.2%	-6.8%
	MEAN QCSDPASS	0.1%	0.2%	0.1%	-2.0%	-7.3%
	MEAN WCVI	0.2%	0.8%	0.3%	-2.0%	-7.2%
	MEAN SOG	0.4%	1.4%	7.5%	-9.7%	-7.6%

Chum Figures
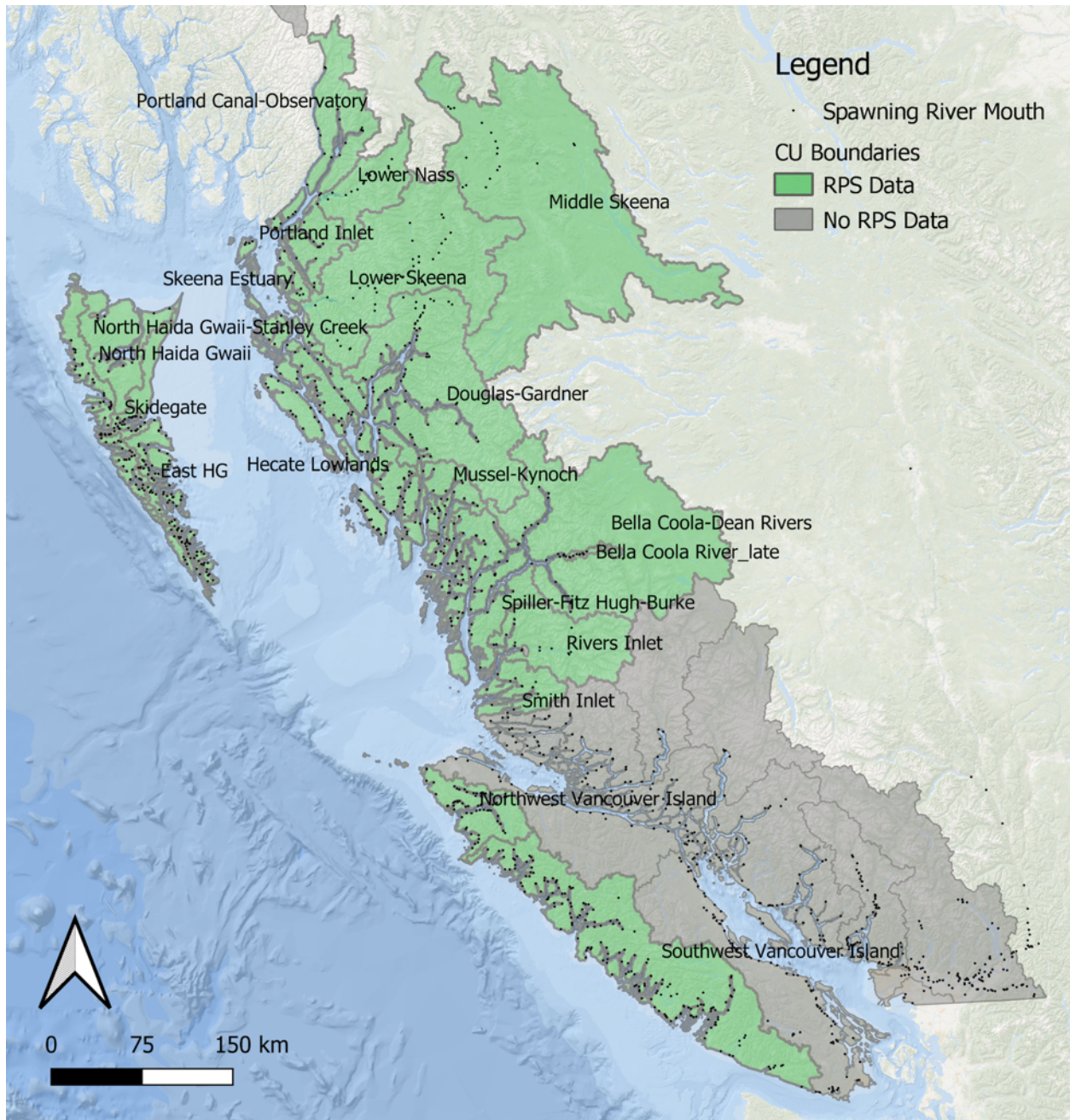
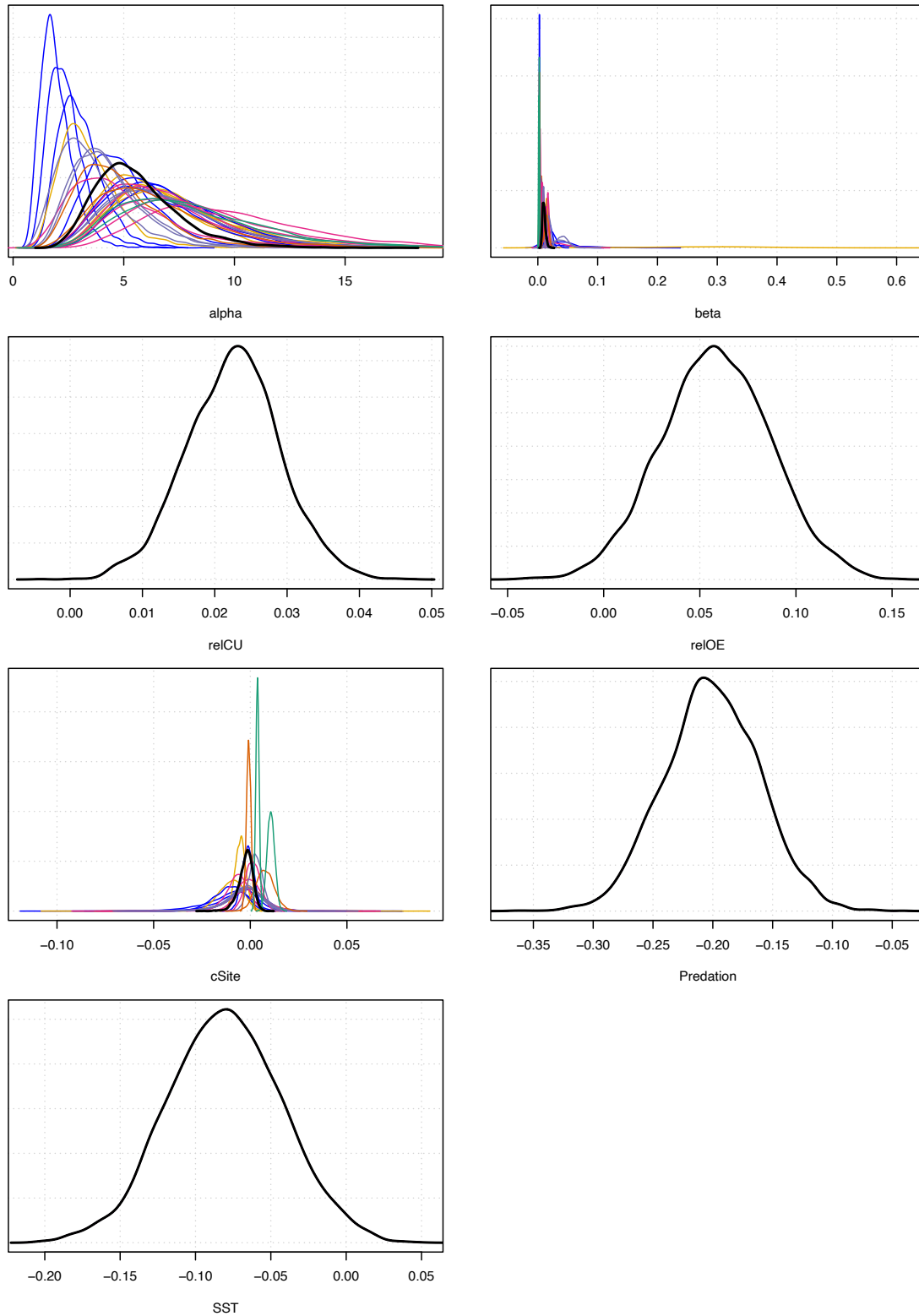Figure CM.1. Locations of Conservation Units with recruits per spawner (RPS) data for Chum models.

Figure CM.2. Posterior distribution of coefficient estimates for intrinsic productivity (α), density dependence (β), hatchery (H^{relCU}, H^{relOE}, H^{cSite}), predation, and sea surface temperature (SST) for full Chum model. Colors indicate different regions for Chum populations (NC= blue, HG=yellow, CC=pink, QCSDPASS=purple, WCVI=orange, SOG=green)
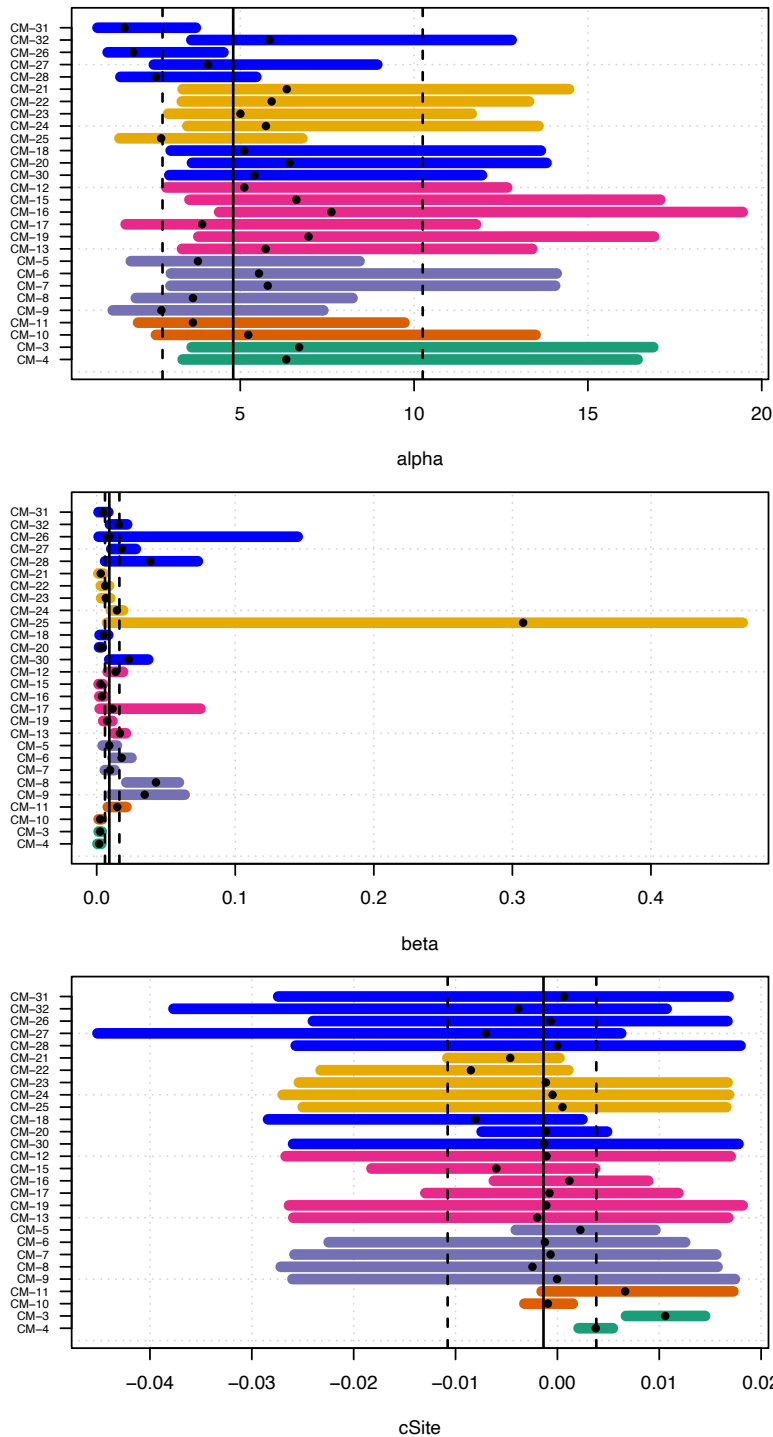
Fig CM.3. Coefficient estimates for α, β, cumulative hatchery release sites (H^{cSite}) for full Chum model. The circles indicate population specific mean posterior estimates along with 95% credible intervals, while the vertical lines indicate the mean posterior for the average effect across all populations (vertical solid black line) with 95% credible intervals (vertical dotted black lines). Colors indicate different regions for Chum populations (NC= blue, HG=yellow, CC=pink, QCSDPASS=purple, WCVI=orange, SOG=green)
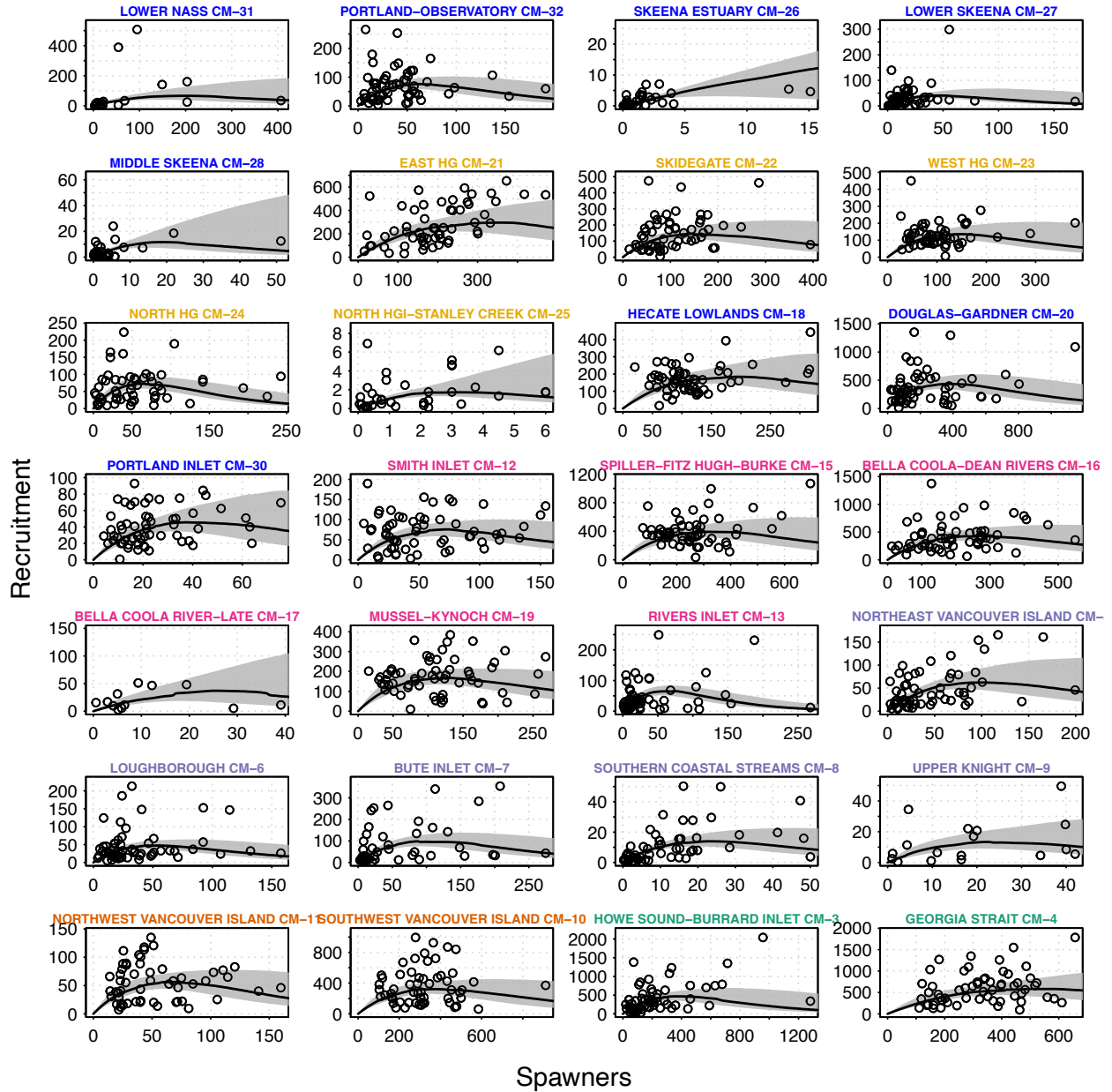
Fig CM.4. Median posterior (black line) and 95% credible intervals (shaded area) spawner-recruit curve from top Chum multi-population Ricker model with cumulative release sites and seal density covariate. Colors for population names indicate different regions for Chum populations (NC= blue, HG=yellow, CC=pink, QCSDPASS=purple, WCVI=orange, SOG=green).
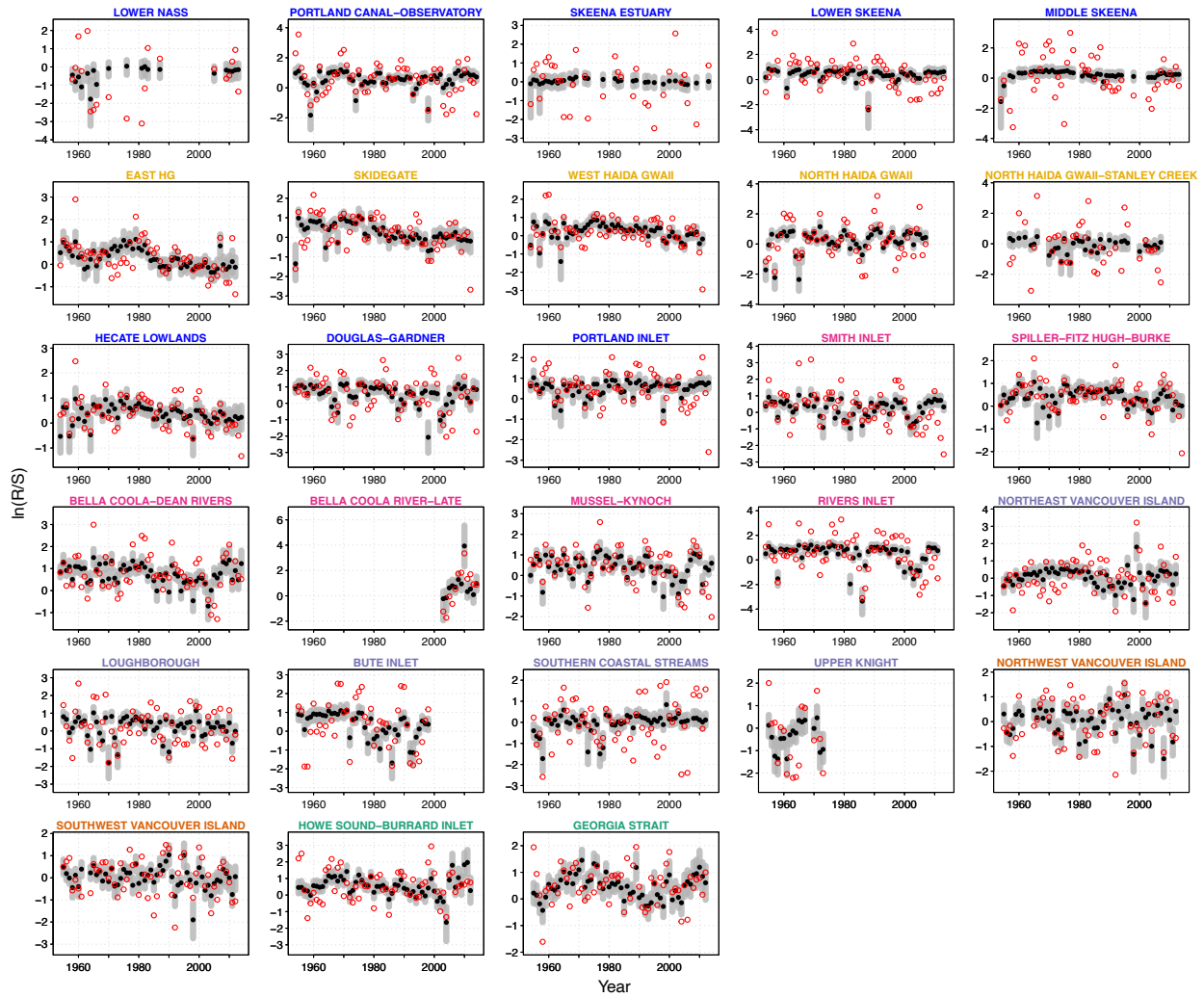
Figure CM.5. Log recruits-per-spawner observations (red circles) by brood year and median estimates (black dots) with 95% credible intervals (grey lines) from top Coho Model with cumulative hatchery release sites and seal density covariates.

Appendix HS – Harbour Seal population modelling

Regional Harbour Seal populations in BC were estimated via deterministic generalized logistic growth models of the form

(HS.1) $\quad N_{s,t+1} = N_{s,t} + r_s N_{s,t}\left(1 - \left(\frac{N_{s,t}}{K_s}\right)^{\theta_s}\right) - C_{s,t}$

where $N_{s,t}$ is the number of adult seals in year t for region s, $C_{s,t}$ is the annual number of seals killed in region s during year t, r is the intrinsic growth rate of the population, K is the population carrying capacity, and θ is the shape parameter that determines the biomass at maximum net productivity level (MNPL). Model notation and equations are provided in Table 1 and Table 2, respectively. A standard logistic model assumes that MNPL occurs at K/2, whereas the shape parameter on the generalized logistic model produces MNPL above K/2 when $\theta > 1$. For all populations, we could not estimate parameters assuming an unexploited state in 1950, so initial numbers were estimated as a scalar multiple κ of the carrying capacity K.

The generalised logistic model was specified in Template Model Builder (TMB, Kristensen et al. 2016), and leading model parameters r, K, θ, and κ were estimated via Hamiltonian Monte-Carlo using the tmbstan package (Monnahan and Kristensen 2018). Posterior log-density functions were the sum of log-likelihood functions for observational indices, and normal prior density functions for leading model parameters r, K, and θ. The initialization scalar κ was freely estimated.

Observational data for the likelihood function calculation were indices of abundance for surveys $g \in \{1,2\}$, modeled via a linear observation model

(HS.2) $\quad I_{t,g} = q_g B_t e^{\xi_{t,g}}$

where q_g is catchability and $\xi_{t,g}$ is a normally distributed random observation deviation in year t for survey index g, with observation deviation variance τ_g^2. Nuisance parameters q_g and τ_g^2 were derived from model residuals as conditional maximum likelihood estimates (E2.9-2.10), resulting in a concentrated data likelihood (E2.11).

Harbour Seal population models were fit from 1950-2014 and projected forward to 2020 for $s = 9$ regions: 7 in Strait of Georgia (Howe Sound, Gulf Islands, Southern Gulf, Northeast Gulf, Fraser River, Northwest Gulf, Boundary Bay), 1 in the Skeena, and 1 for the BC population outside the Strait of Georgia (Outside SOG). For each region, the model was fit to two indices of abundance: (1) a relative abundance index from 1950-1972 based on a backwards model extrapolation (similar to stock reduction analysis) used to reconstruct historical abundance for all of BC ($g = $1, Fig. 2 in DFO 2010), and (2) an absolute region-specific abundance index from1966-2014 provided from DFO survey data ($g = $2, S. Tucker, DFO, pers. comm). Abundance indices were equally weighted for SOG regions ($w_{t,g} = $ 1), while the coastwide historical abundance index ($g = $1) was down-weighted to 50% for Outside SOG ($w_{t,1} = $ 2, $w_{t,2} = 1$) and 30% for Skeena ($w_{t,1} = 3, w_{t,2} = 1$) to allow estimation of θ shape parameter.

Annual removals of Harbour Seals were based on historical data for seal pelts processed, bounties paid for seal pelts, and predator control records (Olesiuk 2009) as

(HS.3) $C_t = \frac{(B_t + P_t)}{R} + D_t + P_k \cdot D_t'$

where B_t is bounties paid for seal pelts, P_t is additional processed seal pelts, $R = 0.65$ is the recovery rate of carcasses, D_t and D_t' are, respectively, the confirmed and probable numbers of dead seals killed by Fisheries and Oceans predator control actions, and $P_k = 0.75$ is the assumed death rate of probable kills during predator control (Eq 13 and Table 7 in Olesiuk 2009). Coastwide catches for BC were subdivided among the Strait of Georgia (SOG) and Outside SOG areas according to the mean proportion of Harbour Seal abundance from 1976-2008 survey years (Figure 16, Olesiuk 2009), excluding years with missing data for one of the areas. SOG catches were then further

subdivided among the seven SOG and the Skeena survey subareas according to mean proportion of region-specific abundance estimates from the survey from 1988-2014 for SOG and 1977-2005 for Skeena.

For each SOG region s we set mean priors for K (μ^K) as mean abundance estimates from 1996-2014 with a 100% CV (i.e., $\sigma^K = \mu^K$), as survey data indicates regional populations approached carrying capacity during this period. For Skeena we use mean abundance from 1987-2005, since fits from Olesiuk 2009 indicate the population was at carrying capacity circa 1990. The outside SOG population uses a vague normal prior with 100% CV for K, with $\mu^K = \sigma^K = 60{,}000$, which is the 2008 coastwide abundance estimate for British Columbia (DFO 2010), chosen beacuse logistic models indicated populations in Strait of Georgia and outer BC were at or near carrying capacity, respectively (Olesiuk 2010). We use intrinsic rate of growth r prior hyperparameters $\mu^r = 0.13$ with $\sigma^r = 0.013$ for SOG areas and $\mu^r = 0.17$ with $\sigma^r = 0.051$ (representing an assumed 30% CV) for outside SOG and Skeena populations, based on average r estimates from Olesiuk (2010). Shape parameter prior hyperparameters of $\mu^\theta = 6.8$ were used for all population models (Olesiuk 2009) with $\sigma^\theta = 2$, which represents an assumed 30% CV.

Abundance for ocean entry regions outside SOG was estimated from the Outside SOG model based on the mean proportion of seals in each survey region from historical surveys from 1976-2008 (19% WCVI, 25% QCSJSDP, 11% CC, 23% NC, 22% HG). SOG abundance was calculated by summing population numbers from the 7 SOG areas modelled. For each ocean entry region we calculated time series of seal density by dividing by estimates of shoreline lengths for each region (3751 km in WCVI, 4786 km in QCSJSDP, 5259 km in CC, 7120 km in NC, 3170 km HG, unpublished data, C. Nordstrom, DFO). Model fits for subareas and Outside SOG are provided in Figs. HS.1-2.

Harbour Seal Tables

Table HS.1. Notation for the generalized logistic population dynamics model for Harbour Seals

Symbol	Description
	Indices and index ranges
T	Year in which stock assessment is performed
t	Year, where $t = t_1, \ldots, T$
g	Survey index where $g = 1, \ldots, G$
n_g	Number of non-missing observations for the index g
	Data
C_t	Catch numbers removed during year t
$I_{t,g}$	Stock relative or absolute abundance observation for year t and index g
$w_{t,g}$	scalar for observation error standard deviations for year t and gear g
	Leading model parameters
K	Carrying capacity
r	Intrinsic growth rate
θ	Shape parameter
κ	Initial population scalar
	Nuisance parameters
q_g	Catchability coefficient for abundance index g
τ	average observation error standard deviation
	State variables
N_t	Numbers at the beginning of year t
	Prior distributions
$N(\mu^r, \sigma^r)$	Normal prior on r
$N(\mu^K, \sigma^K)$	Normal prior on $\boldsymbol{K}$
$N(\mu^\theta, \sigma^\theta)$	Normal prior on θ
	Error distributions
$\xi_{t,g} \sim N(0, \tau^2)$	Observation error in year t for index g

Table HS.2. Generalized logistic population dynamics model for Harbour Seals

|	
Model parameters	
E2.1	$$\Phi = (K', r', \theta', \log \kappa)$$
Parameter transformations	
E2.2	$$K = \exp(K')$$
E2.3	$r = \exp(r')$
E2.4	$\theta = \exp(\theta')$
E2.5	$$\kappa = exp(log\,\kappa)$$
Population dynamics model	
E2.6	$$N_{t_1} = \kappa \cdot K$$ $$N_{t+1} = N_t + rN_t\left(1 - \left(\frac{N_t}{K}\right)^{\theta}\right) - C_t, \quad t > t_1$$
Observation model Residuals	
E2.7	$\xi_{t,g} = \ln(I_{t,g}/N_t)$
Conditional maximum likelihood estimates	
E2.8	$$n_g = \sum_{t=t_1}^{T} \mathbb{1}\left(I_{t,g} > 0\right)$$
E2.9	$$\widehat{\ln q_g} = \frac{1}{n_g} \sum_{t=t_1}^{T} \mathbb{1}\left(I_{t,g} > 0\right) \cdot \xi_{t,g}$$
E2.10	$$\widehat{\tau_g^2} = \frac{1}{n_g} \sum_{t=t_1}^{T} \mathbb{1}\left(I_{t,g} > 0\right) \left(\frac{\xi_{t,g} - \widehat{\ln q_g}}{w_{t,g}}\right)^2$$
Negative log-likelihood and objective function	
E2.9	$$l(\Phi|I_{t,g}) = \frac{\sum n_g}{2} \ln \tau^2$$
E2.10	$$G(\Phi|I_{t,g}) \propto l(\Phi|I_{t,g}) + \frac{1}{2(\sigma^K)^2}(K - \mu^K) + \frac{1}{2(\sigma^r)^2}(r - \mu^r) + \frac{1}{2(\sigma^\theta)^2}(\theta - \mu^\theta)$$
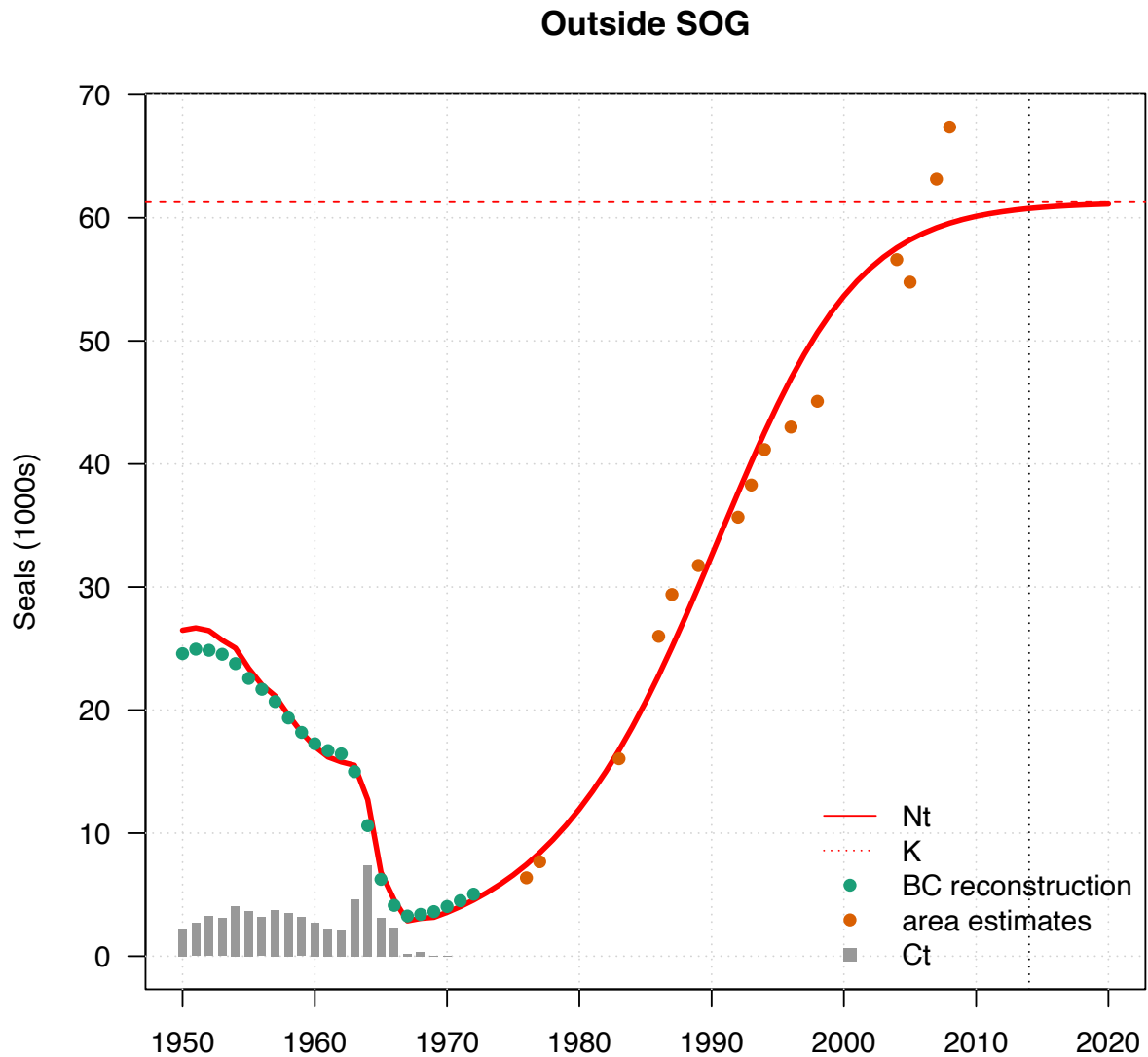
Outside SOG

Figure HS.1. Harbour Seal abundance MLE (red lines) in areas outside Strait of Georgia (SOG) from 1950 until 2014 (vertical dashed line), projected until 2020. Points show the abundance indices as described in the figure legend and text, while grey bars at the bottom of the plot show removals.
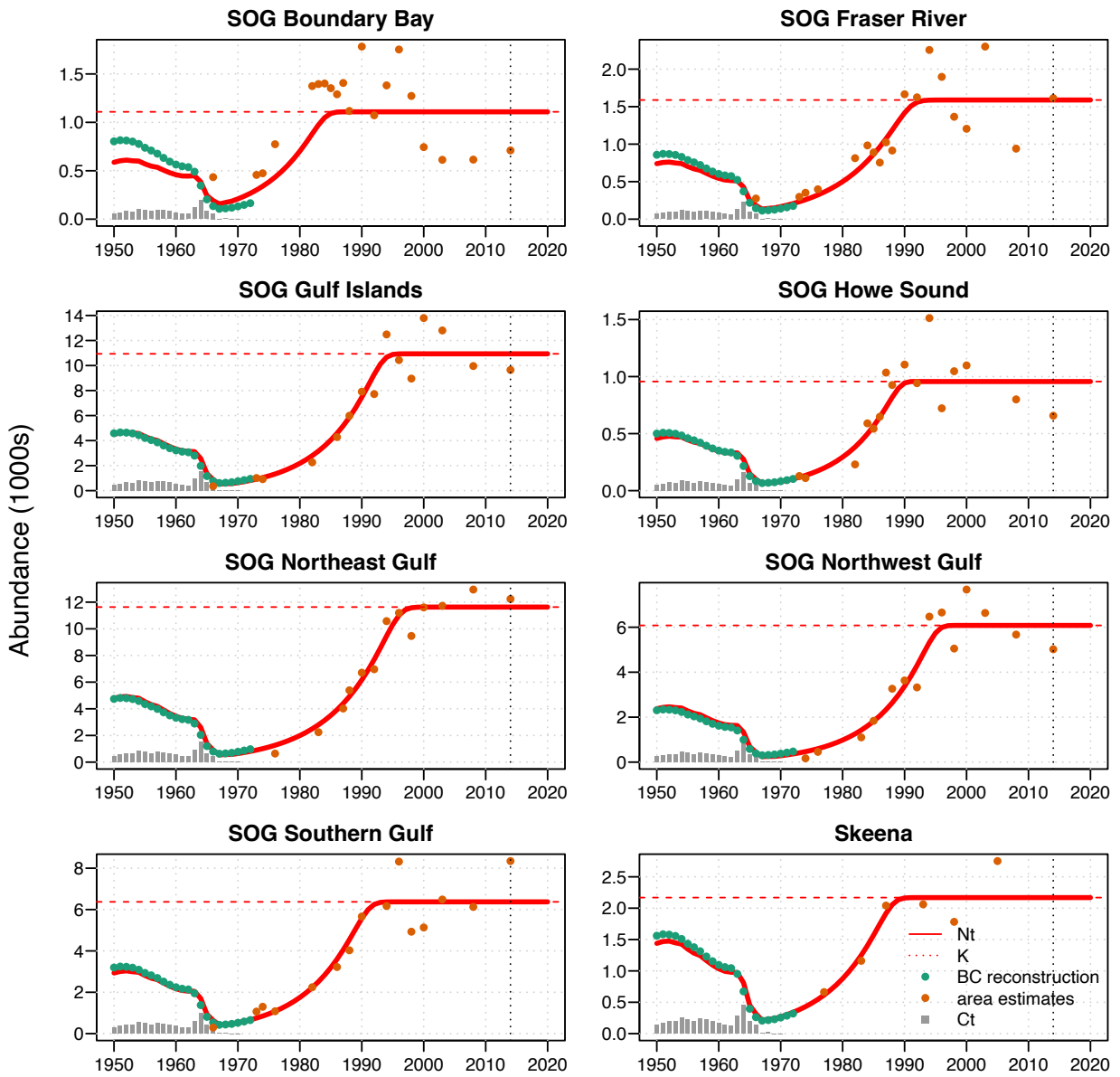
Figure HS.2. Harbour Seal abundance MLE (red lines) for 7 subareas in Strait of Georgia (SOG) and the Skeena from 1950 until 2014 (vertical dashed lines), projected until 2020. Points show the abundance indices as described in the figure legend and text, while grey bars at the bottom of the plot show removals.

Appendix SR

This section summarizes the data, methods, and potential for bias in estimates of catch, escapement, and recruits per spawner (RPS) for Chinook, Coho, and Chum populations included in Ricker models (Tables SR.1-SR.3). The variation and bias in catch or escapement numbers varies by area depending on methods and data availability, while bias in recruits-per-spawner depends on the levels (and sources) of bias in catch and escapement records. Recruits-per-spawner is calculated as:

$$RPS_t = \frac{R_t}{S_t} = \frac{C_R + S_R}{S_t}$$

where RPS is recruits-per-spawner from brood year t and S_t is the spawner escapement in brood year t. R_t is total adult returns from brood year t, which are the sum of spawner escapement S_R and catch C_R of adult returns across multiple years from the same brood year t.

For most populations (Tables SR.1-SR.3) catch estimates, or significant portions thereof, are derived from escapement numbers and estimated exploitation rates from indicator stocks, e.g.:

$$S_R = \sum_{a=A^{Min}}^{A^{Max}} S_{t+a,a}$$

$$R_t = \sum_{a=A^{Min}}^{A^{Max}} \frac{S_{t+a,a}}{1 - U_{t+a}}$$

Where $S_{t+a,a}$ is the number of spawners from each return year t+a, U_{t+a} is the exploitation rate for each year, and A^{Min} and A^{Max} represent the range of age-at-maturity for each species. In this case, any bias in spawner estimates will also be reflected in catch estimates and, therefore, total adult returns, which will cancel out when dividing returns by spawners to calculate RPS.

If all or a portion of catch is estimated by other methods (e.g., genetic sampling to apportion marine catch, in-river catch monitoring) than catch estimates may have no bias or less bias than escapement, in which case RPS would be negatively biased (i.e., underestimated). To evaluate potential bias in RPS in such instances, we simulated estimates of RPS across multiple scenarios varying harvest rates, total spawner abundance, and bias in escapement, assuming catch records were unbiased (Figure SR.1). Simulation results showed that negative bias increased for larger harvest rates, larger escapement bias (i.e., differences between catch and escapement bias), and lower spawner abundance. A negative bias in RPS, caused by increased hatchery returns on spawning grounds in turn biasing escapement estimates, could generate a perceived negative effect of hatchery activity on productivity, or if there is a negative effect from hatchery activity it could overestimated. Based on our review of data and methods for generating RPS datasets (Tables SR.1-SR.3), we identified potential for negative bias in RPS estimates for Chinook populations from Nass, Skeena, and Central Coast, and Chum populations for Inner South Coast and Strait of Georgia.

Table SR.1. Summary of data sources (indicated by footnotes), methods, and potential for bias for spawner-recruit data for BC Chinook populations. The Strait of Georgia and Fraser River Chinook data are for specific stocks, whereas all other data are for Conservation Units (CUs). For more details on data sources refer to PSF 2021. Abbreviations are: ER=exploitation rates, NCC= North and Central Coast, CWT= Coded Wire Tag, CU= Conservation Unit.

Regions	CU/Stock Name	Method		Potential for Bias		
		Escapement	Catch	Escapement	Catch	RPS
Nass	PORTLAND SOUND-OBSERVATORY INLET-LOWER NASS [1,2]	Run reconstructions from NCC database[1]. Expansion factors are used to i) infill indicator streams not monitored in a given year based on historical proportion of spawners in CU, ii) expand data from monitored streams to non-monitored streams in CU, and iii) adjust for observer efficiency[12]	In-river catch monitoring and estimates for marine fisheries provided by Nisga'a Joint Technical Committee (NJTC)	Potential to overestimate escapement by counting straying hatchery fish on spawning grounds in CUs. This is less likely for CUs without hatchery releases of Chinook (Upper Nass, Ecstall, NCC - late timing, Docee, and Dean River), although hatchery fish could stray from nearby CUs.	Potential to overestimate wild harvest for portion of catch generated via ERs and escapement estimates, since escapement can include some hatchery returns. This is less likely for CUs without hatchery releases of Chinook (Upper Nass, Ecstall, NCC - late timing, Docee, and Dean River).	Potential for negative bias in RPS because returns (catch + escapement) may have less bias than spawners (escapement). Both escapement numbers and catch may be overestimated due to counting hatchery fish on spawning grounds; however less so for catch when only a portion is derived from ER-based estimates.
	UPPER NASS [1,2]					
Skeena	ECSTALL [1,2]		Harvest estimated via i) ERs derived from CWT recovery data for Kitsumkalum River indicator stock[11], ii) creel surveys for terminal fisheries for commercial gillnet, sport and First Nations catch[11], and iii) assumptions to fill in data for missing years using average ratios of catch to escapement for years with data[1]			
	LOWER SKEENA [1,2]					
	KALUM-EARLY TIMING [1,2]					
	KALUM-LATE TIMING [1,2]					
	MIDDLE SKEENA-LARGE LAKES [1,2]					
	MIDDLE SKEENA-MAINSTEM TRIBUTARIES [1,2]					
	UPPER BULKLEY RIVER [1,2]					
Central Coast	NORTH & CENTRAL COAST-LATE TIMING [1,2]		Harvest estimated via i) expansion of CWT return data, ii) ERs derived from CWT recovery data for Canadian and Alaskan fisheries, iii) assumptions about First Nations and commercial catch as a proportion of total escapement, iv) assumptions to fill in data for missing years using average ERs or ratios of catch to escapement for years with data.			
	NORTH & CENTRAL COAST-EARLY TIMING [1,2]					
	DOCEE [1,2]					
	BELLA COOLA-BENTINCK [1,2]					
	DEAN RIVER [1,2]					
	RIVERS INLET [1,2]					
	WANNOCK [1,2]					
Strait of Georgia	QUINSAM RIVER [3,4,8,10]	Spawning ground counts	Estimated via stock-specific annual exploitation rates	Potential to overestimate escapement by	Same bias as escapement since catch is derived	Low potential for bias in RPS, since any bias in escapement would
	COWICHAN RIVER [3,4,5,10]					

			estimated from CWT data for indicator stocks	counting hatchery fish on spawning grounds	from ERs and escapement numbers	also be included in the catch.
	PUNTLEDGE RIVER – FALL [2,3,4,6,10]					
	NANAIMO RIVER – FALL [3,4,7,10]					
	QUALICUM RIVER [2,3,4,9,10]					
Fraser	HARRISON RIVER [2,3,4,9,10]					
	SHUSWAP RIVER [2,3,4,9,10]					
	CHILLIWACK RIVER – FALL [2,3,4,9,10]					

Sources: 1. English et al. 2016; 2. NuSEDS Database (www.npafc.org); 3. PSC (2015*a*, 2015*b*); 4. PSC (2016); 5. Tompkins et al. (2005); 6. Trites et al. 1996; 7. Lam and Carter (2010); 8. Bennett et al. (2010); 9. NMFS (1997); 10. Nelson et al. 2019; 11. PSC 2016; 12. PSF 2021

Table SR.2. Summary of data sources (indicated by footnotes), methods, and potential for bias for spawner-recruit data for Coho Conservation Units. For more details on data sources refer to PSF 2021. Abbreviations are: ER=exploitation rates, NCC= North and Central Coast, CWT= Coded Wire Tag, CU= Conservation Unit.

Regions	CU Name	Methods		Potential for bias		
		Escapement	Catch	Escapement	Catch	RPS
Haida Gwaii	HG-EAST [1,2]	Run reconstructions from NCC database[1]. Expansion factors are used to i) infill indicator streams not monitored in a given year based on historical proportion of spawners in CU, ii) expand data from monitored streams to non-monitored streams in CU, and iii) adjust for observer efficiency[5]	Estimated via stock-specific annual ERs estimated from CWT data for Coho indicator stocks (Deena River, Toboggan Creek, Zolzap Creek) and estimates for Babine River Coho[6]. Assumptions to fill in data for missing years use i) average ERs for years with data, ii) ERs from nearby areas, iii) 20-60% of ER estimates from Babine/Area 4 Coho, iv) historical ratios of Canadian ERs to Alaskan ERs to estimate Alaskan ER.	Potential to overestimate escapement by counting hatchery fish on spawning grounds	Same bias as escapement since catch is derived from ERs and escapement numbers	Low potential for bias in RPS, since any bias in escapement would also be included in the catch.
	HG-WEST[1,2]					
	HG-GRAHAM ISLAND LOWLANDS[1,2]					
Nass	LOWER NASS[1,2]					
	UPPER NASS[1,2]					
	PORTLAND SOUND-OBSERVATORY INLET-PORTLAND CANAL[1,2]					
Skeena	SKEENA ESTUARY[1,2]					
	LOWER SKEENA[1,2]					
	MIDDLE SKEENA[1,2]					
	UPPER SKEENA[1,2]					
	HECATE STRAIT MAINLAND[1,2]					
	DOUGLAS CHANNEL-KITIMAT ARM[1,2]					
	NORTHERN COASTAL STREAMS[1,2]					
Central Coast	BRIM-WAHOO[1,2]					
	SMITH INLET[1,2]					
	BELLA COOLA-DEAN RIVERS[1,2]					
	MUSSEL-KYNOCH[1,2]					
	RIVERS INLET[1,2]					
Strait of Georgia	INTERIOR FRASER[3]	Majority of escapement estimates	Catch estimates are derived using i)	Potential to overestimate	Similar bias to escapement from	Low potential for bias in RPS for 1975-1996
	FRASER CANYON[3]					

| LOWER THOMPSON[3] | are from visual surveys of spawning grounds, while some streams use fence counts and mark-recapture. Assumptions are used to estimate escapements for some streams in years when they were not surveyed. Not all spawning streams are surveyed and included in escapement estimates. Attempts are made to remove hatchery fish counts from wild escapements numbers.[4] | assumed ER of 68% (1975-1985), ii) ERs from CWT data (1986-1996), iii) genetic sampling to estimate stock-specific catch for different fisheries and areas (1998-2000), and iv) model-based estimates of ERs (2001-2012)[4]. | escapement by counting hatchery fish on spawning grounds. Attempts are made to adjust escapements for any hatchery fish, but the proportion of hatchery fish in wild escapement is likely underestimated[3].Only 2% of fry and 23% of smolts released by hatcheries since 1998 were marked with removal of adipose fins[4].

Potential to underestimate escapement based on spawning streams that are not surveyed[3]. | 1975-1996 and 2001-2012 since catch is derived from ERs and escapement numbers.

Low bias in catch from 1998-2000 when it was estimated via genetic sampling for stock identification of fisheries catch. | and 2001-2012, since any bias in escapement would also be included in the catch.

Potential for bias in RPS for 1998-2000 because returns (catch +escapement) may have different levels of bias than spawners (escapement). Escapement numbers may be overestimated or underestimated, while catch should not be. |
| SOUTH THOMPSON[3] | | | | | |
| NORTH THOMPSON[3] | | | | | |

Sources: 1. English et al. 2016; 2. NuSEDS Database (www.npafc.org); 3. Korman et al. 2019; 4. Decker et al. 2014; 5. PSF 2021; 6. Holtby 1999

Table SR.3. Summary of data sources (indicated by footnotes), methods, and potential for bias for spawner-recruit data for Chum Conservation Units. For more details on data sources refer to PSF 2021. Abbreviations are: ER=exploitation rates, NCC= North and Central Coast, CWT= Coded Wire Tag, CU= Conservation Unit.

Regions	CU Name	Methods		Potential for bias		
		Escapement	Catch	Escapement	Catch	RPS
Haida Gwaii	EAST HG[1,2]	Run reconstructions from NCC database[1]. Expansion factors are used to i) infill indicator streams not monitored in a given year based on historical proportion of spawners in CU, ii) expand data from monitored streams to non-monitored streams in CU, and iii) adjust for observer efficiency[5].	Estimated via stock-specific annual ERs estimated from CWT data for indicator stocks. Assumed Alaskan ERs were zero	Potential to overestimate escapement by counting hatchery fish on spawning grounds	Same bias as escapement since catch is derived from ERs and escapement numbers	Low potential for bias in RPS, since any bias in escapement would also be included in the catch.
	SKIDEGATE[1,2]					
	WEST HAIDA GWAII[1,2]					
	NORTH HAIDA GWAII[1,2]					
	NORTH HAIDA GWAII-STANLEY CREEK[1,2]					
Nass	LOWER NASS[1,2]		No direct measures of Chum harvest rates. Estimated via ERs for pink stocks prior to 1982 and weekly ERs for area 3-5 Sockeye stocks with a Chum run-timing model. Assumed Alaskan ERs were equal to Alaskan ERs for Pink Salmon.			
	PORTLAND CANAL-OBSERVATORY[1,2]					
Skeena	SKEENA ESTUARY[1,2]					
	LOWER SKEENA[1,2]					
	MIDDLE SKEENA[1,2]					
Central Coast	HECATE LOWLANDS[1,2]		Estimated via stock-specific annual ERs estimated from CWT data for indicator stocks. Assumed Alaskan ERs were zero			
	DOUGLAS-GARDNER[1,2]					
	PORTLAND INLET[1,2]					
	SMITH INLET[1,2]					
	SPILLER-FITZ HUGH-BURKE[1,2]					
	BELLA COOLA-DEAN RIVERS[1,2]					
	BELLA COOLA RIVER-LATE[1,2]					
	MUSSEL-KYNOCH[1,2]					
	RIVERS INLET[1,2]					

WCVI	NORTHWEST VANCOUVER ISLAND[3]	Method for generating escapement time series unclear. Data excludes hatchery returns	Estimated via stock-specific annual ERs estimated from CWT data for indicator stocks.			
	SOUTHWEST VANCOUVER ISLAND[3]					
Inner South Coast	NORTHEAST VANCOUVER ISLAND[2,4]	Reconstructed escapement time series based on annual spawner surveys. Observed escapements from surveys are expanded to account for non-monitored streams in CU in each year.	Genetic Stock Identification (GSI) from tissue samples from mixed fisheries catch are used to estimate stock-specific catch for different fisheries and weekly periods. The average stock compositions are used to apportion catch for years that were not samples (1953-1982)	Potential to overestimate escapement by counting straying hatchery fish on spawning grounds in CUs. This is less likely for CUs with no or few hatchery releases of Chum (Bute Inlet, Southern Coastal Streams, Upper Knight), although hatchery fish could stray from nearby CUs.	Low, since catch is estimated via genetic sampling for stock identification of fisheries catch and not using escapement	Potential for negative bias in RPS because returns (catch + escapement) have less bias than spawners (escapement). Escapement numbers may be overestimated, while catch should not be.
	LOUGHBOROUGH[2,4]					
	BUTE INLET[2,4]					
	SOUTHERN COASTAL STREAMS[2,4]					
	UPPER KNIGHT[2,4]					
	HOWE SOUND-BURRARD INLET[2,4]					
Strait of Georgia	GEORGIA STRAIT[2,4]					

Sources: 1. English et al. 2016; 2. NuSEDS Database (www.npafc.org); 3. Holt et al. 2018; 4. Inner South Coast Chum Stock Reconstructions (unpublished data, Pieter Van Will, DFO); 5. PSF 2021.
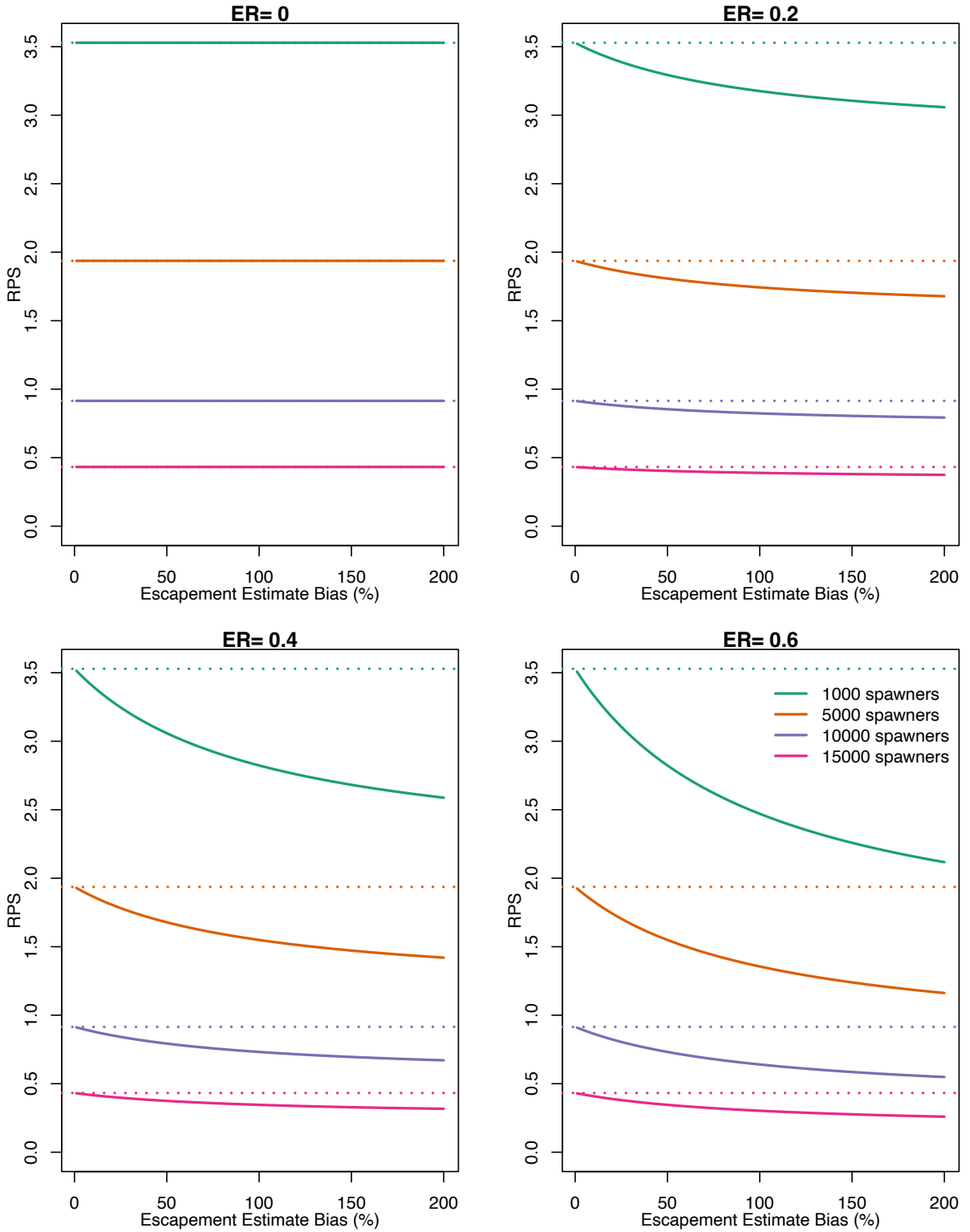
Figure SR.1. Simulated estimates (solid lines) and true values (dotted lines) for recruits-per-spawner (RPS) for data scenarios with no bias in catch estimates and varying levels of exploitation rates (ERs), spawner abundance, and bias in escapement estimates. The true RPS values are generated using a Ricker spawner-recruit relationship with mean values from the 24-population Chinook model with no additional covariates (α =4.1, β =0.15).

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