DSM TN 40. Changes in delta smelt population parameters since the inception of the Formal Endangered Species Act Consultation on the Proposed Coordinated Operations of the Central Valley Project (CVP) and State Water Project (SWP)

Version 6, September 24, 2019

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Summary

In 2009 the Formal Endangered Species Act Consultation on the Proposed Coordinated Operations of the Central Valley Project (CVP) and State Water Project (SWP) (henceforth referred to as the "BiOp") went into effect. This BiOp, among other things, called for a number of life stage specific management actions related to delta smelt. How population parameters such as recruitment, life stage specific survival, and annual growth rate, have changed since the BiOp inception (but not necessarily implementation) is of interest. Two population dynamics model approaches were applied to gain insight into any such changes. The first model is a stage structred state-space model that allows quantification of recruitment and life stage specific survival and process noise for each of these stages, and was fit to four time series of sequentially recorded life stage abundance data since 1995. This model allows a test about whether life stage specific vital rates have changed between pre- to post-BiOp time period cohorts, and estimation of the subsequent cohort specific growth rate (the product of the vital rates). A second model type describing annual changes in adult abundance, with and without a change point in model parameters to occur in 2009, was also constructed and fit to data since 2002. The change point model does not allow inference about life stage specific vital rates, but does allow for a change in both the exptected growth rate and process noise variance parameters between the pre- and post-BiOp time periods, providing a second about whether the annual growth rate changed from pre- to post-BiOp time periods. A number of simpler models were also considered, mostly for confirmation of performance of the more complex ones. The key findings were

- All models closely agreed in estimated historic abundance estimates and cohort specific population growth rates. All models predict continued decline of the delta smelt population, reflecting the trend observations from empirical abudance indices.

- The stage-structed model found no evidence for changes in expected recruitment between pre- to post-BiOp time frames, while there was some evidence for declines in both summer and fall survival. The most pronounced statistical result as a significant increase in adult winter survival in post-BiOp cohorts compared with pre-BiOp cohorts. The combined effects of the changes from pre- to post-BiOp expected values appear to have resulted in population growth rates below one since the 2012 cohort.

- The change point annual time step model found a positive change in the expected growth rate from 2002-2008 (pre-BiOp) to post-BiOp time periods. However, the process noise also increased, resulting in predictions with a less rapid decline but allowing for more stochasticity.

- Simulations 10 years into the future starting from the 2017 estimated adult abundance based on pre- and post-BiOp based vital rate paremeters from the stage structured and

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annual change point model all showed continued declines of delta smelt. The models indicated opposite effects of the BiOp as measured by the median growth rate, although substantial process noise prohibits very clear distinctions between model predictions.

1   Data

All models were fit using abundance estimates provided in Polansky et al. (2019) (Table 1 shows the adult abundances from 2002 to 2017). For the stage structured model, the abundance estimates and measures of uncertainty came from the 1995 through 2016 data of the 20-mm May survey for life stage 1 (post-larva), STN July-Aug survey for life stage 2 (juveniles), and FMWT Oct-Nov survey for life stage 3 (sub-adults); 1995 through 2001 SpMWT Feb-Mar survey for life stage 4 (adults); and 2002 through 2017 SKT Feb-Mar data for life stage 4. For the annual time step model, only the SKT Feb-Mar stage 4 data from 2002 through 2017 was used (Table 1). These estimates correspond to the 1995 through 2016 cohorts plus the addition of adult estimates from the 1994 cohort.

Table 1: Adult abundance estimates (N), standard errors (SE), coefficients of variation (CV), and empirical growth rates (λ), based on February-March pooled SKT data.

Year	N	SE	CV	λ
2002	933982.05	225097.30	0.24	
2003	1167662.36	165503.81	0.14	1.25
2004	763619.13	161572.62	0.21	0.65
2005	329721.62	101264.13	0.31	0.43
2006	301735.06	45389.15	0.15	0.92
2007	375069.53	124450.83	0.33	1.24
2008	207930.46	82196.37	0.40	0.55
2009	217409.35	72908.01	0.34	1.05
2010	278254.65	90567.51	0.33	1.28
2011	232899.42	83946.62	0.36	0.84
2012	1105082.20	388558.53	0.35	4.74
2013	316805.68	93219.19	0.29	0.29
2014	250095.17	80597.19	0.32	0.79
2015	162446.29	74258.13	0.46	0.65
2016	21730.15	8900.90	0.41	0.13
2017	30887.73	9560.98	0.31	1.42

2   Models

The models were generally state-space models of the kind described in Newman et al. (2014). State-space models consist of a process model and an observation model, allowing inference about vital rates and process noise while accounting for (possibly complex) sampling biases and inclusion of sampling uncertainty. Some regression models based on the adult abundance estimates following Dennis et al. (1991) were also applied mostly as a comparative tool, but will not be discussed in any detail here. Sections 2.1 and 2.2 below describe state process models of interest here. Section 2.3 describes the observation model that is common in stochastic structure to all process models.

2.1 Stage structured process model

The first model considered was a stage-structured state-space model of the kind described in Newman et al. (2014). An advantage of using a stage-structured model is that it facilitates understanding drivers of population abundances at a finer biological resolution on understanding where BiOp effects may occur. This can be advantageous when management actions are set to target specific portions of an organisms life cycle, such as specified in the BiOp. If a coarse grain approach is taken as was done in the annual time step models described below, an effects analysis may not be well suited to identify the success or failure of an action because changes in other vital rates may mask the effect.

Given an initial abundance of stage class $S4$ (adults) individuals $N_{S4,0}$, the state process model describes a series of life stage transitions within and across cohorts. At the end of the time period over which eggs are spawned, hatched and recruit into stage class S1 individuals, the number of stage class $S1$ (post-larvae) individuals $N_{S1,c}$ in cohort c depends on the number of $S4$ individuals in the previous cohort $N_{S4,c-1}$ and a stochastic recruitment function ρ_c. At the end of the time period assigned to the $S1$ life stage, the number of stage class $S2$ (junviles) individuals $N_{S2,c}$ depends on $N_{S1,c}$ and the stage class $S1$ survival rate for that cohort $\phi_{1,c}$. The survival rates for susequent life stages are analogously defined, giving the set of update equations

$$N_{S1,c} = \rho_c N_{S4,c-1} \tag{1}$$
$$N_{S2,c} = \phi_{1,c} N_{S1,c} \tag{2}$$
$$N_{S3,c} = \phi_{2,c} N_{S2,c} \tag{3}$$
$$N_{S4,c} = \phi_{3,c} N_{S3,c} \tag{4}$$

Recruitment is modeled as a log-normal random variable

$$\rho_c \sim \text{Log-normal}\left(\mu = \zeta_0 + \zeta_1 X_{R,c}, \sigma_R^2\right) \tag{5}$$

where $X_{R,c} = 0$ if $c < 2008$ and 1 for $c \geq 2009$. The survival rates are logit-normal random variables

$$\phi_{1,c} \sim \text{Logit-normal}\left(\mu = \beta_0 + \beta_1 X_{S1,c}, \sigma_{S1}^2\right) \tag{6}$$
$$\phi_{2,c} \sim \text{Logit-normal}\left(\mu = \eta_0 + \eta_1 X_{S2,c}, \sigma_{S2}^2\right) \tag{7}$$
$$\phi_{3,c} \sim \text{Logit-normal}\left(\mu = \gamma_0 + \gamma_1 X_{S3,c}, \sigma_{S3}^2\right) \tag{8}$$

where $X_{S1,c} = X_{S2,c} = 0$ if $c < 2008$ and 1 for $c \geq 2009$, and $X_{S3,c} = 0$ if $c < 2007$ and 1 for $c \geq 2008$.

Irrespective of how each of the recruitment and survival rates are modeled, a term of interest is the historically realized annual population growth rate

$$\lambda_c = N_{S4,c}/N_{S4,c-1} = \rho_c \phi_{1,c} \phi_{2,c} \phi_{3,c} \tag{9}$$

2.2 Annual time step process model

The state-space process model is

$$N_{S4,c+1} = N_{S4,c} e^{\mu + \epsilon_t}, \epsilon_t \sim N(0, \sigma^2) \tag{10}$$

The annual time step change point process model conditions the parameter values in Eqn. 10 on whether predicted abundances are before the 2008 cohort (which includes 2009 adult abundance estimates) or after,

$$N_{S4,c+1} = \begin{cases} N_{S4,c}e^{\mu_1+\epsilon_c}, \epsilon_c \sim N(0,\sigma_1^2) & \text{if } c < 2007 \\ N_{S4,c}e^{\mu_2+\epsilon_c}, \epsilon_c \sim N(0,\sigma_2^2) & \text{if } c \geq 2008 \end{cases} \tag{11}$$

Similarly to Eqn. 9, the historically realized (including the random effect of process noise) population growth rate for each cohort is estimated as

$$\lambda_c = N_{S4,c}/N_{S4,c-1} = e^{\mu.+\epsilon_c} \tag{12}$$

where $\mu.$ can be one of μ, μ_1, or μ_2. The population growth rate prior to any random effects is $\exp\mu.$.

2.3 Observation model

The observation models are similar, in that the estimated abundance indices $\widehat{N}$ are treated as log-normal random variables

$$\widehat{N} \sim \text{Log-normal}\left(\mu = \ln(\psi N), \sigma = \sqrt{\ln(1 + \widehat{CV}^2)}\right) \tag{13}$$

where $\widehat{CV} = \widehat{se}_{\widehat{N}}/\hat{N}$ is the empirical abundance estimate coefficient of variation and where the life stage and cohort indices on latent abundance indices N, estimated abundance indices $\widehat{N}$, and estimated coefficients of variation $\widehat{CV}$ of the $\widehat{N}$, have been omitted for clarity. The survey specific parameter $\psi \in (0,1)$ is fixed at 1 for all $S1$ observations, $S4$ observations starting in 2002. For all $S2$ and $S3$ observations, and for $S4$ observations prior to 2002, it is estimated. Details can be found in Polansky et al. (DSM TN9).

3 Model inference

Paremeter inference was conducted using Bayesian methods implemented in JAGS version 4.3.0 (Plummer 2017) within in R (R Development Core Team 2018) using the R2jags library (Su and Yajima 2015). Each posterior was sampled using 10 chains sampling 1,000 sequential values from the Gibbs sampler after a burnin of 99,000 iterations each. Gelman-Rubin diagnostics, traceplots, and graphical checks were applied to assess model fit.

4 Results

4.1 Historic time series

The geometric mean growth rate from the adult empirical time series since 2002 is 0.80, reflecting the downard trend in abundances. All time series models showed comparable estimates of latent abundances and uncertainty (Figure 1). Other model checking procedures (e.g Gelman-Rubin statistic and traceplots) indicated appropriate mixing of the MCMC samples.

4.2 Stage structured model

A positive change in winter survival since 2009 has the most statistical support, with some weak evidence for declines in summer and fall survival (Table 2 and Figure 2). The realized vital

rate values on the natural scale for each cohort are shown in Figure 3. These further indicate the consistent increased winter survival since 2009. From 2012 to 2015, the cohort population growth rate has been lower than one (Figure 3), the apparent result of either very low summer survival (2012), fall survival (2013), or recruitment and "not great" subsequent summer and fall survival. 2016 appears to have slightly better recruitment and near average (since 2012) summer and fall survival, leading to a slightly positive population growth rate for that cohort.

Table 2: Stage structured model posterior summaries of the BiOp effect parameter for each vital rate. Evidence is the proportion of the posterior above zero.

Parameter	Mean	Std. Dev.	2.5%	97.5%	Evidence
ζ_1	0.05	0.17	-0.29	0.39	0.62
β_1	-0.60	0.43	-1.49	0.25	0.08
η_1	-0.30	0.41	-1.10	0.54	0.22
γ_1	1.07	0.59	0.06	2.37	0.98

4.3   Annual time step models

Both annual time step models showed similar estimates in the μ parameter (the natural log of the population growth rate), with a slightly lower estimate for pre-BiOp cohorts compared with post-BiOp cohorts (Table 3 and Figure 4). In contrast, the process noise variance parameters varied across models and time periods, with estimates being much larger for post-BiOp cohort dynamics compared to pre-BiOp cohorts (Table 3 and Figure 4).

Posterior distributions of the population growth rates were similar across the annual time step models (Table 3 and Figure 5), which in turn were comparable to the stage structured model estimates (Figure 6).

Table 3: Annual time step model parameter posterior summaries. Evidence is the proportion of the posterior above zero. No evidence values for the process noise variance posteriors are given because these have no prior probability for values ≤ 0.

Parameter	Mean	Std. Dev.	2.5%	97.5%	Evidence
μ	-0.22	0.16	-0.54	0.12	0.08
μ_1	-0.30	0.12	-0.50	-0.00	0.02
μ_2	-0.19	0.29	-0.77	0.39	0.23
σ^2	0.41	0.27	0.12	1.08	-
σ_1^2	0.07	0.16	0.00	0.44	-
σ_2^2	0.89	0.73	0.20	2.76	-

Table 4: Annual time step model population growth rate estimates prior to the effects of process noise, e^{μ}.

Model	Mean	Median	2.5%	97.5%
No change point	0.81	0.80	0.58	1.13
Change point (pre-BiOp)	0.75	0.73	0.61	1.00
Change point (post-BiOp)	0.86	0.82	0.46	1.48

5 Future abundance simulations

Future abundances based on several of the fitted state process models and accounting for parameter estimate uncertainty were simulated. The models used were the stage structured model with either pre- or post-BiOp vital rate parameter distributions, or the annual time step change point model with either the pre- or post-BiOp growth rate and process noise parameter distributions. For each model, 1,000 abundance simulations over 10 years starting at an initial adult abundance value equal to the 2017 calendar year estimate of 30,888 (rounded) were done. The simulations accounted for process noise and parameter uncertainty. Adult abundances were used to summarize future predictions.

All models predicted continued future declines in abundance, regardless of whether pre- or post-BiOp parameters were used (Figure 7). It should be noted that prediction uncertainty is extreme, as illustrated in Table 5.

Table 5: Selected simulated abundance percentiles, values below which the corresponding percentage of simulations fell below, of the 1,000 simulated future abundances based on the stage structured model using post-BiOp parameters.

	Percentage				
Year	2.5%	25%	50%	75%	97.5%
2018	3.46e+02	7.24e+03	2.35e+04	7.42e+04	3.58e+05
2019	2.82e+01	2.73e+03	1.64e+04	7.98e+04	1.00e+06
2020	4.56e+00	1.09e+03	1.05e+04	8.37e+04	2.41e+06
2021	1.03e+00	4.95e+02	8.42e+03	9.30e+04	6.10e+06
2022	2.15e-01	2.58e+02	5.15e+03	1.10e+05	1.12e+07
2023	3.81e-02	1.10e+02	3.63e+03	1.07e+05	1.59e+07
2024	4.65e-03	5.79e+01	2.28e+03	1.01e+05	3.94e+07
2025	7.43e-04	2.47e+01	1.92e+03	9.49e+04	1.23e+08
2026	3.66e-04	1.30e+01	1.22e+03	1.15e+05	1.61e+08
2027	1.13e-04	5.34e+00	9.76e+02	8.97e+04	2.35e+08

6 Remarks, caveats and areas of further work

- The way in which the BiOp came into existence and is implemented is not binary, as treated here. For example, from 2005 through 2008 an "Interim Remedy" version was implemented, the consequences of which may partially explain the elevated winter survival observed in 2006 through 2008. Using some measure of the implementation of the intent of the BiOp could provide a clearer understanding of the relationship between a regulatory document, the Delta ecosystem, and actual delta smelt population dynamics.

- More insightful analyses about possible causal factors impacting population parameters has been achieved by using physical and biological covariates germane to delta smelt vital rates as predictor variables. This is the topic of Polansky et al. (DSM TN9).

- It may be interesting to identify if covariate effects of system variables interact with the BiOp. For example, recruitment and early life stage survival may show dependence on an interaction between flow, temperature, and whether or not the BiOp was in place.

- Only minimal checks on model performance and fitting were made by exploring how well latent abundance estimate time series matched with observed ones, traceplots, and examining Gelman-Rubin statistics. More exhaustive model building approaches could lead to improved models.

- The lack of density dependence has several implications for the simulation study. First, unrealisitcally large abundance predictions (related to the lack of compensatory density-dependent feedbacks) can and did occur. Second, possible Allee effects resultsing from depensatory processes (e.g. individuals not being able to find each other during spawning) may result in realized abundances decreasing more rapidly than is predicted.

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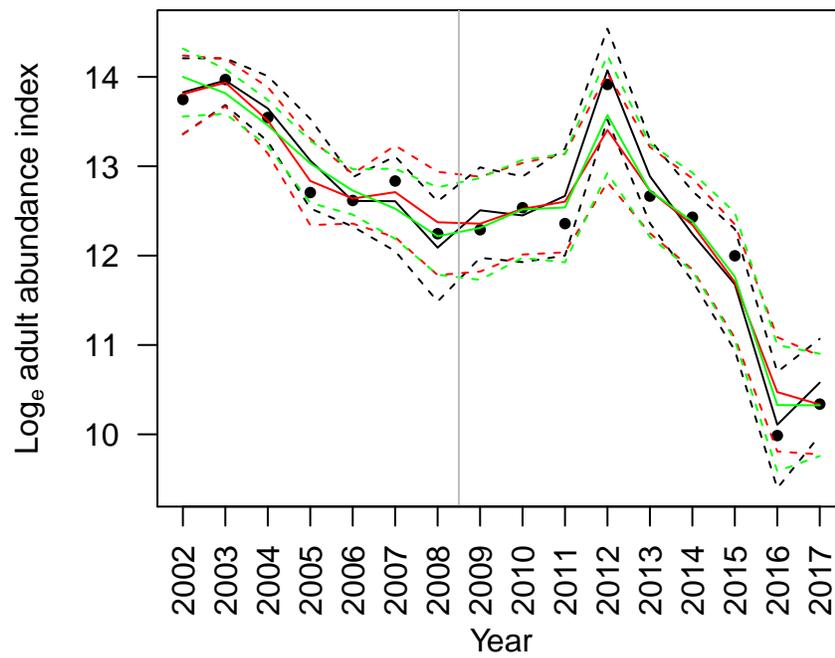
Figure 1: Estimated adult abundance indices on the natural log scale by calendar year (points). Solid lines show mean posterior predicted abundances, and dashed lines show the corresponding 95% central Bayesian credible intervals, for the stage structured (black), annual model without a change point (red), and annual model with a change point (green).
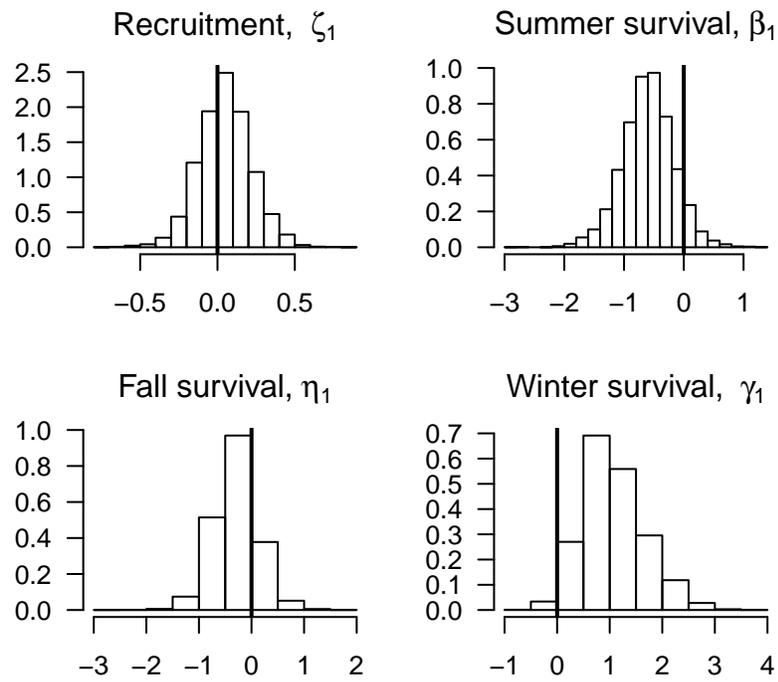
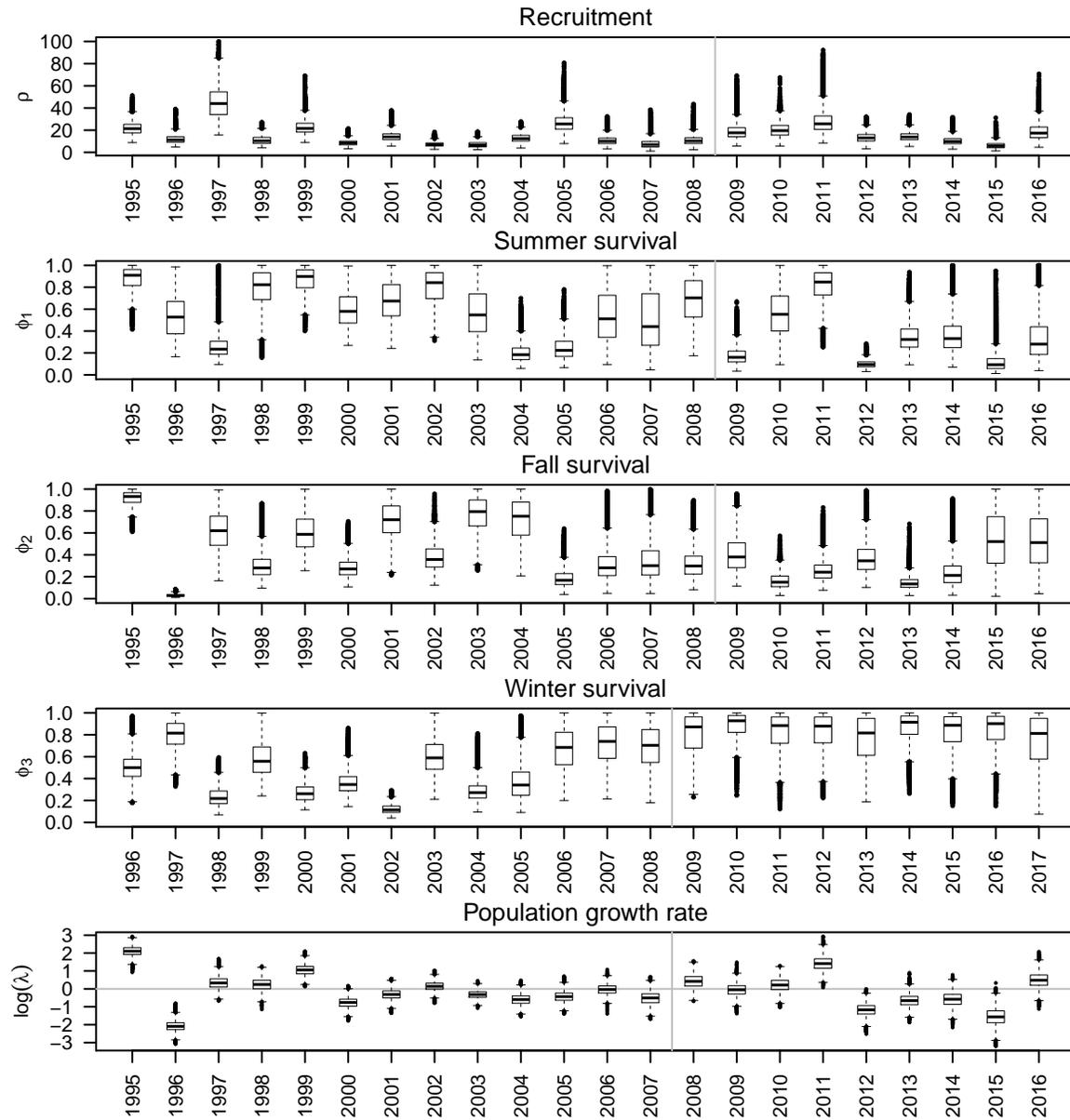Figure 2: Posterior distributions showing the stage structured model BiOp effect parameters. Vertical lines are drawn at 0. Compare with Table 2.

Figure 3: Posterior distributions of the stage structured model vital rates estimates by calendar year. Note winter survival rates are for the subsequent calendar year relative to the other vital rates for the cohort, which can be seen by vertical comparison of boxplots across panels. The bottom panel shows the posterior of the overall population growth rate $\lambda = \rho * \phi_{\text{summer}} * \phi_{\text{fall}} * \phi_{\text{winter}}$ on the natural log scale; values above and below 0 indicate postivitve and negative population growth for the year. Vertical lines distinguish vital rates derived from either pre- or post-BiOp data. The x-axis labels show cohort year, which includes data from winter adults of the subsequent calendar year.
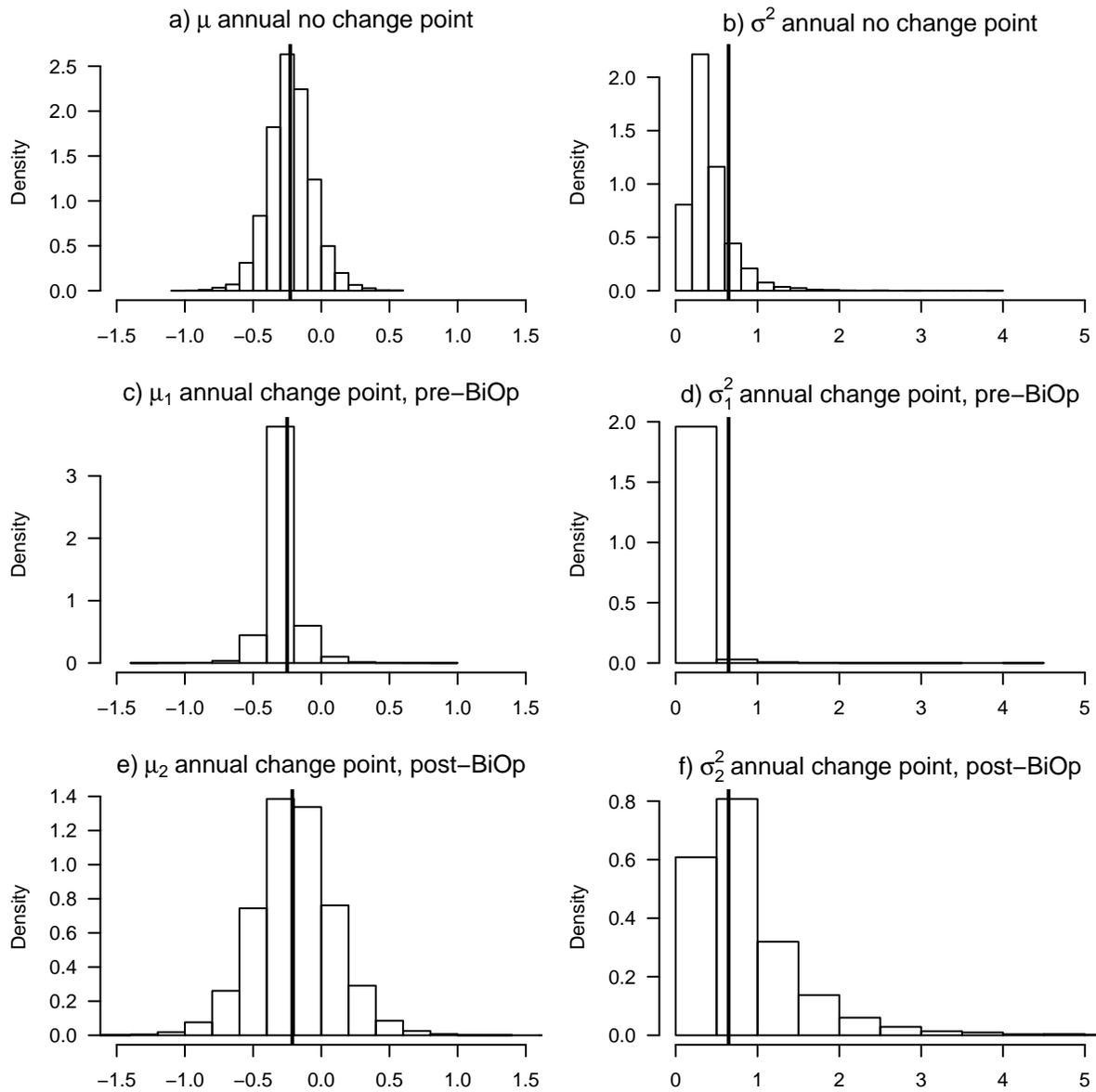
Figure 4: Histograms of the annual time step model posterior parameter distributions. Bold vertical lines show linear least squares regression parameter estimates.
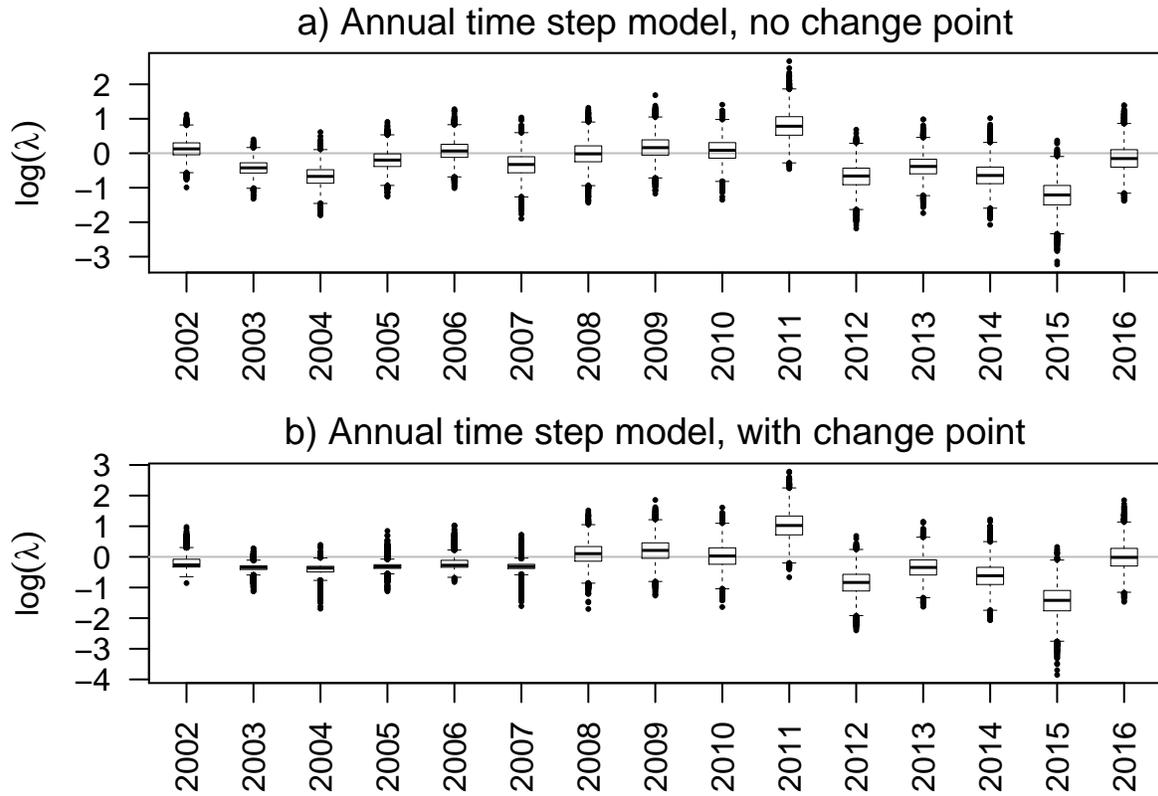
a) Annual time step model, no change point

b) Annual time step model, with change point

Figure 5: Boxplots of the annual growth rate esimate posteriors from the annual time step models on the natural log scale. Light vertical grey line delimits cohorts pre and post BiOp implementation.
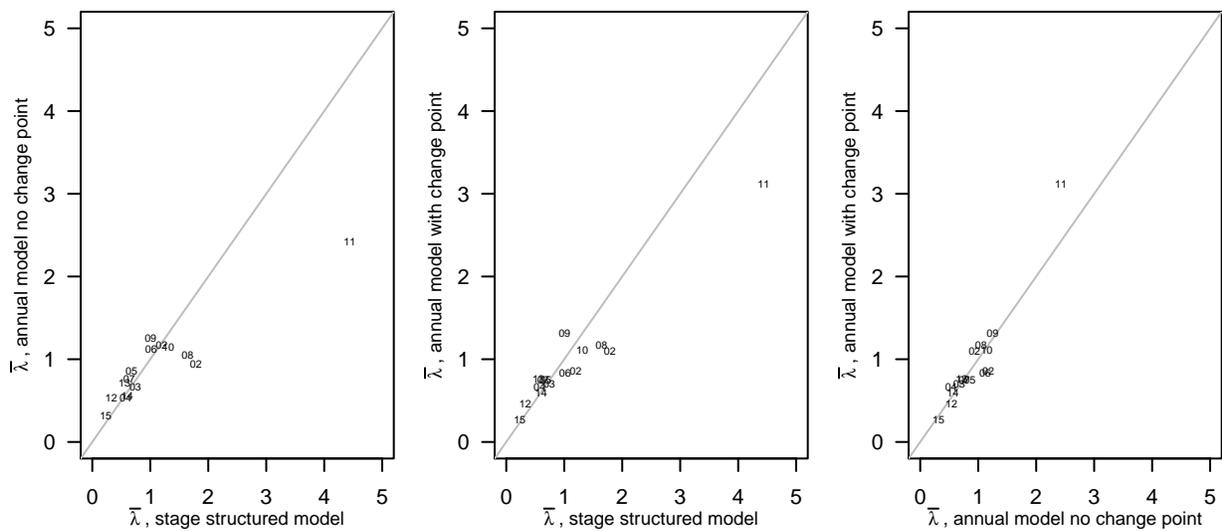

Figure 6: Scatter plots of the posterior mean annual growth rates $\bar{\lambda}$ for the different pairs of models. Text indicates the cohort year of the growth rate.
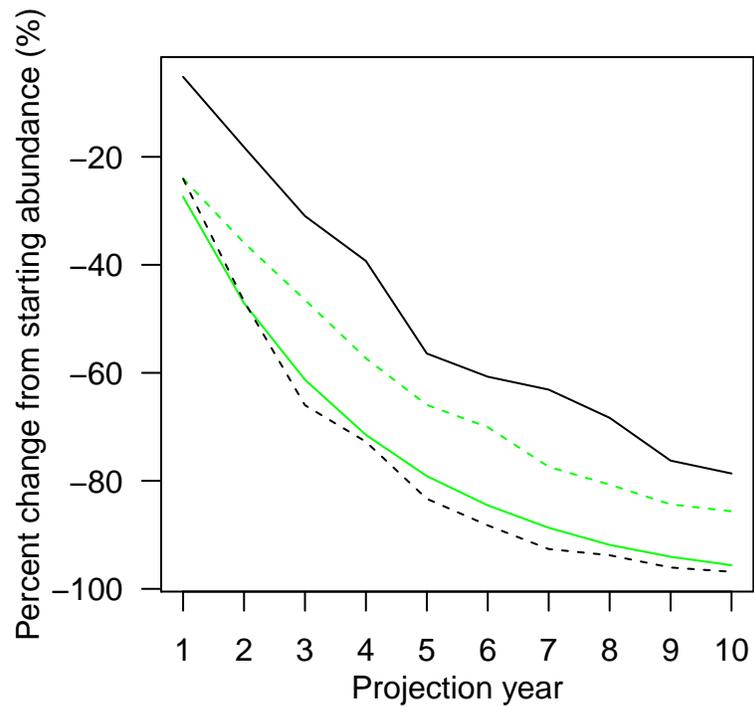
Figure 7: Percent change of median future abundance predictions relative to the starting value of 30,887.73 over 10 projection years based on the stage structured (black lines) and annual change point model (green lines), using vital rates from pre (solid lines) and post (dashed lines) BiOp model parameters. Projection year 1 corresponds to calendar year 2018.