2017 Crab Modeling Workshop Report for Tanner Crab

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1.0 Introduction

The purpose of this paper is to report on recent developments in the new Tanner crab stock assessment model code (now “TCSAM02”, formerly “TCSAM2015”) and provide a direct comparison between equivalent models run with the new code and models run with the code used for the 2016 assessment (“TCSAM2013”; Stockhausen, 2016). Like TCSAM2013, TCSAM02 provides a size-structured integrated assessment environment based on AD Model Builder (Fournier et al., 2012), a suite of C++ libraries for developing models fit to data using automatic differentiation methods. TCSAM02, under development for the past two years, provides a much more flexible environment to TCSAM2013 for defining alternative models based on a set of model configuration files. TCSAM02 can fit new data types not available in TCSAM2013: molt increment (growth) and male chela height (maturity) data. It also provides the option to calculate the OFL and associated quantities directly within the model, thus results retain full model uncertainty when calculated using MCMC (using TCSAM2013, the OFL is calculated in a separate projection model and incorporates uncertainty only in recruitment and end-year mature biomass).

Although a number of options for configuring the assessment model have been incorporated into the TCSAM2013 model code over the past few years (see the 2014, 2015, and 2016 Tanner crab SAFE chapters), many features in the code remain “hard-wired” and cannot be changed without substantially re-writing it—in particular, the number and type of fisheries and surveys incorporated in the model, the likelihood components defined in the model, the time periods defined for model parameters, and the alternative functions used to describe selectivity. Using TCSAM02, the number of fisheries and surveys, as well as their associated data types and likelihood components, is specified in the configuration files, as are the time periods assigned to different model processes and parameters. A variety of alternative prior probability functions can also be assigned to any model parameter using the configuration files. Similarly, a number of alternative selectivity functions can be assigned to any fishery or survey, different selectivity functions can be assigned in different time periods, and the same selectivity parameter can be assigned to different functions.

As noted previously, the purpose of this paper is to report on recent developments in TCSAM02 and to provide a direct comparison between equivalent models run with the 2016 assessment data using TCSAM02 and TCSAM2013, with the expectation that this comparison will provide sufficient rationale for adopting TCSAM02 for the 2017 stock assessment and discontinuing further use of TCSAM2013. In order to achieve this direct comparison, it was necessary to add several additional options to TCSAM2013 and run the resulting TCSAM2013 model with these options turned “on”. The resulting “directly-comparable” model will be proposed at the May CPT meeting as the “base model” for the 2017 assessment.

In Section 2, I provide an overview of the TCSAM02 model code and features. A more detailed discussion of the model code is provided in Appendix A. In Section 3, I discuss the changes made to the TCSAM2013 code to achieve a direct comparison with TCSAM02 and provide results from a series of

TCSAM2013 models which document the incremental changes used to obtain the directly-comparable TCSAM2013 model from the 2016 assessment model. In Section 4, I discuss results from the "directly-comparable" TCSAM02 and TCSAM2013 models using fixed parameter values. In Section 5, I discuss results from the "directly-comparable" TCSAM02 and TCSAM2013 models when parameter estimation is turned "on". Finally, I discuss recommendations for continued work in Section 6.

2. An overview of differences between TCSAM02 and TCSAM2013

The TCSAM02 model code is available on GitHub; the current development version is on the "AddingNewDataTypes" branch (committed on Jan. 10, 2017[1]). A detailed description of the model equations is provided in Appendix A. The equations used in the model to calculate the equilibrium size distribution, the basis for calculating the OFL, are provided in Appendix B. The TCSAM2013 model code is also available on GitHub; the 2016 assessment model is on the "2016AssessmentModel" branch[2] while a version more "directly-comparable" to TCSAM02 is on the "After2016AssessmentA" branch[3]. A detailed description of the 2016 assessment model is provided in Appendix C.

The key features that make TCSAM02 an improvement on the current TCSAM2013 code are: 1) the ability to specify multiple time blocks for any model parameter in control files; 2) the ability to assign prior probabilities to any model parameter for each associated time block; 3) the ability to specify multiple fleets and associated data in control files; 4) the ability to specify data likelihood functions in control files, 5) the integration of growth (molt increment) and maturity (chela height) data into the model fitting process; 6) more selectivity function options; 7) numerous prior probability function options, 8) a more numerically-stable approach to growth, and 9) implementation of OFL calculations directly within the model.

It is possible to configure a TCSAM02 model to reproduce results from a TCSAM2013 model run by using an equivalent model configuration (selectivity functions, prior probability functions, likelihood types, etc.) and judiciously fixing parameter values (see Section 4). However, it also appears that current differences in the parameterization of several model processes result in the convergence of otherwise-equivalent TCSAM02 and TCSAM2013 models to different states (see Section5). As such, I focus here on describing model processes that have different parameterizations in TCSAM2013 and TCSAM02, including natural mortality, growth, survey catchability, and directed fishery selectivity prior to 1991.

Natural mortality

In TCSAM2013, the natural mortality rate on crab of sex *x* in maturity state *m* in year *y* ($M_{y,x,m}$, independent of shell condition and size) is given by:

$$M_{y,x,m} = \begin{cases} M^{base} \cdot \delta M_{x,m} & otherwise \\ M^{base} \cdot \delta M_{x,m} \cdot \delta M^{T}_{x,MAT} & 1980 \le y \le 1984 \end{cases}$$

where $M^{base}$is the (fixed) base rate (= 0.23), $\delta M_{x,m}$ is a sex- and maturity state-specific multiplier, and $\delta M^{T}_{x,MAT}$ is a sex-specific multiplier on mature crab during the "enhanced mortality" period from 1980 to 1984. In addition, the two values of $\delta M_{x,m}$ for immature crab are constrained to be identical. Priors on the $\delta M_{x,m}$ are applied assuming N(1,0.05) distributions.

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[1] SHA = 66db6ea0157212c3a7e6af9214b8ff3ae39fe1b6

[2] SHA = 5f5125054e31dc282f1296a2e5656df6690ebb24

[3] SHA = 787a79c23748ee23a44223727e848b192938694f

In TCSAM02, ln-scale natural mortality rate on crab of sex *x* in maturity state *m* in year *y* ($lnM_{y,x,m}$) is described by five parameters (the μ's) using

$$lnM_{y,x,m} = \mu^0 + \mu_t^0 + \delta_{m,MAT} \cdot \mu_t^{MAT} + \delta_{x,FEM} \cdot \mu_t^{FEM} + \delta_{x,FEM} \cdot \delta_{m,MAT} \cdot \mu_t^{FEM,MAT}$$

where μ^0 is the base (ln-scale) rate for all crab, μ_t^0 is a constant offset for all crab for time block *t*, μ_t^{MAT} is a constant offset for all mature crab, μ_t^{FEM} is a constant offset for all female crab, and $\mu_t^{MAT,FEM}$ is a constant offset for all female crab. Here, *t* may refer to different time blocks for different parameters. Parameterization on the ln-scale was chosen to ensure that the corresponding arithmetic-scale rate was positive. While it is possible to find sets of parameter values that duplicate the natural mortality rates in TCSAM2013 using this parameterization, it does not allow one to specify priors that are exactly equivalent to those used in TCSAM2013.

Growth

In both TCSAM02 and TCSAM2013, mean post-molt size $\bar{z}_{y,x,z}$ is modeled as a power function of size *z*, with sex-specific parameters a_x and b_x using

$$\bar{z}_{y,x,z} = e^{a_x} \cdot z^{b_x}$$

where time blocks can be assigned to a_x and b_x in TCSAM02 to incorporate time-varying growth. Sex-specific normal priors are defined for the parameters in TCSAM2013; these can be duplicated in TCSAM02.

The sex-specific growth transition matrix, $\Theta_{y,x,z,z'}$, in TCSAM2013 is given by

$\Theta_{y,x,z,z'} = c_{x,z} \cdot \Delta_{z,z'}{}^{\alpha_{x,z}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_x}}$	Sex-specific (*x*) transition matrix for growth from pre-molt *z* to post-molt z', with $z' \geq z$
$c_{x,z} = \left[\sum_{z'} \Delta_{z,z'}{}^{\alpha_{x,z}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_x}}\right]^{-1}$	Normalization constant so $1 = \sum_{z'} \Theta_{x,z,z'}$
$\Delta_{z,z'} = z' - z$	Actual growth increment
$\alpha_{x,z} = [\bar{z}_{x,z} - z]/\beta_x$	Mean molt increment, scaled by β_x

where β_x is a fixed (not-estimated) scale factor. TCSAM02 includes this growth model as an option (mainly to match TCSAM2013 for testing), but its preferred growth model is similar to the one used in GMACS:

$\Theta_{y,x,z,z'} = c_{y,x,z} \cdot \int_{z'-bin/2}^{z'+bin/2} \Gamma\left(\frac{z'' - \bar{z}_{x,z}}{\beta_x}\right) dz''$	Sex-specific (*x*) transition matrix for growth from pre-molt *z* to post-molt z', with $z' \geq z$

$c_{y,x,z} = \left[\int_{z}^{\infty} \Gamma\left(\frac{z'' - \bar{z}_{y,x,z}}{\beta_{y,x}}\right) dz''\right]^{-1}$	Normalization constant so $1 = \sum_{z'} \Theta_{y,x,z,z'}$

where the integral represents the cumulative gamma distribution across the z' size bin. The TCSAM2013 approach was intended as an approximation to the TCSAM02 approach; the latter may be more stable numerically from a convergence perspective.

Survey catchability

In TCSAM2013, fully-selected survey catchability for the annual NMFS EBS bottom trawl survey is parameterized by sex in two time periods

$$q_{y,x} = \begin{cases} q_x^I & y < 1982 \\ q_x^{II} & 1982 \leq y \end{cases}$$

Priors are placed on the parameters q_x^t using normal distributions.

In TCSAM02, fully-selected catchability $q_{v,y,x,m}$ for survey v in year $y \in t$ is parameterized on the ln-scale using

$$q_{v,y,x,m,s} = \exp\left(pLnQ_v + pLnDQT_{v,t} + \delta_{m,IMM} \cdot pLnDQM_{v,t} + \delta_{x,FEM} \cdot pLnDQX_{v,t} + \delta_{x,FEM} \cdot \delta_{m,IMM} \cdot pLnDQXM_{v,t}\right)$$

where $pLnQ_v$ is the baseline ln-scale capture rate (for mature males), $pLnDQT_{v,t}$ is an additive modifier for time block *t*, $pLnDQM_{v,t}$ is an additive modifier for immature crab, $pLnDQX_{v,t}$ is an additive modifier for females, and $pLnDQXM_{v,t}$ is an additive modifier for immature females. As with natural mortality, the ln-scale was chosen to provide positive-definite estimates of survey catchability. In contrast to natural mortality, however, it is possible to provide priors identical to those used in TCSAM2013 as well as achieve equivalent values.

Directed fishery selectivity prior to 1991

In TCSAM2013, total catch selectivity for males in the directed fishery is characterized as logistic across three time periods: before 1991, from 1991 to 1996, and after 1996. The logistic functions in each period are defined by two values: 1) β, a parameter characterizing the slope of the function and 2) z_{50}, the size at 50% selected. Two values of β, are estimated: one applying to the fishery before 1997, the other applying to the fishery after 1996. After 1990, z_{50} is estimated annually and is parameterized using

$$z_{50_y} = e^{pLnZ_{50} + \delta Z_{50_y}}$$

where $pLnZ_{50}$ is the ln-scale mean parameter and the δZ_{50_y} are annual ln-scale “devs”. Prior to 1991, z_{50} is set to the average z_{50_y} from 1991 to 1996.

In TCSAM02, a similar approach can be taken, except that the value for z_{50} prior to 1991 cannot be calculated as an average over some time period; instead, it must be estimated (or fixed) as a parameter.

3. Changes to TCSAM2013 to achieve comparability with TCSAM02

Changes from the 2016 assessment model to achieve a version of TCSAM2013 that can be compared directly with TCSAM02 are provided in this section. The 2016 assessment model is referred to in the discussion below as “AM”.

All models discussed in this section were evaluated using 200 runs with “jittered” parameter values to provide a range of initial starting locations for the objective function minimizing procedure. The run resulting in the smallest objective function value and smallest maximum parameter gradient value was taken to be the global minimum solution. This jittering approach has been found to reduce the possibility that the minimum found by the minimization procedure is only a local minimum on the multidimensional surface of the objective function, not the global minimum.

Model AMa: Fitting to “uncorrected” survey size composition data

Old shell male crab observed in the NMFS trawl survey have been classified as “mature” based on the dual assumptions that: 1) the “old shell” classification indicates that a crab has not molted in the year prior to observation and 2) immature crab molt every year. Thus, old shell male crab must have undergone their terminal molt and can be classified as “mature”. However, there is some chance that immature crab that molt annually may be mistakenly classified as “old shell”. To address this concern, prior to fitting the survey size compositions, the 2016 assessment model applied a size-specific correction for the fraction of old shell crab (Fig. 1) that were mature vs. immature to observed survey size compositions for male crab classified as mature old shell. This correction was also performed in the 2012-2015 assessments.

The effect of the correction is to increase the number of male crab classified as “immature” relative to those classified as “mature” in any given size bin, but its impact for a size bin depends on both the size-specific correction and the relative number of mature crab classified as new shell vs. old shell. Because most old shell male crab in the survey are larger than 90 mm CW, the effects are rather small (Fig. 2). This correction is not applied in TCSAM02, so the 2016 assessment model (“AM”) was re-run without it (“AMa”).

Compared with AMa, estimated natural mortality rates for mature males were somewhat higher during the “enhanced mortality” period of 1980-1984 for AM (Fig. 3), the estimated size-specific probability of terminal molt for males was slightly smaller for AM (Fig. 4), as was the estimated mean post-molt size for males (Fig. 5). Results for females were practically identical for the two models. Estimated recruitment trends exhibited very small differences between the two models (Fig. 6), as did population abundance trends by sex and maturity state (Fig. 7)—although mature male abundance was somewhat larger for AMa across all years relative to AM. Mature male biomass (Fig. 8) was slightly larger for AMa, relative to AM, across all years (~80,000 t for AMa vs. ~72,000 t for AM in 2015). Estimated trawl survey biomass (Fig. 9) was almost identical across all years, with slightly higher estimates for both sexes in AMa during the early 1970s (before observed data) while estimated retained catch biomass in the directed fishery was essentially identical between the two models (Fig. 10). Estimated total catch biomass in the directed fishery (Fig. 11) was slightly higher for AMa than AM for both sexes during 1978 and 1979, but was otherwise similar for the two models. Very small differences existed between the two models for estimated total by catch biomass in the snow crab (Fig. 12), groundfish (Fig. 13), and BBRKC (Fig. 14) fisheries. A more comprehensive set of model comparisons, summarized here, can be found in the accompanying online document “ModelComparisons.AM-AMa.pdf”.

Changes to the likelihood components for the converged models (Table 1) were small except for those components involving the survey size compositions: the change to AMa resulted in a better fit to the size compositions for immature males (31.7 likelihood units) but worse fits for mature males (-26.7 likelihood units) and immature females (-5.5).

Model AMb: AMa + fitting to fishery size compositions as total capture size compositions
TCSAM02 fits fishery *capture* size compositions to the observed *capture* size compositions, based on at-sea observer data, in the likelihood whereas the 2016 assessment model fits predicted fishery *mortality* size compositions to (supposed) fishery mortality size compositions derived from the observed total capture size compositions. These two approaches are equivalent for the bycatch fisheries because the "observed" fishery mortality size compositions are simply scaled (by discard mortality) versions of the capture size compositions. However, this is not the case for male size compositions in the directed fishery because retention mortality is size-specific. In fact, the 2016 assessment model fit predicted size compositions for total male *mortality* in the directed fishery to observed size compositions for total male *capture* because the retained and discarded components of the at-sea observer size composition data can not be disaggregated to apply discard mortality correctly for the directed fishery. This approach was used in previous assessments as well, but no alternative existed for those assessments because those models directly estimated fishery selectivity functions associated with fishing mortality, whereas the 2016 assessment model estimated fishery selectivity functions associated with total capture and subsequently derived total mortality size compositions based on aggregating size-specific retained and discard mortality predicted separately. In retrospect for 2016, this was not the best use of the observed fishery size composition data, which reflected total capture size compositions. Consequently, an option aws added to TCSAM2013 to fit predicted total capture size compositions to observed total capture size compositions—consistent with TCSAM02. Model "AMb" implemented this option, but was otherwise identical to AMa.

The effect of the change from fitting predicted total mortality size comps to observed total catch (i.e., capture) size comps (AMa) to the more consistent practice of fitting predicted total catch size comps to observed total catch size comps (AMb) is apparent in Fig.s 15 and 16. The predicted total mortality size comps in AMa are slightly right-shifted to larger sizes than the predicted total catch size comps in AMb (Fig. 15) while the corresponding predicted total catch size comps in AMa are slightly left-shifted to smaller sizes relative to AMb (Fig. 16). This resulted in large changes in the likelihood components for retained catch and total male catch size compositions in the directed fishery (Table 1). The total objective function was substantially reduced in AMb relative to AMa (151.5 likelihood units), reflecting much better fits to the size compositions for retained males (55.6 units) and captured males (102.1 units) in the directed fishery for AMb (Table 1). Somewhat offsetting these improvements, AMb exhibited poorer fits to survey size compositions for mature crab (males: -10.2 units, females: -8.4 units).

Compared with AMa, estimated natural mortality rates for mature males were somewhat higher during the "enhanced mortality" period of 1980-1984 for AMb (Fig. 17) while the estimated size-specific probability of terminal molt for males was slightly smaller for AMb (Fig. 18). Results for females were practically identical for the two models, as were estimated mean post-molt sizes for both sexes (Fig. 19). Estimated recruitment in AMb was slightly smaller than in AMa prior to 1988, but essentially identical afterwards (Fig. 20), as were population abundance trends by sex and maturity state (Fig. 21) and mature biomass (Fig. 22). Estimated trawl survey biomass (Fig. 23) was smaller in AMb than AMa before 1980 for both sexes, but again was almost identical in the two models afterwards. Estimated retained catch biomass in the directed fishery was essentially identical in all years for the two models (Fig. 24). Estimated total catch (capture) biomass in the directed fishery (Fig. 25) was somewhat higher in AMa than AMb for both sexes from 1965 to 1980 (although the absolute difference was much smaller for females), but was otherwise similar for the two models. Very small (absolute) differences exist between the two models for estimated total by catch biomass in the snow crab (Fig. 26), groundfish (Fig. 27), and BBRKC (Fig. 28) fisheries. A comprehensive set of model comparisons, summarized here, can be found in the accompanying online document "ModelComparisons.AMa-AMb.pdf".

Model AMc: AMb + fitting to fishery biomass time series as total capture biomass time series
TCSAM02 fits time series of predicted total capture biomass in the fisheries to time series of observed (based on at-sea and dockside observer data) total capture biomass, whereas the 2016 assessment model fit time series of predicted total biomass mortality in the fisheries to time series of observed (based on at-sea and dockside-based observer data) total biomass mortality. Consequently, an option was added to TCSAM2013 to fit time series of predicted total capture biomass in the fisheries to time series of observed total capture biomass. Model “AMc” implemented this option, but was otherwise identical to AMb.

Estimated natural mortality rates (Fig. 29), terminal molt probabilities (Fig. 30), and mean growth increments (Fig. 31) were almost identical for the two models. Estimated annual recruitment (Fig. 32), population abundance trends (Fig. 33), mature biomass-at-mating (Fig. 34), and survey biomass (Fig. 35) were also very similar for the two models. Estimated retained catch biomass (Fig. 36) was practically identical in the two models prior to 1993, but estimates were slightly higher for AMC relative to AMb from 1993-2010 while they were slightly lower in 2014 and 2015.

Estimated captured biomass for males in the directed fishery (Fig. 37) was smaller for AMc relative to AMb across all years, by ~25,000 t in 1979, the year of largest catch, but differences were generally much smaller. Estimated captured (bycatch) biomass for females in the directed fishery (Fig. 37) was larger prior to 1985 for AMc relative to AMb (by ~4,000 t in 1979, the year of largest catch), but slightly smaller in years after 1985 (differences < 1,000 t). Estimated captured biomass in the snow crab fishery (Fig. 38) was similar in the two models across all years for males, but smaller across all years for females in AMc, while estimated captured biomass in the groundfish fisheries (Fig. 39) was almost identical across all years. The two models exhibited large relative, and opposite, differences in captured biomass for males and females in the BBRKC fishery (Fig. 40). Fig.s 41-44 illustrate the equivalent plots for estimated total catch mortality (in terms of biomass), as well as the “observed” total catch mortality obtained by applying handling mortality to observed discard biomass (used in the model fitting process in AMb but not AMc). The figures suggest that the “observed” catch mortality biomass is matched as well using AMc as AMb (in which it was directly fit), if not better (Fig. 44 for BBRKC). A comprehensive set of model comparisons, summarized here, can be found in the accompanying online document “ModelComparisons.AMb-AMc.pdf”.

The total objective function was substantially larger for AMc than for AMb (by 146.8 likelihood units; Table 1), but the likelihoods for fishery catch biomass are not comparable from a model selection perspective because the data being fit is different in the two models. However, as illustrated in Fig.s 41-44, the fishery catch mortality biomass data used to fit AMb is actually better fit by the equivalent estimated time series from AMc, even though AMc was fit using observed total fishery captured biomass.

Model AMd: AMc + applying natural mortality after molt-to-maturity
Finally, TCSAM02 applies natural mortality rates for mature crab to immature crab immediately following their molt to maturity whereas the 2016 assessment model continued to apply natural mortality rates for previously immature crab after their terminal molt (now new shell mature crab) until the end of the year in which the terminal molt occurred. Consequently, an option was added to TCSAM2013 to apply natural mortality rates for mature crab to immature crab immediately following their molt to maturity, consistent with TCSAM02. Model “AMd” implemented this option, but was otherwise identical to AMc.

Estimated natural mortality rates (Fig. 45) were very slightly lower for immature crab in AMd, compared with AMc, while rates for mature crab were very slightly higher during 1980-1984 (the enhanced mortality period) but otherwise identical. The probabilities for undergoing terminal molt (Fig. 46) and the mean molt increment (Fig. 47) were essentially identical in the two models. Estimated annual recruitment

(Fig. 48) was slightly smaller in AMd, compared with AMc, as was the annual abundance of sex- and maturity-state population components (Fig. 49). Estimated annual mature biomass-at-mating (Fig. 50) was also slightly smaller in AMd relative to AMc. The two models also exhibited almost identical results for estimated survey biomass (Fig. 51), retained catch biomass (Fig. 52), and total catch biomass in the directed and bycatch fisheries (Fig.s 53-56). A more comprehensive set of model comparisons, summarized here, can be found in the accompanying online document "ModelComparisons.AMc-AMd.pdf".

Fits to survey size compositions were better for immature males crab (by 20.3 likelihood units; Table 1), but worse for mature crab (by -20.7 units), for AMd relative to AMc. The fit to mature survey catch biomass was improved in AMd relative to AMc (by 8 likelihood units; Table 1).

4. TCSAM02 vs. TCSAM2013: Directly-comparable model results with fixed parameters

To directly compare TCSAM02 to TCSAM2013 model results, with the expectation that the results would be (almost) identical, parameter values were taken from TCSAM2013 model AMd and used to create equivalent initial parameter values for a TCSAM02 model (T02a) using identical biological constants (weights-at-size, etc.), survey and fishery data, equivalent likelihood component weights, and model configuration (size bins, etc.). Because TCSAM02 and TCSAM2013 differ in model parameterization for some processes (e.g., natural mortality), T02a was run with parameter estimation turned off in order to compare results directly with those from AMd.

As expected, values for model processes (e.g., natural mortality rates), population quantities (e.g., recruitment and population abundance trends) and survey and fishery quantities (e.g., catch abundance trends) are essentially identical for the two models (Fig.s 57-62). A more comprehensive set of comparison plots for the model results are available in the accompanying online document "ModelComparisons.AMd-T02a.pdf".

Although some small differences can be found between the likelihood components for the two models (Table 2), these are attributed to small differences in parameter values between the two models arising from truncation of the printed parameter values from AMd that were used to set the values for those in T02a.

5. TCSAM02 vs. TCSAM2013: Fitting equivalent models

The previous section showed that TCSAM02 can reproduce TCSAM2013 results when equivalent model configurations and fixed parameter values are used. With this test passed, I turned "on" parameter estimation in the TCSAM02 model (referred to here as "T02" to distinguish the results with estimated parameters from the results with fixed parameters). The "converged" model for T02 was obtained by evaluating 200 model runs with jittered initial parameter values and selecting the run with the smallest objective function and maximum parameter gradient values. One issue that quickly became apparent was that the TCSAM2013 growth model (ported to TCSAM02) was unstable for unknown reasons: no model run successfully converged. Model convergence was only achieved when the growth model was switched to the TCSAM02 growth model (based on the GMACS growth formulation).

When parameters were estimated, natural mortality rates from the two models (Fig. 63) were fairly different (Fig.s 63) for all sex and maturity state combinations, as well as in the 1980-1984 "enhanced mortality" time period. The estimated size-specific probabilities of terminal molt (Fig. 64) were fairly similar, but the probability of undergoing terminal molt at intermediate post-molt sizes was larger for both males and females in T02, compared with AMd. Mean growth curves (Fig. 65) for both sexes were identical for females and almost identical for males for the two models, but the use of different functions for the growth probabilities resulted in slightly different growth transition matrices (e.g., Fig. 66). Estimated annual recruitment (Fig. 67) was up to 2.5 times as large in T02 as in AMd, driving substantial differences in annual abundance of various population components (Fig. 68) and mature biomass-at-mating (Fig. 69). Differences between the two models for these quantities were greatest in the period prior to 1990, but were somewhat smaller after 1990. This was somewhat due to differences between the two models in survey catchability (Fig. 70) and selectivity (Fig. 71).

Estimated retained catch biomass (Fig. 73) was the same in both models—not surprising given the weight placed on this component in the model likelihood—while estimated captured biomass in the directed fishery (Fig. 74) was up to 3 time larger in T02 than AMd prior to 1991 for males; the reverse was true for females during 1976-1979. This behavior in estimated catch biomass is due, in part, to differences between the two models in estimated fishery catchability (Fig. 75) and, for males, capture selectivity (Fig. 76) prior to 1990, as well as differences in population abundance. Differences in fishery catchability between the two models for females, with no differences in selectivity functions, would suggest AMd would exhibit estimated female captured biomasses up to 4 times that of T02 during the late 1970s. The higher female population abundance trends in T02 during this time period ameliorate this difference somewhat. For males, the patterns in fishery catchability are similar to those for females, but differences in captured selectivity curves prior to 1991, as well as differences in estimated abundance levels, leads to higher captured biomass estimates for males in T02 during the entire period prior to 1991.

Estimated captured biomass in the snow crab fishery (Fig. 77) was similar for both sexes in both models, except during 1978-1982, when T02 estimated somewhat more females and fewer males than in AMd. Estimated captured biomass in the groundfish fisheries (Fig. 78) was also similar in both models after 1972. Estimated captured biomass in the BBRKC fishery (Fig. 79) was similar in both models after 1986; before 1986, somewhat larger captured biomasses for both sexes were estimated in T02 compared to AMd. A more comprehensive set of comparison plots for the model results are available in the accompanying online document “ModelComparisons.AMd-T02.pdf”.

It thus appears that equivalent model configurations in the two model codes do not result in identical results when parameter estimation is turned on. This is likely due to differences between TCSAM02 and TCSAM2013 in the way several model processes are parameterized (including fishery capture selectivity in the directed fishery pre-1991). Resolving this issue will require more work.

7. Recommendations

Although it is possible to reproduce results from a TCAM2013 model using TCSAM02 by selecting equivalent selectivity function options, prior probability function options, likelihood component options, likelihood weights, and other model configuration details, as well as judiciously fixing parameter values, differences between TCSAM02 and TCSAM2013 in the details of the parameterization of several population processes (e.g., natural mortality) appear to lead to different solutions when parameter estimation is turned on (see Section 5). As such, it may be worth adding parameterization options in TCSAM02 that more closely reflect those in TCSAM2013 for the processes that currently are parameterized differently. Additionally, it appears that the manner in which the fishery capture selectivity function for males in the directed fishery prior to 1991 is problematic, but can probably be dealt with by “sharing” the mean (or median) size-at-50%-selected parameter from the post-1991 period. Addressing these issues will provide the opportunity to move forward with adopting TCSAM02 for future assessments and the transition to GMACS while ensuring compatibility with the current assessment.

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Tables

Table 1. Comparison of objective function components and model differences for all TCSAM2013 models. Green highlighting indicates differences in objective function component values > 5 units, red highlighting indicates differences < -5 units.

Model	AM	AMa	AMb	AMc	AMd	AM-AMa	AMa-AMb	AMb-AMc	AMc-AMd	AM-AMd	description
penalties	0.12	0.12	0.11	0.11	0.12	0.00	0.00	0.00	0.00	0.00	recruitment penalty
	48.35	48.37	48.42	48.47	48.47	-0.02	-0.05	-0.05	-0.01	-0.13	historic recruitment penalty
	-1.49	-1.48	-1.63	-1.48	-2.05	-0.01	0.15	-0.15	0.58	0.57	natural mortality penalty (immatures)
	3.54	1.37	2.59	4.37	3.48	2.17	-1.22	-1.79	0.90	0.06	natural mortality penalty (mature males)
	34.34	34.39	33.12	34.10	36.00	-0.05	1.27	-0.98	-1.90	-1.66	natural mortality penalty (mature females)
	2.33	2.31	2.27	2.07	2.18	0.02	0.05	0.20	-0.10	0.16	maturity curve smoothness (females)
	0.79	0.76	0.81	0.81	0.81	0.03	-0.05	0.00	0.00	-0.02	maturity curve smoothness (males)
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	z50 devs for male selectivity in TCF (AR1)
	126.61	128.31	125.92	129.46	127.83	-1.70	2.40	-3.54	1.62	-1.22	penalty on F-devs in directed fishery
	29.53	29.52	29.14	32.09	32.06	0.01	0.38	-2.95	0.03	-2.54	penalty on F-devs in snow crab fishery
	132.46	132.44	132.41	147.25	147.28	0.02	0.03	-14.84	-0.03	-14.83	penalty on F-devs in BBRKC fishery
	52.49	52.43	52.37	53.33	53.34	0.07	0.06	-0.97	0.00	-0.85	penalty on F-devs in groundfish fishery
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	z50 devs for male selectivity in TCF (norm2)
priors	2.90	4.05	4.22	4.74	3.07	-1.15	-0.17	-0.52	1.67	-0.17	survey q penalty
	27.03	28.06	28.67	31.24	27.49	-1.03	-0.61	-2.57	3.75	-0.46	female survey q penalty
	-0.48	-0.48	-0.48	-0.48	-0.48	0.00	0.00	0.00	0.00	0.00	female growth parameter a
	-2.13	-2.13	-2.11	-2.07	-2.12	0.00	-0.01	-0.05	0.05	-0.01	female growth parameter b
	-2.54	-2.22	-2.33	-2.26	-2.24	-0.32	0.11	-0.07	-0.02	-0.30	male growth parameter a
	-1.35	-1.35	-1.35	-1.35	-1.35	-0.01	0.00	0.00	0.00	-0.01	male growth parameter b
size comp likelihoods	308.98	309.53	253.89	261.28	260.89	-0.55	55.64	-7.38	0.39	48.09	fishery: TCF retained males
	184.30	183.25	81.13	91.83	91.82	1.05	102.12	-10.70	0.01	92.48	fishery: TCF total males
	9.70	9.76	9.27	9.05	8.98	-0.06	0.49	0.22	0.07	0.72	fishery: TCF discarded females
	52.63	52.58	52.88	53.39	53.31	0.05	-0.31	-0.51	0.08	-0.68	fishery: SCF males
	12.49	12.43	12.34	12.37	12.44	0.06	0.10	-0.04	-0.06	0.05	fishery: SCF females
	26.69	26.25	27.59	34.38	34.57	0.44	-1.34	-6.80	-0.19	-7.88	fishery: RKC males
	2.25	2.24	2.19	2.01	2.02	0.01	0.05	0.18	-0.01	0.24	fishery: RKC females
	463.33	464.45	469.84	479.07	474.28	-1.12	-5.39	-9.23	4.79	-10.96	fishery: GTF males+females
	269.49	237.83	230.44	235.86	220.16	31.65	7.40	-5.43	15.70	49.32	survey: immature males
	250.07	276.82	287.03	289.05	297.95	-26.76	-10.21	-2.02	-8.90	-47.88	survey: mature males
	281.23	286.70	283.21	290.61	285.96	-5.47	3.49	-7.40	4.64	-4.74	survey: immature females
	128.52	132.18	140.56	137.77	149.59	-3.66	-8.38	2.80	-11.82	-21.07	survey: mature females
catch biomass likelihoods	199.10	198.63	198.43	197.96	189.76	0.47	0.19	0.47	8.20	9.34	survey: mature crab
	18.47	18.37	15.63	41.44	41.46	0.10	2.74	-25.80	-0.02	-22.99	fishery: TCF retained males
	11.54	11.35	9.45	14.21	14.25	0.19	1.90	-4.76	-0.04	-2.71	fishery: TCF male total catch biomass
	5.11	5.13	4.84	33.90	34.08	-0.02	0.30	-29.07	-0.18	-28.97	fishery: TCF female catch biomass
	6.21	6.01	5.94	24.68	25.03	0.21	0.06	-18.73	-0.35	-18.82	fishery: SCF total catch biomass
	12.81	12.69	12.40	7.15	7.19	0.12	0.29	5.25	-0.03	5.63	fishery: RKF total catch biomass
	2.43	2.30	2.26	1.82	1.84	0.14	0.04	0.44	-0.02	0.59	fishery: GTF total catch biomass
total	2,697.82	2,702.96	2,551.44	2,698.23	2,679.45	-5.14	151.52	-146.79	18.79	18.37	total

Table 2. Comparison of objective function components for TCSAM2013 model AMd and TCSAM02 model T02a.

type	fleet	data	stock component	Objective function values		
				T02a	AMd	AMd-T02a
index	NMFS survey	survey biomass	all	192.72	189.76	-2.96
		size composition	immature females	285.88	285.96	0.08
			mature females	149.67	149.59	-0.08
			immature males	220.01	220.16	0.15
			mature males	298.07	297.95	-0.12
retained catch	TCF	biomass	all	42.04	41.46	-0.58
		size composition	all	259.85	260.89	1.04
Total catch	GTF	biomass	all	1.90	1.84	-0.06
		size composition	all	474.20	474.28	0.08
	RKF	biomass	all	6.37	7.19	0.82
		size composition	all	36.58	36.59	0.00
	SCF	biomass	all	25.03	25.03	0.00
		size composition	all	65.74	65.74	0.00
	TCF	biomass	all	48.54	48.33	-0.21
		size composition	all	101.51	100.80	-0.71

Table 3. Comparison of objective function components for TCSAM2013 model AMd and TCSAM02 model T02.

type	fleet	data	stock component	Objective function values		
				T02a	AMd	AMd-T02
index	NMFS survey	survey biomass	all	170.07	189.76	19.69
		size composition	immature females	304.08	285.96	-18.12
			mature females	141.44	149.59	8.15
			immature males	204.55	220.16	15.61
			mature males	245.07	297.95	52.88
retained catch	TCF	biomass	all	45.15	41.46	-3.69
		size composition	all	242.50	260.89	18.39
Total catch	GTF	biomass	all	1.66	1.84	0.18
		size composition	all	451.45	474.28	22.83
	RKF	biomass	all	4.83	7.19	2.36
		size composition	all	33.00	36.59	3.59
	SCF	biomass	all	29.05	25.03	-4.02
		size composition	all	66.73	65.74	-0.98
	TCF	biomass	all	54.40	48.33	-6.07
		size composition	all	102.50	100.80	-1.71

Figures

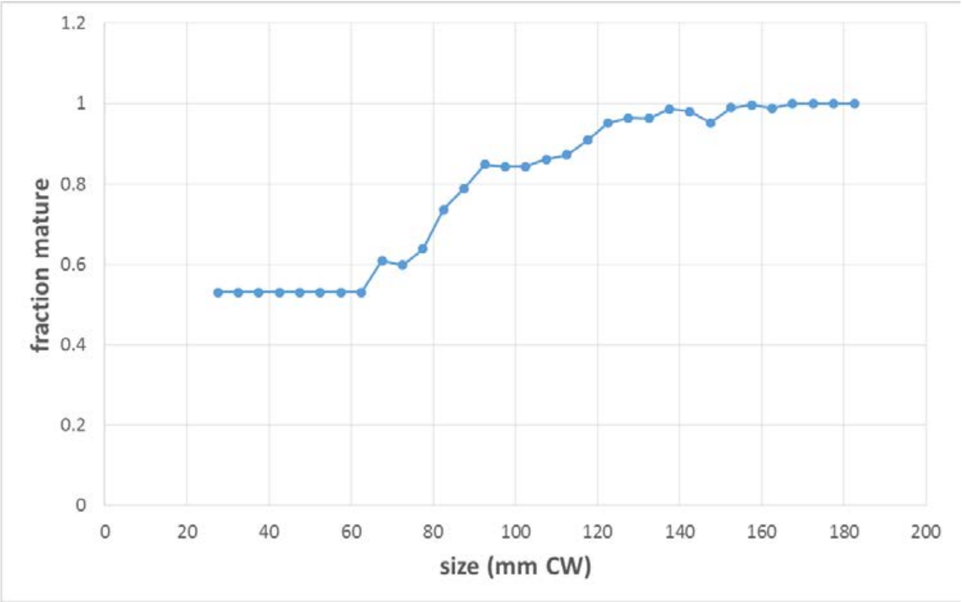

Figure 1. Empirical fraction, by size, of male crab classified as “old shell” that are mature.

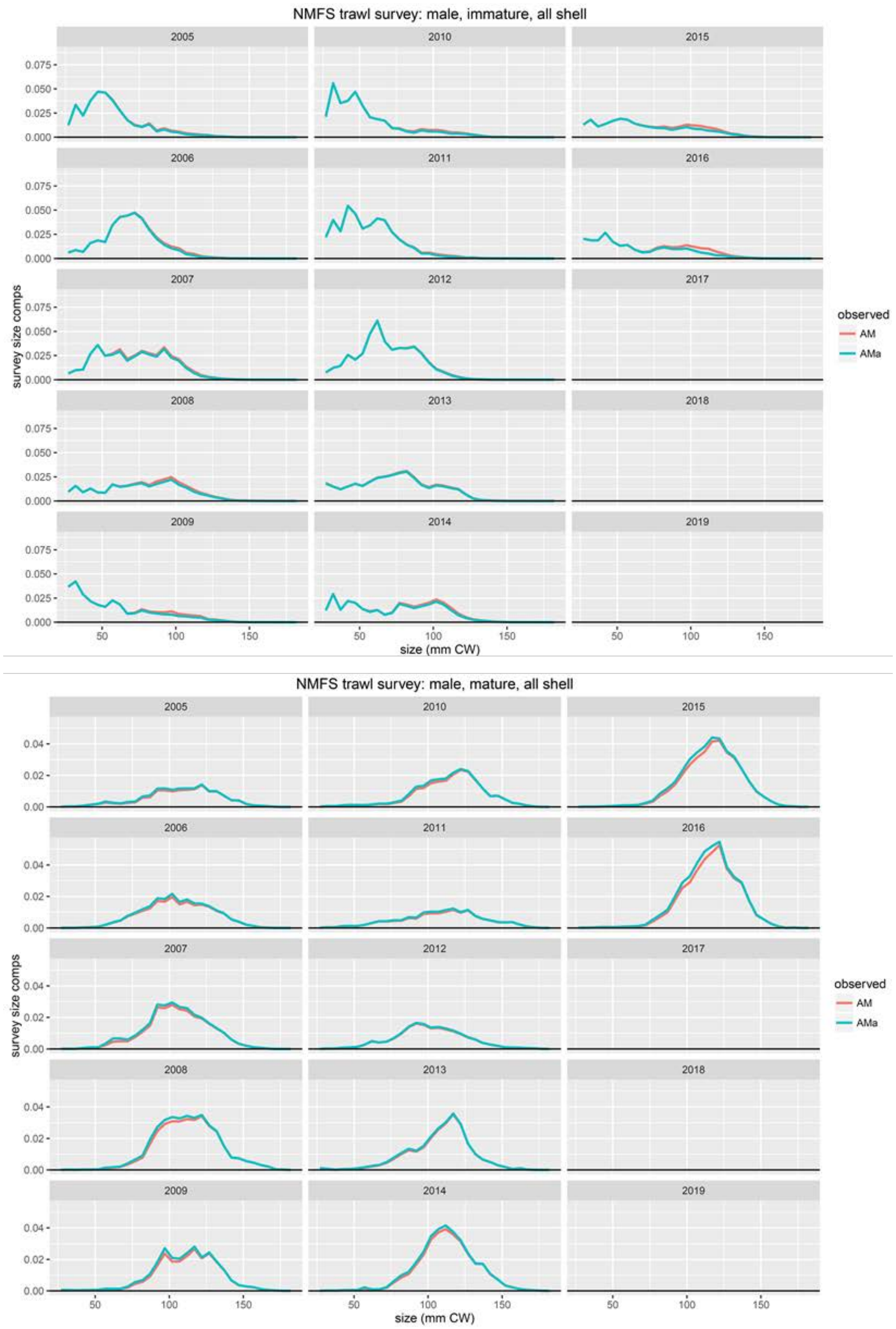

Figure 2. Comparison of recent survey size compositions corrected (AM) and uncorrected (AMa) for old shell classification.

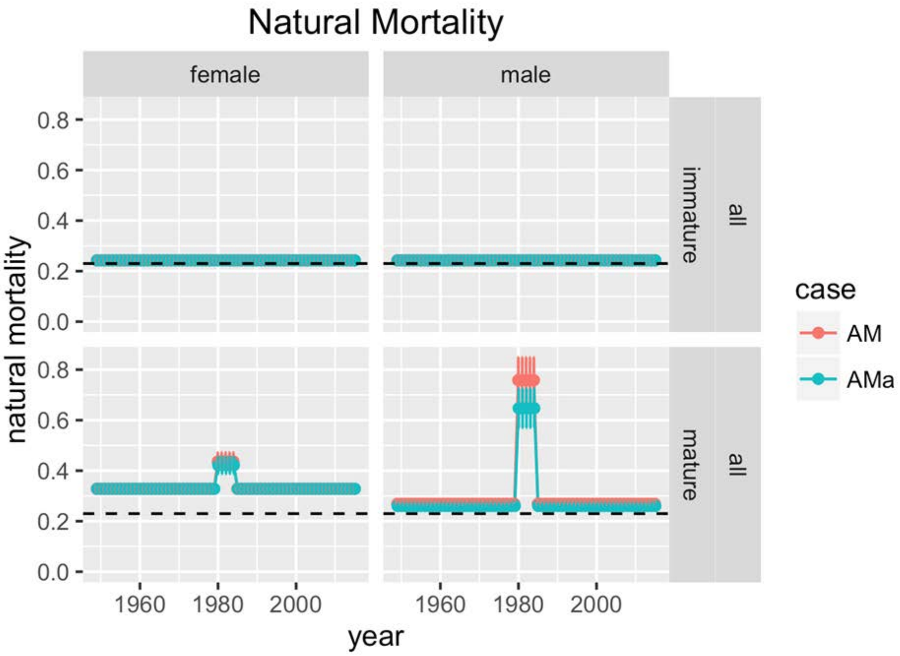

Figure 3. Comparison of estimated natural mortality rates from TCSAM2013 models AM and AMa.

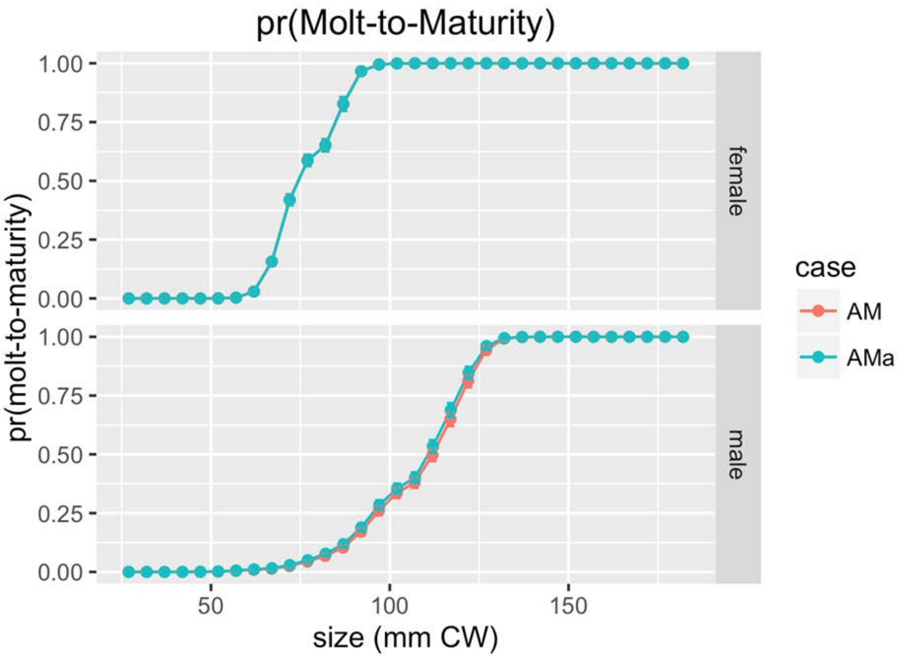

Figure 4. Comparison of estimated probabilities of molt-to-maturity from TCSAM2013 models AM and AMa.

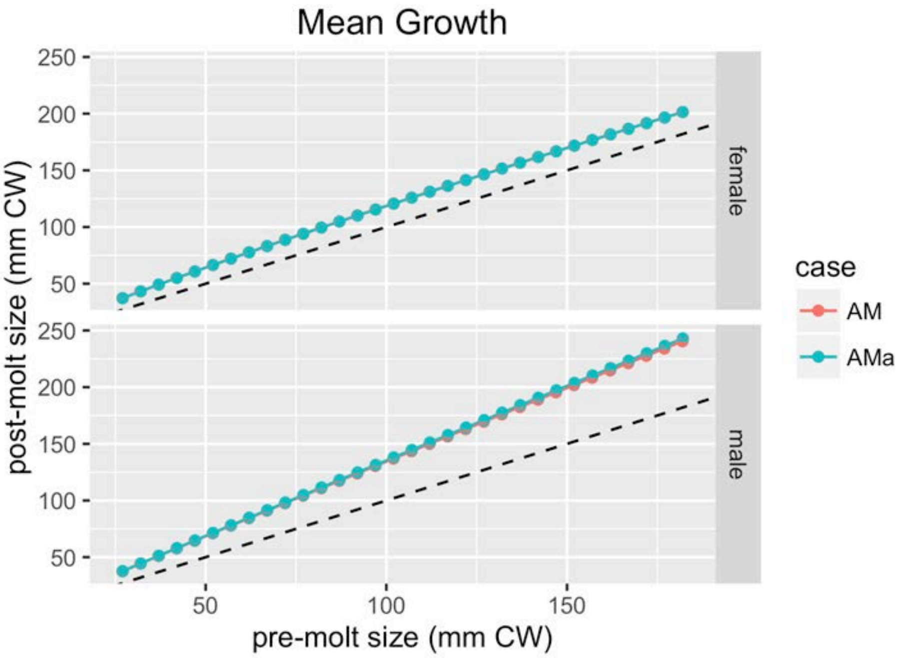

Figure 5. Comparison of estimated mean post-molt size from TCSAM2013 models AM and AMa.

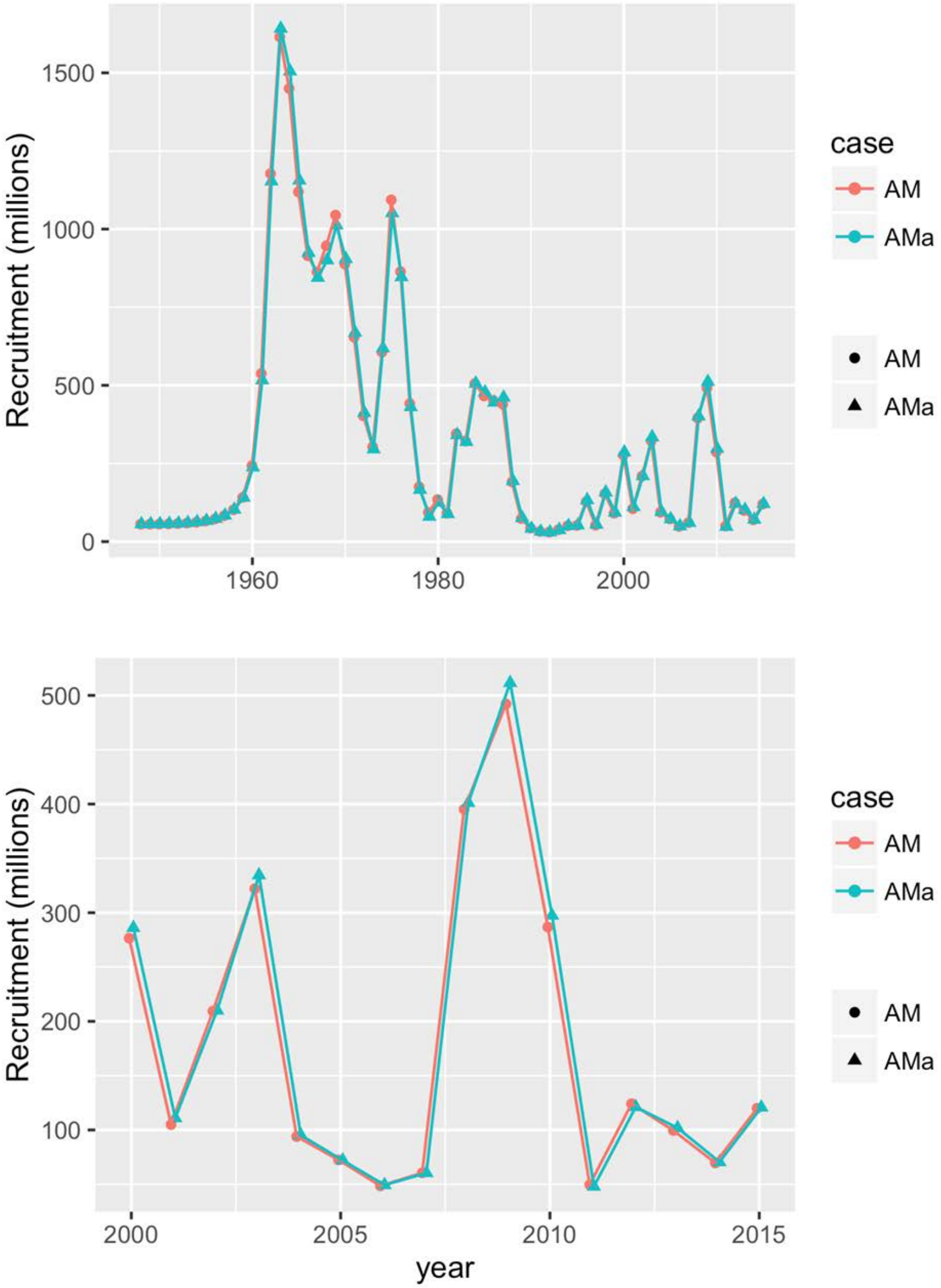

Figure 6. Comparison of estimated recruitment from TCSAM2013 models AM and AMa.

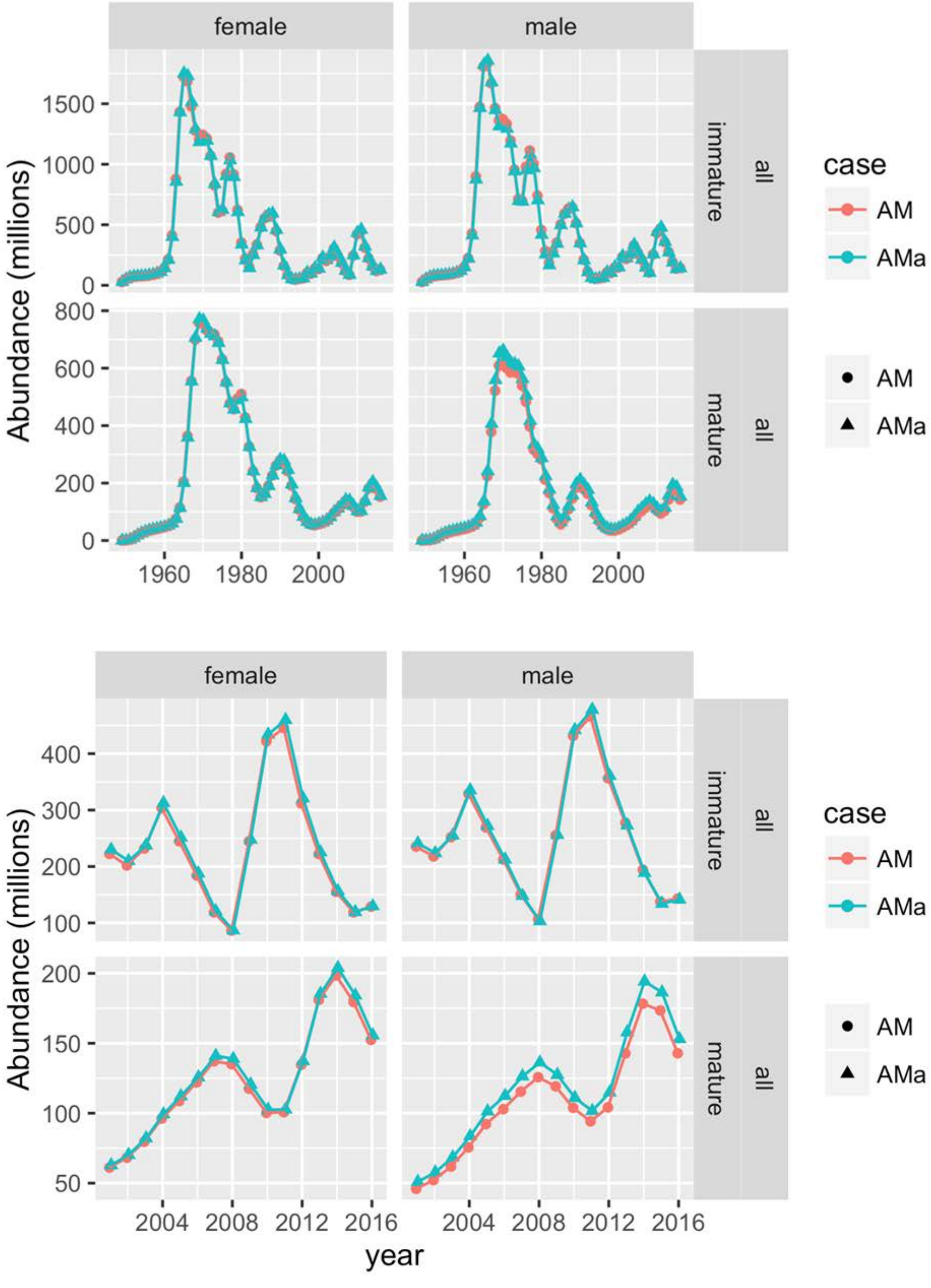

Figure 7. Comparison of estimated population abundance from TCSAM2013 models AM and AMa.

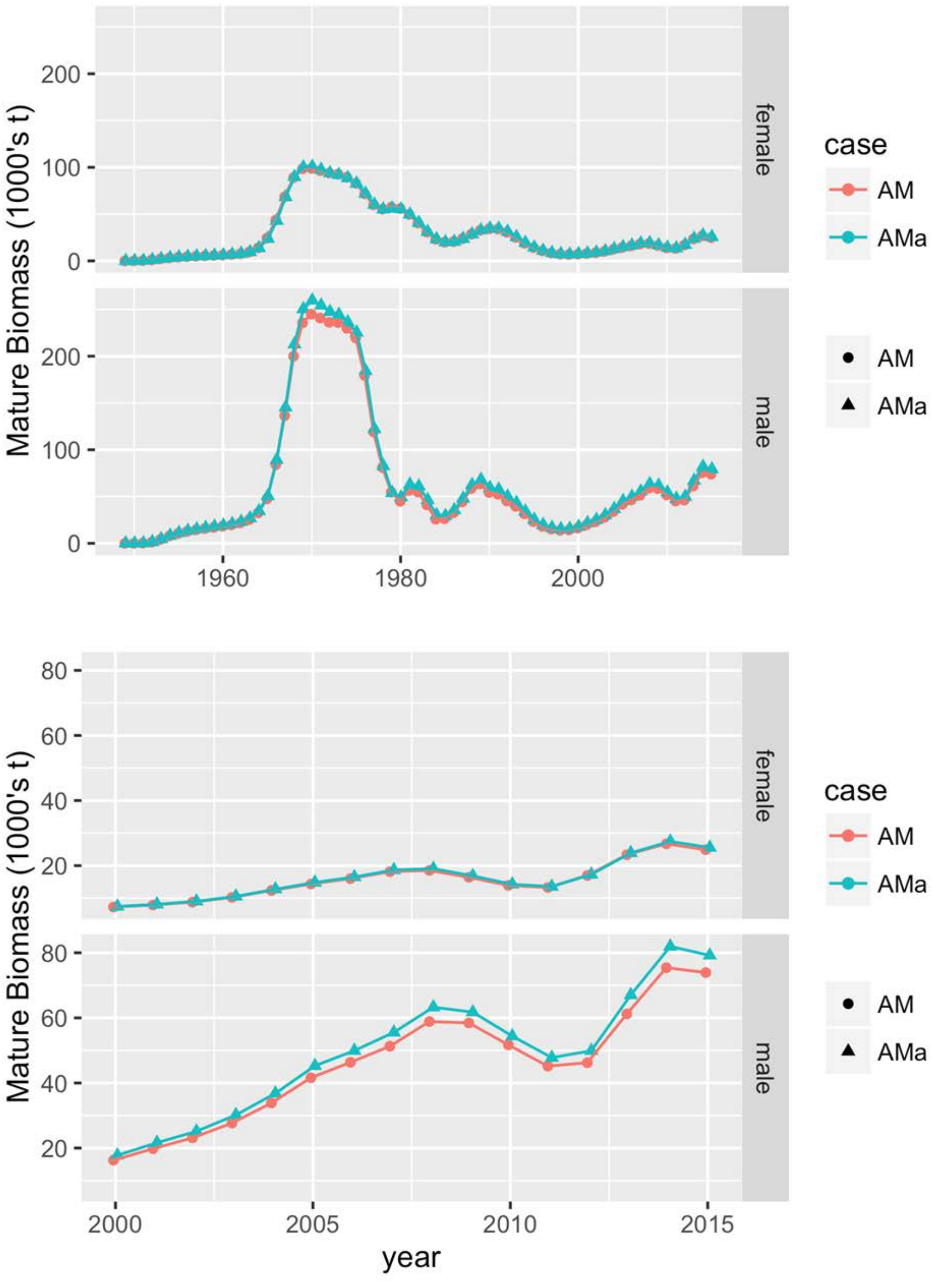

Figure 8. Comparison of estimated mature biomass from TCSAM2013 models AM and AMa.

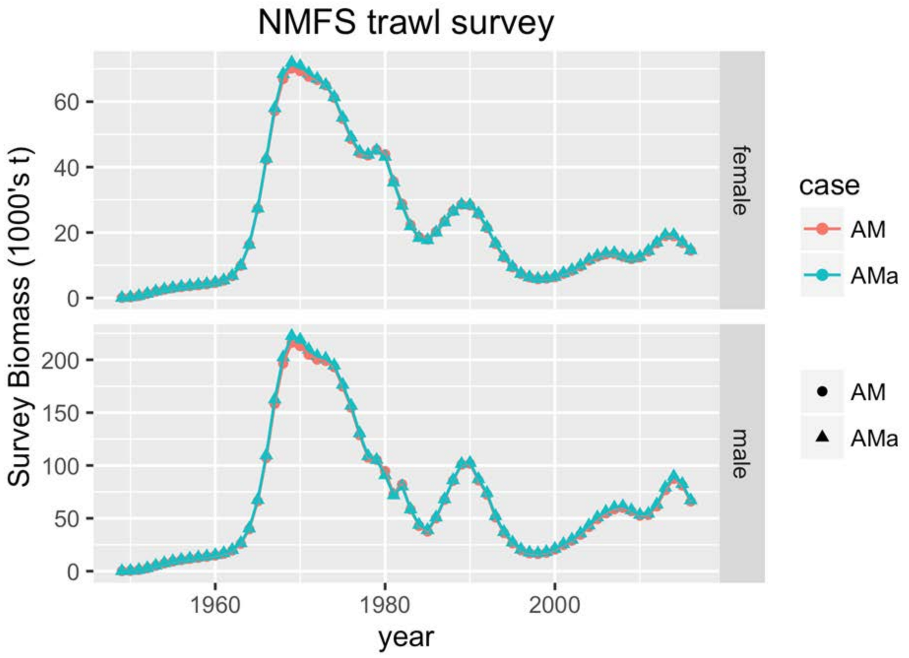

Figure 9. Comparison of estimated survey biomass from TCSAM2013 models AM and AMa.

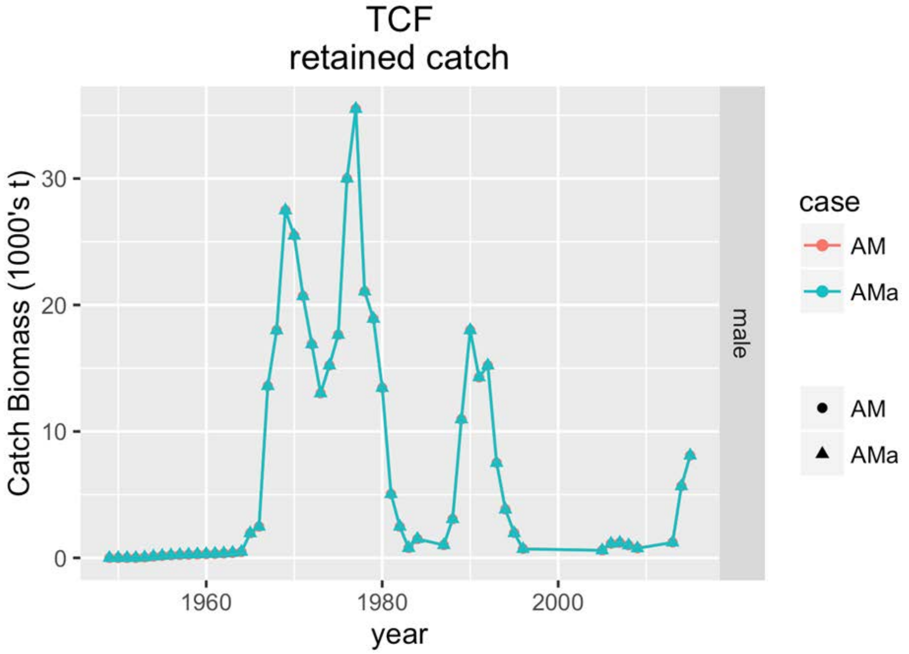

Figure 10. Comparison of estimated retained catch biomass for the directed fishery (TCF) from TCSAM2013 models AM and AMa.

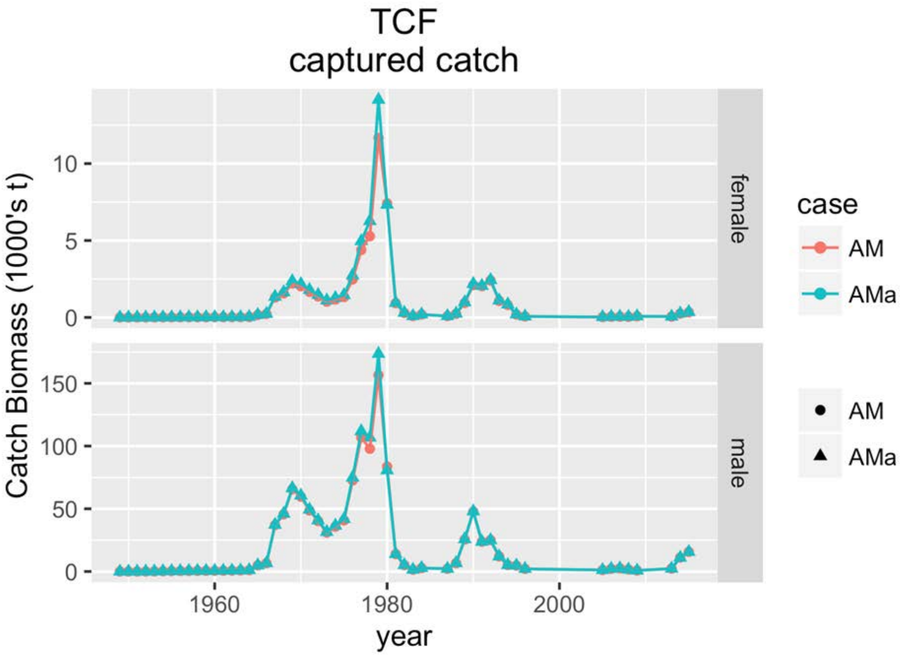

Figure 11. Comparison of estimated total catch (captured) biomass for the directed fishery (TCF) from TCSAM2013 models AM and AMa.

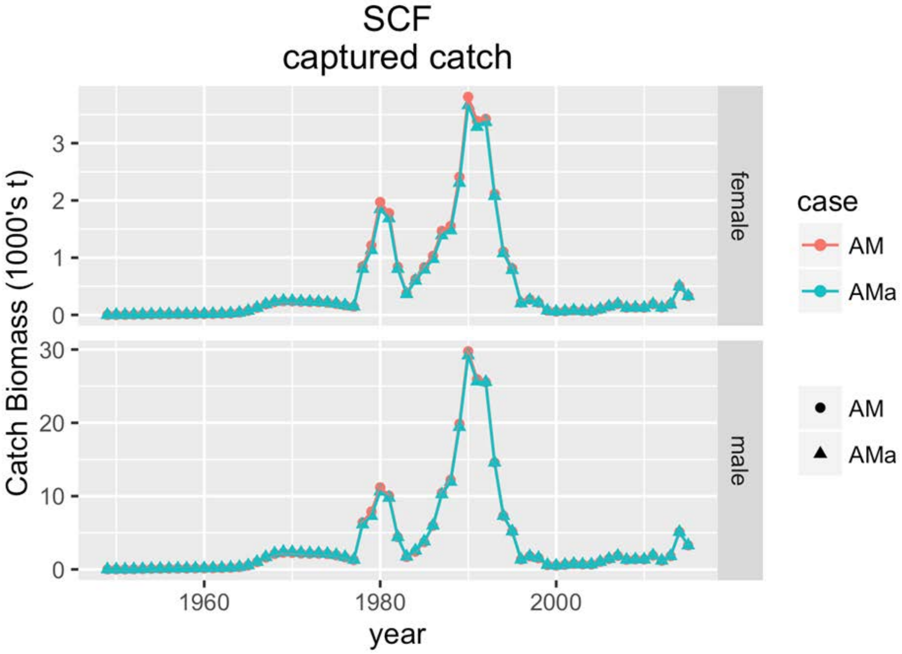

Figure 12. Comparison of estimated total bycatch (captured) biomass for the snow crab fishery (SCF) from TCSAM2013 models AM and AMa.

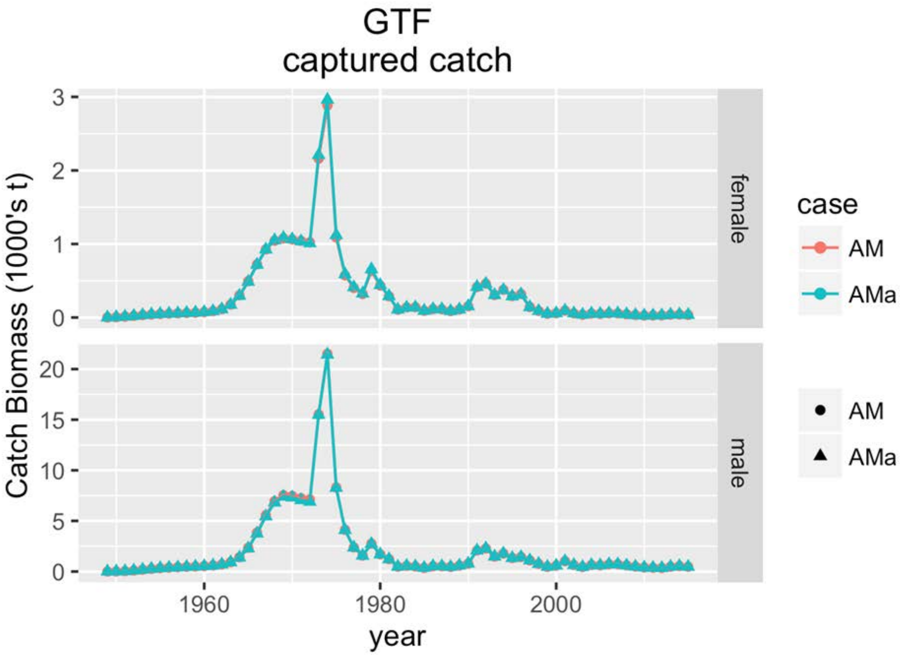

Figure 13. Comparison of estimated total bycatch (captured) biomass for the groundfish fisheries (GTF) from TCSAM2013 models AM and AMa.

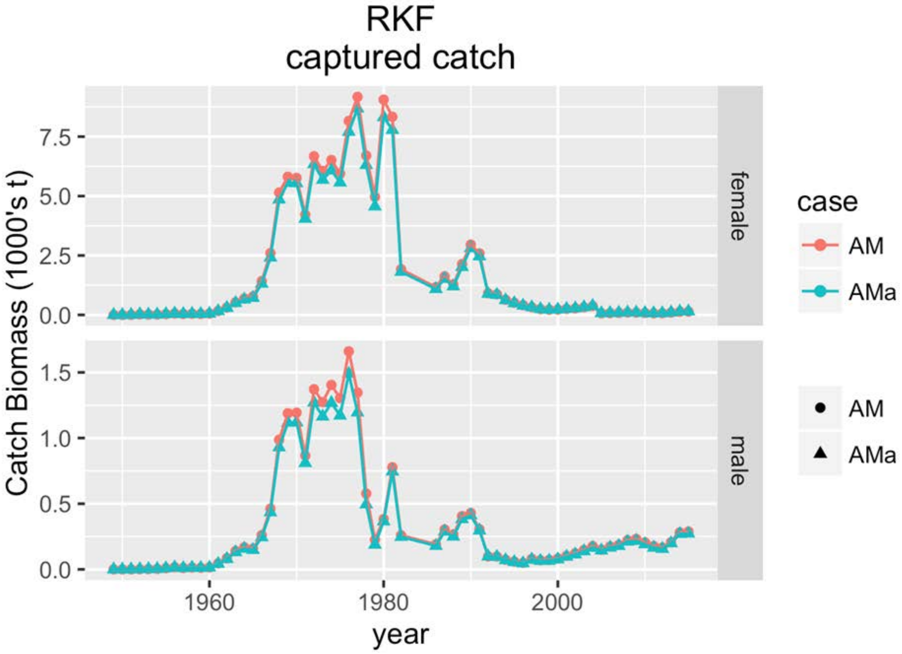

Figure 14. Comparison of estimated total bycatch (captured) biomass for the BBRKC fishery (RKF) from TCSAM2013 models AM and AMa.

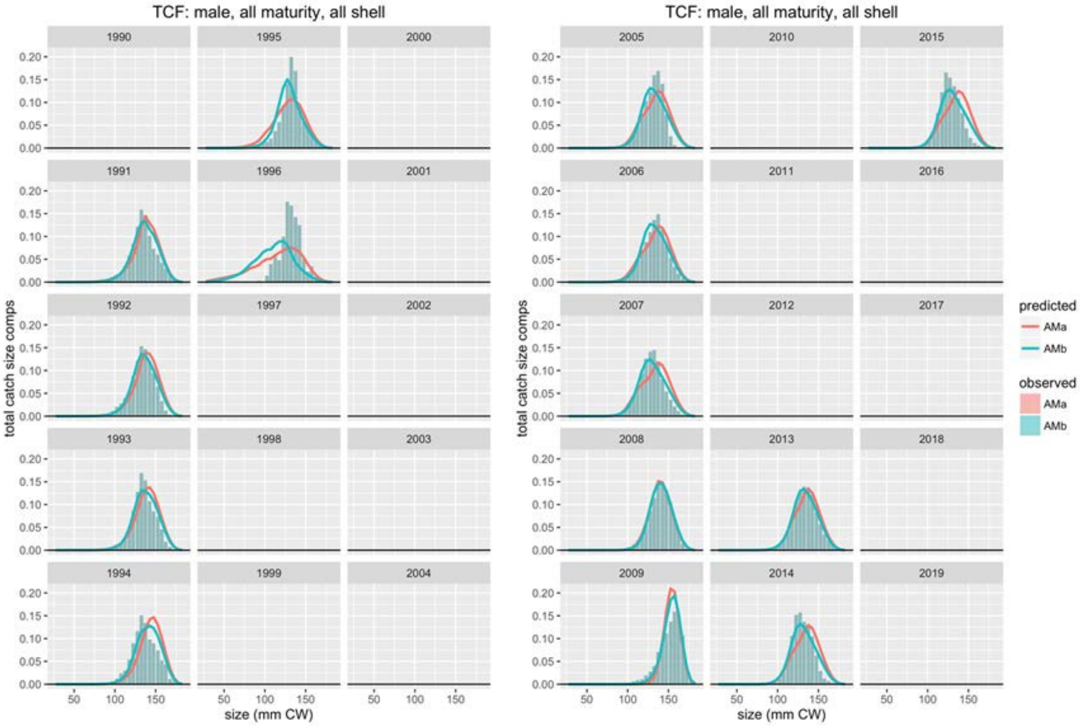

Figure 15. Comparison of model fits to total catch size comps for males in the directed fishery from TCSAM2013 models AMa and AMb. Predicted size comps shown are “total capture” size comps for AMb but “total mortality” size comps for AMa.

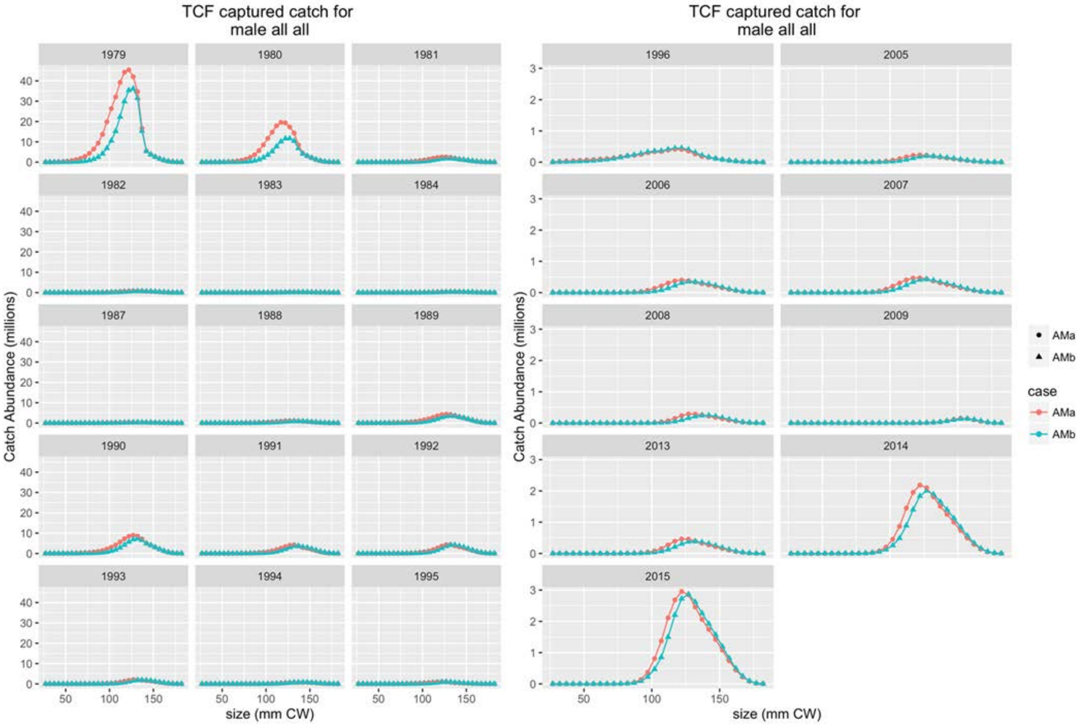

Figure 16. Comparison of model fits to total catch size comps for males in the directed fishery from TCSAM2013 models AMa and AMb. Predicted size comps shown are “total capture” size comps for AMb but “total mortality” size comps for AMa.

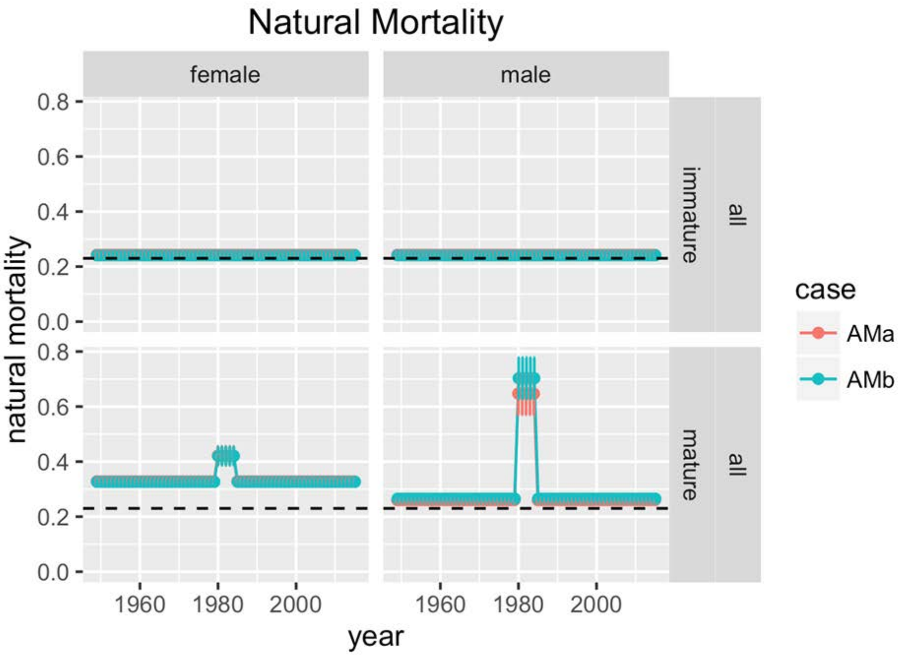

Figure 17. Comparison of estimated natural mortality rates from TCSAM2013 models AMa and AMb.

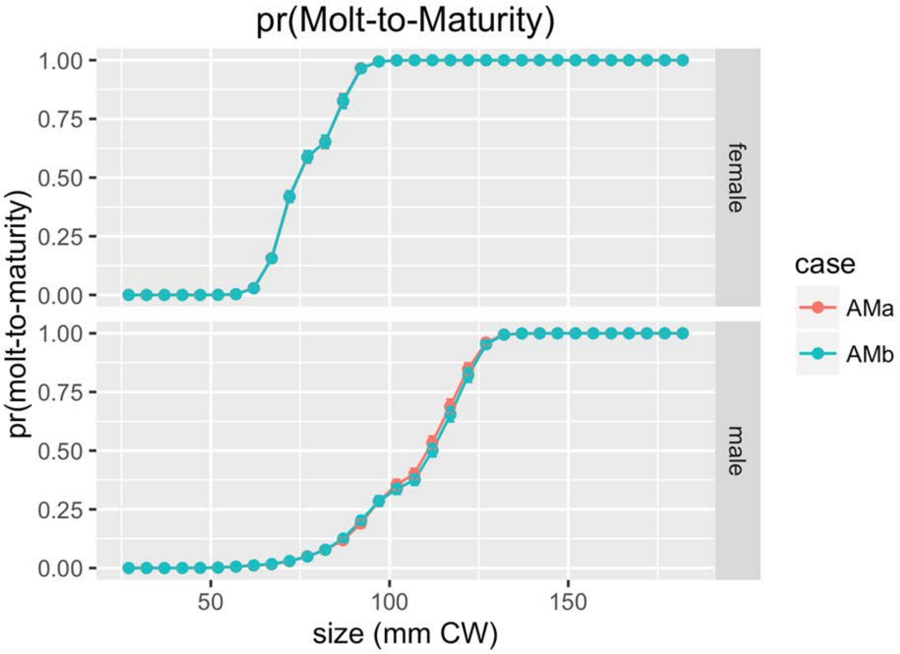

Figure 18. Comparison of estimated probabilities of molt-to-maturity from TCSAM2013 models AMa and AMb.

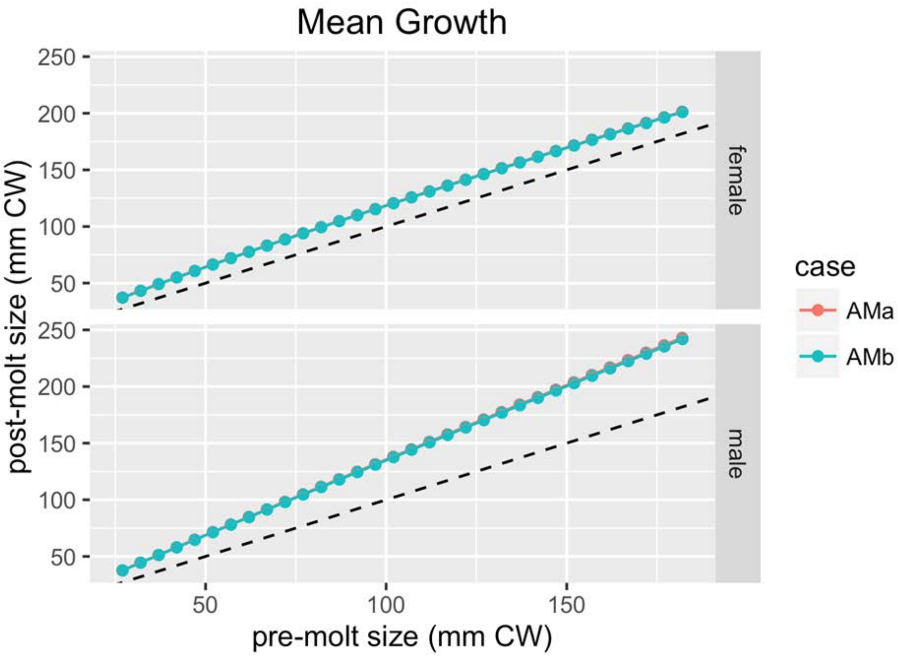

Figure 19. Comparison of estimated mean post-molt size from TCSAM2013 models AMa and AMb.

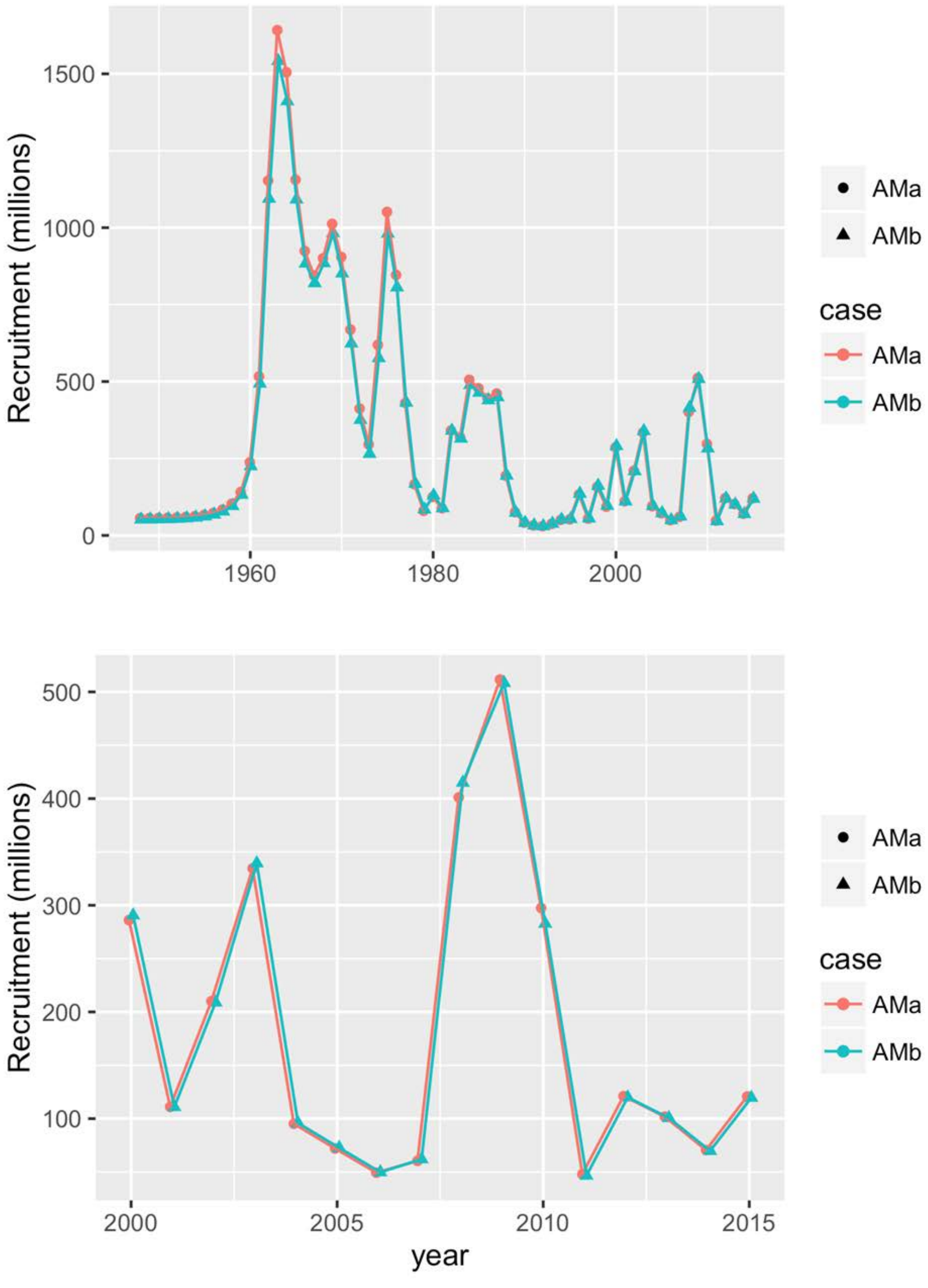

Figure 20. Comparison of estimated recruitment from TCSAM2013 models AMa and AMb.

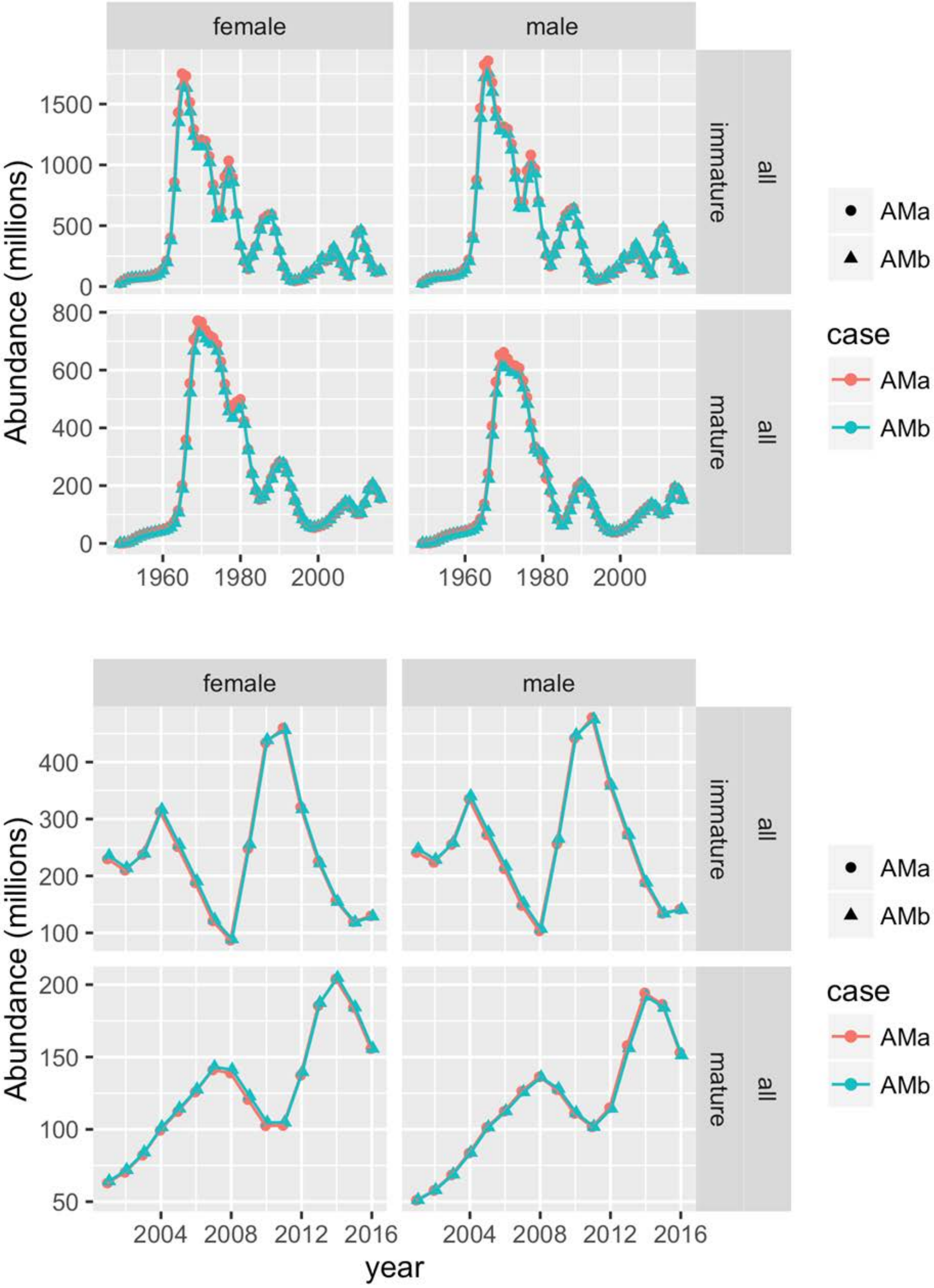

Figure 21. Comparison of estimated population abundance from TCSAM2013 models AMa and AMb.

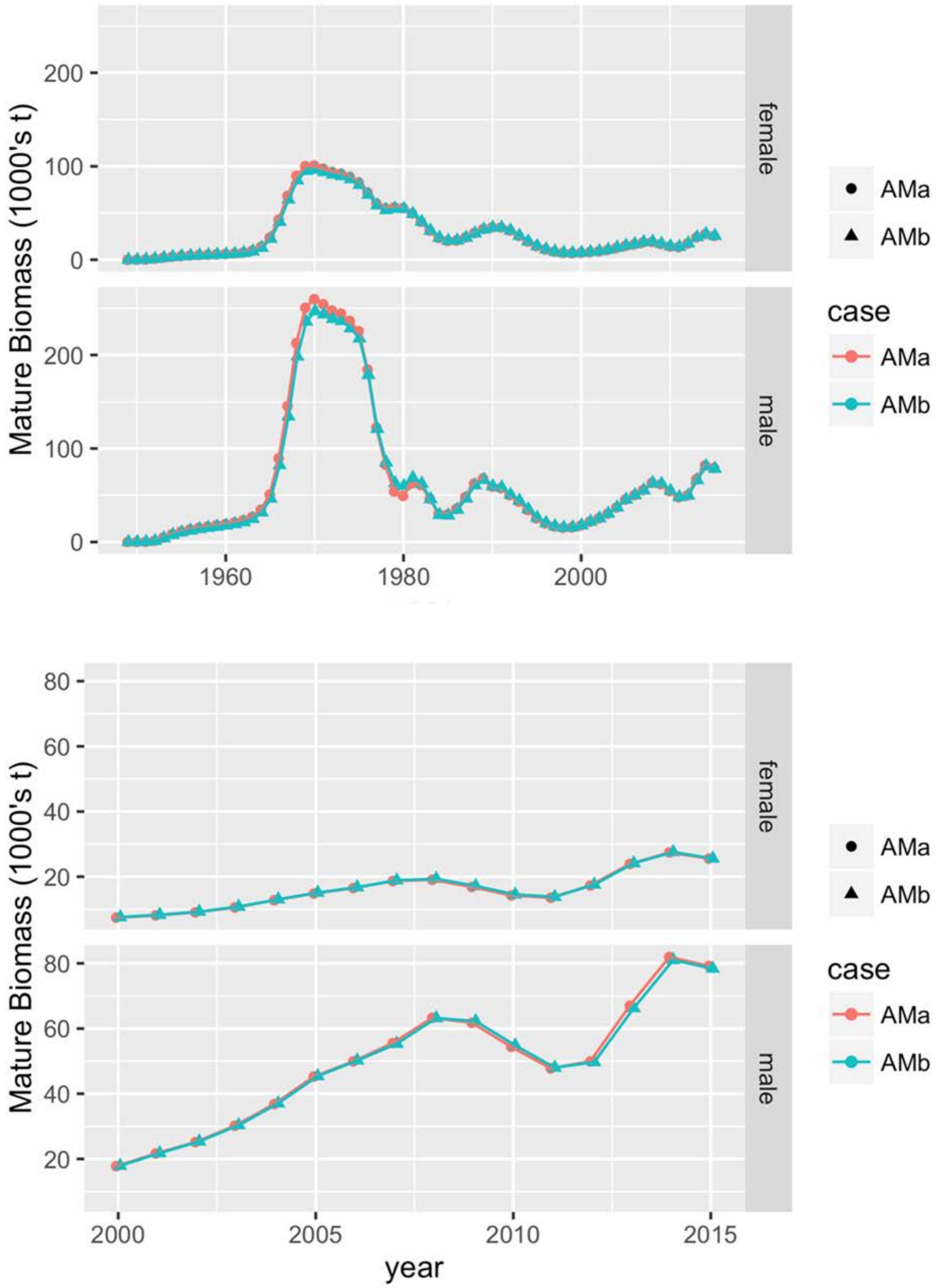

Figure 22. Comparison of estimated mature biomass from TCSAM2013 models AMa and AMb.

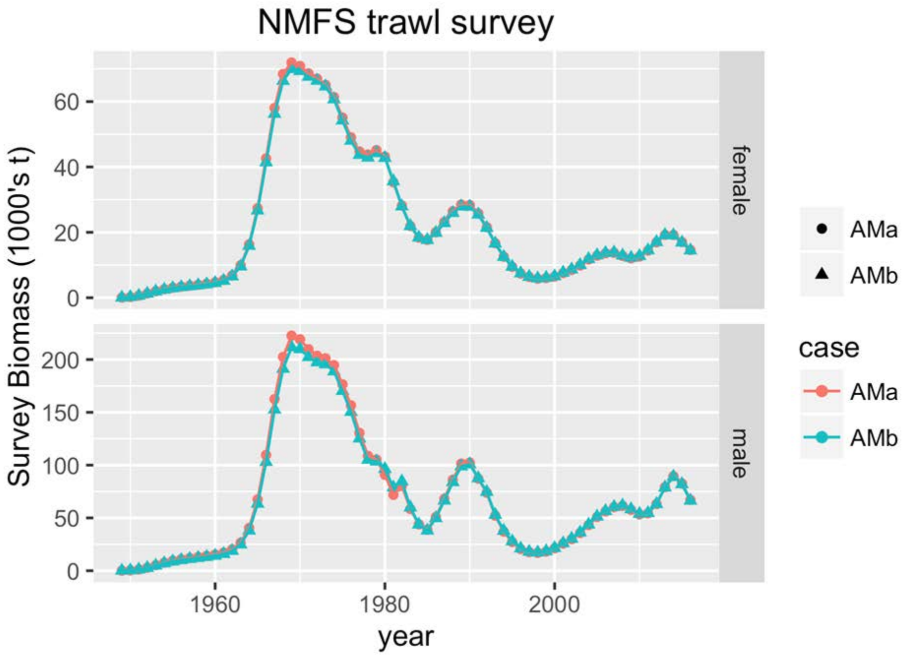

Figure 23. Comparison of estimated survey biomass from TCSAM2013 models AMa and AMb.

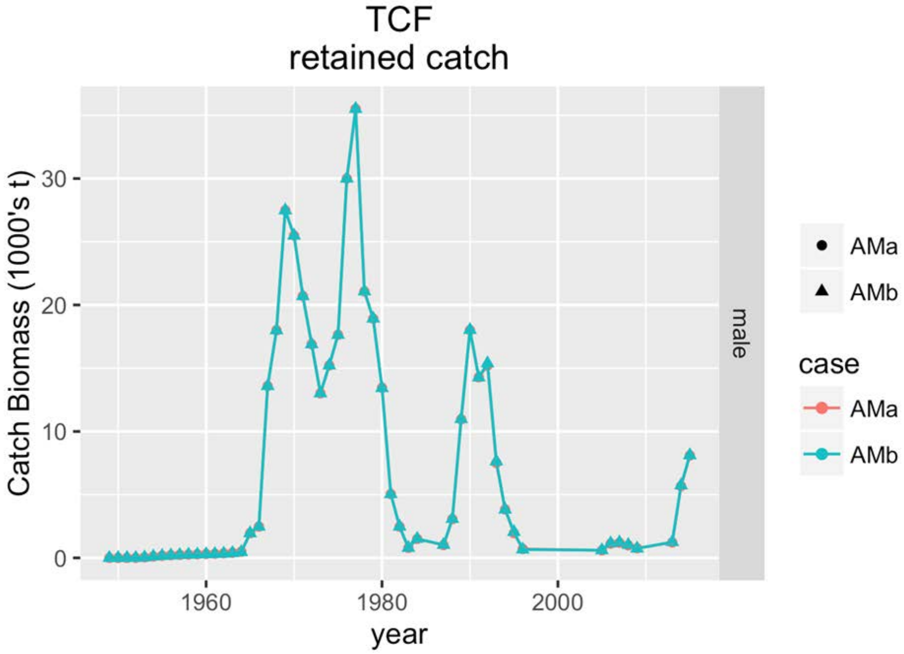

Figure 24. Comparison of estimated retained catch biomass for the directed fishery (TCF) from TCSAM2013 models AMa and AMb.

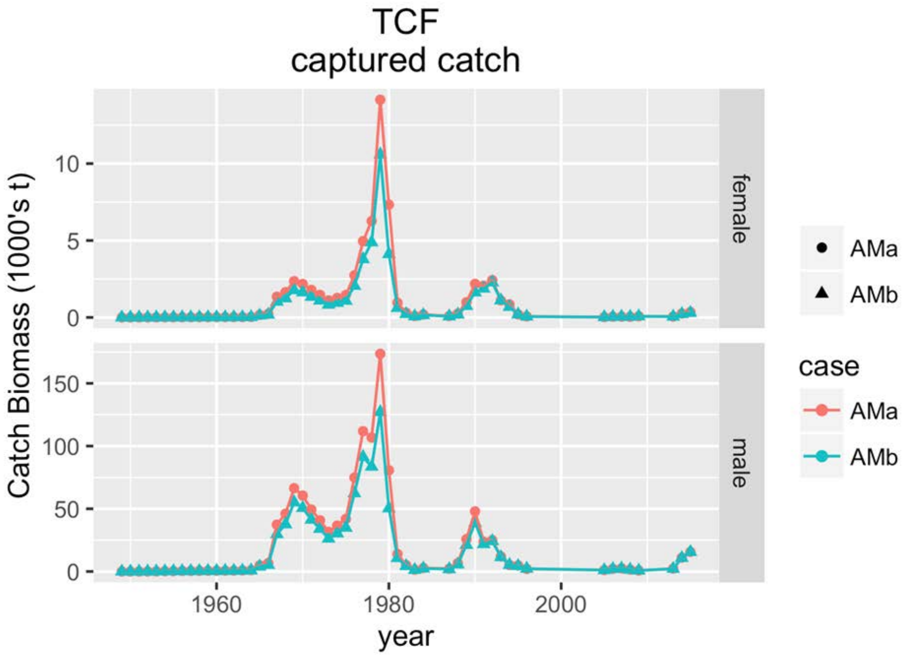

Figure 25. Comparison of estimated total catch (captured) biomass for the directed fishery (TCF) from TCSAM2013 models AMa and AMb.

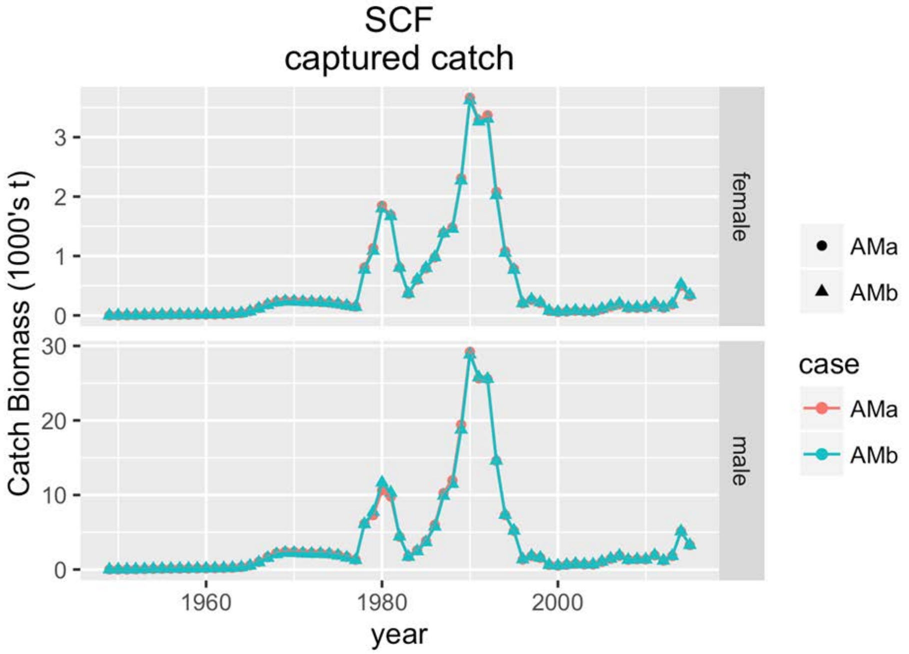

Figure 26. Comparison of estimated total bycatch (captured) biomass for the snow crab fishery (SCF) from TCSAM2013 models AMa and AMb.

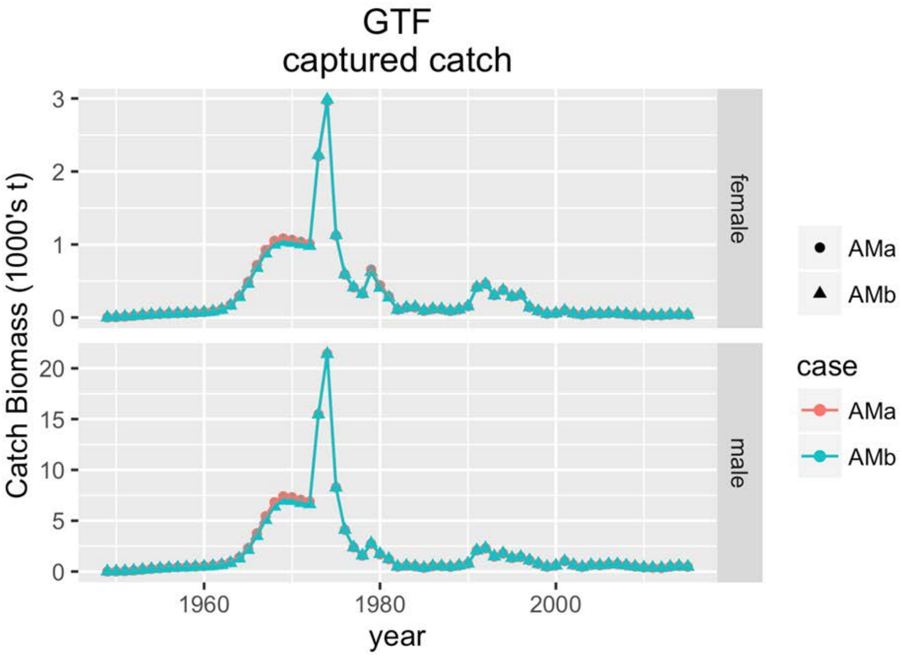

Figure 27. Comparison of estimated total bycatch (captured) biomass for the groundfish fisheries (GTF) from TCSAM2013 models AMa and AMb.

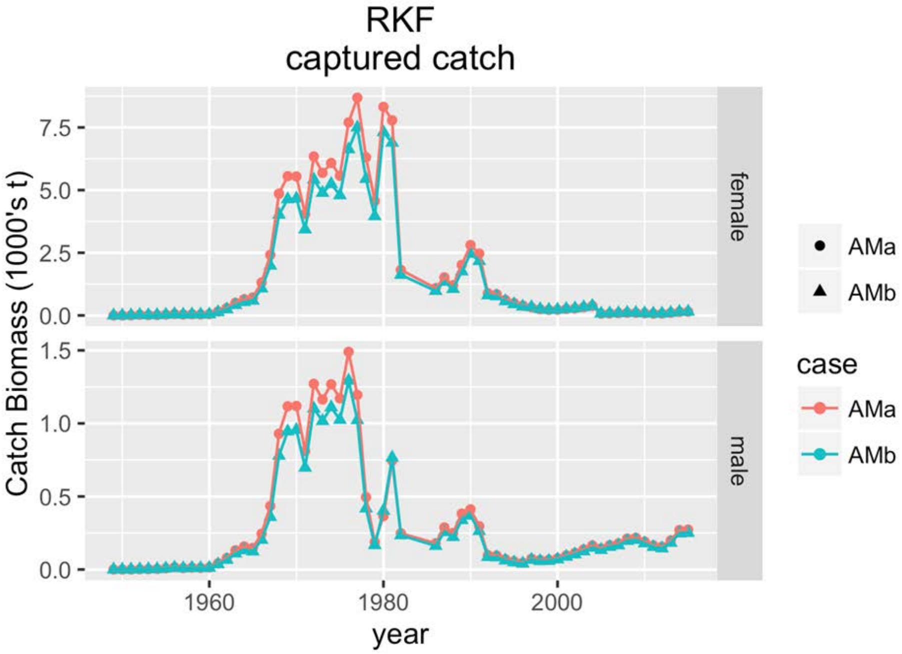

Figure 28. Comparison of estimated total bycatch (captured) biomass for the BBRKC fishery (RKF) from TCSAM2013 models AMa and AMb.

Figure 29. Comparison of estimated natural mortality rates from TCSAM2013 models AMb and AMc.

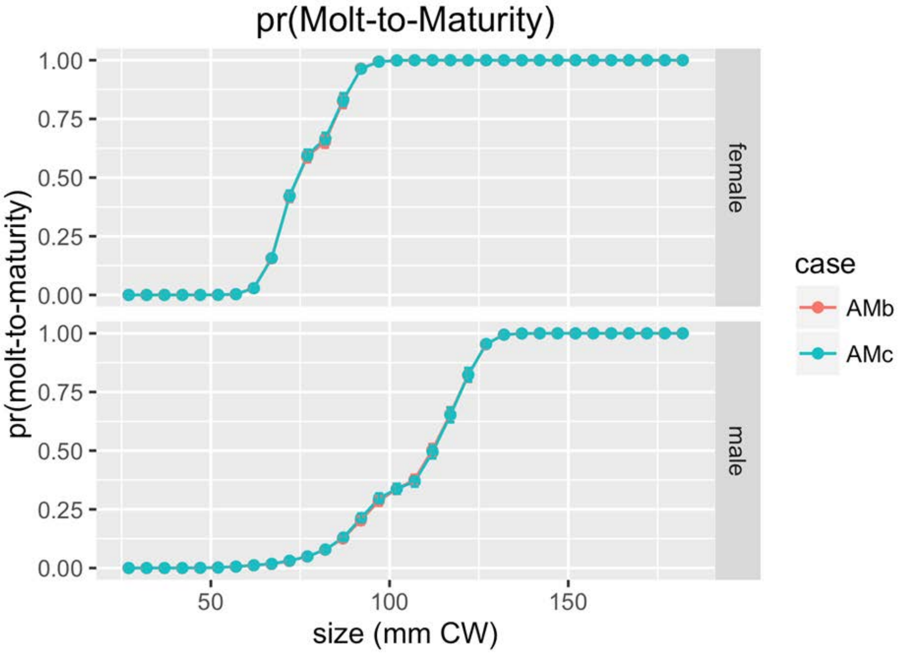

Figure 30. Comparison of estimated probabilities of molt-to-maturity from TCSAM2013 models AMb and AMc.

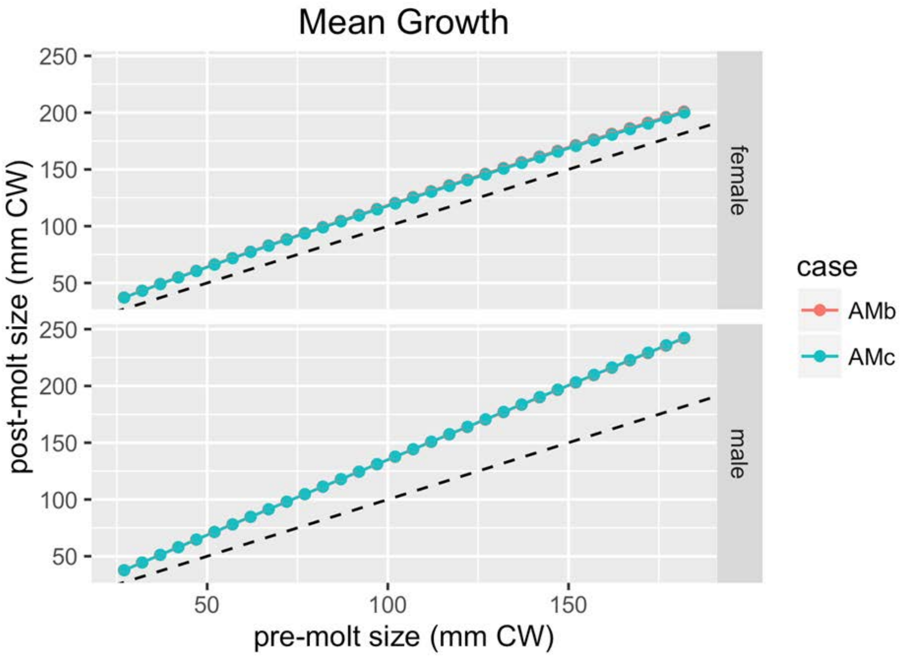

Figure 31. Comparison of estimated mean post-molt size from TCSAM2013 models AMb and AMc.

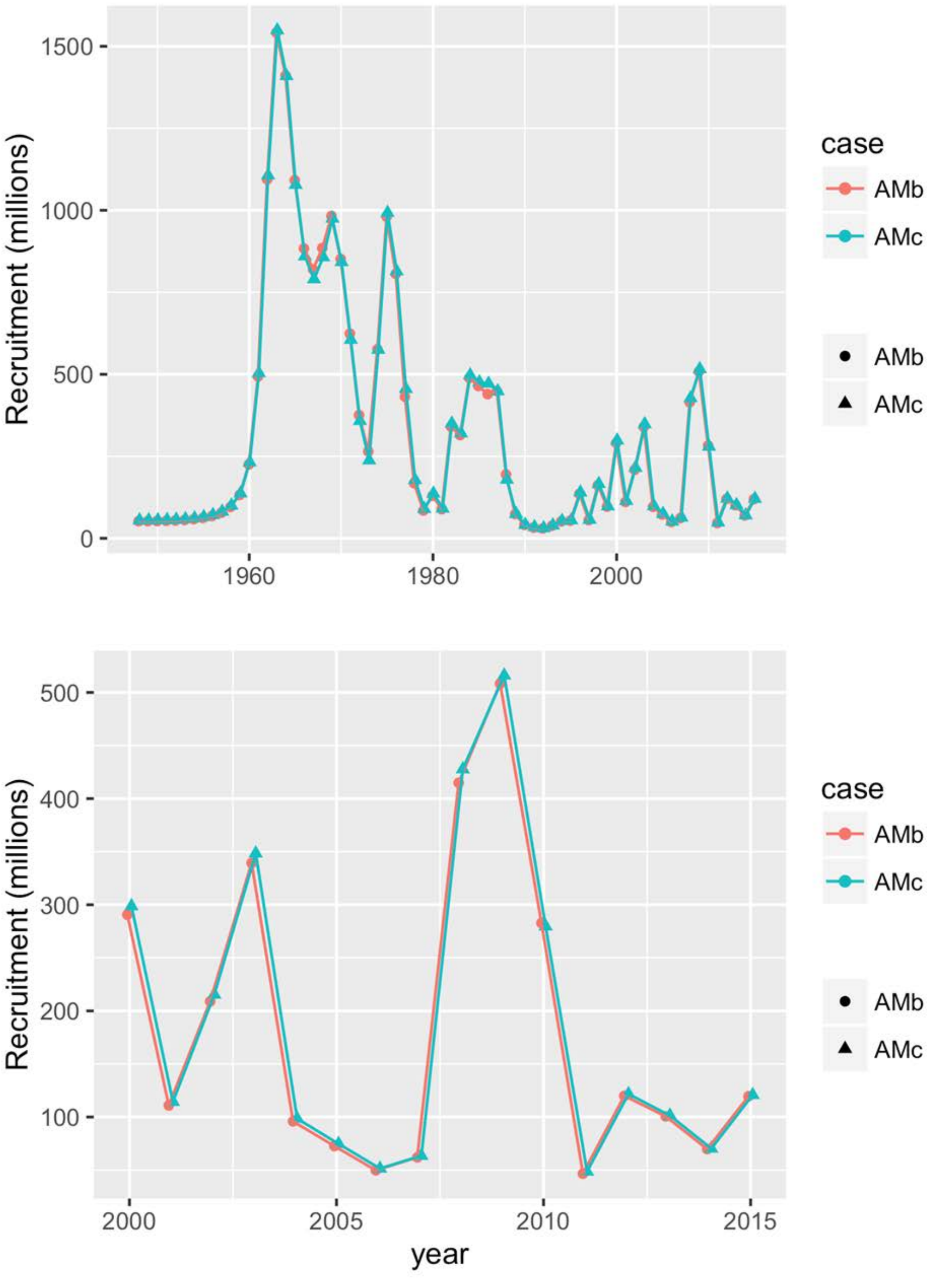

Figure 32. Comparison of estimated recruitment from TCSAM2013 models AMb and AMc.

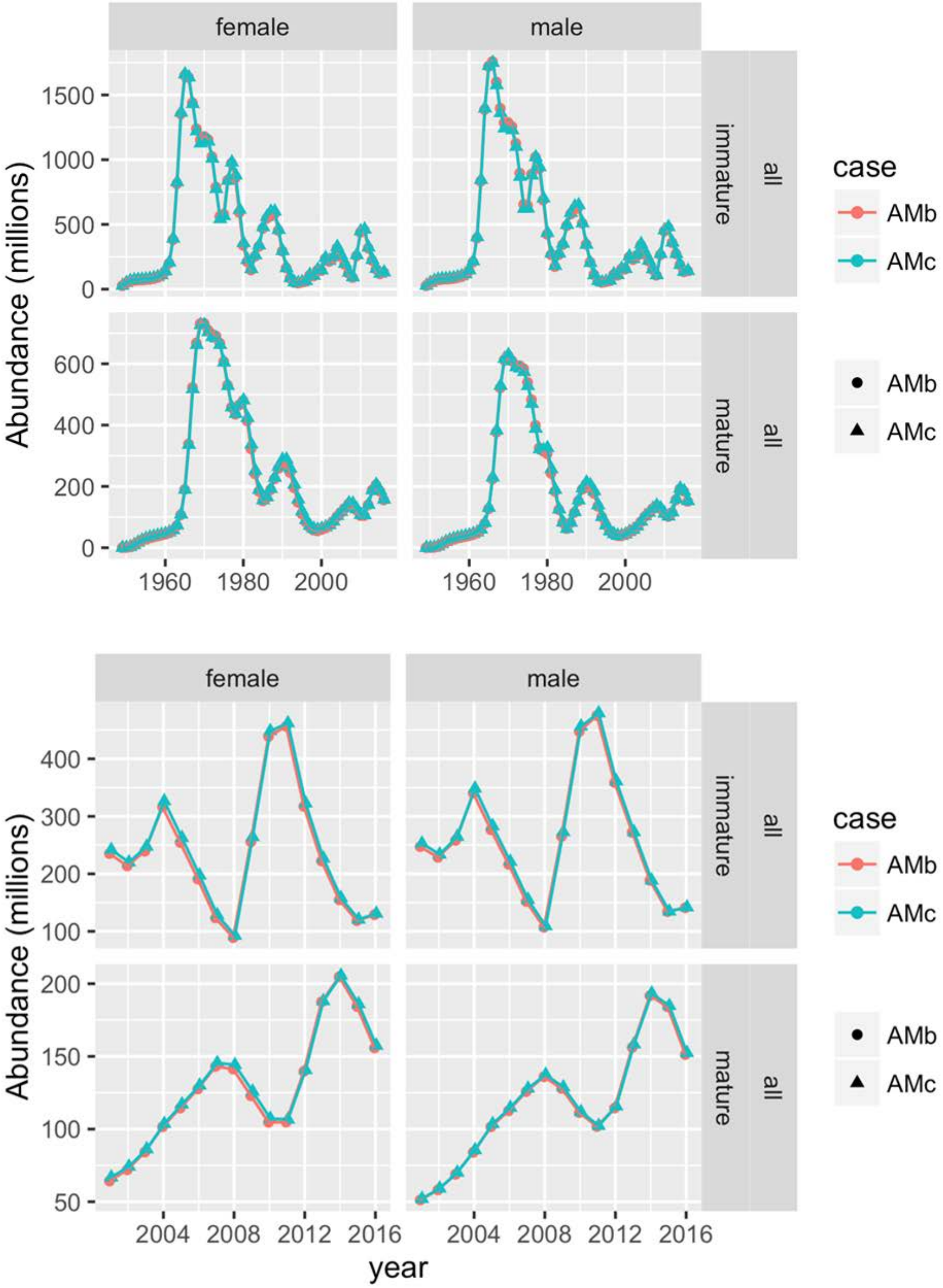

Figure 33. Comparison of estimated population abundance from TCSAM2013 models AMb and AMc.

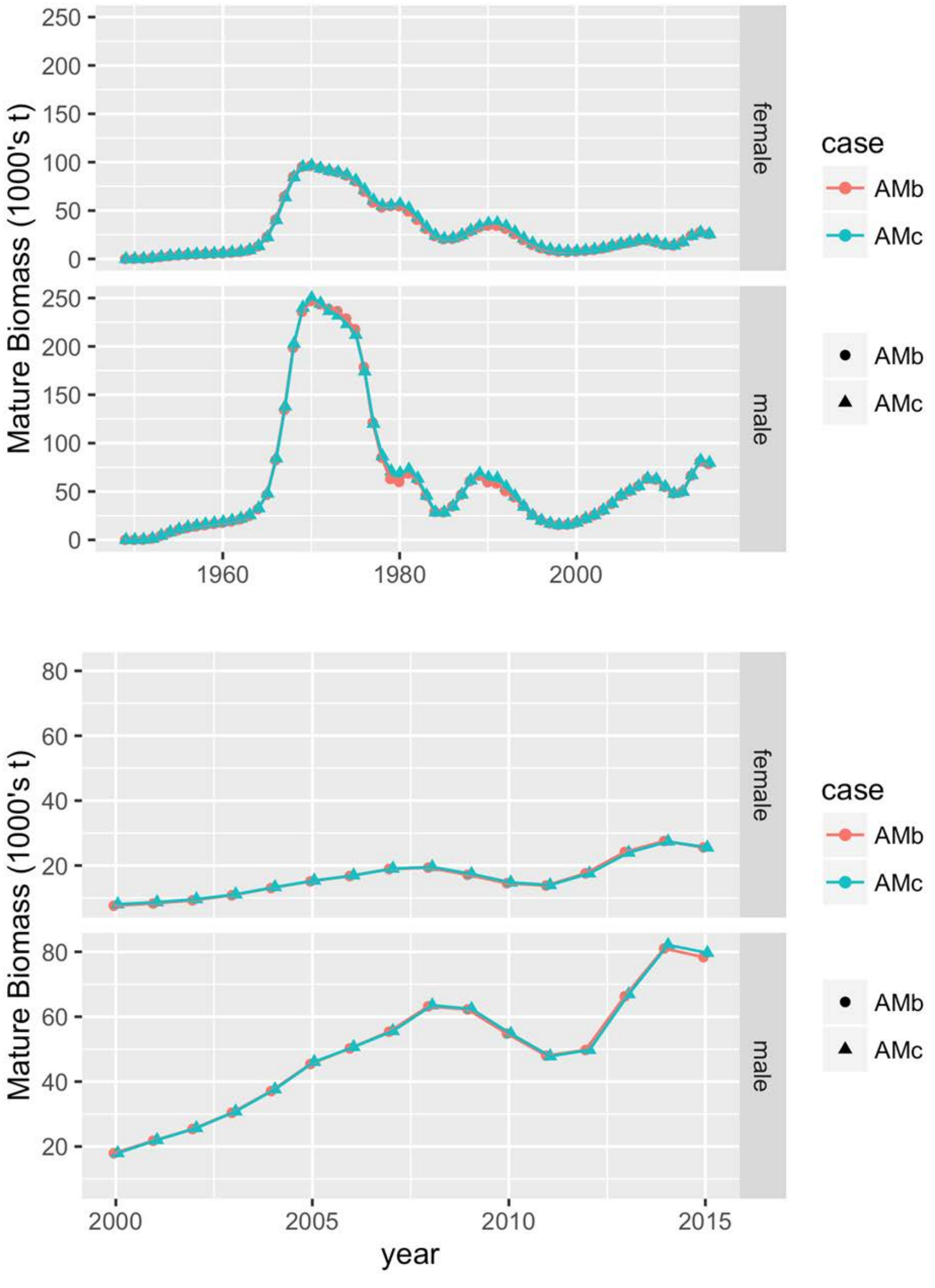

Figure 34. Comparison of estimated mature biomass-at-mating from TCSAM2013 models AMb and AMc.

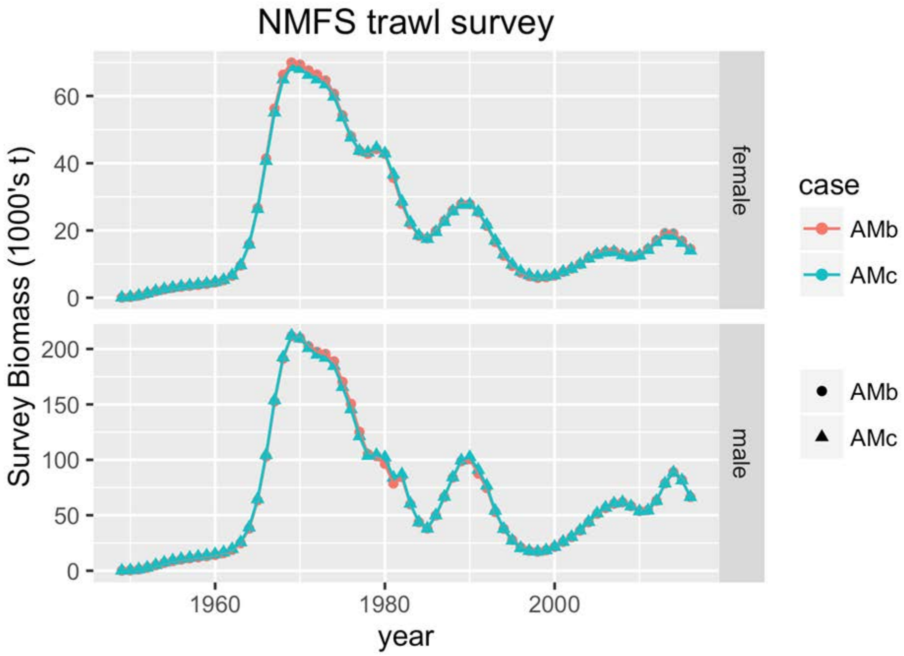

Figure 35. Comparison of estimated survey biomass from TCSAM2013 models AMb and AMc.

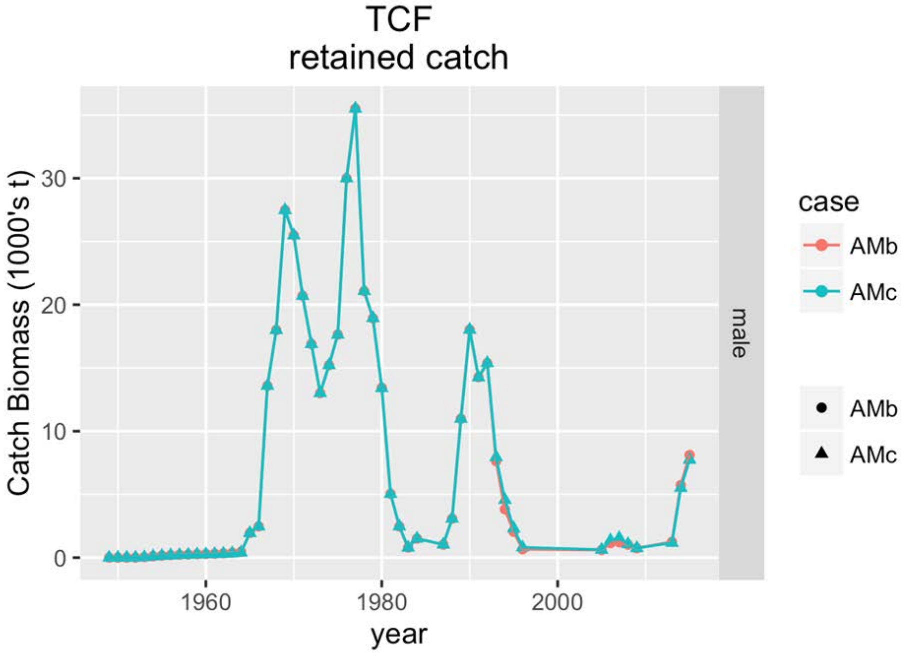

Figure 36. Comparison of estimated retained catch biomass for the directed fishery (TCF) from TCSAM2013 models AMb and AMc.

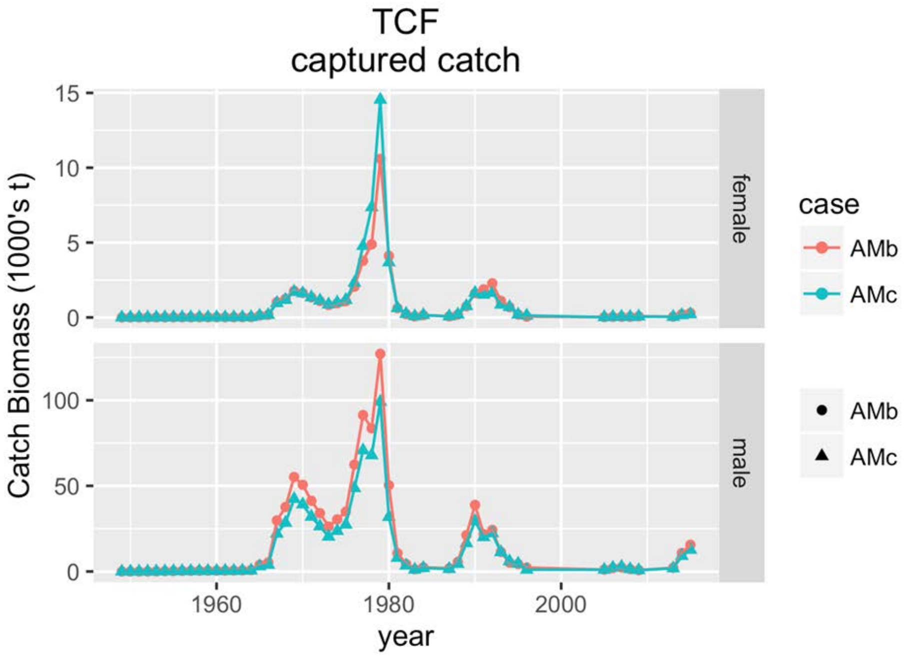

Figure 37. Comparison of estimated total catch (captured) biomass for the directed fishery (TCF) from TCSAM2013 models AMb and AMc.

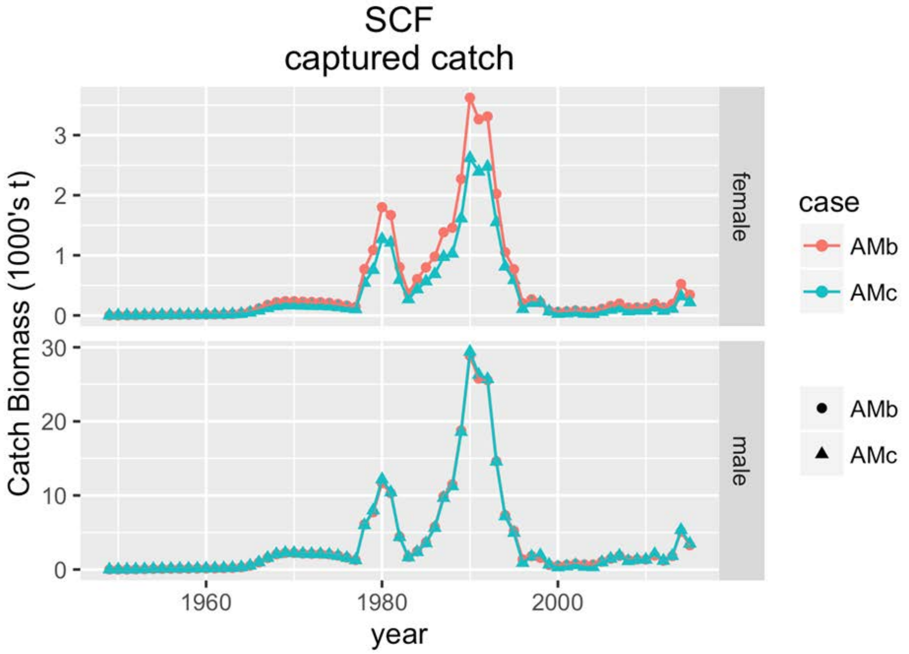

Figure 38. Comparison of estimated total bycatch (captured) biomass for the snow crab fishery (SCF) from TCSAM2013 models AMb and AMc.

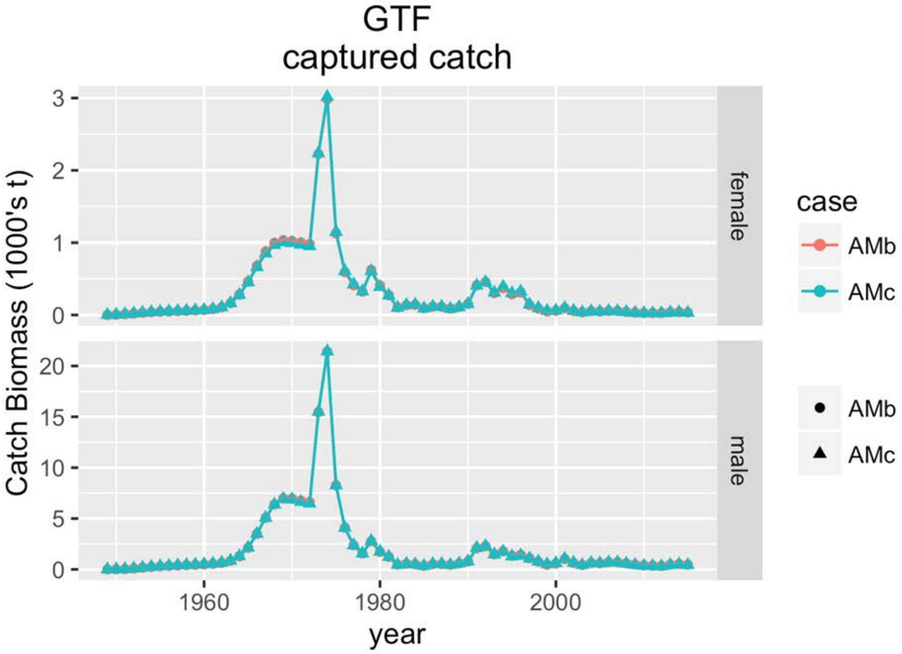

Figure 39. Comparison of estimated total bycatch (captured) biomass for the groundfish fisheries (GTF) from TCSAM2013 models AMb and AMc.

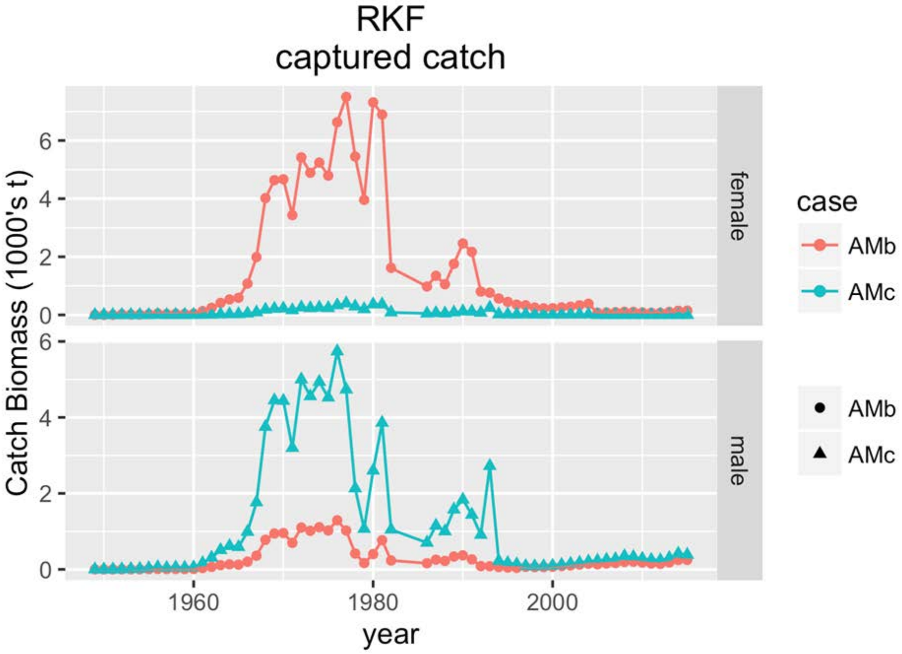

Figure 40. Comparison of estimated total bycatch (captured) biomass for the BBRKC fishery (RKF) from TCSAM2013 models AMb and AMc.

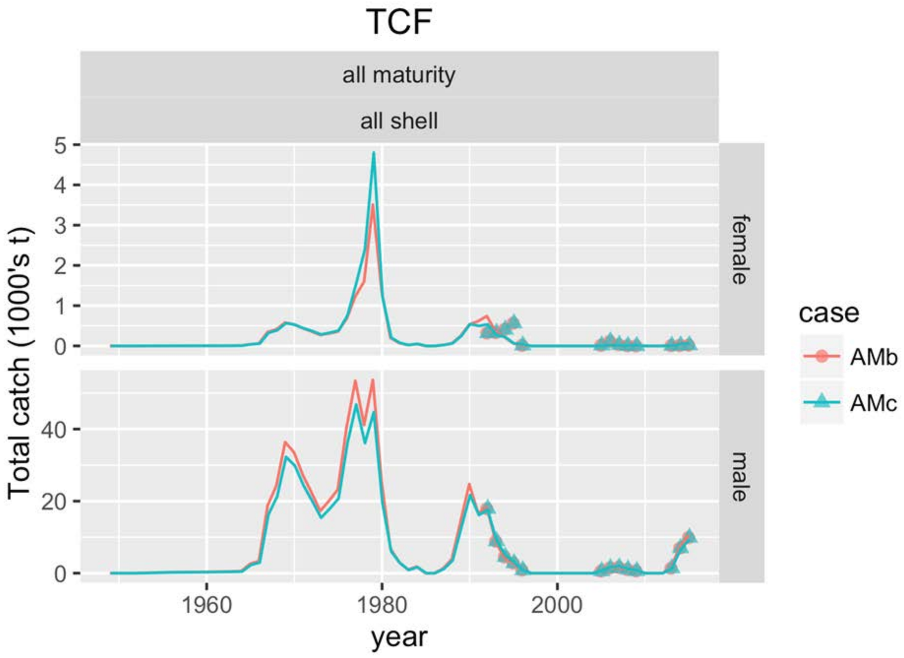

Figure 41. Comparison of estimated (lines) and "observed" (points) total catch mortality biomass for the directed fishery (TCF) from TCSAM2013 models AMb and AMc.

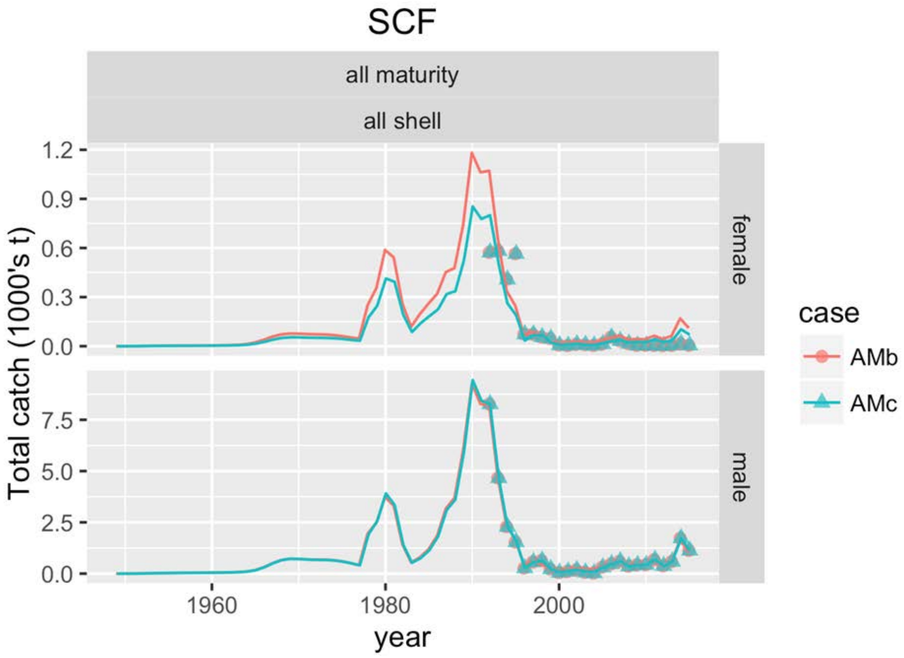

Figure 42. Comparison of estimated (lines) and "observed" (points) total bycatch mortality biomass for the snow crab fishery (SCF) from TCSAM2013 models AMb and AMc.

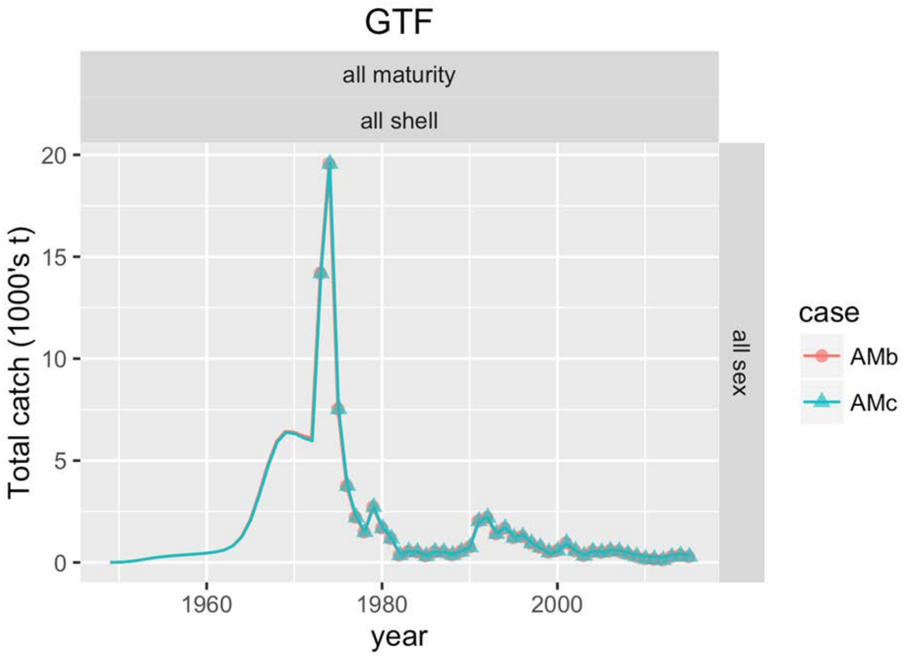

Figure 43. Comparison of estimated (lines) and "observed" (points) total bycatch mortality biomass for the groundfish fisheries (GTF) from TCSAM2013 models AMb and AMc.

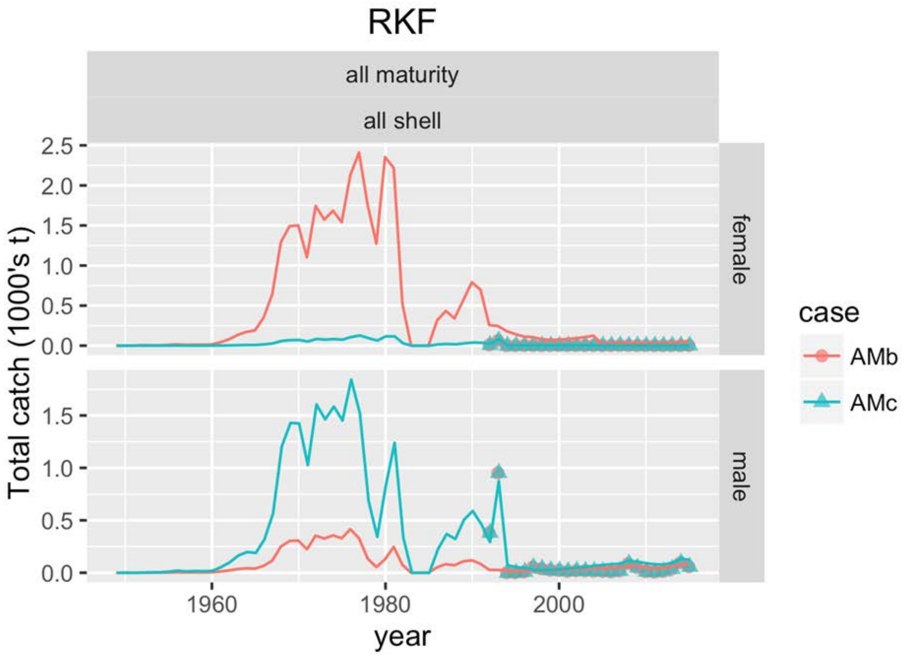

Figure 44. Comparison of estimated (lines) and "observed" (points) total bycatch mortality biomass for the BBRKC fishery (RKF) from TCSAM2013 models AMb and AMc.

Figure 45. Comparison of estimated natural mortality rates from TCSAM2013 models AMc and AMd.

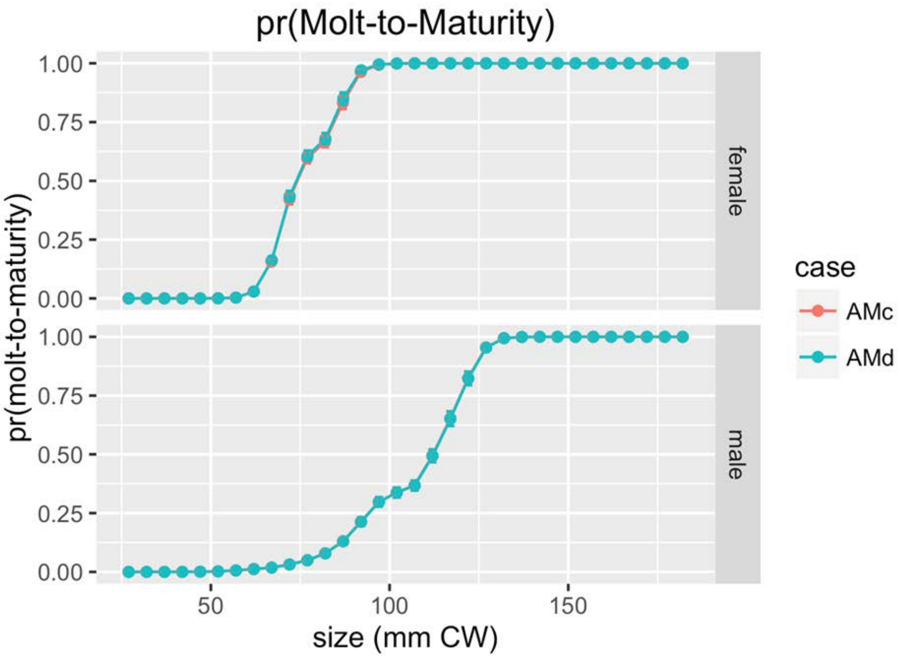

Figure 46. Comparison of estimated probabilities of molt-to-maturity from TCSAM2013 models AMc and AMd.

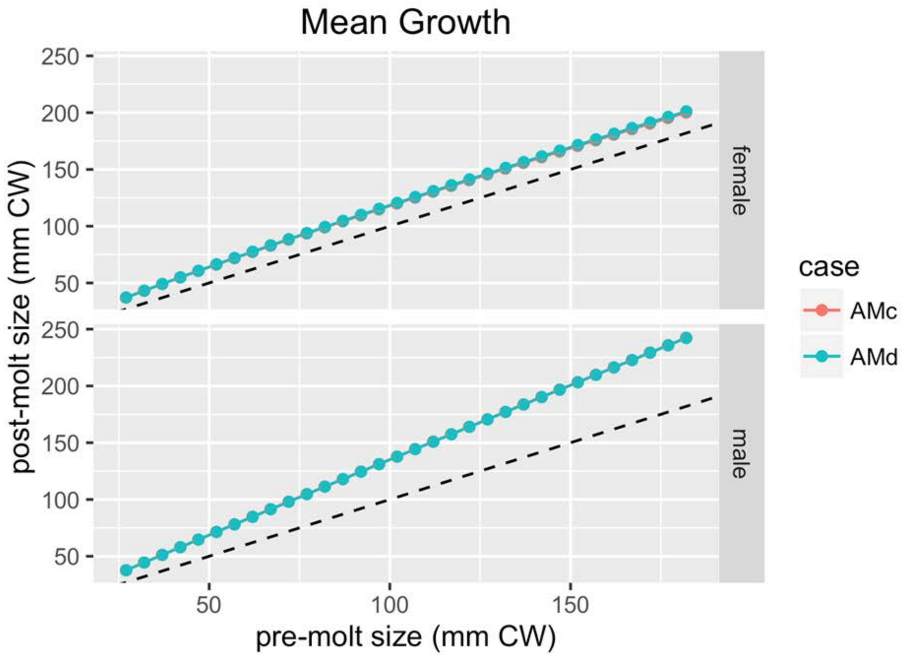

Figure 47. Comparison of estimated mean post-molt size from TCSAM2013 models AMc and AMd.

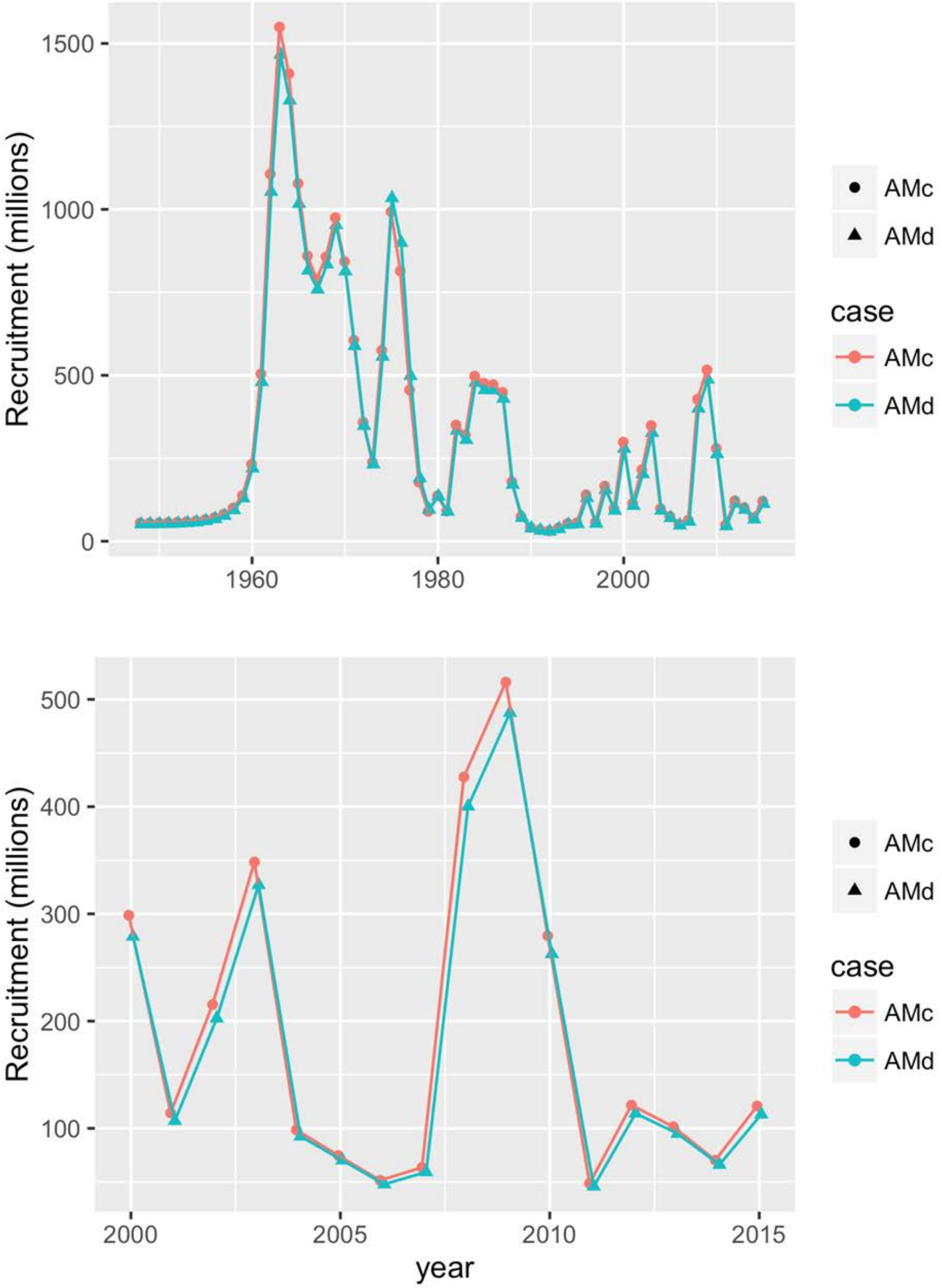

Figure 48. Comparison of estimated recruitment from TCSAM2013 models AMc and AMd.

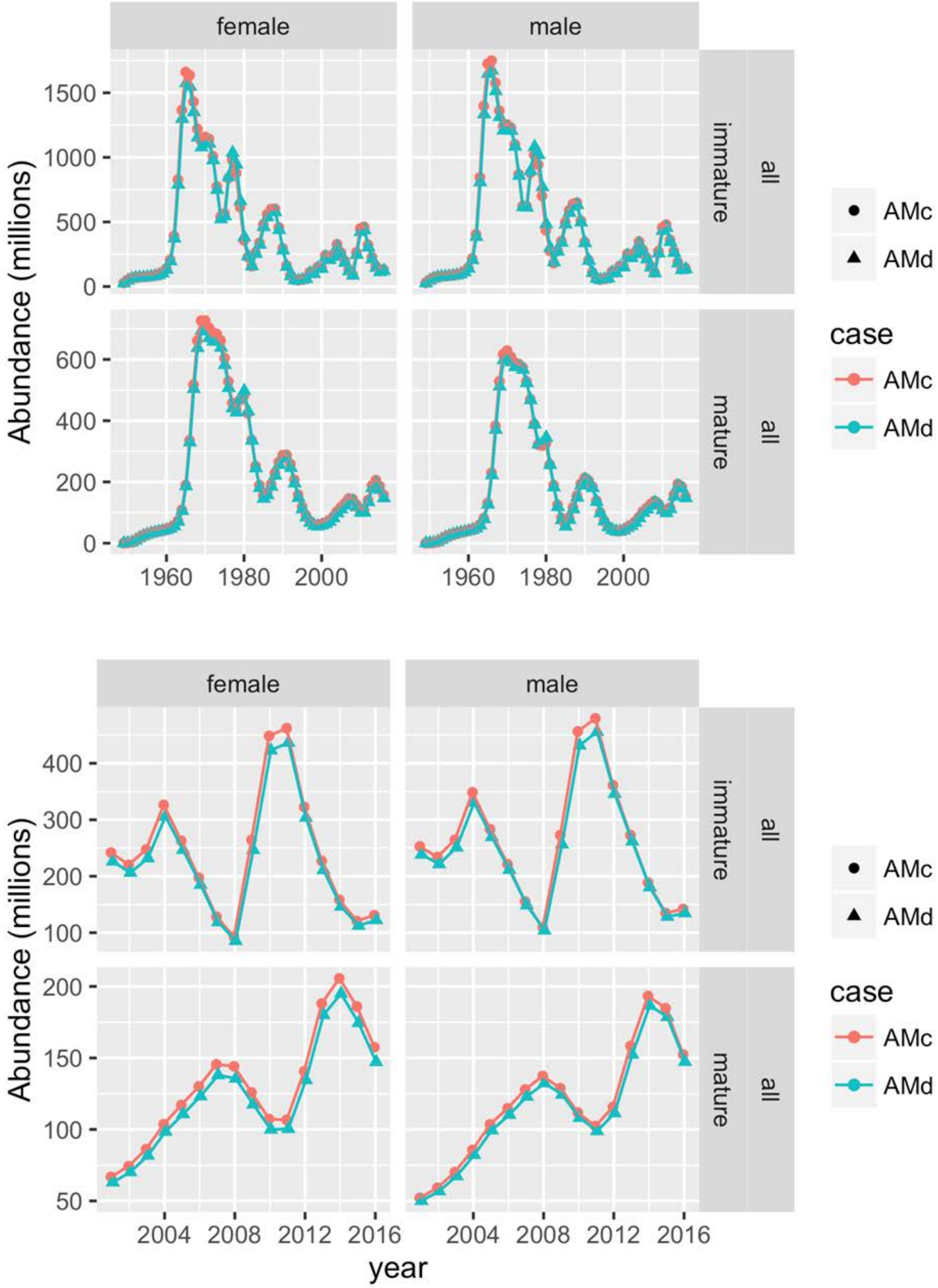

Figure 49. Comparison of estimated population abundance from TCSAM2013 models AMc and AMd.

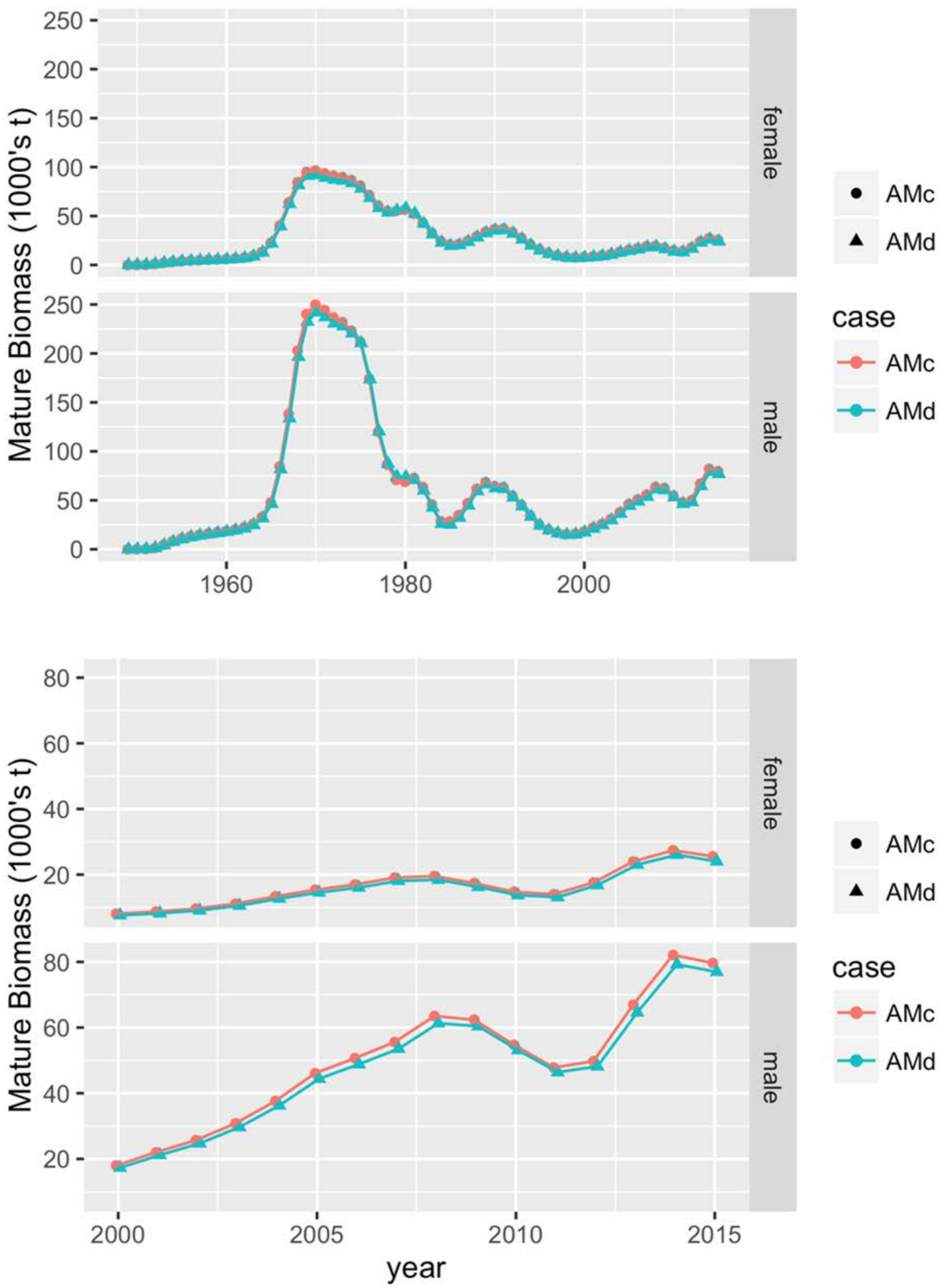

Figure 50. Comparison of estimated mature biomass-at-mating from TCSAM2013 models AMc and AMd.

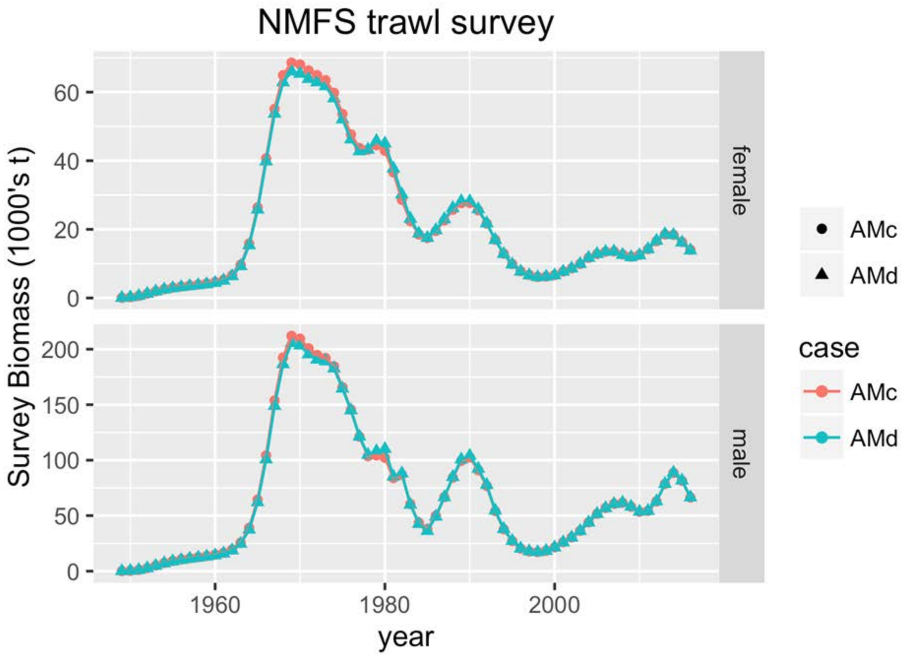

Figure 51. Comparison of estimated survey biomass from TCSAM2013 models AMc and AMd.

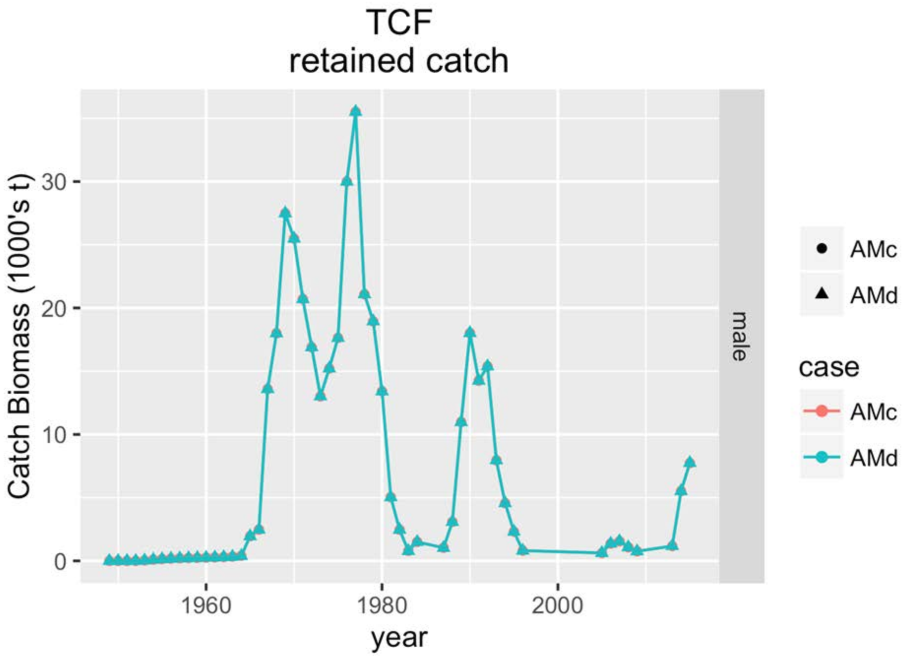

Figure 52. Comparison of estimated retained catch biomass for the directed fishery (TCF) from TCSAM2013 models AMc and AMd.

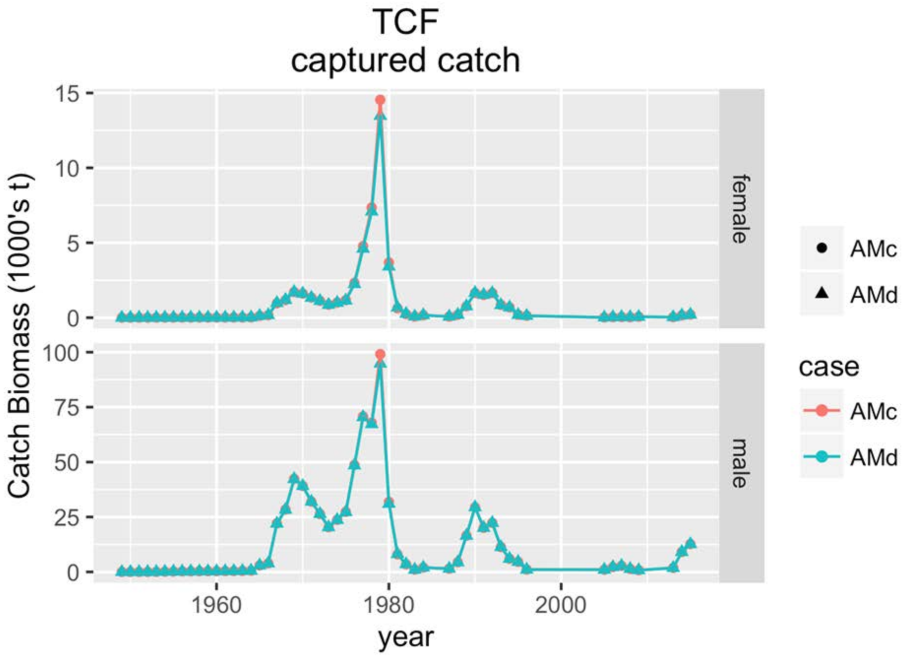

Figure 53. Comparison of estimated total catch (captured) biomass for the directed fishery (TCF) from TCSAM2013 models AMc and AMd.

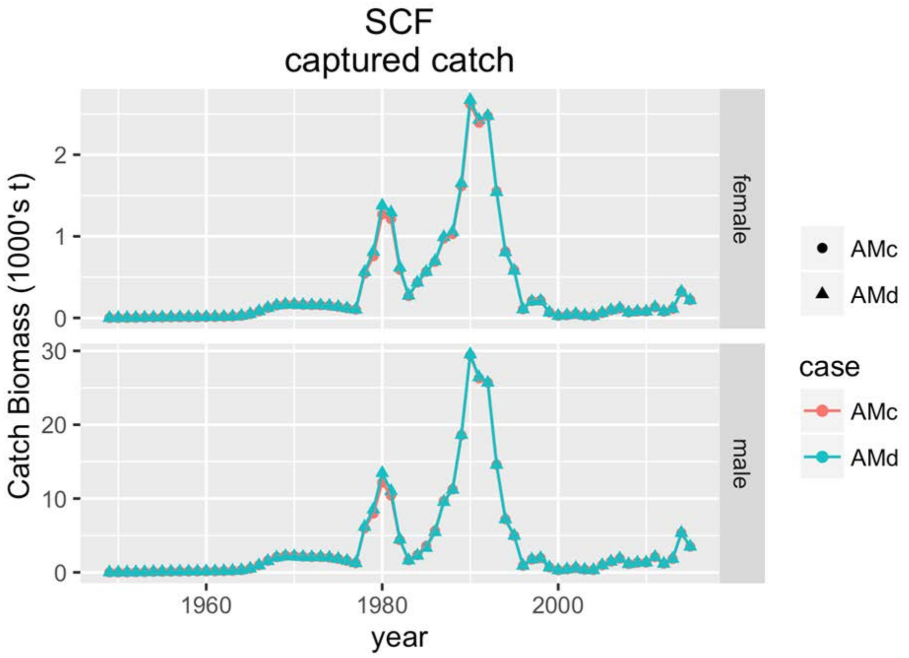

Figure 54. Comparison of estimated total bycatch (captured) biomass for the snow crab fishery (SCF) from TCSAM2013 models AMc and AMd.

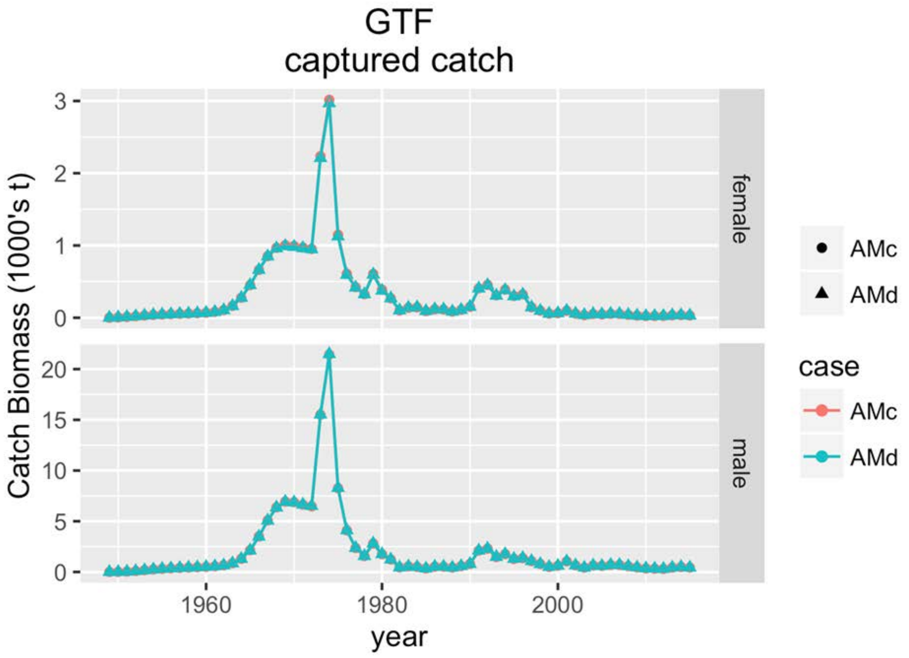

Figure 55. Comparison of estimated total bycatch (captured) biomass for the groundfish fisheries (GTF) from TCSAM2013 models AMc and AMd.

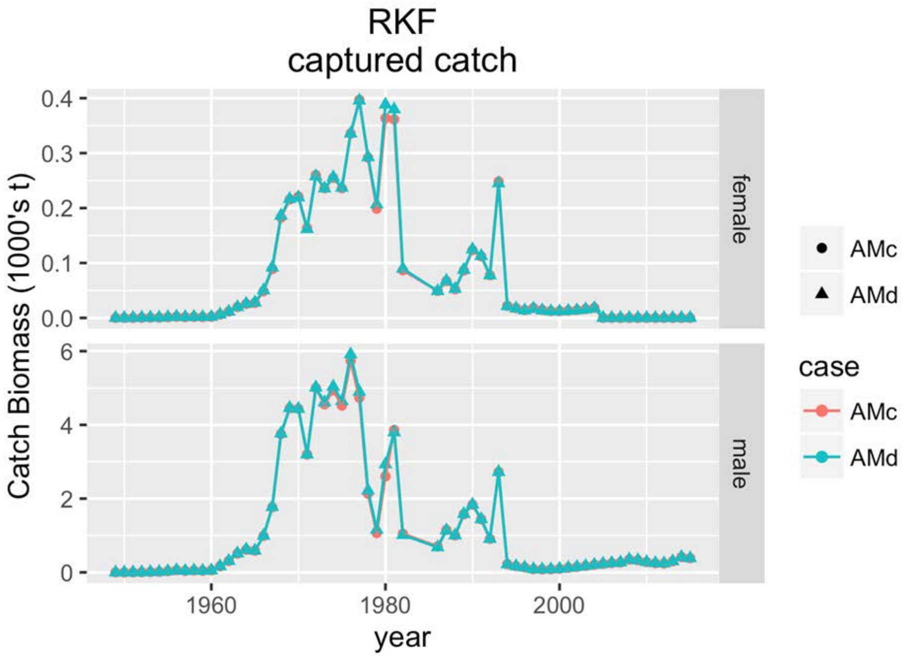

Figure 56. Comparison of estimated total bycatch (captured) biomass for the BBRKC fishery (RKF) from TCSAM2013 models AMc and AMd.

Figure 57. Comparison of estimated natural mortality rates from TCSAM2013 model AMd and TCSAM02 model T02a.

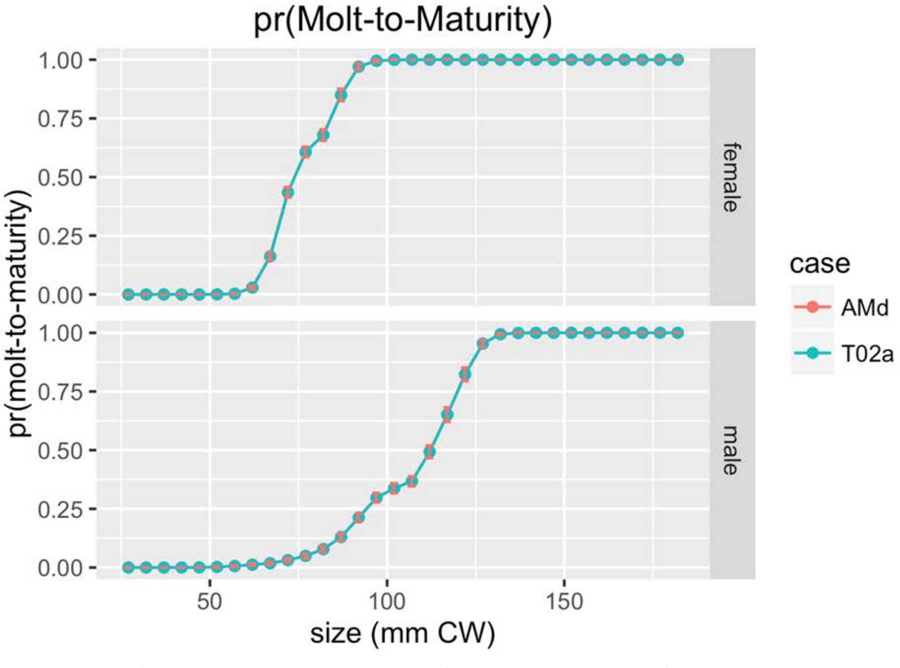

Figure 58. Comparison of estimated probabilities of molt-to-maturity from TCSAM2013 model AMd and TCSAM02 model T02a.

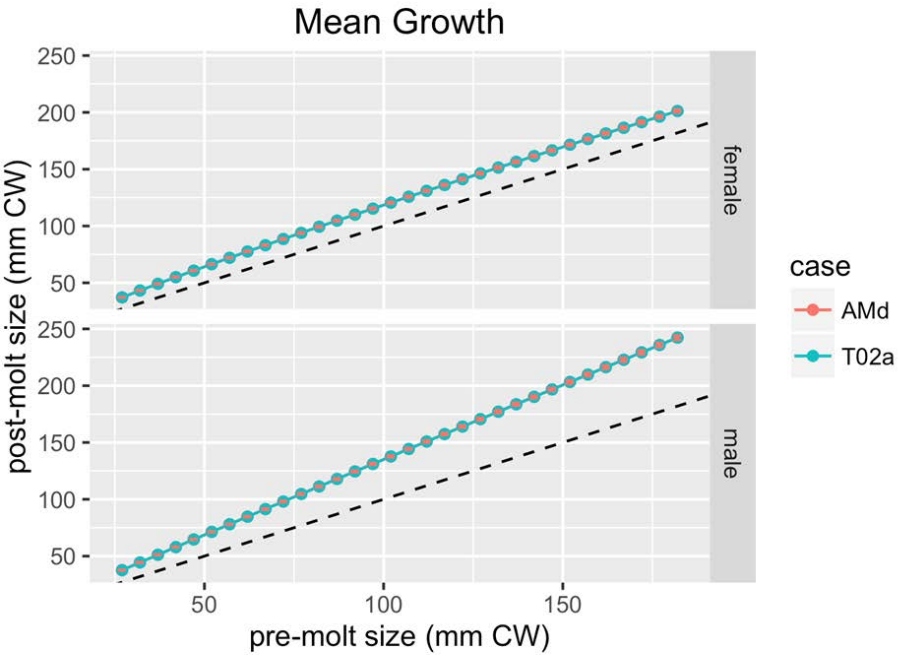

Figure 59. Comparison of estimated mean post-molt size from TCSAM2013 model AMd and TCSAM02 model T02a.

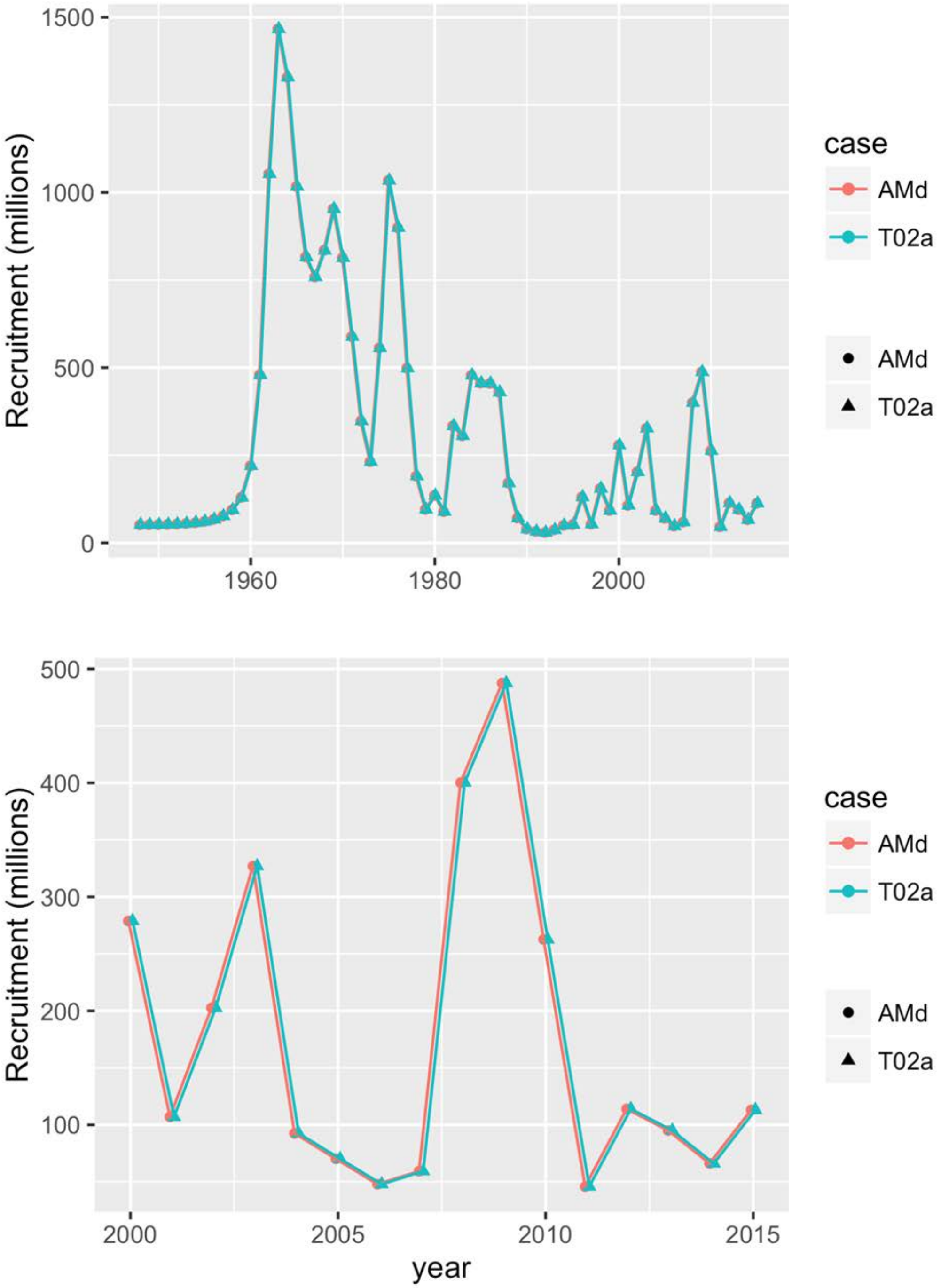

Figure 60. Comparison of estimated recruitment from TCSAM2013 model AMd and TCSAM02 model T02a.

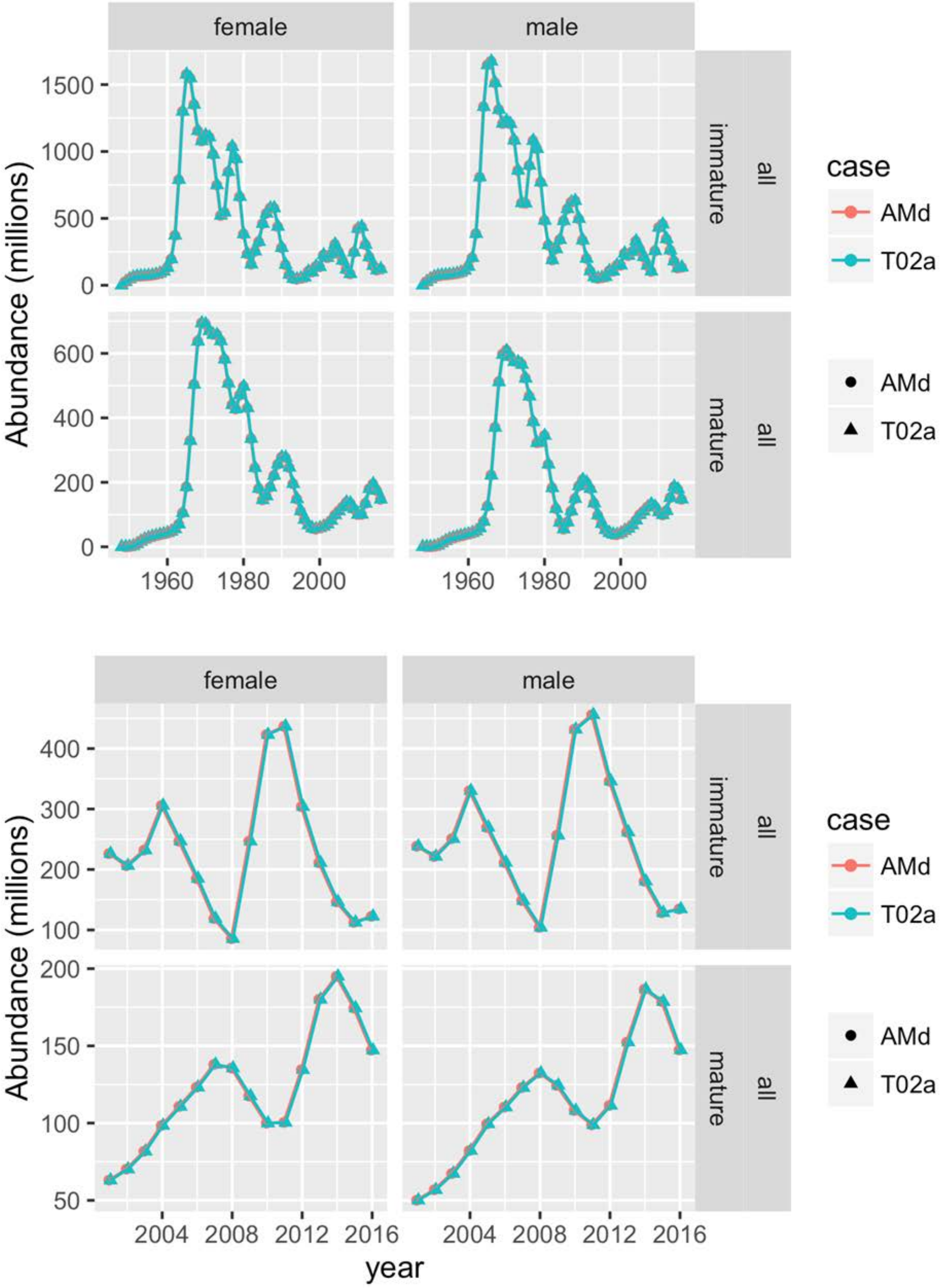

Figure 61. Comparison of estimated population abundance from TCSAM2013 model AMd and TCSAM02 model T02a.

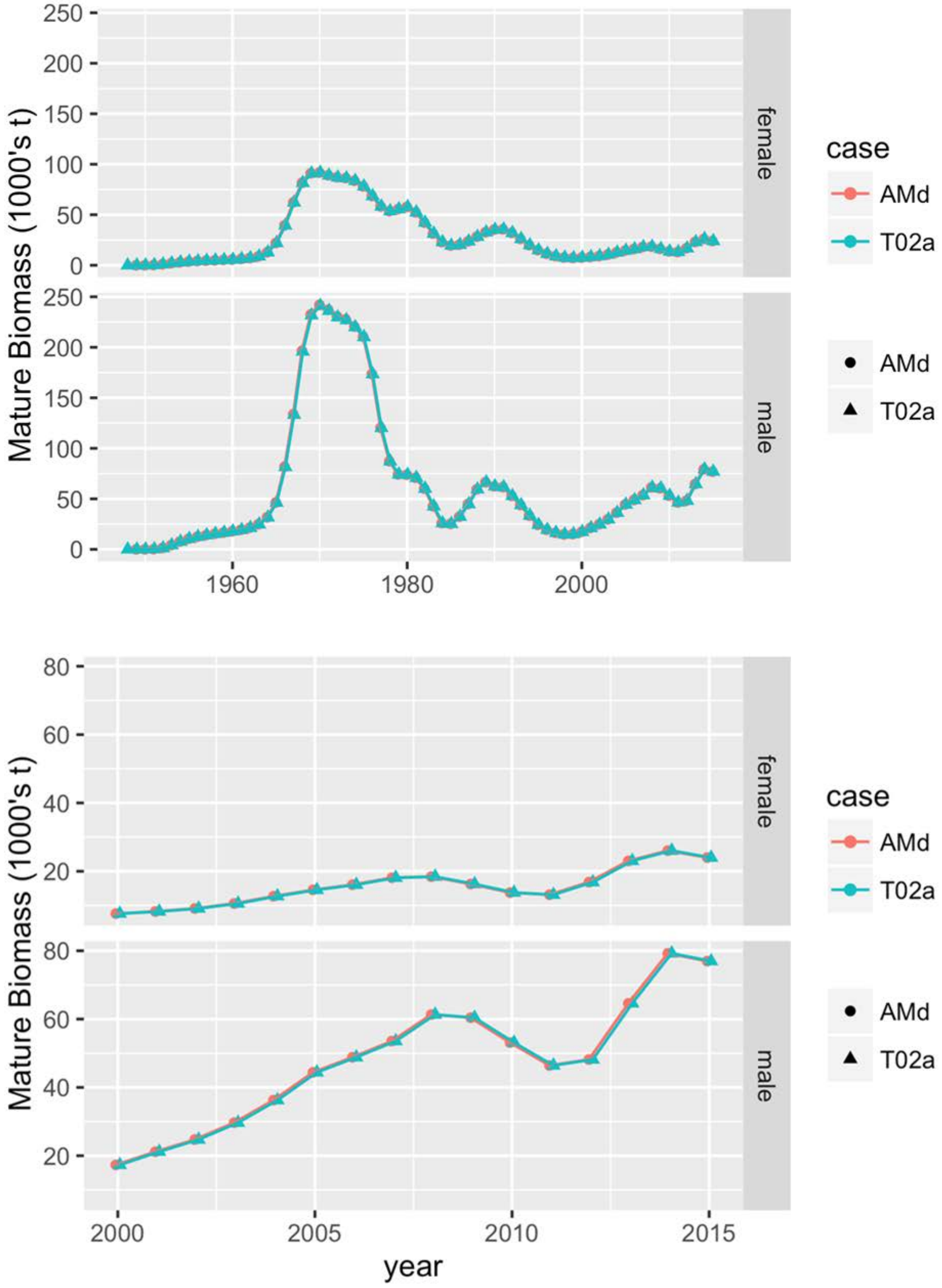

Figure 62. Comparison of estimated mature biomass from TCSAM2013 model AMd and TCSAM02 model T02a.

Figure 63. Comparison of estimated natural mortality rates from TCSAM2013 model AMd and TCSAM02 model T02a.

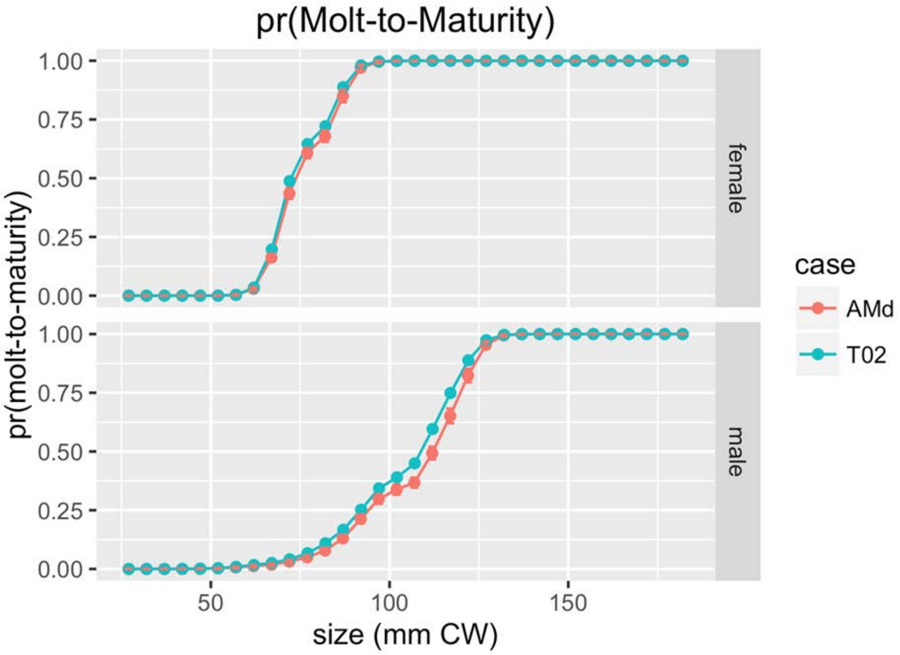

Figure 64. Comparison of estimated probabilities of molt-to-maturity from TCSAM2013 model AMd and TCSAM02 model T02a.

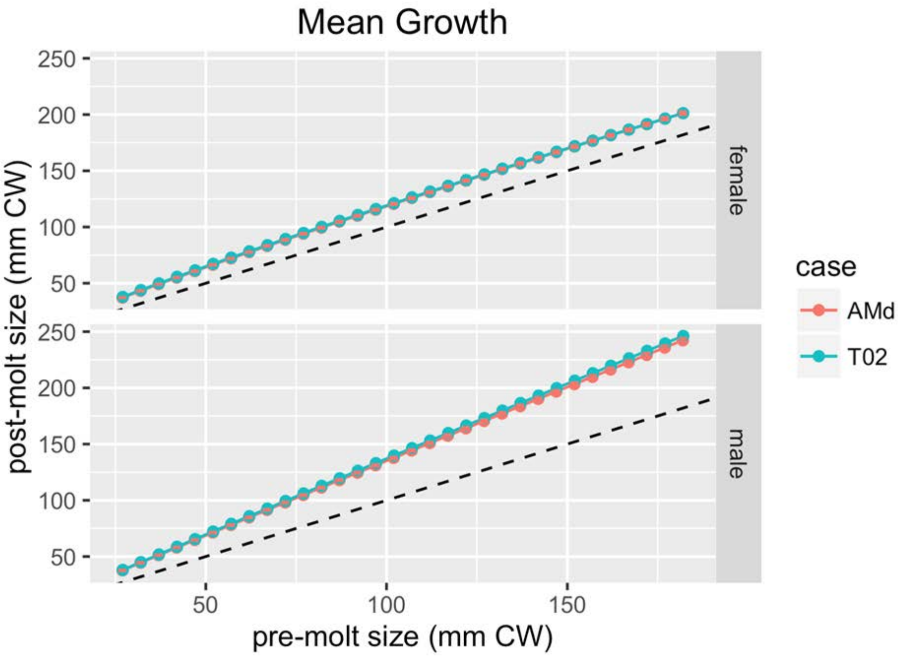

Figure 65. Comparison of estimated mean post-molt size from TCSAM2013 model AMd and TCSAM02 model T02a..

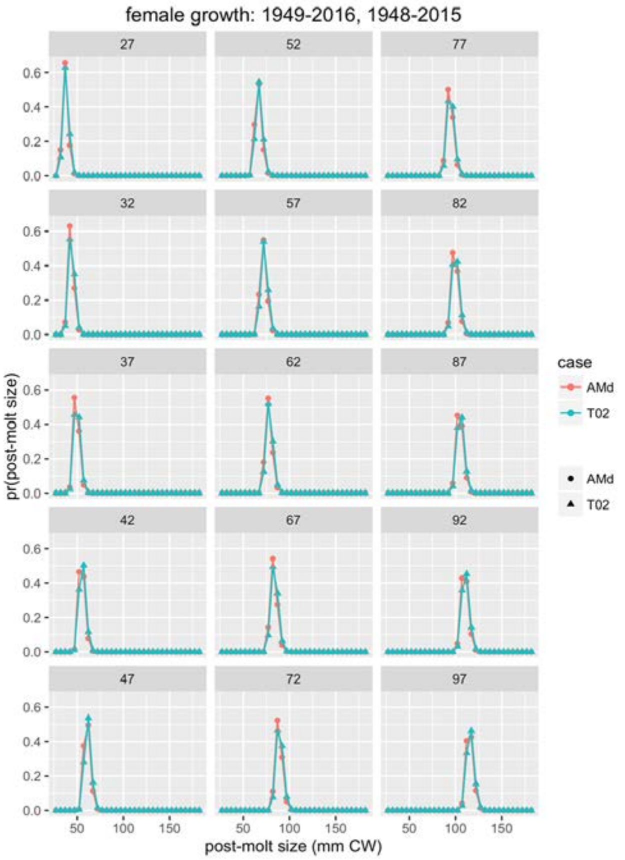

Figure 66. Comparison of estimated growth probabilities from TCSAM2013 model AMd and TCSAM02 model T02a.

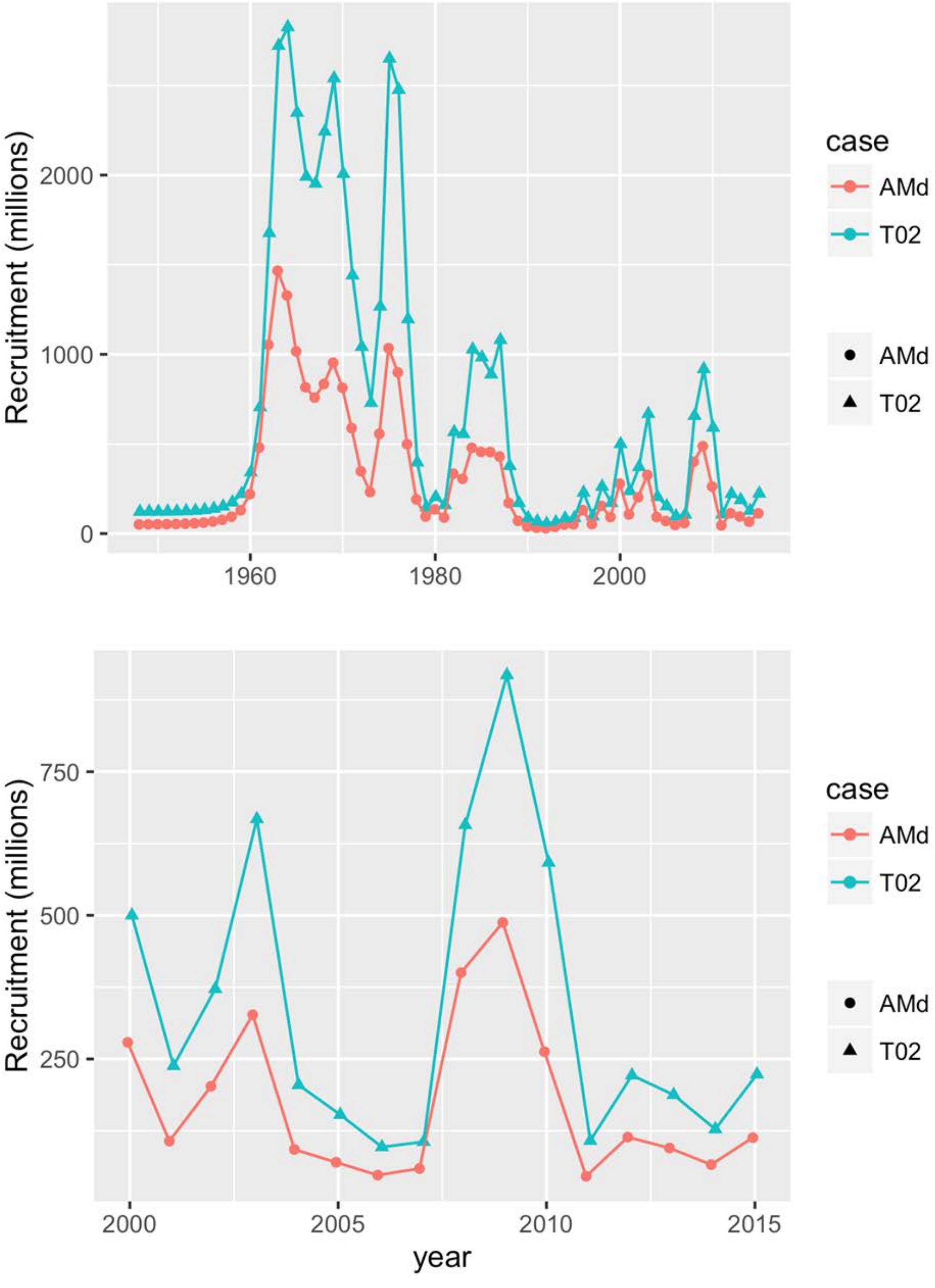

Figure 67. Comparison of estimated recruitment from TCSAM2013 model AMd and TCSAM02 model T02a.

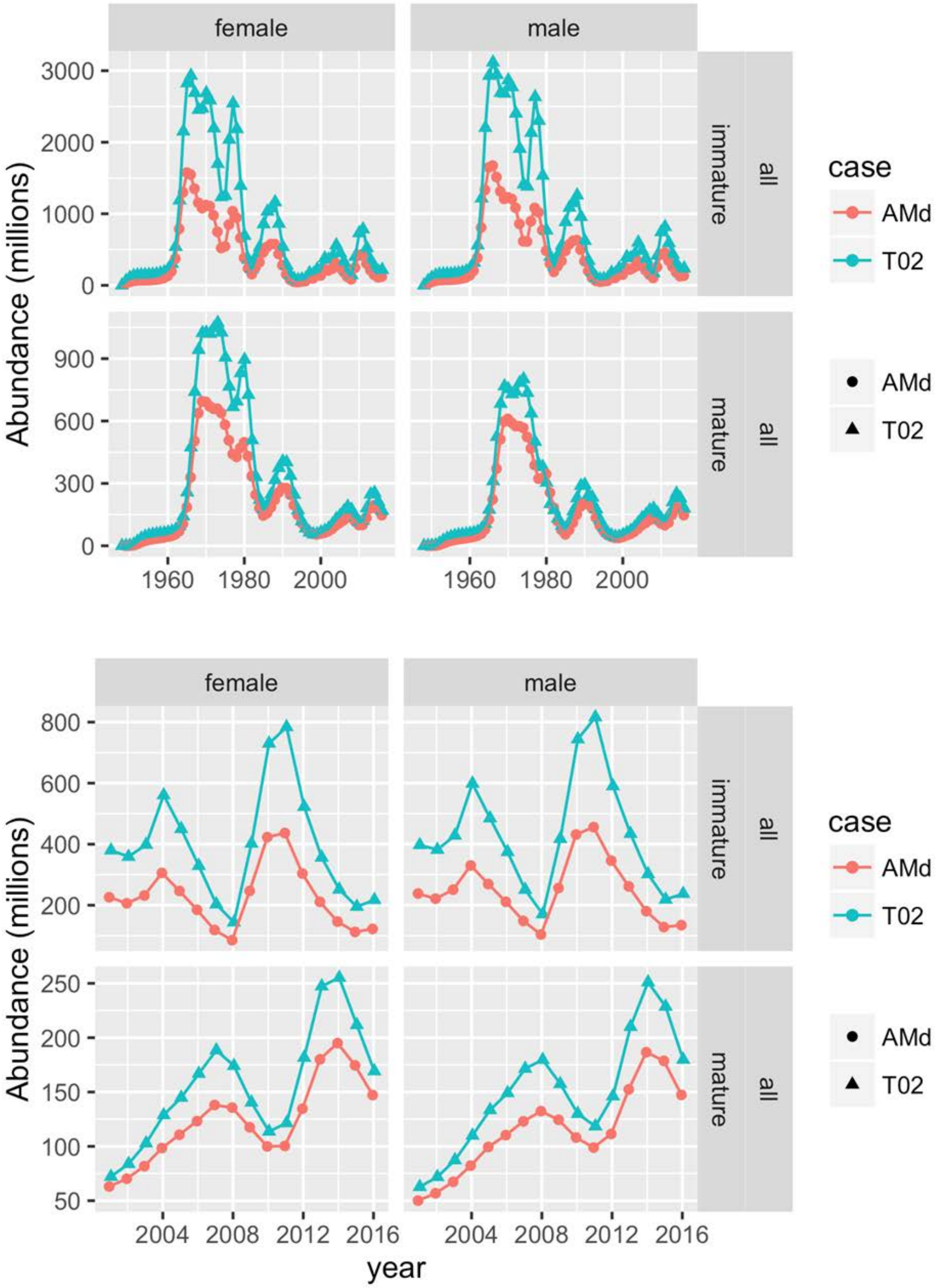

Figure 68. Comparison of estimated population abundance from TCSAM2013 model AMd and TCSAM02 model T02a.

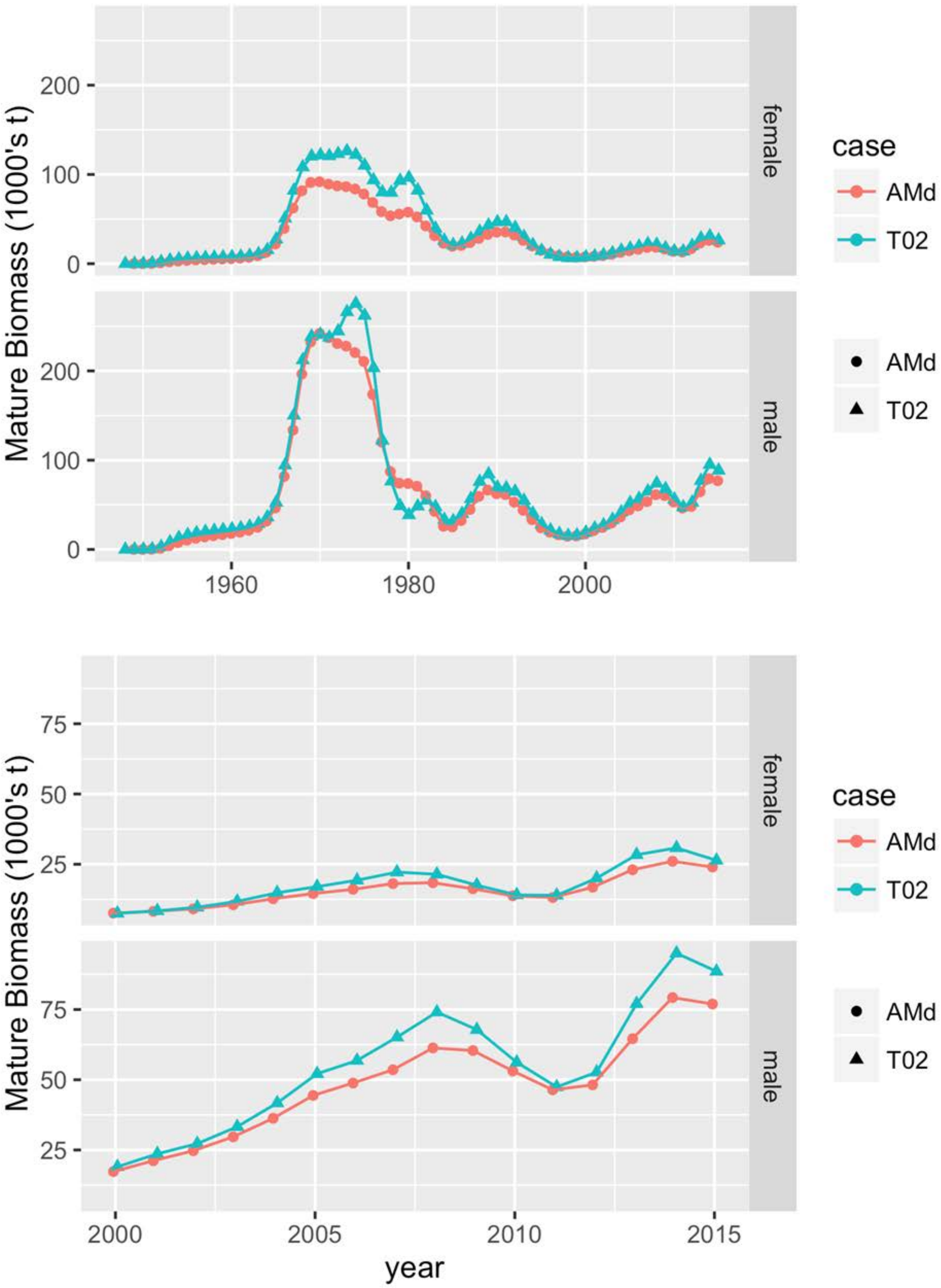

Figure 69. Comparison of estimated mature biomass-at-mating from TCSAM2013 model AMd and TCSAM02 model T02a.

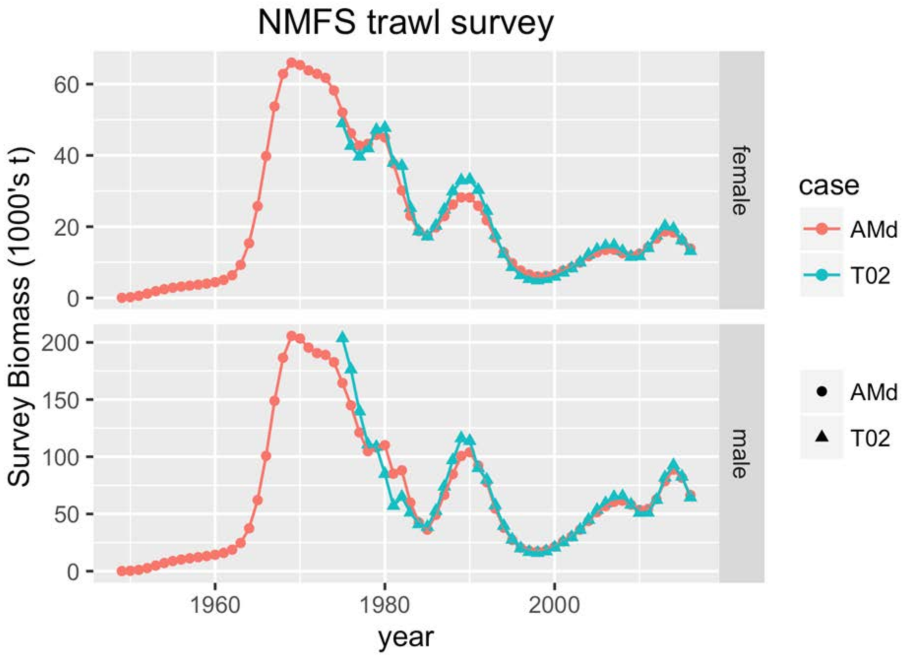

Figure 70. Comparison of estimated survey biomass from TCSAM2013 model AMd and TCSAM02 model T02a.

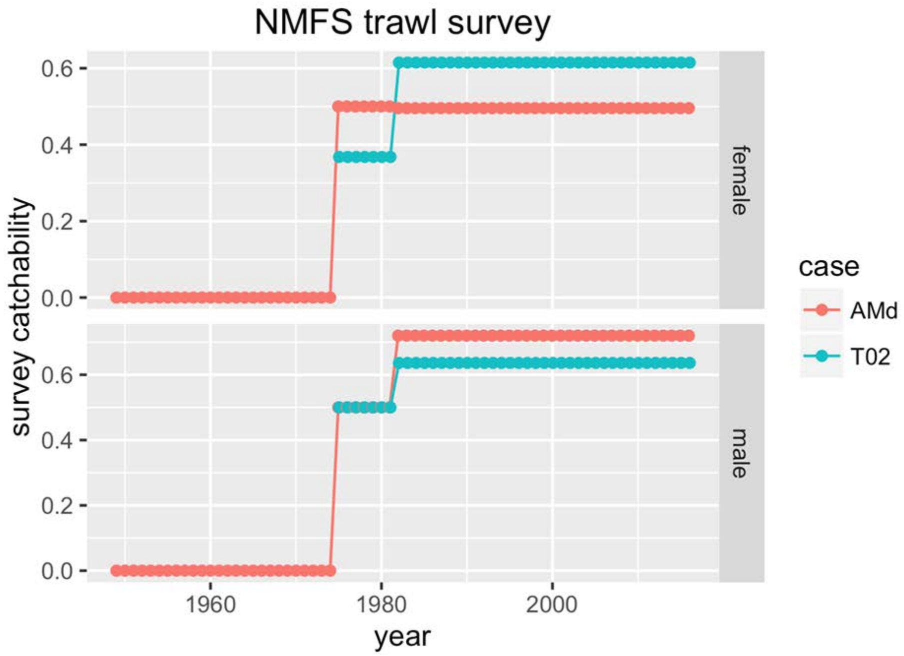

Figure 71. Comparison of estimated survey catchabilities from TCSAM2013 model AMd and TCSAM02 model T02a.

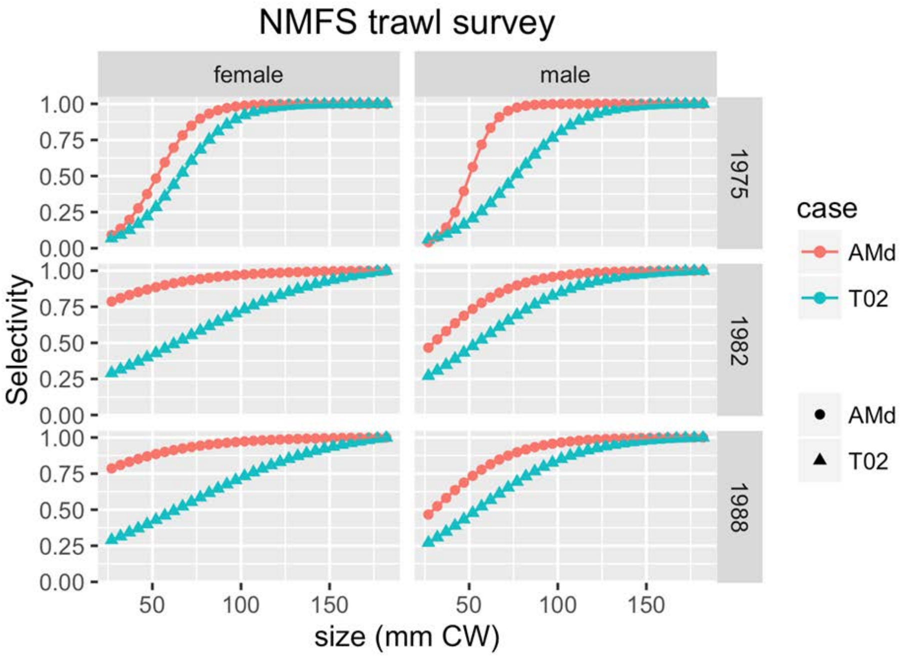

Figure 72. Comparison of estimated survey selectivity functions from TCSAM2013 model AMd and TCSAM02 model T02a.

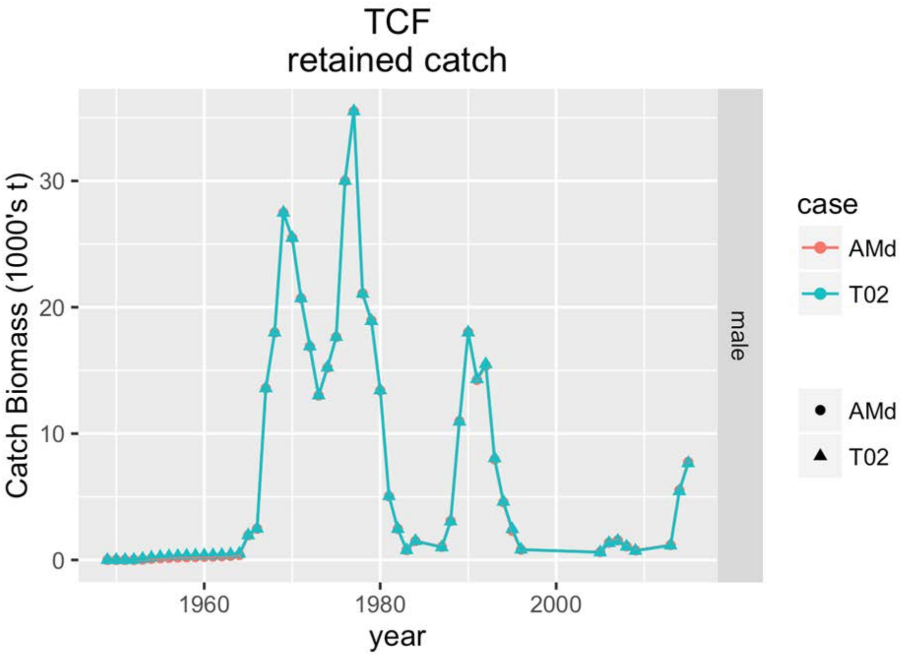

Figure 73. Comparison of estimated retained catch biomass for the directed fishery (TCF) from TCSAM2013 model AMd and TCSAM02 model T02a.

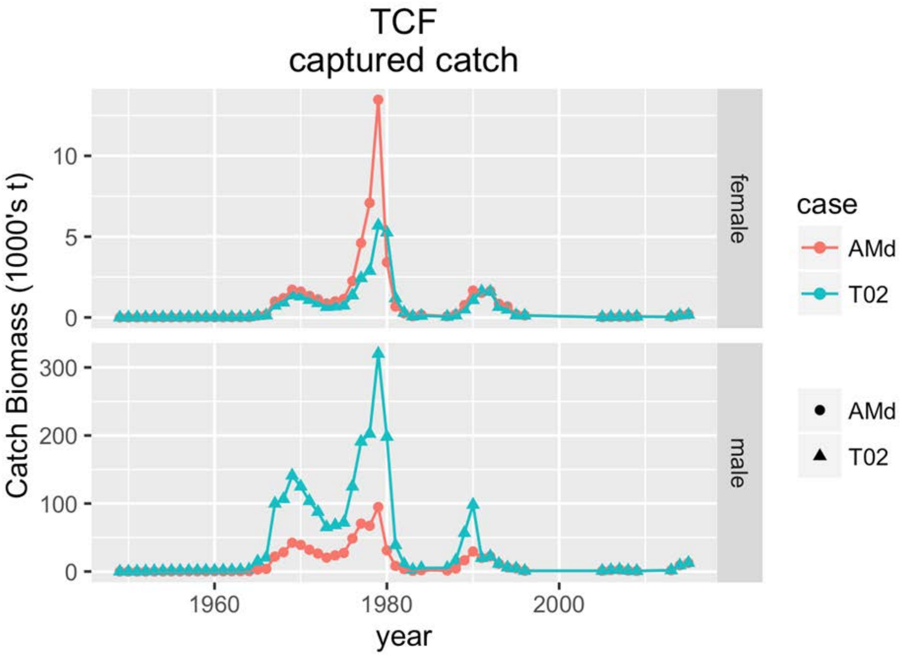

Figure 74. Comparison of estimated total catch (captured) biomass for the directed fishery (TCF) from TCSAM2013 model AMd and TCSAM02 model T02a.

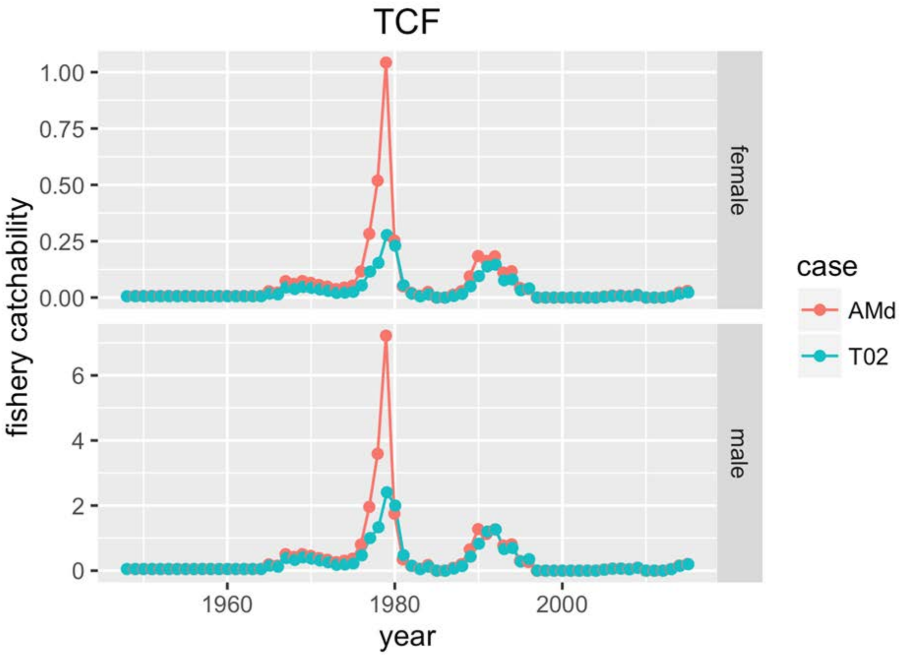

Figure 75. Comparison of estimated catchability for the directed fishery (TCF) from TCSAM2013 model AMd and TCSAM02 model T02a.

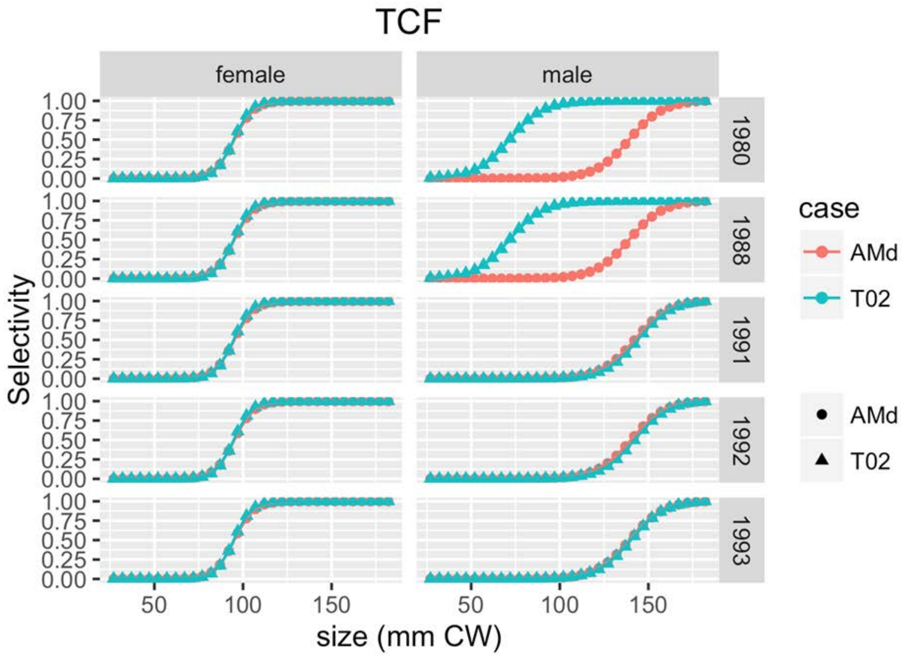

Figure 76. Comparison of estimated total catch selectivity functions for the directed fishery (TCF) from TCSAM2013 model AMd and TCSAM02 model T02a.

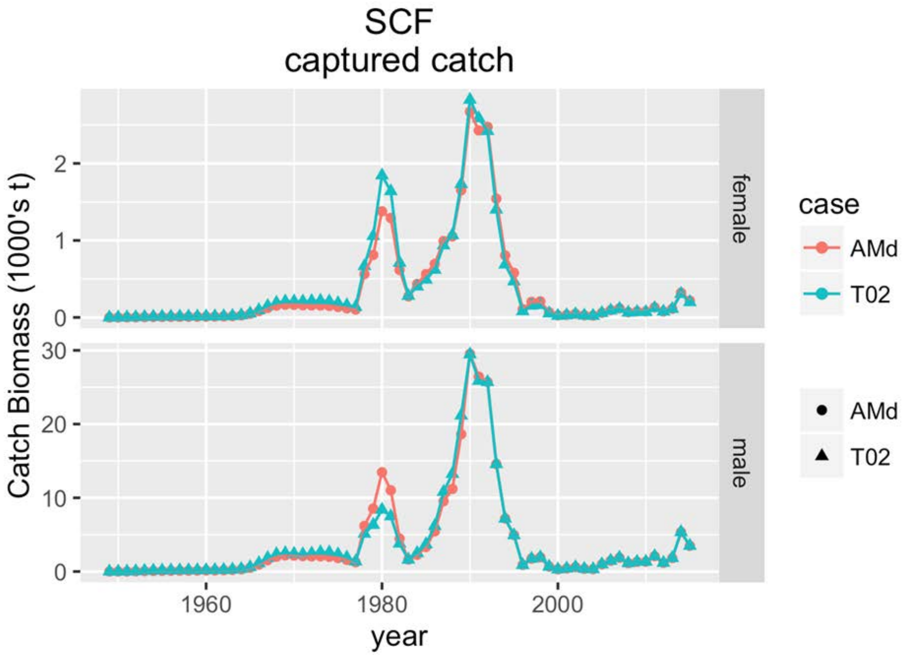

Figure 77. Comparison of estimated total bycatch (captured) biomass for the snow crab fishery (SCF) from TCSAM2013 model AMd and TCSAM02 model T02a.

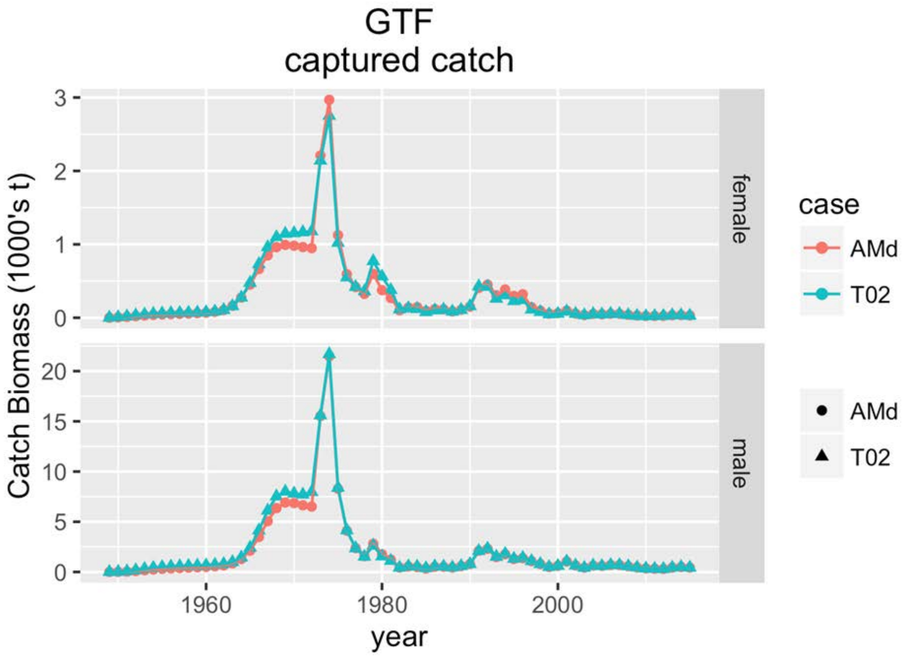

Figure 78. Comparison of estimated total bycatch (captured) biomass for the groundfish fisheries (GTF) from TCSAM2013 model AMd and TCSAM02 model T02a.

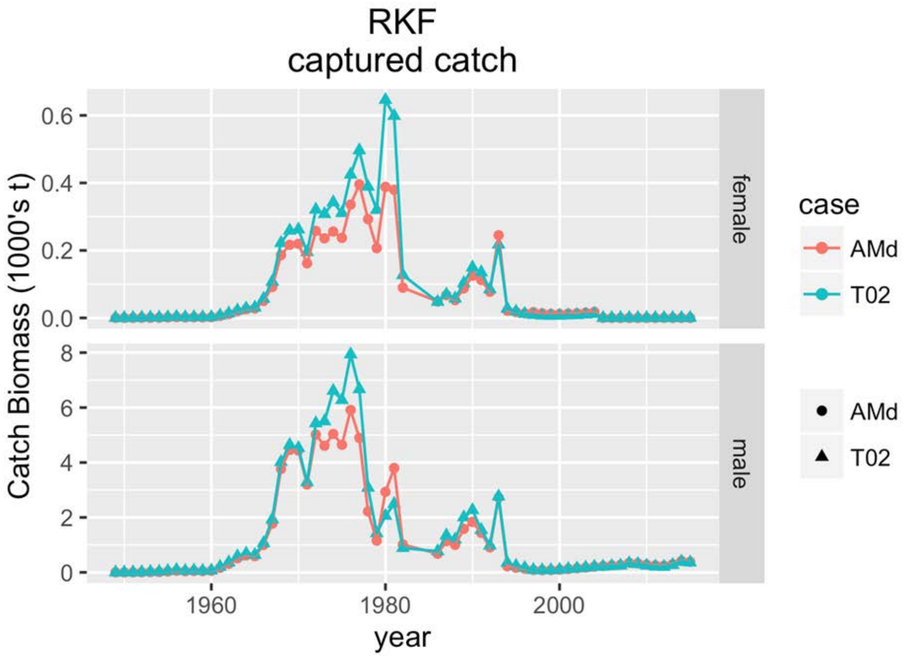

Figure 79. Comparison of estimated total bycatch (captured) biomass for the BBRKC fishery (RKF) from TCSAM2013 model AMd and TCSAM02 model T02a.

Appendix A: TCSAM02 (Tanner Crab Stock Assessment Model, version 02) Description

A. General population dynamics

Population abundance at the start of year *y* in the model, $n_{y,x,m,s,z}$, is characterized by sex *x* (male, female), maturity state *m* (immature, mature), shell condition *s* (new shell, old shell), and size *z* (carapace width, CW). Changes in abundance due to natural mortality, molting and growth, maturation, fishing mortality and recruitment are tracked on an annual basis. Because the principal crab fisheries occur during the winter, the model year runs from July 1 to June 30 of the following calendar year.

The order of calculation steps to project population abundance from year *y* to *y*+1 depends on the assumed timing of the fisheries (δt_y^F) relative to molting (δt_y^m) within year y. The steps when $\delta t_y^F \leq \delta t_y^m$ are outlined below first (Steps A1.1-A1.4), followed by the steps when $\delta t_y^m < \delta t_y^F$. (Steps A2.1-A2.4).

A1. Calculation sequence when $\delta t_y^F \leq \delta t_y^m$

Step A1.1: Survival prior to fisheries

Natural mortality is applied to the population from the start of the model year (July 1) until just prior to prosecution of pulse fisheries for year *y* at δt_y^F. The numbers surviving at δt_y^F in year *y* are given by:

$$n_{y,x,m,s,z}^1 = e^{-M_{y,x,m,s,z} \cdot \delta t_y^F} \cdot n_{y,x,m,s,z} \tag{A1.1}$$

where *M* represents the annual rate of natural mortality in year *y* on crab classified as *x*, *m*, *s*, *z*.

Step A1.2: Prosecution of the fisheries

The directed fishery and bycatch fisheries are modeled as pulse fisheries occurring at δt_y^F in year *y*. The numbers that remain after the fisheries are prosecuted are given by:

$$n_{y,x,m,s,z}^2 = e^{-F_{y,x,m,s,z}^T} \cdot n_{y,x,m,s,z}^1 \tag{A1.2}$$

where $F_{y,x,m,s,z}^T$ represents the total fishing mortality (over all fisheries) on crab classified as *x*, *m*, *s*, *z* in year *y*.

Step A1.3: Survival after fisheries to time of molting/mating

Natural mortality is again applied to the population from just after the fisheries to the time at which molting/mating occurs for year *y* at δt_y^m (generally Feb. 15). The numbers surviving at δt_y^m in year *y* are then given by:

$$n_{y,x,m,s,z}^3 = e^{-M_{y,x,m,s,z} \cdot (\delta t_y^m - \delta t_y^F)} \cdot n_{y,x,m,s,z}^2 \tag{A1.3}$$

where, as above, *M* represents the annual rate of natural mortality in year *y* on crab classified as *x*, *m*, *s*, *z*.

Step A1.4: Molting, growth, and maturation

The changes in population structure due to molting, growth and maturation of immature (new shell) crab, as well as the change in shell condition for new shell mature crab due to aging, are given by:

$$n_{y,x,MAT,NS,z}^4 = \phi_{y,x,z} \cdot \sum_{z'} \Theta_{y,x,z,z'} \cdot n_{y,x,IMM,NS,z'}^3 \tag{A1.4a}$$

$$n^{4}_{y,x,IMM,NS,z} = (1-\phi_{y,x,z}) \cdot \sum_{z'} \Theta_{y,x,z,z'} \cdot n^{3}_{y,x,IMM,NS,z'} \tag{A1.4b}$$

$$n^{4}_{y,x,MAT,OS,z} = n^{3}_{y,x,MAT,OS,z} + n^{3}_{y,x,MAT,NS,z} \tag{A1.4c}$$

where $\Theta_{y,x,z,z'}$ is the growth transition matrix in year *y* for an immature (new shell) crab of sex *x* and pre-molt size *z'* to post-molt size *z* and $\phi_{y,x,z}$ is the probability that a just-molted crab of sex *x* and post-molt size *z* has undergone its terminal molt to maturity. Additionally, all crab that underwent their terminal molt to maturity the previous year are assumed to change shell condition from new shell to old shell (A1.4c). Note that the numbers of immature old shell crab are identically zero in the current model because immature crab are assumed to molt each year until they undergo the terminal molt to maturity, consequently the corresponding equation for *m=IMM*, *s=OS* above is unnecessary.

Step A1.5: Survival to end of year, recruitment, and update to start of next year
Finally, population abundance at the start of year *y*+1 due to natural mortality on crab from the time of molting in year *y* until the end of the model year (June 30) and recruitment of immature new shell (IMM, NS) crab at the end of year *y* ($R_{y,x,z}$) are given by:

$$n_{y+1,x,m,s,z} = \begin{cases} e^{-M_{y,x,IMM,NS,z} \cdot (1-\delta t^{m}_{y})} \cdot n^{4}_{y,x,IMM,NS,z} + R_{y,x,z} & m = IMM, s = NS \\ e^{-M_{y,x,m,s,z} \cdot (1-\delta t^{m}_{y})} \cdot n^{4}_{y,x,m,s,z} & otherwise \end{cases} \tag{A1.5}$$

Note: in TCSAM2013 (Appendix C), recruitment in year y is added to the population at the beginning of year y, whereas here it is added to the population at the beginning of year y+1. Thus, recruitment time series from TCSAM2013 models must be lagged by one year to compare with those from TCSAM02.

A2. Calculation sequence when $\delta t^{m}_{y} < \delta t^{F}_{y}$

Step A2.1: Survival prior to molting/mating
As in the previous sequence, natural mortality is first applied to the population from the start of the model year (July 1), but this time until just prior to molting/mating in year *y* at δt^{m}_{y} (generally Feb. 15). The numbers surviving at δt^{m}_{y} in year *y* are given by:

$$n^{1}_{y,x,m,s,z} = e^{-M_{y,x,m,s,z} \cdot \delta t^{m}_{y}} \cdot n_{y,x,m,s,z} \tag{A2.1}$$

where *M* represents the annual rate of natural mortality in year *y* on crab classified as *x*, *m*, *s*, *z*.

Step A2.2: Molting, growth, and maturation
The changes in population structure due to molting, growth and maturation of immature (new shell) crab, as well as the change in shell condition for new shell mature crab due to aging, are given by:

$$n^{2}_{y,x,MAT,NS,z} = \phi_{y,x,z} \cdot \sum_{z'} \Theta_{y,x,z,z'} \cdot n^{1}_{y,x,IMM,NS,z'} \tag{A2.2a}$$

$$n^{2}_{y,x,IMM,NS,z} = (1-\phi_{y,x,z}) \cdot \sum_{z'} \Theta_{y,x,z,z'} \cdot n^{1}_{y,x,IMM,NS,z'} \tag{A2.2b}$$

$n^2_{y,x,MAT,OS,z} = n^1_{y,x,MAT,OS,z} + n^1_{y,x,MAT,NS,z}$	A2.2c

where $\Theta_{y,x,z,z'}$ is the growth transition matrix in year *y* for an immature (new shell) crab of sex *x* and pre-molt size *z'* to post-molt size *z* and $\phi_{y,x,z}$ is the probability that a just-molted crab of sex *x* and post-molt size *z* has undergone its terminal molt to maturity. Additionally, crabs that underwent their terminal molt to maturity the previous year are assumed to change shell condition from new shell to old shell (A2.2c). Again, the numbers of immature old shell crab are identically zero in the current model because immature crab are assumed to molt each year until they undergo the terminal molt to maturity, consequently the corresponding equation for *m=IMM*, *s=OS* above is unnecessary.

Step A2.3: Survival after molting/mating to prosecution of fisheries

Natural mortality is again applied to the population from just after molting/mating to the time at which the fisheries occur for year *y* (at δt^F_y). The numbers surviving at δt^F_y in year *y* are then given by:

$n^3_{y,x,m,s,z} = e^{-M_{y,x,m,s,z}\cdot(\delta t^F_y - \delta t^m_y)} \cdot n^2_{y,x,m,s,z}$	A2.3

where, as above, *M* represents the annual rate of natural mortality in year *y* on crab classified as *x*, *m*, *s*, *z*.

Step A2.4: Prosecution of the fisheries

The directed fishery and bycatch fisheries are modeled as pulse fisheries occurring at δt^F_y in year *y*. The numbers that remain after the fisheries are prosecuted are given by:

$n^4_{y,x,m,s,z} = e^{-F^T_{y,x,m,s,z}} \cdot n^3_{y,x,m,s,z}$	A2.4

where $F^T_{y,x,m,s,z}$ represents the total fishing mortality (over all fisheries) on crab classified as *x*, *m*, *s*, *z* in year *y*.

Step A2.5: Survival to end of year, recruitment, and update to start of next year

Finally, population abundance at the start of year *y*+1 due to natural mortality on crab from just after prosecution of the fisheries in year *y* until the end of the model year (June 30) and recruitment of immature new (IMM, NS) shell crab at the end of year *y* ($R_{y,x,z}$) and are given by:

$n_{y+1,x,m,s,z} = \begin{cases} e^{-M_{y,x,IMM,NS,z}\cdot(1-\delta t^F_y)} \cdot n^4_{y,x,IMM,NS,z} + R_{y,x,z} & m = IMM, s = NS \\ e^{-M_{y,x,m,s,z}\cdot(1-\delta t^F_y)} \cdot n^4_{y,x,m,s,z} & otherwise \end{cases}$	A2.5

B. Model processes: natural mortality

At its most general, natural mortality $M_{y,x,m,s,z}$ is parameterized as a time-varying (in blocks of years) function of sex, maturity state, and size using the following functional form:

$lnM_{y,x,m} = \mu^0 + \mu^0_t + \delta_{m,MAT} \cdot \mu^{MAT}_t + \delta_{x,FEM} \cdot \mu^{FEM}_t + \delta_{x,FEM} \cdot \delta_{m,MAT} \cdot \mu^{FEM,MAT}_t$	B.1
$M_{y,x,m,s,z} = \begin{cases} \exp\left(lnM_{y,x,m}\right) & if\ Lorenzen\ option\ is\ not\ selected\ for\ block\ t \\ \exp\left(lnM_{y,x,m}\right) \cdot \frac{z_{base}}{z} & if\ Lorenzen\ option\ is\ selected\ for\ block\ t \end{cases}$	B.2a B.2b

where y falls into time block t, the μ's are (potentially) estimable parameters on the ln-scale, and $\delta_{i,j}$ is the delta function (1 if i=j, 0 otherwise). μ^0 represents the baseline (ln-scale) natural mortality rate on immature males, while μ_t^0 is the offset on immature males in time block t, μ_t^{MAT} is the offset for mature crab in time block t, μ_t^{FEM} is the offset for females in time block t, and $\mu_t^{FEM,MAT}$ is the offset for mature females in time block t. As an option, one can include (by time block) size dependence in natural mortality using Lorenzen's approach (eq. B.2b), where z_{base} is a specified reference size (mm CW).

This parameterization for natural mortality differs from that in TCSAM2013 (Appendix C, Section B). In TCSAM2013, sex/maturity-state variations to the base mortality rate are estimated on the arithmetic scale, whereas here they are estimated on the ln-scale. The latter approach may be preferable in terms of model convergence properties because the arithmetic-scale parameter values must be constrained to be positive by placing limits on their values whereas the ln-scale parameter values do not. However, the use of strong priors on the arithmetic-scale parameters in TCSAM2013 (Appendix C, eq. B3) probably addresses this issue satisfactorily. TCSAM2013 also incorporates the ability to estimate additional effects on natural mortality during the 1980-1984 time period, but this time block is hard-wired in the code; thus investigating how changes to this time block affect the assessment require modifying and recompiling the code for every alternative time block considered. A similar study using TCSAM02 would not require modifying the model code because time blocks can be defined for any model process (e.g., natural mortality) in the model input files.

C. Model processes: growth

Annual growth of immature crab in TCSAM02 is implemented using to approaches, the first based on Gmacs and the second (mainly for comparability purposes) based on TCSAM2013 (Appendix C). In TCSAM02, growth can vary by time block, so it is expressed by sex-specific transition matrices $\Theta_{t,x,z,z'}$ that specify the probability that crab in pre-molt size bin z grow to post-molt size bin z' during time block t.

In the GMACS-like approach, the sex-specific growth matrices are given by:

$\Theta_{t,x,z,z'} = c_{t,x,z} \cdot \int_{z'-bin/2}^{z'+bin/2} \Gamma\left(\frac{z''-\bar{z}_{t,x,z}}{\beta_{t,x}}\right) dz''$	Sex-specific (x) transition matrix for growth from pre-molt z to post-molt z', with $z' \geq z$	C.1
$c_{t,,x,z} = \left[\int_{z}^{\infty} \Gamma\left(\frac{z''-\bar{z}_{t,,x,z}}{\beta_{t,x}}\right) dz''\right]^{-1}$	Normalization constant so $1 = \sum_{z'} \Theta_{t,x,z,z'}$	C.2
$\bar{z}_{t,x,z} = e^{a_{t,x}} \cdot z^{b_{t,x}}$	Mean size after molt, given pre-molt size z	C.3

where the integral represents the cumulative gamma distribution across the z' size bin. This approach may have better numerical stability properties than the TCSAM2013 approach below.

The TCSAM2013 approach is really an approximation to the Gmacs approach, where the sex-specific growth matrices $\Theta_{t,x,z,z'}$ are given by

$\Theta_{t,x,z,z'} = c_{t,x,z} \cdot \Delta_{z,z'}{}^{\alpha_{t,x,z}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_{t,x}}}$	Sex-specific (x) transition matrix for growth from pre-molt z to post-molt z', with $z' \geq z$	C.4
$c_{x,z} = \left[\sum_{z'} \Delta_{z,z'}{}^{\alpha_{t,x,z}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_{t,x}}}\right]^{-1}$	Normalization constant so $1 = \sum_{z'} \Theta_{x,z,z'}$	C.5
$\Delta_{z,z'} = z' - z$	Actual growth increment	C.6
$\alpha_{t,x,z} = \left[\bar{z}_{t,x,z} - z\right]/\beta_{t,x}$	Mean molt increment, scaled by β_x	C.7
$\bar{z}_{t,x,z} = e^{a_{t,x}} \cdot z^{b_{t,x}}$	Mean size after molt, given pre-molt size z	C.8

In both approaches, the $a_{t,x}$, $b_{t,x}$, and $\beta_{t,x}$ are arithmetic-scale parameters.

$\Theta_{t,x,z,z'}$ is used to update the numbers-at-size for immature crab, $n_{y,x,z}$, from pre-molt size z to post-molt size z' using:

$n^{+}_{y,x,z'} = \sum_{z} n_{y,x,z} \cdot \Theta_{t,x,z,z'}$		C.9

where y falls within time block t.

Priors using normal distributions are imposed on $a_{t,x}$ and $b_{t,x}$ in TCSAM2013, with the values of the hyper-parameters hard-wired in the model code (App. C, Section C). While priors may be defined for the associated parameters here, these are identified by the user in the model input files and are not hard-wired in the model code.

D. Model processes: maturity (terminal molt)

Maturation of immature crab in TCSAM02 is based on a similar approach to that taken in TCSAM2013, except that the sex- and size-specific probabilities of terminal molt for immature crab, $\phi_{t,x,z}$ (where size z is post-molt size), can vary by time block. After molting and growth, the numbers of (new shell) crab at post-molt size z remaining immature, $n^{+}_{y,x,IMM,NS,z}$, and those maturing, $n^{+}_{x,MAT,NS,z}$, are given by:

$n^{+}_{y,x,IMM,NS,z} = (1 - \phi_{t,x,z}) \cdot n_{y,x,IMM,NS,z}$		D.1a
$n^{+}_{y,x,MAT,NS,z} = \phi_{t,x,z} \cdot n_{y,x,IMM,NS,z}$		D.1b

where y falls in time block t and $n_{y,x,IMM,NS,z}$ is the number of immature, new shell crab of sex x at post-molt size z.

The sex- and size-specific probabilities of terminal molt, $\phi_{t,x,z}$, are related to the logit-scale model parameters $p^{mat}_{t,x,z}$ by:

$\phi_{t,FEM,z} = \begin{cases} \frac{1}{1+e^{p^{mat}_{t,FEM,z}}} & z \le z^{mat}_{t,FEM} \\ 1 & z > z^{mat}_{t,FEM} \end{cases}$	female probabilities of maturing at post-molt size *z*	D.2a
$\phi_{t,MALE,z} = \begin{cases} \frac{1}{1+e^{p^{mat}_{t,MALE,z}}} & z \le z^{mat}_{t,MALE} \\ 1 & z > z^{mat}_{t,MALE} \end{cases}$	male probabilities of maturing at post-molt size *z*	D.2b

where the $z^{mat}_{t,x}$ are constants specifying the minimum pre-molt size at which to assume all immature crab will mature upon molting. The $z^{mat}_{t,x}$ are used here pedagogically; in actuality, the user specifies the *number* of logit-scale parameters to estimate (one per size bin starting with the first bin) for each sex, and this determines the $z^{mat}_{t,x}$ used above. This parameterization is similar to that implemented in TCSAM2013 for the 2016 assessment model (App. C, Section D).

Second difference penalties are applied to the parameter estimates in TCSAM2013's objective function to promote relatively smooth changes in these parameters with size. Similar penalties (smoothness, non-decreasing) can be applied in TCSAM02.

E. Model processes: recruitment

Recruitment of immature (new shell) crab in TCSAM02 has a similar functional form to that used in TCSAM2013(App. 1, Section E), except that the sex ratio at recruitment is not fixed at 1:1 and multiple time blocks can be specified in the new model (not just the "historical" and "current" blocks defined in TCSAM2013). Recruitment in year y of sex *x* crab at size *z* is specified as

$R_{y,x,z} = \dot{R}_y \cdot \ddot{R}_{y,x} \cdot \dddot{R}_{y,z}$	recruitment of immature, new shell crab	E.1

where $\dot{R}_y$ represents total recruitment in year *y* and $\ddot{R}_{y,x}$ represents the fraction of sex x crab recruiting, and $\dddot{R}_{y,z}$is the size distribution of recruits, which is assumed identical for males and females.

Total recruitment in year *y*, $\dot{R}_y$, is parameterized as

$\dot{R}_y = e^{pLnR_t + \delta R_{t,y}} \quad y \in t$	total recruitment	E.2

where *y* falls within time block *t*, $pLnR_t$ is the ln-scale mean recruitment parameter for *t*, and $\delta R_{t,y}$is an element of a "devs" parameter vector for *t* (constrained such that the elements of the vector sum to zero).

The fraction of crab recruiting as sex *x* in year *y* in time block *t* is parameterized using the logistic model

$\ddot{R}_{y,x} = \begin{cases} \frac{1}{1+e^{pLgtRx_t}} & x = MALE \\ 1-\ddot{R}_{y,MALE} & x = FEMALE \end{cases} \quad y \in t$	sex-specific fraction recruiting	E.3

where $pLgtRx_t$ is the logit-scale parameter determining the sex ratio in time block *t*.

The size distribution for recruits in time block *t*, $\dddot{R}_{t,z}$, is based on a gamma-type distribution and is parameterized as

$\dddot{R}_{t,z} = c^{-1} \cdot \Delta_z^{\frac{\alpha_t}{\beta_t}-1} \cdot e^{-\frac{\Delta_z}{\beta_t}}$	size distribution of recruiting crab	E.4

$c = \sum_z \Delta_z^{\frac{\alpha_t}{\beta_t}-1} \cdot e^{-\frac{\Delta_z}{\beta_t}}$	normalization constant so that $1 = \sum_z \ddot{R}_{t,z}$	E.5
$\Delta_z = z + \delta z/2 - z_{min}$	offset from minimum size bin	E.6
$\alpha_t = e^{pLnRa_t}$	gamma distribution location parameter	E.7
$\beta_t = e^{pLnRb_t}$	gamma distribution shape parameter	E.8

where $pLnRa_t$ and $pLnRb_t$ are the ln-scale location and shape parameters and the constant δz is the size bin spacing.

A final time-blocked parameter, *pLnRCV$_t$*, is associated with the recruitment processes. This parameter represents the ln-scale coefficient of variation (cv) in recruitment variability in time block *t*. These parameters are used in a penalty/prior on the recruitment “devs” in the model likelihood function.

F. Selectivity and retention functions

Selectivity and retention functions in TCSAM02 are specified independently from fisheries and surveys in TCSAM02, but subsequently assigned to them. This allows a single selectivity function to be “shared” among multiple fisheries and/or surveys, and among time blocks and sexes, if so desired.

Currently, the following selectivity/retention functions are available for use in the model:

$S_z = \left\{1 + e^{-\beta \cdot (z - z_{50})}\right\}^{-1}$	standard logistic	F.1
$S_z = \left\{1 + e^{-\ln(19) \cdot \frac{(z - z_{50})}{\Delta z_{95-50}}}\right\}^{-1}$	logistic w/ alternative parameterization	F.2
$S_z = \left\{1 + e^{-\beta \cdot (z - \exp(lnZ_{50}))}\right\}^{-1}$	logistic w/ alternative parameterization	F.3
$S_z = \left\{1 + e^{-\ln(19) \cdot \frac{(z - z_{50})}{\exp(ln\Delta z_{95-50})}}\right\}^{-1}$	logistic w/ alternative parameterization	F.4
$S_z = \frac{1}{1 + e^{-\beta_a \cdot (z - z_{a50})}} \cdot \frac{1}{1 + e^{\beta_d \cdot (z - z_{d50})}}$	double logistic	F.5
$S_z = \frac{1}{1 + e^{-\ln(19) \cdot \frac{(z - z_{a50})}{\Delta z_{a(95-50)}}}} \cdot \frac{1}{1 + e^{\ln(19) \cdot \frac{(z - z_{d50})}{\Delta z_{d(95-50)}}}}$	double logistic with alt. parameterization	F.6

A double normal selectivity function (requiring 6 parameters to specify) has also been implemented as an alternative to the double logistic functions. In the above functions, all symbols (e.g., β, Δz_{95-50}) represent parameter values, except “z” which represents crab size.

Selectivity parameters are defined independently of the functions themselves, and subsequently assigned. It is thus possible to “share” parameters across multiple functions. The “parameters” used in selectivity functions are further divided into mean parameters across a time block and annual deviations within the time block. Thus, for example, z_{50} in eq. F1 is actually expressed as $z_{50,y} = \bar{z}_{50} + \delta z_{50,y}$ in terms of model parameters *pS1* and *pDevsS1$_y$*, where $\bar{z}_{50} = pS1$ is the mean size-at-50%-selected over the time period and $\delta z_{50,y} = pDevsS1_y$ is the annual deviation. To accommodate the 6-parameter double normal equation, six "mean" parameter sets (*pS1*, *pS2*,…, *pS6*) and six associated sets of "devs" parameter vectors (*pDevsS1*, *pDevsS2*,…, *pDevsS6*) are defined in the model to specify the parameterization of individual selectivity/retention functions.

Finally, three different options to normalize individual selectivity curves are provided: 1) no normalization, 2) specifying a fully-selected size, and 3) re-scaling such that the maximum value of the re-scaled function is 1. A normalization option must be specified in the model input files for each defined selectivity/retention curve.

G. Fisheries

Unlike TCSAM2013, which explicitly models 4 fisheries that catch Tanner crab (one as a directed fishery, three as bycatch), there is no constraint in TCSAM02 on the number of fisheries that can be incorporated in the model. The only requirement is that each model fishery defined in the input files has a corresponding data component from which parameters can be estimated.

TCSAM02 uses the Gmacs approach to modeling fishing mortality (also implemented in TCSAM2013). The total (retained + discards) fishing mortality rate, $F_{f,y,x,m,s,z}$, in fishery *f* during year *y* on crab in state *x*, *m*, *s*, and *z* (i.e., sex, maturity state, shell condition, and size) is related to the associated fishery capture rate $\phi_{f,y,x,m,s,z}$ by

$F_{f,y,x,m,s,z} = \left[h_{f,t} \cdot \left(1-\rho_{f,y,x,m,s,z}\right) + \rho_{f,y,x,m,s,z}\right] \cdot \phi_{f,y,x,m,s,z}$	fishing mortality rate	G.1

where $h_{f,t}$ is the handling (discard) mortality for fishery *f* in time block t (which includes year *y*) and $\rho_{f,y,x,m,s,z}$ is the fraction of crabs in state *x*, *m*, *s*, *z* that were caught and retained (i.e., the retention function). The retention function is identically 0 for females in a directed fishery and for both sexes in a bycatch fishery. For a directed fishery, the retention function for males is selected from one of the selectivity/retention functions discussed in the previous section.

If $n_{y,x,m,s,z}$ is the number of crab classified as *x*, *m*, *s*, *z* in year *y* just prior to the prosecution of the fisheries, then

$c_{f,y,x,m,s,z} = \frac{\phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1-e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$	number of crab captured	G.2

is the number of crab classified in that state that were *captured* by fishery *f*, where $F^T_{y,x,m,s,z} = \sum_f F_{f,y,x,m,s,z}$ represents the total (across all fisheries) fishing mortality on those crab. The number of crab retained in fishery *f* classified as *x*, *m*, *s*, *z* in year *y* is given by

$r_{f,y,x,m,s,z} = \frac{\rho_{f,y,x,m,s,z} \cdot \phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1-e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$	number of retained crab	G.3

while the number of discarded crab, $d_{f,y,x,m,s,z}$, is given by

$d_{f,y,x,m,s,z} = \frac{\left(1-\rho_{f,y,x,m,s,z}\right) \cdot \phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1-e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$	number of discarded crab	G.4

and the discard mortality, $dm_{f,y,x,m,s,z}$, is

$dm_{f,y,x,m,s,z} = \frac{h_{f,y} \cdot \left(1-\rho_{f,y,x,m,s,z}\right) \cdot \phi_{f,y,x,m,s,z}}{F^{T}_{y,x,m,s,z}} \cdot \left[1-e^{-F^{T}_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$	discard mortality (numbers)	G.5

The biomass associated with the above components is obtained by multiplying each by $w_{x,m,z}$, the associated individual crab weight (estimated outside the model).

The capture rate $\phi_{f,y,x,m,s,z}$ (*not* the fishing mortality rate $F_{f,y,x,m,s,z}$) is modeled as a function separable into separate year and size components such that

$\phi_{f,y,x,m,s,z} = \phi_{f,y,x,m,s} \cdot S_{f,y,x,m,s,z}$	fishing capture rate	G.6

where $\phi_{f,y,x,m,s}$ is the fully-selected capture rate in year *y* and $S_{f,y,x,m,s,z}$ is the size-specific selectivity.

The fully-selected capture rate $\phi_{f,y,x,m,s}$ for *y* in time block *t* is parameterized in the following manner:

$\phi_{f,y,x,m,s} = \exp\left(\overline{lnC}_{f,t,x,m} + pDevsC_{f,t,y}\right)$	G.7

where the $pDevsC_{f,t,y}$ are elements for year *y* of time block *t* of model parameter "devs" vectors representing annual variations from the ln-scale mean fully-selected capture rate $\overline{lnC}_{f,t,x,m}$. The latter is expressed in terms of model parameters as

$\overline{lnC}_{f,t,x,m} = pLnC_{f} + pLnDCT_{f,t} + \delta_{m,IMM} \cdot pLnDCM_{f,t} + \delta_{x,FEM} \cdot pLnDCX_{f,t} + \delta_{x,FEM} \cdot \delta_{m,IMM} \cdot pLnDCXM_{f,t}$	G.8

where $pLnC_{f}$ is the baseline ln-scale capture rate (for mature males), $pLnDCT_{f,t}$ is an additive modifier for time block *t*, $pLnDCM_{f,t}$ is an additive modifier for immature crab, $pLnDCX_{f,t}$ is the additive modifier for females, and $pLnDCXM_{f,t}$ is the additive modifier for immature females.

H. Surveys

If $n_{y,x,m,s,z}$ is the number of crab classified as *x*, *m*, *s*, *z* in year *y* just prior to the prosecution of a survey, then the abundance, $a_{v,y,x,m,s,z}$, and biomass, $b_{v,y,x,m,s,z}$, for crab classified in that state by survey *v* is given by

$a_{v,y,x,m,s,z} = q_{v,y,x,m,s,z} \cdot n_{y,x,m,s,z}$	survey abundance	H.1
$b_{v,y,x,m,s,z} = w_{x,m,z} \cdot q_{v,y,x,m,s,z} \cdot n_{y,x,m,s,z}$	survey biomass	H.2

where $q_{v,y,x,m,s,z}$ is the size-specific survey catchability on this component of the population and $w_{x,m,z}$ is the associated individual crab weight (estimated outside the model).

The survey catchability $q_{v,y,x,m,s,z}$ is decomposed in the usual fashion into separate time block and size components such that, for *y* in time block *t*:

$q_{v,y,x,m,s,z} = q_{v,t,x,m,s} \cdot S_{v,t,x,m,s,z}$	survey catchability	H.3

where $q_{v,t,x,m,s}$ is the fully-selected catchability in time block *t* and $S_{v,t,x,m,s,z}$ is the size-specific survey selectivity.

The fully-selected catchability $q_{v,t,x,m,s}$ is parameterized in a fashion similar to that for fully-selected fishery capture rates (except that annual "devs" are not included) in the following manner:

$q_{v,t,x,m,s} = \exp\big(pLnQ_v + pLnDQT_{v,t} + \delta_{m,IMM} \cdot pLnDQM_{v,t} + \delta_{x,FEM} \cdot pLnDQX_{v,t} + \delta_{x,FEM} \cdot \delta_{m,IMM} \cdot pLnDQXM_{v,t}\big)$	H.4

where $pLnQ_v$ is the baseline ln-scale capture rate (for mature males), $pLnDQT_{v,t}$ is an additive modifier for time block *t*, $pLnDQM_{v,t}$ is an additive modifier for immature crab, $pLnDQX_{v,t}$ is an additive ln-scale modifier for females, and $pLnDQXM_{v,t}$ is an additive modifier for immature females.

I. Model fitting: objective function equations

The TCSAM02 model is fit by minimizing an objective function, $\mathscr{o}$, with additive components consisting of: 1) negative log-likelihood functions based on specified prior probability distributions associated with user-specified model parameters, and 2) several negative log-likelihood functions based on input data components, of the form:

$\mathscr{o} = -2\sum_p \lambda_p \cdot \ln(\wp_p) - 2\sum_l \lambda_l \cdot \ln(\mathcal{L}_l)$	model objective function	I.1

where $\wp_p$ represents the *p*th prior probability function, $\mathcal{L}_l$ represents the *l*th likelihood function, and the λ's represent user-adjustable weights for each component.

Prior Probability Functions

Prior probability functions can be associated with each model parameter or parameter vector by the user in the model input files (see Section L below for examples on specifying priors).

Likelihood Functions

The likelihood components included in the model's objective function are based on normalized size frequencies and time series of abundance or biomass from fishery or survey data. Survey data optionally consists of abundance and/or biomass time series for males, females, and/or all crab (with associated survey cv's), as well as size frequencies by sex, maturity state, and shell condition. Fishery data consists of similar data types for optional retained, discard, and total catch components.

Size frequency components

Likelihood components involving size frequencies are based on multinomial sampling:

$\ln(\mathcal{L}) = \sum_y n_{y,c} \cdot \sum_z \{p^{obs}_{y,c,z} \cdot \ln(p^{mod}_{y,c,z} + \delta) - p^{obs}_{y,c,z} \cdot \ln(p^{obs}_{y,c,z} + \delta)\}$	multinomial log-likelihood	I.2

where the *y*'s are years for which data exists, "*c*" indicates the population component classifiers (i.e., sex, maturity state, shell condition) the size frequency refers to, $n_{y,c}$ is the classifier-specific effective sample size for year y, $p^{obs}_{y,c,z}$ is the observed size composition in size bin *z* (i.e., the size frequency normalized to sum to 1 across size bins for each year), $p^{mod}_{y,c,z}$ is the corresponding model-estimated size composition, and δ is a small constant. The manner in which the observed and estimated size frequencies for each data component are aggregated (e.g., over shell condition) prior to normalization is specified by the user in the model input files. Data can be entered in input files at less-aggregated levels of than will be used in the model; it will be aggregated in the model to the requested level before fitting occurs.

Aggregated abundance/biomass components

Likelihood components involving aggregated (over size, at least) abundance and or biomass time series can be computed using one of three potential likelihood functions: the normal, the lognormal, and the "norm2". The likelihood function used for each data component is user-specified in the model input files.

The ln-scale normal likelihood function is

$\ln(\mathcal{L}^{N})_c \;=-\frac{1}{2}\sum_y \left\{\frac{\left[a_{y,c}^{obs}-a_{y,c}^{mod}\right]^2}{\sigma_{y,c}^2}\right\}$	normal log-likelihood	I.3

where $a_{y,c}^{obs}$ is the observed abundance/biomass value in year y for aggregation level c, $a_{y,c}^{mod}$ is the associated model estimate, and $\sigma_{y,c}^2$ is the variance associated with the observation.

The ln-scale lognormal likelihood function is

$\ln(\mathcal{L}^{LN})_c \;=-\frac{1}{2}\sum_y \left\{\frac{\left[ln\left(a_{y,c}^{obs}+\delta\right)-ln\left(a_{y,c}^{mod}+\delta\right)\right]^2}{\sigma_{y,c}^2}\right\}$	lognormal log-likelihood	I.4

where $a_{y,c}^{obs}$ is the observed abundance/biomass value in year y for aggregation level c, $a_{y,c}^{mod}$ is the associated model estimate, and $\sigma_{y,c}^2$ is the ln-scale variance associated with the observation.

For consistency with TCSAM2013, a third type, the "norm2", may also be specified

$\ln(\mathcal{L}^{N2})_x \;=-\frac{1}{2}\sum_y \left[a_{y,x}^{obs}-a_{y,x}^{mod}\right]^2$	"norm2" log-likelihood	I.5

This is equivalent to specifying a normal log-likelihood with $\sigma_{y,x}^2 \equiv 1.0$. This is the standard likelihood function applied tin TCSAM2013 to fishery catch time series.

Aggregation fitting levels

A number of different ways to aggregate input data and model estimates prior to fitting likelihood functions have been implemented in TCSAM02. These include:

Abundance/Biomass	Size Conpositions	
by	by	extended by
total	total	x
x		x, m
x, mature only	x	--
x, m		m
x, s		s
x, m, s	x, m	--
		s
	x, s	
	x, m, s	

where x, m, s refer to sex, maturity state and shell condition and missing levels are aggregated over. For size compositions that are "extended by" x, m, s, or $\{x, m\}$, this involves appending the size compositions corresponding to each combination of "extended by" factor levels, renormalizing the extended composition to sum to 1, and then fitting the extended composition using a multinomial likelihood.

K. Devs vectors

For TCSAM02 to accommodate arbitrary numbers of fisheries and time blocks, it is necessary to be able to define arbitrary numbers of devs vectors. This is currently not possible in ADMB, so TCSAM02 uses an alternative implementation of "devs" vectors from that implemented in ADMB. In TCSAM02, an *n*-element "devs" vector is implemented using an (*n*-1)-element bounded parameter vector, with the final element of the "devs" vector defined as $-\sum_{n-1} v_i$, where v_i is the ith value of the parameter (or devs) vector, so that the sum over all elements of the devs vector is identically 0. Penalties are placed on the the final element of the devs vector to ensure it is bounded in the same manner as the parameter vector.

L. Parameter specification for model processes

Parameter specification in TCSAM02 occurs entirely within the model input files and is extremely flexible in terms of setting initial values, defining upper and lower limits on estimated parameter values, specifying prior distributions and hyper-prior parameters for use in the model likelihood function, and defining time blocks across which parameters related to a given model process are combined. Parameters are organized in the input files to the model according to the model process (e.g., recruitment, fishing mortality, etc.) the parameter group affects.

Two types of parameters are currently incorporated in TCSAM02, "number_vector"s and "vector_vector"s. Parameters of the first kind, number_vectors (i.e., a vector of parameter numbers), are used to define and estimate different values (numbers) associated with the same parameter in different time blocks. Different characteristics (e.g., upper and lower limits, initial value, estimation phase) can be associated with each value of a number_vector-type parameter. Parameters of the second kind, vector_vectors (i.e., a vector of parameter vectors), are used to define and estimate different vectors associated with a parameter vector (e.g., a "devs" vector) across different time blocks. Different characteristics (e.g., upper and lower limits, initial value, estimation phase) can be associated with each vector of a vector_vector-type parameter.

Text Box 1 illustrates an example specification for the recruitment process involving the model parameters *pLnR*, *pLnRCV*, *pLgtRX*, *pLnRa*, *pLnRb* (all number_vectors) and the "devs" parameter vector *pDevsLnR* (implemented as a vector_vector). Time blocks are defined for the recruitment process, not for individual parameters. The latter can be used across multiple time blocks. Time blocks are defined in the PARAMETER_COMBINATIONS section (lines 2-6 in the example), and individual parameters are assigned using indices. In the example, two parameter combinations are defined, specifying combinations of the recruitment-associated parameters to two time blocks ("[-1:1974]", i.e. model start year to 1974, and "[1975:-1]", i.e. 1975 to model end year). Recruitment in the first time block is a function of the first parameter definition (id=1) for each of the recruitment parameters, while it is a function of the second parameter definitions (id=2) for *pLnR* and *pDevsLnR* and the first definition for the remaining parameters in the second time block. In the example, the two time blocks are continuous, but it is also possible to define discontinuous blocks (e.g., "[1965:1971; 1980:1990]"). Default index values (-1) correspond to the minimum or maximum index value used for the index type in the model, depending on position in the block definition. For year indices, it is also possible to use "-2" to refer to the current assessment year (-1 refers to the current fishery year).

For each number_vector-type parameter (e.g., *pLnR*, starting at line 8), the user specifies (line 9) the number of different values that will be assigned in the PARAMETER_COMBINATIONS section. For each number, the user specifies (e.g. line 11) the "lower" and "upper" bounds on the value, the default initial value (“init_val”), the “phase” in the model convergence scheme at which the value is first estimated, the likelihood multiplier (“prior_wgt”) on the prior associated with the value, the name of the prior to use (“prior_type”; e.g. ‘normal’ or ‘none’), the hyper-parameters associated with the prior (“prior_params”; e.g., mean and standard deviation for a ‘normal’ prior) and any additional constants required for the function used as the prior. In addition, options (“jitter?”, “resample?”) for setting the initial value can be turned on or off. If both are “OFF”, then the default (“init_val”) is used. If jittering is “ON”, the initial value will be a random draw between the lower and upper bounds set for the number. If resampling is turned “ON”, the initial value will be a random draw based on the prior distribution.

A similar logic applies to parameter vector_vectors (e.g., *pDevsLnR*), except that the user must also specify the type of indexing (“idx.type”; e.g., line 32) used for each vector (one of the model index types: “YEAR”, “SEX”, “MATURITY_STATE”, “SHELL_CONDITION”, “SIZE”, “FISHERY” or “SURVEY”) and define the range for the indices as a “block”. The indices the block defines need not be continuous.

Text Boxes

```
 1| recruitment #parameter group name
 2| PARAMETER_COMBINATIONS #required keyword
 3| 2  #number of rows defining parameter combinations
 4| #id  YEAR_BLOCK  pLnR   pLnRCV  pLgtRX   pLnRa   pLnRb  pDevsLnR
 5|   1  [-1:1974]     1      1       1        1       1        1    #model spin-up period
 6|   2  [1975:-1]     2      1       1        1       1        2    #data-informed model
period
 7|. PARAMETERS #required keyword
 8| pLnR #parameter name; ln-scale mean recruitment parameter
 9| 2  #number of parameters
10| #id lower upper jitter? init_val  phase resample? prior_wgt prior_type prior_params
prior_consts
11|  1    0    20     OFF       8       1     OFF        1       normal      10 3
#spin-up period
12|  2    0    20     OFF      11.4     1     OFF        1       normal      10 3
#model period
13| pLnRCV #parameter name; ln-scale parameter for cv of recruitment
14| 1  #number of parameters
15| #id lower  upper jitter? init_val    phase   resample?   prior_wgt   prior_type
prior_params  prior_consts
16|  1   -2.0   2.0   OFF  -0.43275213    -1       OFF           1        none    #full model
period (init_val equiv. to var=0.5)
17| pLgtRX #parameter name; logit-scale parameter for male sex ratio
18| 1  #number of parameters
19| #id lower  upper jitter? init_val  phase   resample?  prior_wgt   prior_type  prior_params
prior_consts
20|  1   -1      1    OFF       0       -1       OFF          1         normal      0  0.2
#full model period
21| pLnRa #ln-scale gamma distribution location parameter for pr(size-at-recruitment)
22| 1  #number of parameters
23| #id  lower  upper jitter? init_val    phase   resample?   prior_wgt   prior_type
prior_params    prior_consts
24|  1     1     4     ON    2.442347     -1      OFF           1        normal       2.5 1
#init_val = ln(11.50)
```

Text Box 1. Example parameter specification for recruitment in TCSAM02. Input values are in black text, comments are in green. Line numbers (text in blue) are shown for reference purposes.

Appendix B: Equilibrium population size distribution for Tanner crab

This appendix documents the equations I developed to describe the single-sex population equilibrium size distribution for Tanner crab, assuming that recruitment is independent of stock size (e.g., as for a Tier 3 stock). These equations form the basis in TCSAM02 for calculating the Tier 3 OFL. It should be noted that these equations are also applicable to other crab with a terminal molt categorized as immature/mature and new shell/old shell, such as snow crab.

Population states

The Tanner crab population on July 1 can be characterized by abundance-at-size in four population states:

in– immature new shell crab
io– immature old shell crab
mn – mature new shell crab
mo – mature old shell crab

where each of these states represents a vector of abundance-at-size (i.e., a vector subscripted by size).

Population processes

The following processes then describe the dynamics of the population over a year:

S_1 – survival from start of year to time of molting/growth of immature crab, possibly including fishing mortality (a diagonal matrix)
S_2 – survival after time of molting/growth of immature crab to end of year, possibly including fishing mortality (a diagonal matrix)
Φ – probability of an immature crab molting (pr(molt|*z*), where *z* is pre-molt size; a diagonal matrix) (pr(molt|*z*) is assumed to be 1 in TCSAM02).
Θ – probability that a molt was terminal (pr(molt to maturity|*z*, molt), where *z* is post-molt size; a diagonal matrix)
T – size transition matrix (a non-diagonal matrix)
1 – identity matrix
R –number of recruits by size (a vector)

The matrices above are doubly –subscripted, and *R* is singly-subscripted, by size. Additionally, the matrices above (except for the identity matrix) can also be subscripted by population state (*in*, *io*, *mn*, *mo*) for generality. For example, survival of immature crab may differ between those that molted and those that skipped.

Population dynamics

The following equations then describe the development of the population from the beginning of one year to the beginning of the next:

$$in^{+} = R + S_{2in} \cdot \{(1 - \Theta_{in}) \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + T_{io} \cdot (1 - \Theta_{io}) \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \quad (1)$$
$$io^{+} = S_{2io} \cdot \{(1 - \Phi_{in}) \cdot S_{1in} \cdot in + (1 - \Phi_{io}) \cdot S_{1io} \cdot io\} \quad (2)$$
$$mn^{+} = S_{2mn} \cdot \{\Theta_{in} \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + \Theta_{io} \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \quad (3)$$
$$mo^{+} = S_{2mo} \cdot \{S_{1mn} \cdot mn + S_{1mo} \cdot mo\} \quad (4)$$

where "+" indicates year+1 and all recruits (*R*) are assumed to be new shell.

Equilibrium equations

The equations reflecting equilibrium conditions (i.e., $in^{+} = in$, etc.) are simply:

$$in = R + S_{2in} \cdot \{(1 - \Theta_{in}) \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + (1 - \Theta_{io}) \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \quad (5)$$

$$io = S_{2io} \cdot \{(1 - \Phi_{in}) \cdot S_{1in} \cdot in + (1 - \Phi_{io}) \cdot S_{1io} \cdot io\} \tag{6}$$
$$mn = S_{2mn} \cdot \{\Theta_{in} \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + \Theta_{io} \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \tag{7}$$
$$mo = S_{2mo} \cdot \{S_{1mn} \cdot mn + S_{1mo} \cdot mo\} \tag{8}$$

where *R* above is now the equilibrium (longterm average) number of recruits-at-size vector.

Equilibrium solution
The equilibrium solution can be obtained by rewriting the above equilibrium equations as:

$$in = R + A \cdot in + B \cdot io \tag{9}$$
$$io = C \cdot in + D \cdot io \tag{10}$$
$$mn = E \cdot in + F \cdot io \tag{11}$$
$$mo = G \cdot mn + H \cdot mo \tag{12}$$

where *A, B, C, D, E, F, G*, and *H* are square matrices. Solving for *io* in terms of *in* in eq. 10, one obtains

$$io = \{1 - D\}^{-1} \cdot C \cdot in \tag{13}$$

Plugging eq. 13 into 9 and solving for *in* yields

$$in = \{1 - A - B \cdot [1 - D]^{-1} \cdot C\}^{-1} \cdot R \tag{14}$$

Equations 13 for *io* and 14 for *in* can simply be plugged into eq. 11 to yield *mn* while eq. 12 can then be solved for *mo*, yielding

$$mo = \{1 - H\}^{-1} \cdot G \cdot mn \tag{15}$$

where (for completeness):

$$A = S_{2in} \cdot (1 - \Theta_{in}) \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \tag{16}$$
$$B = S_{2in} \cdot (1 - \Theta_{io}) \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \tag{17}$$
$$C = S_{2io} \cdot (1 - \Phi_{in}) \cdot S_{1in} \tag{18}$$
$$D = S_{2io} \cdot (1 - \Phi_{io}) \cdot S_{1io} \tag{19}$$
$$E = S_{2mn} \cdot \Theta_{in} \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \tag{20}$$
$$F = S_{2mn} \cdot \Theta_{io} \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \tag{21}$$
$$G = S_{2mo} \cdot S_{1mn} \tag{22}$$
$$H = S_{2mo} \cdot S_{1mo} \tag{23}$$

Note that Θ, the size-specific conditional probability of a molt being the terminal molt-to-maturity, is defined above on the basis of post-molt, not pre-molt, size. This implies that whether or not a molt is terminal depends on the size a crab grows into, not the size it at which it molted. An alternative approach would be to assume that the conditional probability of terminal molt is determined by pre-molt size. This would result in an alternative set of equations, but these can be easily obtained from the ones above by simply reversing the order of the terms involving *T* and Θ (e.g., the term $(1 - \Theta_{in}) \cdot T_{in}$ becomes $T_{in} \cdot (1 - \Theta_{in})$).

Appendix C: 2016 Assessment Model Description (TCSAM2013)

Introduction

The 2016 Tanner crab stock assessment model (TCSAM2013) is an integrated assessment model developed in C++ using AD Model Builder (Fournier et al., 2012) libraries that is fit to multiple data sources. The 2016 assessment model code is publicly available on GitHub (on branch "2016AssessmentModel"). While a number of options have been added to the code in recent years, TCSAM2013 suffers "structural" difficulties with a number of hard-wired time periods and other constraints that cannot really be addressed without re-writing the code. The model described herein is the version used in the Sept. 2016 assessment (Stockhausen, 2016).

Model parameters in TCSAM2013 are estimated using a maximum likelihood approach, with Bayesian-like priors on some parameters and penalties for smoothness and regularity on others. Data components entering the likelihood include fits to survey biomass, survey size compositions, retained catch, retained catch size compositions, discard mortality in the bycatch fisheries, and discard size compositions in the bycatch fisheries. Population abundance at the start of year *y* in the model, $n_{y,x,m,s,z}$, is characterized by sex *x* (male, female), maturity state *m* (immature, mature), shell condition *s* (new shell, old shell), and size *z* (carapace width, CW). Changes in abundance due to natural mortality, molting and growth, maturation, fishing mortality and recruitment are tracked on an annual basis. Because the principal crab fisheries occur during the winter, the model year runs from July 1 to June 30 of the following calendar year.

A. Calculation sequence

Step A1: Survival prior to fisheries

Natural mortality is applied to the population from the start of the model year (July 1) until just prior to prosecution of the pulse fisheries for year *y* at δt_y^F. The numbers surviving at δt_y^F in year *y* are given by:

$$n_{y,x,m,s,z}^1 = e^{-M_{y,x,m,s,z} \cdot \delta t_y^F} \cdot n_{y,x,m,s,z} \tag{A1}$$

where *M* represents the annual rate of natural mortality in year *y* on crab classified as *x*, *m*, *s*, *z*.

Step A2: Prosecution of the fisheries

The directed fishery and bycatch fisheries are modeled as pulse fisheries occurring at δt_y^F in year *y*. The numbers that remain after the fisheries are prosecuted are given by:

$$n_{y,x,m,s,z}^2 = \left(1 - e^{-F_{y,x,m,s,z}^T}\right) \cdot n_{y,x,m,s,z}^1 \tag{A2}$$

where F^T represents total (across all fisheries) annual fishing mortality in year *y* on crab classified as *x*, *m*, *x*, *z*.

Step A3: Survival after fisheries to time of molting/mating

Natural mortality is again applied to the population from just after the fisheries to the time at which molting/mating occurs for year *y* at δt_y^m. The numbers surviving at δt_y^m in year *y* are then given by:

$$n_{y,x,m,s,z}^3 = e^{-M_{y,x,m,s,z} \cdot (\delta t_y^m - \delta t_y^F)} \cdot n_{y,x,m,s,z}^2 \tag{A3}$$

where, as above, *M* represents the annual rate of natural mortality in year *y* on crab classified as *x*, *m*, *s*, *z*. In the 2012 and 2013 assessments, molting and mating were taken to occur on Feb. 15 each year ($\delta t_y^m = 0.625$), and the pulse fisheries were taken to occur just prior to this ($\delta t_y^F = 0.625$, also), so the term in the exponent in eq. A3 was 0 for all years.

Step A4: Molting, growth, and maturation
The changes in population structure due to molting, growth and maturation of immature (new shell) crab, as well as the change in shell condition for new shell mature crab due to aging, are given by:

$n^4_{y,x,MAT,NS,z} = \phi_{y,x,z} \cdot \sum_{z'} \Theta_{y,x,z,z'} \cdot n^3_{y,x,IMM,NS,z'}$	A4a
$n^4_{y,x,IMM,NS,z} = (1 - \phi_{y,x,z'}) \cdot \sum_{z'} \Theta_{y,x,z,z'} \cdot n^3_{y,x,IMM,NS,z'}$	A4b
$n^4_{y,x,MAT,OS,z} = n^3_{y,x,MAT,OS,z} + n^3_{y,x,MAT,NS,z}$	A4c

where $\phi_{y,x,z}$ is the probability that an immature (new shell) crab of sex *x* and size *z* will undergo its terminal molt to maturity and $\Theta_{y,x,z,z'}$ is the growth transition matrix from size *z'* to *z* for that crab. Additionally, crabs that underwent their terminal molt to maturity the previous year are assumed to change shell condition from new shell (*NS*) to old shell (*OS*; A.4c). Note that the numbers of immature, old shell crab are identically zero in the current model because immature crab are assumed to molt each year until they undergo the terminal molt to maturity; consequently, an equation for *m=IMM*, *s=OS* above is unnecessary.

Step A5: Survival to end of year, recruitment, and update to start of next year
Finally, population abundance at the start of year *y*+1 due to recruitment of immature new shell crab at the beginning of the new year *y+1* ($r_{y,x,z}$) and natural mortality on crab from the time of molting in year *y* until the end of the model year (June 30) are given by:

$r_{y,x,z} = R_y \cdot \rho_{y,x} \cdot \eta_z$	A5a
$n_{y+1,x,m,s,z} = \begin{cases} e^{-M_{y,x,IMM,NS,z} \cdot (1-\delta t^m_y)} \cdot n^4_{y,x,IMM,NS,z} + r_{y+1,x,z} & m = IMM, s = NS \\ e^{-M_{y,x,m,s,z} \cdot (1-\delta t^m_y)} \cdot n^4_{y,x,m,s,z} & otherwise \end{cases}$	A5b

B. Model processes: natural mortality

Natural mortality rates in TCSAM2013 vary across 3 year blocks (model start-1979, 1980-1984,1985-model end) within which they are sex- and maturity state-specific but do not depend on shell condition or size. They are parameterized in the following manner:

$M_{y,x,m,s,z} = \begin{cases} M^{base}_{x,m,s} \cdot \delta M_{x,m} & otherwise \\ M^{base}_{x,m,s} \cdot \delta M_{x,m} \cdot \delta M^T_{x,m} & 1980 \le y \le 1984 \end{cases}$	natural mortality rates	B1 B2

where *y* is year, *x* is sex, *m* is maturity state and *s* is shell condition, the $M^{base}_{x,m,s}$ are user constants (not estimated), and the $\delta M_{x,m}$ and $\delta M^T_{x,m}$ are parameters (although not all are estimated).

Priors are imposed on the $\delta M_{x,m}$ parameters in the likelihood using:

$\Pr(\delta M_{x,m}) =\cdot e^{-\frac{(\delta M_{x,m}-\mu_{x,m})}{2\cdot\sigma^2_{x,m}}}$	Prior probability function for $\delta M_{x,m}$	B3

The μ's and σ^2 , along with bounds, initial values and estimation phases used for the parameters, as well as the values for the constants, used in the 2016 assessment model are:

parameters/constants	$\mu_{x,m}$	$\sigma^2_{x,m}$	lower bound	upper bound	initial value	phase	code name
$M^{base}_{x,m,s}$	--	--	--	--	0.23	NA	`baseM_msx`
$\delta M_{x,IMM}$	1.0	0.05	0.2	2.0	1.0	7	`pMfac_Imm`
$\delta M_{MALE,MAT}$	1.0	0.05	0.1	1.9	1.0	7	`pMfac_MatM`
$\delta M_{FEMALE,MAT}$	1.0	0.05	0.1	1.9	1.0	7	`pMfac_MatF`
$\delta M^{T}_{x,IMM}$	--	--	--	--	1.0	NA	`--`
$\delta M^{T}_{MALE,MAT}$			0.1	10.0	1.0	7	`pMfac_Big(MALE)`
$\delta M^{T}_{FEMALE,MAT}$			0.1	10.0	1.0	7	`pMfac_Big (FEMALE)`

where constants have phase = NA and estimated parameters have phase > 0. When no corresponding variable exists in the model (i.e., the code name is NA), the effective value of the parameter/constant is given.

C. Model processes: growth

Growth of immature crab in TCSAM2013 is based on sex-specific transition matrices that specify the probability that crab in pre-molt size bin *z* grow to post-molt size bin z'. The sex-specific growth matrix $\Theta_{x,z,z'}$ is related to the sex-specific parameters a_x, b_x, and β_x by the following equations:

$\Theta_{x,z,z'} = c_{x,z}\cdot{\Delta_{z,z'}}^{\alpha_{x,z}-1}\cdot e^{-\frac{\Delta_{z,z'}}{\beta_x}}$	Sex-specific (*x*) transition matrix for growth from pre-molt *z* to post-molt z', with $z' \geq z$	C1
$c_{x,z} = \left[\sum_{z'}{\Delta_{z,z'}}^{\alpha_{x,z}-1}\cdot e^{-\frac{\Delta_{z,z'}}{\beta_x}}\right]^{-1}$	Normalization constant so $1 = \sum_{z'}\Theta_{x,z,z'}$	C2
$\Delta_{z,z'} = z' - z$	Actual growth increment	C3

$\alpha_{x,z} = [\bar{z}_{x,z} - z]/\beta_x$	Mean molt increment, scaled by β_x	C4
$\bar{z}_{x,z} = e^{a_x} \cdot z^{b_x}$	Mean size after molt, given pre-molt size *z*	C5

$\Theta_{x,z,z'}$ is used to update the numbers-at-size for immature crab following molting using:

$n_{x,z'}^{+} = \sum_{z} n_{x,z} \cdot \Theta_{x,z,z'}$		C6

where *z* is the pre-molt size and z' is the post-molt size.

Sex-specific priors are imposed on the estimated values $\hat{a}_x$ and $\hat{b}_x$ for the a_x and b_x parameters using:

$\Pr(\hat{a}_x) =\cdot e^{-\frac{(\hat{a}_x-\mu_{a_x})}{2\cdot\sigma_{a_x}^2}}$	Prior probability function for a's	C7
$\Pr(\hat{b}_x) =\cdot e^{-\frac{(\hat{b}_x-\mu_{b_x})}{2\cdot\sigma_{b_x}^2}}$	Prior probability function for b's	C8

The μ's and σ^2 , along with the bounds, initial values and estimation phases used for the parameters are:

parameter	sex (*x*)	μ_x	σ_x^2	lower bound	upper bound	initial value	phase	code name
a_x	female	0.56560241	0.100	0.4	0.7	0.55	8	`pGrAF1`
	male	0.43794100	0.025	0.3	0.6	0.45	8	`pGrAM1`
b_x	female	0.9132661	0.025	0.6	1.2	0.90	8	`pGrBF1`
	male	0.9487000	0.100	0.7	1.2	0.95	8	`pGrBM1`
β_x	both	NA	NA	0.75000	0.75001	0.750005	-2	`pGrBeta_x`

Note that the β_x are treated as constants because the associated estimation phases are negative.

D. Model processes: maturity (terminal molt)

Maturation of immature crab in TCSAM2013 is based on sex- and size-specific probabilities of maturation, $\phi_{x,z}$, where size *z* is post-molt size. After molting and growth, the numbers of crab remaining immature, $n_{x,IMM,NS,z}^{+}$, and those maturing, $n_{x,MAT,NS,z}^{+}$, at post-molt size *z* are given by:

$n^{+}_{x,IMM,NS,z} = (1-\phi_{x,z}) \cdot n_{x,IMM,NS,z}$ $n^{+}_{x,MAT,NS,z} = \phi_{x,z} \cdot n_{x,IMM,NS,z}$		D1a D1b

where $n_{x,IMM,NS,z}$ is the number of immature, new shell crab of sex *x* at post-molt size *z*.

Two options are now available to parameterize $\phi_{x,z}$ relative to model parameters $p^{mat}_{x,z}$. In the old parameterization, the $p^{mat}_{x,z}$ are log-scale parameters related to the $\phi_{x,z}$ by:

$\phi_{FEMALE,z} = \begin{cases} e^{p^{mat}_{FEMALE,z}} & z \le 100\ mm\ CW \\ 1 & z > 100\ mm\ CW \end{cases}$	female probabilities of maturing at pre-molt size *z*	D2a
$\phi_{MALE,z} = e^{p^{mat}_{MALE,z}}$	male probabilities of maturing at pre-molt size *z*	D2b

whereas, for the option used in the 2016 assessment model, the $p^{mat}_{x,z}$ are logit-scale parameters related to the $\phi_{x,z}$ by:

$\phi_{FEMALE,z} = \begin{cases} 1/(1+e^{p^{mat}_{FEMALE,z}}) & z \le 100\ mm\ CW \\ 1 & z > 100\ mm\ CW \end{cases}$	female probabilities of maturing at pre-molt size *z*	D3c
$\phi_{MALE,z} = 1/(1+e^{p^{mat}_{MALE,z}})$	male probabilities of maturing at pre-molt size *z*	D3d

For both options, each $p^{mat}_{FEMALE,z}$ is an estimated parameter (16 parameters), as is each $p^{mat}_{MALE,z}$ (32 parameters).

Second difference penalties, $P2^{mat}_{x}$, on the parameter estimates are applied in the model's objective function to promote relatively smooth changes with size. Penalties on negative first differences, $P1^{mat}_{x}$, are applied to avoid a decline in the probability of molting-to-maturity at larger sizes. These penalties are of the form

$P1^{m}_{x} = posfun(\nabla p^{mat}_{x,z})$	1st-difference penalties for decreasing probabilities with size	D4a
$P2^{m}_{x} = \sum_{z} [\nabla(\nabla p^{mat}_{x,z})]^2$	2nd-difference (smoothness) likelihood penalty	D4b
$\nabla p^{mat}_{x,z} = p^{mat}_{x,z} - p^{mat}_{x,z-1}$	first differences	D4c

The bounds, initial values and estimation phases used for the parameters in the 2016 assessment model for the standard option were:

parameters	lower bound	upper bound	initial value	phase	code name
$p^{mat}_{MALE,z}$	-15	15	0	5	`pPrM2MF`

$p^{mat}_{FEMALE,z}$	-15	15	0	5	`pPrM2MF`

E. Model processes: recruitment

Recruitment of immature (new shell) crab in TCSAM2013 has the functional form:

$R_{y,x,z} = \dot{R}_{y,x} \cdot \ddot{R}_z$	recruitment of immature, new shell crab	E1

where *y* is year, *x* is sex, and *z* is size. $\dot{R}_{y,x}$ represents total sex-specific recruitment in year y and $\ddot{R}_z$ represents the size distribution of recruits, which is assumed identical for males and females.

Sex-specific recruitment, $\dot{R}_{y,x}$, is parameterized as

$\dot{R}_{y,x} = \begin{cases} e^{pLnR^H + \delta R^H_y} & y < y_{rec}\ (historic\ recruitment) \\ e^{pLnR + \delta R_y} & y_{rec} \le y\ (current\ recruitment) \end{cases}$	sex-specific recruitment of immature, new shell crab	E2

where y_{rec} is the first year of "current" recruitment, the sex ratio at recruitment is assumed to be 1:1 and the δR_y and δR^H_y are "devs" parameter vectors, with the constraint that the elements of a "devs" vector sums to zero. Prior to the 2016 assessment, y_{rec} was hard-wired to 1974, but it is now an input in the model control file. Independent parameter sets are used for the "historic" period during model spin-up (1949-1973) and the "current" period (1974-2013).

The size distribution for recruits, $\ddot{R}_z$, is based on a gamma-type distribution and is parameterized as

$\ddot{R}_z = c^{-1} \cdot \Delta_z^{\frac{\alpha}{\beta}-1} \cdot e^{-\frac{\Delta_z}{\beta}}$	size distribution of recruiting crab	E3

where α and β are parameters, $\Delta_z = z + 2.5 - z_{min}$, and $c = \sum_z \Delta_z^{\frac{\alpha}{\beta}-1} \cdot e^{-\frac{\Delta_z}{\beta}}$ is a normalization constant so that $1 = \sum_z \ddot{R}_z$. z_{min} is the smallest model size bin (27 mm) and the constant 2.5 represents one-half the size bin spacing.

Penalties are imposed on the "devs" parameter vectors δR_y and δR^H_y in the objective function as follows:

$\mathrm{P}(\delta R) = \sum_y {\delta R_y}^2$	Penalty function on δR_y	E4
$\mathrm{P}(\delta R^H) = \sum_y \left(\delta R^H_y - \delta R^H_{y-1}\right)^2$	1st difference penalty function on δR^H_y	E5

The bounds, initial values and estimation phases used for the parameters used in the 2016 assessment model are:

parameters	lower bound	upper bound	initial value	phase	code name

$pLnR^H$	--	--	0.0	1	`pMnLnRecHist`
$pLnR$	--	--	4.49	1	`pMnLnRec`
δR_y^H	-15	15	0	1	`pRecDevsHist`
δR_y	-15	15	0	1	`pRecDevs`
α	11.49	11.51	11.50	-8	`pRecAlpha`
β	3.99	4.01	4.00	-8	`pRecBeta`

where parameters with phase < 0 are not estimated (i.e., treated as constants).

F. Model processes: fisheries

Four fisheries that catch Tanner crab are included in TCSAM2013: 1) the directed Tanner crab fishery, 2) the snow crab fishery, 3) the BBRKC fishery and 4) the various groundfish fisheries (lumped as one bycatch fishery). Crab (males only) are assumed to be retained exclusively in the directed fishery. Bycatch of non-retained Tanner crab (males and females) is assumed to occur in all four fisheries; discard mortality fractions for the (discarded) bycatch are assumed to differ between the crab and groundfish fisheries due to the differences in gear used (pots vs. primarily bottom trawl).

Two options now exist in the TCSAM2013 code to model fishing mortality: the old option (used in assessments prior to 2016) and the Gmacs(Whitten et al., 2013) option (used in the 2016 assessment). For both options, the predicted number of crab killed in fishery *f* by year in TCSAM2016 assessment model has the functional form:

$m_{y,x,m,s,z}^f = \frac{F_{y,x,m,s,z}^f}{F_{y,x,m,s,z}^T} \cdot \left[1 - e^{-F_{y,x,m,s,z}^T}\right] \cdot n_{y,x,m,s,z}^1$	estimated crab mortality in fishery *f*	F1

where *y* is year, *x* is sex, *m* is maturity state, *s* is shell condition and *z* is size, $F_{y,x,m,s,z}^f$ is sex/maturity state/shell condition/size-specific fishing mortality in year *y*, and $F_{y,x,m,s,z}^T = \sum_f F_{y,x,m,s,z}^f$ is total fishing mortality sex *x* crab in maturity state *m* and shell condition *s* at size *z* at the time the fisheries occur in year *y*. Note that $m_{y,x,m,s,z}^f$ represents the estimated *mortality* in numbers associated with fishery *f*, not the numbers *captured* (i.e., brought on deck). These differ because discard mortality is not 100% in the fisheries).

In the standard option, the total fishing *mortality* rate $F_{y,x,m,s,z}^f$ for each fishery is decomposed into two multiplicative components: 1) the mortality rate on fully-selected crab, FM_y^f, and 2) a size-specific selectivity function $S_{y,x,m,s,z}^f$, as follows:

$F_{y,x,m,s,z}^f = FM_{y,x}^f \cdot S_{y,x,m,s}^f$	fishing mortality rate in fishery *f*	F2s

In the Gmacs option, the total *capture* $C^f_{y,x,m,s,z}$rate for each fishery is similarly decomposed into two multiplicative components: 1) the capture rate on fully-selected crab, FC^f_y, and 2) a size-specific selectivity function $S^f_{y,x,m,s,z}$, as follows:

$C^f_{y,x,m,s,z} = FC^f_{y,x} \cdot S^f_{y,x,m,s}$	fishing mortality rate in fishery *f*	F2s

For the Gmacs option, the fishing mortality rate $F^f_{y,x,m,s,z}$ is related to the capture rate $C^f_{y,x,m,s,z}$ by

$F^f_{y,x,m,s,z} = (r^f_{y,x,m,s,z} + hm_f \cdot [1 - r^f_{y,x,m,s,z}]) \cdot C^f_{y,x,m,s,z}$	fishing mortality rate in fishery *f*	F2g

where $r^f_{y,x,m,s,z}$ is the "retention" function and hm_f is the rate of handling mortality on discarded (non-retained) crab.

Fully-selected fishing mortality

The manner in which the fully-selected fishing mortality (or capture) rate is further decomposed is time-dependent and specific to each fishery. Consequently, this decomposition is discussed below specific to each fishery.

Considering total fishing mortality (retained + discards) in the directed Tanner crab fishery (TCF) first, the fully-selected fishing mortality is modeled differently in three time periods. In the standard FMM, total sex-specific fishing mortality is parameterized as

$FM^{TCF}_{y,x} = \begin{cases} 0.05 & y < 1965 \\ 0 & 1965 \leq y, fishery\ closed \\ e^{p\overline{LnF}^{TCF} + \delta F^{TCF}_y + pLnF^{TCF}_x} & 1965 \leq y, fishery\ open \end{cases}$	fully-selected fishing mortality rate in the directed Tanner crab fishery	F3s

where $p\overline{LnF}^{TCF}$is a parameter representing the mean ln-scale fishing mortality in the Tanner crab fishery since 1964 (catch data for this fishery begins in 1965), δF^{TCF}_y represents a "devs" parameter vector with elements defined for each year the fishery was open, and $pLnF^{TCF}_x$ is an optional female-only log-scale offset (i.e., $pLnF^{TCF}_{MALE} \equiv 0$) added this year. Prior to 1965, a small directed fishing mortality rate (0.05) is assumed.

The parameterization for sex-specific capture rates in the Gmacs FMM looks identical, but the parameters have different interpretations:

$FC^{TCF}_{y,x} = \begin{cases} 0.05 & y < 1965 \\ 0 & 1965 \leq y, fishery\ closed \\ e^{p\overline{LnF}^{TCF} + \delta F^{TCF}_y + pLnF^{TCF}_x} & 1965 \leq y, fishery\ open \end{cases}$	fully-selected capture rate in the directed Tanner crab fishery	F3g

For Tanner crab bycatch in the snow crab fishery (SCF), the fully-selected discard fishing mortality is modeled differently in three time periods using:

$FM_{y,x}^{SCF} = \begin{cases} 0.01 & y < 1978 \\ r^{SCF} \cdot E_y^{SCF} \cdot e^{pLnF_x^{SCF}} & 1978 \le y \le 1991 \\ e^{p\overline{LnF}^{SCF} + \delta F_y^{SCF} + pLnF_x^{SCF}} & 1992 \le y \end{cases}$	fully-selected discard fishing mortality rate in the snow crab fishery	F4s

where $p\overline{LnF}^{SCF}$ is a parameter representing the mean ln-scale bycatch fishing mortality in the snow crab fishery since 1992 (when reliable observer-based Tanner crab discard data in the snow crab fishery first became available), δF_y^{SCF} represents a “devs” parameter vector with elements defined for each year in this time period, and $pLnF_x^{SCF}$ is an optional female-only log-scale offset (i.e., $pLnF_{MALE}^{SCF} \equiv 0$) added this year. Prior to 1978, a small annual discard mortality rate associated with this fishery (0.01) is assumed. Annual effort data (total potlifts, E_y^{SCF}) is used to extend predictions of Tanner crab discard mortality in this fishery into the period 1978-1991. To do this, the assumption is made that effort in the snow crab fishery is proportional to Tanner crab discard fishing mortality and estimate the proportionality constant, r^{SCF}, using a ratio estimator between effort and discard mortality in the period 1992-present:

$r^{SCF} = \dfrac{\left\{\frac{1}{N}\sum_{y=1992}^{present} FM_y^{SCF}\right\}}{\left\{\frac{1}{N}\sum_{y=1992}^{present} E_y^{SCF}\right\}}$	ratio estimator relating fishing mortality rate to effort in the snow crab fishery	F5

where *N* is the number of years, 1992-present.

For Tanner crab bycatch in the BBRKC fishery (RKF), the fully-selected discard fishing mortality when the fishery was open is modeled differently in three time periods using:

$FM_{y,x}^{RKF} = \begin{cases} 0.02 & y < 1953 \\ max\left\{0.01, -ln\left[1 - r^{RKF} \cdot E_y^{RKF} \cdot e^{pLnF_x^{RKF}}\right]\right\} & 1953 \le y \le 1991 \\ e^{p\overline{LnF}^{RKF} + \delta F_y^{RKF} + pLnF_x^{RKF}} & 1992 \le y \end{cases}$	fully-selected discard fishing mortality rate in the BBRKC fishery	F6

where $p\overline{LnF}^{RKF}$ is a parameter representing the mean ln-scale bycatch fishing mortality in the BBRKC fishery since 1992 (when observer-based Tanner crab discard data in the BBRKC fishery first became available), δF_y^{RKF} represents a “devs” parameter vector with elements defined for each year in this period that the fishery was open, and $pLnF_x^{RKF}$ is an optional female-only log-scale offset (i.e., $pLnF_{MALE}^{RKF} \equiv 0$) added this year.. Prior to 1953, a small annual discard mortality rate associated with this fishery (0.02) was assumed. Annual effort data (total potlifts, E_y^{RKF}) was used to extend predictions of Tanner crab discard mortality in this fishery into the period 1953-1991. To do this, we made the assumption that effort in the BBRKC fishery is proportional to Tanner crab discard fishing mortality and estimate the proportionality constant, r^{RKF}, using a ratio estimator between effort and discard mortality in the period 1992-present:

$r^{RKF} = \dfrac{\left\{\frac{1}{N}\sum_{y=1992}^{present} \left[1 - e^{-FM_y^{RKF}}\right]\right\}}{\left\{\frac{1}{N}\sum_{y=1992}^{present} E_y^{RKF}\right\}}$	ratio estimator relating fishing mortality rate to effort in the BBRKC fishery	F7

where *N* is the number of years, 1992-present, when the BBRKC fishery was open. For any year that the BBRKC fishery was closed, $FM_{y,x}^{RKF}$ was set to 0.

Finally, for Tanner crab bycatch in the groundfish fisheries (GTF), the fully-selected discard fishing mortality in the fishery was modeled differently in two time periods using:

$FM_{y,x}^{GTF} = \begin{cases} \frac{1}{N}\sum_{y=1992}^{present} e^{p\overline{LnF}^{GTF}+\delta F_y^{GTF}+pLnF_x^{GTF}} & y < 1973 \\ e^{p\overline{LnF}^{GTF}+\delta F_y^{GTF}+pLnF_x^{GTF}} & 1973 \leq y \end{cases}$	fully-selected discard fishing mortality rate in the groundfish trawl fisheries	F8

where $p\overline{LnF}^{GTF}$ is a parameter representing the mean fully-selected ln-scale bycatch fishing mortality in the groundfish fisheries since 1973 (when observer-based Tanner crab discard data in the groundfish fisheries first became available), δF_y^{GTF} is a "devs" parameter vector with elements representing the annual ln-scale deviation from the mean, and $pLnF_x^{GTF}$ is an optional female-only log-scale offset (i.e., $pLnF_{MALE}^{GTF} \equiv 0$) added this year. Prior to 1973, the fully-selected discard mortality rate associated with these fisheries was assumed to be constant and equal to the mean over the 1973-present period.

When the Gmacs FMM option is selected instead of the standard FMM, the previous parameterizations apply to the $FC_{y,x}^{f}$'s, not the $FM_{y,x}^{f}$'s.

The bounds (when set), initial values and estimation phases used for the fully-selected fishing mortality parameters and devs vectors in the 2016 assessment model were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\overline{LnF}^{TCF}$	--	--	-0.7	1	`pAvgLnF_TCF`
δF_y^{TCF}	-15	15	0	2	`pF_DevsTCF`
$p\overline{LnF}^{SCF}$	--	--	-3.0	3	`pAvgLnF_SCF`
δF_y^{SCF}	-15	15	0	4	`pF_DevsSCF`
$p\overline{LnF}^{RKF}$	-5.25	-5.25	-5.25	-4	`pAvgLnF_RKF`
δF_y^{RKF}	-15	15	0	-5	`pF_DevsRKF`
$p\overline{LnF}^{GTF}$	--	--	-4.0	2	`pAvgLnF_GTF`
δF_y^{GTF}	-15	15	0	3	`pF_DevsGTF`

where all parameters and parameter vectors were estimated (phase > 0), except for those associated with the BBRKC fishery.

Fishery selectivity

The manner in which fishery selectivity is parameterized is also time-dependent and specific to each fishery, as with the fully-selected fishing mortality. However, the time periods used to define selectivity are not necessarily those used for the fully-selected fishing mortality.

In the directed Tanner crab fishery (TCF), total (retained + discards) selectivity (under the standard FMM) or capture selectivity (under the Gmacs FMM) is modeled using sex-specific ascending logistic functions. For males, in addition, total selectivity is parameterized differently in three time periods, corresponding to differences in information about the fishery (pre-/post-1991) and differences in the fishery itself (pre-/post-rationalization in 2005):

$S^{TCF}_{y,FEMALE,m,s,z} = \left\{1+e^{-p\beta^{TCF}_{FEMALE}\cdot\left(z-pZ_{50}{}^{TCF}_{FEMALE}\right)}\right\}^{-1}$	total selectivity for females in the directed Tanner crab fishery	F9
$S^{TCF}_{y,MALE,m,s,z} = \begin{cases} \left\{1+e^{-p\beta^{TCF(1)}_{MALE}\cdot\left(z-\overline{z_{50}}^{TCF}_{MALE}\right)}\right\}^{-1} & y \le 1990 \\ \left\{1+e^{-p\beta^{TCF(1)}_{MALE}\cdot\left(z-z_{50}{}^{TCF}_{y,MALE}\right)}\right\}^{-1} & 1991 \le y \le 1996 \\ \left\{1+e^{-p\beta^{TCF(2)}_{MALE}\cdot\left(z-z_{50}{}^{TCF}_{y,MALE}\right)}\right\}^{-1} & 2005 \le y \le 2009 \end{cases}$	total selectivity for males in the directed Tanner crab fishery	F10

where the $p\beta^{TCF(t)}_{x}$ are parameters controlling the slopes of the associated logistic selectivity curves, $pZ_{50}{}^{TCF}_{FEMALE}$ is the parameter controlling the size of females at 50% selection, $\overline{z_{50}}^{TCF}_{MALE}$ controls the size of 50%-selected males in the pre-1991 period, and $z_{50}{}^{TCF}_{y,MALE}$ controls the size of 50%-selected males in the post-1990 period. The latter three quantities are functions of estimable parameters as described in the following:

$\overline{z_{50}}^{TCF}_{MALE} = \frac{1}{6}\sum_{y=1991}^{1996} z_{50}{}^{TCF}_{y,MALE}$	male size at 50%-selected used in pre-1991 period	F11
$z_{50}{}^{TCF}_{y,MALE} = e^{pLnZ_{50}{}^{TCF}_{MALE}+\delta Z_{50}{}^{TCF}_{y,MALE}}$	male size at 50%-selected used in post-1990 period	F12

where $pLnZ_{50}{}^{TCF}_{MALE}$ is a parameter controlling the ln-scale mean male size at 50% selectivity post-1990 and $\delta Z_{50}{}^{TCF}_{y,MALE}$ is a parameter vector controlling annual ln-scale deviations in male size at 50% selectivity post-1990. As formulated, selectivity in the directed fishery is not a function of maturity state or shell condition.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 5 parameters describing total selectivity in the directed Tanner crab fishery were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{FEMALE}^{TCF}$	0.1	0.4	0.25	3	`slpTCFF_z50`
$pZ_{50}{}_{FEMALE}^{TCF}$	80	150	115	3	`selTCFF_z50`
$p\beta_{MALE}^{TCF(1)}$	0.05	0.75	0.4	3	`selTCFF_z50`
$p\beta_{MALE}^{TCF(2)}$	0.1	0.4	0.25	3	`fish_slope_yr_3`
$pLnZ_{50}{}_{MALE}^{TCF}$	4.0	5.0	4.5	3	`log_avg_sel50_3`

where all parameters were estimated. The bounds, initial values and estimation phase used in the 2016 assessment model for the ln-scale "devs" parameter vector $\delta Z_{50}{}_{y,MALE}^{TCF}$ describing annual deviations in male size at 50%-selected (1991-1996, 2005-2009) were:

parameters	lower bound	upper bound	initial value	phase	code name
$\delta Z_{50}{}_{y,MALE}^{TCF}$	-0.5	0.5	0	3	`log_sel50_dev_3`

In the snow crab fishery (SCF), bycatch (discard) selectivity is modeled using three time periods (model start to 1996, 1997-2004, 2005 to present). Male selectivity is described using dome-shaped (double logistic) functions in each period, with:

$S_{y,MALE,m,s,z}^{SCF}=\begin{cases}S_{MALE,z}^{SCF(1)} & y\le 1996\\ S_{MALE,z}^{SCF(2)} & 1997\le y\le 2004\\ S_{MALE,z}^{SCF(3)} & 2005\le y\end{cases}$	male selectivity in the snow crab fishery	F13

where the double logistic functions $S_{MALE,z}^{SCF(t)}$ are parameterized using:

$S_{MALE,z}^{SCF(t)}=\left\{1+e^{-p\beta_{MALE}^{SCF(ta)}\cdot\left(z-pZ_{50}{}_{MALE}^{SCF(ta)}\right)}\right\}^{-1}\cdot\left\{1+e^{+p\beta_{MALE}^{SCF(td)}\cdot\left(z-\exp[pZ_{50}{}_{MALE}^{SCF(td)}]\right)}\right\}^{-1}$	dome-shaped	F14

where $p\beta_{x}^{SCF(ta)}$and $pZ_{50}{}_{x}^{SCF(ta)}$ are the 6 parameters controlling the ascending limb of the double logistic function and $p\beta_{x}^{SCF(td)}$and $pZ_{50}{}_{x}^{SCF(td)}$ are the 6 parameters controlling the descending limb for each period *t*. Note that $pZ_{50}{}_{x}^{SCF(td)}$ is evaluate on the log-scale to ensure positivity.

Female selectivity is described using ascending logistic functions in each period, with:

$S^{SCF}_{y,FEMALE,m,s,z} = \begin{cases} S^{SCF(1)}_{FEMALE,z} & y \le 1996 \\ S^{SCF(2)}_{FEMALE,z} & 1997 \le y \le 2004 \\ S^{SCF(3)}_{FEMALE,z} & 2005 \le y \end{cases}$	female selectivity in the snow crab fishery	F15

where the ascending logistic functions $S^{SCF(t)}_{FEMALE,z}$ are parameterized using:

$S^{SCF(t)}_{FEMALE,z} = \left\{1 + e^{-p\beta^{SCF(t)}_{FEMALE}\cdot\left(z - pZ_{50}{}^{SCF(t)}_{FEMALE}\right)}\right\}^{-1}$	ascending logistic selectivity	F16

where the $p\beta^{SCF(p)}_{x}$ are the 3 parameters controlling the slopes of the associated logistic selectivity curves and the $pZ_{50}{}^{SCF(p)}_{x}$ are the 3 parameters controlling size at 50%-selection.

As formulated, selectivity in the snow crab fishery is not a function of maturity state or shell condition.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 12 parameters describing male selectivity in the snow crab fishery were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{MALE}^{SCF(1a)}$	0.01	0.50	0.255	4	`selSCFM_slpA1`
$pZ_{50}{}_{MALE}^{SCF(1a)}$	60	150	122.5	4	`selSCFM_z50A1`
$p\beta_{MALE}^{SCF(1d)}$	0.01	0.50	0.255	4	`selSCFM_slpD1`
$pZ_{50}{}_{MALE}^{SCF(1d)}$	40	200	120	4	`selSCFM_lnZ50D1`
$p\beta_{MALE}^{SCF(2a)}$	0.01	0.50	0.255	4	`selSCFM_slpA2`
$pZ_{50}{}_{MALE}^{SCF(2a)}$	60	150	122.5	4	`selSCFM_z50A2`
$p\beta_{MALE}^{SCF(2d)}$	0.01	0.50	0.255	4	`selSCFM_slpD2`
$pZ_{50}{}_{MALE}^{SCF(2d)}$	40	200	120	4	`selSCFM_lnZ50D2`
$p\beta_{MALE}^{SCF(3a)}$	0.01	0.50	0.255	4	`selSCFM_slpA3`
$pZ_{50}{}_{MALE}^{SCF(3a)}$	60	150	122.5	4	`selSCFM_z50A3`
$p\beta_{MALE}^{SCF(3d)}$	0.01	0.50	0.255	4	`selSCFM_slpD3`
$pZ_{50}{}_{MALE}^{SCF(3d)}$	40	200	120	4	`selSCFM_lnZ50D3`

where all parameters were estimated.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 6 parameters describing female selectivity in the snow crab fishery were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{FEMALE}^{SCF(1)}$	0.05	0.5	0.275	4	`selSCFF_slpA1`
$pZ_{50}{}_{FEMALE}^{SCF(1)}$	50	150	100	4	`selSCFF_z50A1`
$p\beta_{FEMALE}^{SCF(2)}$	0.05	0.5	0.275	4	`selSCFF_slpA2`
$pZ_{50}{}_{FEMALE}^{SCF(2)}$	50	120	85	4	`selSCFF_z50A2`
$p\beta_{FEMALE}^{SCF(3)}$	0.05	0.5	0.275	4	`selSCFF_slpA3`
$pZ_{50}{}_{FEMALE}^{SCF(3)}$	50	120	85	4	`selSCFF_z50A3`

where all parameters were estimated.

In the BBRKC fishery (RKF), bycatch (discard) selectivity is also modeled using the three time periods used to model selectivity in the snow crab fishery (model start to 1996, 1997-2004, 2005 to present), with sex-specific parameters estimated in each period. All sex/period combinations are modeled using ascending logistic functions:

$S_{y,x,m,s,z}^{RKF} = \begin{cases} \left\{1+e^{-p\beta_x^{RKF(1)}\cdot\left(z-pZ_{50}{}_x^{RKF(1)}\right)}\right\}^{-1} & y \le 1996 \\ \left\{1+e^{-p\beta_x^{RKF(2)}\cdot\left(z-pZ_{50}{}_x^{RKF(2)}\right)}\right\}^{-1} & 1997 \le y \le 2004 \\ \left\{1+e^{-p\beta_x^{RKF(3)}\cdot\left(z-pZ_{50}{}_x^{RKF(3)}\right)}\right\}^{-1} & 2005 \le y \end{cases}$	selectivity in the BBRKC fishery	F17

where the $p\beta_x^{RKF(p)}$ are 6 parameters controlling the slopes of the associated logistic selectivity curves and the $pZ_{50}{}_x^{RKF(p)}$ are 6 parameters controlling size at 50%-selection. As formulated, selectivity in the BBRKC fishery is not a function of maturity state or shell condition.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 12 parameters describing male selectivity in the BBRKC fishery were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{MALE}^{RKF(1)}$	0.01	0.50	0.255	3	`selRKFM_slpA1`
$pZ_{50}{}_{MALE}^{RKF(1)}$	95	150	122.5	3	`selRKFM_z50A1`
$p\beta_{MALE}^{RKF(2)}$	0.01	0.50	0.255	3	`selRKFM_slpA2`
$pZ_{50}{}_{MALE}^{RKF(2)}$	95	150	122.5	3	`selRKFM_z50A2`
$p\beta_{MALE}^{RKF(3)}$	0.01	0.50	0.255	3	`selRKFM_slpA3`
$pZ_{50}{}_{MALE}^{RKF(3)}$	95	150	122.5	3	`selRKFM_z50A3`

where all parameters were estimated.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 6 parameters describing female selectivity in the BBRKC fishery were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{FEMALE}^{RKF(1)}$	0.005	0.50	0.2525	3	`selRKFF_slpA1`
$pZ_{50}{}_{FEMALE}^{RKF(1)}$	50	150	100	3	`selRKFF_z50A1`
$p\beta_{FEMALE}^{RKF(2)}$	0.005	0.50	0.255	3	`selRKFF_slpA2`
$pZ_{50}{}_{FEMALE}^{RKF(2)}$	50	150	100	3	`selRKFF_z50A2`
$p\beta_{FEMALE}^{RKF(3)}$	0.01	0.50	0.255	3	`selRKFF_slpA3`
$pZ_{50}{}_{FEMALE}^{RKF(3)}$	50	170	110	3	`selRKFF_z50A3`

where all parameters were estimated.

In the groundfish fisheries (GTF), bycatch (discard) selectivity is also modeled using three time periods (model start to 1986, 1987-1996, 1997 to present), but these are different from those used in the snow crab and BBRKC fisheries. Sex-specific parameters are estimated in each period; all sex/period combinations are modeled using ascending logistic functions:

$S_{y,x,m,s,z}^{GTF} = \begin{cases} \left\{1 + e^{-p\beta_x^{GTF(1)} \cdot \left(z - pZ_{50}{}_x^{GTF(1)}\right)}\right\}^{-1} & y \le 1986 \\ \left\{1 + e^{-p\beta_x^{GTF(2)} \cdot \left(z - pZ_{50}{}_x^{GTF(2)}\right)}\right\}^{-1} & 1987 \le y \le 1996 \\ \left\{1 + e^{-p\beta_x^{GTF(3)} \cdot \left(z - pZ_{50}{}_x^{GTF(3)}\right)}\right\}^{-1} & 1997 \le y \end{cases}$	selectivity in the groundfish fisheries	F18

where the $p\beta_x^{GTF(p)}$ are 6 parameters controlling the slopes of the associated logistic selectivity curves and the $pZ_{50}{}_x^{GTF(p)}$ are 6 parameters controlling size at 50%-selection. As formulated, selectivity in the groundfish fisheries is not a function of maturity state or shell condition.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 12 parameters describing male selectivity in the groundfish fisheries were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{MALE}^{GTF(1)}$	0.01	0.50	0.255	3	`selGTFM_slpA1`
$pZ_{50}{}_{MALE}^{GTF(1)}$	40	120.01	80.005	3	`selGTFM_z50A1`
$p\beta_{MALE}^{GTF(2)}$	0.01	0.50	0.255	3	`selGTFM_slpA2`
$pZ_{50}{}_{MALE}^{GTF(2)}$	40	120.01	80.005	3	`selGTFM_z50A2`
$p\beta_{MALE}^{GTF(3)}$	0.01	0.50	0.255	3	`selGTFM_slpA3`
$pZ_{50}{}_{MALE}^{GTF(3)}$	40	120.01	80.005	3	`selGTFM_z50A3`

where all parameters were estimated.

The bounds, initial values and estimation phases used in the 2016 assessment model for the 6 parameters describing female selectivity in the groundfish fisheries were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta_{FEMALE}^{GTF(1)}$	0.01	0.50	0.255	3	`selGTFF_slpA1`
$pZ_{50}{}_{FEMALE}^{GTF(1)}$	40	125.01	82.505	3	`selGTFF_z50A1`
$p\beta_{FEMALE}^{GTF(2)}$	0.005	0.50	0.255	3	`selGTFF_slpA2`
$pZ_{50}{}_{FEMALE}^{GTF(2)}$	40	250.01	145.005	3	`selGTFF_z50A2`
$p\beta_{FEMALE}^{GTF(3)}$	0.01	0.50	0.255	3	`selGTFF_slpA3`
$pZ_{50}{}_{FEMALE}^{GTF(3)}$	40	150.01	95.005	3	`selGTFF_z50A3`

where all parameters were estimated.

Retention in the directed fishery

Retention of male crab in the directed fishery is modeled as a multiplicative size-specific process "on top" of total (retention + discards) fishing selectivity. The number of crab (males only) retained in the directed Tanner crab fishery is given by

$r_{y,m,s,z}^{TCF} = \dfrac{R_{y,m,s,z}^{TCF}}{F_{y,MALE,m,s,z}^{T}} \cdot \left[1 - e^{-F_{y,MALE,m,s,z}^{T}}\right] \cdot n_{y,MALE,m,s,z}^{1}$	retained male crab (numbers) in the directed fishery	F19

where $R_{y,m,s,z}^{TCF}$ is the retained mortality rate associated with retention, which is related to the total fishing mortality rate on male crab in the directed fishery, $F_{y,MALE,m,s,z}^{TCF}$, by

$\begin{aligned} R_{y,m,s,z}^{TCF} &= \rho_{y,m,s,z}^{TCF} \cdot F_{y,MALE,m,s,z}^{TCF} \\ &= FM_{y}^{TCF} \cdot \rho_{y,m,s,z}^{TCF} \cdot S_{y,MALE,m,s}^{TCF} \end{aligned}$	retained mortality rate in the directed fishery	F20

where $\rho_{y,m,s,z}^{TCF}$ represents size-specific retention of male crab. Retention at size, $\rho_{y,m,s,z}^{TCF}$, in the directed fishery is modeled as an ascending logistic function, with different parameters in two time periods, as follows:

$\rho_{y,m,s,z}^{TCF} = \begin{cases} \left\{1 + e^{-p\beta^{TCFR(1)} \cdot \left(z - pZ_{50}{}^{TCFR(1)}\right)}\right\}^{-1} & y \leq 1990 \\ \left\{1 + e^{-p\beta^{TCFR(2)} \cdot \left(z - pZ_{50}{}^{TCFR(2)}\right)}\right\}^{-1} & 1991 \leq y \end{cases}$	size-specific retention in the directed fishery	F21

where $p\beta^{TCFR(t)}$ is the parameter controlling the slope of the function in the each period (t=1,2) and $pZ_{50}{}^{TCFR(t)}$ is the parameter controlling the size at 50%-selected. As formulated, retention is not a function of maturity state or shell condition.

The bounds, initial values and estimation phases used for the size-specific retention parameters in the 2016 assessment model were:

parameters	lower bound	upper bound	initial value	phase	code name
$p\beta^{TCFR(1)}$	0.25	1.01	0.63	3	`fish_fit_slope_mn1`
${pZ_{50}}^{TCFR(1)}$	85	160	122.5	3	`fish_fit_sel50_mn1`
$p\beta^{TCFR(2)}$	0.25	2.01	1.13	3	`fish_fit_slope_mn2`
${pZ_{50}}^{TCFR(2)}$	85	160	122.5	3	`fish_fit_sel50_mn2`

where all parameters were estimated.

G. Model indices: surveys

The predicted number of crab caught in the survey by year in the 2013 TCSAM model has the functional form:

$n_{y,x,m,s,z}^{srv} = q_{y,x} \cdot S_{y,x,z} \cdot n_{y,x,m,s,z}$	predicted number of crab caught in survey	G1

where *y* is year, *x* is sex, *m* is maturity state, *s* is shell condition and *z* is size, $q_{y,x}$is sex-specific survey catchability in year y, $S_{y,x,z}$ is sex-specific size selectivity in year y, and $n_{y,x,m,s,z}$ is the number of sex *x* crab in maturity state *m* and shell condition *s* at size *z* at the time of the survey in year *y*.

Three time periods that were used to test hypotheses regarding changes in catchability and selectivity in the survey over time are defined in the model. These periods are defined as: 1) $y < 1982$, 2) $1982 \le y \le 1987$, and 3) $1988 \le y$. As parameterized in the 2016 assessment model, catchabilities in periods 2 and 3 were assumed to be identical, so only two sets of sex-specific parameters reflecting catchability were used in the model. In terms of the three time periods, catchability was parameterized using the sex-specific parameters q_x^I and q_x^{II} in the following manner:

$q_{y,x} = \begin{cases} q_x^I & y < 1982 \\ q_x^{II} & 1982 \le y \le 1987 \\ q_x^{II} & 1988 \le y \end{cases}$	survey catchability	G2

The bounds, initial values and estimation phases used for these parameters in the 2016 assessment model were:

parameters	lower bound	upper bound	initial value	phase	code name

q^{I}_{MALE}	0.50	1.001	0.7505	4	`srv2_q`
q^{I}_{FEMALE}	0.50	1.001	0.7505	4	`srv2_femQ`
q^{II}_{MALE}	0.20	2.00	1.1	4	`srv3_q`
q^{II}_{FEMALE}	0.20	1.00	0.6	4	`srv3_femQ`

where all parameters were estimated (phase > 0).

Similarly, survey selectivity in periods 2 and 3 was assumed identical and only two sets of sex-specific parameters were used to describe survey selectivity using logistic functions:

$S_{y,z} = \begin{cases} \left\{1 + e^{-\left[\ln(19)\cdot(z - {z_{50}}_x^{I})/\delta {z_{95}}_x^{I}\right]}\right\}^{-1} & y < 1982 \\ \left\{1 + e^{-\left[\ln(19)\cdot(z - {z_{50}}_x^{II})/\delta {z_{95}}_x^{II}\right]}\right\}^{-1} & 1982 \le y \le 1987 \\ \left\{1 + e^{-\left[\ln(19)\cdot(z - {z_{50}}_x^{II})/\delta {z_{95}}_x^{II}\right]}\right\}^{-1} & 1987 \le y \end{cases}$	survey selectivity	G3

where the z_{50}'s are parameters reflecting the inflection point of the logistic curve (i.e., size at 50% selected) and the δz_{95}'s are parameters reflecting the difference the sizes at 50% and 95% selected.

The bounds, initial values and estimation phases used for the selectivity parameters used in the 2016 assessment model were:

parameters	lower bound	upper bound	initial value	phase	code name
${z_{50}}_{MALE}^{I}$	0	90	45	4	`srv2_sel50`
${z_{50}}_{FEMALE}^{I}$	-200	100.01	-49.005	4	`srv2_sel50_f`
$\delta {z_{95}}_{MALE}^{I}$	0	100	50	4	`srv2_seldiff`
$\delta {z_{95}}_{FEMALE}^{I}$	0	100	50	4	`srv2_seldiff_f`
${z_{50}}_{MALE}^{II}$	0	69	34.5	4	`srv3_sel50`
${z_{50}}_{FEMALE}^{II}$	-50	69	9.5	4	`srv3_sel50_f`
$\delta {z_{95}}_{MALE}^{II}$	0	100	50	4	`srv3_seldiff`
$\delta {z_{95}}_{FEMALE}^{II}$	0	100	50	4	`srv3_seldiff_f`

where all parameters were estimated (phase > 0).

H. Model fitting: objective function equations

The TCSAM2016 assessment model is fit by minimizing an objective function, $\mathscr{o}$, with additive components consisting of: 1) several penalty functions, 2) several negative log-likelihood functions based on assumed prior probability distributions for model parameters, and 3) several negative log-likelihood functions based on input data components, of the form:

$\mathscr{o} = \sum_{f} \lambda_f \cdot \mathcal{F}_f - 2 \sum_{p} \lambda_p \cdot \ln(\wp_p) - 2 \sum_{l} \lambda_l \cdot \ln(\mathcal{L}_l)$	model objective function	H1

where $\mathcal{F}_f$ represents the *f*th penalty function, $\wp_p$ represents the *p*th prior probability function, $\mathcal{L}_l$ represents the *l*th likelihood function, and the λ's represent user-adjustable weights for each component.

Penalty Functions

The penalty functions associated with various model quantities are identified in the section (B-F) concerning the associated process.

Prior Probability Functions

The prior probability functions associated with various model parameters are identified in the section (B-F) concerning the associated parameter.

Likelihood Functions

The model’s objective function includes likelihood components based on 1) retained catch size frequencies (i.e., males only) in the directed fishery from dockside observer sampling; 2) total catch (retained + discarded) size frequencies by sex in each fishery from at-sea observer sampling; 3) size frequencies for immature males, mature males, immature females, and mature females, respectively, from trawl survey data; 4) dockside retained catch biomass (i.e., males only) in the directed fishery from fish ticket data; 5) estimated total catch (retained + discarded) mortality in biomass by sex in the crab and groundfish fisheries from at-sea observer sampling; and 6) estimated mature biomass by sex from trawl survey data. As discussed in more detail below, size frequency-related likelihood components are based on the multinomial distribution while those related to biomass are based on either the normal or lognormal distributions.

Size frequency components

Fishery-related (log-scale) likelihood components involving sex-specific size frequencies are based on the following equation for multinomial sampling:

$\ln(\mathcal{L}^M)^f_x = \sum_y n^f_{y,x} \cdot \sum_z p^{obs.f}_{y,x,z} \cdot \ln\left(p^{mod.f}_{y,x,z} + \delta\right) - p^{obs.f}_{y,x,z} \cdot \ln\left(p^{obs.f}_{y,x,z} + \delta\right)$	multinomial log-likelihood	H2

where *f* indicates the fishery, *x* indicates sex, the *y*’s are years for which data exists, $n^f_{y,x}$ is the sex-specific effective sample size for year y, $p^{obs.f}_{y,x,z}$ is the observed size composition in size bin *z* (i.e., the size frequency normalized to sum to 1 across size bins for each year), $p^{mod.f}_{y,x,z}$ is the corresponding model estimate, and δ is a small constant.

Size compositions for retained catch (male only) in the directed Tanner crab fishery are obtained from dockside observer sampling and calculated from shell condition-specific size frequencies $r^{obs.TCF}_{y,MALE,s,z}$ using:

$p^{obs.TCF}_{y,MALE,z} = \dfrac{\sum_s r^{obs.TCF}_{y,MALE,s,z}}{\sum_s \sum_z r^{obs.TCF}_{y,MALE,s,z}}$	retained size compositions for the directed fishery from dockside observer sampling	H3

where *s* indicates shell condition (new shell, old shell) and *z* indicates the size bin. The corresponding model size compositions are calculated from the predicted numbers retained in the directed fishery $r^{mod.TCF}_{y,MALE,m,s,z}$ using

$p^{mod.TCF}_{y,MALE,z} = \dfrac{\sum_m \sum_s r^{mod.TCF}_{y,MALE,m,s,z}}{\sum_m \sum_s \sum_z r^{mod.TCF}_{y,MALE,m,s,z}}$	model-predicted retained catch size compositions for the directed fishery	H4

where, additionally, *m* is maturity state (immature, mature).

Size compositions for total (retained + discarded) catch in fishery *f* (*f* = 1-4) are sex-specific and are calculated from sex/shell condition-specific size frequencies $r^{obs.f}_{y,x,s,z} + d^{obs.f}_{y,x,s,z}$ obtained from at-sea observer sampling using:

$p^{obs.f}_{y,x,z} = \dfrac{\sum_s \left[r^{obs.f}_{y,x,s,z} + d^{obs.f}_{f,y,x,s,z}\right]}{\sum_s \sum_z \left[r^{obs}_{y,x,s,z} + d^{obs}_{y,x,s,z}\right]}$	sex-specific size compositions for total catch for fishery *f* from at-sea observer sampling	H5

where *s* indicates shell condition (new shell, old shell) and *z* indicates the size bin. In the above equation, $d^{obs.f}_{y,x,s,z}$ has *not* been discounted for discard survival (i.e., it's consistent with setting discard mortality to 100%). The corresponding model size compositions are calculated from the predicted total fishing *mortality* (numbers) in each fishery *f*, $m^{mod.f}_{y,x,m,s,z}(= r^{mod.f}_{y,x,m,s,z} + \delta_f \cdot d^{mod.f}_{y,x,m,s,z})$, using

$p^{mod.f}_{y,x,z} = \dfrac{\sum_m \sum_s m^{mod.f}_{y,x,m,s,z}}{\sum_m \sum_s \sum_z m^{mod.f}_{y,x,m,s,z}}$	model-predicted total catch mortality size compositions for fishery *f*	H6

where, again, the subscript *m* is maturity state (immature, mature). In eq. H6, $m^{mod.f}_{y,x,m,s,z}$ does not assume any particular value for discard mortality.

Log-scale likelihood components for the trawl survey involve size frequencies that are sex- and maturity state-specific, and thus are based on the following equation for multinomial sampling:

$\ln(\mathcal{L}^M)^{srv}_{x,m} = \sum_y n^{srv}_{y,x,m} \cdot \sum_z \left\{ p^{obs.srv}_{y,x,m,z} \cdot \ln\left(p^{mod.srv}_{y,x,m,z} + \delta\right) - p^{obs.srv}_{y,x,mz} \cdot \ln\left(p^{obs.srv}_{y,x,mz} + \delta\right) \right\}$	multinomial log-likelihood	H7

where *x* indicates sex, the *y*'s are years for which data exists, $n^{srv}_{y,x,m}$ is the sex- and maturity-state specific effective sample size for year *y*, $p^{obs.srv}_{y,x,z}$ is the observed size composition in size bin *z* (i.e., the size frequency normalized to sum to 1 across size bins for each year), $p^{mod.srv}_{y,x,z}$ is the corresponding model estimate, and δ is a small constant.

Fishery biomass components

Likelihood components related to fishery biomass totals are based on the assumption of normally-distributed sampling, and generally have the simple form:

$\ln(\mathcal{L}^N)^f_x = -0.5 \sum_y \left[b^{obs.f}_{y,x} - b^{mod.f}_{y,x} \right]^2$	normal log-likelihood	H8

where $b^{obs.f}_{y,x}$ is the sex-specific catch *mortality* (as biomass) in fishery *f* for year *y* and $b^{mod.f}_{y,x}$ is the corresponding value predicted by the model. Components of this sort are calculated for retained biomass in the directed fishery, total (retained + discard) sex-specific fishery-related mortality in the model crab fisheries, and discard-related (not sex-specific) mortality in the groundfish fishery. The observed components of discard-related mortality for each fishery are obtained by multiplying the observed discard biomass by the assumed discard mortality fraction.

This year, an option to apply a lognormal likelihood to fishery biomass totals was implemented using:

$\ln(\mathcal{L}^N)^f_x = -0.5 \sum_y \dfrac{\left[ln\left(b^{obs.f}_{y,x} + \delta\right) - ln\left(b^{mod.f}_{y,x} + \delta\right) \right]^2}{2 \cdot \ln(1 + cv_f^2)}$	lognormal log-likelihood	H9

where the cv_f 's represent assumed error cv's, by fishery.

Survey biomass components

Likelihood components related to survey biomass are based on the assumption of lognormally-distributed sampling errors, and have the form:

$\ln(\mathcal{L}^N)_x^{srv} = -\sum_y \frac{\left[ln\left(b_{y,x}^{obs.srv}+\delta\right) - ln\left(b_{y,x}^{mod.srv}+\delta\right)\right]^2}{2\cdot\ln(1+cv_{y,x}^2)}$	lognormal log-likelihood	H9

where $b_{y,x}^{obs.srv}$ is sex-specific mature biomass estimated from the trawl survey data for year y, $b_{y,x}^{mod.srv}$ is the corresponding value predicted by the model, and $cv_{y,x}$ is the cv of the observation. Survey numbers-at-size $n_{y,x,m,s,z}^{obs.srv}$, classified by sex, shell condition and maturity state, are combined with sex- and maturity state-specific weight-at-size relationships $w_{x,m,z}$ to estimate sex-specific mature biomass $b_{y,x}^{obs.srv}$ using

$b_{y,x}^{obs.srv} = \sum_s \sum_z n_{y,x,MATURE,s,z}^{obs.srv} \cdot w_{x,MATURE,z}$	mature biomass	H10

An equivalent equation is used to calculate $b_{y,x}^{mod.srv}$.

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