BSAI Tanner Crab

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Introduction

Several issues regarding the BSAI Tanner crab stock assessment are addressed in this chapter. These include 1) revisions to data included in the 2014 assessment and their effects vis-a-vis the 2014 assessment, 2) a report on the effect of assumed handling mortality on setting OFL using the 2014 assessment model, 3) a description of a new assessment model (TCSAM2015) developed for Tanner crab using the Gmacs fishing mortality equations, 4) a derivation of a closed-form, deterministic solution to initial numbers-at-size (an option in TCSAM2015) for a crab stock with terminal molt biology, 5) a description of an R-based simulation package, rsimTCSAM, developed to facilitate testing and debugging of TCSAM2015, and 6) results from running the TCSAM2015 model on several simulated datasets, and 7) results from running TCSAM2015 on the data used in the 2014 assessment.

1. Data revisions

1.a 2013 Tanner crab dockside size frequencies

Subsequent to completing the September 2014 assessment, ADF&G revised the size frequencies for Tanner crab retained in the directed fishery during the previous fishing season (2013/14) used in the assessment. While the revised size frequencies are identical for the region east of 166° W longitude to those used in the assessment, they are substantially different for the region west of 166° W (Figure 1a.1). While the overall number of measured crab was similar between the original (2635) and revised (2237) data, the proportion of new shell to old shell crab was substantially different (909:1726 in the original data; 1869:368 in the revised data)—as were the average sizes (original data: 152 mm CW for new shell crab, 153 for old shell crab; revised data: 138 mm CW for new shell crab, 142 for old shell crab).

To address the impact of the revised data on the assessment, I updated the retained size frequencies in the directed fishery, re-ran the accepted 2014 assessment model configuration (TCSAM2014), and compared model outputs. Basically, the revised data had very little impact on the original assessment results. Model-predicted time series for male and female survey biomass are essentially identical (Fig. 1a.2), as are estimated time series for MMB and recruitment (Fig. 1a.3). The estimated male selectivity in the directed fishery was *slightly* different for 2013 between the two models (Fig. 1a.4), while those for other years were essentially identical. Estimates of average recruitment, current and projected MMB, and ABC and OFL were also almost identical (Fig. 1a.5).
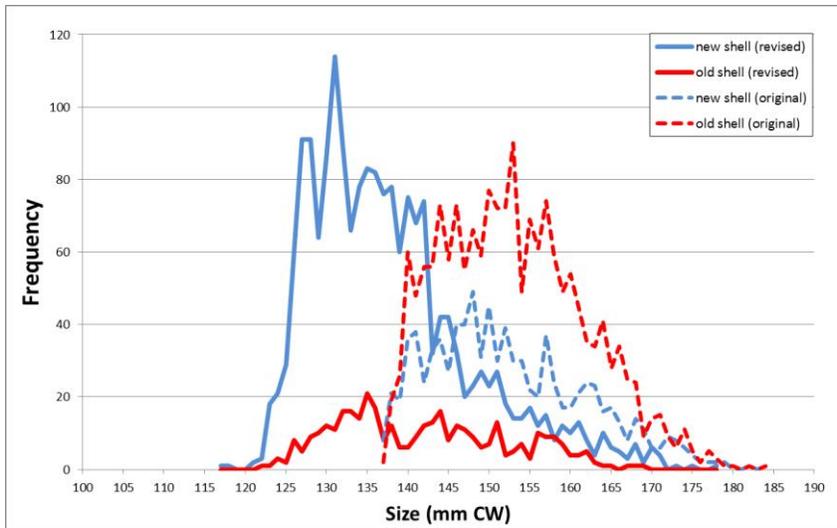
Figure 1a.1. Comparison of dockside size frequencies (1-mm bin size) by shell condition for retained Tanner crab in the directed fishery from 2013/14. Dashed lines: data incorporated into the 2014 assessment; solid lines: revised size frequencies.

a)

b)
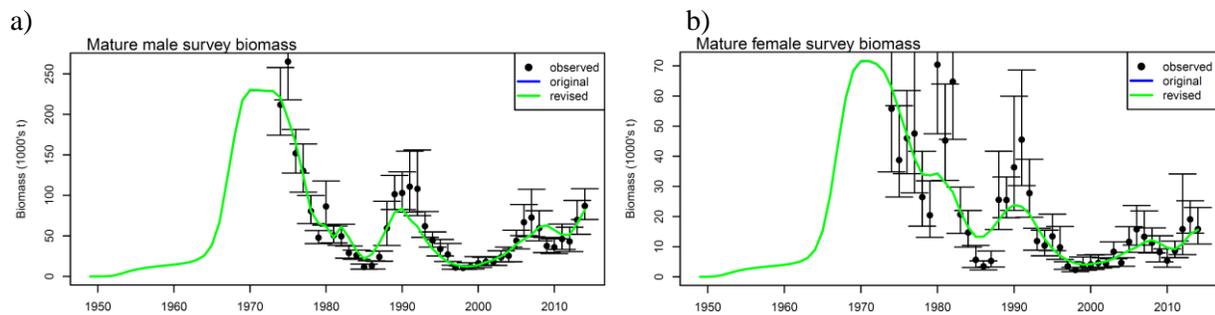
Figure 1a.2. Comparison of fits to mature survey biomass by sex using the 2014 assessment model with the original data (blue line) and with the revised 2013/14 dockside size frequencies (green line). [Note: the results using the original data are completely overlaid by those using the revised data.]

a)

b)
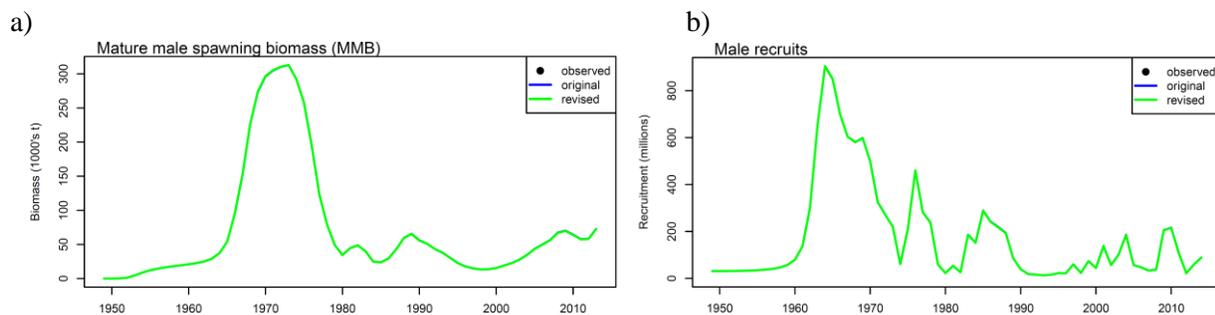
Figure 1a.3. Comparison of time series of a) model-estimated MMB and b) male recruitment using the 2014 assessment model with the original data (blue line) and the revised 2013/14 dockside size frequencies (green line). [Notes: 1) the results using the original data are completely overlaid by those using the revised data; 2) there are no observations for comparison to the models' results.]

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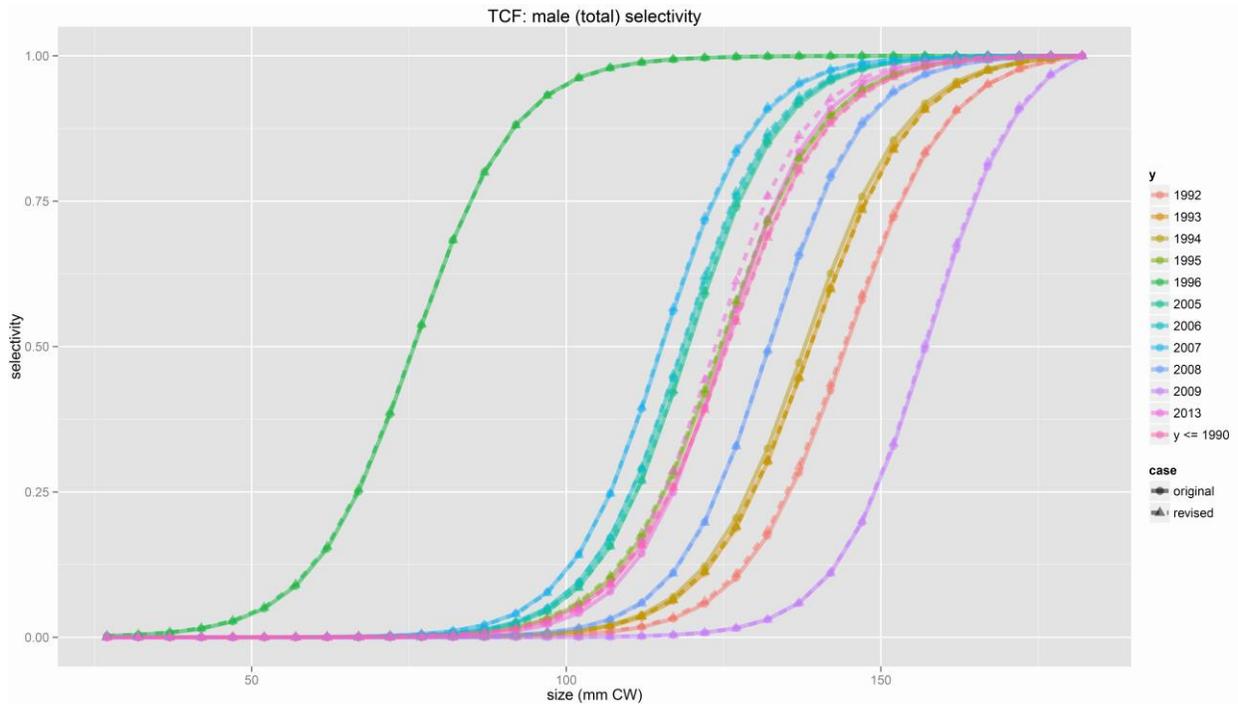
Figure 1a.4. Comparison of male total selectivity functions by year in the directed Tanner crab fishery estimated using the original data (solid lines, circles) and using the revised dockside size frequencies (dashed lines, triangles). Estimated functions for 2013 are slightly different.
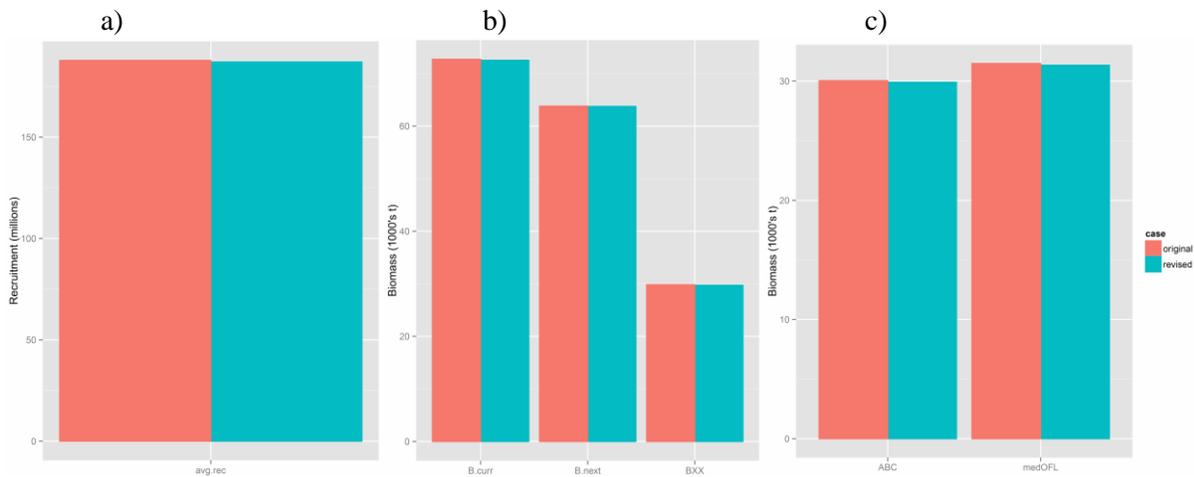

Figure 1a.5. Comparison of a) estimated average recruitment, b) current MMB (B.curr), projected MMB (B.next), and B35%, and c) calculated ABC and median OFL (medOFL) obtained from the 2014 assessment model using the original (coral) and revised (turquoise) data.

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1.b NMFS trawl survey

Annual observations from 1974 to 2014 of Tanner crab abundance, biomass, and population composition from the annual NMFS Eastern Bering Sea Summer Bottom Trawl Survey were included in the 2014 assessment. The bottom trawl survey has been conducted since the 1970s. Starting in 1975, the survey was expanded from Bristol Bay to include the majority of the continental shelf. Prior to 1982, several trawl gear combinations (nets and doors) were used during the survey, but the gear was standardized in 1982. Prior to 1988, the number of stations varied annually and gradually increased until being standardized in 1988. Since 1988, 376 standard stations have been included in the surveys. Between 1994 and 2010, survey stations at which more than 100 legal-sized Tanner or red king crab were considered to be "hot spots". For each "hot spot", additional tows were made within the area corresponding to the station to reduce the variance associated with the large catch. Starting in 2011, this "hot spot" protocol was discontinued. Finally, due to changes in timing of the red king crab reproductive cycle with temperature, some stations in Bristol Bay sampled at the beginning of the survey were re-sampled at the end of the survey in some years to better characterize female red king crab abundance.

An effort is currently being made to "clean up" the survey data used in the crab stock assessments by developing a standardized time series. One aspect of this standardization is that the 1974 survey will be dropped from the standard survey dataset, which will now start in 1975. Another aspect is that multiple tows at a station (e.g., "hot spot" tows) will be eliminated and a single "standard" tow will be selected to represent the station. The extent to which these changes will impact the Tanner crab assessment is addressed in this section.

I chose to address the impact of changes to the survey data on the Tanner crab assessment in a two-step process. Because the changes associated with the revised 2013 dockside size frequencies were very small, I started with the "revised" data discussed above in Section 1.a. (the 2014 assessment data with the 2013 revised dockside size compositions), rather than the exact dataset used in the 2014 assessment, to assess the cumulative implications of the revisions. First, I dropped the 1974 survey from the data used in the model, re-ran the accepted 2014 assessment model configuration (TCSAM2014) with the (now doubly) revised data, and compared model outputs to results from the 2014 assessment. These results are discussed in the Section 1.b.i. Next, I replaced the original survey data for 1975-2014 with the revised version for the same time period, re-ran TCSAM2014 with the (now triply) revised data, and compared model outputs to results from the 2014 assessment. These results are discussed in the Section 1.b.ii.

1.b.i Dropping the 1974 NMFS trawl survey

Dropping the 1974 survey from the data led to fairly small differences between the revised model and 2014 assessment results. Small differences were evident between the two model runs for model-estimated survey biomass (Fig. 1bi.1), MMB (Fig. 1bi.2a), and recruitment time series (Fig. 1bi.2b), but only during the 1965-1976 time period—prior to 1965 and subsequent to 1976 the time series were essentially identical. Estimated average recruitment, current and projected MMB, and ABC and median OFL (Fig. 1bi.3) were also essentially identical between the two model runs.

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a)

b)
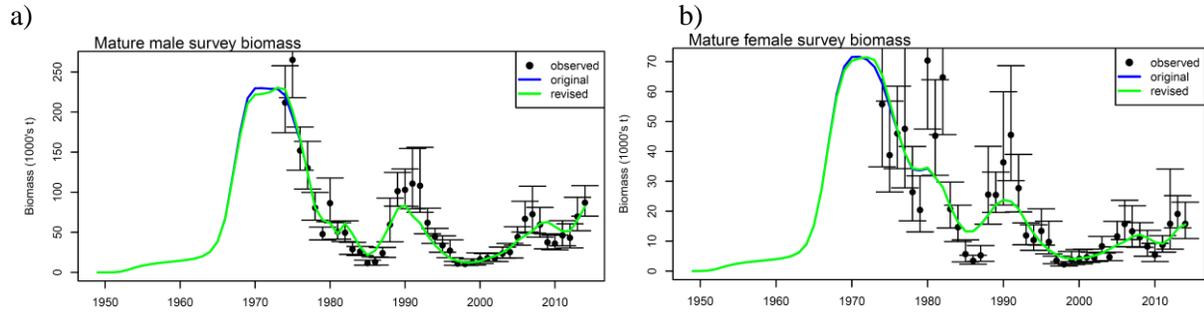
Figure 1bi.1. Comparison of fits to mature survey biomass by sex from the 2014 assessment model using the original data (blue line) and the revised data (green line) with the 1974 survey excluded from the model fitting procedure.

a)

b
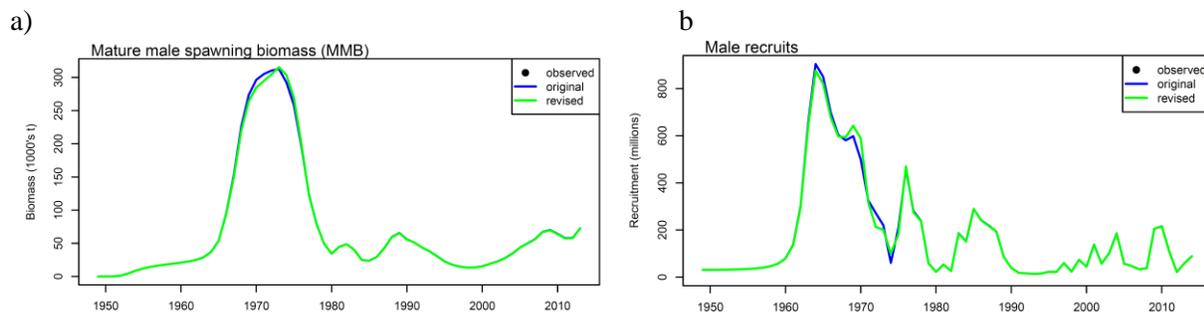
Figure 1bi.2. Comparison of time series of model-estimated MMB from the 2014 assessment model using the original data (blue lines) and the revised data with the 1974 survey excluded from the model fitting procedure.[Note: there are no observations for comparison to the models' results.]
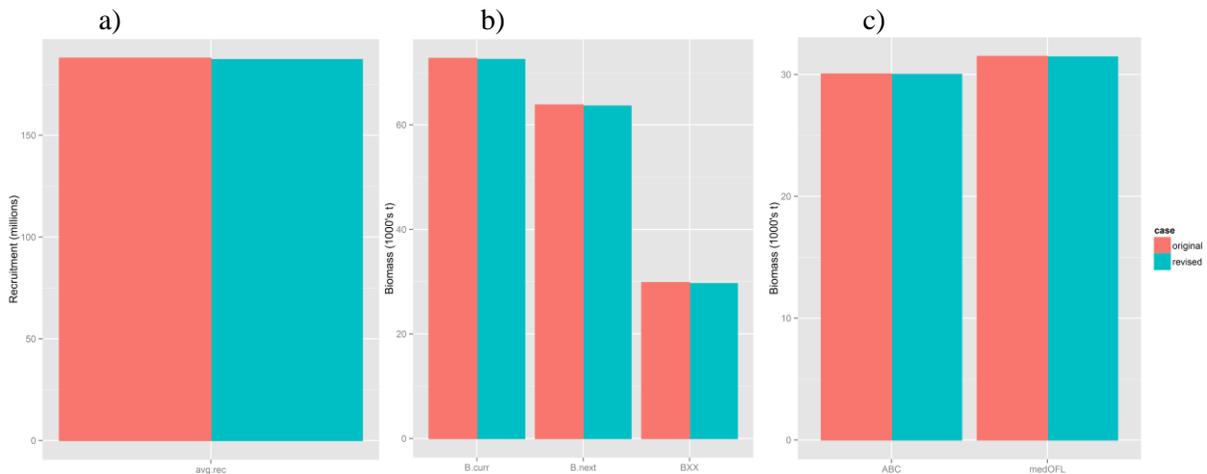
Figure 1bi.3. Comparison of a) estimated average recruitment, b) current MMB ("B.curr"), projected MMB ("B.next"), and B35% ("BXX"), and c) calculated ABC and median OFL ("medOFL") obtained from the 2014 assessment model using the original (coral) and revised (turquoise) data.

1.b.ii Revised 1975-2014 NMFS trawl survey data
To be addressed.

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2. Impact of assumed handling mortality on assessment results

Based on a presentation by D. Urban (NMFS) at the May 2014 Crab Plan Team (CPT) meeting on short term mortality for Tanner crab caught in the crab fisheries and subsequent discussion by the CPT (ref.), the assumed handling mortality used in the assessment model for Tanner crab caught and discarded in the directed and other crab pot fisheries was revised downward from 0.50 (50% mortality) to 0.321 (32.1%). As shown at the September 2014 CPT meeting, the revised value for handling mortality results in lower values for OFL and ABC than would have been obtained using the old value—contrary to expectations. As a follow-up on this issue, I've re-run the accepted 2014 assessment model and data using 25 different values for assumed pot fishery handling mortality ranging from 0.05 (5% mortality on discarded crab) to 1.00 (100% mortality) to better discern the trends in assessment results with changes in the assumed value.

The results of this more comprehensive study are consistent with the trends discerned at the September 2014 CPT meeting. Estimated average recruitment increased with assumed pot fishery handling mortality (Fig. 2.1a), as did current mature male biomass (MMB), projected MMB, and B35% (Fig. 2.1b). F35% was inversely-related to assumed pot-fishery handling mortality (Fig. 2.2a), while ABC and OFL were positively related to it (Fig. 2.2a). The model also exhibited decreasing trends in estimated male survey catchability with increased handling mortality (Fig. 2.3a), as well as decreasing trends in average ln-scale fishing mortality in the directed and groundfish trawl bycatch fisheries (Fig. 2.3b).

The mechanism driving this dependence has not been conclusively identified, and likely reflects the interaction of many components in minimizing the model's objective function. This is not surprising, given the complexity of the model and the myriad tradeoffs it can make by adjusting parameter estimates to suitably fit the data. However, the results are consistent with the model most easily adjusting mean recruitment to reflect changes in the assumed handling mortality. From the population perspective, increased handling mortality should lead to lower population sizes (all else being equal) because fishing mortality is larger. However, the fishery and survey datasets to be fit remain unchanged as assumed pot fishing handling mortality is changed, so the model adjusts parameters to obtain the best fit to these datasets. If all other estimated parameters remained the same, then mean recruitment would necessarily have to increase to offset population losses due to increased handling mortality in order that model-estimated fishery and survey catch levels continue to match the fishery survey catches that constitute the data the model is trying to match. Trends in other model quantities with increased handling mortality (Fig.s 2.2, 2.3) appear to be consistent with the trend in mean recruitment as the driver for these changes. Model quantities related to population biomass (current biomass, projected biomass, and particularly B35%, Fig. 2.1b) scale with mean recruitment and exhibit increasing trends with handling mortality. Conversely, F35% would be expected to be inversely related to handling mortality, and it indeed decreases with increased handling mortality (Fig. 2.2a). ABC and OFL also scale with mean recruitment and, again, exhibit increasing trends with handling mortality (Fig. 2.2b). Because the fisheries capture proportionally fewer small crab than large crab, the impact of handling mortality is proportionally smaller for smaller crab--so the number of small crab will go up with increased handling mortality even if recruitment increased only to exactly match the loss of (larger) crab due through discarding. However, this in turn implies the survey should "see" more small crab as handling mortality (and recruitment) increases—which it doesn't because the survey data doesn't change. One way the model could respond to this conflict is to estimate smaller survey q's (catchability coefficients) as handling mortality increases, which is exactly what happens (Fig. 2.3b). Finally, median fishing mortality rates (not capture rates) in

the snow crab bycatch fishery would be expected to increase with increased discard mortality in the pot fisheries, while fishing mortality due to the groundfish trawl fisheries would be expected to decline, and both do so (Fig. 2.3b). Whether or not the median fishing mortality in the directed fishery would be expected to be positively related to discard mortality probably depends on the fraction of discarded crab relative to retained crab. For the directed fishery, it appears that retention is the greater factor and thus median fishing mortality in the directed fishery is inversely related to discard mortality.

a)

b)
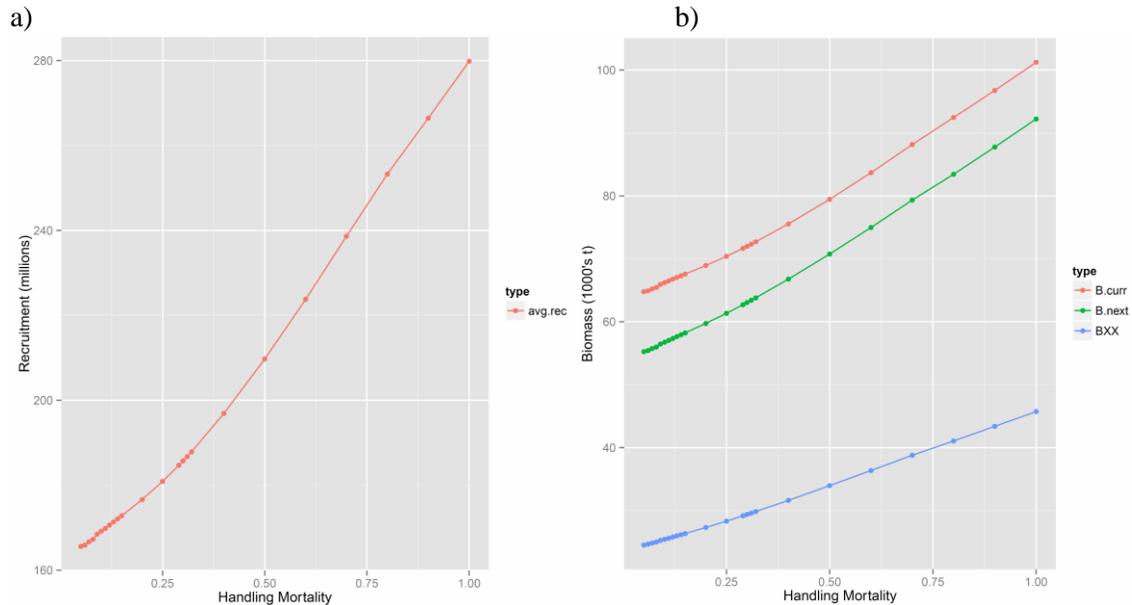
Figure 2.1. Dependence on assumed handling mortality for estimated a) average recruitment (1982-2014) and b) current MMB ('B.curr'), projected MMB ('B.next'), and $B_{35\%}$ ('BXX').

a)

b)
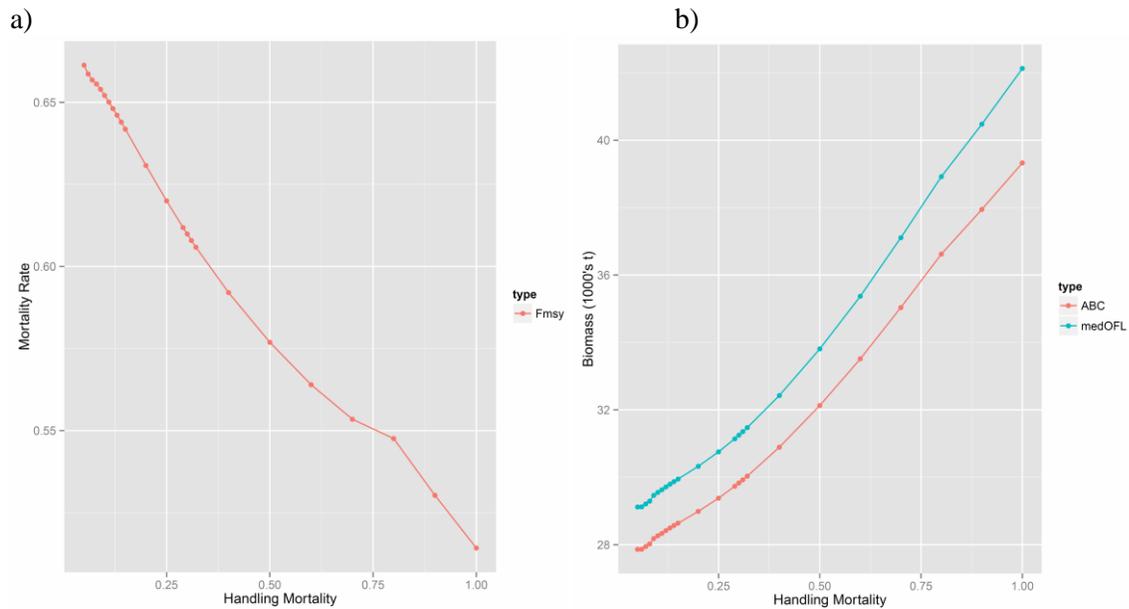
Figure 2.2. Dependence on assumed handling mortality for estimated a) $F_{35\%}$ ('Fmsy') and b) ABC and median OFL ('medOFL').

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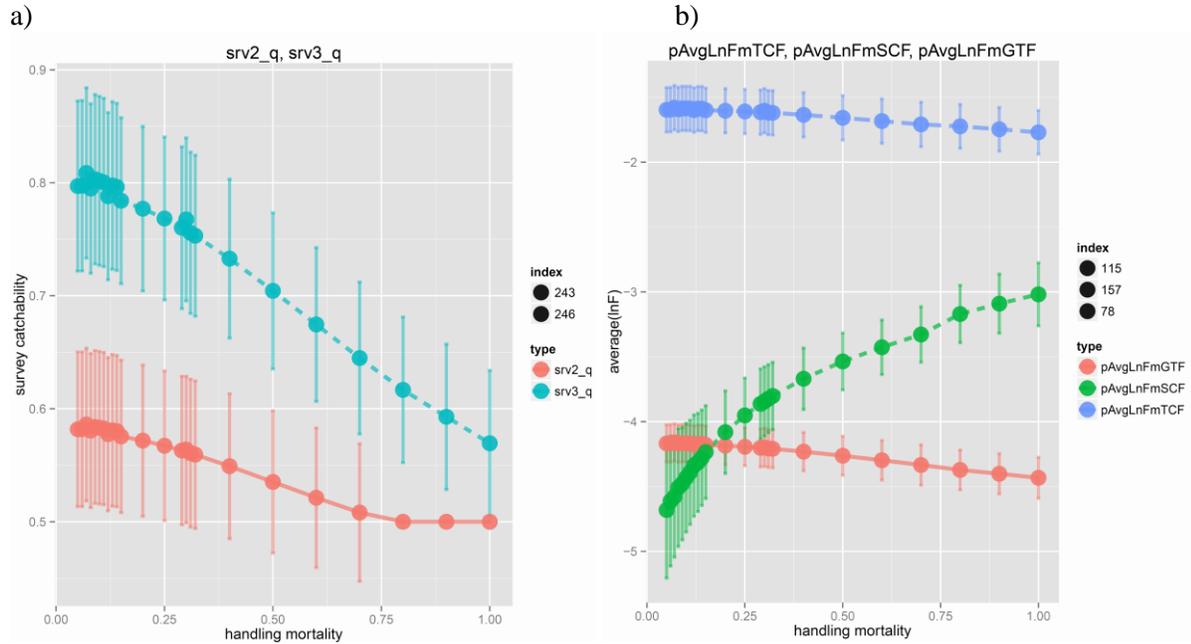
Figure 2.3. Dependence on assumed handling mortality for a) estimated male survey selectivity during 1982-1987 ('srv2_q') and after 1987 ('srv3_q') and b) average ln-scale fishing mortality rate for the directed Tanner crab fishery ('pAvgLnFmTCF'), the snow crab bycatch fishery ('pAvgLnFmSCF'), and the groundfish fishery ('pAvgLnFmGTF').

3. TCSAM (Tanner Crab Stock Assessment Model) 2015 Description

Introduction

TCSAM2015, the 2015 version of the Tanner crab model is an integrated assessment model that is fit to multiple data sources. It was developed by the author in C++ using AD Model Builder (Fournier et al., 2012) libraries. TCSAM2015 is heavily based on the Tanner crab model used in the 2014 stock assessment (Stockhausen, 2014), but it incorporates the Gmacs (Whitten et al., 2013) approach to modeling fishing mortality based on capture rates and is completely new model code and has a format for model input files that differs from the current assessment model.

Model parameters in TCSAM2015 are estimated using a maximum likelihood approach. Data components entering the likelihood include fits to survey abundance or biomass, survey size compositions, retained catch, retained catch size compositions, total catch from at-sea observer sampling, and total catch size compositions from at-sea observer sampling. It is possible to specify Bayesian-like priors on all parameters using the input files to the model. Multiple time blocks can also be defined for any model process (e.g., recruitment, natural mortality) using the input files.

An R-based simulator, rsimTCSAM, has also been developed to provide a completely independent code base for testing TCSAM2015 features, functionality and estimation performance. Additionally, an R-based package, tcsam2015, has been developed to allow plotting of TCSAM2015 model output, comparison of rsimTCSAM and TCSAM2015 models, and comparison of multiple TCSAM2015 models. All code related to TCSAM2015 (the ADMB and C++ code, the rsimTCSAM R-code, and the tcsam2015 R code) is available through the GitHub code repository at https://github.com/wStockhausen. under the repositories "wtsTCSAM2015" (the ADMB code), "wtsADMB" (a required C++ library I developed), "tcsam2015" (the R package/code for post-run visualization), and "rsimTCSAM" (the R package/code for simulating data to test TCSAM2015).

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 $\boldsymbol{\delta t_y^F \leq \delta t_y^m}$

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:

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

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:

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$$n^2_{y,x,m,s,z} = e^{-F^T_{y,x,m,s,z}} \cdot n^1_{y,x,m,s,z} \qquad\qquad\qquad\qquad\qquad \text{A1.2}$$

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 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^m_y (generally Feb. 15). The numbers surviving at δt^m_y in year y are then given by:

$$n^3_{y,x,m,s,z} = e^{-M_{y,x,m,s,z} \cdot (\delta t^m_y - \delta t^F_y)} \cdot n^2_{y,x,m,s,z} \qquad\qquad\qquad \text{A1.3}$$

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:

$$n^4_{y,x,MAT,NS,z} = \sum_{z'} \Theta^{MAT}_{y,x,z,z'} \cdot \phi_{y,x,z'} \cdot n^3_{y,x,IMM,NS,z'} \qquad\qquad \text{A1.4a}$$

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

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

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 $\Theta^m_{y,x,z,z'}$ is the growth transition matrix from size z' to z for that crab, which may depend on whether ($m=MAT$; eq. A1.4a) or not ($m=IMM$; eq. A1.4b) the terminal molt to maturity occurs. Additionally, crabs 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 $m=IMM$, $s=NS$ 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:

$$R_{y,x,z} = \dot{R}_y \cdot \ddot{R}_{y,x} \cdot \dddot{R}_{y,z} \qquad\qquad\qquad\qquad\qquad\qquad \text{A1.5a}$$

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

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A2. Calculation sequence when $\delta t_y^m < \delta t_y^F$

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_y^m (generally Feb. 15). The numbers surviving at δt_y^m in year y are given by:

$$n_{y,x,m,s,z}^1 = e^{-M_{y,x,m,s,z} \cdot \delta t_y^m} \cdot n_{y,x,m,s,z} \qquad \text{A2.1}$$

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:

$$n_{y,x,MAT,NS,z}^2 = \sum_{z'} \Theta_{y,x,z,z'}^{MAT} \cdot \phi_{y,x,z'} \cdot n_{y,x,IMM,NS,z'}^1 \qquad \text{A2.2a}$$

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

$$n_{y,x,MAT,OS,z}^2 = n_{y,x,MAT,OS,z}^1 + n_{y,x,MAT,NS,z}^1 \qquad \text{A2.2c}$$

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 $\Theta_{y,x,z,z'}^m$ is the growth transition matrix from size z' to z for that crab, which may depend on whether ($m=MAT$; eq. A2.2a) or not ($m=IMM$; eq. A2.2b) the terminal molt to maturity occurs. 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 $m=IMM$, $s=NS$ 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_y^F). The numbers surviving at δt_y^F in year y are then given by:

$$n_{y,x,m,s,z}^3 = e^{-M_{y,x,m,s,z} \cdot (\delta t_y^F - \delta t_y^m)} \cdot n_{y,x,m,s,z}^2 \qquad \text{A2.3}$$

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_y^F in year y. The numbers that remain after the fisheries are prosecuted are given by:

$$n_{y,x,m,s,z}^4 = e^{-F_{y,x,m,s,z}^T} \cdot n_{y,x,m,s,z}^3 \qquad \text{A2.4}$$

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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:

$$R_{y,x,z} = \dot{R}_y \cdot \ddot{R}_{y,x} \cdot \dddot{R}_{y,z} \qquad\qquad \text{A2.5a}$$

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

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:

$$lnM_{y,x,m} = \mu^0 + \mu^0_t + \delta_{m,IMM} \cdot \mu^{IMM}_t + \delta_{x,FEM} \cdot \mu^{FEM}_t + \delta_{x,FEM} \cdot \delta_{m,IMM} \cdot \mu^{FEM,IMM}_t \qquad \text{B.1}$$

$$M_{y,x,m,s,z} = \begin{cases} \exp(lnM_{y,x,m}) & \text{if Lorenzen option is not selected for block } t \quad \text{B.2a} \\ \exp(lnM_{y,x,m}) \cdot \dfrac{z_{base}}{z} & \text{if Lorenzen option is selected for block } t \quad \text{B.2b} \end{cases}$$

where y falls into time block t, the μ's are (potentially) estimable parameters on the ln-scale, , $\delta_{i,j}$ is 1 if $i=j$ and 0 otherwise. μ^0 represents the baseline (ln-scale) natural mortality rate on mature males, while μ^0_t is the offset on mature males in time block t, μ^{IMM}_t is the offset for immature crab in time block t, μ^{FEM}_t is the offset for females in time block t, and $\mu^{FEM,IMM}_t$ is the offset for immature 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, ==ref.==), where z_{base} is a specified reference size (mm CW).

This parameterization for natural mortality differs from that in TCSAM2013 (Appendix 1, 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 1, 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 TCSAM2015 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
As a user option, annual growth of immature crab in TCSAM2015 can be based on the same approach used in TCSAM2013 or it can be based on that used in Gmacs. In either case, growth can vary by time block. As such, growth is expressed by sex-specific transition matrices $\Theta_{t,x,z,z'}$ that specify the

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probability that crab in pre-molt size bin z grow to post-molt size bin z' during time block t. The sex-specific growth matrix $\Theta_{t,x,z,z'}$ is given by

$$
\Theta_{t,x,z,z'}
= \begin{cases}
c_{t,x,z} \cdot \Delta_{z,z'}{}^{\alpha_{t,x,z}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_{t,x}}} & (TCSAM2013) \\
c_{t,x,z} \cdot \int_{z}^{z+\Delta z} dz'' \cdot \Delta_{z'',z'}{}^{\alpha_{t,x,z}-1} \cdot e^{-\frac{\Delta_{z'',z'}}{\beta_{t,x}}} & Gmacs
\end{cases}
$$

Sex-specific (x) transition matrix for growth from pre-molt z to post-molt z', with $z' \geq z$ C.1

$$
c_{x,z}
= \begin{cases}
\left[\sum_{z'} \Delta_{z,z'}{}^{\alpha_{t,x,z}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_{t,x}}} \right]^{-1} & TCSAM2013 \\
\left[\int_{z_{min}}^{\infty} dz'' \cdot \Delta_{z'',z'}{}^{\alpha_{t,x,z}-1} \cdot e^{-\frac{\Delta_{z'',z'}}{\beta_{t,x}}} \right]^{-1} & Gmacs
\end{cases}
$$

Normalization constant so

$$1 = \sum_{z'} \Theta_{x,z,z'}$$

C.2

$$\Delta_{z,z'} = z' - z$$ Actual growth increment   C.3

$$\alpha_{t,x,z} = [\bar{z}_{t,x,z} - z]/\beta_{t,x}$$ Mean molt increment, scaled by β_x C.4

$$\bar{z}_{t,x,z} = e^{a_{t,x}} \cdot z^{b_{t,x}}$$ Mean size after molt, given pre-molt size z C.5

where the $a_{t,x}$, $b_{t,x}$, and $\beta_{t,x}$ (parameters in TCSAM2013) are arithmetic-scale versions of the ln-scale model parameters $pLnA_{t,x}$, $pLnB_{t,x}$, and $pLn\beta_{t,x}$:

$$a_{t,x} = e^{pLnA_{t,x}}$$ C.6

$$b_{t,x} = e^{pLnB_{t,x}}$$ C.7

$$\beta_{t,x} = e^{pLn\beta_{t,x}}$$ C.8

Again, because $a_{t,x}$, $b_{t,x}$, and $\beta_{t,x}$ must be non-negative, the associated parameters in TCSAM2015 are estimated on the ln-scale and transformed to the arithmetic scale.

$\Theta_{t,x,z,z'}$ 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. 1, Section C). While priors may be defined for the

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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

Maturation of immature crab in TCSAM2015 is based on a similar approach to that taken in TCSAM2013, except that the sex- and size-specific probabilities of maturation, $\phi_{t,x,z}$ (where size z is pre-molt size), can vary by time block. After molting, but before assessing growth, the numbers of (new shell) crab remaining immature, $n^+_{y,x,IMM,NS,z}$, and those maturing, $n^+_{x,MAT,NS,z}$, at pre-molt size z are given by:

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

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 pre-molt size z.

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

$$\phi_{t,FEM,z} = \begin{cases} \dfrac{1}{1 + e^{p^{mat}_{t,FEM,z}}} & z \leq z^{mat}_{t,FEM} \\ 1 & z > z^{mat}_{t,FEM} \end{cases} \qquad \text{female probabilities of maturing at pre-molt size } z \qquad \text{D.2a}$$

$$\phi_{t,MALE,z} = \begin{cases} \dfrac{1}{1 + e^{p^{mat}_{t,MALE,z}}} & z \leq z^{mat}_{t,MALE} \\ 1 & z > z^{mat}_{t,MALE} \end{cases} \qquad \text{male probabilities of maturing at pre-molt size } z \qquad \text{D.2b}$$

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 differs from that used in TCSAM2013 (App. 1, Section D). In TCSAM2013, the model parameters are estimated on the ln-scale and constrained to be less than 0 so that the resulting maturation probabilities are between 0 and 1. However, the parameters associated with larger size bins frequently hit the 0 upper bound in TCSAM2013, which may affect overall model convergence and stability. The logit-scale parameters used here may be less problematic in this respect.

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 are also applied in TCSAM2015.

E. Model processes: recruitment

Recruitment of immature (new shell) crab in TCSAM2015 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

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

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

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

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

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

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

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

$$c = \sum_z \Delta_z^{\frac{\alpha_t}{\beta_t} - 1} \cdot e^{-\frac{\Delta_z}{\beta_t}} \qquad\qquad \text{normalization constant so that } 1 = \sum_z \dddot{R}_{t,z} \quad \text{E.5}$$

$$\Delta_z = z + \delta z/2 - z_{min} \qquad\qquad \text{offset from minimum size bin} \qquad\qquad \text{E.6}$$

$$\alpha_t = e^{pLnRa_t} \qquad\qquad \text{gamma distribution location parameter} \qquad \text{E.7}$$

$$\beta_t = e^{pLnRb_t} \qquad\qquad \text{gamma distribution shape parameter} \qquad \text{E.8}$$

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 TCSAM2015 are specified independently from fisheries and surveys in TCSAM2015, 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 ascending logistic function

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$$S_z = \frac{1}{1 + e^{-\beta \cdot (z - z_{50})}} \qquad\qquad \text{ascending logistic function} \qquad \text{F.1}$$

with parameters z_{50}, β and the double logistic function

$$S_z = \frac{1}{1 + e^{-\beta_a \cdot (z - z_{a50})}} \cdot \frac{1}{1 + e^{\beta_d \cdot (z - z_{d50})}} \qquad\qquad \text{double logistic} \qquad \text{F.2}$$

with parameters $z_{a50}, \beta_a, z_{d50}, \beta_d$ are available as selectivity/retention functions for use in the model (z represents crab size in the equations). For each function, several alternative parameterizations are available. For the ascending logistic function, these are:

Alternative parameters	relation to standard parameters	
$z_{50}, \Delta z_{(95-50)}$	$\beta = \dfrac{\ln(19)}{\Delta z_{(95-50)}}$	F.3
lnZ_{50}, β	$z_{50} = \exp(lnZ_{50})$	F.4
$z_{50}, ln\Delta z_{(95-50)}$	$\beta = \dfrac{\ln(19)}{\exp(ln\Delta z_{(95-50)})}$	F.5

For the double logistic, these are:

Alternative parameters	relation to standard parameters	
$z_{a50}, \Delta z_{a(95-50)}, z_{d50}, \Delta z_{d(50-95)}$	$\beta_a = \dfrac{\ln(19)}{\Delta z_{a(95-50)}}, \beta_d = \dfrac{\ln(19)}{\Delta z_{d(50-95)}}$	F.6
$z_{a50}, ln\Delta z_{a(95-50)}$ $ln\Delta z_{(d95-a95)}, ln\Delta z_{d(50-95)}$	$\beta_a = \dfrac{\ln(19)}{\exp(ln\Delta z_{a(95-50)})}$ $z_{d50} = z_{a50} + \exp(ln\Delta z_{(d95-a95)}) + \exp(ln\Delta z_{d(50-95)})$ $\beta_d = \dfrac{\ln(19)}{\exp(ln\Delta z_{d(50-95)})}$	F.7

The alternative parameterizations may have better convergence properties in some circumstances than the standard parameterizations. In addition, a double normal selectivity function (requiring 6 parameters to specify) will also be implemented as an alternative to the double logistic function.

In addition, 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 eventually 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. However, parameters that are unused during a model run (e.g., *pS6*) can be easily excluded by setting the associated number of estimated parameter values to 0 in the parameter configuration file.

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 TCSAM2015 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.

TCSAM2015 uses the Gmacs approach to modeling fishing mortality (see App. 2 for a detailed derivation of the basic equations). 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

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

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

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

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. It follows from Appendix 2 that the number of crab retained in fishery f classified as x, m, s, z in year y is given by

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

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

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

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

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

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 in the usual fashion as a function separable into separate year and size components such that

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

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:

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

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

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

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

$$a_{v,y,x,m,s,z} = q_{v,y,x,m,s,z} \cdot n_{y,x,m,s,z} \qquad \text{survey abundance} \qquad \text{H.1}$$

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

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:

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

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:

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

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 TCSAM2015 model is fit by minimizing an objective function, $\mathcal{O}$, 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:

$$\mathcal{O} = -2 \sum_{p} \lambda_p \cdot \ln(\wp_p) - 2 \sum_{l} \lambda_l \cdot \ln(\mathcal{L}_l) \qquad \text{model objective function} \qquad \text{I.1}$$

where $\wp_p$ represents the pth prior probability function, $\mathcal{L}_l$ represents the lth 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 K 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:

$$\ln(\mathcal{L}) = \sum_{y} n_{y,c} \cdot \sum_{z} \{ p_{y,c,z}^{obs} \cdot \ln(p_{y,c,z}^{mod} + \delta) - p_{y,c,z}^{obs} \cdot \ln(p_{y,c,z}^{obs} + \delta) \} \qquad \begin{array}{l} \text{multinomial} \\ \text{log-likelihood} \end{array} \qquad \text{I.2}$$

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, $p_{y,c,z}^{obs}$ 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), $p_{y,c,z}^{mod}$ 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.

Time series components

Likelihood components involving abundance/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

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

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

The ln-scale lognormal likelihood function is

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

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

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

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

This is equivalent to specifying a normal log-likelihood with $\sigma_{y,x}^2 \equiv 1$. This is the likelihood function applied tin TCSAM2013 to fishery catch time series.

K. Parameter specification for model processes

Parameter specification in TCSAM2015 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 TCSAM2015, "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. There are no parameters of the third kind (yet!). Hopefully these terms will be clarified by the following example.

Text Box 3.1 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* (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 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.

Literature cited

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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)
25| pLnRb #ln-scale gamma distribution scale paramter for pr(size-at-recruitment)
26| 1  #number of parameters
27| #id  lower   upper jitter? init_val    phase   resample?   prior_wgt   prior_type prior_params prior_consts
28|  1    0      4    ON    1.386294     -1        OFF          1           normal     1.5  1 #init_val = ln(4.00)
29| pDevsLnR #annual ln-scale recruitment deviations
30| 2      #number of parameter vectors
31| #id idx.type block    read? lower  upper jitter? init_val phase resample? prior_wgt   prior_type prior_params prior_consts
32|  1   YEAR  [-1:1974] FALSE  -10   10    OFF      0       2     OFF        1           none   #spin-up period
33|  2   YEAR  [1975:-1] FALSE  -10   10    OFF      0       2     OFF        1           none   #data period
```

Text Box 3.1. Example parameter specification for recruitment in TCSAM2015. Input values are in black text, comments are in green. Line numbers (text in blue) are shown for reference purposes.

4. Equilibrium size distribution for a terminally-molting crab stock (e.g., Tanner crab)

The following section outlines the equilibrium solution for sex-specific numbers (or proportions)-at-size for a Tier 3 crab stock in which individuals undergo a terminal molt to functional maturity. As formulated, the population is explicitly characterized by maturity state (immature, <u>ma</u>ture) and shell condition (<u>n</u>ew shell, <u>o</u>ld shell). Sex-specific solutions can be obtained by plugging in sex-specific rates to describe the population processes, as well as sex-specific recruitment (or sex ratio, if proportions are desired). The population dynamics used to develop the equilibrium solution are appropriate for a Tier 3 stock (recruitment is independent of stock size), so this solution is not applicable to stocks which have a well-defined stock-recruit relationship (i.e., Tier 1 or 2 stocks). Note also that references to numbered equations here are specific to this section. Vector quantities appear in italicized typeface (e.g., R), matrix quantities appear in italicized bold typeface (e.g. $\boldsymbol{\Phi}$).

Population states (subscripted by size)

$\qquad$ *in*– immature new shell crab (numbers-at-size vector)
$\qquad$ *io*– immature old shell crab (numbers-at-size vector)
$\qquad$ *mn* – mature new shell crab (numbers-at-size vector)
$\qquad$ *mo* – mature old shell crab (numbers-at-size vector)

Population processes (double-subscripted by size)

$\qquad$ $\boldsymbol{S_1}$ – survival from start of year to time of molting/growth of immature crab (diagonal matrix)
$\qquad$ $\boldsymbol{S_2}$ – survival after time of molting/growth of immature crab to end of year (diagonal matrix)
$\qquad$ $\boldsymbol{\Phi}$ – probability of an immature crab molting (pr(molt|z), where z is pre-molt size; diagonal matrix)
$\qquad$ $\boldsymbol{\Theta}$ – probability that a molt is terminal (pr(molt to maturity|z, molt), where z is pre-molt size; diagonal matrix)
$\qquad$ $\boldsymbol{T}$ – size transition matrix (non-diagonal matrix)
$\qquad$ $\boldsymbol{I}$ – identity matrix
$\qquad$ R –(sex-specific) number of recruits by size (vector)

In the following, the above (except for the identity matrix and R) are subscripted by population state (*in*, *io*, *mn*, *mo*) for generality. In particular, if skip-molting of immature crab occurs prior to terminal molt, then the survival of immature crab may differ between those that molted (to new shell condition) and those that skipped (and became immature, old shell crab). For Tanner crab, skip molting is assumed to be negligible and thus all immature crab are "new shell".

Dynamics

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

Numbers recruiting-at-size are assumed immature, new shell. "+" indicates year+1.

Equilibrium equations

In equilibrium, the numbers-at-size in each population category remain the same, so the population dynamics at equilibrium are simply eq.s 1-4 above with the "+" superscripts removed:

$$in = R + \boldsymbol{S_{2in}} \cdot \{\boldsymbol{T_{in}} \cdot (\boldsymbol{1} - \boldsymbol{\Theta_{in}}) \cdot \boldsymbol{\Phi_{in}} \cdot \boldsymbol{S_{1in}} \cdot in + \boldsymbol{T_{io}} \cdot (\boldsymbol{1} - \boldsymbol{\Theta_{io}}) \cdot \boldsymbol{\Phi_{io}} \cdot \boldsymbol{S_{1io}} \cdot io\} \qquad (6)$$
$$io = \boldsymbol{S_{2io}} \cdot \{(\boldsymbol{1} - \boldsymbol{\Phi_{in}}) \cdot \boldsymbol{S_{1in}} \cdot in + (\boldsymbol{1} - \boldsymbol{\Phi_{io}}) \cdot \boldsymbol{S_{1io}} \cdot io\} \qquad (7)$$
$$mn = \boldsymbol{S_{2mn}} \cdot \{\boldsymbol{T_{in}} \cdot \boldsymbol{\Theta_{in}} \cdot \boldsymbol{\Phi_{in}} \cdot \boldsymbol{S_{1in}} \cdot in + \boldsymbol{T_{io}} \cdot \boldsymbol{\Theta_{io}} \cdot \boldsymbol{\Phi_{io}} \cdot \boldsymbol{S_{1io}} \cdot io\} \qquad (8)$$
$$mo = \boldsymbol{S_{2mo}} \cdot \{\boldsymbol{S_{1mn}} \cdot mn + \boldsymbol{S_{1mo}} \cdot mo\} \qquad (9)$$

R above is equilibrium number of recruits-at-size vector

Equilibrium solution

To simplify the solution, the equilibrium equations above can be written in abbreviated form as:

$$in = R + A \cdot in + B \cdot io \tag{10}$$
$$io = C \cdot in + D \cdot io \tag{11}$$
$$mn = E \cdot in + F \cdot io \tag{12}$$
$$mo = G \cdot mn + H \cdot mo \tag{13}$$

where A, B, C, D, E, F, G, and H are square matrices.

Solving for io in terms of in in eq. 11, one obtains

$$io = \{1 - D\}^{-1} \cdot C \cdot in \tag{14}$$

Plugging 14 into 10 and solving for in yields

$$in = \{1 - A - B \cdot [1 - D]^{-1} \cdot C\}^{-1} \cdot R \tag{15}$$

Equations 14 for io and 15 for in can simply be plugged into eq. 12 to yield mn while eq. 13 can then be solved for mo, yielding

$$mo = \{1 - H\}^{-1} \cdot G \cdot mn \tag{16}$$

where (for completeness):

$$A = S_{2in} \cdot T_{in} \cdot (1 - \Theta_{in}) \cdot \Phi_{in} \cdot S_{1in} \tag{17}$$
$$B = S_{2in} \cdot T_{io} \cdot (1 - \Theta_{io}) \cdot \Phi_{io} \cdot S_{1io} \tag{18}$$
$$C = S_{2io} \cdot (1 - \Phi_{in}) \cdot S_{1in} \tag{19}$$
$$D = S_{2io} \cdot (1 - \Phi_{io}) \cdot S_{1io} \tag{20}$$
$$E = S_{2mn} \cdot T_{in} \cdot \Theta_{in} \cdot \Phi_{in} \cdot S_{1in} \tag{21}$$
$$F = S_{2mn} \cdot T_{io} \cdot \Theta_{io} \cdot \Phi_{io} \cdot S_{1io} \tag{22}$$
$$G = S_{2mo} \cdot S_{1mn} \tag{23}$$
$$H = S_{2mo} \cdot S_{1mo} \tag{24}$$

5. rsimTCSAM

"rsimTCSAM" is an R package I developed using RStudio for simulating datasets with which to test TCSAM2015 models. The package, as well as its source code and sample configuration files with which to run a simulation, is hosted in a public repository on GitHub at https://github.com/wStockhausen/rsimTCSAM.git. The current version (as of 4/25/2015) is 0.9.0. rsimTCSAM ("rsim", for short) is intended to be a port of the TCSAM2015 "operating model" (e.g., the TCSAM2015 population dynamics and observation models described in Section 3) to a code base completely independent of the ADMB-based model to facilitate code debugging and model testing. R was selected for the code base because it is a rich and flexible programming, statistical, and visualization environment, as well as because R forms the principal basis for analyzing and visualizing TCSAM2015 model output. Creating an rsim simulation consists of: 1) writing a "model configuration file" that defines the model configuration (range of years, number of sexes, number of fisheries, etc.), parameter values for the population dynamics and observation models, and data-related TCSAM2015 model options and 2) reading in the model configuration file and running the simulation by invoking the R function "runSim.TCSAM()". Model output consists of 1) a set of files suitable for use in a TCSAM2015 model run, 2) a series of plots reflecting the simulated model dynamics (available as a pdf, if so specified), and 3) an R list object encapsulating the configuration and arrays reflecting the model processes, dynamics, and observations for later comparison with TCSAM2015 model runs against the simulated data.

The following text boxes outline a basic "configuration file" for running an rsim simulation. The first section (see Text Box 5.1) of the configuration file begins with the keyword "ModelConfiguration", followed on the next line by "TC", indicating the simulation is for Tanner crab.

Model dimensions are specified in the subsequent section following the "DIMENSIONS" keyword. Because R allows text strings to be evaluated as the configuration file is parsed, it is possible to refer to the variables "mny" and "asy" (and "mxy") in the configuration file after the dimensions section, rather than repeating the values for the start year (mny), assessment year (asy), and final year (mxy=asy-1). This makes it quite simple, for example, to change all time blocks that refer to the final year (fisheries, e.g.) or assessment year (surveys, e.g.) by changing the value in the dimensions section rather than changing the value in every time block.

```
#====================
# rsimTCSAM configuration file
#
# This file runs the model from 1950 to 2014 to test generate
# test files for TCSAM2015. Basic configuration is:
#   1 time period for all biological processes
#   1 fishery, 1 time period for parameters, same F, selectivity for M/F
#   1 survey,  1 time period for parameters, same Q, selectivity for M/F
#====================
#----------------------------------------------------------
ModelConfiguration #keyword
TC      #model type (KC or TC for king crab or Tanner crab)
#----------------------------------------------------------
#-----dimensions
DIMENSIONS  #keyword
1950    #start year
2014    #assessment year (=mxy+1)
25      #min size cutpoint (mm)
185     #max size cutpoint (mm)
5       #size bin size (mm)
2       #number of sexes
'male' 'female'  #labels for sexes
2       #number of maturity states
'immature' 'mature'      #labels for maturity states
2       #number of shell conditions
'new shell' 'old shell' #labels for shell conditions
1       #number of fisheries
'TCF'  #labels for fisheries: Tanner crab directed fishery
1       #number of surveys
'NMFS trawl survey' #names for surveys
#----------------------------------------------------------
#-----parameters
PARAMETERS  #keyword
0.625  #mate time
0.625  #fish time
#--Weight-at-size
watZ   #required keyword
1          #number of time blocks
mny:asy #time block 1 (asy=assessment year)
#sex       maturity      a        b
'female' 'immature'  0.000637   2.794
'female'   'mature'  0.000344   2.956
 'male' 'immature'  0.000163   3.136
 'male'   'mature'  0.000163   3.136
```

Text Box 5.1.

Parameter values for model processes are specified after the "PARAMETERS" keyword. Within-year timing for mating and fishing activities are specified first, using the fraction of a year from July 1 on which the activities occur. Mating and fishing occur at the specified times for all model years. Most

model processes can be defined over several time blocks, using R vector syntax to define each time block (e.g. "c(mny:1965,1970,1980:mxy)"). Parameter values *a* and *b* describing weight-at-size, modeled as $W = aZ^b$, where *W* is weight in grams and *Z* is carapace width in mm, are specified by sex and maturity state for each time block.

Natural mortality (Text Box 5.2) is specified in time blocks by sex and maturity state. A non-zero cv can also be specified to introduce process error in the rate of natural mortality. An annual probability of molting for immature crab by sex and shell condition and be defined in time blocks using a size-specific ascending logistic function characterized by size at 50% probability of molting (z50) and its slope (sdv). Immature Tanner crab are assumed to molt annually, which is achieved in the model by setting z50 to a large number (e.g, 1000). The growth transition matrix for molting crab is specified by time block using sex-specific parameters describing the mean growth increment as a 2-parameter power-law function of size (ln(a) and ln(b)) and a gamma distribution scale factor. Note that ln-scale

```
#--Natural mortality
NaturalMortality  #required keyword
1        #number of time blocks
mny:mxy  #time block 1
#sex          maturity   M     cv
  'male'       'mature' 0.23  0.0
  'male'     'immature' 0.23  0.0
'female'       'mature' 0.23  0.0
'female'     'immature' 0.23  0.0
#--Molting
Molting  #required keyword
1     #number of time blocks
mny:mxy  #time block 1
#sex       shell condition    z50     sdv
  'male'  'new shell'         1000     10
  'male'  'old shell'         1000     10
'female'  'new shell'         1000     10
'female'  'old shell'         1000     10
#--Molt to maturity
MoltToMaturity  #required keyword
1         #number of time blocks
mny:mxy   #time block 1
#sex       z50      sdv
  'male'   100       10
'female'    80       10
#--Growth
Growth  #required keyword
1        #number of time blocks
mny:mxy  #time block 1
#sex       ln(a)          ln(b)           ln(scale)
  'male'   log(0.43)      log(0.97)       log(0.75)
'female'   log(0.70)      log(0.88)       log(0.75)
#--Recruitment
Recruitment  #required keyword
#initialization
#lnR      cvR     lnXR     sdXR    lnAlphaZ     lnBetaZ
log(71)   0.5      0.0      0.0    log(11.5)    log(4.0)
1  #number of time blocks
#years      lnR     cvR     lnXR    sdXR    lnAlphaZ    lnBetaZ
mny:mxy    log(71)   0.5      0.0     0.0   log(11.5)   log(4.0)
```
Text Box 5.2.

parameters can be specified as "log(x)", and the file parser will make the conversion to the ln-scale. Recruitment is treated somewhat differently from other processes, in that parameters describing the equilibrium recruitment pattern used to define the initial size composition of the stock are specified, as

well as parameters describing sex and size-specific recruitment in time blocks. Parameters used to specify recruitment processes include the mean ln-scale recruitment (lnR), the cv for recruitment (cvR), the logit-scale sex ratio (lnXR = ln(pr(male)/pr(female)), annual process error in the sex ratio (sdXR), and parameters describing the size composition of recruiting crab using a gamma distribution (lnAlphaZ and lnBetaZ).

Selectivity functions (Text Box 5.3) are specified *en masse*, irrespective of how they will be used to describe size-specific fishing processes and/or survey selectivity. Each function is assigned an index value by which it can subsequently be assigned to

```
#--Selectivity/Retention functions
Selectivity  #required keyword
3    #number of curves
#index     function       np    params
   1    'asclogistic5095'  3     60   120  182  'NMFS trawl survey' #z50   z95  fsz
   2    'asclogistic5095'  3    138   150  182  'TCF retention'     #z50   z95  fsz
   3    'asclogistic5095'  3     80   120  182  'TCF selectivity'   #z50   z95  fsz
#--Fisheries
Fisheries  #required keyword
#-fishery 1
'TCF'  #Tanner crab directed fishery
#output info: retained catch
#include   aggregate type   pdf type      cv/ss      weighting
   TRUE      BY_TOTAL       LOGNORMAL      0.05        1.0    #abundance
   TRUE      BY_TOTAL       LOGNORMAL      0.10        1.0    #biomass
   TRUE      BY_TOTAL       MULTINOMIAL     50         1.0    #size comps
#output info: discard catch
#include   aggregate type   pdf type      cv/ss      weighting
   TRUE      BY_XS          LOGNORMAL      0.05        1.0    #abundance
   TRUE      BY_XS          LOGNORMAL      0.10        1.0    #biomass
   TRUE      BY_XS          MULTINOMIAL     50         1.0    #size comps
#output info: total catch
#include   aggregate type   pdf type      cv/ss      weighting
   TRUE      BY_XS          LOGNORMAL      0.05        1.0    #abundance
   TRUE      BY_XS          LOGNORMAL      0.10        1.0    #biomass
   TRUE      BY_XS          MULTINOMIAL     50         1.0    #size comps
1   #number of time blocks
#-----time block 1
c(1965:1996,2004:2009,2013:mxy)    #years
#sex    discard mortality   lnF      sd F   SelFcnIndex   RetFcnIndex
  'male'      0.321        log(0.3)    0.4        3             2
'female'      0.321        log(0.3)    0.4        3             0
#--Surveys
Surveys  #required keyword
#-survey 1
'NMFS trawl survey'
#output info
#include   aggregate type   pdf type      cv/ss      weighting
   TRUE      BY_XMS         LOGNORMAL      0.15        1.0    #abundance
   TRUE      BY_XMS         LOGNORMAL      0.20        1.0    #biomass
   TRUE      BY_XMS         MULTINOMIAL     25         1.0    #size comps
1   #number of time blocks
#-----time block 1
1975:asy   #years
#  sex      lnQ       sd Q     selFcnIndex
  'male' log(1.0)     0.0          1
'female' log(1.0)     0.0          1
DONE #keyword
```
Text Box 3.

specific fishery and/or survey components. As in TCSAM2015, two standard selectivity functions are currently implemented: the standard ascending logistic ('asclogistic') and double logistic ('dbllogistic') functions (see Section 3.F), together with a few alternative parameterizations. For the ascending logistic function, these are:

function name	alternative parameters	relation to standard parameters
asclogistic5095	z_{50}, z_{95}	$\beta = \dfrac{\ln(19)}{z_{95} - z_{50}}$
asclogistic50D95	$z_{50}, \Delta z_{(95-50)}$	$\beta = \dfrac{\ln(19)}{\Delta z_{(95-50)}}$

For the double logistic, only one is available:

function name	alternative parameters	relation to standard parameters
dbllogistic5095	$z_{a50}, z_{a95}, z_{d50}, z_{d95}$	$\beta_a = \dfrac{\ln(19)}{z_{a95} - z_{a50}}, \beta_d = \dfrac{\ln(19)}{z_{d50} - z_{d95}}$

While convergence is not an issue for the simulation, the alternative parameterizations may simplify comparisons with TCSAM2015 model results.

It is also required to specify the type of normalization used for each selectivity curve, as well as provide a label for use in plots. Normalization options include: 1) explicitly specifying a fully-selected carapace width, 2) normalizing by the maximum of the function over all size bins in the model, and 3) no normalization.

Fisheries and surveys are defined following the selectivity curves in sections starting with the keywords "Fisheries" and "Surveys", respectively (Text Box 3). Within each section, fisheries and surveys are identified by the names assigned to them in the dimensions section of the configuration file (Text Box 1). For each fishery and each survey, the user specifies the types of data to include in the output files rsimTCSAM creates for input to a TCSAM2015 model run, as well as the aggregation type for fitting data in TCSAM2015, the likelihood function, and the likelihood weight used in the TCSAM model run. For fisheries, three categories of catch data can be included in the output file: retained catch, discarded catch, and total catch. For surveys, only one category of catch data can be included: total catch. In each of these categories, 3 types of time series data may be included: aggregate abundance data (i.e., summed over size bins), aggregate biomass data, and size compositions. For the aggregated data types, the user specifies a cv as the uncertainty measure to be included in the output data files, whereas the user specifies a sample size in the case of size composition data.

The following TCSAM2015 aggregation types can be specified:

Keyword	Aggregation Type	Fit Type (size compositions)
BY_TOTAL	aggregate over all sex, maturity, and shell states	fit total
BY_X	aggregate by sex over all maturity and shell states	fit separately by sex category
BY_XE	aggregate by sex over all maturity and shell states	fit proportions extended across all sex categories
BY_XM	aggregate by sex and maturity state over all shell states	fit separately by each combination of sex, maturity categories

BY_XME	aggregate by sex and maturity state over all shell states	fit proportions extended across all sex, maturity category combinations
BY_XS	aggregate by sex and shell state over all maturity states	fit separately by each combination of sex, shell categories
BY_XSE	aggregate by sex and shell state over all maturity states	fit proportions extended across all sex, shell category combinations
BY_XMS	no aggregation	fit separately by each combination of sex, maturity and shell categories
BY_XMSE	no aggregation	fit proportions extended across all sex, maturity, shell category combinations

The following TCSAM2015 likelihood distribution types can be specified:

Keyword	Likelihood distribution
NONE	no fitting
MULTINOMIAL	multinomial likelihood (for size composition data)
NORMAL	normal likelihood with error cv specified in data file
LOGNORMAL	lognormal likelihood with error cv specified in data file
NORM2	normal likelihood with standard deviation of 1

For each time block defined for a particular fishery, the user specifies sex-specific values for discard (handling) mortality, the mean ln-scale capture rate (lnC), the standard deviation for annual ln-scale devs in capture rate (sd F), and the indices identifying the selectivity and retention (for males in a directed fishery) functions to use. For each time block defined for a particular survey, the user specifies sex-specific values for the mean ln-scale survey catchability (lnQ), the standard deviation in ln-scale devs in survey catchability (sd Q), and the index of the selectivity function to use.

The configuration file is terminated with the keyword "DONE".

As noted above, model output consists of 1) a set of files suitable for use in a TCSAM2015 model run, 2) a series of plots reflecting the simulated model dynamics (available as a pdf, if so specified), and 3) an R list object encapsulating the configuration and arrays reflecting the model processes, dynamics, and observations for later comparison with TCSAM2015 model runs against the simulated data. The output files for use with TCSAM2015 are:

File name	Description
ModelConfig.dat	specifies TCSAM2015 model configuration information
Model.Datasets.dat	specifies file names for datasets to be read in
Model.Data.BioInfo.dat	specifies biological information not estimated in the model (e.g., weight-at-size, timingof mating and fisheries)
Model.Data.Fishery.*name*.dat	fishery data, one file for each fishery
Model.Data.Survey.*name*.dat	survey data, on file for each survey

6. TCSAM2015 model results using simulated datasets

Results from running TCSAM2015 against two datasets simulated using rsimTCSAM are presented in this section. The first simulated dataset addresses a rather simple scenario and incorporates a single model fishery (loosely based on the directed Tanner crab fishery) and a single abundance survey (loosely based on the annual NMFS EBS bottom trawl survey). The simulation and results from running TCSAM2015 on the simulated data are discussed in Sections 6a and 6b, respectively. The second simulated dataset addresses a scenario more closely approximating Tanner crab in the real world and incorporates four model fisheries (loosely based on the directed Tanner crab, snow crab bycatch, Bristol Bay red king crab bycatch, and groundfish trawl bycatch fisheries) and a single abundance survey (loosely based on the annual NMFS EBS bottom trawl survey). The simulation and results from running TCSAM2015 on this more complex simulated data are discussed in Section 6c and 6d, respectively.

6.a. A simple simulated dataset

The first simulated dataset, A1, addresses a rather simple scenario that incorporates a single model fishery (loosely based on the directed Tanner crab fishery) and a single abundance survey (loosely based on the annual NMFS EBS bottom trawl survey). The rsimTCSAM model configuration file used to run the simulation, "rsimTCSAM.Configuration.A1.dat", is available on GitHub at the following URL: https://github.com/wStockhausen/rsimTCSAM.git. It is essentially the same as the file outlined in the Text Boxes in Section 5. I used the random number seed 111111 to run the simulation in a manner that can be duplicated. Plots of model results are provided in the accompanying online material in the file "rsimTCSAM.A1.pdf". The model was run from 1950/51 to 2013/14.

Key features to the simulated data are: 1) the equilibrium size distribution calculation outlined in Section 4 is used to initialize the model (Fig. 6a.1), 2) the cv for recruitment is 0.5, 3) natural mortality is the same (0.23 yr^{-1}) for all population components, 4) parameters describing the mean molt increment and spread are the same as those in the 2014 assessment model (Fig. 6a.2), 5) the probability of molting to maturity is, for simplicity, an ascending logistic function of size (Fig. 6a.3), 6) the fishery and survey selectivity curves are constant with time and the same for both sexes (Fig. 6a.4), 7) the retention curve is constant with time (Fig. 6a.4), 8) the fully-selected fishery capture rate is the same for both sexes, and 9) the fully-selected survey catchability is the same for both sexes (1.0). The fishery starts in 1965 and is closed during the same time periods that the real Tanner crab fishery was closed. The survey starts in 1975 and was "conducted" annually.

The time series of simulated total recruitment is shown in Fig. 6a.5. Recruitment is uncorrelated between years and varies from ~15 million crab to ~180 million. Population abundance, mature biomass and size composition trends are shown in Fig.s 6a.6 and 6a.7. The start of the fishery in 1965 is quite noticeable in the mature male biomass time series in particular, reflecting a rapid "fishing down" effect exacerbated by an exceedingly high capture rate in 1966 (Fig. 6a.8). Simulated ln-scale deviations provided annual variability in fishery capture rates and mortality. Both sexes were subject to the same capture rates. A discard mortality rate of 0.321 (the same as in the 2014 assessment) was used for the simulation. The resulting trends in simulated fishery catch components (capture, discard mortality, retention, and total fishing-related mortality) are illustrated in Fig. 6a.9. The size compositions associated with the fishery catch components are illustrated in Fig. 6a.10.

The simulated survey started in 1975. As noted above, survey catchability was 1 for both sexes, and both were subject to the same survey selectivity. Time series trends in survey abundance (numbers) are shown in Fig. 6a.11 and associated size compositions are shown in Fig. 6a.12.
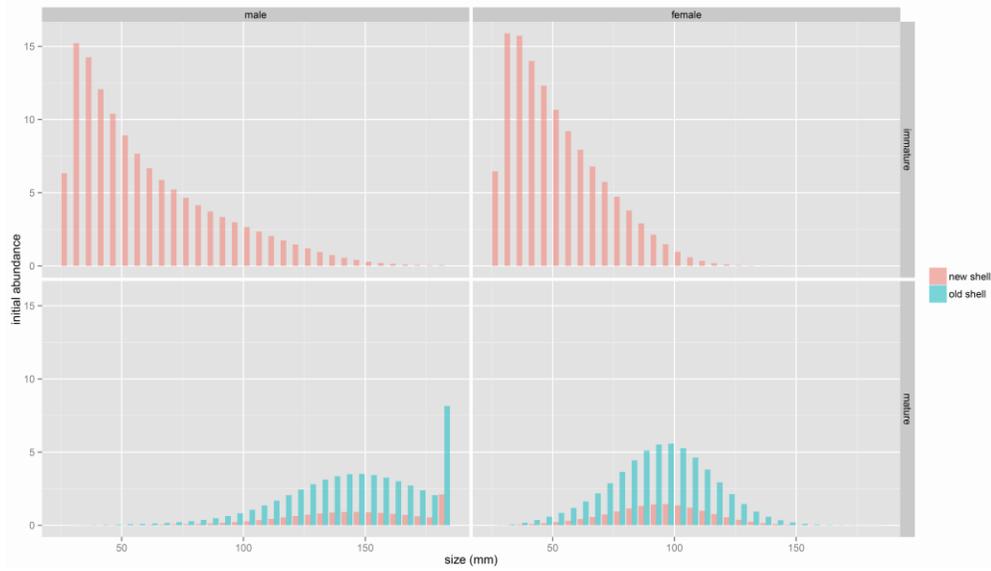
Fig. 6a.1. Initial (simulated) size compositions.
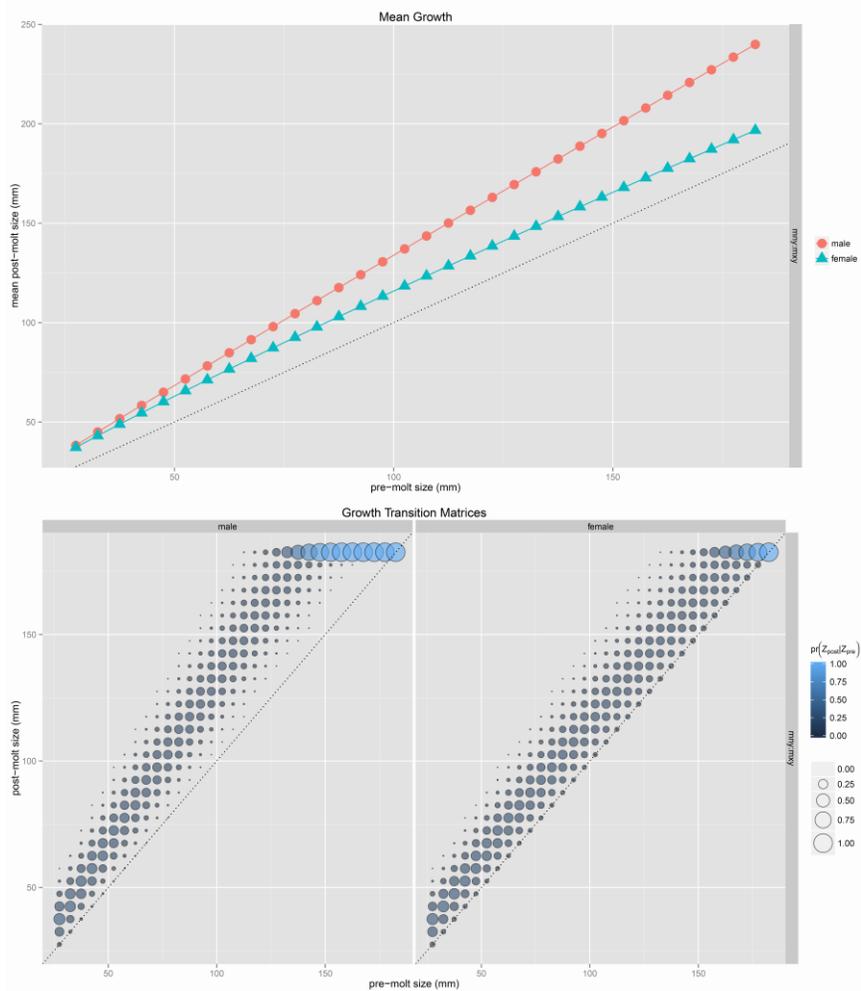
Fig. 6a.2. Mean growth (upper graph) and size transition matrices (lower graph).
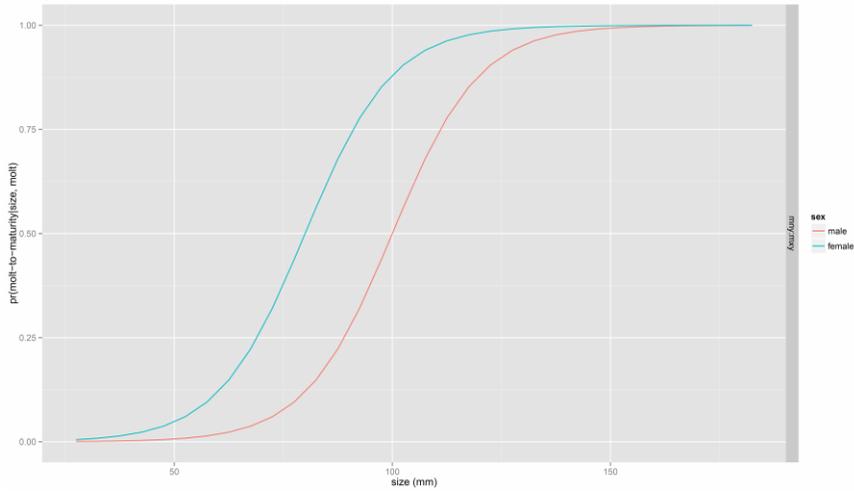
Fig. 6a.3. Probability of molt-to-maturity.
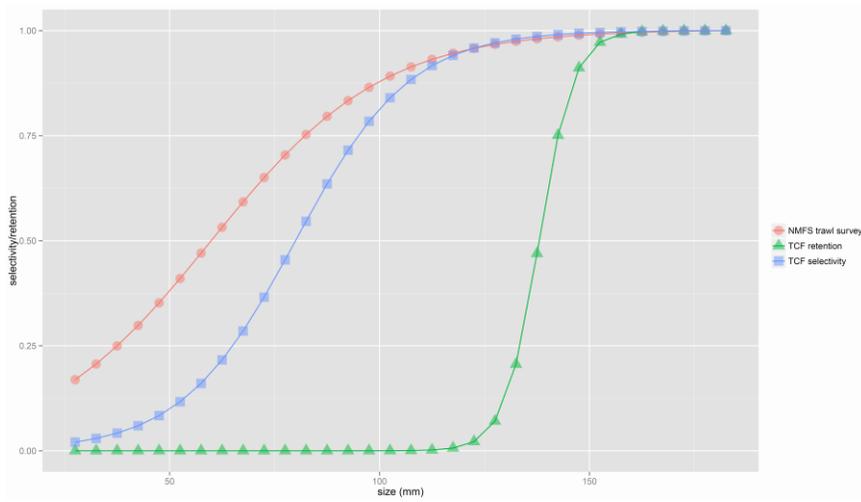
Fig. 6a.4. Selectivity and retention curves in the simulated survey and fishery.
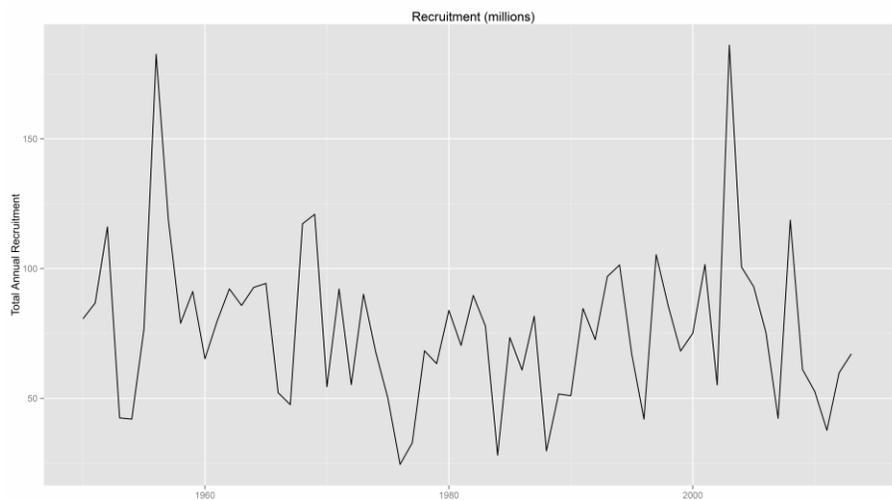
Fig. 6a.5. Time series for simulated recruitment (millions).

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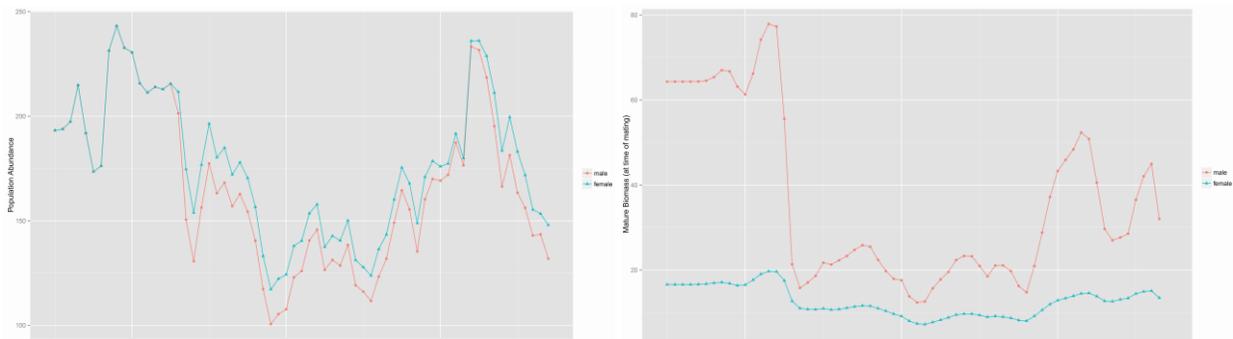
Fig. 6a.6. Time series for simulated population abundance (millions, left) and mature biomasss (1000's t, right).
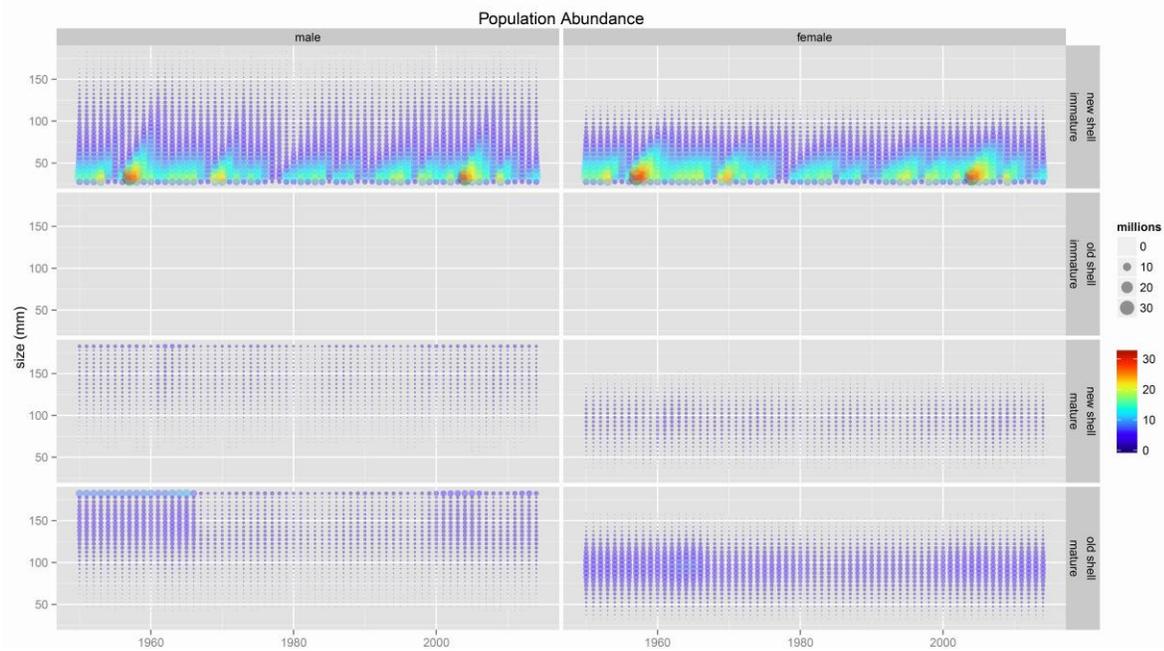
Fig. 6a.7. Time series of size compositions for the simulated population. Disc size and color indicate numbers (in millions).
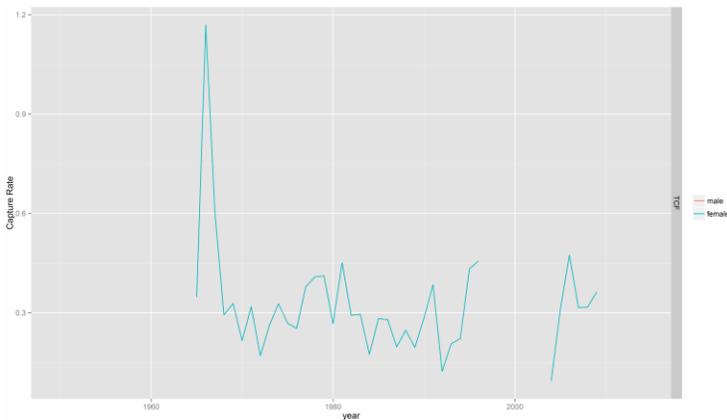
Fig. 6a.8. Time series of fully-selected capture rates for the simulated fishery. (The rate for 2013 is not shown because of the gap between 2009 and 2013).

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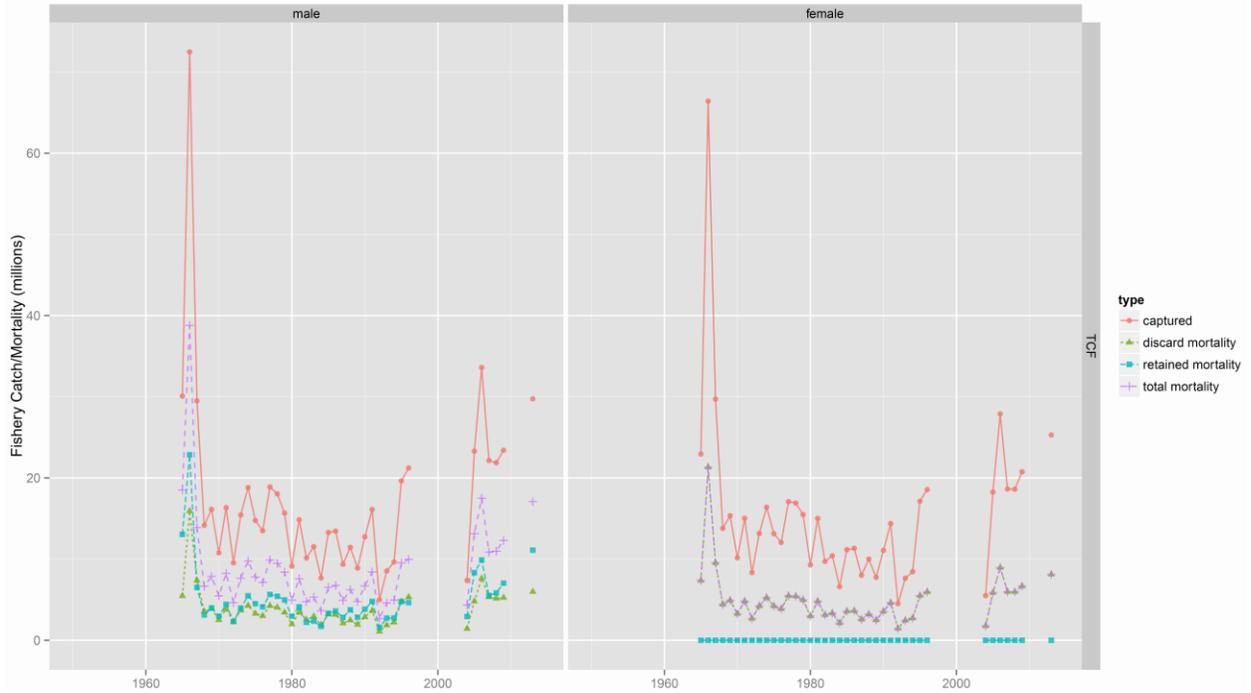
Fig. 6a.9. Time series of simulated fishery catches (coral), discard mortality (green), retained mortality (aqua), and total (fishing-related) mortality (purple), in millions of crab.
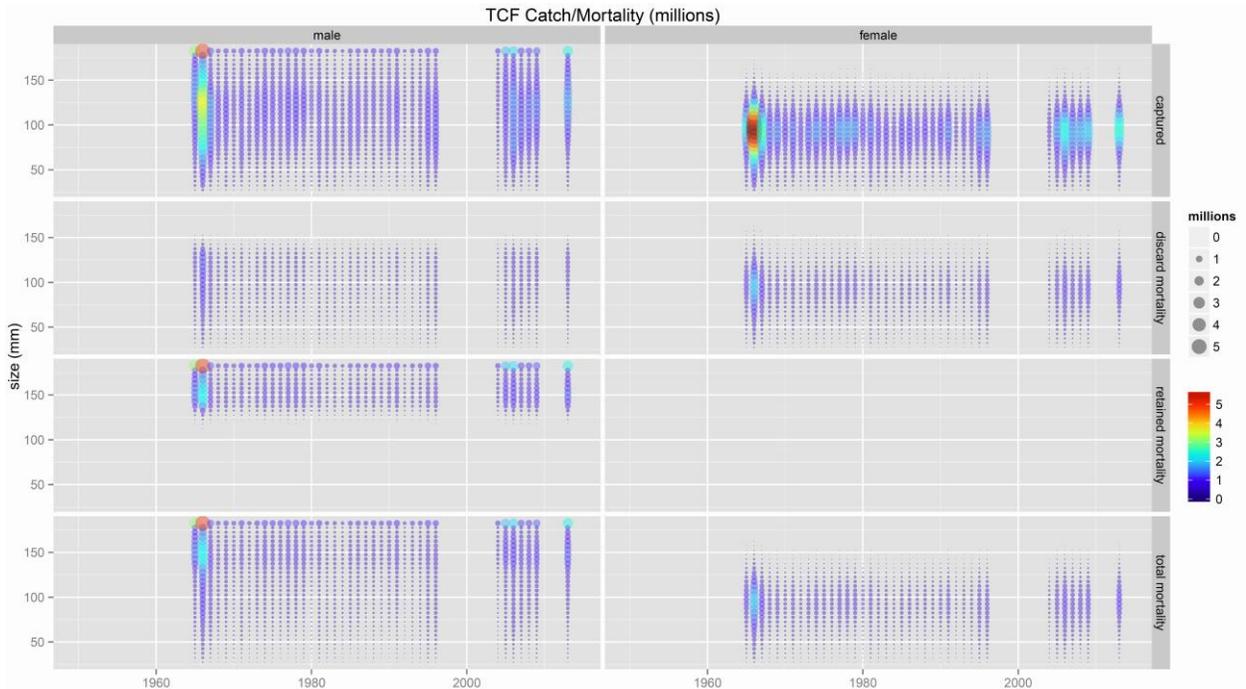
Fig. 6a.10. Time series of size compositions for simulated fishery catch components. Disc size and color indicate numbers (in millions).
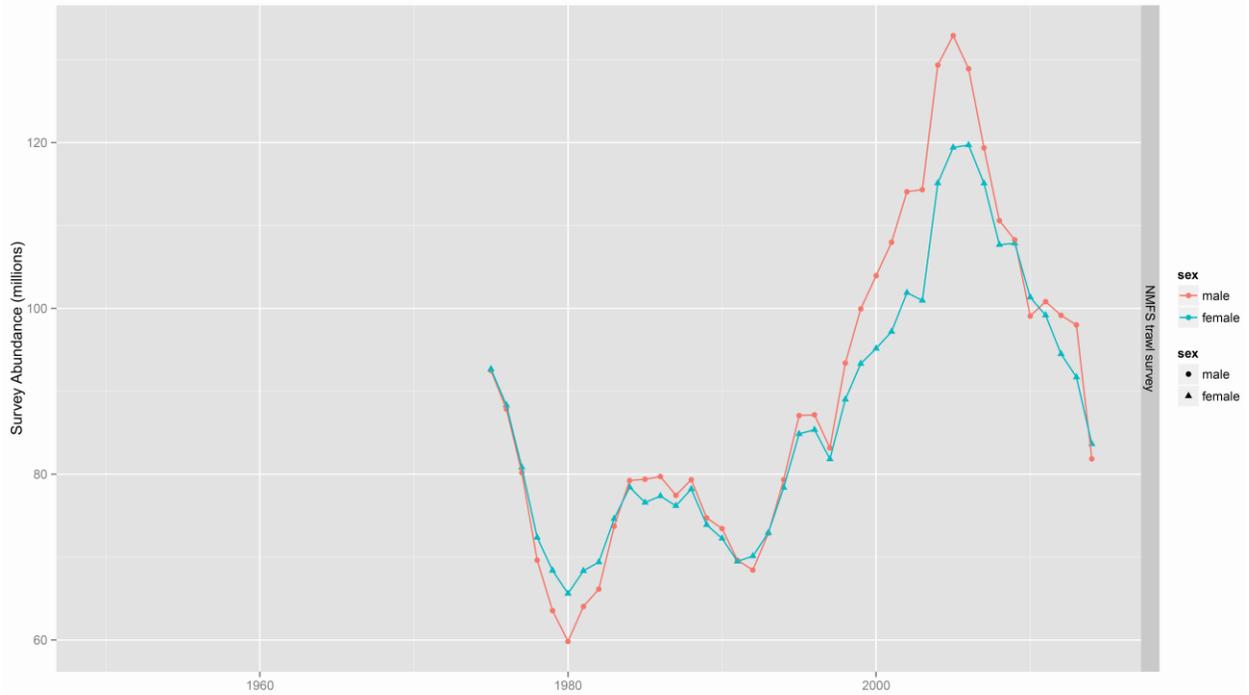
Fig. 6a.11. Time series of simulated survey abundance (in millions).
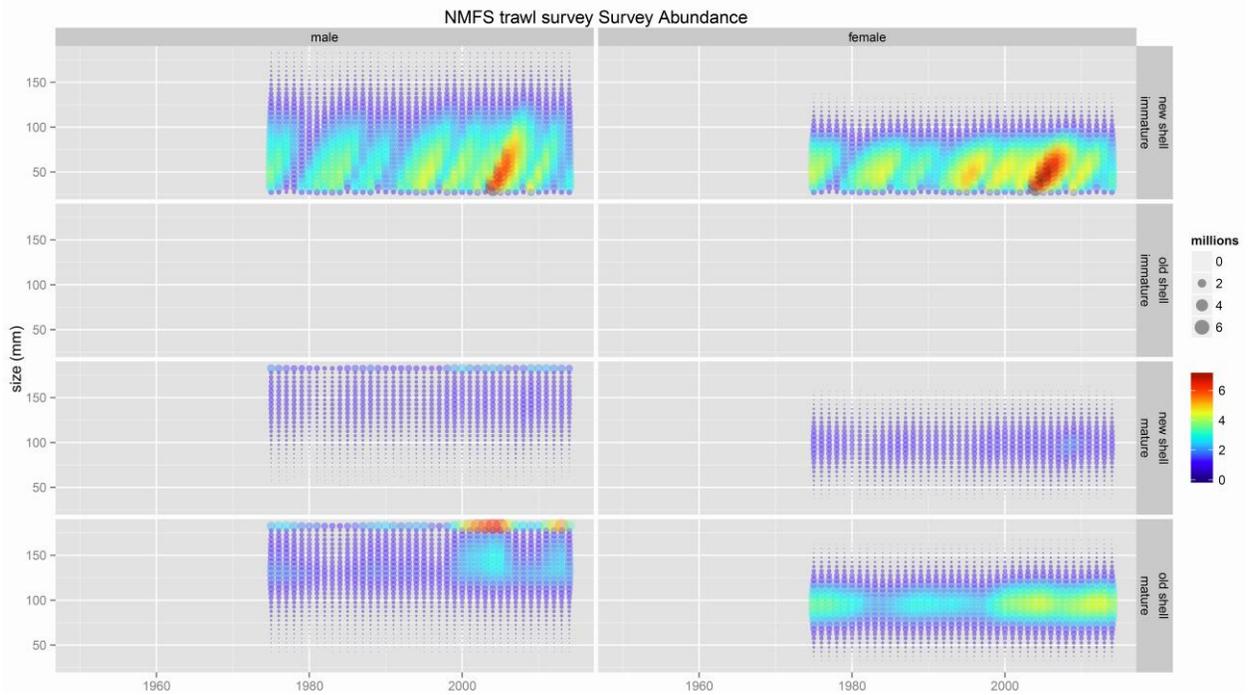
Fig. 6a.12. Time series of size compositions for simulated survey catch components. Disc size and color indicate numbers (in millions).

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6b. A simple simulated dataset: TCSAM2015 results

To test the TCSAM2015 ADMB code for bugs and make an initial evaluation of the model, four model scenarios were run using the simulated data files from the rsimTCSAM simulation described in the previous section (Table 6b.1). In Models A1a and A1b, the recruitment time series was estimated (median and ln-scale deviations), as was the fishing capture rate time series (median "F" and annual ln-scale deviations), as well as all selectivity and retention functions. Baseline survey q (catchability) was fixed at 1, and sex-specific offsets from median "F" (capture rate, not fishing mortality) and q were not estimated. Growth parameters and parameters describing the probability of the molt to maturity were fixed, as were the sex ratio and size composition at recruitment. Models A1c and A1d differed from A1a and A1b by additionally estimating sex-specific offsets to natural mortality, growth parameters, as well as sex-specific "F" and q offsets. The initial size composition was set to zero and the population was built up from annual recruitments in models A1a and A1c, while the initial size composition was calculated using the approach outlined in Section 4 in models A1b and A1d.

Table 6b.1. TCSAM2015 model scenarios.

Process	Component	TCSAM2015 Model Scenario			
		A1a	A1b	A1c	A1d
recruitment	median	estimated	estimated	estimated	estimated
	ln-scale devs	estimated	estimated	estimated	estimated
	sex ratio	fixed	fixed	fixed	fixed
	size composition	fixed	fixed	fixed	fixed
natural mortality	base	fixed	fixed	fixed	fixed
	offsets	fixed	fixed	estimated	estimated
growth		fixed	fixed	estimated	estimated
maturity		fixed	fixed	estimated	estimated
TCF	median F	estimated	estimated	estimated	estimated
(directed fishery)	F offsets	fixed	fixed	estimated	estimated
	ln-scale devs	estimated	estimated	estimated	estimated
	male selectivity	estimated	estimated	estimated	estimated
	female selectivity	estimated	estimated	estimated	estimated
	retention	estimated	estimated	estimated	estimated
Survey	median Q	fixed	fixed	fixed	fixed
	Q offsets	fixed	fixed	estimated	estimated
	male selectivity	estimated	estimated	estimated	estimated
	female selectivity	estimated	estimated	estimated	estimated
initial size composition		0	estimated	0	estimated

Initial parameter values were set to the simulation's equivalents, except for recruitment and fishing capture rate deviations, which were set to zero. Thus model convergence was only moderately tested, but the principal point of these runs was to identify any striking differences (i.e., code bugs) between the simulation and the model.

Time series of simulated fishery abundance, biomass, and size compositions were available by sex and shell condition. The simulated fishery abundance and biomass data were assigned cv's of 5% and 10%, respectively, to represent the quality of observations (although no observation error was added to the data). Fishery size compositions were assigned sample sizes of 50 by sex/shell condition factor combination for retained and discard/total size compositions, respectively. Time series of simulated survey abundance, biomass and size compositions were available by sex, maturity state, and shell condition. Survey abundance and biomass data were assigned cv's of 15% and 20% (similar to values for

the NMFS trawl survey), while survey size compositions were assigned sample sizes of 25 by sex/maturity state/shell condition combination. For model fitting, error distributions for both fishery and survey "bulk" data (size-integrated abundance and biomass) were assumed to be lognormal in structure, while size compositions were multinomial. Retained catch data (bulk and size compositions) were fit after summing over maturity state and shell condition. Fishery discard and total catch data were fit separately for each sex and shell condition combination (4 combinations) after summing over maturity state. Survey data was fit separately for each sex, maturity state, and shell condition combination (6 combinations).

Model runs converged and valid hessians were obtained for all four configurations. TCSAM2015 performance appeared to be excellent in all four model runs, as one would hope. Comprehensive plots of model results and model comparisons are available in the online material (files 'A1a.plots.tcsam.pdf', 'A1b.plots.tcsam.pdf', 'A1c.plots.tcsam.pdf', 'A1d.plots.tcsam.pdf'). Values for objective function components were similar for all models and exceptionally small, indicating very good fits to the simulated data (Figs 6b.1-3). No model achieved an exact fit, but that was not expected given that the stopping procedure was based on a non-zero (even though very small) error criterion for convergence.

It was reassuring to see that allowing parameters influencing natural mortality (Fig. 6b.4), growth (Fig. 6b.5), molt-to-maturity (Fig. 6b.6), initial size composition (Fig. 6b.7), and selectivity and retention curves (Fig. 6b.8) to be estimated did not cause the models to diverge from the simulated data. Values from the models are nearly identical to those from the simulation.

Subsequent to 1960, the population numbers-at-size predicted by the models agree well with those from the simulation (Fig. 6b.9). Prior to 1960, differences are evident, with models A1a and A1c predicting numbers at smaller sizes better than models A1b and A1d, which predicted numbers at larger sizes better. The latter occurred because A1b and A1d estimated initial size compositions using the calculations outlined in Section 4, whereas models A1a and A1c built up their populations from 0 using only recruitment.

The simulated recruitment time series was well-estimated by all the models from 1960 on (Fig. 6b.10). From 1950 to 1960, all the models exhibited rather smooth (correlated) changes in recruitment, reflecting the basic lack of information to the models during this period because the (fishery) data didn't start until 1965. Subsequent to 1960, all the models tracked the annual deviations in recruitment rather well, although they tended to underestimate the extent of the largest changes.

Model-predicted trends in simulated population abundance were nearly identical to the true (simulated) population abundance from 1960 on (Fig. 6b.11). Prior to 1960, model-predicted abundance patterns exhibit smooth trajectories reflecting the smoothness in model-predicted recruitment during this time period. It is notable, because this is what the current assessment model does, that the models (A1a, A1c) that started with initial size compositions at zero and built up their populations strictly from recruitment alone managed to achieve the same population levels within the first 10 years of the model runs as the models that started with equilibrium size compositions. Model-predicted trends in mature biomass were also nearly identical to the true mature biomass, but only after 1963 (Fig. 6b.12). As with other quantities, there was also excellent agreement between the fully-selected fishing rates (Fig. 6b.13), different catch components (Fig. 6b.14), and survey abundance (Fig. 6b.15) predicted by the models and those from the simulation.

The final figure (Fig. 6b.16) in this section addresses an issue that arose in previous Crab Workshops regarding whether the Gmacs fishing mortality model correctly incorporated discard mortality. The figure shows the ratio of total discard mortality (as biomass) to total discard biomass by year for each model and the simulation. To within numerical roundoff error, the ratio is 0.321, which is the value used for the rate of discard mortality in both the simulation and the models. This provides some validation that the gmacs fishing mortality model, which is applied size bin by size bin, is (at least) consistent with an aggregate application of discard mortality such as is used in the current assessment model.
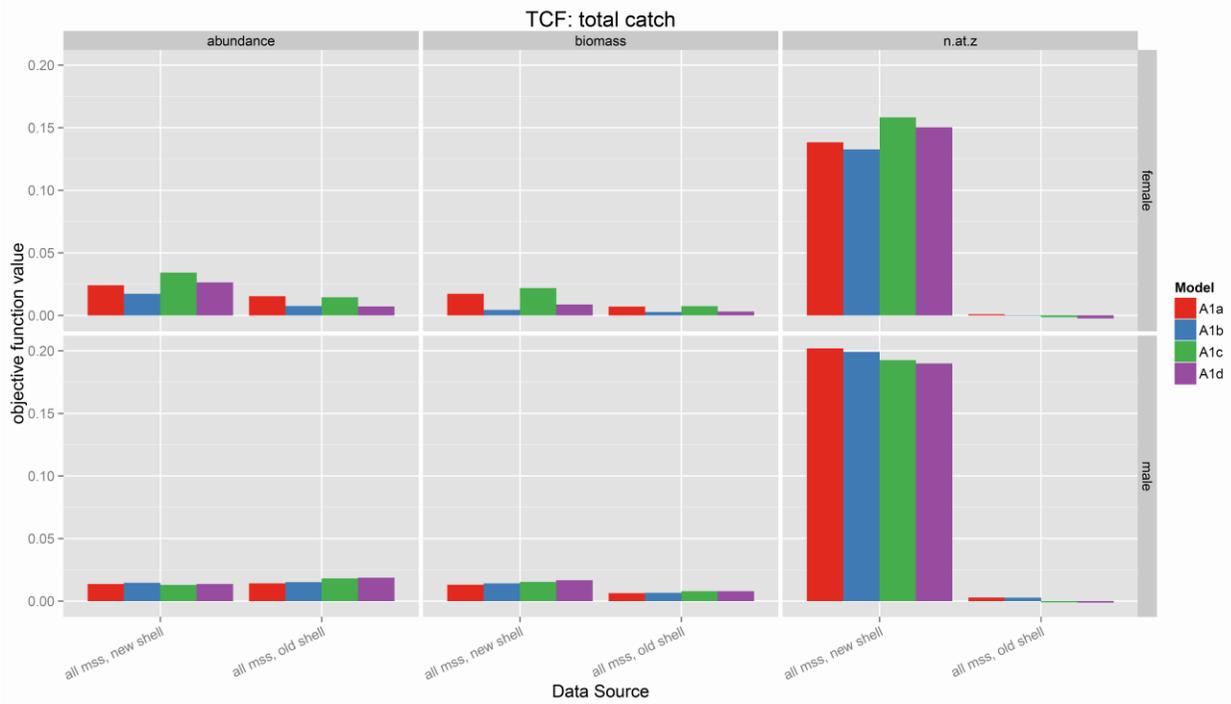
Fig. 6b.1. Objective function values for total catch components in the simulated directed fishery.
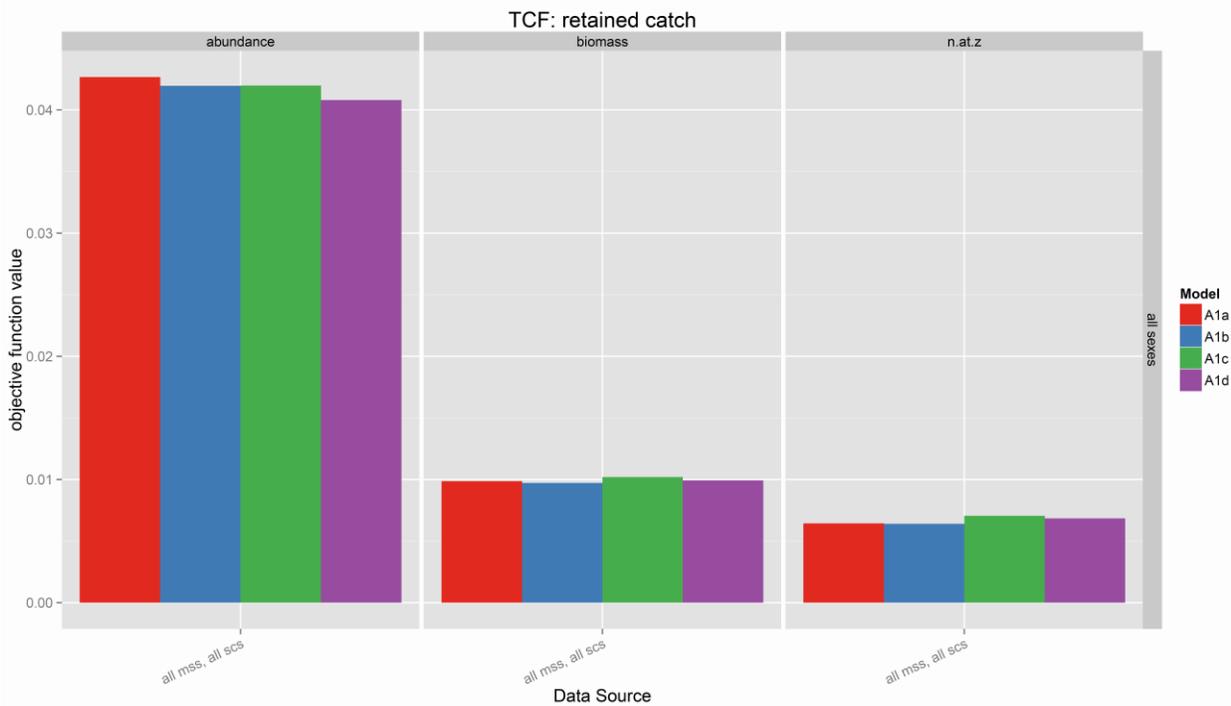
Fig. 6b.2. Objective function values for retained catch components in the simulated directed fishery.
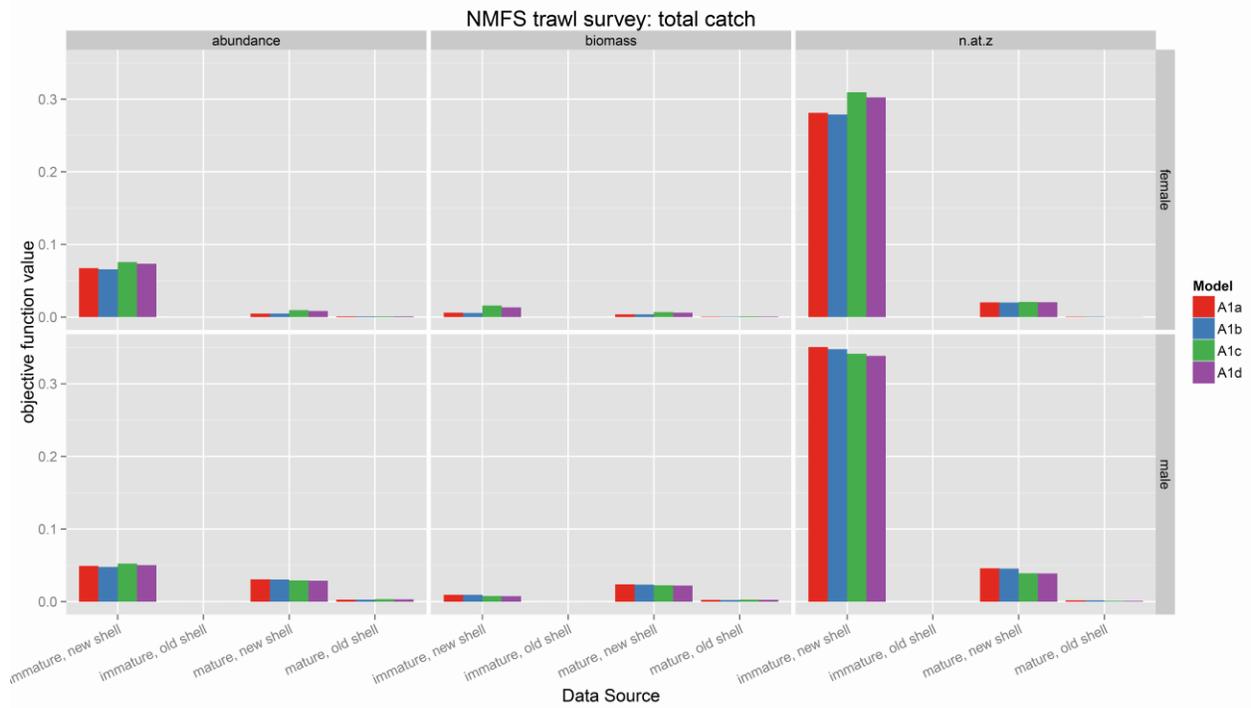
Fig. 6b.3. Objective function values for components from the simulated survey.
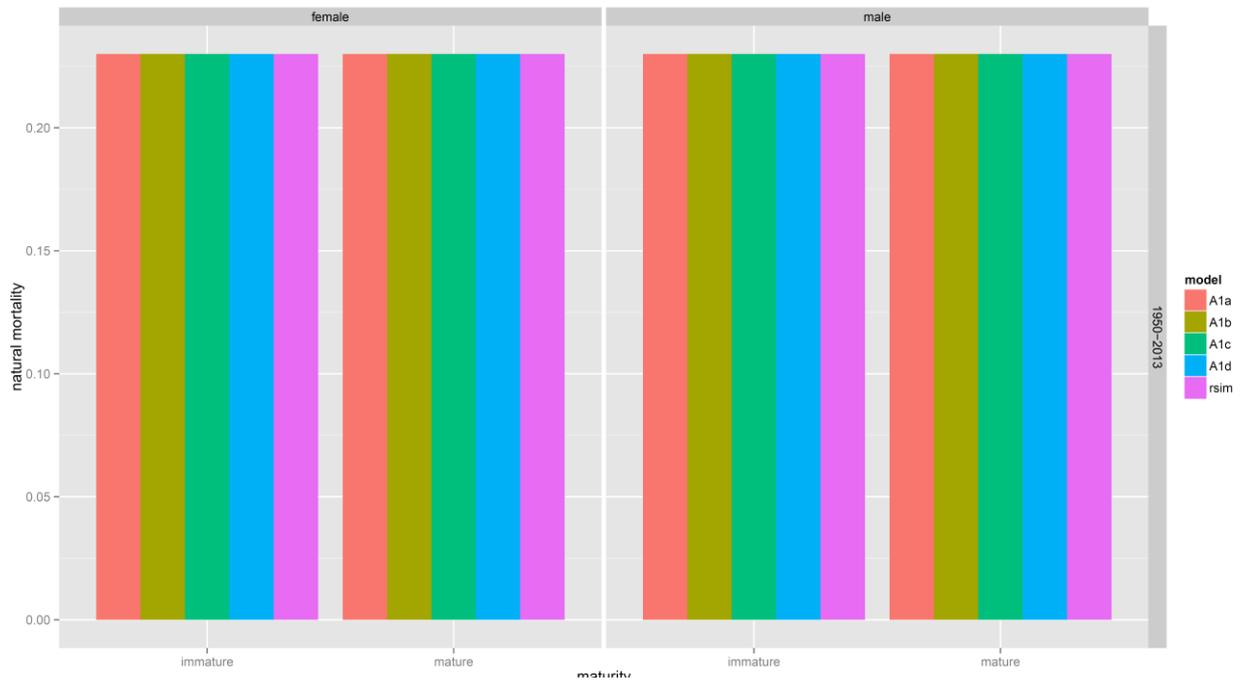
Fig. 6b.4. Natural mortality. Sex-specific offsets fixed for A1a and A1b, estimated for A1c and A1d. "rsim" represents the value in the simulation model.

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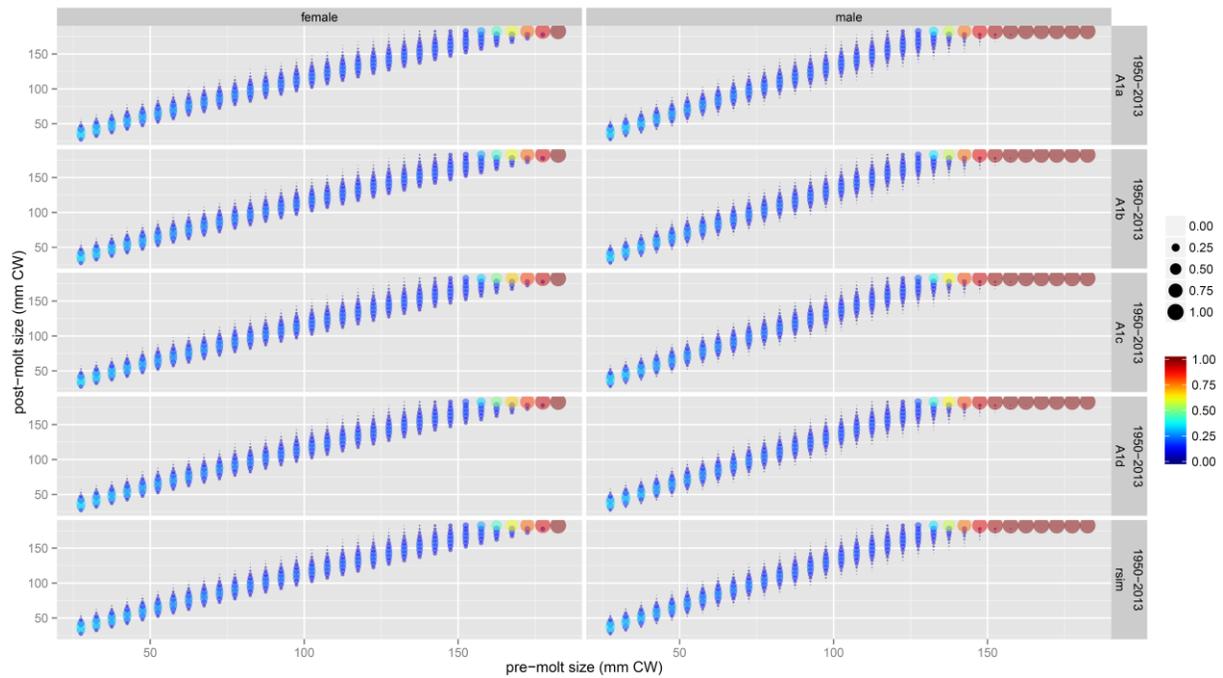
Fig. 6b.5. Size transition matrices for immature crab. Growth parameters were fixed for A1a and A1b, estimated for A1c and A1d. "rsim" denotes the values from the simulation model.
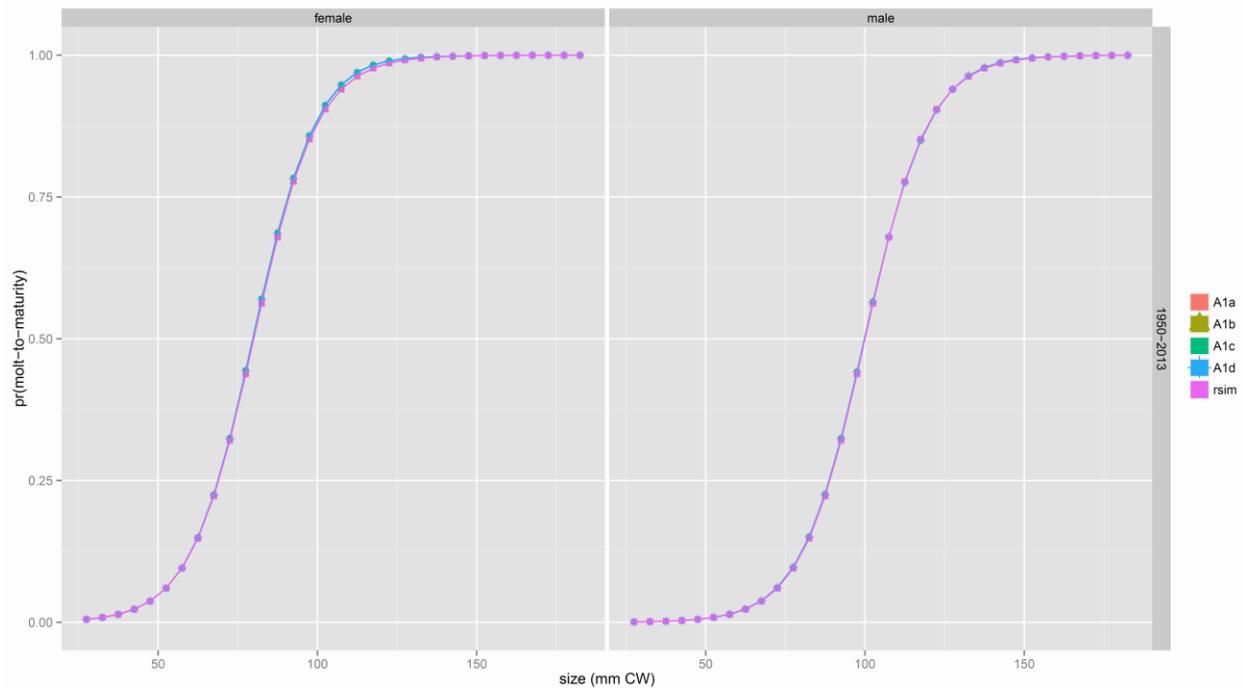
Fig. 6b.6. Probability of molting to maturity as a function of size. Molt-to-maturity parameters were fixed for A1a and A1b, estimated for A1c and A1d. "rsim" denotes the values from the simulation model.
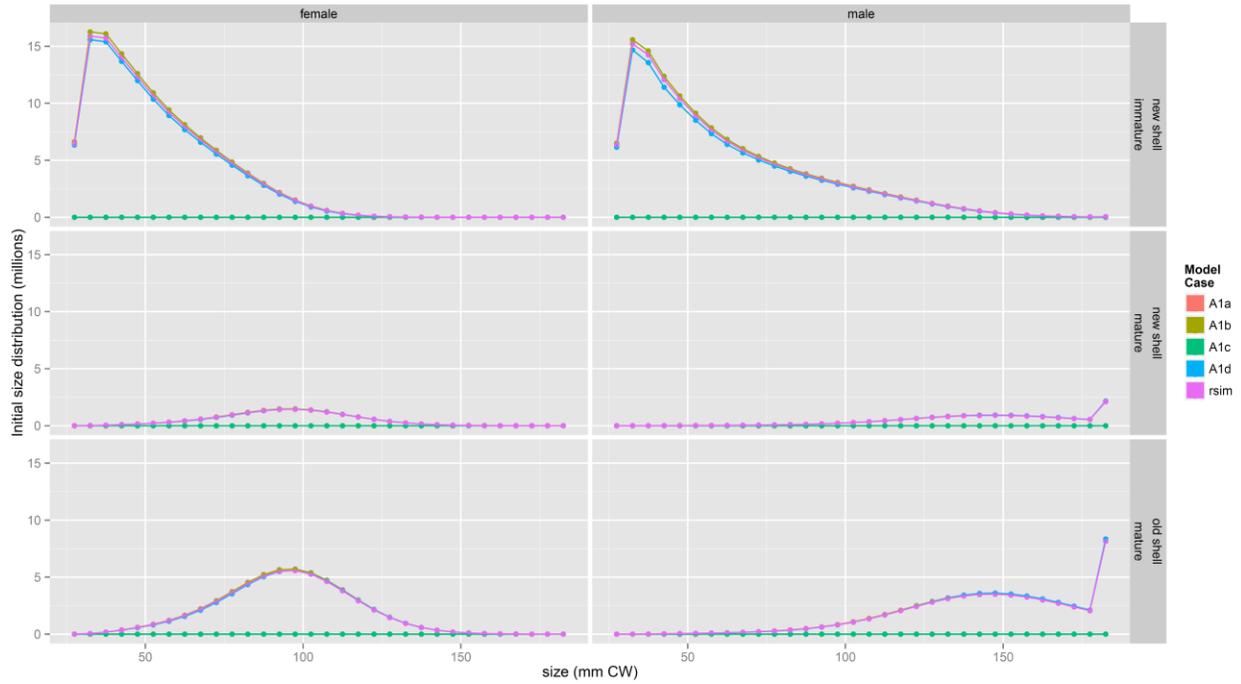
Fig. 6b.7. Initial size compositions. Initial size compositions were identically zero for A1a and A1c and were calculated for A1b and A1d. "rsim" denotes the values from the simulation model.
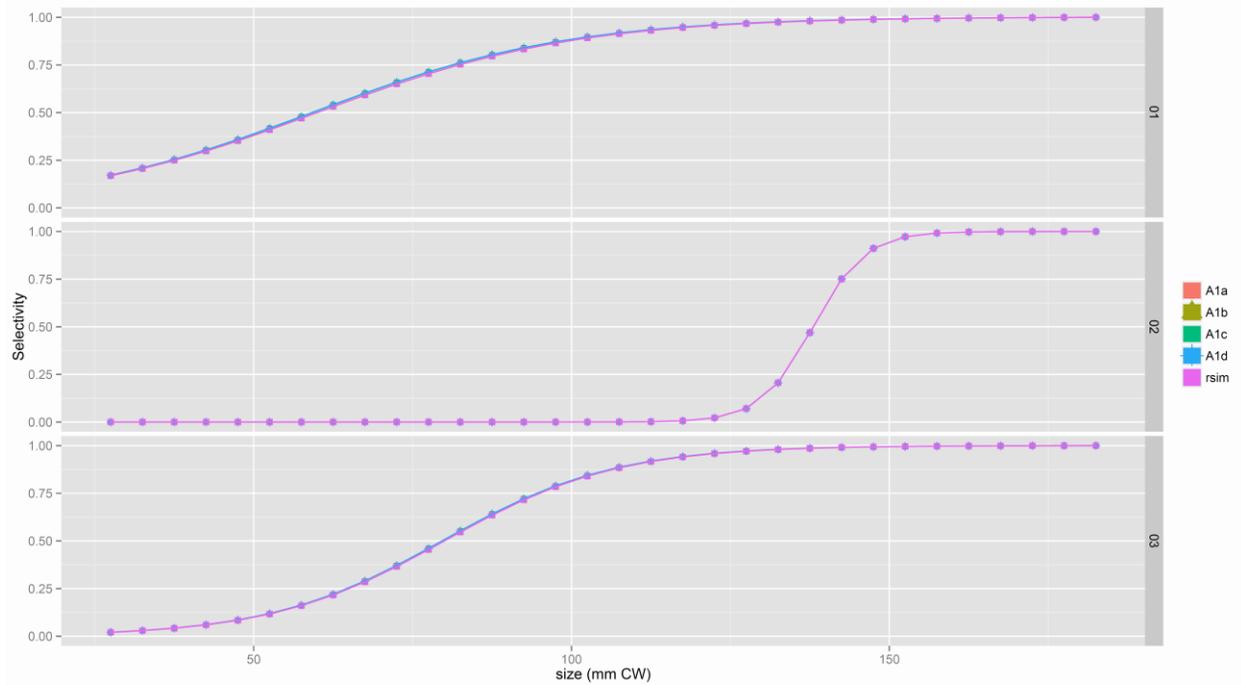
Fig. 6b.8. Estimated selectivity/retention curves. Upper: survey selectivity (both sexes); center: fishery retention; lower: fishery selectivity (both sexes). "rsim" denotes the values from the simulation model.
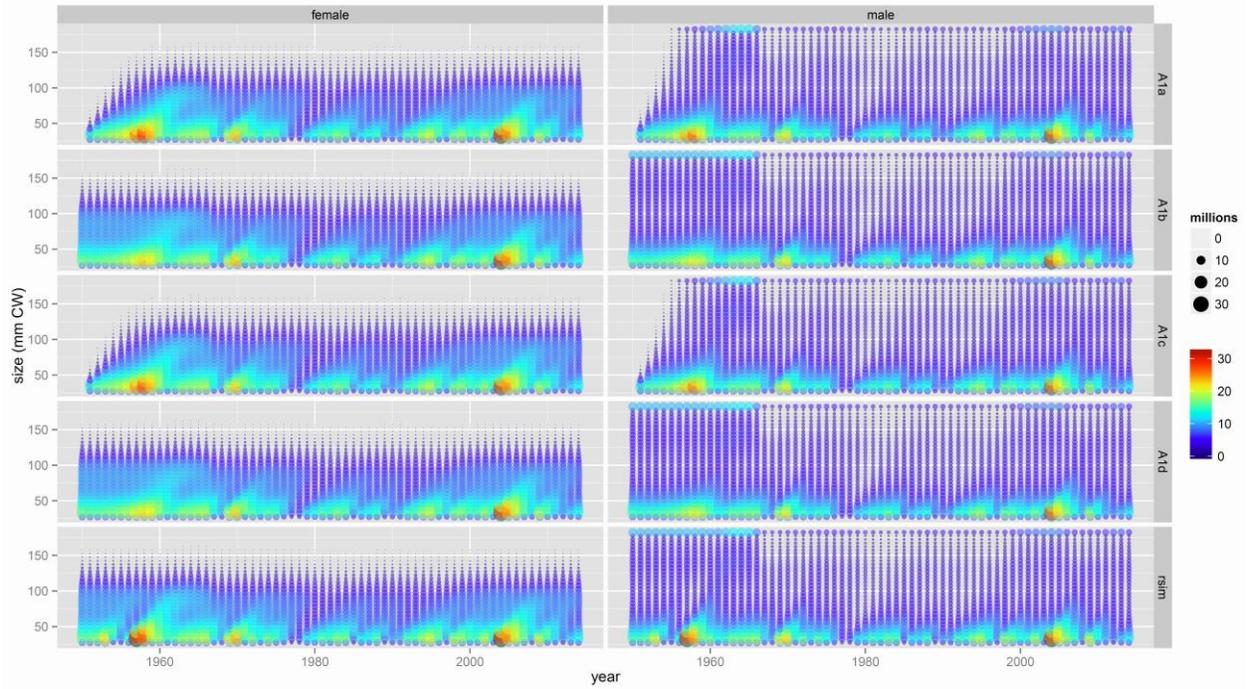
Fig. 6b.9. Estimated population abundance by size bin. "rsim" denotes the values from the simulation model.
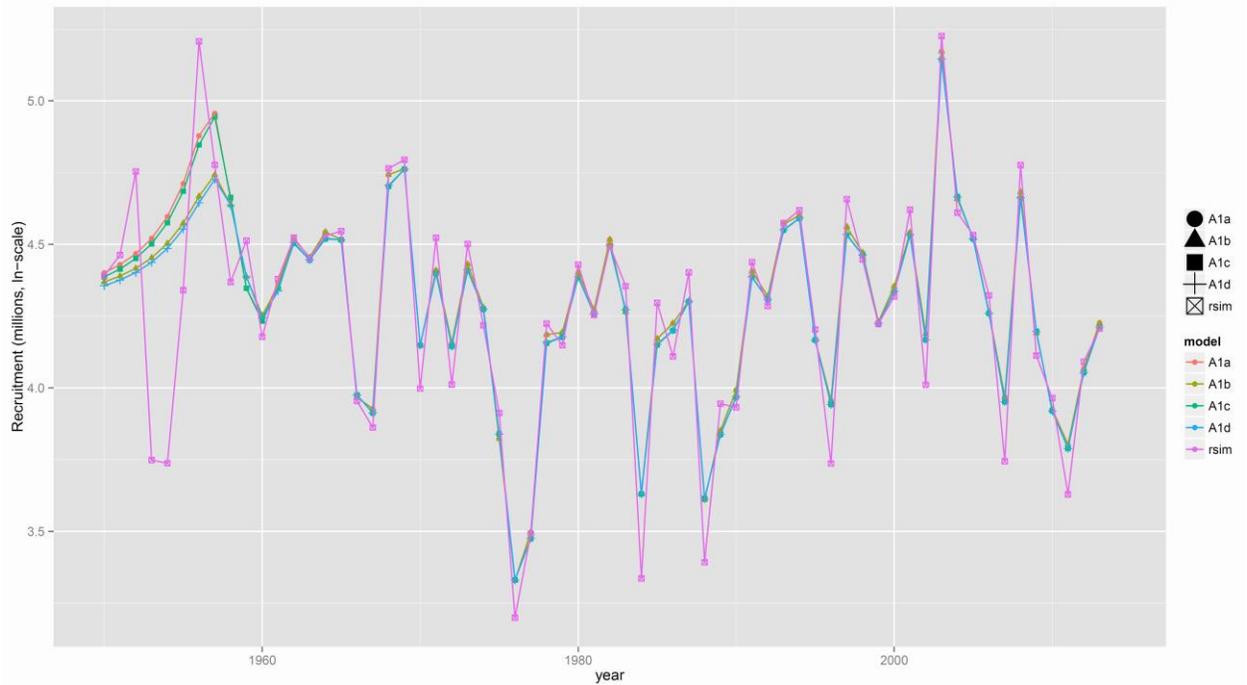
Fig. 6b.10. Estimated recruitment time series. "rsim" denotes the values from the simulation model.
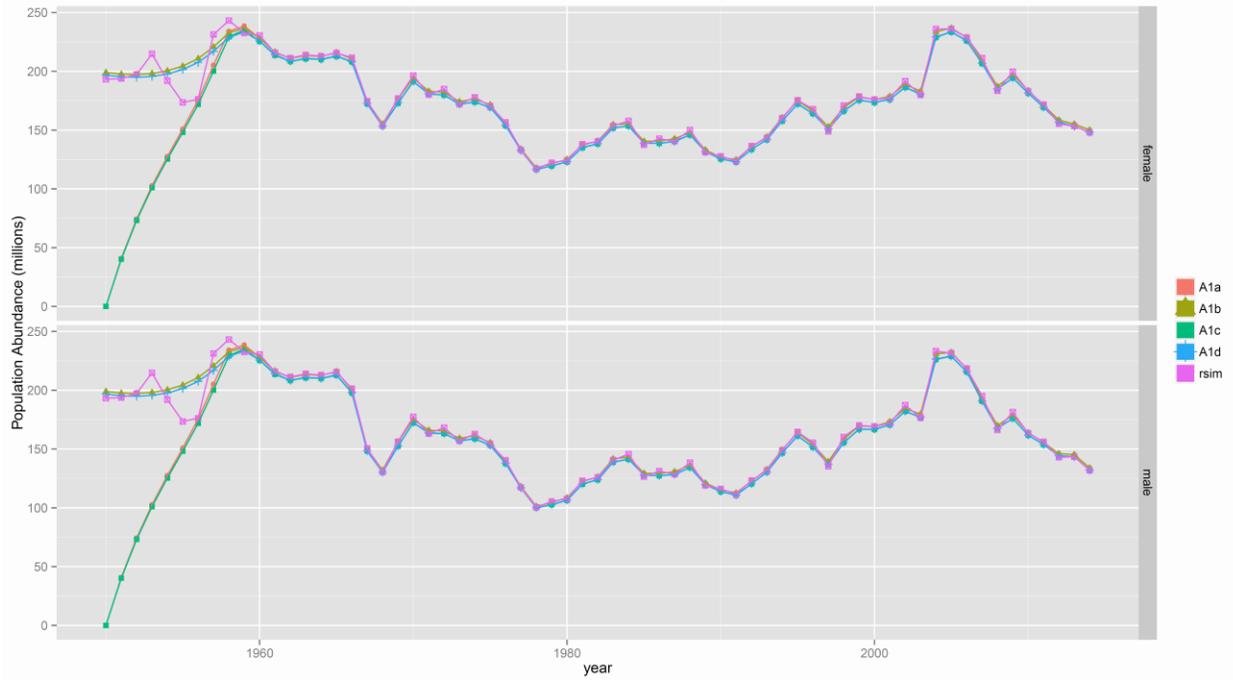
Fig. 6b.11. Population abundance trends. "rsim" denotes the values from the simulation model.
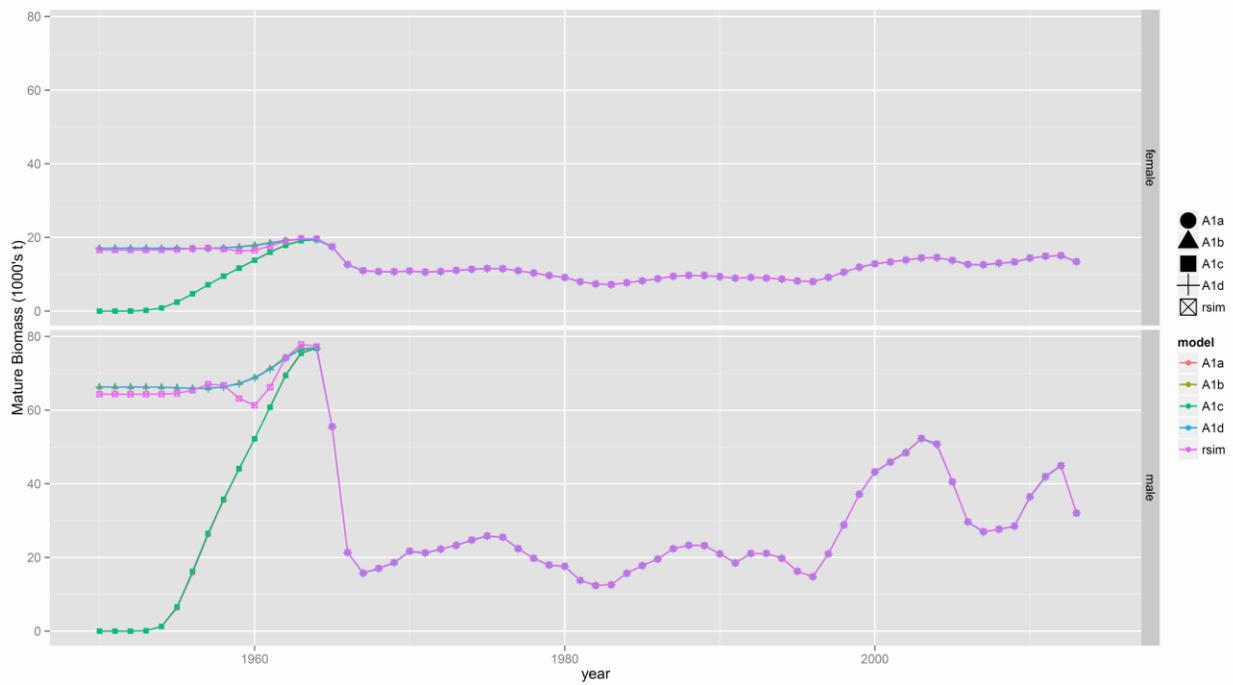
Fig. 6b.12. Mature population biomass trends. "rsim" denotes the values from the simulation model.
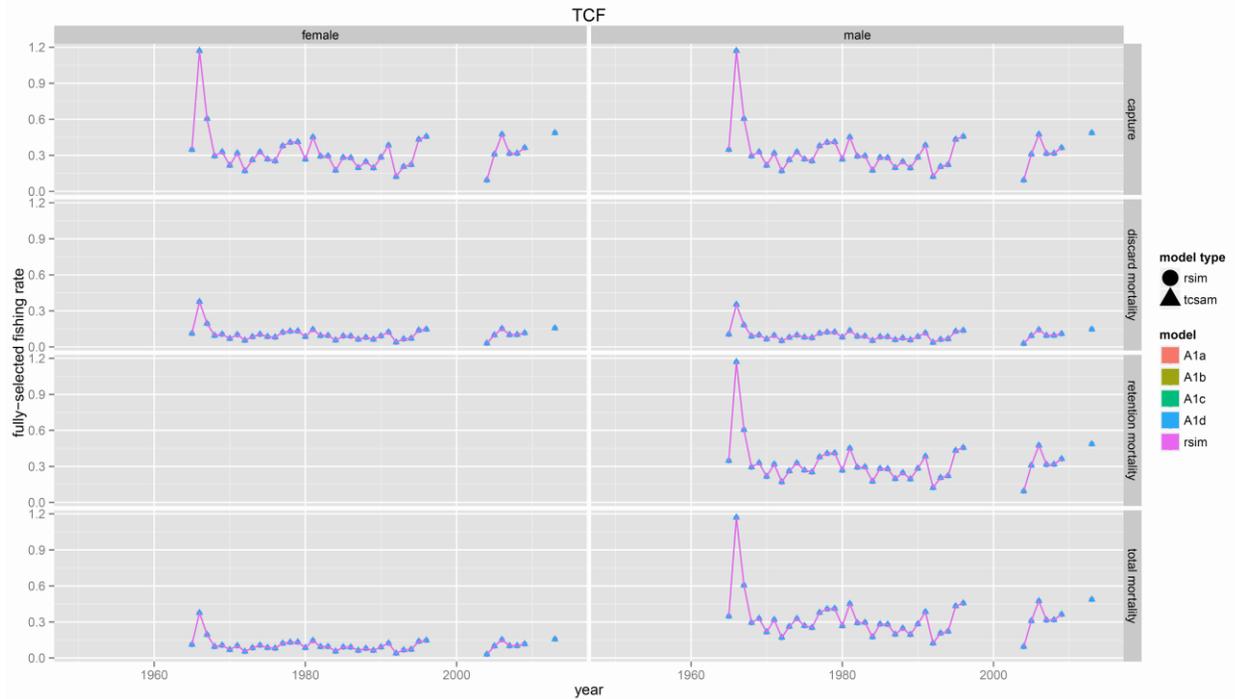
Fig. 6b.13. Estimated fully-selected fishing rates. "rsim" denotes the values from the simulation model.
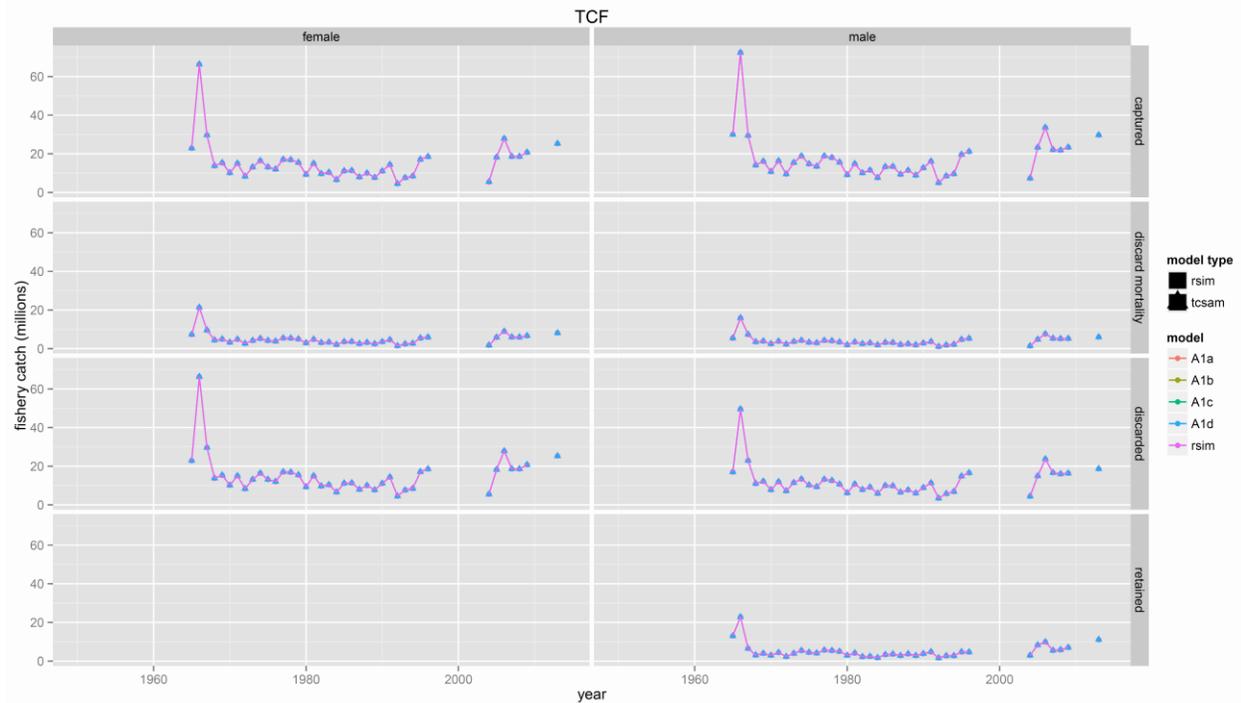

Fig. 6b.14. Estimated fishery catch/mortality. "rsim" denotes the values from the simulation model.

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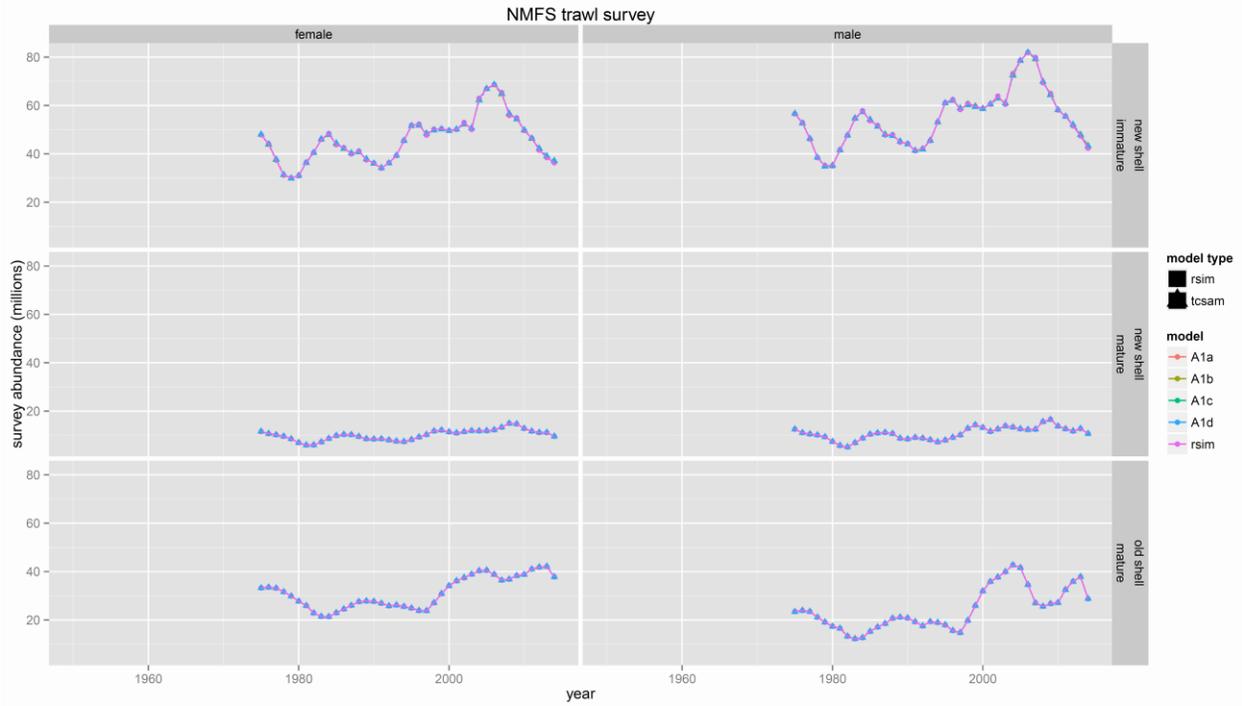
Fig. 6b.15. Estimated survey abundance. "rsim" denotes the values from the simulation model.
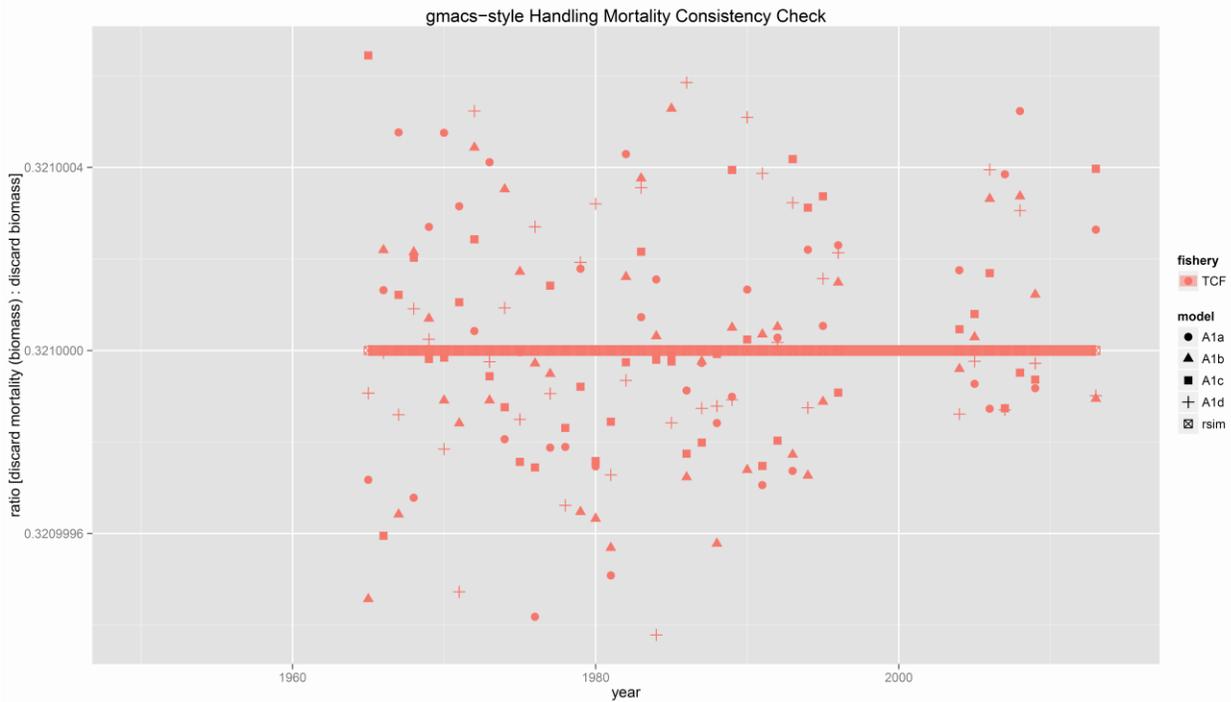

Fig. 6b.16. Estimated ratio of size-aggregated discard mortality (biomass) to discard biomass in the simulated fishery. "rsim" denotes the values from the simulation model.

Sections 6c and 6d are TBD.