NOAA Technical Memorandum NMFS-NWFSC-140

Using Integrated Population Models to Evaluate Fishery and Environmental Impacts on Pacific Salmon Viability

April 2018

U.S. DEPARTMENT OF COMMERCE
National Oceanic and Atmospheric Administration
National Marine Fisheries Service
Northwest Fisheries Science Center

Using Integrated Population Models to Evaluate Fishery and Environmental Impacts on Pacific Salmon Viability

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April 2018

Contents

Figures

Tables

Abstract

Age- or stage-structured population models, also known as life cycle models, are a mainstay of applied ecology and conservation, particularly in fisheries management. The data available to inform parameters in such models are, however, often limited and variable in quality. Ad-hoc, piecemeal approaches to parameter estimation can lead to biased inference about key processes, such as the strength of density dependence and the magnitude of environmental variability in recruitment. Recent statistical advances have facilitated a more rigorous, comprehensive approach to fitting life cycle models by combining all relevant data into a joint likelihood function. Such integrated population models (IPMs) have been widely applied in marine fisheries stock assessment, but are less familiar in salmonid management.

We developed a multipopulation IPM for Pacific salmon (*Oncorhynchus* spp.) that accounts for spatial and temporal variability in adult recruitment and age structure, the presence of hatchery-origin spawners, and observation error in abundance, age-composition, and hatchery-fraction data. The method is analogous to traditional spawner–recruit modeling based on brood-table reconstruction, but the model is fitted to the "raw" data and distinguishes between process and observation error.

We applied the model to 29 populations of spring/summer Chinook salmon in the Snake River and Upper Columbia River Evolutionarily Significant Units (ESUs), and used the estimated parameters and states to simulate the impact of fishery exploitation rate on future abundance and quasi-extinction risk. As expected, predicted abundance declined and quasi-extinction risk increased across a range of fixed harvest rates from 0–0.3. The slope of the decline in abundance, relative to population-specific carrying capacity, was inversely related to intrinsic productivity. Large-scale environmental fluctuations (e.g., ocean conditions and hydrosystem operations, represented by the shared process error) were at least as important as harvest in determining long-term population viability. If future environmental conditions are relatively poor, and especially if they are assumed to have undergone a persistent state shift at some point in the last 60 years, then quasi-extinction risks are dramatically elevated even in the absence of harvest. We see potential for the further development of IPMs (e.g., the inclusion of more detailed stage structure) and their application to salmon conservation problems throughout the Pacific Northwest.

Acknowledgments

Introduction

Managing at-risk species requires understanding the degree to which population dynamics are governed by density dependence versus other environmental drivers. In many cases, however, the data necessary to complete a comprehensive assessment are spatially and temporally limited, which creates unique challenges for identifying the underlying demographic causes of population declines. For example, errors in population censuses from incomplete surveys, when not appropriately modeled, may lead to underestimates of recruitment (Sanz-Aguilar et al. 2016) or overestimates of the strength of density dependence (Knape and de Valpine 2012). Similarly, imprecision in the estimated age composition of a population can bias the estimated strength of density dependence (Zabel and Levin 2002). In turn, any management decisions based on such models could be misguided, potentially hindering recovery of the population. Therefore, proper consideration of all sources of uncertainty in the data is necessary to design robust conservation strategies.

Life cycle models are commonly used to evaluate the potential response(s) of populations to various scenarios of future conditions. Traditionally, their development follows a two-step process, whereby: 1) population growth rates and demographic rates are informed by multiple data sources with separate likelihoods, and 2) the estimated parameters and data are then used as inputs into population projection models or stock assessments (Schaub and Abadi 2011, Maunder and Punt 2013). This approach suffers from several drawbacks. First, the available raw data are used inefficiently (i.e., information is lost when summarized to calculate demographic rates), which creates problems for determining the appropriate likelihood functions and evaluating model diagnostics. Second, there is no formal assessment of the variance and covariance within and among model parameters, which would require some form of joint likelihood based on all available data. Third, failure to acknowledge trade-offs among parameters—and the fact that any given type of data (e.g., age structure) may contain information on multiple aspects of population dynamics (e.g., recruitment and survival)—can lead to biased parameter estimates.

More recently, so-called integrated population models (IPMs) have been used to address these shortcomings. IPMs are based on a joint likelihood constructed from each of the individual data likelihoods, which ideally captures the full uncertainty in the data (Schaub and Abadi 2011, Maunder and Punt 2013) and improves the precision and accuracy of parameter estimates (Tavecchia et al. 2009, Johnson et al. 2010). IPMs are closely linked to state-space models (de Valpine and Hilborn 2005), which are hierarchical models consisting of a process model (a stochastic description of the true but unobservable population dynamics) and an observation model (a model of the noisy data, conditional on the true state of the population). Furthermore, if IPMs are set up in a hierarchical fashion to model multiple populations simultaneously, information "borrowed" from data-rich populations helps to improve the precision of parameter estimates in relatively data-poor ones (Punt et al. 2011, Jiao et al. 2011).

IPMs have been used in a variety of studies related to conservation of birds (Schaub et al. 2007, Oppel et al. 2014) and the management of exploited mammals (Tavecchia et al. 2009, Johnson et al. 2010) and marine fishes (Ianelli 2002, Punt et al. 2010), but they are less familiar in salmonid management and conservation. The IPM for Pacific salmon that we describe here shares some features with the models of Newman et al. (2006), Su and Peterman (2012), Fleischman et al. (2013), and Winship et al. (2014), but we expand upon previous analyses in two ways. First, we allow for the possibility that a spawning population might include hatchery-origin fish, treating their abundance as an unknown state to be estimated. Second, we extend the process model to represent an ensemble of populations with potentially correlated process errors, using a hierarchical framework.

In this report, we use this model to evaluate the effects of alternative assumptions about harvest mortality on the abundance and quasi-extinction risk of populations in the Snake River spring/summer and Upper Columbia River spring Chinook salmon Evolutionarily Significant Units (ESUs). These analyses were conducted at the request of the NMFS West Coast Region and are intended to be helpful for evaluating alternative management actions.

We took several steps to adapt and enhance our models for use in evaluating harvest actions. The models were already under development with an objective of being available to inform future Federal Columbia River Power System (FCRPS) evaluations. This modeling framework has recently been reviewed by the Independent Scientific Advisory Board.[1] For the purposes of this report, and given the relatively short time frame available for model development, the application presented here focuses solely on harvest mortality and does not include detailed components for directly assessing other factors such as tributary habitat actions, hatchery supplementation, or alternative hydropower actions. Development of those components will continue for future assessments in support of recovery planning and evaluation of tributary habitat strategies. In addition, the models are designed to assess only a hypothetical constant harvest mortality rate, and do not take into account abundance-based harvest control rules. With respect to these simplifications, our approach is similar to the analysis of "recovery exploitation rates" (RERs) that has previously been conducted for the Puget Sound and Lower Columbia River Chinook salmon ESUs (NMFS 2004, Ford et al. 2007).

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[1] https://www.nwcouncil.org/fw/isab/isab2017-1/

Methods

Traditional run reconstruction

The traditional approach to spawner–recruit analysis for salmonids begins by reconstructing the time series of recruits from annual observations of spawner abundance, age structure, hatchery fraction, and harvest rate (the "brood table"). The paired values of spawners and recruits are then used as independent and dependent variables, respectively, in a regression model to estimate the parameters representing the expected distribution of recruits for a given number of spawners. Specifically, recruits born in spawning year t are calculated as the sum of returning spawners in subsequent years weighted by age structure, expanded to include harvest, and discounted by the fraction of hatchery-origin spawners so only natural-origin recruits are counted:

$$R_t^{\mathrm{obs}} = \sum_a \frac{S_{t+a}^{\mathrm{obs}} q_{t+a,a}^{\mathrm{obs}} \left(1 - p_{\mathrm{HOS},t}^{\mathrm{obs}}\right)}{1 - F_{t,a}^{\mathrm{obs}}}.$$

Here, S_t^{obs} is spawner abundance in year t, $q_{t,a}^{\mathrm{obs}}$ is the proportion of spawners of age-a, $F_{t,a}^{\mathrm{obs}}$ is the (possibly age-specific) harvest rate, $p_{\mathrm{HOS},t}^{\mathrm{obs}}$ is the proportion of hatchery-origin spawners, and the summation is over all adult ages. The superscripts indicate that these are observed or measured quantities (i.e., data or sample statistics). The regression model is then

$$R_t^{\mathrm{obs}} = f(S_t^{\mathrm{obs}} \mid \boldsymbol{\theta}) e^{\varepsilon_t},$$

where f is the spawner–recruit function with parameter vector $\boldsymbol{\theta}$ and $\varepsilon_t \sim \mathrm{N}(0, \sigma^2)$ is a residual error.

Integrated population model

The traditional run-reconstruction regression approach treats the observed spawner abundance (the "independent variable") as a quantity that is known precisely. By conditioning the predicted recruitment on observed spawner abundance in each cohort, it implicitly assumes that the residual deviations are due to process error alone (Hilborn and Mangel 1997), yet it is not truly a process-error model because it does not account for the biological and mathematical dependence of S_t^{obs} on the "dependent variable," R_t^{obs}. This leads to the well known time-series and errors-in-variables biases (Ludwig and Walters 1981, Walters and Ludwig 1981), which can severely affect estimates of the spawner–recruit parameters and management reference points.

Furthermore, a single missing observation of any of the quantities in the brood table induces multiple missing recruitment estimates (equal to the number of adult age classes), and the regression framework simply omits these missing values. In particular, if $a_{\max}$ is the age of the oldest spawners, then the final $a_{\max} - 1$ years of recruits will be missing, because the complete

cohorts have not yet returned to spawn and be counted. As a result, short-term forecasts cannot be conditioned on the most recent (and perhaps most informative) observations. If, instead, missing observations of age structure are imputed using spatial or temporal averages, as is often done in Columbia River populations when age-frequency sample sizes are small or zero, then the recruitment from small spawning cohorts may be overestimated, biasing estimates of productivity and density dependence (Zabel and Levin 2002).

As an alternative approach, we develop an IPM to describe the complete life cycle (i.e., adult-to-adult) dynamics of one or more salmon populations. The process model begins with the spawner–recruit function,

$$R_t = f(S_t \mid \boldsymbol{\theta}) e^{\varepsilon_t},$$

but here the variables S_t and R_t represent the true, unknown state of the population, and $\varepsilon_t \sim N(0, \sigma^2)$ is interpreted as a process error deviation. In the application discussed below, we use the Beverton–Holt model:

$$R_t = \frac{\alpha S_t}{1 + \alpha S_t / R_{\max}} e^{\varepsilon_t}, \tag{1}$$

where α is intrinsic productivity and $R_{\max}$ is the asymptotic maximum recruitment. (Although we do not present model selection results here in the interest of space, previous analyses using this IPM framework found stronger support for the Beverton–Holt than the Ricker model for the data set described below.) The recruits from cohort t return to spawn in subsequent years, with the proportion of surviving adults returning at each age given by the cohort-specific vector $\mathbf{p}_t$. For example, in the case of Interior Columbia Basin spring/summer Chinook salmon, adults return at ages 3–5, so $\mathbf{p}_t = (p_{t,3}, p_{t,4}, p_{t,5})$. By parameterizing the recruit age distribution conditional on survival to adulthood, we avoid having to estimate or specify annual survival and maturation probabilities during ocean residence, which are not identifiable from the data typically available for wild populations. The vector of age proportions in each cohort is drawn from a multivariate logistic normal distribution (Aitchison 1982) with mean vector $\boldsymbol{\gamma}$ and covariance matrix $\boldsymbol{\Sigma}_\mathbf{p}$:

$$\mathrm{alr}(\mathbf{p}_t) \sim \mathrm{MVN}(\boldsymbol{\gamma}, \boldsymbol{\Sigma}_\mathbf{p}), \tag{2}$$

where the additive log ratio transformation is $\mathrm{alr}(\mathbf{p}_t) = \left(\log(p_{t,a_{\min}} / p_{t,a_{\max}}), \ldots, \log(p_{t,a_{\max}-1} / p_{t,a_{\max}})\right)$. The vector of log ratios is then easily transformed back to the simplex space of proportions. Note that the use of $a_{\max}$ as the reference age class is arbitrary; equivalent distributions on the simplex of proportions are obtained regardless of the choice of reference class (Aitchison 1982).

The number of natural-origin (or "wild") spawners in year t is then simply the sum over age classes of recruits minus losses to terminal fisheries (represented by the mortality rate, $F_{t,a}^{\mathrm{obs}}$) and any adults removed for hatchery broodstock (represented by the number taken, B_t):

$$S_t^{\mathrm{W}} = \left[\sum_a R_{t-a} p_{t-a,a} \left(1 - F_{t,a}^{\mathrm{obs}}\right)\right] - B_t. \tag{3}$$

We assume broodstock removals are measured without error, since these are typically small numbers of fish that are well documented. For simplicity, we assume $F_{t,a}^{\text{obs}}$ represents the true harvest rate, although in principle this assumption could be relaxed. The spawning population may also include hatchery-origin fish that are either deliberately or inadvertently allowed to reproduce naturally. We did not attempt to develop a process submodel describing life history trajectories of hatchery-born fish following their release as juveniles (i.e., survival to adulthood, age distribution, harvest mortality and broodstock removal, and natural dispersal or outplanting into natal or non-natal rivers). Instead we simply define $p_{\text{HOS},t}$, the proportion of hatchery-origin spawners in year t, as a parameter, so that

$$S_t^{\text{H}} = S_t^{\text{W}} p_{\text{HOS},t} / (1 - p_{\text{HOS},t}).$$

The total spawner abundance is then $S_t = S_t^{\text{W}} + S_t^{\text{H}}$.

We can extend the process model to describe the dynamics of an ensemble of populations by adopting a hierarchical framework (Clark 2005, Gelman et al. 2014). This entails two modifications to Equation 1. First, the Beverton–Holt parameters for each population i are assumed to follow a bivariate lognormal hyperdistribution, allowing them to be correlated:

$$\left(\log(\alpha_i), \log(R_{\text{max},i}) \right) \sim \text{MVN}\left(\boldsymbol{\mu}_{\alpha,R_{\text{max}}}, \boldsymbol{\Sigma}_{\alpha,R_{\text{max}}} \right).$$

Second, in addition to the population-specific recruitment process error ε_{it}, we include a process error term that is shared among all populations, representing common environmental drivers (e.g., ocean conditions or hydrosystem operations). These shared productivity anomalies $\boldsymbol{\phi}$ are modeled as an AR(1) process on the log scale,

$$\begin{aligned} \log(\phi_t) &= \mathbf{x}_t \boldsymbol{\beta} + v_t \\ v_t &\sim \text{N}\left(\rho v_{t-1}, \sigma_\phi^2 \right) \end{aligned}, \tag{4}$$

where ρ is the autocorrelation coefficient of the process error innovations $\mathbf{v}$, and the time-varying mean is parameterized by a $1 \times K$ vector of covariates $\mathbf{x}_t$ and a corresponding $K \times 1$ vector of regression coefficients $\boldsymbol{\beta}$. This regression formulation provides a way to explicitly model the effects of environmental factors (including time trends or step changes) while accounting for any "unexplained" common fluctuations via autocorrelated noise. Thus, the full model for the cohort born in year t in population i,

$$R_{it} = \frac{\alpha_i S_{it}}{1 + \alpha_i S_{it} / R_{\text{max},i}} \phi_t e^{\varepsilon_{it}}, \tag{5}$$

decomposes the variation in recruitment into spatial (among-population), temporal (among-year), and idiosyncratic (residual) components.

The model for the time-varying cohort age distributions (Equation 2) also needs to be expanded in the multi-population context. We allow each population to have its own average (on the log-ratio scale) adult age proportions γ_i, so the age vector for cohort t is drawn from a multivariate logistic normal distribution with covariance matrix Σ_p shared among populations:

$$\text{alr}(\mathbf{p}_{it}) \sim \text{MVN}(\gamma_i, \Sigma_p). \tag{6}$$

The population-level mean vector of log ratios γ_i is, in turn, drawn from a multivariate normal hyperdistribution,

$$\gamma_i \sim \text{MVN}(\mu_\gamma, \Sigma_\gamma), \tag{7}$$

where the mean vector μ_γ represents the average age structure (on the log-ratio scale) of the multi-population ensemble, and the covariance matrix Σ_γ represents the among-population heterogeneity in average adult age distributions.

The observation model consists of three likelihood components. First, the observed or estimated total spawner abundance is lognormally distributed around the true abundance with observation error standard deviation σ_{obs}:

$$\log(S_t^{\text{obs}}) \sim \text{N}(\log(S_t), \sigma_{\text{obs}}^2). \tag{8}$$

Second, the observed age composition of natural-origin spawners is typically based on subsamples of carcasses or live fish handled at weirs. These sampling methods produce a vector of age frequencies which we assume to follow a multinomial distribution,

$$\left[n_{t,a_{\min}}^{\text{obs}}, \ldots, n_{t,a_{\max}}^{\text{obs}} \right] \sim \text{Multinomial}\left(\sum_a n_{t,a}^{\text{obs}}; q_{t,a_{\min}}, \ldots, q_{t,a_{\max}} \right), \tag{9}$$

where $n_{t,a}^{\text{obs}}$ is the observed count of age-a adults in year t, the sample size for the multinomial is the total number of fish aged, and the expected probability of age a in year t, $q_{t,a}$, is found by normalizing the number of age-a spawners by the total natural-origin spawner abundance (Equation 3).

The third observation likelihood component is the frequency of hatchery- and wild-origin spawners, typically based on recovery of marks (e.g., adipose fin clips) on carcasses or fish passed over weirs. Again, these sampling methods produce counts, $n_{t,\text{W}}^{\text{obs}}$ and $n_{t,\text{H}}^{\text{obs}}$, which we assume to follow a binomial distribution with expected probability given by the true fraction of hatchery spawners:

$$n_{t,\text{H}}^{\text{obs}} \sim \text{Bin}(n_{t,\text{H}}^{\text{obs}} + n_{t,\text{W}}^{\text{obs}}, p_{\text{HOS},t}). \tag{10}$$

Note that we make no assumptions about the age structure of hatchery-origin adults; in principle, this could be incorporated into the observation model, but age frequencies of hatchery-origin fish are not widely available.

Parameter estimation

We estimate model parameters for the multiple-population IPM in a Bayesian framework (Gelman et al. 2014). The joint posterior distribution is the product of: 1) the prior on the hyperparameters (μ_α, $\mu_{R_{max}}$, σ_α, $\sigma_{R_{max}}$, $\rho_{\alpha,R_{max}}$, σ, $\boldsymbol{\beta}$, ρ, σ_ϕ, $\boldsymbol{\mu_\gamma}$, $\boldsymbol{\Sigma_\gamma}$, $\boldsymbol{\Sigma_p}$, and $\mathbf{p}_{HOS}$), 2) the probability density of the population-level random effects (spawner–recruit parameters and age structure means) and latent states (shared productivity anomalies, annual recruitment, and age structure) given their hyperparameters, 3) the prior on the initial states, and 4) the observation likelihood.

We used vague priors for all hyperparameters with the exception of the autocorrelation coefficient ρ, which was given a power-exponential prior that regularizes the tails of the posterior away from -1 and 1 to ensure stationarity:

$$p(\rho) \propto \exp\left[\left(\frac{|\rho|}{0.85}\right)^{50}\right]. \tag{11}$$

We explored alternate values of the shape and scale in this prior and found that they had fairly minor effects on the mean and bulk of the posterior mass. We also need to specify a prior on the initial states. Spawner abundance and age structure in the first $1{:}a_{max}$ years of each population's data series cannot be predicted based on previous states (recruitment and age structure), so for $t = 1, ..., a_{max}$ we assumed that $\log(S_{it}) \sim N(0{,}5^2)$ and $\mathbf{q}_{it}$, the vector of spawner age proportions, was distributed uniformly on the simplex. The prior on the initial shared process error innovation was the stationary distribution,

$$\log(\nu_t) \sim N\left(0, \frac{\sigma_\phi^2}{1-\rho^2}\right).$$

We simulated 1,500 draws from the posterior distribution in each of three randomly initiated Markov chains using the Hamiltonian Monte Carlo algorithm (HMC; Monnahan et al. 2017) implemented in Stan 2.14.0 (Stan Development Team 2016) as run from R 3.3.3 (R Development Core Team 2017). The first 500 iterations of each chain were used as warmup and discarded, resulting in a total saved sample of 3,000 draws. We assessed convergence by visual inspection of traceplots and by verifying that Gelman and Rubin's (1992) potential scale reduction factor was <1.1 for all parameters, and that there were no divergent transitions. Code for all analyses is available online as part of the R package `salmonIPM`.[2]

Forward simulation

Simulating future population trajectories under the IPM is straightforward; the process model is simply iterated for the desired number of years past the end of the time series of observations, generating a posterior predictive distribution of future states conditioned on the historical data.

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[2] Available from E. R. Buhle, NWFSC, upon request.

In particular, predicted future spawner abundance and age structure are conditioned on the incomplete cohorts at the end of the data series (i.e., those cohorts from which one or more older age classes have not yet returned to spawn). The IPM therefore assimilates the same information traditionally used in a sibling regression (Peterman 1982), in which linear relationships between age-class abundance within cohorts are used to predict older-aged adult returns given the observed younger-aged returns. In contrast to sibling regression, however, the IPM does not assume a fixed age structure, but allows the cohort age distribution to vary through time.

For all of the future simulations, we set broodstock removal and hatchery spawner abundance to zero to represent a baseline projection of risk in the absence of supplementation. We examined the impact of harvest-related mortality on population viability by varying the future harvest rate $F_{t,a}$ over a range of values. The harvest mortality rate was constant within each simulated trajectory (i.e., $F_{t,a} = F_a$ for all t), corresponding to a fixed-rate policy that does not depend on population size. Each set of parameters and states sampled from the joint posterior was used to generate multiple future trajectories, one for each value of F_a.

Application to Snake River spring/summer and Upper Columbia River spring Chinook salmon

We examined 26 populations of Chinook salmon in the Snake River spring/summer ESU and three populations in the Upper Columbia River spring ESU. In total, the data set includes 1,696 cases (distinct population/year combinations) spanning six decades, from 1952 to 2016 (Table 1). We obtained population-specific annual estimates of age and hatchery/wild frequencies from state and tribal assessment biologists around the region. In many cases, this entailed retrieving information from historical reports and field records of spawning ground surveys. The majority of adults are age 4 or 5, with a smaller proportion of three-year-olds (almost entirely male); six-year-old spawners were observed in very few cases, so we omit this age class in the analysis. Spawner observations were missing in 67 cases, and age-frequency data were missing in 864 cases, predominantly in the early years of the time series. These missing data pose no problems for the IPM approach, as the process model automatically imputes the underlying states.

Hatchery-origin spawners have been recorded in roughly two-thirds of the populations at some point during their history, but in most cases, hatchery programs were not operational before the mid-1980s. We therefore fixed $p_{\text{HOS},t}$ at zero except in populations and time periods when hatchery-origin adults were known to be present. We used estimates of the area of potential spawning habitat in each watershed to standardize spawner abundance among populations. That is, we used spawners/ha as the state variable in the spawner–recruit model, and then multiplied by area to obtain total spawners as required for the observation model. While not strictly necessary, this approach scales $R_{\text{max},i}$ to standardized units of spawners/ha for all populations, removing variation due to overall population size and bolstering the assumption of exchangeability of the random effects.

Table 1. Summary of Snake River spring/summer (SRSS) and Upper Columbia River spring (UCS) Chinook salmon data, including the range of sampling years (some years may have missing data), minimum viable abundance target (MAT) designated by the TRT, and the median (5th and 95th) percentiles for both the total observed spawner abundance and the proportion of hatchery-origin spawners (p_{HOS}). MATs marked with an asterisk indicate populations designated as "maintained," meaning that the recovery plan does not require them to exceed the MAT.

Population	ESU	Years	MAT	Spawners	p_{HOS}
Catherine (GRCAT)	SRSS	1955–2013	1,000	430 (43–1,926)	0.22 (0–0.78)
Lostine (GRLOS)	SRSS	1952–2013	1,000	664 (95–1,792)	0.18 (0–0.75)
Minam (GRMIN)	SRSS	1954–2013	750	550 (102–1,499)	0.08 (0–0.5)
Upper Grande Ronde (GRUMA)	SRSS	1955–2013	1,000*	238 (21–1,016)	0.23 (0–0.95)
Wenaha (GRWEN)	SRSS	1952–2013	750	541 (85–2,488)	0.11 (0–0.78)
Imnaha (IRMAI)	SRSS	1952–2013	750	1,452 (349–3,569)	0.2 (0–0.65)
Bear Valley (MFBEA)	SRSS	1957–2016	750	503 (59–2,004)	0
Big (MFBIG)	SRSS	1957–2016	1,000	246 (19–773)	0.02 (0–0)
Camas (MFCAM)	SRSS	1957–2016	500*	81(9–476)	0
Chamberlain (MFCHA)	SRSS	1957–2016	750	520 (77–1,372)	0
Loon (MFLOO)	SRSS	1957–2016	500	82 (9–697)	0
Marsh (MFMAR)	SRSS	1957–2016	500	382 (23–1,349)	0
Sulphur (MFSUL)	SRSS	1957–2016	500*	101 (2–478)	0
Upper Middle Fork Salmon (MFUMA)	SRSS	1957–2016	750*	133 (11–703)	0
East Fork South Fork Salmon (SFEFS)	SRSS	1960–2015	1,000*	442 (120–1,241)	0.15 (0–0.7)
South Fork Salmon (SFMAI)	SRSS	1957–2016	1,000	1,192 (267–3,047)	0.2 (0–0.64)
Secesh (SFSEC)	SRSS	1960–2016	750	408 (140–1,214)	0.02 (0–0.07)
Tucannon (SNTUC)	SRSS	1957–2016	500	436 (104–1,182)	0.22 (0–0.65)
East Fork Salmon (SREFS)	SRSS	1957–2016	1,000	488 (28–2,433)	0.05 (0–0.36)
Lemhi (SRLEM)	SRSS	1957–2016	2,000	322 (45–2,259)	0
Lower Mainstem Salmon (SRLMA)	SRSS	1957–2016	2,000*	181 (38–888)	0.02 (0–0.1)
North Fork Salmon River (SRNFS)	SRSS	1957–2016	500*	108 (8–432)	0
Pahsimeroi (SRPAH)	SRSS	1989–2016	1,000	207 (41–676)	0.41 (0.01–0.93)
Upper Salmon (SRUMA)	SRSS	1957–2016	1,000	874 (94–2,228)	0.13 (0–0.43)
Valley (SRVAL)	SRSS	1957–2016	500	153 (13–1,036)	0
Yankee (SRYFS)	SRSS	1957–2016	500*	117 (2–1,497)	0.03 (0–0.11)
Entiat (UCENT)	UCS	1960–2016	500	341 (71–1,020)	0.18 (0–0.55)
Methow (UCMET)	UCS	1960–2016	2,000	1,376 (102–3,188)	0.31 (0–0.86)
Wenatchee (UCWEN)	UCS	1960–2016	2,000	1,890 (260–4,115)	0.23 (0–0.79)

Harvest mortality, whether observed or simulated, was assumed to affect age-4 and 5 spawners equally; age-3 spawners were not subject to harvest. All harvest was assumed to occur in terminal fisheries as adults returned to spawn. In forward simulations, the constant harvest mortality ranged from 0 to 0.3 in increments of 0.05. (For comparison, the current management regime is designed to limit harvest impacts to 5–17% of the aggregate adult spring/summer Chinook salmon return to the Columbia River.)

To explore the interactive effects of harvest mortality and environmental stochasticity on viability, we fit two versions of the IPM, making different assumptions about the historical pattern of average environmental conditions common to all populations (Equation 4). In the constant baseline model, the shared productivity anomalies are stationary, with mean zero ($x_t = 0$ for all t), so the simulated future distribution of ϕ_t resembles the distribution of all estimated past values (Figure 1A). The step change model, by contrast, assumes that underlying environmental conditions shifted permanently at some point during the historical record (e.g., due to changes in the hydropower system or climatic regime), so in the future, $\log(\phi_t)$ will have the same mean as the latter part of the estimated time series (Figure 1B). In this case, x_t is a dummy indicator variable taking on one value before and another value after the step change (the values are centered to mean zero over the fitted time series). The change point was identified as the year 1970, based on post-hoc analysis of the posterior mean series $\log(\phi_{1952:2016})$ from the constant baseline model. This was the most recent year in which a *t*-test found a significant difference
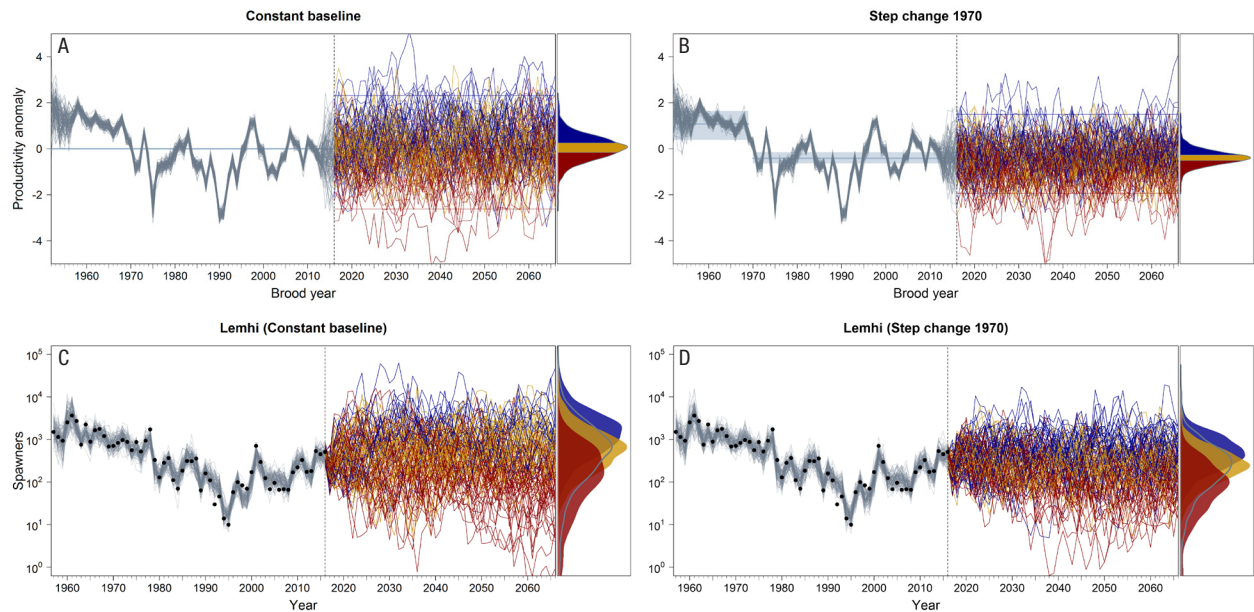
Figure 1. Procedure for summarizing simulated future population trajectories based on average environmental conditions. Productivity anomalies represent environmental fluctuations common to all populations, and are modeled as a first-order autoregressive process. In the constant baseline model (A), this AR(1) process has a constant zero mean, whereas in the step change model (B), the mean differs before and after the change point (the year 1970); the respective estimates and 95% credible intervals are shown as gray bands. Given the estimated anomalies over the period of observed data (gray lines to the left of the vertical bar), each trajectory in the posterior sample is extended into the future by simulating from the AR(1) process. Each future trajectory is characterized by its average environmental conditions (e.g., the blue and red horizontal lines in A and B), and the distribution of these averages is divided into equal thirds representing relatively good (blue), intermediate (yellow), or bad (red) conditions. These labels are then applied to the corresponding trajectories of future population size (C and D), allowing viability metrics to be computed either unconditionally or conditioned on average environmental conditions. For example, the overlapping histograms in C and D show the posterior predictive distribution of total spawners in year 50 in the future given that conditions are good, intermediate, or bad, while the gray curve shows the unconditional distribution.

between the earlier and later means. For each model structure, viability reference points were evaluated both unconditionally (over the full joint posterior) and conditional on average future environmental states. Each simulated future trajectory was characterized as "good," "intermediate," or "bad" for large-scale average productivity, corresponding to mean $\log(\phi_t)$ values falling in the upper, middle, or lower third, respectively, of the distribution of such values (Figures 1A and 1B). Posterior summaries were then calculated separately for each category of future average environmental conditions (Figures 1C and 1D).

From each simulated trajectory, we evaluated three population-specific management reference points related to viability: 1) total wild spawner abundance in a given year, 2) total wild spawner abundance in a given year as a proportion of the minimum abundance target (MAT; Table 1) determined by the Interior Columbia Technical Recovery Team (ICTRT 2007), and 3) quasi-extinction, where the quasi-extinction threshold (QET) was defined in terms of the four-year running mean of total wild spawner abundance. The QET does not represent absolute extinction, but a threshold below which demographic and genetic risks and associated uncertainties become non-negligible. ICTRT (2007) used QET = 50 spawners based on the scarcity of historical observations of <50 spawners and consistency with applications by the Puget Sound and Lower Columbia/Willamette Technical Recovery Teams. Quasi-extinction occurs if the running mean falls below QET at least once, and the posterior predictive probability of quasi-extinction (PQE) for a given harvest rate is the proportion of trajectories where this occurs. The time horizon for forward simulations was 50 years past the end of the data series, and the three viability reference points were evaluated at 25 and 50 years.

As an additional reference point, we calculated the maximum harvest mortality that each population could sustain, in a purely deterministic model, before the growth rate falls below replacement:

$$F_{\text{max},i} = 1 - \frac{1}{\alpha_i}. \tag{12}$$

Because our model (and reality) includes environmental stochasticity and potentially regime shifts, F_{max} should not be overinterpreted; it provides an adjunct to help contextualize the results of the direct simulations.

Results and Discussion

The multi-population IPM did a good job of capturing the historical dynamics of Snake River spring/summer and Upper Columbia River spring Chinook salmon populations (Figure 2). In the constant baseline model, the coefficient of determination between the median of the estimated log-spawners and the observed log-spawners across the entire data set was 0.92, and 99% of the observed values fell within the 95% credible interval based on the observation error distribution. Observation error in spawner abundance was greater (posterior mean and 95% confidence interval of σ_{obs}: 0.55, 0.50–0.60) than the unique process error in recruitment (σ: 0.46, 0.41–0.51). However, overall recruitment process error was dominated by the shared component, whose standard deviation was $\sigma_\phi / \sqrt{1-\rho^2} = 1.14$ (0.87–1.50) and which was strongly autocorrelated (ρ: 0.75, 0.60–0.85). This can be seen in Figure 2, where the trajectories of different populations are highly synchronous. These results were nearly identical under the step change model except for the autocorrelation in the shared process errors, which was lower (ρ: 0.54, 0.28–0.79), as expected.

Estimated spawner–recruit curves varied considerably among populations (Figure 3, Table 2). Maximum recruitment was more variable (CV of R_{max}: 184%) than maximum per capita productivity (CV of α: 61%), despite being standardized by the amount of spawning habitat. Nonetheless, there was consistent evidence of density dependence over the range of densities observed (Figure 3A). Posterior distributions of R_{max} (Figure 3C) had well defined modes and right tails, indicating that the data ruled out arbitrarily large values (i.e., density independence).

Future projections of population viability were highly sensitive to environmental conditions and harvest-related mortality. Mean spawner abundance declined linearly with harvest mortality (hence the relationship appears convex on the log scale shown in Figure 4 for four populations representing a range of abundance and productivity). Indeed, this linearity is expected, based on simple equilibrium analysis of any deterministic, non-age-structured spawner–recruit model subjected to fixed-rate harvest. In the case of the Beverton–Holt,

$$R = \frac{\alpha S}{1 + \alpha S / R_{max}}(1 - F),$$

the equilibrium is

$$S^* = \frac{R_{max}(\alpha - 1)}{\alpha} - R_{max} F.$$

The unfished carrying capacity K (the intercept) depends on both maximum recruitment and maximum productivity, and a larger population (higher R_{max}) will experience larger absolute declines for a given increase in harvest rate. If we consider the equilibrium as a proportion of K,

$$\frac{S^*}{K} = 1 - \frac{\alpha}{\alpha - 1} F,$$

the decline in abundance relative to the unfished baseline is still linear, but with a slope that depends on intrinsic productivity such that the less productive the population, the steeper the decline with increasing harvest rate.
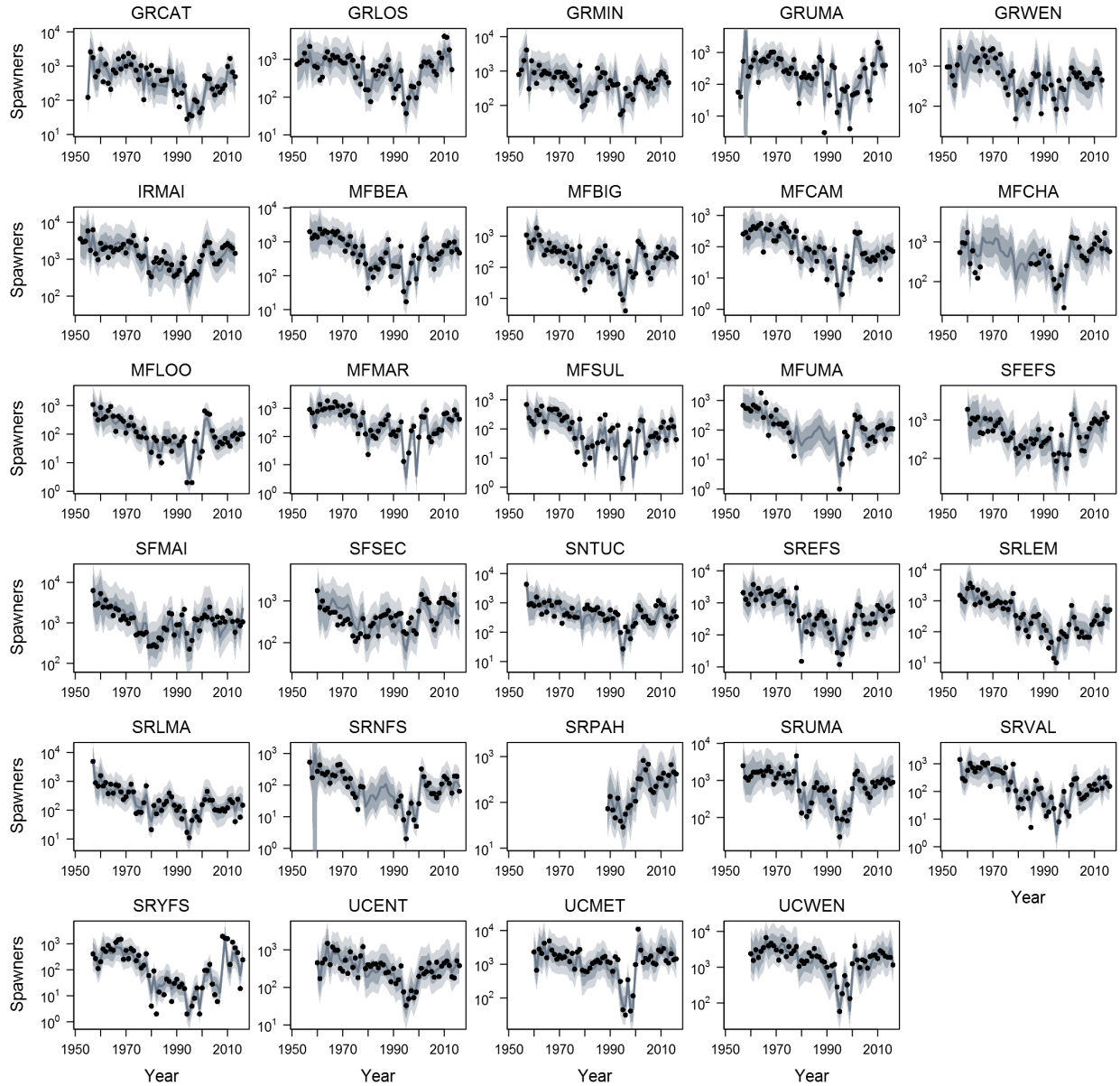
Figure 2. Time series of observed (points) and estimated spawner abundance for each of 29 populations of Snake River spring/summer and Upper Columbia River spring Chinook salmon. The posterior median (solid gray line) is from the multipopulation IPM with constant baseline productivity. Posterior 95% credible intervals indicate process (dark shading) and observation (light shading) uncertainties.
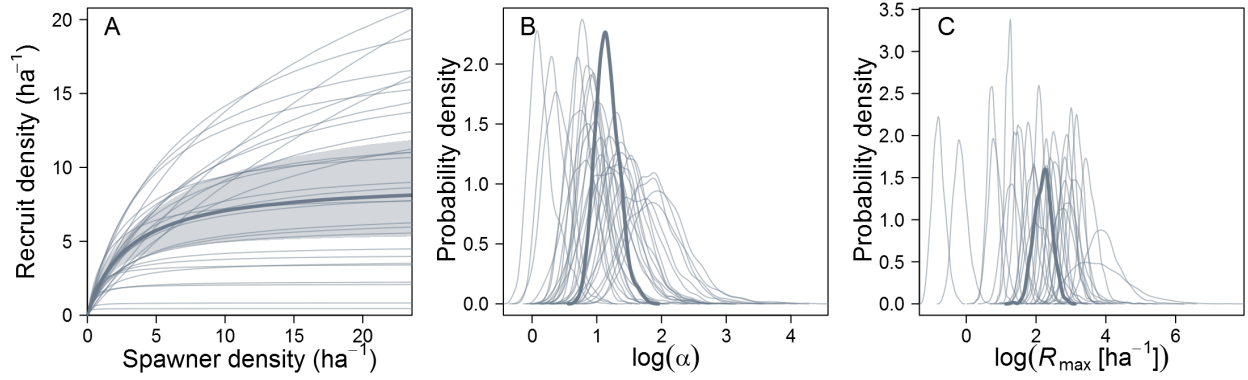
Figure 3. Estimated spawner–recruit relationship (A) and intrinsic productivity (B) and capacity (C) parameters for the multipopulation IPM with constant baseline productivity. Thin lines correspond to each of 29 populations of Snake River spring/summer and Upper Columbia River spring Chinook salmon; thick lines represent hyper-means across populations. In 3A, each curve is a posterior median and the shaded region represents the 95% credible interval of the hyper-mean curve (uncertainty around the population-specific curves is omitted for clarity).

Table 2. Posterior summaries (medians and 95% credible intervals) of population-specific intrinsic productivity (α) and asymptotic recruitment (R_{max}), as well as their hyperparameters (log-mean and log-SD), under the multipopulation IPM with constant baseline productivity. Also shown is F_{max}, the maximum harvest mortality that could be sustained in the absence of environmental stochasticity, which is a function of α.

Population	α	R_{max} (spawners/ha)	F_{max}
GRCAT	1.37 (0.99–2.21)	49.98 (24.01–144.58)	0.27 (0–0.55)
GRLOS	3.11 (1.8–6.74)	10.19 (7.09–16.96)	0.68 (0.44–0.85)
GRMIN	3.93 (2.26–8.61)	20.21 (14.61–30.43)	0.75 (0.56–0.88)
GRUMA	1.48 (1–2.4)	16.69 (9.58–46.55)	0.32 (0–0.58)
GRWEN	2.1 (1.41–3.62)	23.29 (14.89–40.56)	0.52 (0.29–0.72)
IRMAI	3.46 (2.1–8.31)	24.3 (17.5–35.29)	0.71 (0.52–0.88)
MFBEA	3.73 (2.38–7.01)	12.59 (9.03–18.87)	0.73 (0.58–0.86)
MFBIG	6.52 (3.56–13.92)	2.1 (1.59–2.9)	0.85 (0.72–0.93)
MFCAM	2.61 (1.64–4.71)	3.73 (2.3–6.82)	0.62 (0.39–0.79)
MFCHA	4.75 (2.69–10.73)	11.72 (7.79–20.44)	0.79 (0.63–0.91)
MFLOO	3.89 (2.29–9.08)	2.29 (1.6–3.68)	0.74 (0.56–0.89)
MFMAR	2.52 (1.75–4)	17.9 (11.96–29.18)	0.6 (0.43–0.75)
MFSUL	2.04 (1.42–3.29)	16.85 (10.68–29.47)	0.51 (0.3–0.7)
MFUMA	5.1 (2.41–13.17)	0.84 (0.58–1.36)	0.8 (0.58–0.92)
SFEFS	3.48 (2.12–7.14)	4.75 (3.41–7.05)	0.71 (0.53–0.86)
SFMAI	7.3 (3.63–20.23)	3.47 (2.77–4.49)	0.86 (0.72–0.95)
SFSEC	6.2 (3.23–15.43)	8.15 (6.21–11.39)	0.84 (0.69–0.94)
SNTUC	2.39 (1.55–4.09)	32.82 (22.09–58.53)	0.58 (0.35–0.76)
SREFS	2.9 (1.99–4.83)	13.23 (8.73–21.69)	0.65 (0.5–0.79)
SRLEM	2.44 (1.72–3.75)	6.65 (4.17–11.26)	0.59 (0.42–0.73)
SRLMA	6.4 (3–21.34)	0.45 (0.33–0.68)	0.84 (0.67–0.95)
SRNFS	4.44 (2.64–8.52)	4.14 (2.9–6.1)	0.77 (0.62–0.88)
SRPAH	3.13 (1.67–7.03)	8.73 (4.72–27.24)	0.68 (0.4–0.86)
SRUMA	4.2 (2.54–8.41)	18.05 (13.01–28.01)	0.76 (0.61–0.88)
SRVAL	2.62 (1.86–4.16)	10.04 (6.58–16.55)	0.62 (0.46–0.76)
SRYFS	2.21 (1.64–3.16)	7.09 (4.53–11.86)	0.55 (0.39–0.68)
UCENT	2.3 (1.28–5.25)	19.78 (12.18–51.65)	0.56 (0.22–0.81)
UCMET	2.77 (1.54–4.98)	6.09 (4.35–10.16)	0.64 (0.35–0.8)
UCWEN	1.13 (0.85–1.93)	43.09 (13.87–296.84)	0.12 (0–0.48)
μ_θ	1.15 (0.84, 1.56)	2.21 (1.74, 2.68)	
σ_θ	0.55 (0.38, 0.84)	1.17 (0.91, 1.58)	
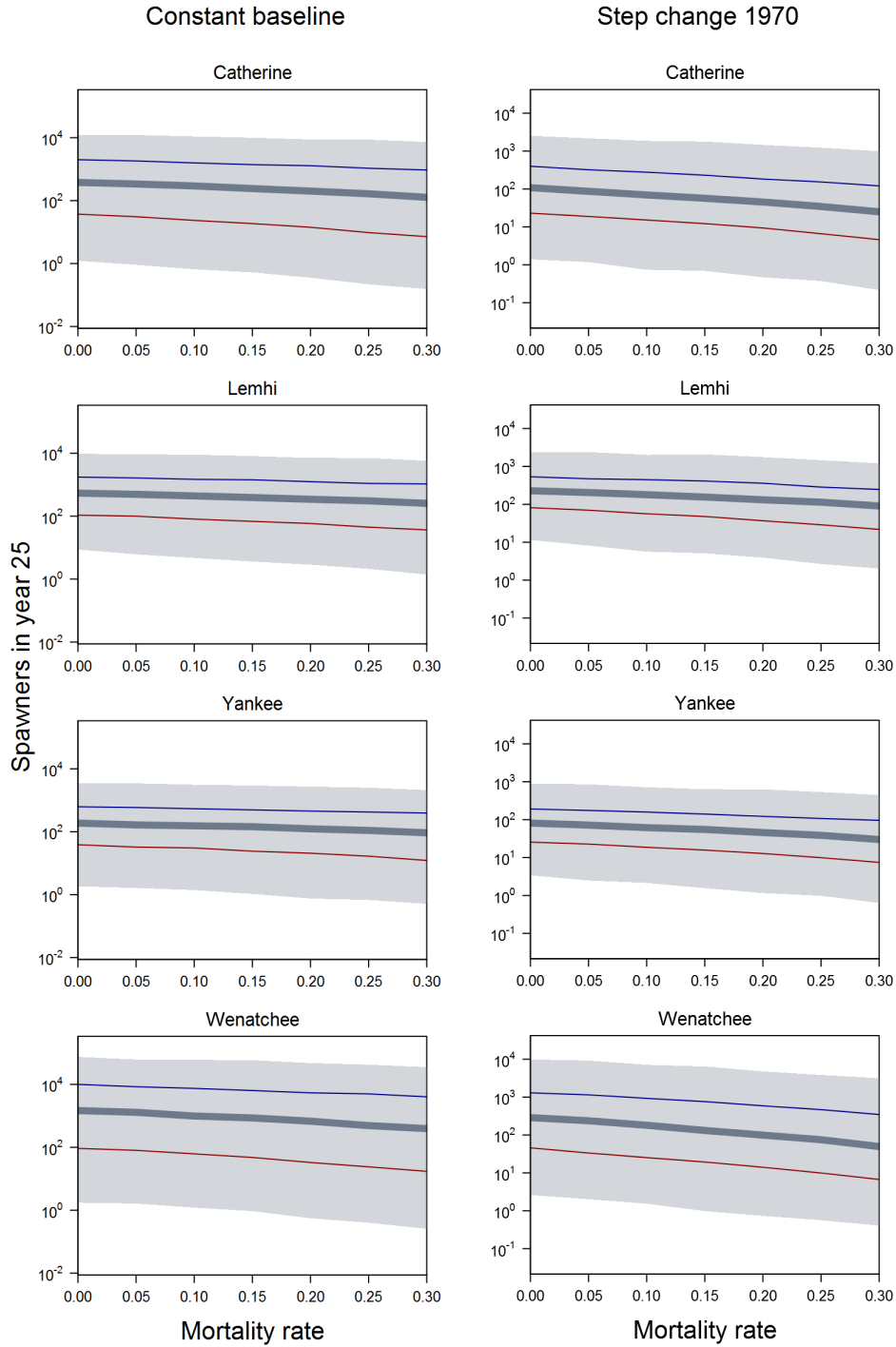
Figure 4. Posterior predictive distributions of total wild spawners, 25 years in the future, for four Chinook salmon populations as a function of harvest mortality rate and average environmental conditions (green = good, red = bad, thick gray = unconditional; intermediate scenario omitted for clarity). Harvest is modeled as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. Lines are posterior medians, and shading indicates the 95% credible interval of the unconditional posterior. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

These linear declines in average abundance may nonetheless translate into nonlinear increases in quasi-extinction risk (Figure 5), because the PQE acts as a cumulative distribution function applied to the posterior predictive distribution of abundance. For two populations (Catherine Creek and Wenatchee, Table 2), the highest modeled harvest mortality of 0.3 exceeded the posterior median of F_{max}, indicating a probability >0.5 that this mortality rate would, if sustained, cause long-term declines even in the absence of environmental fluctuations or regime shifts. One additional population (Upper Mainstem Grande Ronde) had a posterior median of F_{max} that was barely above 0.3. For all other populations, the probability of $F_{max} < 0.3$ was less than 0.05 (Table 2). However, a population in a stochastic environment may experience quasi-extinction even if its deterministic equilibrium is nonzero (or above the QET), which is why the simulations generally indicate nontrivial quasi-extinction risk at harvest mortality rates well below F_{max}.

Regardless of whether the historical pattern of environmental fluctuations was assumed to reflect variation around a constant baseline or a shift to a lower-productivity regime beginning in 1970 (Figure 1), future environmental conditions were generally at least as influential as harvest mortality. In the cases shown in Figure 4, for example, the difference in total spawner abundance as the environmental background goes from good to bad exceeds the difference between harvest mortality of zero and 30%. The contrast in quasi-extinction risk across environmental scenarios is even more striking, due to the nonlinear shape of the PQE function (Figure 5). Populations subjected to bad average conditions (in the lowest third of the distribution) had severely elevated risks compared to the overall unconditional distribution. The impacts of environmental regime and harvest mortality on the stationary distribution of abundance were generally multiplicative (i.e., additive on the log scale shown in Figure 4), but again, this translated into synergistic or antagonistic interactive effects on quasi-extinction risk (Figure 5). As expected, the step change model gave more pessimistic forecasts than the constant baseline model. The effect of a persistent shift to a less-favorable regime was, however, partly mitigated by reduced uncertainty (e.g., compare Figures 1C and 1D). That is, the step change model ruled out the most extreme excursions in both the positive and negative directions.

Populations varied widely in their baseline viability and resilience to worsening environmental conditions and harvest mortality (Tables 3–7). Some (e.g., Yankee Fork) had substantial risks of quasi-extinction in as little as 25 years, even under favorable environmental conditions and no harvest. Others (e.g., Lemhi) could sustain harvest mortality up to 30% (with relatively low 25-year quasi-extinction risk) as long as conditions remained good and one assumed a constant environmental baseline, but became increasingly sensitive to harvest impacts if conditions were intermediate or poor or if the baseline was assumed to have shifted in 1970. Assuming a permanent environmental change in 1970, many populations had at least a moderate risk of quasi-extinction in 50 years even with no harvest and "good" environmental conditions (Table 7).
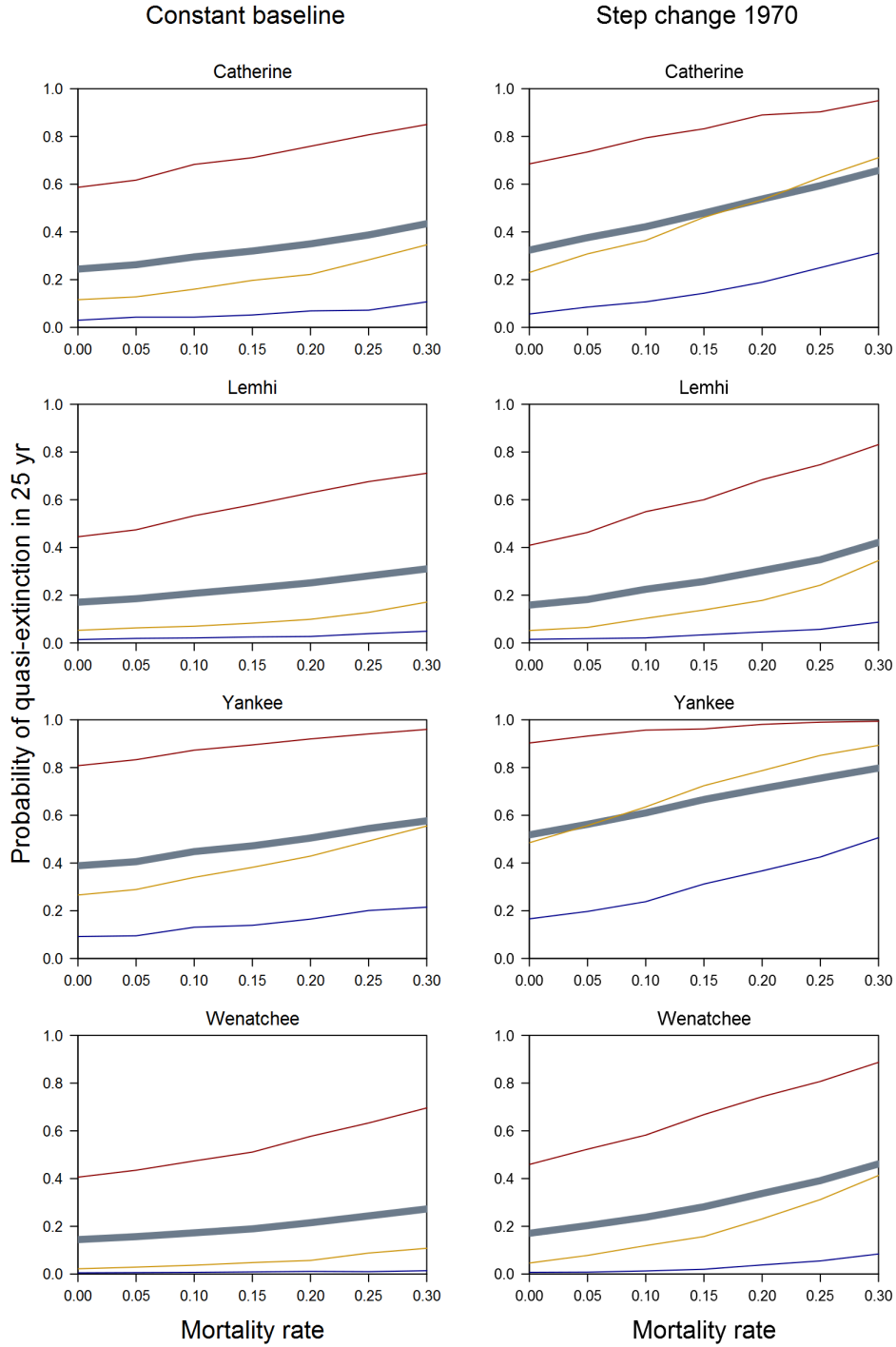
Figure 5. Posterior predictive probabilities of quasi-extinction, 25 years in the future, for four Chinook salmon populations as a function of harvest mortality rate and average environmental conditions (blue = good, yellow = intermediate, red = bad, thick gray line = unconditional). Harvest is modeled as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. The quasi-extinction threshold is a four-year running average of 50 spawners. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

It is important to remember that this is not an equilibrium analysis. Under our density-dependent model, population size will eventually converge to a stochastic equilibrium represented by a stationary distribution (which could be a point mass at zero, if the maximum productivity falls below replacement), but it is not guaranteed to approach stationarity within a 50-year time horizon. In particular, if the realized growth rate is barely above or below replacement, then the transient dynamics could be very prolonged. An example of this is the Wenatchee, a relatively large population whose intrinsic productivity has a posterior distribution that straddles replacement (α: 1.13, 0.85–1.93). F_{max} is quite low (0.12, 0–0.48), indicating that modest harvest impacts might not be sustainable even in a purely deterministic world, and the decline in simulated abundance as a function of harvest mortality is relatively steep at year 25 (Figure 4), yet quasi-extinction within this time horizon is far from assured (Figure 5). By year 50, however, abundance has declined further (compare Tables 3 and 4). The lesson is that the analysis presented here is concerned with dynamics over time scales relevant to recovery planning. Over the longer term, the inherent structural uncertainty related to "slow variables" not included in these models, such as climatic change and shifts in species interactions, will likely exceed the uncertainty that we can anticipate based on the observed and modeled stochastic dynamics.

Two caveats, stated previously, should be borne in mind when interpreting the results presented here. First, we simulated a fixed harvest-rate policy despite the fact that the current and likely future management system involves a sliding-scale harvest control rule based on the aggregate adult abundance of upriver spring/summer Chinook salmon entering the Columbia River. This modeling decision was made in the interest of tractability and avoiding additional assumptions, given that our model may not include all the populations comprising the aggregate run. As a result, our projections of harvest impacts are likely pessimistic, since a sliding-scale rule would reduce the mortality rate as abundance declines. However, in practice, the effects of such a rule at the population scale will depend on the degree of synchrony among populations. Strongly synchronous dynamics, such as we found, make it more likely that all populations will experience simultaneous declines, and thus will individually benefit from reduced harvest rates under a control rule based on aggregate abundance. Second, our simulations assume an absence of hatchery supplementation, also for reasons of tractability. Several of the populations studied here do in fact have ongoing supplementation programs, which may play an important role in buffering variability in abundance (e.g., Winship et al. 2014). For these populations, our results may again be pessimistic, although any demographic enhancement from hatchery-origin spawners may incur a cost to productivity (Naish et al. 2007, Christie et al. 2014, Scheuerell et al. 2015). A more detailed evaluation of this potential tradeoff is beyond the scope of this study. On the other hand, roughly half of the modeled populations have no history of hatchery supplementation, so in these cases our results apply cleanly.

Life cycle models are commonly used to predict population responses to scenarios of future conditions. As such, the degree to which they can accurately and precisely capture retrospective patterns in population dynamics is critical to evaluating how much faith one should place in any future forecasts. Although IPMs have been used more widely in terrestrial and marine environments (Schaub and Abadi 2011, Maunder and Punt 2013), they have not yet been widely applied to studies of Pacific salmon. Here we have demonstrated how the development and application of an IPM sheds new light on the current and future status of at-risk populations. In particular, we see several advantages to this approach: 1) a unified framework for both the retrospective and prospective phases of analysis, 2) a full accounting of the uncertainties inherent in the available data, and 3) statistically consistent, probabilistic estimates of parameters and derived quantities of interest, such as quasi-extinction risks, and the abundance and productivity metrics specified under the Viable Salmonid Population recovery criteria (McElhany et al. 2000). In addition, the hierarchical nature of our IPM allows us to effectively borrow information from data-rich populations to help inform parameter estimation among the data-poor populations (Jiao et al. 2011, Punt et al. 2011).

Our IPM is presently based upon adult data only, but there is nothing precluding an expansion of the model to include any applicable juvenile data as well. For example, there are snorkel counts of stream-resident parr for a subset of the populations we analyzed here, which we have used successfully in other related analyses (Thorson et al. 2014). As noted above, efforts are underway to extend the adult-to-adult IPM described here to accommodate additional life history complexity. Including age or stage structure in the IPM framework can improve the accuracy and precision of parameter estimates such as the strength of density dependence and the variance of stochastic elements (Schaub and Abadi 2011), so these efforts could potentially lead to improved forecasts of harvest impacts as well as the ability to evaluate tributary habitat strategies, supplementation actions, and hydropower management alternatives.

Quantitative population viability analyses (PVAs) for Pacific salmon are negatively affected by a number of factors that mask the true population status, including observation errors, nonstationary age composition, and hatchery supplementation (Holmes 2004). Meta-analyses have shown that failing to adequately address observation errors leads to overestimates of the strength of density dependence (e.g., Freckleton et al. 2006, Knape and de Valpine 2012), which implies greater resilience to any potential disturbance. Furthermore, statistical models such as our IPM typically outperform much more detailed mechanistic models when estimating quasi-extinction rates (Holmes et al. 2007) or forecasting future abundance (Ward et al. 2014). Our IPM provides estimates of intrinsic productivity and carrying capacity at both the population and larger ESU levels, the latter of which is the domain where any (de)listing decisions are made. Thus, we see potential for the further development of IPMs and their application to salmon conservation problems throughout the Pacific Northwest.

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Table 3. Posterior predictive distributions (median and 95% credible interval) of total wild spawners, 25 years in the future, for 29 Chinook salmon populations as a function of harvest mortality rate (*Mort.*) and average environmental conditions. Harvest is simulated as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
GRCAT	0	379 (1–12189)	1998 (163–25293)	37 (0–604)	108 (1–2532)	398 (43–4907)	23 (0–269)
	0.1	293 (1–10971)	1581 (154–22508)	24 (0–466)	70 (1–1866)	277 (23–3912)	15 (0–195)
	0.2	201 (0–8775)	1288 (87–18764)	14 (0–319)	45 (0–1458)	183 (14–3049)	9 (0–135)
	0.3	127 (0–7313)	942 (60–15514)	7 (0–225)	25 (0–995)	121 (6–2282)	5 (0–66)
GRLOS	0	530 (13–7417)	1510 (172–13863)	128 (3–1319)	252 (21–1980)	535 (98–3844)	103 (7–672)
	0.1	448 (11–7590)	1301 (159–13770)	101 (2–1149)	205 (14–1891)	459 (76–3933)	83 (6–536)
	0.2	369 (6–6159)	1122 (148–11631)	79 (1–810)	165 (10–1719)	393 (63–3357)	63 (3–460)
	0.3	300 (4–5080)	962 (124–10739)	59 (1–668)	125 (5–1332)	296 (51–2430)	42 (2–302)
GRMIN	0	569 (19–8957)	1648 (181–16132)	171 (5–1412)	300 (29–2425)	595 (100–4478)	138 (13–762)
	0.1	481 (14–7368)	1398 (163–14907)	132 (3–1240)	241 (20–2094)	483 (93–3895)	112 (10–715)
	0.2	427 (10–6056)	1146 (126–11973)	104 (2–1097)	206 (15–1815)	402 (79–3936)	84 (6–551)
	0.3	350 (6–5265)	1016 (130–9656)	74 (1–886)	168 (10–1478)	356 (61–2727)	61 (4–424)
GRUMA	0	185 (1–5000)	777 (84–9795)	21 (0–397)	54 (1–1054)	179 (24–2279)	13 (0–119)
	0.1	135 (1–4055)	662 (58–8066)	14 (0–205)	38 (1–887)	137 (16–1875)	9 (0–98)
	0.2	96 (0–3518)	507 (49–7498)	8 (0–124)	26 (0–581)	95 (9–1364)	6 (0–65)
	0.3	66 (0–2946)	421 (27–5638)	5 (0–112)	15 (0–494)	63 (6–914)	3 (0–39)
GRWEN	0	548 (5–10487)	2033 (210–20564)	96 (1–1286)	218 (8–2919)	579 (85–5342)	72 (3–546)
	0.1	445 (3–9036)	1665 (203–21187)	72 (1–986)	172 (5–2307)	451 (74–4267)	53 (2–392)
	0.2	354 (2–8490)	1407 (140–15921)	48 (0–746)	124 (3–1781)	342 (50–3584)	33 (1–377)
	0.3	269 (1–6600)	1214 (120–12439)	27 (0–574)	83 (2–1421)	261 (30–2620)	20 (0–237)
IRMAI	0	992 (33–14694)	2789 (330–28404)	287 (9–2304)	494 (42–4602)	1029 (199–8277)	218 (18–1326)
	0.1	877 (21–13473)	2620 (309–27117)	230 (5–2338)	412 (31–3822)	875 (156–7151)	169 (13–1089)
	0.2	734 (15–12014)	2216 (267–23850)	187 (4–1694)	336 (21–3216)	760 (146–5569)	135 (7–856)
	0.3	604 (10–10937)	1963 (210–18590)	128 (2–1175)	266 (14–2535)	604 (101–4477)	98 (6–679)
MFBEA	0	697 (22–10088)	1772 (245–20322)	221 (7–1764)	351 (28–2894)	679 (124–4848)	158 (14–834)
	0.1	584 (17–9001)	1627 (182–18241)	177 (5–1853)	290 (24–2873)	600 (94–4155)	135 (12–760)
	0.2	508 (12–7319)	1348 (184–16190)	143 (3–1240)	244 (17–2301)	481 (84–3921)	105 (7–611)
	0.3	405 (7–6920)	1258 (136–12922)	101 (2–928)	187 (10–1902)	390 (63–3057)	72 (4–511)
MFBIG	0	263 (14–3309)	642 (79–6039)	106 (6–892)	145 (18–1117)	252 (43–2020)	84 (12–440)
	0.1	227 (11–2858)	554 (73–5846)	90 (4–691)	130 (16–929)	222 (43–1441)	71 (9–352)
	0.2	205 (9–2686)	486 (69–5310)	77 (4–656)	106 (14–857)	199 (38–1449)	56 (8–295)
	0.3	173 (7–2333)	463 (59–4437)	60 (2–557)	90 (9–677)	169 (28–1108)	46 (4–267)
MFCAM	0	137 (2–2429)	410 (47–4990)	30 (1–323)	64 (3–626)	142 (23–1102)	24 (1–162)
	0.1	111 (1–2109)	367 (44–3979)	25 (0–236)	48 (2–492)	114 (18–941)	17 (1–123)
	0.2	94 (1–1796)	317 (36–3552)	18 (0–211)	37 (1–414)	96 (16–700)	11 (0–91)
	0.3	71 (0–1518)	272 (28–3495)	12 (0–135)	27 (1–354)	68 (11–688)	7 (0–65)
MFCHA	0	717 (28–10640)	1755 (213–17288)	262 (7–2350)	381 (41–3097)	679 (124–6061)	189 (20–1157)
	0.1	624 (19–9507)	1547 (189–19020)	205 (5–2057)	321 (31–2716)	597 (114–4852)	157 (14–866)
	0.2	537 (14–7533)	1391 (148–14781)	166 (4–1820)	267 (23–2431)	509 (93–4503)	125 (11–791)
	0.3	457 (12–7087)	1231 (159–14231)	127 (2–1322)	221 (15–1966)	432 (67–3945)	98 (8–611)
MFLOO	0	132 (4–1905)	336 (39–3720)	41 (1–364)	67 (6–587)	122 (23–1002)	31 (3–168)
	0.1	116 (4–1798)	306 (41–3491)	36 (1–332)	56 (4–510)	109 (19–754)	26 (2–141)
	0.2	98 (2–1427)	254 (34–3016)	26 (1–247)	46 (3–433)	89 (17–821)	20 (1–122)
	0.3	79 (1–1330)	235 (29–2324)	20 (0–204)	37 (2–337)	75 (14–557)	14 (1–100)
MFMAR	0	443 (8–7635)	1486 (156–15631)	102 (2–1075)	198 (9–2051)	450 (75–3257)	71 (3–517)
	0.1	380 (6–6792)	1234 (145–13326)	78 (1–710)	161 (7–1773)	379 (68–3323)	52 (3–405)
	0.2	306 (3–5794)	1008 (121–11585)	56 (1–603)	125 (4–1504)	297 (49–2556)	36 (1–325)
	0.3	235 (1–4867)	878 (115–10006)	38 (0–408)	83 (2–1052)	235 (36–1865)	23 (1–209)

Table 3 (continued). Posterior predictive distributions of total wild spawners, 25 years in the future, for 29 Chinook salmon populations.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
MFSUL	0	116 (1–2346)	406 (47–4569)	21 (0–234)	46 (1–574)	117 (17–852)	13 (0–118)
	0.1	93 (1–2119)	341 (41–4249)	15 (0–164)	36 (1–469)	98 (14–808)	9 (0–90)
	0.2	70 (0–1800)	307 (32–3954)	10 (0–107)	26 (0–364)	72 (9–747)	6 (0–57)
	0.3	53 (0–1554)	239 (28–3144)	6 (0–98)	17 (0–289)	52 (6–623)	3 (0–42)
MFUMA	0	140 (6–1935)	351 (45–3443)	54 (2–480)	76 (8–597)	137 (24–1169)	39 (4–211)
	0.1	123 (5–1730)	299 (43–3786)	43 (1–396)	65 (7–551)	118 (22–889)	33 (3–190)
	0.2	108 (3–1579)	275 (37–2866)	34 (1–303)	54 (5–451)	98 (16–801)	26 (2–163)
	0.3	88 (2–1366)	234 (26–2328)	26 (1–256)	44 (3–368)	83 (16–645)	20 (2–147)
SFEFS	0	409 (12–6569)	1139 (174–12223)	130 (3–1143)	212 (15–1894)	429 (73–3029)	99 (8–492)
	0.1	371 (9–5705)	1031 (157–11259)	101 (2–1035)	180 (12–1549)	354 (60–2469)	75 (6–406)
	0.2	318 (6–4486)	918 (125–9340)	77 (1–677)	149 (8–1360)	300 (53–2151)	58 (3–305)
	0.3	258 (4–4232)	784 (106–7457)	57 (1–538)	109 (5–1176)	256 (39–1892)	41 (2–242)
SFMAI	0	975 (59–11910)	2169 (288–24232)	393 (23–3648)	560 (73–3977)	913 (161–6593)	321 (42–1496)
	0.1	872 (48–10675)	2070 (272–22607)	339 (17–2894)	492 (59–3563)	847 (152–5299)	279 (34–1400)
	0.2	777 (41–10138)	1728 (222–18408)	275 (14–2714)	428 (51–3128)	742 (155–4934)	230 (29–1136)
	0.3	648 (30–8080)	1523 (209–16205)	229 (8–1934)	360 (42–2696)	621 (125–4383)	193 (23–1062)
SFSEC	0	542 (26–5764)	1171 (140–10637)	207 (10–1643)	283 (34–2012)	481 (87–3171)	152 (21–716)
	0.1	449 (20–5606)	1092 (152–10346)	167 (9–1588)	245 (28–1864)	420 (80–3068)	126 (13–679)
	0.2	397 (16–5250)	908 (130–9762)	141 (5–1463)	208 (22–1633)	377 (74–2462)	103 (11–522)
	0.3	334 (11–4700)	847 (117–8829)	119 (3–985)	174 (16–1396)	311 (62–2231)	85 (9–493)
SNTUC	0	437 (4–8602)	1381 (163–15756)	86 (1–1038)	184 (8–2088)	419 (69–3667)	62 (3–505)
	0.1	357 (3–6803)	1223 (116–13908)	66 (1–674)	139 (5–1758)	354 (56–3030)	44 (2–375)
	0.2	283 (1–5878)	1057 (132–10933)	47 (0–557)	105 (3–1457)	266 (44–2686)	28 (1–278)
	0.3	214 (1–5386)	800 (90–10006)	29 (0–448)	71 (2–1209)	198 (28–2138)	17 (0–182)
SREFS	0	752 (16–11963)	2129 (251–20246)	205 (5–1790)	347 (18–3628)	679 (128–5576)	134 (7–914)
	0.1	601 (10–10390)	1913 (232–21812)	154 (2–1438)	284 (13–3049)	607 (99–5255)	100 (5–713)
	0.2	499 (7–9006)	1645 (210–17169)	118 (2–1067)	222 (8–2352)	508 (84–3946)	73 (4–554)
	0.3	404 (5–7398)	1345 (153–15113)	80 (1–751)	159 (5–1701)	389 (58–3301)	48 (2–413)
SRLEM	0	540 (9–9633)	1753 (201–19569)	108 (2–1319)	228 (11–2392)	534 (84–3887)	82 (4–576)
	0.1	441 (5–8998)	1482 (149–16280)	81 (1–891)	180 (6–2025)	447 (68–3781)	56 (2–434)
	0.2	344 (3–7097)	1248 (133–15171)	59 (0–757)	132 (4–1765)	360 (52–2799)	37 (2–349)
	0.3	256 (1–5773)	1060 (106–13938)	37 (0–404)	91 (2–1201)	246 (35–2404)	22 (1–250)
SRLMA	0	241 (14–3101)	597 (83–6003)	92 (5–815)	136 (17–1014)	226 (43–1735)	73 (10–380)
	0.1	216 (11–2874)	492 (58–5288)	82 (4–732)	118 (14–907)	194 (39–1416)	63 (7–347)
	0.2	193 (8–2171)	452 (62–4720)	66 (3–595)	102 (11–755)	176 (33–1341)	51 (6–318)
	0.3	159 (6–2282)	410 (54–3904)	51 (2–500)	85 (9–622)	157 (27–1007)	42 (4–230)
SRNFS	0	115 (5–1660)	274 (37–3156)	40 (1–380)	62 (6–494)	106 (21–806)	30 (3–173)
	0.1	97 (4–1421)	259 (35–2865)	32 (1–331)	52 (4–416)	93 (17–698)	25 (2–158)
	0.2	87 (2–1308)	219 (33–2629)	25 (1–252)	41 (3–368)	83 (14–677)	19 (2–109)
	0.3	70 (1–1072)	193 (23–2273)	18 (0–190)	33 (2–328)	64 (12–555)	14 (1–90)
SRPAH	0	411 (8–6625)	1151 (123–14641)	105 (2–1188)	184 (12–1829)	354 (65–3529)	76 (4–557)
	0.1	329 (6–5842)	987 (110–12112)	81 (2–831)	155 (8–1577)	320 (63–2865)	59 (3–416)
	0.2	270 (4–5187)	856 (82–10657)	62 (1–630)	121 (5–1371)	270 (46–2478)	43 (2–301)
	0.3	219 (2–4004)	721 (72–8412)	41 (0–580)	91 (3–1053)	208 (34–1973)	29 (1–204)
SRUMA	0	1122 (42–15808)	2938 (412–31284)	387 (15–3764)	592 (61–4769)	1076 (186–8298)	298 (27–1564)
	0.1	1014 (32–15442)	2489 (342–25263)	310 (10–3072)	515 (44–4197)	908 (180–7257)	240 (23–1271)
	0.2	861 (23–12004)	2291 (305–23117)	252 (6–2358)	411 (33–3786)	786 (127–6093)	179 (13–1089)
	0.3	682 (17–11003)	1853 (255–18373)	190 (5–1802)	332 (22–2974)	681 (118–5498)	137 (8–764)
SRVAL	0	254 (5–4653)	785 (98–9092)	61 (1–542)	119 (7–1069)	247 (45–1921)	42 (2–296)
	0.1	201 (3–4039)	669 (92–7802)	50 (1–432)	92 (4–974)	209 (37–1628)	29 (2–243)
	0.2	167 (2–3129)	557 (77–6143)	34 (0–372)	68 (3–822)	165 (24–1449)	22 (1–172)
	0.3	130 (1–2721)	469 (59–5217)	22 (0–231)	49 (2–670)	131 (19–1219)	13 (1–116)

Table 3 (continued). Posterior predictive distributions of total wild spawners, 25 years in the future, for 29 Chinook salmon populations.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
SRYFS	0	188 (2–3515)	622 (73–8120)	39 (0–407)	81 (3–890)	191 (30–1615)	26 (1–186)
	0.1	154 (1–3125)	538 (61–5883)	30 (0–289)	62 (2–717)	159 (25–1215)	19 (1–140)
	0.2	124 (1–2715)	454 (56–5750)	21 (0–225)	46 (1–631)	122 (23–1101)	13 (0–106)
	0.3	93 (1–2107)	394 (44–4856)	12 (0–144)	30 (1–446)	96 (14–808)	7 (0–70)
UCENT	0	338 (4–6095)	1177 (139–11943)	69 (1–696)	140 (6–1489)	340 (54–2600)	49 (3–348)
	0.1	282 (2–5271)	962 (113–12799)	48 (0–578)	112 (3–1446)	269 (47–2461)	34 (1–274)
	0.2	217 (2–4352)	785 (86–10649)	34 (0–451)	83 (2–1122)	214 (28–1908)	22 (1–205)
	0.3	165 (1–3713)	656 (81–8806)	21 (0–313)	57 (1–840)	175 (22–1427)	13 (0–152)
UCMET	0	874 (15–15948)	2405 (318–28031)	222 (3–2646)	402 (20–3680)	813 (130–5842)	152 (8–1167)
	0.1	732 (10–13784)	2178 (264–24477)	180 (1–1795)	310 (15–3339)	705 (121–5863)	110 (6–943)
	0.2	584 (6–10447)	1810 (244–24070)	124 (1–1439)	250 (9–3069)	558 (89–4560)	86 (3–733)
	0.3	436 (3–9490)	1521 (207–19164)	91 (1–912)	178 (5–2205)	447 (68–3768)	54 (2–479)
UCWEN	0	1471 (2–74486)	9987 (796–196590)	92 (0–1904)	287 (3–9857)	1295 (108–21396)	46 (1–664)
	0.1	985 (1–60143)	7458 (614–139277)	62 (0–1326)	181 (2–7117)	926 (71–19148)	25 (1–465)
	0.2	675 (1–47531)	5384 (416–103719)	33 (0–889)	99 (1–4765)	589 (36–11796)	14 (0–276)
	0.3	392 (0–35276)	4013 (276–94554)	17 (0–460)	50 (0–3141)	347 (19–9325)	7 (0–178)

Table 4. Posterior predictive distributions (median and 95% credible interval) of total wild spawners, 50 years in the future, for 29 Chinook salmon populations as a function of harvest mortality rate and average environmental conditions. Harvest is simulated as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
GRCAT	0	344 (0–13850)	1666 (86–33854)	18 (0–1122)	55 (0–2216)	289 (13–5883)	5 (0–179)
	0.1	264 (0–12494)	1340 (57–29032)	8 (0–556)	30 (0–1761)	179 (7–4421)	2 (0–108)
	0.2	163 (0–10109)	1017 (43–23681)	3 (0–380)	12 (0–1139)	102 (3–2903)	1 (0–47)
	0.3	88 (0–7726)	794 (28–20562)	1 (0–152)	4 (0–687)	52 (1–2058)	0 (0–25)
GRLOS	0	524 (6–9830)	1303 (119–19325)	149 (1–2666)	231 (8–2428)	480 (63–4593)	103 (2–841)
	0.1	454 (4–7721)	1073 (101–16643)	121 (0–2081)	186 (6–1946)	396 (50–4527)	79 (1–651)
	0.2	364 (2–7455)	958 (74–18188)	92 (0–1658)	145 (3–1674)	353 (35–3721)	53 (0–489)
	0.3	288 (1–6629)	781 (57–13009)	58 (0–1310)	106 (1–1337)	257 (33–2665)	32 (0–324)
GRMIN	0	571 (13–10023)	1287 (103–19028)	211 (2–2975)	286 (20–2747)	531 (76–4985)	156 (7–1006)
	0.1	495 (9–8463)	1154 (103–19861)	166 (2–2431)	240 (15–2161)	450 (64–3828)	114 (4–759)
	0.2	425 (4–7783)	970 (82–17427)	126 (1–2096)	200 (9–2029)	402 (55–3526)	93 (2–681)
	0.3	341 (3–6570)	855 (68–12895)	90 (0–1737)	151 (5–1692)	309 (41–3003)	67 (1–513)
GRUMA	0	163 (0–5360)	579 (36–13331)	12 (0–436)	33 (0–1002)	139 (9–1825)	4 (0–118)
	0.1	109 (0–4741)	504 (24–10387)	6 (0–421)	18 (0–742)	93 (5–1927)	2 (0–75)
	0.2	77 (0–3886)	402 (20–8493)	2 (0–212)	9 (0–471)	62 (2–1206)	1 (0–44)
	0.3	47 (0–3073)	302 (12–8201)	1 (0–118)	3 (0–381)	30 (1–840)	0 (0–20)
GRWEN	0	536 (1–13666)	1645 (127–31225)	94 (0–2198)	190 (2–2867)	502 (50–5256)	51 (0–622)
	0.1	449 (1–11160)	1312 (83–19749)	62 (0–1782)	131 (1–2458)	398 (32–5145)	27 (0–457)
	0.2	316 (0–9063)	1185 (74–18793)	33 (0–1210)	87 (0–1913)	296 (24–3806)	13 (0–337)
	0.3	232 (0–7641)	893 (55–16342)	16 (0–768)	48 (0–1382)	211 (12–2648)	5 (0–153)
IRMAI	0	997 (16–18108)	2359 (194–32867)	329 (3–4681)	484 (30–4615)	933 (120–7331)	233 (8–1769)
	0.1	903 (9–15324)	2216 (188–28171)	261 (2–4442)	404 (16–4228)	796 (107–7128)	178 (4–1440)
	0.2	750 (5–14619)	1832 (159–25710)	203 (1–3744)	325 (8–3676)	662 (75–6618)	134 (1–1027)
	0.3	589 (3–12047)	1453 (128–23899)	142 (0–2772)	245 (4–2827)	530 (59–5210)	90 (1–809)

Table 4 (continued). Posterior predictive distributions of total wild spawners, 50 years in the future, for 29 Chinook salmon populations.

		Constant baseline			Step change 1970		
Population	Mort.	Unconditional	Good	Bad	Unconditional	Good	Bad
MFBEA	0	690 (16–12392)	1586 (117–25660)	263 (3–3350)	365 (25–2694)	624 (79–4349)	171 (10–1401)
	0.1	607 (11–9724)	1510 (105–21102)	214 (1–2436)	297 (18–2477)	566 (62–3699)	139 (5–1202)
	0.2	494 (8–9083)	1227 (93–17487)	160 (1–2217)	238 (10–2052)	443 (55–3881)	100 (2–900)
	0.3	384 (3–6697)	1030 (73–13319)	122 (0–1473)	174 (6–1825)	355 (43–3370)	67 (1–713)
MFBIG	0	269 (12–3704)	567 (51–6114)	122 (4–1179)	155 (17–1097)	245 (31–1665)	91 (10–593)
	0.1	232 (10–3155)	504 (44–5254)	110 (2–1017)	135 (15–895)	225 (33–1441)	76 (8–544)
	0.2	203 (8–2982)	458 (38–5685)	93 (2–783)	111 (11–762)	185 (28–1270)	63 (5–459)
	0.3	168 (6–2412)	375 (32–4946)	73 (1–807)	95 (8–718)	159 (21–1092)	53 (3–416)
MFCAM	0	138 (1–2450)	376 (24–4539)	40 (0–550)	59 (2–622)	126 (14–959)	21 (0–207)
	0.1	116 (0–2098)	317 (20–4388)	30 (0–487)	45 (1–525)	112 (10–875)	14 (0–146)
	0.2	92 (0–1808)	285 (17–3822)	21 (0–321)	34 (0–377)	80 (8–766)	9 (0–122)
	0.3	69 (0–1594)	223 (15–3632)	13 (0–217)	22 (0–330)	63 (5–583)	4 (0–88)
MFCHA	0	717 (23–11194)	1588 (126–21649)	317 (4–3315)	400 (32–2928)	638 (96–4429)	223 (16–1653)
	0.1	632 (16–9851)	1425 (122–19215)	255 (3–2741)	326 (23–2399)	531 (86–4198)	176 (9–1367)
	0.2	531 (11–8399)	1295 (109–13456)	207 (1–2320)	282 (18–2179)	475 (63–3284)	150 (7–1018)
	0.3	441 (6–7189)	1029 (78–11465)	166 (1–1997)	220 (10–1973)	411 (53–3427)	106 (2–941)
MFLOO	0	129 (3–1897)	308 (23–3820)	51 (0–530)	66 (5–513)	114 (15–828)	33 (2–251)
	0.1	111 (2–1901)	266 (22–3290)	41 (0–441)	58 (3–438)	105 (14–733)	29 (1–251)
	0.2	95 (1–1657)	250 (20–3223)	32 (0–391)	48 (2–382)	87 (12–630)	22 (0–201)
	0.3	80 (1–1342)	201 (15–2629)	23 (0–303)	38 (1–325)	70 (8–554)	15 (0–130)
MFMAR	0	441 (3–8173)	1211 (74–18940)	125 (1–1788)	192 (5–1987)	420 (50–3389)	67 (1–680)
	0.1	375 (2–7164)	1118 (74–14548)	90 (0–1382)	146 (2–1723)	366 (35–2708)	44 (0–499)
	0.2	295 (1–6098)	805 (56–13934)	62 (0–1082)	104 (1–1337)	280 (23–2371)	28 (0–411)
	0.3	210 (0–5337)	728 (47–13088)	32 (0–698)	64 (0–1030)	203 (18–1796)	14 (0–258)
MFSUL	0	115 (0–2612)	356 (22–5591)	25 (0–394)	40 (0–515)	116 (10–904)	10 (0–146)
	0.1	88 (0–2157)	304 (18–3641)	15 (0–308)	28 (0–411)	85 (6–861)	6 (0–97)
	0.2	69 (0–1835)	250 (14–3859)	9 (0–218)	18 (0–355)	62 (5–646)	3 (0–67)
	0.3	48 (0–1533)	204 (11–3736)	4 (0–133)	9 (0–242)	43 (2–505)	1 (0–40)
MFUMA	0	145 (4–2104)	337 (25–3732)	62 (1–607)	77 (7–578)	131 (18–795)	43 (4–332)
	0.1	122 (3–1963)	278 (22–4225)	52 (1–525)	65 (6–528)	113 (13–828)	37 (3–248)
	0.2	102 (2–1512)	241 (19–2848)	41 (0–453)	55 (4–453)	97 (10–661)	28 (2–235)
	0.3	88 (1–1467)	210 (19–2571)	33 (0–377)	43 (2–348)	79 (9–559)	20 (1–175)
SFEFS	0	435 (7–6787)	970 (77–13073)	157 (1–1872)	205 (12–1863)	395 (48–3361)	107 (4–706)
	0.1	369 (3–6828)	847 (69–13123)	126 (0–1623)	176 (8–1686)	348 (43–2558)	82 (2–687)
	0.2	305 (2–5876)	784 (57–11412)	95 (0–1283)	139 (5–1327)	294 (32–2230)	57 (1–531)
	0.3	251 (1–5098)	618 (51–8094)	68 (0–909)	105 (2–1050)	231 (27–1877)	37 (0–388)
SFMAI	0	972 (45–12726)	2014 (156–23810)	526 (13–4327)	582 (61–3658)	891 (135–5093)	353 (41–2228)
	0.1	888 (42–12447)	1848 (185–22662)	425 (14–4203)	509 (52–3633)	817 (119–4780)	290 (29–1991)
	0.2	778 (35–10146)	1638 (146–20500)	369 (8–3285)	442 (42–3204)	702 (97–4367)	252 (21–1586)
	0.3	649 (27–9486)	1473 (145–16842)	290 (4–2487)	362 (33–2435)	577 (83–3981)	210 (16–1295)
SFSEC	0	528 (23–7300)	1157 (91–14171)	230 (6–2264)	292 (28–1916)	459 (65–2841)	161 (17–1314)
	0.1	449 (18–6087)	981 (88–12315)	202 (5–1787)	255 (25–1773)	404 (61–2337)	141 (15–1121)
	0.2	393 (13–5514)	857 (64–10290)	169 (3–1618)	217 (16–1580)	366 (49–2489)	116 (7–836)
	0.3	342 (7–4802)	745 (73–9638)	142 (2–1308)	183 (13–1331)	294 (38–1763)	99 (6–733)
SNTUC	0	412 (1–8974)	1183 (77–17164)	95 (0–1797)	167 (2–2062)	395 (38–2890)	51 (0–565)
	0.1	343 (1–7368)	1048 (63–16014)	66 (0–1140)	127 (1–1535)	317 (28–2779)	30 (0–490)
	0.2	265 (0–6183)	866 (50–13974)	37 (0–976)	87 (0–1260)	249 (21–2486)	17 (0–320)
	0.3	188 (0–4851)	698 (36–11582)	19 (0–685)	49 (0–917)	168 (11–1963)	7 (0–220)
SREFS	0	712 (9–12254)	1974 (154–22834)	248 (1–2875)	335 (12–3435)	667 (79–6058)	142 (3–1147)
	0.1	617 (4–11348)	1532 (126–20211)	193 (0–2796)	270 (9–2719)	530 (69–4899)	99 (2–1052)
	0.2	502 (3–10021)	1344 (87–20927)	137 (0–1876)	198 (4–2143)	426 (51–4667)	67 (1–626)
	0.3	390 (1–9069)	1149 (61–17699)	83 (0–1541)	135 (1–1701)	348 (31–3237)	33 (0–490)

Table 4 (continued). Posterior predictive distributions of total wild spawners, 50 years in the future, for 29 Chinook salmon populations.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
SRLEM	0	553 (3–10211)	1529 (98–21024)	139 (0–2022)	219 (5–2129)	490 (57–3468)	71 (1–702)
	0.1	443 (2–9129)	1320 (86–20075)	91 (0–1717)	166 (2–1802)	386 (36–3268)	47 (0–560)
	0.2	342 (1–7659)	1101 (66–15379)	62 (0–1374)	112 (1–1609)	324 (28–3172)	24 (0–424)
	0.3	247 (0–6177)	877 (53–12294)	35 (0–885)	69 (0–1184)	226 (19–2103)	11 (0–247)
SRLMA	0	247 (11–3614)	550 (51–6071)	115 (3–1044)	137 (14–979)	222 (34–1348)	81 (8–532)
	0.1	219 (7–3078)	468 (36–5491)	96 (3–980)	119 (11–868)	204 (27–1302)	69 (5–451)
	0.2	185 (6–2615)	429 (35–5067)	78 (2–735)	105 (8–772)	168 (21–1113)	59 (4–397)
	0.3	155 (4–2323)	351 (30–4464)	64 (1–716)	86 (6–577)	141 (18–960)	47 (2–348)
SRNFS	0	114 (3–1820)	268 (24–3974)	49 (1–492)	62 (4–490)	106 (16–676)	32 (2–254)
	0.1	98 (2–1609)	233 (19–3312)	41 (0–487)	51 (3–411)	90 (12–626)	26 (2–189)
	0.2	85 (1–1388)	207 (14–2640)	31 (0–346)	43 (2–354)	79 (10–564)	20 (1–165)
	0.3	70 (1–1136)	174 (15–2542)	24 (0–271)	33 (1–307)	60 (6–447)	15 (0–126)
SRPAH	0	384 (4–7315)	986 (71–16064)	130 (1–2285)	183 (6–1608)	360 (46–3122)	76 (1–657)
	0.1	325 (3–6965)	837 (57–14276)	96 (0–1371)	144 (3–1440)	297 (35–2449)	58 (1–516)
	0.2	259 (1–5857)	733 (53–12285)	70 (0–1226)	114 (1–1286)	239 (27–2066)	39 (0–455)
	0.3	211 (1–4402)	627 (42–9682)	45 (0–894)	80 (1–948)	190 (21–2068)	22 (0–295)
SRUMA	0	1122 (28–15778)	2494 (214–27355)	468 (6–4739)	607 (48–4637)	1052 (121–6717)	334 (16–2241)
	0.1	982 (21–14021)	2210 (167–25360)	388 (4–4190)	514 (34–4568)	894 (116–7129)	265 (11–2051)
	0.2	849 (16–12395)	1965 (153–24967)	317 (2–3464)	399 (21–3249)	754 (114–5117)	197 (7–1604)
	0.3	706 (8–10834)	1787 (153–22316)	226 (1–2978)	319 (12–2866)	623 (76–4290)	142 (3–1311)
SRVAL	0	251 (2–4772)	658 (43–9588)	81 (0–961)	108 (3–1171)	231 (25–1721)	41 (1–385)
	0.1	208 (1–3774)	571 (44–8946)	56 (0–940)	85 (2–1013)	189 (22–1634)	28 (0–315)
	0.2	168 (0–3526)	518 (33–6803)	38 (0–590)	63 (1–767)	162 (17–1543)	17 (0–206)
	0.3	125 (0–3034)	437 (29–5962)	22 (0–432)	40 (0–509)	119 (11–983)	9 (0–135)
SRYFS	0	189 (1–3674)	557 (34–7547)	42 (0–721)	76 (1–900)	167 (20–1409)	19 (0–286)
	0.1	150 (0–3355)	461 (30–6188)	33 (0–568)	54 (0–663)	148 (13–1221)	12 (0–198)
	0.2	123 (0–2858)	406 (23–6398)	19 (0–435)	35 (0–523)	110 (11–943)	6 (0–131)
	0.3	84 (0–2411)	322 (20–5432)	10 (0–255)	21 (0–384)	82 (7–869)	3 (0–74)
UCENT	0	329 (1–6576)	950 (57–13893)	72 (0–1296)	126 (1–1451)	284 (33–2624)	36 (0–524)
	0.1	262 (1–5419)	787 (51–11671)	52 (0–857)	96 (1–1178)	249 (25–2097)	24 (0–397)
	0.2	197 (0–5042)	668 (47–10348)	30 (0–724)	65 (0–874)	185 (13–1708)	12 (0–238)
	0.3	149 (0–4362)	561 (29–8080)	16 (0–493)	40 (0–738)	127 (6–1296)	5 (0–184)
UCMET	0	843 (5–15109)	2161 (172–33360)	248 (0–3419)	376 (8–3543)	743 (76–6222)	142 (1–1347)
	0.1	715 (2–12939)	1919 (144–25384)	195 (0–3046)	304 (4–3254)	661 (71–5728)	110 (1–1262)
	0.2	558 (1–11563)	1668 (110–23237)	124 (0–2007)	223 (2–2473)	500 (42–4404)	68 (0–819)
	0.3	418 (0–9781)	1349 (77–21088)	75 (0–1841)	142 (0–1841)	394 (29–2833)	33 (0–546)
UCWEN	0	1263 (0–94186)	9177 (373–207481)	33 (0–2335)	95 (0–9299)	942 (34–23954)	4 (0–368)
	0.1	789 (0–65070)	7536 (246–144594)	15 (0–1315)	40 (0–4910)	527 (11–15624)	1 (0–144)
	0.2	427 (0–52773)	5461 (158–161662)	5 (0–587)	12 (0–3089)	265 (2–10434)	0 (0–74)
	0.3	186 (0–41522)	3084 (85–93054)	1 (0–240)	3 (0–2069)	89 (1–5811)	0 (0–25)

Table 5. Posterior predictive distributions (median and 95% credible interval) of total wild spawners as a percentage of MAT, 25 years in the future, for 29 Chinook salmon populations as a function of harvest mortality rate and average environmental conditions. Harvest is simulated as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
GRCAT	0	38 (0–1219)	200 (16–2529)	4 (0–60)	11 (0–253)	40 (4–491)	2 (0–27)
	0.1	29 (0–1097)	158 (15–2251)	2 (0–47)	7 (0–187)	28 (2–391)	2 (0–19)
	0.2	20 (0–877)	129 (9–1876)	1 (0–32)	5 (0–146)	18 (1–305)	1 (0–14)
	0.3	13 (0–731)	94 (6–1551)	1 (0–22)	2 (0–100)	12 (1–228)	0 (0–7)
GRLOS	0	53 (1–742)	151 (17–1386)	13 (0–132)	25 (2–198)	54 (10–384)	10 (1–67)
	0.1	45 (1–759)	130 (16–1377)	10 (0–115)	21 (1–189)	46 (8–393)	8 (1–54)
	0.2	37 (1–616)	112 (15–1163)	8 (0–81)	17 (1–172)	39 (6–336)	6 (0–46)
	0.3	30 (0–508)	96 (12–1074)	6 (0–67)	12 (1–133)	30 (5–243)	4 (0–30)
GRMIN	0	76 (3–1194)	220 (24–2151)	23 (1–188)	40 (4–323)	79 (13–597)	18 (2–102)
	0.1	64 (2–982)	186 (22–1988)	18 (0–165)	32 (3–279)	64 (12–519)	15 (1–95)
	0.2	57 (1–807)	153 (17–1596)	14 (0–146)	27 (2–242)	54 (11–525)	11 (1–73)
	0.3	47 (1–702)	135 (17–1287)	10 (0–118)	22 (1–197)	48 (8–364)	8 (1–56)
GRUMA	0	19 (0–500)	78 (8–979)	2 (0–40)	5 (0–105)	18 (2–228)	1 (0–12)
	0.1	13 (0–405)	66 (6–807)	1 (0–21)	4 (0–89)	14 (2–187)	1 (0–10)
	0.2	10 (0–352)	51 (5–750)	1 (0–12)	3 (0–58)	9 (1–136)	1 (0–7)
	0.3	7 (0–295)	42 (3–564)	0 (0–11)	2 (0–49)	6 (1–91)	0 (0–4)
GRWEN	0	73 (1–1398)	271 (28–2742)	13 (0–171)	29 (1–389)	77 (11–712)	10 (0–73)
	0.1	59 (0–1205)	222 (27–2825)	10 (0–131)	23 (1–308)	60 (10–569)	7 (0–52)
	0.2	47 (0–1132)	188 (19–2123)	6 (0–99)	17 (0–237)	46 (7–478)	4 (0–50)
	0.3	36 (0–880)	162 (16–1659)	4 (0–77)	11 (0–189)	35 (4–349)	3 (0–32)
IRMAI	0	132 (4–1959)	372 (44–3787)	38 (1–307)	66 (6–614)	137 (27–1104)	29 (2–177)
	0.1	117 (3–1796)	349 (41–3616)	31 (1–312)	55 (4–510)	117 (21–953)	23 (2–145)
	0.2	98 (2–1602)	296 (36–3180)	25 (0–226)	45 (3–429)	101 (19–743)	18 (1–114)
	0.3	81 (1–1458)	262 (28–2479)	17 (0–157)	35 (2–338)	81 (13–597)	13 (1–90)
MFBEA	0	93 (3–1345)	236 (33–2710)	29 (1–235)	47 (4–386)	91 (17–646)	21 (2–111)
	0.1	78 (2–1200)	217 (24–2432)	24 (1–247)	39 (3–383)	80 (13–554)	18 (2–101)
	0.2	68 (2–976)	180 (25–2159)	19 (0–165)	33 (2–307)	64 (11–523)	14 (1–81)
	0.3	54 (1–923)	168 (18–1723)	13 (0–124)	25 (1–254)	52 (8–408)	10 (1–68)
MFBIG	0	26 (1–331)	64 (8–604)	11 (1–89)	14 (2–112)	25 (4–202)	8 (1–44)
	0.1	23 (1–286)	55 (7–585)	9 (0–69)	13 (2–93)	22 (4–144)	7 (1–35)
	0.2	21 (1–269)	49 (7–531)	8 (0–66)	11 (1–86)	20 (4–145)	6 (1–30)
	0.3	17 (1–233)	46 (6–444)	6 (0–56)	9 (1–68)	17 (3–111)	5 (0–27)
MFCAM	0	27 (0–486)	82 (9–998)	6 (0–65)	13 (1–125)	28 (5–220)	5 (0–32)
	0.1	22 (0–422)	73 (9–796)	5 (0–47)	10 (0–98)	23 (4–188)	3 (0–25)
	0.2	19 (0–359)	63 (7–710)	4 (0–42)	7 (0–83)	19 (3–140)	2 (0–18)
	0.3	14 (0–304)	54 (6–699)	2 (0–27)	5 (0–71)	14 (2–138)	1 (0–13)
MFCHA	0	96 (4–1419)	234 (28–2305)	35 (1–313)	51 (5–413)	91 (17–808)	25 (3–154)
	0.1	83 (3–1268)	206 (25–2536)	27 (1–274)	43 (4–362)	80 (15–647)	21 (2–115)
	0.2	72 (2–1004)	186 (20–1971)	22 (0–243)	36 (3–324)	68 (12–600)	17 (2–106)
	0.3	61 (2–945)	164 (21–1897)	17 (0–176)	30 (2–262)	58 (9–526)	13 (1–81)
MFLOO	0	26 (1–381)	67 (8–744)	8 (0–73)	13 (1–117)	24 (5–200)	6 (1–34)
	0.1	23 (1–360)	61 (8–698)	7 (0–66)	11 (1–102)	22 (4–151)	5 (0–28)
	0.2	20 (0–285)	51 (7–603)	5 (0–49)	9 (1–87)	18 (3–164)	4 (0–24)
	0.3	16 (0–266)	47 (6–465)	4 (0–41)	7 (0–67)	15 (3–111)	3 (0–20)
MFMAR	0	89 (2–1527)	297 (31–3126)	20 (0–215)	40 (2–410)	90 (15–651)	14 (1–103)
	0.1	76 (1–1358)	247 (29–2665)	16 (0–142)	32 (1–355)	76 (14–665)	10 (1–81)
	0.2	61 (1–1159)	202 (24–2317)	11 (0–121)	25 (1–301)	59 (10–511)	7 (0–65)
	0.3	47 (0–973)	176 (23–2001)	8 (0–82)	17 (0–210)	47 (7–373)	5 (0–42)

Table 5 (continued). Posterior predictive distributions of total wild spawners as a percentage of MAT, 25 years in the future, for 29 Chinook salmon populations.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
MFSUL	0	23 (0–469)	81 (9–914)	4 (0–47)	9 (0–115)	23 (3–170)	3 (0–24)
	0.1	19 (0–424)	68 (8–850)	3 (0–33)	7 (0–94)	20 (3–162)	2 (0–18)
	0.2	14 (0–360)	61 (6–791)	2 (0–21)	5 (0–73)	14 (2–149)	1 (0–11)
	0.3	11 (0–311)	48 (6–629)	1 (0–20)	3 (0–58)	10 (1–125)	1 (0–8)
MFUMA	0	19 (1–258)	47 (6–459)	7 (0–64)	10 (1–80)	18 (3–156)	5 (1–28)
	0.1	16 (1–231)	40 (6–505)	6 (0–53)	9 (1–73)	16 (3–119)	4 (0–25)
	0.2	14 (0–211)	37 (5–382)	5 (0–40)	7 (1–60)	13 (2–107)	4 (0–22)
	0.3	12 (0–182)	31 (4–310)	4 (0–34)	6 (0–49)	11 (2–86)	3 (0–20)
SFEFS	0	41 (1–657)	114 (17–1222)	13 (0–114)	21 (1–189)	43 (7–303)	10 (1–49)
	0.1	37 (1–571)	103 (16–1126)	10 (0–104)	18 (1–155)	35 (6–247)	8 (1–41)
	0.2	32 (1–449)	92 (13–934)	8 (0–68)	15 (1–136)	30 (5–215)	6 (0–31)
	0.3	26 (0–423)	78 (11–746)	6 (0–54)	11 (0–118)	26 (4–189)	4 (0–24)
SFMAI	0	98 (6–1191)	217 (29–2423)	39 (2–365)	56 (7–398)	91 (16–659)	32 (4–150)
	0.1	87 (5–1068)	207 (27–2261)	34 (2–289)	49 (6–356)	85 (15–530)	28 (3–140)
	0.2	78 (4–1014)	173 (22–1841)	28 (1–271)	43 (5–313)	74 (15–493)	23 (3–114)
	0.3	65 (3–808)	152 (21–1621)	23 (1–193)	36 (4–270)	62 (12–438)	19 (2–106)
SFSEC	0	72 (4–769)	156 (19–1418)	28 (1–219)	38 (4–268)	64 (12–423)	20 (3–96)
	0.1	60 (3–747)	146 (20–1380)	22 (1–212)	33 (4–249)	56 (11–409)	17 (2–90)
	0.2	53 (2–700)	121 (17–1302)	19 (1–195)	28 (3–218)	50 (10–328)	14 (1–70)
	0.3	45 (1–627)	113 (16–1177)	16 (0–131)	23 (2–186)	42 (8–297)	11 (1–66)
SNTUC	0	87 (1–1720)	276 (33–3151)	17 (0–208)	37 (2–418)	84 (14–733)	12 (1–101)
	0.1	71 (1–1361)	245 (23–2782)	13 (0–135)	28 (1–352)	71 (11–606)	9 (0–75)
	0.2	57 (0–1176)	211 (26–2187)	9 (0–111)	21 (1–291)	53 (9–537)	6 (0–56)
	0.3	43 (0–1077)	160 (18–2001)	6 (0–90)	14 (0–242)	40 (6–428)	3 (0–36)
SREFS	0	75 (2–1196)	213 (25–2025)	20 (1–179)	35 (2–363)	68 (13–558)	13 (1–91)
	0.1	60 (1–1039)	191 (23–2181)	15 (0–144)	28 (1–305)	61 (10–526)	10 (0–71)
	0.2	50 (1–901)	164 (21–1717)	12 (0–107)	22 (1–235)	51 (8–395)	7 (0–55)
	0.3	40 (0–740)	134 (15–1511)	8 (0–75)	16 (1–170)	39 (6–330)	5 (0–41)
SRLEM	0	27 (0–482)	88 (10–978)	5 (0–66)	11 (1–120)	27 (4–194)	4 (0–29)
	0.1	22 (0–450)	74 (7–814)	4 (0–45)	9 (0–101)	22 (3–189)	3 (0–22)
	0.2	17 (0–355)	62 (7–759)	3 (0–38)	7 (0–88)	18 (3–140)	2 (0–17)
	0.3	13 (0–289)	53 (5–697)	2 (0–20)	5 (0–60)	12 (2–120)	1 (0–13)
SRLMA	0	12 (1–155)	30 (4–300)	5 (0–41)	7 (1–51)	11 (2–87)	4 (0–19)
	0.1	11 (1–144)	25 (3–264)	4 (0–37)	6 (1–45)	10 (2–71)	3 (0–17)
	0.2	10 (0–109)	23 (3–236)	3 (0–30)	5 (1–38)	9 (2–67)	3 (0–16)
	0.3	8 (0–114)	20 (3–195)	3 (0–25)	4 (0–31)	8 (1–50)	2 (0–11)
SRNFS	0	23 (1–332)	55 (7–631)	8 (0–76)	12 (1–99)	21 (4–161)	6 (1–35)
	0.1	19 (1–284)	52 (7–573)	6 (0–66)	10 (1–83)	19 (3–140)	5 (0–32)
	0.2	17 (0–262)	44 (7–526)	5 (0–50)	8 (1–74)	17 (3–135)	4 (0–22)
	0.3	14 (0–214)	39 (5–455)	4 (0–38)	7 (0–66)	13 (2–111)	3 (0–18)
SRPAH	0	41 (1–662)	115 (12–1464)	10 (0–119)	18 (1–183)	35 (6–353)	8 (0–56)
	0.1	33 (1–584)	99 (11–1211)	8 (0–83)	16 (1–158)	32 (6–287)	6 (0–42)
	0.2	27 (0–519)	86 (8–1066)	6 (0–63)	12 (1–137)	27 (5–248)	4 (0–30)
	0.3	22 (0–400)	72 (7–841)	4 (0–58)	9 (0–105)	21 (3–197)	3 (0–20)
SRUMA	0	112 (4–1581)	294 (41–3128)	39 (1–376)	59 (6–477)	108 (19–830)	30 (3–156)
	0.1	101 (3–1544)	249 (34–2526)	31 (1–307)	51 (4–420)	91 (18–726)	24 (2–127)
	0.2	86 (2–1200)	229 (31–2312)	25 (1–236)	41 (3–379)	79 (13–609)	18 (1–109)
	0.3	68 (2–1100)	185 (25–1837)	19 (0–180)	33 (2–297)	68 (12–550)	14 (1–76)
SRVAL	0	51 (1–931)	157 (20–1818)	12 (0–108)	24 (1–214)	49 (9–384)	8 (0–59)
	0.1	40 (1–808)	134 (18–1560)	10 (0–86)	18 (1–195)	42 (7–326)	6 (0–49)
	0.2	33 (0–626)	111 (15–1229)	7 (0–74)	14 (1–164)	33 (5–290)	4 (0–34)
	0.3	26 (0–544)	94 (12–1043)	4 (0–46)	10 (0–134)	26 (4–244)	3 (0–23)

Table 5 (continued). Posterior predictive distributions of total wild spawners as a percentage of MAT, 25 years in the future, for 29 Chinook salmon populations.

| Population | Mort. | Constant baseline | | | Step change 1970 | | |
		Unconditional	Good	Bad	Unconditional	Good	Bad
SRYFS	0	38 (0–703)	124 (15–1624)	8 (0–81)	16 (1–178)	38 (6–323)	5 (0–37)
	0.1	31 (0–625)	108 (12–1177)	6 (0–58)	12 (1–143)	32 (5–243)	4 (0–28)
	0.2	25 (0–543)	91 (11–1150)	4 (0–45)	9 (0–126)	24 (5–220)	3 (0–21)
	0.3	19 (0–421)	79 (9–971)	2 (0–29)	6 (0–89)	19 (3–162)	1 (0–14)
UCENT	0	68 (1–1219)	235 (28–2389)	14 (0–139)	28 (1–298)	68 (11–520)	10 (1–70)
	0.1	56 (0–1054)	192 (23–2560)	10 (0–116)	22 (1–289)	54 (9–492)	7 (0–55)
	0.2	43 (0–870)	157 (17–2130)	7 (0–90)	17 (0–224)	43 (6–382)	4 (0–41)
	0.3	33 (0–743)	131 (16–1761)	4 (0–63)	11 (0–168)	35 (4–285)	3 (0–30)
UCMET	0	44 (1–797)	120 (16–1402)	11 (0–132)	20 (1–184)	41 (7–292)	8 (0–58)
	0.1	37 (1–689)	109 (13–1224)	9 (0–90)	16 (1–167)	35 (6–293)	5 (0–47)
	0.2	29 (0–522)	90 (12–1203)	6 (0–72)	13 (0–153)	28 (4–228)	4 (0–37)
	0.3	22 (0–475)	76 (10–958)	5 (0–46)	9 (0–110)	22 (3–188)	3 (0–24)
UCWEN	0	74 (0–3724)	499 (40–9829)	5 (0–95)	14 (0–493)	65 (5–1070)	2 (0–33)
	0.1	49 (0–3007)	373 (31–6964)	3 (0–66)	9 (0–356)	46 (4–957)	1 (0–23)
	0.2	34 (0–2377)	269 (21–5186)	2 (0–44)	5 (0–238)	29 (2–590)	1 (0–14)
	0.3	20 (0–1764)	201 (14–4728)	1 (0–23)	2 (0–157)	17 (1–466)	0 (0–9)

Table 6. Posterior predictive distributions (median and 95% credible interval) of total wild spawners as a percentage of MAT, 50 years in the future, for 29 Chinook salmon populations as a function of harvest mortality rate and average environmental conditions. Harvest is simulated as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

| Population | Mort. | Constant baseline | | | Step change 1970 | | |
		Unconditional	Good	Bad	Unconditional	Good	Bad
GRCAT	0	34 (0–1385)	167 (9–3385)	2 (0–112)	6 (0–222)	29 (1–588)	0 (0–18)
	0.1	26 (0–1249)	134 (6–2903)	1 (0–56)	3 (0–176)	18 (1–442)	0 (0–11)
	0.2	16 (0–1011)	102 (4–2368)	0 (0–38)	1 (0–114)	10 (0–290)	0 (0–5)
	0.3	9 (0–773)	79 (3–2056)	0 (0–15)	0 (0–69)	5 (0–206)	0 (0–3)
GRLOS	0	52 (1–983)	130 (12–1932)	15 (0–267)	23 (1–243)	48 (6–459)	10 (0–84)
	0.1	45 (0–772)	107 (10–1664)	12 (0–208)	19 (1–195)	40 (5–453)	8 (0–65)
	0.2	36 (0–745)	96 (7–1819)	9 (0–166)	15 (0–167)	35 (3–372)	5 (0–49)
	0.3	29 (0–663)	78 (6–1301)	6 (0–131)	11 (0–134)	26 (3–266)	3 (0–32)
GRMIN	0	76 (2–1336)	172 (14–2537)	28 (0–397)	38 (3–366)	71 (10–665)	21 (1–134)
	0.1	66 (1–1128)	154 (14–2648)	22 (0–324)	32 (2–288)	60 (8–510)	15 (1–101)
	0.2	57 (1–1038)	129 (11–2324)	17 (0–280)	27 (1–271)	54 (7–470)	12 (0–91)
	0.3	45 (0–876)	114 (9–1719)	12 (0–232)	20 (1–226)	41 (5–400)	9 (0–68)
GRUMA	0	16 (0–536)	58 (4–1333)	1 (0–44)	3 (0–100)	14 (1–182)	0 (0–12)
	0.1	11 (0–474)	50 (2–1039)	1 (0–42)	2 (0–74)	9 (0–193)	0 (0–8)
	0.2	8 (0–389)	40 (2–849)	0 (0–21)	1 (0–47)	6 (0–121)	0 (0–4)
	0.3	5 (0–307)	30 (1–820)	0 (0–12)	0 (0–38)	3 (0–84)	0 (0–2)
GRWEN	0	72 (0–1822)	219 (17–4163)	12 (0–293)	25 (0–382)	67 (7–701)	7 (0–83)
	0.1	60 (0–1488)	175 (11–2633)	8 (0–238)	18 (0–328)	53 (4–686)	4 (0–61)
	0.2	42 (0–1208)	158 (10–2506)	4 (0–161)	12 (0–255)	40 (3–507)	2 (0–45)
	0.3	31 (0–1019)	119 (7–2179)	2 (0–102)	6 (0–184)	28 (2–353)	1 (0–20)
IRMAI	0	133 (2–2414)	315 (26–4382)	44 (0–624)	65 (4–615)	124 (16–977)	31 (1–236)
	0.1	120 (1–2043)	295 (25–3756)	35 (0–592)	54 (2–564)	106 (14–950)	24 (1–192)
	0.2	100 (1–1949)	244 (21–3428)	27 (0–499)	43 (1–490)	88 (10–882)	18 (0–137)
	0.3	79 (0–1606)	194 (17–3187)	19 (0–370)	33 (1–377)	71 (8–695)	12 (0–108)

Table 6 (continued). Posterior predictive distributions of total wild spawners as a percentage of MAT, 50
years in the future, for 29 Chinook salmon populations.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
MFBEA	0	92 (2–1652)	211 (16–3421)	35 (0–447)	49 (3–359)	83 (11–580)	23 (1–187)
	0.1	81 (2–1296)	201 (14–2814)	29 (0–325)	40 (2–330)	75 (8–493)	19 (1–160)
	0.2	66 (1–1211)	164 (12–2332)	21 (0–296)	32 (1–274)	59 (7–517)	13 (0–120)
	0.3	51 (0–893)	137 (10–1776)	16 (0–196)	23 (1–243)	47 (6–449)	9 (0–95)
MFBIG	0	27 (1–370)	57 (5–611)	12 (0–118)	15 (2–110)	24 (3–167)	9 (1–59)
	0.1	23 (1–315)	50 (4–525)	11 (0–102)	14 (1–89)	22 (3–144)	8 (1–54)
	0.2	20 (1–298)	46 (4–568)	9 (0–78)	11 (1–76)	18 (3–127)	6 (1–46)
	0.3	17 (1–241)	37 (3–495)	7 (0–81)	9 (1–72)	16 (2–109)	5 (0–42)
MFCAM	0	28 (0–490)	75 (5–908)	8 (0–110)	12 (0–124)	25 (3–192)	4 (0–41)
	0.1	23 (0–420)	63 (4–878)	6 (0–97)	9 (0–105)	22 (2–175)	3 (0–29)
	0.2	18 (0–362)	57 (3–764)	4 (0–64)	7 (0–75)	16 (2–153)	2 (0–24)
	0.3	14 (0–319)	45 (3–726)	3 (0–43)	4 (0–66)	13 (1–117)	1 (0–18)
MFCHA	0	96 (3–1493)	212 (17–2887)	42 (1–442)	53 (4–390)	85 (13–591)	30 (2–220)
	0.1	84 (2–1313)	190 (16–2562)	34 (0–365)	44 (3–320)	71 (11–560)	23 (1–182)
	0.2	71 (1–1120)	173 (15–1794)	28 (0–309)	38 (2–291)	63 (8–438)	20 (1–136)
	0.3	59 (1–959)	137 (10–1529)	22 (0–266)	29 (1–263)	55 (7–457)	14 (0–126)
MFLOO	0	26 (1–379)	62 (5–764)	10 (0–106)	13 (1–103)	23 (3–166)	7 (0–50)
	0.1	22 (0–380)	53 (4–658)	8 (0–88)	12 (1–88)	21 (3–147)	6 (0–50)
	0.2	19 (0–331)	50 (4–645)	6 (0–78)	10 (0–76)	17 (2–126)	4 (0–40)
	0.3	16 (0–268)	40 (3–526)	5 (0–61)	8 (0–65)	14 (2–111)	3 (0–26)
MFMAR	0	88 (1–1635)	242 (15–3788)	25 (0–358)	38 (1–397)	84 (10–678)	13 (0–136)
	0.1	75 (0–1433)	224 (15–2910)	18 (0–276)	29 (0–345)	73 (7–542)	9 (0–100)
	0.2	59 (0–1220)	161 (11–2787)	12 (0–216)	21 (0–267)	56 (5–474)	6 (0–82)
	0.3	42 (0–1067)	146 (9–2618)	6 (0–140)	13 (0–206)	41 (4–359)	3 (0–52)
MFSUL	0	23 (0–522)	71 (4–1118)	5 (0–79)	8 (0–103)	23 (2–181)	2 (0–29)
	0.1	18 (0–431)	61 (4–728)	3 (0–62)	6 (0–82)	17 (1–172)	1 (0–19)
	0.2	14 (0–367)	50 (3–772)	2 (0–44)	4 (0–71)	12 (1–129)	1 (0–13)
	0.3	10 (0–307)	41 (2–747)	1 (0–27)	2 (0–48)	9 (0–101)	0 (0–8)
MFUMA	0	19 (1–281)	45 (3–498)	8 (0–81)	10 (1–77)	17 (2–106)	6 (0–44)
	0.1	16 (0–262)	37 (3–563)	7 (0–70)	9 (1–70)	15 (2–110)	5 (0–33)
	0.2	14 (0–202)	32 (3–380)	5 (0–60)	7 (1–60)	13 (1–88)	4 (0–31)
	0.3	12 (0–196)	28 (3–343)	4 (0–50)	6 (0–46)	11 (1–75)	3 (0–23)
SFEFS	0	43 (1–679)	97 (8–1307)	16 (0–187)	20 (1–186)	39 (5–336)	11 (0–71)
	0.1	37 (0–683)	85 (7–1312)	13 (0–162)	18 (1–169)	35 (4–256)	8 (0–69)
	0.2	30 (0–588)	78 (6–1141)	9 (0–128)	14 (1–133)	29 (3–223)	6 (0–53)
	0.3	25 (0–510)	62 (5–809)	7 (0–91)	11 (0–105)	23 (3–188)	4 (0–39)
SFMAI	0	97 (5–1273)	201 (16–2381)	53 (1–433)	58 (6–366)	89 (13–509)	35 (4–223)
	0.1	89 (4–1245)	185 (19–2266)	43 (1–420)	51 (5–363)	82 (12–478)	29 (3–199)
	0.2	78 (4–1015)	164 (15–2050)	37 (1–329)	44 (4–320)	70 (10–437)	25 (2–159)
	0.3	65 (3–949)	147 (14–1684)	29 (0–249)	36 (3–243)	58 (8–398)	21 (2–130)
SFSEC	0	70 (3–973)	154 (12–1890)	31 (1–302)	39 (4–255)	61 (9–379)	21 (2–175)
	0.1	60 (2–812)	131 (12–1642)	27 (1–238)	34 (3–236)	54 (8–312)	19 (2–149)
	0.2	52 (2–735)	114 (9–1372)	23 (0–216)	29 (2–211)	49 (6–332)	15 (1–111)
	0.3	46 (1–640)	99 (10–1285)	19 (0–174)	24 (2–177)	39 (5–235)	13 (1–98)
SNTUC	0	82 (0–1795)	237 (15–3433)	19 (0–359)	33 (0–412)	79 (8–578)	10 (0–113)
	0.1	69 (0–1474)	210 (13–3203)	13 (0–228)	25 (0–307)	63 (6–556)	6 (0–98)
	0.2	53 (0–1237)	173 (10–2795)	7 (0–195)	17 (0–252)	50 (4–497)	3 (0–64)
	0.3	38 (0–970)	140 (7–2316)	4 (0–137)	10 (0–183)	34 (2–393)	1 (0–44)
SREFS	0	71 (1–1225)	197 (15–2283)	25 (0–287)	34 (1–343)	67 (8–606)	14 (0–115)
	0.1	62 (0–1135)	153 (13–2021)	19 (0–280)	27 (1–272)	53 (7–490)	10 (0–105)
	0.2	50 (0–1002)	134 (9–2093)	14 (0–188)	20 (0–214)	43 (5–467)	7 (0–63)
	0.3	39 (0–907)	115 (6–1770)	8 (0–154)	14 (0–170)	35 (3–324)	3 (0–49)

Table 6 (continued). Posterior predictive distributions of total wild spawners as a percentage of MAT, 50 years in the future, for 29 Chinook salmon populations.

Population	Mort.	Constant baseline			Step change 1970		
		Unconditional	Good	Bad	Unconditional	Good	Bad
SRLEM	0	28 (0–511)	76 (5–1051)	7 (0–101)	11 (0–106)	24 (3–173)	4 (0–35)
	0.1	22 (0–456)	66 (4–1004)	5 (0–86)	8 (0–90)	19 (2–163)	2 (0–28)
	0.2	17 (0–383)	55 (3–769)	3 (0–69)	6 (0–80)	16 (1–159)	1 (0–21)
	0.3	12 (0–309)	44 (3–615)	2 (0–44)	3 (0–59)	11 (1–105)	1 (0–12)
SRLMA	0	12 (1–181)	28 (3–304)	6 (0–52)	7 (1–49)	11 (2–67)	4 (0–27)
	0.1	11 (0–154)	23 (2–275)	5 (0–49)	6 (1–43)	10 (1–65)	3 (0–23)
	0.2	9 (0–131)	21 (2–253)	4 (0–37)	5 (0–39)	8 (1–56)	3 (0–20)
	0.3	8 (0–116)	18 (1–223)	3 (0–36)	4 (0–29)	7 (1–48)	2 (0–17)
SRNFS	0	23 (1–364)	54 (5–795)	10 (0–98)	12 (1–98)	21 (3–135)	6 (0–51)
	0.1	20 (0–322)	47 (4–662)	8 (0–97)	10 (1–82)	18 (2–125)	5 (0–38)
	0.2	17 (0–278)	41 (3–528)	6 (0–69)	9 (0–71)	16 (2–113)	4 (0–33)
	0.3	14 (0–227)	35 (3–508)	5 (0–54)	7 (0–61)	12 (1–89)	3 (0–25)
SRPAH	0	38 (0–731)	99 (7–1606)	13 (0–229)	18 (1–161)	36 (5–312)	8 (0–66)
	0.1	33 (0–696)	84 (6–1428)	10 (0–137)	14 (0–144)	30 (4–245)	6 (0–52)
	0.2	26 (0–586)	73 (5–1228)	7 (0–123)	11 (0–129)	24 (3–207)	4 (0–45)
	0.3	21 (0–440)	63 (4–968)	5 (0–89)	8 (0–95)	19 (2–207)	2 (0–30)
SRUMA	0	112 (3–1578)	249 (21–2736)	47 (1–474)	61 (5–464)	105 (12–672)	33 (2–224)
	0.1	98 (2–1402)	221 (17–2536)	39 (0–419)	51 (3–457)	89 (12–713)	26 (1–205)
	0.2	85 (2–1240)	197 (15–2497)	32 (0–346)	40 (2–325)	75 (11–512)	20 (1–160)
	0.3	71 (1–1083)	179 (15–2232)	23 (0–298)	32 (1–287)	62 (8–429)	14 (0–131)
SRVAL	0	50 (0–954)	132 (9–1918)	16 (0–192)	22 (1–234)	46 (5–344)	8 (0–77)
	0.1	42 (0–755)	114 (9–1789)	11 (0–188)	17 (0–203)	38 (4–327)	6 (0–63)
	0.2	34 (0–705)	104 (7–1361)	8 (0–118)	13 (0–153)	32 (3–309)	3 (0–41)
	0.3	25 (0–607)	87 (6–1192)	4 (0–86)	8 (0–102)	24 (2–197)	2 (0–27)
SRYFS	0	38 (0–735)	111 (7–1509)	8 (0–144)	15 (0–180)	33 (4–282)	4 (0–57)
	0.1	30 (0–671)	92 (6–1238)	7 (0–114)	11 (0–133)	30 (3–244)	2 (0–40)
	0.2	25 (0–572)	81 (5–1280)	4 (0–87)	7 (0–105)	22 (2–189)	1 (0–26)
	0.3	17 (0–482)	64 (4–1086)	2 (0–51)	4 (0–77)	16 (1–174)	1 (0–15)
UCENT	0	66 (0–1315)	190 (11–2779)	14 (0–259)	25 (0–290)	57 (7–525)	7 (0–105)
	0.1	52 (0–1084)	157 (10–2334)	10 (0–171)	19 (0–236)	50 (5–419)	5 (0–79)
	0.2	39 (0–1008)	134 (9–2070)	6 (0–145)	13 (0–175)	37 (3–342)	2 (0–48)
	0.3	30 (0–872)	112 (6–1616)	3 (0–99)	8 (0–148)	25 (1–259)	1 (0–37)
UCMET	0	42 (0–755)	108 (9–1668)	12 (0–171)	19 (0–177)	37 (4–311)	7 (0–67)
	0.1	36 (0–647)	96 (7–1269)	10 (0–152)	15 (0–163)	33 (4–286)	5 (0–63)
	0.2	28 (0–578)	83 (6–1162)	6 (0–100)	11 (0–124)	25 (2–220)	3 (0–41)
	0.3	21 (0–489)	67 (4–1054)	4 (0–92)	7 (0–92)	20 (1–142)	2 (0–27)
UCWEN	0	63 (0–4709)	459 (19–10374)	2 (0–117)	5 (0–465)	47 (2–1198)	0 (0–18)
	0.1	39 (0–3254)	377 (12–7230)	1 (0–66)	2 (0–246)	26 (1–781)	0 (0–7)
	0.2	21 (0–2639)	273 (8–8083)	0 (0–29)	1 (0–154)	13 (0–522)	0 (0–4)
	0.3	9 (0–2076)	154 (4–4653)	0 (0–12)	0 (0–103)	4 (0–291)	0 (0–1)

Table 7. Posterior predictive quasi-extinction probability, over a 25- or 50-year time horizon, for 29 Chinook salmon populations as a function of harvest mortality rate and average environmental conditions (*Unc.* = unconditional probability). Harvest is simulated as a fixed, density-independent mortality rate, and populations are assumed to receive no input of naturally spawning hatchery-origin adults. The quasi-extinction threshold is a four-year running average of 50 spawners. Results are shown for the constant baseline and step change versions of the multipopulation IPM.

| | | 25 years | | | | | | 50 years | | | | | |
| | | Constant baseline | | | Step change 1970 | | | Constant baseline | | | Step change 1970 | | |
Population	Mortality	Unc.	Good	Bad	Unc.	Good	Bad	Unc.	Good	Bad	Unc.	Good	Bad
GRCAT	0	0.24	0.03	0.59	0.32	0.06	0.68	0.41	0.1	0.84	0.63	0.26	0.96
	0.1	0.3	0.04	0.68	0.42	0.11	0.79	0.48	0.13	0.9	0.74	0.38	0.99
	0.2	0.35	0.07	0.76	0.54	0.19	0.89	0.56	0.18	0.95	0.84	0.57	1
	0.3	0.43	0.11	0.85	0.66	0.31	0.95	0.65	0.26	0.98	0.9	0.72	1
GRLOS	0	0.13	0.01	0.35	0.1	0	0.27	0.25	0.05	0.56	0.24	0.05	0.53
	0.1	0.16	0.02	0.4	0.14	0.02	0.35	0.3	0.06	0.65	0.31	0.08	0.65
	0.2	0.19	0.02	0.47	0.2	0.02	0.47	0.34	0.07	0.72	0.42	0.14	0.78
	0.3	0.24	0.03	0.57	0.29	0.05	0.62	0.41	0.11	0.81	0.55	0.22	0.89
GRMIN	0	0.11	0.01	0.29	0.07	0	0.19	0.2	0.03	0.47	0.17	0.03	0.4
	0.1	0.13	0.01	0.34	0.1	0.01	0.26	0.25	0.05	0.56	0.23	0.05	0.5
	0.2	0.16	0.02	0.41	0.15	0.02	0.37	0.3	0.06	0.64	0.32	0.08	0.65
	0.3	0.21	0.02	0.5	0.21	0.03	0.48	0.36	0.1	0.73	0.43	0.13	0.8
GRUMA	0	0.37	0.08	0.78	0.53	0.18	0.89	0.59	0.21	0.96	0.82	0.53	1
	0.1	0.43	0.11	0.84	0.63	0.27	0.94	0.65	0.27	0.99	0.89	0.68	1
	0.2	0.51	0.16	0.91	0.73	0.4	0.97	0.71	0.36	1	0.93	0.8	1
	0.3	0.58	0.23	0.94	0.82	0.55	0.99	0.79	0.48	1	0.97	0.9	1
GRWEN	0	0.15	0.01	0.4	0.15	0.01	0.37	0.29	0.04	0.65	0.34	0.08	0.7
	0.1	0.19	0.02	0.48	0.21	0.02	0.5	0.34	0.06	0.74	0.45	0.12	0.83
	0.2	0.24	0.03	0.57	0.29	0.05	0.63	0.41	0.1	0.82	0.57	0.22	0.92
	0.3	0.3	0.05	0.67	0.4	0.1	0.77	0.49	0.15	0.9	0.69	0.34	0.96
IRMAI	0	0.06	0	0.16	0.03	0	0.09	0.12	0.01	0.32	0.09	0.01	0.23
	0.1	0.07	0	0.2	0.05	0	0.13	0.15	0.02	0.38	0.13	0.02	0.32
	0.2	0.09	0	0.26	0.07	0	0.19	0.2	0.03	0.47	0.18	0.03	0.42
	0.3	0.13	0.01	0.34	0.11	0.01	0.29	0.25	0.04	0.57	0.27	0.06	0.59
MFBEA	0	0.09	0	0.24	0.06	0	0.16	0.17	0.02	0.42	0.13	0.02	0.32
	0.1	0.11	0	0.31	0.08	0	0.22	0.21	0.03	0.51	0.19	0.03	0.44
	0.2	0.14	0.01	0.38	0.12	0	0.33	0.26	0.05	0.6	0.27	0.06	0.59
	0.3	0.18	0.01	0.47	0.18	0.02	0.46	0.32	0.06	0.7	0.37	0.1	0.72
MFBIG	0	0.26	0.04	0.6	0.26	0.05	0.57	0.43	0.14	0.8	0.46	0.18	0.81
	0.1	0.3	0.06	0.67	0.34	0.09	0.68	0.47	0.18	0.84	0.55	0.26	0.88
	0.2	0.35	0.08	0.75	0.42	0.12	0.8	0.54	0.23	0.91	0.67	0.37	0.95
	0.3	0.41	0.11	0.82	0.52	0.18	0.88	0.61	0.29	0.95	0.75	0.47	0.98
MFCAM	0	0.57	0.26	0.93	0.74	0.45	0.98	0.73	0.45	0.98	0.9	0.72	1
	0.1	0.62	0.32	0.94	0.8	0.57	0.99	0.79	0.53	1	0.94	0.82	1
	0.2	0.68	0.37	0.97	0.87	0.69	1	0.83	0.6	1	0.97	0.9	1
	0.3	0.75	0.46	0.99	0.92	0.79	1	0.89	0.7	1	0.98	0.95	1
MFCHA	0	0.09	0	0.25	0.05	0	0.13	0.17	0.02	0.4	0.11	0.02	0.26
	0.1	0.11	0.01	0.29	0.07	0	0.19	0.19	0.03	0.45	0.15	0.02	0.36
	0.2	0.13	0.01	0.36	0.1	0	0.27	0.24	0.04	0.54	0.21	0.05	0.46
	0.3	0.17	0.01	0.44	0.14	0.01	0.36	0.29	0.06	0.63	0.29	0.07	0.6
MFLOO	0	0.56	0.24	0.94	0.74	0.45	0.97	0.75	0.48	0.99	0.9	0.75	1
	0.1	0.61	0.29	0.95	0.8	0.54	0.99	0.79	0.54	1	0.94	0.84	1
	0.2	0.67	0.36	0.98	0.87	0.67	1	0.85	0.64	1	0.97	0.92	1
	0.3	0.73	0.43	0.99	0.91	0.76	1	0.89	0.72	1	0.98	0.95	1
MFMAR	0	0.17	0.01	0.45	0.17	0.02	0.44	0.3	0.06	0.68	0.35	0.08	0.72
	0.1	0.22	0.02	0.53	0.23	0.02	0.56	0.36	0.08	0.76	0.45	0.12	0.84
	0.2	0.26	0.03	0.64	0.32	0.04	0.72	0.43	0.12	0.84	0.57	0.21	0.92
	0.3	0.32	0.05	0.73	0.44	0.1	0.85	0.51	0.17	0.92	0.7	0.36	0.98

Table 7 (continued). Posterior predictive quasi-extinction probability, over a 25- or 50-year time horizon, for 29 Chinook salmon populations.

| Population | Mortality | 25 years | | | | | | 50 years | | | | | |
| | | Constant baseline | | | Step change 1970 | | | Constant baseline | | | Step change 1970 | | |
		Unc.	Good	Bad	Unc.	Good	Bad	Unc.	Good	Bad	Unc.	Good	Bad
MFSUL	0	0.59	0.28	0.94	0.79	0.53	0.99	0.76	0.49	0.99	0.93	0.82	1
	0.1	0.65	0.34	0.96	0.85	0.64	0.99	0.82	0.57	1	0.96	0.88	1
	0.2	0.71	0.41	0.99	0.9	0.74	1	0.86	0.66	1	0.98	0.94	1
	0.3	0.77	0.49	0.99	0.94	0.84	1	0.91	0.75	1	0.99	0.97	1
MFUMA	0	0.51	0.19	0.89	0.67	0.37	0.95	0.71	0.4	0.98	0.87	0.68	1
	0.1	0.57	0.24	0.94	0.76	0.49	0.98	0.76	0.48	0.99	0.92	0.78	1
	0.2	0.63	0.31	0.96	0.83	0.6	0.99	0.81	0.56	1	0.96	0.88	1
	0.3	0.71	0.4	0.99	0.89	0.72	1	0.87	0.68	1	0.98	0.94	1
SFEFS	0	0.16	0.01	0.43	0.13	0.01	0.35	0.29	0.07	0.64	0.28	0.06	0.6
	0.1	0.2	0.02	0.49	0.19	0.01	0.48	0.34	0.08	0.7	0.37	0.1	0.74
	0.2	0.23	0.03	0.58	0.26	0.03	0.6	0.39	0.11	0.79	0.48	0.17	0.85
	0.3	0.29	0.04	0.68	0.35	0.07	0.71	0.47	0.15	0.88	0.6	0.27	0.93
SFMAI	0	0.04	0	0.11	0.02	0	0.05	0.09	0.01	0.23	0.04	0.01	0.1
	0.1	0.05	0	0.14	0.03	0	0.07	0.11	0.01	0.27	0.06	0.01	0.15
	0.2	0.07	0	0.18	0.04	0	0.11	0.13	0.02	0.34	0.08	0.01	0.21
	0.3	0.09	0	0.24	0.05	0	0.15	0.17	0.02	0.4	0.12	0.02	0.29
SFSEC	0	0.11	0.01	0.29	0.07	0	0.2	0.2	0.04	0.47	0.16	0.02	0.37
	0.1	0.13	0.01	0.35	0.1	0	0.26	0.24	0.05	0.53	0.21	0.04	0.46
	0.2	0.17	0.02	0.43	0.14	0.02	0.36	0.3	0.07	0.62	0.27	0.08	0.56
	0.3	0.21	0.03	0.52	0.21	0.02	0.48	0.35	0.09	0.71	0.37	0.12	0.69
SNTUC	0	0.2	0.02	0.51	0.21	0.03	0.52	0.35	0.08	0.72	0.41	0.11	0.78
	0.1	0.25	0.03	0.6	0.29	0.05	0.64	0.4	0.1	0.81	0.51	0.17	0.88
	0.2	0.29	0.04	0.68	0.37	0.07	0.78	0.47	0.13	0.88	0.63	0.26	0.95
	0.3	0.35	0.05	0.78	0.51	0.15	0.88	0.54	0.18	0.94	0.76	0.45	0.99
SREFS	0	0.09	0	0.26	0.07	0	0.2	0.18	0.02	0.44	0.17	0.02	0.41
	0.1	0.13	0.01	0.36	0.11	0	0.28	0.24	0.04	0.57	0.24	0.04	0.56
	0.2	0.15	0.01	0.4	0.16	0	0.41	0.28	0.05	0.64	0.33	0.06	0.71
	0.3	0.2	0.02	0.52	0.23	0.03	0.57	0.35	0.07	0.74	0.46	0.13	0.84
SRLEM	0	0.17	0.01	0.44	0.16	0.02	0.41	0.28	0.05	0.64	0.32	0.07	0.7
	0.1	0.21	0.02	0.53	0.22	0.02	0.55	0.34	0.07	0.72	0.43	0.1	0.83
	0.2	0.25	0.03	0.63	0.3	0.05	0.68	0.41	0.1	0.82	0.54	0.19	0.92
	0.3	0.31	0.05	0.71	0.42	0.09	0.83	0.49	0.15	0.9	0.67	0.31	0.97
SRLMA	0	0.3	0.06	0.66	0.32	0.08	0.65	0.46	0.16	0.84	0.53	0.24	0.85
	0.1	0.34	0.08	0.73	0.38	0.12	0.72	0.52	0.21	0.89	0.62	0.34	0.91
	0.2	0.4	0.1	0.8	0.49	0.18	0.84	0.58	0.26	0.94	0.71	0.43	0.97
	0.3	0.45	0.13	0.84	0.6	0.27	0.92	0.66	0.34	0.97	0.82	0.58	0.99
SRNFS	0	0.61	0.27	0.95	0.79	0.53	0.99	0.79	0.52	0.99	0.93	0.82	1
	0.1	0.66	0.33	0.97	0.84	0.61	1	0.84	0.6	1	0.96	0.9	1
	0.2	0.72	0.4	0.99	0.9	0.74	1	0.88	0.7	1	0.98	0.94	1
	0.3	0.78	0.5	1	0.94	0.82	1	0.92	0.79	1	0.99	0.96	1
SRPAH	0	0.2	0.03	0.5	0.21	0.03	0.49	0.34	0.09	0.69	0.38	0.12	0.73
	0.1	0.24	0.03	0.58	0.27	0.05	0.62	0.39	0.11	0.78	0.48	0.18	0.83
	0.2	0.28	0.05	0.66	0.35	0.08	0.72	0.45	0.14	0.86	0.58	0.26	0.92
	0.3	0.35	0.06	0.77	0.46	0.14	0.85	0.54	0.2	0.93	0.71	0.38	0.98
SRUMA	0	0.05	0	0.14	0.02	0	0.06	0.1	0.01	0.26	0.06	0	0.16
	0.1	0.06	0	0.17	0.03	0	0.1	0.12	0.01	0.32	0.08	0.01	0.22
	0.2	0.08	0	0.22	0.05	0	0.15	0.16	0.02	0.4	0.12	0.02	0.31
	0.3	0.1	0	0.27	0.08	0	0.22	0.2	0.03	0.48	0.18	0.03	0.43
SRVAL	0	0.32	0.07	0.7	0.38	0.09	0.77	0.48	0.16	0.87	0.61	0.28	0.95
	0.1	0.36	0.08	0.77	0.48	0.14	0.87	0.55	0.2	0.93	0.72	0.4	0.99
	0.2	0.43	0.12	0.85	0.58	0.22	0.94	0.62	0.26	0.97	0.81	0.55	1
	0.3	0.5	0.16	0.91	0.69	0.34	0.98	0.69	0.34	0.99	0.9	0.72	1

Table 7 (continued). Posterior predictive quasi-extinction probability, over a 25- or 50-year time horizon, for 29 Chinook salmon populations.

| | | 25 years | | | | | | 50 years | | | | | |
| | | Constant baseline | | | Step change 1970 | | | Constant baseline | | | Step change 1970 | | |
Population	Mortality	Unc.	Good	Bad	Unc.	Good	Bad	Unc.	Good	Bad	Unc.	Good	Bad
SRYFS	0	0.39	0.09	0.81	0.52	0.17	0.9	0.57	0.23	0.94	0.75	0.41	0.99
	0.1	0.45	0.13	0.87	0.61	0.24	0.96	0.64	0.29	0.97	0.84	0.57	1
	0.2	0.5	0.16	0.92	0.71	0.37	0.98	0.7	0.36	0.99	0.9	0.73	1
	0.3	0.58	0.22	0.96	0.8	0.51	0.99	0.77	0.47	1	0.95	0.85	1
UCENT	0	0.24	0.03	0.58	0.28	0.04	0.63	0.4	0.09	0.81	0.51	0.18	0.88
	0.1	0.29	0.04	0.68	0.36	0.08	0.74	0.46	0.13	0.88	0.61	0.28	0.93
	0.2	0.34	0.05	0.76	0.47	0.12	0.85	0.53	0.18	0.93	0.72	0.39	0.98
	0.3	0.4	0.08	0.84	0.58	0.2	0.93	0.59	0.23	0.96	0.81	0.54	0.99
UCMET	0	0.09	0	0.25	0.07	0	0.19	0.18	0.02	0.44	0.17	0.02	0.41
	0.1	0.11	0	0.31	0.1	0	0.27	0.22	0.03	0.52	0.24	0.04	0.53
	0.2	0.14	0.01	0.4	0.14	0.01	0.38	0.27	0.04	0.63	0.31	0.06	0.66
	0.3	0.18	0.01	0.49	0.2	0.01	0.5	0.34	0.06	0.73	0.43	0.12	0.8
UCWEN	0	0.14	0	0.41	0.17	0.01	0.46	0.28	0.03	0.68	0.46	0.07	0.89
	0.1	0.17	0.01	0.47	0.24	0.01	0.58	0.33	0.04	0.77	0.57	0.15	0.95
	0.2	0.22	0.01	0.58	0.34	0.04	0.74	0.4	0.06	0.88	0.69	0.29	0.98
	0.3	0.27	0.01	0.7	0.46	0.08	0.89	0.49	0.09	0.95	0.8	0.48	1

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