Appendix K:
Description of the Tanner Crab Stock Assessment Model (ver. 2)

Introduction

The computer code used in the 2016 Tanner crab stock assessment (Stockhausen, 2016), referred to here as "TCSAM2013" (i.e., an acronym for Tanner Crab Stock Assessment Model, 2013), evolved directly from the assessment model code developed by Rugolo and Turnock (2011, 2012a) used in the 2012 stock assessment (Rugolo and Turnock, 2012b), as rewritten and revised by Stockhausen for the 2013 and subsequent stock assessments (Stockhausen et al., 2013; Stockhausen, 2014; Stockhausen, 2015; Stockhausen, 2016). TCSAM2013, no longer used for assessments, was an integrated assessment model that estimated model parameters in a maximum likelihood framework using AD Model Builder C++ libraries (Fournier et al., 2012) for automatic differentiation to fit to time series of survey (fishery-independent) biomass and size compositions, retained catch biomass and size compositions in the directed fishery, and catch biomass and size compositions in several fisheries that take Tanner crab as bycatch. The computer code for the TCSAM2013 is available on GitHub (the 2016 assessment model version is on the "2016AssessmentModel" branch). While a number of model options could be configured "on-the-fly" using a control file, assessment models developed using the TCSAM2013 computer code were constrained in a number of ways, including the number of directed fisheries (1) and bycatch fisheries (3) that can be accommodated, the type of surveys that can accommodated (1), and the number and type of time blocks that are defined for model parameters (most are hard-wired in the code). Additionally, status determination and overfishing limit (OFL) calculations required a separate "projection model" code to be run separately using a results file from a successful TCSAM2013 model run.

The "TCSAM02" (Tanner Crab Stock Assessment Model, version 2) modeling framework was developed "from scratch" to eliminate many of the constraints imposed on potential future assessment models by TCSAM2013. Like TCSAM2013, TCSAM02 uses AD Model Builder libraries as the basis for model optimization using a maximum likelihood (or Bayesian) approach. The model code for TCSAM02 is available on GitHub (the current development branch is "After201705CPT"). TCSAM02 was first used for the Tanner crab assessment in 2017 (Stockhausen, 2017) and will be used until a transition is made to Gmacs (the Generalized Model for Alaska Crab Stocks). Gmacs is intended to be used for all crab stock assessments conducted for the North Pacific Fisheries Management Council (NPFMC), including both lithodid (king crab) and *Chionoecetes* (Tanner and snow crab) stocks, while TCSAM02 is specific to *Chionoecetes* biology (i.e., terminal molt)..

TCSAM02 is referred to here as a "modeling framework" because, somewhat similar to Stock Synthesis (Methot and Wetzel, 2013), model structure and parameters are defined "on-the-fly" using control files—rather than editing and re-compiling the underlying code. In particular, the number of fisheries and surveys, as well as their associated data types (abundance, biomass, and /or size compositions) and the number and types of time blocks defined for every model parameter, are defined using control files in TCSAM02 and have not been pre-determined. Priors can be placed on any model parameter. New data types (e.g., growth data) can also be included in the model optimization that could not be fit with TCSAM2013. Additionally, status determination and OFL calculations can be done directly within a TCSAM02 model run, rather having to run a separate "projection model".

Model Description

A. General population dynamics

TCSAM02 is a stage/size-based population dynamics model. Population abundance at the start (July 1) 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, shell aging, 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/growth/mating (δt_y^m) in year y. The steps when the fisheries occur before molting/growth/mating ($\delta t_y^F \leq \delta t_y^m$) are outlined below first (Steps A1.1-A1.4), followed by the steps when molting/growth/mating occurs after the fisheries ($\delta t_y^m < \delta t_y^F$; Steps A2.1-A2.4).
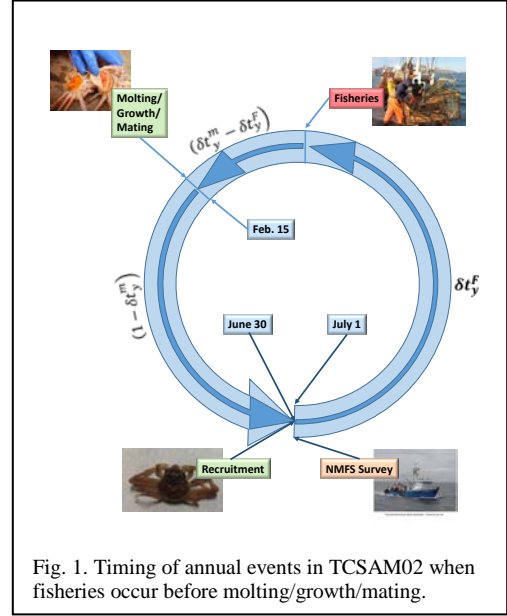

Fig. 1. Timing of annual events in TCSAM02 when fisheries occur before molting/growth/mating.

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

Step A1.1: Survival prior to fisheries

Natural mortality is applied to the population from the start of the model year (July 1) until just prior to prosecution of pulse fisheries for year y at δt_y^F. The numbers surviving to 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 and bycatch fisheries are modeled as simultaneous pulse fisheries occurring at δt_y^F in year y. The numbers that remain after the fisheries are prosecuted are given by:

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

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

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

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

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

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 mature new shell (MAT, NS) crab to mature old shell (MAT, OS) crab due to aging, are given by:

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

where $\Theta_{y,x,z,z'}$ is the growth transition matrix in year *y* for an immature new shell (IMM, NS) crab of sex *x* and pre-molt size *z'* to post-molt size *z* and $\phi_{y,x,z}$ is the probability that a just-molted crab of sex *x* and post-molt size *z* has undergone its terminal molt to maturity (MAT). All crab that molted remain new shell (NS) crab. Additionally, all mature crab that underwent 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 (IMM, OS) 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 "missing" equation for *m=IMM, s=OS* is unnecessary.

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

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

A2. Calculation sequence when $\delta t^m_y < \delta t^F_y$

Step A2.1: Survival prior to molting/growth/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/growth/mating in year *y* at δt^m_y (generally Feb. 15). The numbers surviving at δt^m_y in year *y* are given by:

$$n^1_{y,x,m,s,z} = e^{-M_{y,x,m,s,z} \cdot \delta t^m_y} \cdot n_{y,x,m,s,z}$$	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 (IMM, NS) crab, as well as the change in shell condition for mature new shell (MAT, NS) crab to mature old shell (MAT, OS) crab due to aging, are given by:

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

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

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

where $\Theta_{y,x,z,z'}$ is the growth transition matrix in year y for an immature new shell (IMM, NS) crab of sex x and pre-molt size z' to post-molt size z and $\phi_{y,x,z}$ is the probability that a just-molted crab of sex x and post-molt size z has undergone its terminal molt to maturity. Additionally, mature new shell (MAT, NS) crab 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 because immature crab are assumed to molt each year until they undergo the terminal molt to maturity.

Step A2.3: Survival after molting/growth/mating to prosecution of fisheries
Natural mortality is again applied to the population from just after molting/growth/mating to the time at which the fisheries occur for year y (at δt^F_y). The numbers surviving at δt^F_y in year y are then given by:

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

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

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

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

Step A2.5: Survival to end of year, recruitment, and update to start of next year
Finally, population abundance at the start of year $y+1$ due to natural mortality on crab from just after prosecution of the fisheries in year y until the end of the model year (June 30) and recruitment of immature new (IMM, NS) shell crab at the end of year y ($R_{y,x,z}$) and are given by:

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

B. Parameter specification

Because parameterization of many model processes (e.g., natural mortality, fishing mortality) in TCSAM02 is fairly flexible, it is worthwhile discussing how model processes and their associated parameters are configured in TCSAM02 before discussing details of the model processes themselves. Each type of model process has a set of (potentially estimable) model parameters and other information associated with it, but different "elements" of a model process can be defined that apply, for example, to different segments of the population and/or during different time blocks. In turn, several "elements" of a model parameter associated with a model process may also be defined (and applied to different elements of the process). At least one combination of model parameters and other information associated with a model process must be defined—i.e., one process element must be defined.

Model processes and parameters are configured in a "ModelParametersInfo" file, one of the three control files required for a model run (the others are the "ModelConfiguration" file and the "ModelOptions" file). As an example of the model processes and parameter specification syntax, Text Box 1 presents the part of a "ModelParametersInfo" file concerned with specifying fishing processes in the directed Tanner crab fishery.

In Text Box 1, the keyword "fisheries" identifies the model process in question. The first section, following the "PARAMETER_COMBINATIONS" keyword (up to the first set of triple blue dots), specifies the indices associated with fishing process parameters (pHM, pLnC, pDC1, pDC2, pDC3, pDC4, pDevsLnC, pLnEffX, pLgtRet), selectivity and retention functions (idxSelFcn, idxRetFcn), and effort averaging time period (effAvgID) that apply to a single fishing process element. In this example, the indices for the selectivity and retention functions, as well as those for the effort averaging time period, constitute the "other information" specified for each fishing process element. Each fishing process element in turn applies to a specific fishery (FISHERY=1 indicates the directed fishery, in this case), time block (specified by YEAR_BLOCK), and components of the model population (specified by SEX, MATURITY STATE, and SHELL CONDITION). Using indices to identify which parameters and selectivity and retention functions apply to a given combination of fishery/time block/sex/maturity state/shell condition allows one to "share" individual parameters and selectivity and retention functions across different fishery/time block/sex/maturity state/shell condition combinations.

The second section (following the "PARAMETERS" keyword) determines the characteristics for each of the fishing process parameters, organized by parameter name (note: the parameters associated with the different selectivity and retention functions are specified in a different section of the ModelParametersInfo file). Here, each parameter name corresponds to an ADMB "param_init_bounded_number_vector" in the model code—the exception being pDevsLnC, which corresponds to an ADMB "param_init_bounded_vector_vector".

Each row under a "non-devs" parameter name in the fisheries section (e.g., pLnC) specifies the index used to associate an element of the parameter with the fishing processes defined in the PARAMETER_COMBINATIONS section, as well as characteristics of the element in the associated ADMB number_vector (upper and lower bounds, initial value, and initial estimation phase), various flags for initialization ("jitter", "resample"), definition of an associated prior probability distribution, and a label. Each row under a "devs" parameter name (e.g., pDevsLnC) specifies much the same information for the associated ADMB devs vector, with the "read" flag replacing the "initial value" entry. If "read?" is TRUE, then a vector of initial values is read from the file after all "info" rows for the devs parameter have

been read. The "jitter" flag (if set to TRUE) provides the ability to change the initial value for an element of a non-devs parameter using a randomly selected value based on the element's upper and lower bounds. For a devs parameter, an element with jitter set to TRUE is initialized using a vector of randomly-generated numbers (subject to being a devs vector within the upper and lower bounds). The "resample" flag was intended to specify an alternative method to providing randomly-generated initial values (based on an element's prior probability distribution, rather than its upper and lower bounds), but this has not yet been fully implemented.

Some model processes apply only to specific segments of the population (e.g., growth only applies to immature, new shell crab). In general, though, a model process element can be defined to apply to any segment of the population (by specifying SEX, MATURITY STATE, and SHELL CONDITION appropriately) and range of years (by specifying YEAR_BLOCK). In turn, an element of a parameter may be "shared" across multiple processes by specifying the element's index in multiple rows of a PARAMETERS_COMBINATION block.

```
#------------------------------
# Fishery parameters
#------------------------------
fisheries #process name
PARAMETER_COMBINATIONS
42  #number of rows defining parameter combinations for all fisheries
#Directed Tanner Crab Fishery (TCF)
#                                    |MATURITY|SHELL|                               |pDevs| pLn | pLgt| idx   | idx   | eff   |
#id  FISHERY  YEAR_BLOCK             SEX | STATE  |COND |  pHM  pLnC pDC1 pDC2 pDC3 pDC4 |  LnC  | EffX| Ret |SelFcn|RetFcn| AvgID |  label
1     1       [-1:1964]              MALE     ALL    ALL    1    1    0    0    0    0      0      0    0     9      5       0     TCF:_M_T1
2     1       [1965:1984;1987:1990]  MALE     ALL    ALL    1    2    0    0    0    0      1      0    0     9      5       0     TCF:_M_T2
3     1       [1991:1996]            MALE     ALL    ALL    1    2    0    0    0    0      1      0    0     10     6       0     TCF:_M_T3
4     1       [2005:2009]            MALE     ALL    ALL    1    2    0    0    0    0      1      0    1     11     7       0     TCF:_M_T4
5     1       [2013:-1]              MALE     ALL    ALL    1    2    0    0    0    0      1      0    1     12     8       0     TCF:_M_T5
6     1       [-1:1964]              FEMALE   ALL    ALL    1    1    0    1    0    0      0      0    0     13     0       0     TCF:_F_T1
7     1       [1965:1984;1987:1996]  FEMALE   ALL    ALL    1    2    0    1    0    0      1      0    0     13     0       0     TCF:_F_T2
8     1       [2005:2009;2013:-1]    FEMALE   ALL    ALL    1    2    0    1    0    0      1      0    0     14     0       0     TCF:_F_T3
...
PARAMETERS
pHM #handling mortality (0-1)
3     #number of parameters
#   |    limits    |        | initial | start |          |-     priors       -|
#id |lower   upper|jitter?| value  | phase |resample?| wgt| type| params| consts|  label
1      0      1     OFF    0.321     -1       OFF        1   none   none    none     handling_mortality_for_crab_pot_fisheries
...
pLnC #base (ln-scale) capture rate (mature males)
9     #number of parameters
#   |    limits    |        | initial  | start |          |-     priors       -|
#id |lower   upper|jitter?|  value   | phase |resample?| wgt| type| params| consts|  label
1    -15     15     OFF    -2.995732274  -1      OFF        1   none  none    none     TCF:_base_capture_rate,_pre-1965_(=0.05)
2    -15     15     ON     -1.164816291   1      OFF        1   none  none    none     TCF:_base_capture_rate,_1965+
...
pDC1 #main temporal ln-scale capture rate offset
0     #number of parameters
pDC2 #ln-scale capture rate offset for female crabs
6     #number of parameters
#   |    limits    |        | initial  | start |          |-     priors       -|
#id |lower  upper |jitter?|  value   | phase |resample?| wgt  type  params  consts|  label
1    -5.0   5.0     ON     -2.058610432   1      OFF        1.0  none   none    none    TCF:_female_offset
...
pDevsLnC #annual ln-scale capture rate deviations
6         #number of parameter vectors
#   | index |                index                   |       | limits    |          |initial |start |          |-      priors         -|
#id |  type |                block                   | read? |lower   upper| jitter?| value  |phase |resample?| wgt | type | params | consts |label
1     YEAR   [1965:1984;1987:1996;2005:2009;2013:-1]  FALSE   -15    15     ON       0        1       OFF       2.0  normal   0 1     none    TCF:_T2345
...
```

Text Box 1. Abbreviated example of process and parameter specifications in a "ModelParametersInfo" file for fishing mortality in TCSAM02. Only parameter combinations and parameters relevant to the directed fishery are shown. Input values are in black text, comments are in green, triple blue dots indicate additional input lines not shown.

C. Model processes: natural mortality

The natural mortality rate applied to crab of sex x, maturity state m, shell condition s, and size z in year y, $M_{y,x,m,s,z}$, can be specified using one of two parameterizations. The first parameterization option uses a ln-scale parameterization with an option to include an inverse- size dependence using Lorenzen's approach:

$$lnM_{y,x,m,s} = \mu^0_{y,x,m,s} + \sum_{i=1}^{4} \delta\mu^i_{y,x,m,s}$$	C.1a
$$M_{y,x,m,s,z} = \begin{cases} \exp(lnM_{y,x,m,s}) & \textit{if Lorenzen option is not selected} \\ \exp(lnM_{y,x,m,s}) \cdot \dfrac{z_{base}}{z} & \textit{if Lorenzen option is selected} \end{cases}$$	C.1b C.1c

where the μ^0 and the $\delta\mu^i$'s are (potentially) estimable parameters defined for time block T, sex S (MALE, FEMALE, or ANY), maturity M (IMMATURE, MATURE, or ANY), and shell condition S (NEWSHELL, OLDSHELL, or ANY), and $\{y,x,m,s\}$ falls into the set $\{T,X,M,S\}$. In Eq. C.1c, z_{base} denotes the specified reference size (mm CW) for the inverse-size dependence.

The second parameterization option uses an arithmetic parameterization in order to provide backward compatibility with the 2016 assessment model based on TCSAM2013. In TCSAM2013, the natural mortality rate $M_{y,x,m,s,z}$ was parameterized using:

$$M_{y,x,m=IMM,s,z} = M^{base} \cdot \delta M_{IMM}$$	C.2a
$$M_{y,x,m=MAT,s,z} = \begin{cases} M^{base} \cdot \delta M_{x,MAT} & \textit{otherwise} \\ M^{base} \cdot \delta M_{x,MAT} \cdot \delta M^T_{x,MAT} & 1980 \leq y \leq 1984 \end{cases}$$	C.2b

where M^{base} was a fixed value (0.23 yr^{-1}), δM_{IMM} was a multiplicative factor applied for all immature crab, the $\delta M_{x,MAT}$ were sex-specific multiplicative factors for mature crab, and the $\delta M^T_{x,MAT}$ were additional sex-specific multiplicative factors for mature crab during the 1980-1984 time block (which has been identified as a period of enhanced natural mortality on mature crab, the mechanisms for which are not understood). While it would be possible to replicate Eq.s C.2a and C.2b using ln-scale parameters, TCSAM2013 also placed informative arithmetic-scale priors on some of these parameters—and this could not be duplicated on the ln-scale. Consequently, the second option uses the following parameterization, where the parameters (and associated priors) are defined on the arithmetic-scale:

$$lnM_{y,x,m,s} = \ln[\mu^0_{y,x,m,s}] + \sum_{i=1}^{4} \ln[\delta\mu^i_{y,x,m,s}]$$	C.3a

A system of equations identical to C.2a-b can be achieved under the following assignments:

$$\mu^0_{\{y,x,m,s\}\in\{T=ALL,X=ALL,M=ALL,S=ALL\}} = M^{base}$$	C.4a
$$\delta\mu^1_{\{y,x,m,s\}\in\{T=ALL,X=ALL,M=IMM,S=ALL\}} = \delta M_{IMM}$$	C.4e
$$\delta\mu^1_{\{y,x,m,s\}\in\{T=ALL,X=x,M=MAT,S=ALL\}} = \delta M_{x,MAT}$$	C.4f
$$\delta\mu^2_{\{y,x,m,s\}\in\{T=1980-1984,X=x,M=MAT,S=ALL\}} = \delta M^T_{x,MAT}$$	C.4g

where unassigned $\delta\mu^i_{y,x,m,s}$ are set equal to 1. Pending further model testing using alternative model configurations, the TCSAM2013 option is standard.

It is worth noting explicitly that, given the number of potential parameters above that could be used, extreme care must be taken when defining a model to achieve a set of parameters that are not confounded and are, at least potentially, estimable.

D. Model processes: growth

Because Tanner crab are assumed to undergo a terminal molt to maturity, in TCSAM02 only immature crab experience growth. Annual growth of immature crab is implemented as using two options, the first based on a formulation used in Gmacs and the second (mainly for purposes of backward compatibility) based on that used in TCSAM2013. In TCSAM02, growth can vary by time block and sex, so it is expressed by sex-specific transition matrices for time block t, $\Theta_{t,x,z,z'}$, that specify the probability that crab of sex x in pre-molt size bin z' grow to post-molt size bin z at molting.

In the Gmacs-like approach (the standard approach as of May, 2017), the sex-specific growth matrices are given by:

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

where the integral represents a cumulative gamma distribution across the post-molt (z) size bin. This approach may have better numerical stability properties than the TCSAM2013 approach below.

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

$\Theta_{t,x,z,z'} = c_{t,x,z'} \cdot \Delta_{z,z'}^{\alpha_{t,x,z'}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_{t,x}}}$	Sex-specific (x) transition matrix for growth from pre-molt z' to post-molt z, with $z \geq z'$	D.2a
$c_{t,x,z'} = \left[\displaystyle\sum_{z'} \Delta_{z,z'}^{\alpha_{t,x,z'}-1} \cdot e^{-\frac{\Delta_{z,z'}}{\beta_{t,x}}}\right]^{-1}$	Normalization constant so $1 = \displaystyle\sum_z \Theta_{t,x,z,z'}$	D.2b
$\Delta_{z,z'} = z - z'$	Actual growth increment	D.2c
$\alpha_{t,x,z'} = [\bar{z}_{t,x,z'} - z']/\beta_{t,x}$	Mean molt increment, scaled by $\beta_{t,x}$	D.2d
$\bar{z}_{t,x,z'} = e^{a_{t,x}} \cdot z'^{b_{t,x}}$	Mean size after molt, given pre-molt size z'	D.2e

In both approaches, the $a_{t,x}$, $b_{t,x}$, and $\beta_{t,x}$ are arithmetic-scale parameters with imposed bounds. $\Theta_{t,x,z,z'}$ 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:

$$n_{y,x,z}^+ = \sum_{z'} \Theta_{t,x,z,z'} \cdot n_{y,x,z'}$$	numbers at size of immature crab after growth	D.3

where y falls within time block t (see also Eq.s A1.4a-b and A2.2a-b).

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. While priors may be defined for the associated parameters here, these are identified by the user in the model input files and are not hard-wired in the model code.

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

$$n_{y,x,IMM,NS,z}^+ = (1 - \phi_{t,x,z}) \cdot n_{y,x,IMM,NS,z}$$	crab remaining immature	E.1a
$$n_{y,x,MAT,NS,z}^+ = \phi_{t,x,z} \cdot n_{y,x,IMM,NS,z}$$	crab maturing (terminal molt)	E.1b

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

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

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

where the $z_{t,x}^{mat}$ are constants specifying the minimum pre-molt size at which to assume all immature crab will mature upon molting. The $z_{t,x}^{mat}$ 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 $z_{t,x}^{mat}$ used above. This parameterization is similar to that implemented in TCSAM2013 for the 2016 assessment model.

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

F. Model processes: recruitment
Recruitment in TCSAM02 consists of immature new shell crab entering the population at the end of the model year (June 30). Recruitment in TCSAM02 has a similar functional form to that used in TCSAM2013, except that the sex ratio at recruitment is not fixed at 1:1 and multiple time blocks can be specified. In TCSAM2013, two time blocks were defined: "historical" (model start to 1974) and "current" (1975-present), with "current" recruitment starting in the first year of NMFS survey data. In TCSAM02, recruitment in year y of immature new shell crab of sex x at size z is specified as

$R_{y,x,z} = \dot{R}_y \cdot \ddot{R}_{y,x} \cdot \ddot{R}_{y,z}$	recruitment of immature, new shell crab by sex and size bin	F.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 $\ddot{R}_{y,z}$ is the size distribution of recruits, which is assumed identical for males and females.

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

$\dot{R}_y = e^{pLnR_t + \delta R_{t,y}} \quad y \in t$	total recruitment in year y	F.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 over the time block).

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

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

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

The size distribution for recruits in time block t, $\ddot{R}_{t,z}$, is assumed to be a gamma distribution and is parameterized as

$\ddot{R}_{t,z} = c^{-1} \cdot \Delta_z^{\frac{\alpha_t}{\beta_t} - 1} \cdot e^{-\frac{\Delta_z}{\beta_t}}$	size distribution of recruiting crab	F.4
$c_t = \sum_z \Delta_z^{\frac{\alpha_t}{\beta_t} - 1} \cdot e^{-\frac{\Delta_z}{\beta_t}}$	normalization constant so that $1 = \sum_z \ddot{R}_{t,z}$	F.5
$\Delta_z = z + \delta z/2 - z_{min}$	offset from minimum size bin	F.6
$\alpha_t = e^{pLnRa_t}$	gamma distribution location parameter	F.7
$\beta_t = e^{pLnRb_t}$	gamma distribution shape parameter	F.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 process representing the ln-scale coefficient of variation (cv) in recruitment variability in time block t. These parameters are used to apply priors on the recruitment "devs" in the model likelihood function.

G. Selectivity and retention functions
Selectivity and retention functions in TCSAM02 are specified independently from the fisheries and surveys to which they are subsequently applied. This allows a single selectivity function to be "shared" among multiple fisheries and/or surveys, as well as among multiple time block/sex/maturity state/shell condition categories, if so desired.

Currently, the following functions are available for use as selectivity or retention curves in a model:

$S_z = \{1 + e^{-\beta \cdot (z - z_{50})}\}^{-1}$	standard logistic	G.1
$S_z = \{1 + e^{-\beta \cdot (z - \exp(lnZ_{50}))}\}^{-1}$	logistic w/ alternative parameterization	G.2
$S_z = \left\{1 + e^{-\ln(19) \cdot \frac{(z - z_{50})}{\Delta z_{95-50}}}\right\}^{-1}$	logistic w/ alternative parameterization	G.3
$S_z = \left\{1 + e^{-\ln(19) \cdot \frac{(z - z_{50})}{\exp(ln\Delta z_{95-50})}}\right\}^{-1}$	logistic w/ alternative parameterization	G.4
$S_z = \left\{1 + e^{-\ln(19) \cdot \frac{(z - \exp(lnZ_{50}))}{\exp(ln\Delta z_{95-50})}}\right\}^{-1}$	logistic w/ alternative parameterization	G.5
$S_z = \dfrac{1}{1 + e^{-\beta_a \cdot (z - z_{a50})}} \cdot \dfrac{1}{1 + e^{\beta_d \cdot (z - z_{d50})}}$	double logistic	G.6
$S_z = \dfrac{1}{1 + e^{-\ln(19) \cdot \frac{(z - z_{a50})}{\Delta z_{a(95-50)}}}} \cdot \dfrac{1}{1 + e^{\ln(19) \cdot \frac{(z - z_{d50})}{\Delta z_{d(95-50)}}}}$	double logistic with alt. parameterization	G.7
$S_z = \dfrac{1}{1 + e^{-\ln(19) \cdot \frac{(z - z_{a50})}{\exp(ln\Delta z_{a(95-50)})}}} \cdot \dfrac{1}{1 + e^{\ln(19) \cdot \frac{(z - z_{d50})}{\exp(ln\Delta z_{d(95-50)})}}}$ $where\ z_{d50} = [z_{a50} + \exp(ln\Delta z_{a(95-50)}) + \exp(ln\Delta z_{d(95-50)})]$	double logistic with alt. parameterization	G.8
$S_z = \dfrac{1}{1 + e^{-\ln(19) \cdot \frac{(z - \exp(lnz_{a50}))}{\exp(ln\Delta z_{a(95-50)})}}} \cdot \dfrac{1}{1 + e^{\ln(19) \cdot \frac{(z - z_{d50})}{\exp(ln\Delta z_{d(95-50)})}}}$ $where\ z_{d50} = [\exp(lnz_{a50}) + \exp(ln\Delta z_{a(95-50)}) + \exp(ln\Delta z_{d(95-50)})]$	double logistic with alt. parameterization	G.9
$S_z = \dfrac{1}{1 + e^{-\beta_a \cdot (z - z_{a50})}} \cdot \dfrac{1}{1 + e^{\beta_d \cdot (z - [z_{a50} + \exp(lnZ_{d50-a50})])}}$	double logistic with alt. parameterization	G.10

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

Selectivity parameters are defined independently of the functions themselves, and subsequently assigned. It is thus possible to "share" parameters across multiple functions. The "parameters" used in selectivity functions are further divided into mean parameters across a time block and annual deviations within a time block. To accommodate the 6-parameter double normal equation, six "mean" parameter sets (*pS1*, *pS2*,…, *pS6*) and six associated sets of "devs" parameter vectors (*pDevsS1*, *pDevsS2*,…, *pDevsS6*) are defined to specify the parameterization of individual selectivity/retention functions. 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.

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.

H. Fisheries

Unlike TCSAM2013, which explicitly models 4 fisheries that catch Tanner crab (one as a directed fishery, three as bycatch), there is no constraint in TCSAM02 on the number of fisheries that can be incorporated in the model. All fisheries are modeled as "pulse" fisheries occurring at the same time.

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

$F_{f,y,x,m,s,z} = \left[h_{f,t} \cdot \left(1 - \rho_{f,y,x,m,s,z}\right) + \rho_{f,y,x,m,s,z}\right] \cdot \phi_{f,y,x,m,s,z}$	fishing mortality rate	H.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 assumed to be identically 0 for females in a directed fishery and for both sexes in a bycatch fishery.

In TCSAM2013, the same retention function (in each of two time blocks) was applied to male crab regardless of maturity state or shell condition. Additionally, full retention of large males was assumed, such that the retention function essentially reached 1 at large sizes. In TCSAM02, different retention functions can be applied based on maturity state and/or shell condition, and "max retention" is now an (potentially) estimable logit-scale parameter. Thus, in TCSAM02, the retention function $\rho_{f,y,x,m,s,z}$ is given by

$\rho_{f,y,x,m,s,z} = \dfrac{1}{1 + e^{\rho_{f,t,x,m,s}}} \cdot R_{f,y,x,m,s,z}$	retention function	H.2

where f corresponds to the directed fishery, y is in time block t, x=MALE, $\rho_{f,t,x,m,s}$ is the corresponding logit-scale "max retention" parameter, and $R_{f,y,x,m,s,z}$ is the associated selectivity/retention curve.

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

$c_{f,y,x,m,s,z} = \dfrac{\phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1 - e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$	number of crab captured	H.3

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

$r_{f,y,x,m,s,z} = \dfrac{\rho_{f,y,x,m,s,z} \cdot \phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1 - e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$	number of retained crab	H.4

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

$$d_{f,y,x,m,s,z} = \frac{(1 - \rho_{f,y,x,m,s,z}) \cdot \phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1 - e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$$ | number of discarded crab | H.5

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

$$dm_{f,y,x,m,s,z} = \frac{h_{f,y} \cdot (1 - \rho_{f,y,x,m,s,z}) \cdot \phi_{f,y,x,m,s,z}}{F^T_{y,x,m,s,z}} \cdot \left[1 - e^{-F^T_{y,x,m,s,z}}\right] \cdot n_{y,x,m,s,z}$$ | discard mortality (numbers) | H.6

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

$$\phi_{f,y,x,m,s,z} = \phi_{f,y,x,m,s} \cdot S_{f,y,x,m,s,z}$$ | fishing capture rate | H.7

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:

$$\phi_{f,y,x,m,s} = \exp\left(\overline{lnC}_{f,t,x,m,s} + pDevsC_{f,y,x,m,s}\right)$$ | | H.8

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

$$\overline{lnC}_{f,t,x,m,s} = pLnC_{f,t,x,m,s} + \sum_{i=1}^{4} \delta C^i_{f,t,x,m,s}$$ | | H.9

where the $pLnC_{f,t,x,m,s}$ is the mean ln-scale capture rate (e.g., for mature males) and the $\delta C^i_{f,t,x,m,s}$ are ln-scale offsets.

I. 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 survey abundance, $a_{v,y,x,m,s,z}$, of crab classified in that state by survey v is given by

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

where $q_{v,y,x,m,s,z}$ is the size-specific survey catchability on this component of the population.

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

$$q_{v,y,x,m,s,z} = q_{v,t,x,m,s} \cdot S_{v,t,x,m,s,z}$$ | survey catchability | I.2

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:

$$q_{v,t,x,m,s} = \exp\left(pLnQ_{v,t,x,m,s} + \sum_{i=1}^{4} \delta Q_{v,t,x,m,s}^i\right) \qquad \text{I.3}$$

where the $pLnQ_{v,t,x,m,s}$ is the mean ln-scale catchability (e.g., for mature males) and the $\delta Q_{v,t,x,m,s}^i$ are ln-scale offsets.

J. Model fitting: objective function equations
The TCSAM02 model is fit by minimizing an objective function, σ, 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:

$$\sigma = -2 \sum_p \lambda_p \cdot \ln(\wp_p) - 2 \sum_l \lambda_l \cdot \ln(\mathcal{L}_l) \qquad \text{model objective function} \qquad \text{J.1}$$

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

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

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

Size frequency components
Likelihood components involving size frequencies are based on multinomial sampling:

$$\ln(\mathcal{L}) = \sum_y n_{y,c} \cdot \sum_z \left\{p_{y,c,z}^{obs} \cdot \ln\left(p_{y,c,z}^{mod} + \delta\right) - p_{y,c,z}^{obs} \cdot \ln\left(p_{y,c,z}^{obs} + \delta\right)\right\} \qquad \text{multinomial log-likelihood} \qquad \text{J.2}$$

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. Data can be entered in input files at less-aggregated levels of than will be used in the model; it will be aggregated in the model to the requested level before fitting occurs.

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

The ln-scale normal likelihood function is

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

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

The ln-scale lognormal likelihood function is

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

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

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

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

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

Growth data
Growth (molt increment) data can be fit as part of a TCSAM02 model. Multiple datasets can be fit at the same time. The likelihood for each dataset (L_d) is based on the same gamma distribution used in the growth model:

$$L_d = -\sum_{i \in d} ln\left\{\Gamma\left(\frac{\tilde{z}_i - \bar{z}_{y_i,x_i,z_i}}{\beta_{y_i,x_i}}\right)\right\}$$	gamma log-likelihood	J.6

where z_i and $\tilde{z}_i$ are the pre-molt and post-molt sizes for individual i (of sex x_i collected in year y_i) in dataset d, respectively, $\bar{z}_{y_i,x_i,z_i}$ is the predicted mean post-molt size for individual i, and β_{y_i,x_i} is the scale factor for the gamma distribution corresponding to individual i.

Maturity ogive data
Annual maturity ogive data, the observed proportions-at-size of mature crab in a given year, can also be fit as part of a TCSAM02 model. This data consists of proportions of mature crab observed within a size bin, as well as the total number of observations for that size bin. The proportions are assumed to represent the fraction of new shell mature crab (i.e., having gone through terminal molt within the previous growth season) to all new shell crab within the size bin in that year. Multiple datasets can be fit at the same time. The likelihood for each observation is based on a binomial distribution with sample size equal to the

number of observations within the corresponding size bin, so the likelihood for each dataset (L_m) is given by:

$L_m = \sum_{y,z} n_{y,z} \cdot \{p_{y,z}^{obs} \cdot \ln(p_{y,z}^{mod} + \delta) + (1 - p_{y,z}^{obs}) \cdot \ln(1 - p_{y,z}^{mod} + \delta)\}$	binomial log-likelihood	J.7

where y is a year, z is a size bin, $n_{y,z}$ is the total number of classified crab in size bin z in year y, $p_{y,z}^{obs}$ is the observed ratio of mature, new shell males to total new shell males in size bin z in year y, $p_{y,z}^{obs}$ is the corresponding model-predicted ratio, and δ is a small constant to prevent trying to calculate $\ln(0)$.

Effort data
In both TCSAM2013 and TCSAM02, fishery-specific effort data is used to predict annual fully-selected fishery capture rates for Tanner crab bycatch in the snow crab and Bristol Bay red king crab fisheries in the period before at-sea observer data is available (i.e., prior to 1991), based on the assumed relationship

$$F_{f,y} = q_f \cdot E_{f,y}$$

where $F_{f,y}$ is the fully-selected capture rate in fishery f in year y, q_f is the estimated catchability in fishery f, and $E_{f,y}$ is the reported annual, fishery-specific effort (in pots). In TCAM2013, the fishery q's are estimated directly from the ratio of fishery mean F to mean E over the time period (t_f) when at-sea observer data is available from which to estimate the $F_{f,y}$'s as parameters:

$$q_f = \frac{\sum_{y \in t_f} F_{f,y}}{\sum_{y \in t_f} E_{f,y}}.$$

Note that, in this formulation, the fishery q's are not parameters (i.e., estimated via maximizing the likelihood) in the model. In TCSAM2013, the time period over which q is estimated for each fishery is hard-wired. This approach is also available as an option in TCSAM02, although different time periods for the averaging can be specified in the model options file.

A second approach to effort extrapolation in which the fishery q's are fully-fledged parameters estimated as part of maximizing the likelihood is provided in TCSAM02 as an option, as well. In this case, the effort data is assumed to have a lognormal error distribution and the following negative log-likelihood components are included in the overall model objective function:

$$L_f = \sum_y \frac{\left(\ln(E_{f,y} + \delta) - \ln\left(\frac{F_{f,y}}{q_f} + \delta\right)\right)^2}{2 \cdot \sigma_f^2}$$

where σ_f^2 is the assumed ln-scale variance associated with the effort data and δ is a small value so that the arguments of the ln functions do not go to zero.

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

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

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

K. Devs vectors

For TCSAM02 to accommodate arbitrary numbers of fisheries and time blocks, it is necessary to be able to define arbitrary numbers of "devs" vectors. This is currently not possible using the ADMB C++ libraries, so TCSAM02 uses an alternative implementation of devs vectors from that implemented in ADMB. For the 2017 assessment, an *n*-element "devs" vector was implemented using an *n*-element bounded parameter vector. with the final element of the "devs" vector defined as $-\sum_{n-1} v_i$, where v_i was the ith value of the parameter (or devs) vector, so that the sum over all elements of the devs vector was identically 0. Penalties were placed on the final element of the devs vector to ensure it was bounded in the same manner as the parameter vector. However, this approach was problematic when initializing the model with the values for the *n*-1 elements that defined the n-element devs vector, the value of the n-th element $(-\sum_{n-1} v_i)$ was not guaranteed to satisfy the bounds placed on the vector. Thus, this approach was revised to allow specification of all n element values (the $v_n = -\sum_{n-1} v_i$ constraint was removed) while the likelihood penalty was changed to ensure the sum of the elements was 0. The new approach also has the advantage that it more closely follows the one used in ADMB to define "devs" vectors. Test runs with both approaches showed no effect on convergence to the MLE solution.

L. Priors for model parameters

A prior probability distribution can be specified for any element of model parameter. The following distributions are available for use as priors:

indicator	parameters	constants	description
none	none	none	no prior applied
ar1_normal	μ, σ	none	random walk with normal deviates
cauchy	x_0, γ	none	Cauchy pdf
chisquare	υ	none	χ^2 pdf
constant	min, max	none	uniform pdf
exponential	λ	none	exponential pdf
gamma	r, μ	none	gamma pdf
invchisquare	υ	none	inverse χ^2 pdf

invgamma	r, μ	none	inverse gamma pdf
invgaussian	μ, λ	none	inverse Gaussian pdf
lognormal	median, CV	none	lognormal pdf
logscale_normal	median, CV	none	normal pdf on ln-scale
normal	μ, σ	none	normal pdf
scaled_invchisquare	υ, s	none	inverse χ^2 scaled pdf
scaledCV_invchisquare	υ, CV	none	inverse χ^2 pdf, scaled by CV
t	υ	none	t distribution
truncated_normal	μ, σ	min, max	truncated normal pdf

M. Parameters and other information determined outside the model

Several nominal model parameters are not estimated in the model, rather they are fixed to values determined outside the model. These include Tanner crab handling mortality rates for discards in the crab fisheries (32.1%), the groundfish trawl fisheries (80%), and the groundfish pot fisheries (50%), as well the base rate for natural mortality (0.23 yr^{-1}). Sex- and maturity-state-specific parameters for individual weight-at-size have also been determined outside the model, based on fits to data collected on the NMFS EBS bottom trawl survey (Daly et al., 2016). Weight-at-size, $w_{x,m,z}$, is given by

$$w_{x,m,z} = a_{x,m} \cdot z^{b_{x,m}}$$

where

sex	maturity state	$a_{x,m}$	$b_{x,m}$
male	all states	0.000270	3.022134
female	immature	0.000562	2.816928
	mature	0.000441	2.898686

and size is in mm CW and weight is in kg.

N. OFL calculations and stock status determination

Overfishing level (OFL) calculations and stock status determination for Tanner crab are based on Tier 3 considerations for crab stocks as defined by the North Pacific Fishery Management Council (NPFMC; NPFMC 2016). Tier 3 considerations require life history information such as natural mortality rates, growth, and maturity but use proxies based on a spawner-per-recruit approach for F_{MSY}, B_{MSY}, and MSY because there is no reliable stock-recruit relationship. Equilibrium recruitment is assumed to be

Fig. 2. The F_{OFL} harvest control rule.

equal to the average recruitment over a selected time period (1982-present for Tanner crab). For Tier 3 stocks, the proxy for B_{MSY} is defined as 35% of longterm (equilibrium) mature male biomass (MMB) for the unfished stock (B_0). The proxy F_{MSY} for Tier 3 stocks is then the directed fishing mortality rate that results in $B_{35\%}$ (i.e., $F_{35\%}$), while the MSY proxy is the longterm total (retained plus discard) catch mortality resulting from fishing at F_{MSY}. The OFL calculation for the upcoming year is based on a sloping
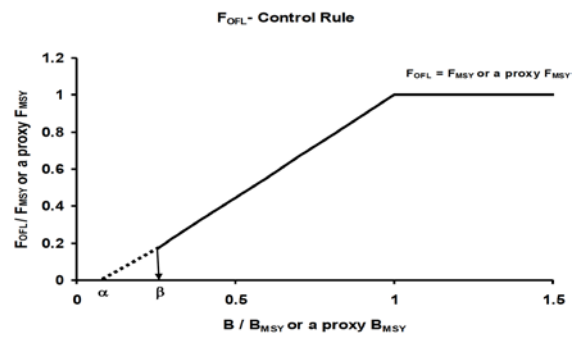
harvest control rule for F_{OFL} (Fig. 2), the directed fishing mortality rate that results in the OFL. If the "current" MMB (projected to Feb. 15 of the upcoming year under the F_{OFL}) is above B_{MSY} ($B_{35\%}$), then $F_{OFL}=F_{MSY}=F_{35\%}$. If the current MMB is between $\beta \cdot B_{MSY}$ and B_{MSY}, then F_{OFL} is determined from the slope of the control rule. In either of these cases, the OFL is simply the projected total catch mortality under directed fishing at F_{OFL}. If current MMB is less than $\beta \cdot B_{MSY}$, then no directed fishing is allowed ($F_{OFL}=0$) and the OFL is set to provide for stock rebuilding with bycatch in non-directed fisheries. Note that if current MMB is less than B_{MSY}, then the process of determining F_{OFL} is generally an iterative one.

Stock status is determined by comparing "current" MMB with the Minimum Stock Size Threshold (MSST), which is defined as $0.5x B_{MSY}$: if "current" MMB is below the MSST, then the stock is overfished—otherwise, it is not overfished.

N.1 Equilibrium conditions
Both OFL calculations and stock status determination utilize equilibrium considerations, both equilibrium under unfished conditions (to determine B_0 and $B_{35\%}$) and under fished conditions (to determine $F_{35\%}$). For Tier 3 stocks, because there is no reliable stock-recruit relationship, analytical solutions can be found for equilibrium conditions for any fishing mortality conditions. These solutions are described below (the notation differs somewhat from that used in previous sections).

N.1.1 Population states
The Tanner crab population on July 1 can be characterized by abundance-at-size in four population states:

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

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

N.1.2 Population processes
The following processes then describe the dynamics of the population over a year:

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

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

N.1.3 Population dynamics

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

$$in^+ = R + S_{2in} \cdot \{(1 - \Theta_{in}) \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + T_{io} \cdot (1 - \Theta_{io}) \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \tag{N.1}$$

$$io^+ = S_{2io} \cdot \{(1 - \Phi_{in}) \cdot S_{1in} \cdot in + (1 - \Phi_{io}) \cdot S_{1io} \cdot io\} \tag{N.2}$$

$$mn^+ = S_{2mn} \cdot \{\Theta_{in} \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + \Theta_{io} \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \tag{N.3}$$

$$mo^+ = S_{2mo} \cdot \{S_{1mn} \cdot mn + S_{1mo} \cdot mo\} \tag{N.4}$$

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

N.1.4 Equilibrium equations

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

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

$$io = S_{2io} \cdot \{(1 - \Phi_{in}) \cdot S_{1in} \cdot in + (1 - \Phi_{io}) \cdot S_{1io} \cdot io\} \tag{N.6}$$

$$mn = S_{2mn} \cdot \{\Theta_{in} \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \cdot in + \Theta_{io} \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \cdot io\} \tag{N.7}$$

$$mo = S_{2mo} \cdot \{S_{1mn} \cdot mn + S_{1mo} \cdot mo\} \tag{N.8}$$

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

N.1.5 Equilibrium solution

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

$$in = R + A \cdot in + B \cdot io \tag{N.9}$$

$$io = C \cdot in + D \cdot io \tag{N.10}$$

$$mn = E \cdot in + F \cdot io \tag{N.11}$$

$$mo = G \cdot mn + H \cdot mo \tag{N.12}$$

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

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

Plugging eq. 13 into 9 and solving for in yields

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

Equations 13 for io and 14 for in can simply be plugged into eq. 11 to yield mn:

$$mn = E \cdot in + F \cdot io \tag{N.15}$$

while eq. 12 can then be solved for mo, yielding:

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

where (for completeness):

$$A = S_{2in} \cdot (1 - \Theta_{in}) \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \tag{N.17}$$

$$B = S_{2in} \cdot (1 - \Theta_{io}) \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \tag{N.18}$$

$$C = S_{2io} \cdot (1 - \Phi_{in}) \cdot S_{1in} \tag{N.19}$$

$$D = S_{2io} \cdot (1 - \Phi_{io}) \cdot S_{1io} \tag{N.20}$$

$$E = S_{2mn} \cdot \Theta_{in} \cdot T_{in} \cdot \Phi_{in} \cdot S_{1in} \tag{N.21}$$

$$F = S_{2mn} \cdot \Theta_{io} \cdot T_{io} \cdot \Phi_{io} \cdot S_{1io} \tag{N.22}$$
$$G = S_{2mo} \cdot S_{1mn} \tag{N.23}$$
$$H = S_{2mo} \cdot S_{1mo} \tag{N.24}$$

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

N.2 OFL calculations
Because a number of the calculations involved in determining the OFL are iterative in nature, the OFL calculations do not involve automatically-differentiated (AD) variables. Additionally, they are only done after model convergence or when evaluating an MCMC chain. The steps involved in calculating the OFL are outlined as follows:

1. The initial population numbers-at-sex/maturity state/shell condition/size for the upcoming year are copied to a non-AD array.
2. Mean recruitment is estimated over a pre-determined time frame (currently 1982-present).
3. The arrays associated with all population rates in the final year are copied to non-AD arrays for use in the upcoming year.
4. Calculate the average selectivity and retention functions for all fisheries over the most recent 5-year period.
5. Determine the average maximum capture rates for all fisheries over the most recent 5-year period.
6. Using the equilibrium equations, calculate B_0 for unfished stock (B35% = 0.35*B_0).
7. Using the equilibrium equations, iterate on the maximum capture rate for males in the directed fishery to find the one ($F_{35\%}$) that results in the equilibrium MMB = $B_{35\%}$.
8. Calculate "current" MMB under directed fishing at F=$F_{35\%}$ by projecting initial population (1) to Feb. 15.
   a. If current MMB > $B_{35\%}$, F_{OFL} = $F_{35\%}$. The associated total catch mortality is OFL.
   b. Otherwise
      i. set directed F based on the harvest control rule and the ratio of the calculated current MMB to $B_{35\%}$
      ii. recalculate current MMB
      iii. iterate i-iii until current MMB doesn't change between iterations. Then $F_{OFL} = F$ ($< F_{35\%}$) and the OFL is the associated total (retained plus discard) catch mortality.

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