

Effect of data weighting on the mature male biomass estimate for Alaskan golden king crab

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Abstract

Size-structured integrated population dynamics models are used to estimate the time-trajectories of mature male biomass (MMB) of Alaska crab stocks for stock status determination and harvest allocation. Lack of annual biomass surveys makes it difficult to assess the status and biomass of the Aleutian Islands golden king crab (*Lithodes aequispinus*). The assessment for this stock relies on commercial catch, size-composition, crab bycatch in groundfish (trawl and fish pot) fisheries, effort, catch-per-unit of effort, and tagging data to determine the biomass and other stock assessment parameters. The effect of data re-weighting (i.e., stage-2 weighting) methods on MMB estimates was investigated for this stock in relation to the sensitivity of the trends in MMB to the data re-weighting method. The McAllister and Ianelli, and Francis methods were used to re-weight the size-composition data and Punt's method was applied to re-weight the tagging data. Model misspecification (e.g., natural mortality and growth) and the effect of omitting a potentially conflicting data source on estimates of MMB were also investigated. Re-weighting and model misspecification changed the magnitude of estimated values for MMB and their coefficients of variation, but not the MMB trends. The stage-2 weighting of tagging data led to slightly lower estimates of MMB. Under the robust multinomial likelihood for size-composition data, there was not much of a difference between the results of the McAllister and Ianelli method, which ignores correlations in residuals for size-compositions, and the Francis method, which explicitly accounts for these correlations. Specifically, both re-weighting methods led to similar trends, precision, and point estimates of MMB. The R_0 profiles indicated that there was information for abundance estimation when all the data were considered under base or variable growth increment scenarios. The CPUE indices were more informative about absolute abundance than the size-composition data. Hence the issue of data weighting should continue to be explored using case studies.

Keywords: Alaska, data weighting, golden king crab, mature male biomass

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Highlights

- Stage-2 weighting methods for size-compositions and tagging data discussed.
- Effect of stage-2 weighting on MMB explored.
- Stage-2 weighting changed the magnitude, but not MMB trends.
- MMB patterns may depend on the particular data analyzed.

1. Introduction

Due to the difficulties in ageing crustaceans, size-structured population dynamics models, which model cohorts moving through various size-classes over time, have been used for assessment of several crustacean stocks (e.g., Chen et al., 2005; Punt et al., this volume; Zheng et al., 1995). The size-transition matrix, which governs the probability of animals moving from one size-class to the others, plays an important role in size-structured models (Hillary, 2011; Siddeek et al., 2016). Tagging and size-composition data provide information to estimate the size-transition matrix (Punt et al., 1997, 2013). Those data have been used in combination with catch, bycatch, effort, and indices of abundance (e.g., catch-per-unit-effort) data within integrated models to estimate quantities of management importance, such as mature male biomass, fishing mortality, and recruitment (e.g., Zheng and Siddeek, 2015; Turnock and Rugolo, 2015). Tagging data are not available for many crustacean stocks. For those stocks, growth-increment estimates from related species can be used in addition to size-composition data to determine the size-transition matrix (e.g., eastern Bering Sea Tanner crab, Stockhausen, 2016).

Francis (2011) provides two main reasons why data weighting is important in stock assessment: (1) it can substantially change the results, and (2) it affects all the usual tools of statistical inference that are used in stock assessment such as hypothesis tests and calculation of confidence intervals. Francis (2011) argues that greater emphasis should be placed on mimicking abundance indices than size-composition data when assigning weights to data sets. He recommends that process error should be accounted for when setting the ‘stage-2’ effective sample sizes based on the ‘stage-1’ sample sizes when fitting to size-composition data. He emphasizes that stage-1 fitting only accounts for observation errors resulting from data measurements and the sampling design. We follow his suggestion and estimate stage-2 effective sample sizes for size-composition data and extend his advice to re-weighting tagging data following Punt et al. (this volume), while keeping the weights assigned to the abundance data fixed at values used in the stock assessment (Siddeek et al., 2015). The stage-2 fitting of size-composition and tagging data affects the estimation of the size-transition matrix. We apply re-weighting procedures to the specific case of the pot fishery for golden king crab (*Lithodes aequispinus*) in the Aleutian Islands region of Alaska (henceforth ‘AI golden king crab’).

Annual stock status determination and catch allocation for AI golden king crab rely on fishery-dependent data, such as catch, effort, catch-per-unit-effort, and catch size-composition given the absence of annual fishery-independent survey data (Pengilly, 2015). Crab fisheries in the Bering Sea and Aleutian Islands, Alaska, are male-only, with minimum size limits. Most stocks lack essential reproductive biological information to determine a spawning biomass index based on female reproductive potential. Hence, management advice is based on mature male biomass (MMB) as the measure of spawning potential (NPFMC, 2008).

This paper investigates the effects of stage-2 weighting of size-composition and tagging data on trends in MMB estimated using a size-structured model applied to data for the eastern sub-stock of AI golden king crab. The effects are investigated for model scenarios defined by a range of natural mortality values (low to high), halving and doubling mean growth increment from the best estimate, and including or not including highly uncertain groundfish bycatch (trawl and fish pot) size-composition data. R_0

profiles (e.g. Wang et al., 2014) were also constructed to investigate the information content of various data components for abundance estimation.

2. Materials and methods

2.1 Model and data sources

The size-structured model is outlined in Appendix A while the estimated parameters are listed in Appendix B. Siddeek et al. (2015) provide full details of the model. The assessment was implemented using AD Model Builder (Fournier et al., 2012). The data sets included in the assessment are summarized in Table 1. Each data set was weighted, with arbitrarily large weights assigned to catch biomass (to ensure the model mimics the observed removals closely), and sample variance-based weights for standardized observer catch-per-unit-effort (CPUE) indices (Table 1).

2.2 Effective sample size for length composition

The annual number of length measurements in each category of catch (retained, total, and groundfish crab bycatch) is extremely large (thousands) and heterogeneous among years. It is a common practice to use the number of sets/pot lifts or another measure of sampling effort as a starting point for sample sizes instead of the number of length measurements when applying integrated stock assessment methods (Thorson, 2014). Consequently, the initial (stage-1) effective sample sizes were set to the number of days fished by the sampled vessels for the retained and total catch size-composition data, but number of sampled trips for the groundfish crab bycatch. The groundfish fishery uses a variety of gears and hence it is difficult to use ‘day’ as the initial effective sample size unit. We refer to the stage-1 effective samples sizes for the size-composition of the retained catch, total catch, and the groundfish crab bycatch for year t as $\tau_{1,t}^r$, $\tau_{1,t}^T$, and $\tau_{1,t}^{Tr}$ respectively.

Based on the assumption that the size-composition data are a multinomial sample, McAllister and Ianelli (1997) provided an estimator for the stage-2 effective sample sizes (referred to as stage2a weights) based on the ratio of the theoretical variance of expected proportions to the actual variance of proportions,

$$\frac{\sum_l \hat{P}_l - \hat{P}_t}{\sum_l - \hat{P}_t} \quad (1)$$

where $\hat{P}_{t,l}$ and \hat{P}_t are the estimated and observed proportions of the catch during year t in size-class l , and $\tau_{2,t}$ is the stage-2 effective sample size for year t .

McAllister and Ianelli (1997) set the effective sample size for each size-composition data set for eastern Bering Sea yellowfin sole (*Limanda aspera*) as the arithmetic mean of $\tau_{2,t}$ over years t (i.e., a year-invariant effective sample size) and iterated the model fitting, updating the effective sample sizes, until convergence occurred. Equation 1 ignores correlation among the residuals for the catch proportions so likely overestimates effective sample sizes (Francis, 2011). Punt (this volume) suggests using the harmonic mean of $\tau_{2,t}$ if the McAllister and Ianelli formula is used. A harmonic mean (constant) multiplier was consequently used to update the effective sample sizes at each iteration of model fitting until convergence occurred; i.e.

$$\left\{ \frac{1}{\sum_t \left[\frac{1}{\tau_{2,t}} \right]} \right\} \quad (2)$$

where $\tau_{2,t,i}$ is the stage-2 effective sample size for year t in iteration i ($\tau_{2,t,0} = \tau_{1,t}$) and $\hat{\tau}$ is the result of applying Equation 1. Convergence of the process of setting the stage-2 effective sample sizes using Equation 2 was visually assessed by plotting $\tau_{2,t,i-1}$ vs. $\tau_{2,t,i}$ at the final iteration.

Francis' (2011) mean-length based re-weighting method (i.e., Francis formula TA1.8, Punt, this volume) was considered as another way to re-weight the size-composition data (stage-2b) for iteratively re-weighting the initial (stage-1) effective sample sizes. Francis (2011)'s procedure accounts for correlation among catch length proportion residuals using the formula:

$$W^{-1} = \text{var} \left\{ \frac{\bar{l}_t - \hat{l}_t}{\sqrt{\text{var}(\hat{l}_t)}} \right\} \quad (3)$$

where \bar{l}_t and \hat{l}_t are respectively the observed and model-predicted mean lengths for year t :

$$\bar{l}_t = \sum_i \hat{l}_t \hat{p}_{t,i} \quad (4)$$

\hat{l}_t is the mid-point of length-class i , $\text{var}(\hat{l}_t)$ is the variance of the predicted mean length for year t :

$$\text{var}(\hat{l}_t) = \frac{\sum_i \hat{p}_{t,i} (1 - \hat{p}_{t,i})}{S_t} \quad (5)$$

S_t is the effective sample size in year t . Francis (in press) suggested that a good stopping criterion for the iteration process is when there is no appreciable change in the key outputs. Hence, we considered a stopping criterion of no appreciable change in W , terminal year MMB (Equation A10), and retained catch overfishing level (OFL, Equations A11a – A11c). S_t is related to the initial (stage-1) effective sample size according to:

$$S_t = \tau_{2,t,i} \quad (6)$$

where $\tau_{2,t,i}$ is the effective sample size for year t in iteration i and $\hat{p}_{t,i}$ is the Francis weight calculated using Equation 3 during iteration i .

2.3 Weights for the tagging data

Stage-1 weighting of the tagging data (i.e., $\lambda_{y,tag}$ in Equation A16 equal to 1) treats each recapture as an independent Bernoulli trial. Because overdispersion of data points cannot be ruled out, Punt et al. (this volume) propose a stage-2 weighting approach for tagging data based on the variability of errors in predicted mean length (*sensu* Francis, 2011). The stage-2 weighting of the tagging data for each time-at-liberty (there were six times-at-liberty, 1–6 years; Siddeek et al., 2016; Punt et al., this volume) was therefore:

$$\left\{ \frac{(\bar{P} - \hat{P})}{(\hat{P})} \right\} \quad (7)$$

where, \bar{P}_l^{obs} is the observed mean recapture length for release length l , \hat{P}_l is the predicted mean recapture length for release length l , W is the likelihood weight, and SE is the standard error. Thus, under stage-2 weighting of the tagging data, $\lambda_{y,tag}$ is set to W in Equation A16.

2.4 Growth increment

Siddeek et al. (2016) describe how the size-transition matrix was calculated for AI golden king crab. It is a function of three components: 1) moult probability as a function of size, 2) mean growth increment as a function of size, and 3) individual variability in growth increment (Equations A5–A7). The moult probability was modeled using a logistic function, mean growth increment using a linear model, and the variability in the growth increment using the normal distribution. One aspect of this study was to explore the impact of changing the mean growth increment, μ_i (Equation A6), on MMB and its asymptotic CV.

2.5 Scenarios

Table 2 lists the scenarios considered. The scenarios reflect assumptions regarding (a) the weighting for the size-composition and tagging data (either stage-1 or stage-2), (b) the value assumed for natural mortality [two steps incrementing the currently-assumed value for M of 0.18yr^{-1} (Zheng and Siddeek, 2016) by 0.06yr^{-1}], (c) whether the parameters defining the mean growth increment were pre-specified at half or double the values obtained when these parameters were estimated (with the best estimates of growth increment based on scenarios 7 to 12), and (d) whether or not the groundfish (trawl and fish pot) bycatch size-composition data were included in the assessment. The latter scenario was considered because the contribution of groundfish bycatch to total golden king crab catch is very small and the numbers of size measurements are also small, not covering all size-classes in every year (Siddeek et al., 2015). Hence some scenarios without groundfish bycatch size-compositions were considered assuming the groundfish selectivity to be 1.0 for all size-classes. Attempts to estimate groundfish selectivity produced imprecise parameter estimates and a curve that approached 1.0 for most size-classes (Siddeek et al., 2015).

2.6 Diagnostic measures

The scenarios were summarized by the estimates of MMB, the CVs for the estimates of MMB and the confidence intervals for MMB. The confidence intervals of MMB were determined assuming lognormality (Burnham et al., 1987), i.e.:

$$\begin{aligned} U_t &= MMB_t e^{1.96SE(MMB_t)} \\ L_t &= MMB_t e^{-1.96SE(MMB_t)} \end{aligned} \quad (8)$$

where U_t is the upper limit and L_t is the lower limit of the mature male biomass in year t , and the standard error of the logarithm of MMB for year t is $\sqrt{\ln(1+CV_t^2)}$, where CV_t is the coefficient of variation of the estimate of MMB for year t .

2.7 R_0 profile

Likelihood profiling of individual data components across a parameter has been argued to provide a way to evaluate the influence of data (Maunder, 1998, Francis, 2011, Maunder and Piner, this volume) and Wang et al. (2014) argue that such profiles can detect data conflicts. Likelihood profiles were developed for R_0 for three of the scenarios (7, 19, and 25), i.e. for a scenario where all parameters were estimated and when the growth increment was set to half or double the value for scenario 7.

3. Results and discussion

Scenarios 1 to 18 and 31 to 42 were assigned to one set (hereafter referred to as “set 1”) and scenarios 19 to 30 were assigned to a second set (hereafter referred to as “set 2”) for discussion of results. All of the parameters were re-estimated for the set 1 scenarios, whereas growth increments [at 103 and 138 mm CL respectively] were pre-specified either half or double of those estimated for one of scenarios 7 to 12 and all of the parameters were re-estimated subject to this constraint for the set 2 scenarios. Thus, the set 2 scenarios explore the impact of growth on estimates and uncertainty of MMB under stage-1 and stage-2 effective sample sizes.

Catch-rates are the key input data source that scale the biomass in the absence of fishery-independent surveys. All of the set 1 and part (half mean growth increment, green curves in the lower panel of Fig. 1) of the set 2 scenarios mimicked the catch-rate indices about equally well. However, the model-predicted catch-rate trends did not mimic the catch-rate data well when the mean growth increments were doubled (orange curves in the lower panel of Fig. 1). The model matches the catch-rate data better when the weight assigned to the catch-rate likelihood was increased five-fold (the black lines corresponding to scenarios 37 to 42; lower panel of Fig. 1). Overall, the fits indicate that all models were consistent with the catch-rate data, except when the mean growth increment was doubled.

The convergence of the stage-2a effective sample sizes for the size-composition data for the McAllister and Ianelli method was verified for all scenarios using visual plots (see Supplementary Fig. 1 for examples of 1:1 plots for scenarios 9, 10, 39, and 40). The convergence of the re-weighting (stage-2b) parameter, W , under Francis method is demonstrated for scenarios 5, 6, 11, 12, 17, 18, 35, 36, 41, and 42 in Supplementary Table 1. Convergence was achieved after 2 to 4 iterations. Francis re-weighting reduced the input effective sample sizes by ~ 15%– 25%, ~50%, and ~55% for retained, total, and groundfish bycatch size-compositions, respectively, for scenarios 5, 6, 11, 12, 17, 18, 23, 24, 29, 30, 35, 36, 41, and 42. On the other hand, the stage-2a method increased the input effective sample sizes for retained and total size-compositions by ~ 105% and ~10%, respectively, and reduced those for groundfish bycatch by ~45% for scenarios 3, 4, 9, 10, 15, 16, 21, 22, 27, 28, 33, 34, 39, and 40. The MMB estimates under Francis re-weighting were lower compared to the stage-1 weights for the size-composition data except for the largest M (Table 2; Fig. 3). In addition, the estimates of MMB values increased with increased M .

The median CVs of MMB were lower when stage-2a (i.e., McAllister and Ianelli method) weighting was used for the size-composition data instead of stage-1 or stage-2b (Francis method) weighting. This is expected given the stage-2a weighting process increased the weight assigned to the size-composition data. Increasing the weight assigned to the catch-rate likelihood five-fold also reduced the median CVs of MMB compared to the other scenarios (Fig. 2), as expected. Doubling the mean growth

increments increased the median CVs of MMB and led to many outlying CVs (Fig. 2), further confirming that high growth increments are not consistent with the data for AI golden king crab.

Stage-2 (2a and 2b) weighting of size-compositions and the tagging data did not appreciably affect the trends in MMB, although MMB was slightly lower for stage-2 weighting of tagging data for most scenarios (Fig. 3). Stage-2a and stage-2b weighting of the size-composition data narrowed the confidence intervals for MMB (Figs. 3 and 4). Though Francis method of re-weighting (stage-2b) has merit over the McAllister and Ianelli method of re-weighting (stage-2a) because it takes account of correlations in residuals among size-classes, both methods of re-weighting led to similar precisions and trends in MMB. It is possible that the use of robust multinomial model for fitting size-composition data negates the effect of correlations in residuals among size-classes, but this needs further investigation.

The MMB trends and their confidence intervals when the mean growth increment was halved were similar to those for the base scenarios (scenarios 7 to 12). Stage-2 weighting of the tagging data again led to slightly lower estimates of MMB when the mean growth increment was halved (Fig. 4 scenarios 19 vs. 20, 21 vs. 22, and 23 vs. 24). Nevertheless, the trends in MMB did not change dramatically when the tagging data were reweighted. The magnitude of MMB, but not the trends, reduced dramatically when the growth increment was doubled (Table 2 and Fig. 4 scenarios 25 vs. 26, 27 vs. 28, and 29 vs. 30), while stage-2 weighting of tagging data led to slightly higher estimates of MMB when the mean growth increments were doubled. However, as noted above, the fits for these scenarios are poor.

The R_0 profiles (Fig. 5) indicate that the primary determinant of R_0 are the CPUE data, although the penalty on the recruitment deviations also has an important influence on determination of R_0 . There is no evidence for data conflicts for scenarios 7 (Figs 5a, b) and 19 (Figs 5c, d). However, the minimum of the profile for the length data is outside of the 95% confidence interval for the estimate of R_0 for scenario 25 (Figs 5e, f), indicating a data conflict when the growth increments are doubled.

In summary, changes to M , the weight assigned to the catch-rate likelihood, and omitting the groundfish bycatch size-composition data from the models did not substantially affect the trends in MMB, but the magnitude of MMB was lower and precision higher under stage-2 weighting of either size-composition or tagging data. Halving mean growth increment did not affect the magnitude or trend in MMB. However, doubling mean growth increment drastically reduced the MMB estimates, but not the trend. Based on the precision of MMB estimates, stage-2 weighting of size-composition and tagging data is appropriate for assessments of the AI golden king crab. However, there is no clear choice between the McAllister and Ianelli (stage-2a) and the Francis (stage-2b) methods for re-weighting size composition data.

Francis (2011) argues that the purpose of stage-2 weighting is to make the data weights more consistent with the model output. Furthermore, Francis (in press) stresses that there is no 'correct' method of weighting size-composition data with the multinomial likelihood because it does not allow for substantial correlations in size-composition data. We agree with both comments. Re-weighting of size-composition data, accounting for correlations may lead to mixed results, depending on the selected likelihood model. We demonstrate that using two methods for stage-2 weighting of size-composition data for

the robust multinomial likelihood that there was not much of a difference between the results for the stage-2a method, which ignores correlations in residuals between size-compositions, and the stage-2b method, which accounts for such correlations. However, the MMB patterns shown in this paper may depend on this particular data. So this issue should continue to be explored for specific cases.

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Appendix A: Key equations included in the stock assessment model for golden king crab

Basic population dynamics

The annual male abundances by size are modeled using the equation:

$$= \sum_{i=1}^j [N_{t,i} e^{-M} - (\hat{C}_{t,i} + \hat{D}_{t,i} + \hat{T}r_{t,i}) e^{(y_t-1)M}] X_{i,j} + R_{t+1,j} \quad (\text{A1})$$

where $N_{t,i}$ is the number of male crab in size-class i on 1 July (the start of the biological year) of year t , $\hat{C}_{t,i}$, $\hat{D}_{t,i}$, and \hat{r} are respectively the model-predicted pot (target) fishery retained, pot fishery discard dead, and groundfish fishery discard dead catches in size-class i during year t , $X_{i,j}$ is the (i,j) element of the size-transition matrix, y_t is elapsed time from 1 July to the mid-point of the fishery during year t , $R_{t,j}$ is the recruitment to size-class j at the start of year t , and M is (size- and year-independent) instantaneous rate of natural mortality.

The catches by size-class are predicted using the equations:

$$\hat{C} = \frac{F_t s_{t,j} Z_{t,j}}{F_t s_{t,j} + M} \quad (\text{A2a})$$

$$\hat{D} = \frac{F_t s_{t,j}^r Z_{t,j}}{F_t s_{t,j}^r + M} \quad (\text{A2b})$$

$$\hat{T}r = \frac{F_t s_{t,j} Z_{t,j}}{F_t s_{t,j} + M} \quad (\text{A2c})$$

where $Z_{t,j}$ is total fishery-related mortality on animals in size-class j during year t :

$$Z_{t,j} = F_t s_{t,j} + F_t s_{t,j}^r + M \quad (\text{A3})$$

F_t is the full selection fishing mortality for the pot fishery during year t , F_t^r is the full selection fishing mortality for the groundfish fishery during year t , $s_{t,j}$ is the total selectivity for animals in size-class j by the pot fishery during year t , $s_{t,j}^r$ is the selectivity for animals in size-class j by the groundfish (trawl and fish pot) fishery, and $s_{t,j}^r$ is the probability of retention for animals in size-class j by the pot fishery during year t . The mortality of discards for the pot fishery of 0.2yr^{-1} and the mortality of discards in groundfish fishery bycatch of 0.65yr^{-1} (average of mortalities for the trawl (0.8yr^{-1}) and fish pot (0.5yr^{-1}) components of the groundfish fishery) were assumed known (Siddeek et al., 2015; Zheng and Siddeek, 2016).

Selectivity and retention

Selectivity and retention are both assumed to be logistic functions of size:

$$s_{t,j} = \frac{1}{1 + e^{-\ln(50)(L_j - L_{50})}} \quad (\text{A4})$$

where Δ and θ_{50} are the parameters of the total selectivity / retention pattern, and l_i is the midpoint of size-class i . The superscripts “T” and “r” are used to indicate total and retention selectivity in Appendix B. Selectivity changes in blocks for the pot fishery: block 1: 1985/86 to 2004/05 and block 2: 2005/06 to 2015/16. Groundfish fishery selectivity is fixed at 1 for all size-classes (see the text and Siddeek et al., 2015 for justification).

Growth matrix

The growth matrix \mathbf{X} is modeled as follows:

$$\left\{ \begin{matrix} \\ \\ \\ \end{matrix} \right\}^P \tag{A5}$$

where:

$$\begin{matrix} \int & | \mu \\ \int_j & | \mu \\ \int_j & | \mu \end{matrix} ,$$

$$x | \mu \sim \frac{1}{\sqrt{2}} \frac{1}{\sqrt{2}} , \text{ and}$$

is the mean growth increment for male crab in size-class i :

$$\tag{A6}$$

a , b , and σ are estimable parameters, and j_1 and j_2 are the lower and upper limits of the receiving length-class j (in mm CL), l_i is the mid-point of the contributing length-interval i , and n is the number of size-classes. The quantity m_i is the moult probability for size-class i :

$$\frac{1}{c(t-d)} \tag{A7}$$

where c and d are parameters.

Catch-per-unit-effort (CPUE)

The retained catch CPUE is predicted using the equation:

$$\widehat{CPUE} = \sum (N \cdot 5 [\widehat{C}_t \widehat{D}_t \widehat{Tr}_{t,j}]) e \tag{A8}$$

where q_k is the catchability coefficient during the k -th time period ($k=1$: 1985/86 to 2004/05; $k=2$: 2005/06 to 2014/15).

Initial conditions

The initial size-composition corresponded to a population at unfished equilibrium, i.e.:

$$\text{---} \tag{A9}$$

where \mathbf{X} is the growth matrix, \mathbf{S} is a matrix with diagonal elements given by e^{-M} , \mathbf{I} is the identity matrix, and \mathbf{R} is the product of average recruitment and relative proportion of total recruitment to each size-class.

Mature male biomass (MMB)

Mature male biomass at the (assumed) 15 February spawning time in the following year (NPFMC, 2008) is computed using equation

$$\sum_j w_j \hat{C}_j \hat{D}_j \hat{Tr}_j (y')^M \quad (\text{A10})$$

where y' is 0.627, the proportion of a year from 1 July to 15 February, and w_j is the weight of male crab in size-class j .

Overfishing level mortality (F_{OFL})

$$(a) \text{ if } \overline{MMB} < \gamma M, \quad (\text{A11a})$$

$$(b) \text{ if } \overline{MMB} > \gamma M \text{ and } \overline{MMB} < \frac{\alpha}{\left(\frac{t}{\overline{MMB}}\right)}, \quad (\text{A11b})$$

$$(c) \text{ if } \overline{MMB} > \gamma M, \quad (\text{A11c})$$

where γ is a constant multiplier of M (currently assumed to be 1), α is a parameter, and \overline{MMB} is the mean mature male biomass estimated for a selected time period (1985–2015) and used as a B_{MSY} proxy (NPFMC, 2008). The overfishing level directed fishery catch (OFL) is estimated using Equations (A2a) and (A2b) and the overfishing level groundfish bycatch is estimated using Equation (A2c) with an average groundfish fishing mortality rate for 1989–1994.

The likelihood function

Size-composition data

The size-composition data enter the objective function in the form of the robust normal for proportions negative log-likelihood (Fournier et al., 1998), i.e. generically:

$$LL_r^{LF} = 0.5 \sum_t \sum_j \ln(2\pi\sigma_{t,j}^2) - \sum_t \sum_j \ln \left[\exp \left(-\frac{(P_{t,j} - \hat{P}_{t,j})^2}{2\sigma_{t,j}^2} \right) + 0.01 \right] \quad (\text{A12})$$

where $P_{t,j}$ is the observed proportion of male crab in size-class j in the catch during year t , $\hat{P}_{t,j}$ is the model-estimate corresponding to $P_{t,j}$, i.e.:

$$\hat{P}_{t,j} = \frac{\hat{C}_j}{\sum_i \hat{C}_{t,i}}; \hat{P}_{t,i} = \frac{(\hat{C}_i \hat{D}_{t,j})}{\sum_i (\hat{C}_i \hat{D}_{t,i})}; \hat{P}_{t,r} = \frac{\hat{Tr}_j}{\sum_i \hat{Tr}_i} \quad (\text{A13})$$

where $\hat{P}_{t,j}^r$ is the retained, $\hat{P}_{t,j}^T$ is the total, and $\hat{P}_{t,j}^{Tr}$ is the groundfish model-estimate of retained catch proportions of male crab in size-class j in year t , $\sigma_{t,j}^2$ is the variance of $P_{t,j}$:

$$\frac{1}{n} \sum_j \left[\frac{1}{\sigma_{t,j}^2} \right] \quad (A14)$$

is the effective sample size for year t , and n is the number of size-classes.

Catch-rate indices

The catch-rate indices are assumed to be lognormally distributed about the model predictions. The negative log-likelihood is:

$$\left\{ 0.5 \sum_t \left[2\pi(\sigma_{r,t}^2) \right] \sum_t \left(\frac{CPUE_t^r - \widehat{CPUE}_t^r}{2(\sigma_{r,t}^2 + \frac{c}{e})} \right) \right\} \quad (A15)$$

where $CPUE_t^r$ is the standardized retained catch-rate index for year t , $\sigma_{r,t}$ is standard error of the logarithm of $CPUE_t^r$, and \widehat{CPUE}_t^r is the model-estimate corresponding to $CPUE_t^r$, σ_e is the extent of over-dispersion, c is a small constant to prevent zero values (0.001), and e is the weight assigned to the catch-rate data (5 for scenarios 37–42 and 1 for the other scenarios).

Tagging data

Let $\mathbf{V}_{j,t,y}$ be the number of tagged male crab that were released during year t that were in size-class j when they were released and were recaptured after y years, and $\underline{\rho}_{j,t,y}$ be the vector of recaptures by size-class from the males that were released in year t that were in size-class j when they were released and were recaptured after y years. The log-likelihood corresponding to the multinomial distribution for the tagging data is then:

$$\sum_j \sum_t \sum_y \sum_i \ln \hat{\rho}_{j,t,y,i} \quad (A16)$$

where e is the weight assigned to the tagging data for recapture year y , $\hat{\rho}_{j,t,y,i}$ is the proportion in size-class i of the recaptures of males that were released during year t that were in size-class j when they were released and were recaptured after y years:

$$\hat{\rho}_{j,t,y,i} \propto \underline{s}^T [\mathbf{X}]^y \underline{Z}^{(j)} \quad (A17)$$

where \underline{s} is a vector with $\mathbf{V}_{j,t,y}$ at element j and 0 otherwise, and \underline{S}^T is the vector of total selectivities for tagged male crab by the pot fishery. This log-likelihood function is predicated on the assumption that all recaptures are in the pot fishery and the reporting rate is independent of the size of crab.

Penalty functions

Penalties are imposed on the deviations of annual pot fishing mortality (F) about mean pot fishing mortality, annual groundfish fishing mortality (F^{Tr}) about mean groundfish

fishing mortality, recruitment (R) about mean recruitment, and growth increment (G , for a few scenarios):

$$P_1 = \lambda_F \sum_t (\ln F_t - \ln \bar{F})^2 \quad (\text{A18})$$

$$P_2 = \lambda_{F^{Tr}} \sum_t (\ln F_t^{Tr} - \ln \bar{F}^{Tr})^2 \quad (\text{A19})$$

$$P_3 = \lambda_R \sum_t (\ln \varepsilon_t)^2 \quad (\text{A20})$$

where P_1 , P_2 , and P_3 are penalty terms; λ_F , $\lambda_{F^{Tr}}$, and λ_R are the weights assigned to pot fishing mortality (0.001), groundfish fishing mortality (0.001), and recruitment (2.0), respectively.

Appendix B: Pre-specified and estimated parameters of the population dynamics model.

Parameter	Number of parameters
Initial conditions:	
Length-specific equilibrium abundance	n (estimated)
Fishing mortalities:	
Pot fishery deviations, F_t	1985–2015 (estimated)
Mean pot fishery fishing mortality, \bar{F}	1 (estimated)
Groundfish fishery deviations, F_t^{Tr}	1989–2015 (the mean F for 1989 to 1994 was used to estimate groundfish discards back to 1985 (estimated)
Mean groundfish fishery fishing mortality, \bar{F}^{Tr}	1 (estimated)
Selectivity and retention:	
Pot fishery total selectivity θ	2 (1985–2004; 2005+) (estimated)
Pot fishery total selectivity difference,	2 (1985–2004; 2005+) (estimated)
Pot fishery retention θ	1 (1985+) (estimated)
Pot fishery retention difference, Δ	1 (1985+) (estimated)
Groundfish fishery selectivity	fixed at 1 for all size-classes
Growth:	
Expected growth increment, a, b	2 (estimated)
Variability in growth increment, σ	1 (estimated)
Molt probability (size transition matrix with tag data) c	1 (estimated)
Molt probability (size transition matrix with tag data) d	1 (estimated)
Natural mortality, M	1 (pre-specified)
Recruitment:	
Number of recruiting length-classes	5 (pre-specified)
Distribution to length-class, α_r, β_r	2 (estimated)
Median recruitment, \bar{R}	1 (estimated)
Recruitment deviations, ε_t	56 (1961–2016) (estimated)
Over fishing level pot fishery mortality,	1 (calculated using Equations A11a – A11c)
Fishery catchability, q	2 (1985–2004; 2005+) (estimated)
Additional CPUE indices standard deviation,	1 (estimated)
Likelihood weights (coefficient of variation)	Pre-specified, varies among scenarios

Table 1. Data used in the assessment for AI golden king crab, along with the weighting approaches. Note: 1985/86 refers to the fishery prosecuted between July 1985 and June 1986.

Data set	Year range	Data type(s)	Likelihood / weight
Retained pot catch	1985/86–2015/16	Catch in weight	Log-normal, CV 0.032
Retained pot catch	1985/86–2015/16	Size-composition	Robust normal, Scenario-dependent
Total pot catch	1990/91–2015/16	Catch in weight (numbers derived from observer total catch CPUE and fishing effort and converted to weight)	Log normal, CV scaled to a maximum of 0.045 based on the annual number of pots sampled by observers
Total pot catch	1990/91–2015/16	Size-composition	Robust normal, Scenario-dependent
Groundfish discarded bycatch	1989/90–2015/16	Catch in weight	Lognormal, CV 3.344
Groundfish discarded bycatch	1989/90–2015/16	Size-composition	Robust normal, Scenario-dependent
Observer legal size crab CPUE	1991/92–2015/16	Annual CPUE indices with standard errors estimated using a negative binomial GLM (Zuur et al., 2009)	Log-normal with a CV^2 of $\frac{\sigma^2}{\mu^2}$, where μ is estimated from the GLM and σ^2 is an additional (estimated) constant variance
Tag recapture	1991, 1997, 2000, 2003, and 2006 releases	Release and recapture lengths and time-at-large up to 2012 recoveries	Multinomial, Stage-1: weight = 1 for each data point Stage-2: scenario-dependent

Table 2. Model scenarios for eastern Aleutian Islands golden king crab. The last two columns report the estimate of terminal year (2015) MMB and its estimated CV. Stage-2a: McAllister and Ianelli method; Stage-2b: Francis method

Scenario	Size-composition weighting method	Tagging data weighting method	Growth increment / size data	Natural mortality ($M yr^{-1}$)	Terminal MMB (t)	Asymptotic CV of terminal MMB
1	Stage-1	Stage-1	Estimated	0.18	9,526	0.161
2	Stage-1	Stage-2	Estimated	0.18	9,267	0.165
3	Stage-2a	Stage-1	Estimated	0.18	9,090	0.180
4	Stage-2a	Stage-2	Estimated	0.18	8,888	0.183
5	Stage-2b	Stage-1	Estimated	0.18	9,105	0.164
6	Stage-2b	Stage-2	Estimated	0.18	8,779	0.168
7	Stage-1	Stage-1	Estimated	0.24	11,471	0.166
8	Stage-1	Stage-2	Estimated	0.24	11,071	0.170
9	Stage-2a	Stage-1	Estimated	0.24	11,608	0.176
10	Stage-2a	Stage-2	Estimated	0.24	11,210	0.178
11	Stage-2b	Stage-1	Estimated	0.24	10,894	0.168
12	Stage-2b	Stage-2	Estimated	0.24	10,398	0.171
13	Stage-1	Stage-1	Estimated	0.30	13,470	0.170
14	Stage-1	Stage-2	Estimated	0.30	12,911	0.173
15	Stage-2a	Stage-1	Estimated	0.30	13,696	0.181
16	Stage-2a	Stage-2	Estimated	0.30	13,377	0.177
17	Stage-2b	Stage-1	Estimated	0.30	13,923	0.182
18	Stage-2b	Stage-2	Estimated	0.30	13,177	0.184
19	Stage-1	Stage-1	Half mean growth increment (based on scenario 7)	0.24	12,161	0.157
20	Stage-1	Stage-2	Half mean growth increment (based on scenario 8)	0.24	12,595	0.156
21	Stage-2a	Stage-1	Half mean growth increment (based on scenario 9)	0.24	12,168	0.159
22	Stage-2a	Stage-2	Half mean growth increment (based on scenario 10)	0.24	12,156	0.154
23	Stage-2b	Stage-1	Half mean growth increment (based on scenario 11)	0.24	11,906	0.165
24	Stage-2b	Stage-2	Half mean growth increment (based on scenario 12)	0.24	12,079	0.158
25	Stage-1	Stage-1	Double mean growth increment (based on scenario 7)	0.24	9,592	0.285
26	Stage-1	Stage-2	Double mean growth increment (based on scenario 8)	0.24	3,701	0.200
27	Stage-2a	Stage-1	Double mean growth increment (based on scenario 9)	0.24	4,019	0.207
28	Stage-2a	Stage-2	Double mean growth increment (based on scenario 10)	0.24	3,309	0.220

Table 2 continued

29	Stage-2b	Stage-1	Double mean growth increment (based on scenario 11)	0.24	3,649	0.192
30	Stage-2b	Stage-2	Double mean growth increment (based on scenario 12)	0.24	4,056	0.202
31	Stage-1	Stage-1	Groundfish bycatch size-composition data excluded	0.24	11,414	0.169
32	Stage-1	Stage-2	Groundfish bycatch size-composition data excluded	0.24	11,123	0.171
33	Stage-2a	Stage-1	Groundfish bycatch size-composition data excluded	0.24	11,499	0.175
34	Stage-2a	Stage-2	Groundfish bycatch size-composition data excluded	0.24	11,074	0.176
35	Stage-2b	Stage-1	Groundfish bycatch size-composition data excluded	0.24	11,591	0.169
36	Stage-2b	Stage-2	Groundfish bycatch size-composition data excluded	0.24	11,121	0.171
37	Stage-1	Stage-1	Estimated (five-fold weight on catch-rate likelihood)	0.24	12,525	0.103
38	Stage-1	Stage-2	Estimated (five-fold weight on catch-rate likelihood)	0.24	12,227	0.109
39	Stage-2a	Stage-1	Estimated (five-fold weight on catch-rate likelihood)	0.24	14,234	0.097
40	Stage-2a	Stage-2	Estimated (five-fold weight on catch-rate likelihood)	0.24	13,694	0.102
41	Stage-2b	Stage-1	Estimated (five-fold weight on catch-rate likelihood)	0.24	11,771	0.103
42	Stage-2b	Stage-2	Estimated (five-fold weight on catch-rate likelihood)	0.24	11,251	0.109

Figure Titles

Figure 1. Comparison of the observed (open circles with $\exp(\pm 2 \sqrt{\ln(1 + CV_t^2)})$), and the model-predicted CPUE indices (colored solid lines) for scenarios (Sc) 1 to 18 (upper panel) and 7, and 19 to 42 (lower panel). The results for Scenario 7 curve are included in lower panel for comparison.

Figure 2. Box plots of the coefficient of variation (CV) of the among-year variation in mature male biomass (MMB) for scenarios (Sc) 1 to 42.

Figure 3. Comparison of the trends in mature male biomass (MMB with log-normal confidence intervals based $\exp(\pm 2 \sqrt{\ln(1 + CV_t^2)})$) for scenarios (Sc) 1 to 18 and 31 to 42. Pairwise plots compare MMB trends between stage-1 (solid curves with shaded 95% confidence intervals) and stage-2 (dashed curves with dotted lines indicating 95% confidence intervals) weighting of the tagging data.

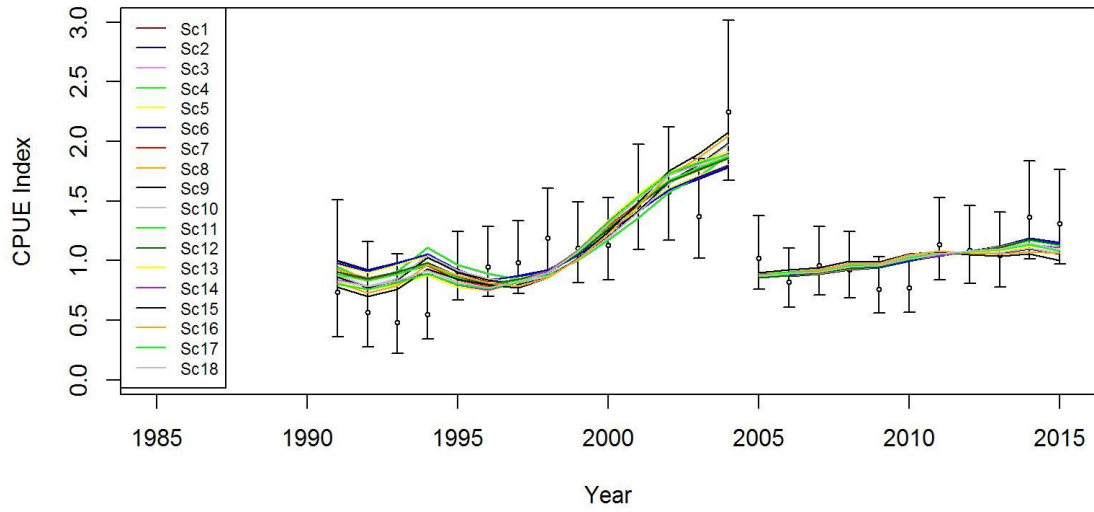
Figure 4. Comparison of the trends in mature male biomass (MMB with log-normal confidence intervals based $\exp(\pm 2 \sqrt{\ln(1 + CV_t^2)})$) for scenarios (Sc) 19 to 30 (i.e., changes to the assumptions regarding the mean growth increment). Pairwise plots compare MMB trends between stage-1 (solid curves with shaded 95% confidence intervals) and stage-2 (dashed curves with dotted lines indicating 95% confidence intervals) weighting of the tagging data.

Figure 5. Total negative log-likelihood and negative log-likelihood by data component as a function of $\log(R_0)$ for the base model [scenario 7, plots (a), and (b)], and scenarios in which the growth increment is set to half [scenario 19, plots (c), and (d)], and double [scenario 25, plots (e), and (f)] the base model estimates. The negative log likelihood values were zero adjusted. The red horizontal line denotes the cut-off for a 95% confidence interval for $\log(R_0)$.

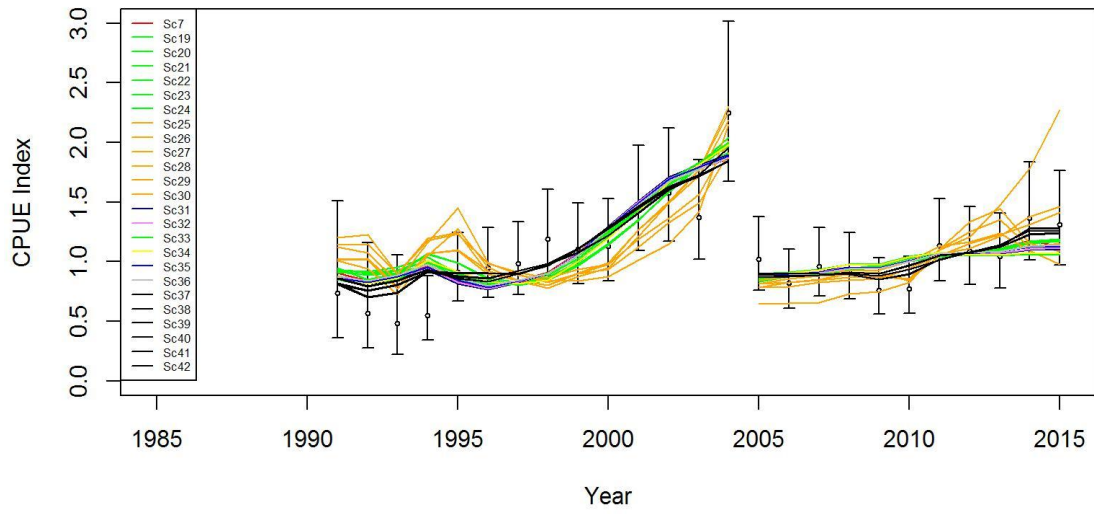
Supplementary figure:

Supplementary Figure 1. Predicted $i-1^{\text{th}}$ step input effective sample size versus the $i-1^{\text{th}}$ step stage-2 effective sample size for retained catch, total catch, and groundfish bycatch size-composition under McAllister and Ianelli method for scenarios (Sc) 9, 10, 39 and 40. The red line is the 1:1 line.

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Figure 1. Color

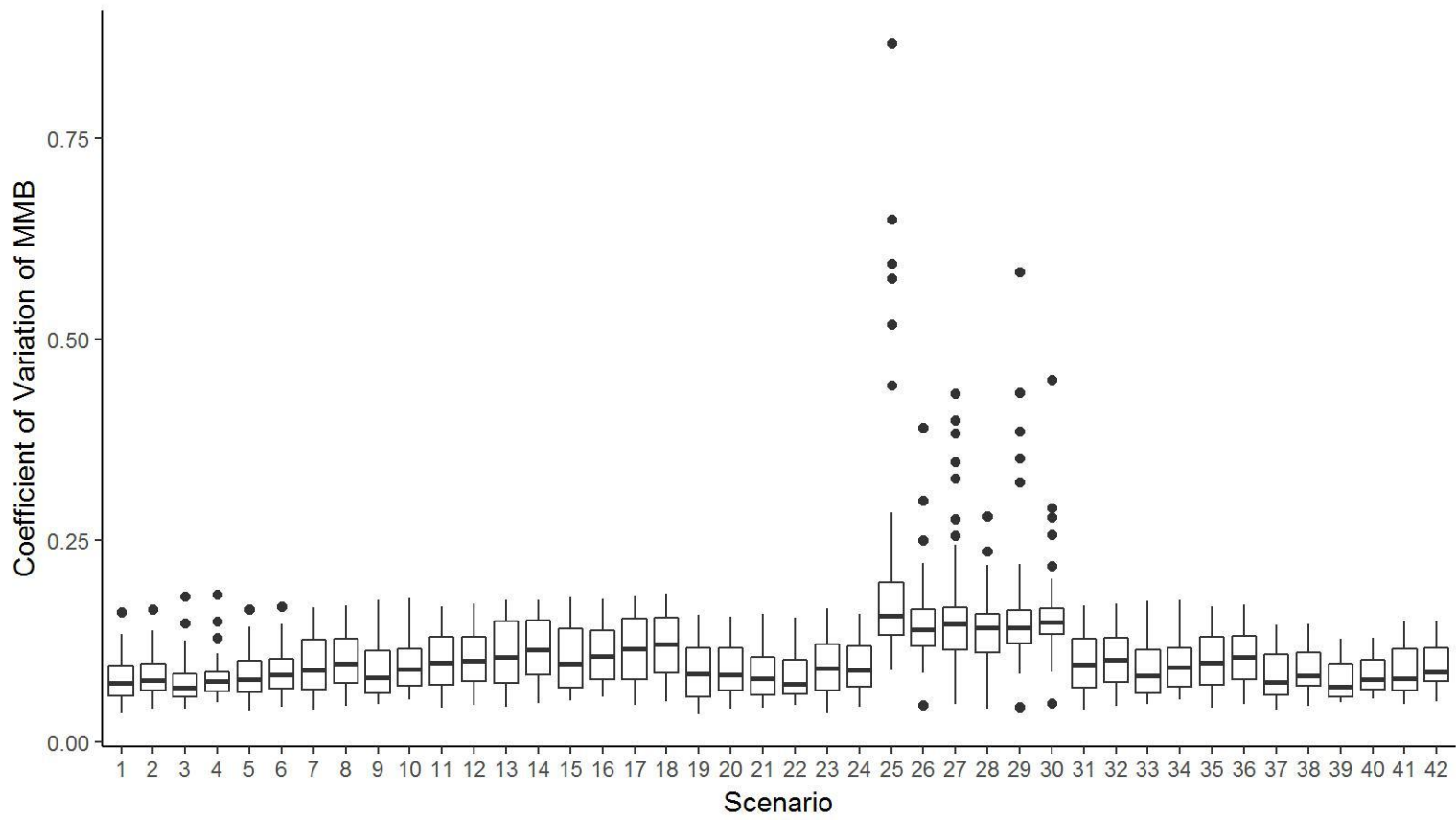


Figure 2.

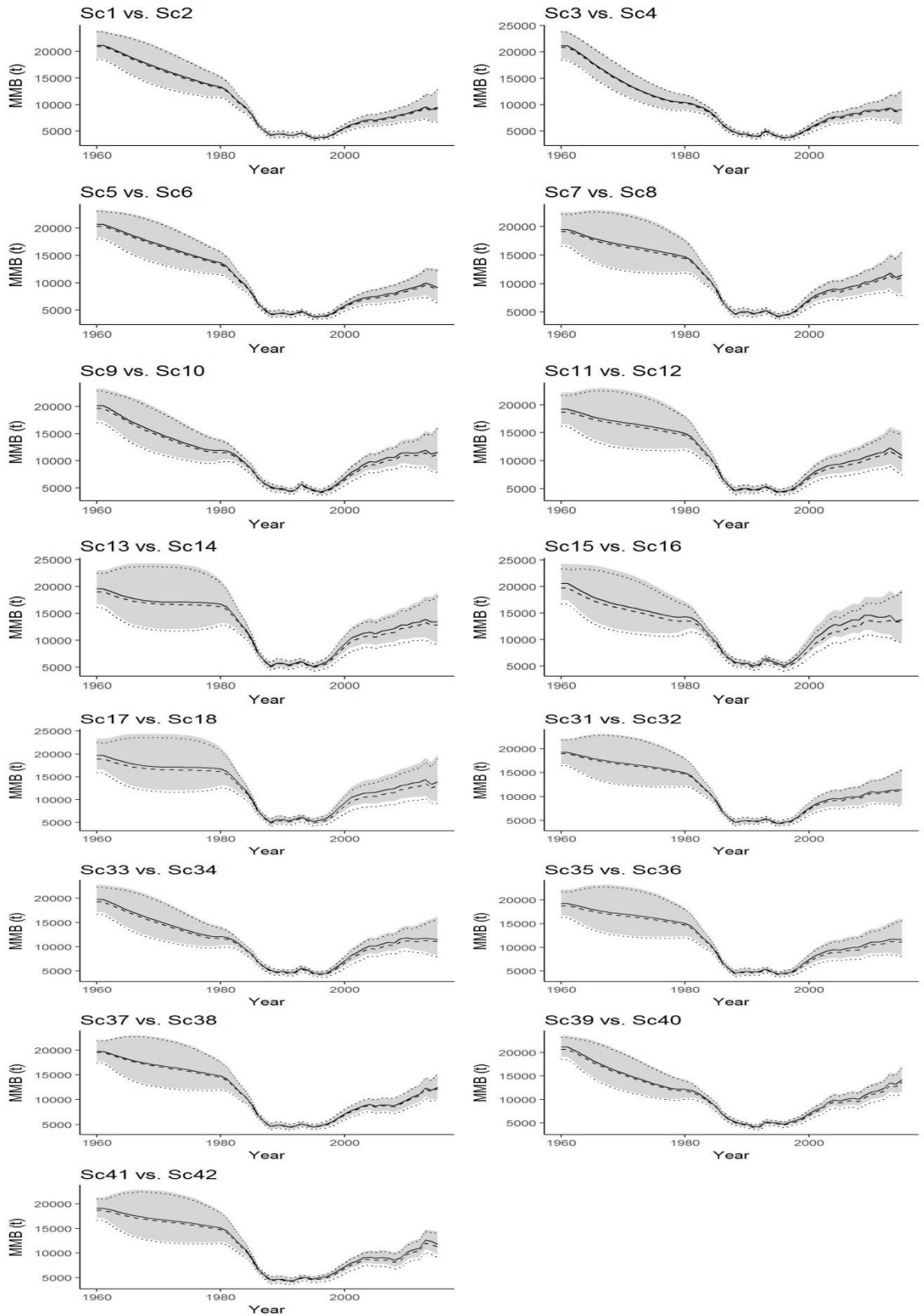
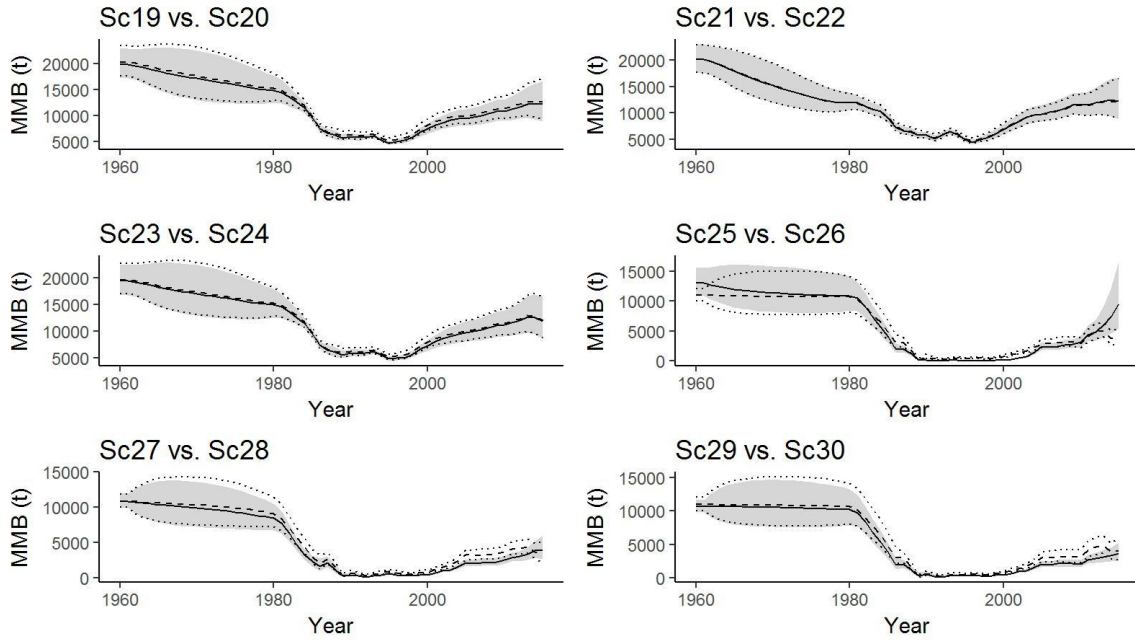


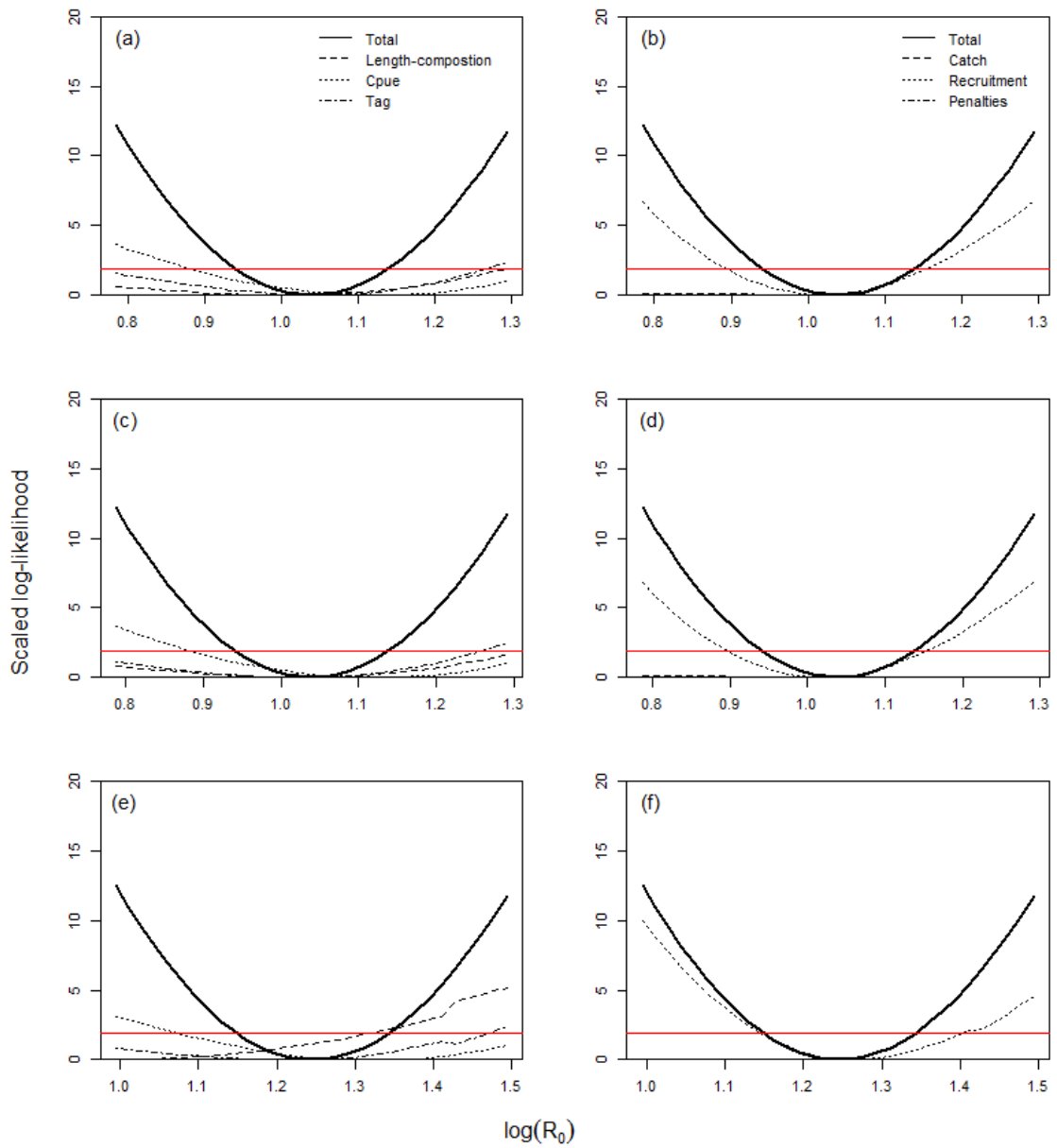
Figure 3.

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Figure 4.



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Figure 5.