# Appendix 3: TCSAM (Tanner Crab Stock Assessment Model) 2014 Description

## Introduction

The 2014 version of the Tanner crab model (TCSAM2014) 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. TCSAM2014 is heavily based on the Tanner crab model used in the 2013 stock assessment (Stockhausen et al., 2013; Appendix 1 here) but incorporates the Gmacs (Whitten et al., 2013) approach to modeling fishing mortality based on capture rates and is completely new model code.

Model parameters in TCSAM2014 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.

## A. General population dynamics

Population abundance at the start of year *y* in the model, , 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 () relative to molting () within year y. The steps when are outlined below first (Steps A1.1-A1.4), followed by the steps when . (Steps A2.1-A2.4).

## A1. Calculation sequence when

### 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 . The numbers surviving at in year *y* are given by:

|  |  |
| --- | --- |
|  | 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 in year *y*. The numbers that remain after the fisheries are prosecuted are given by:

|  |  |
| --- | --- |
|  | A1.2 |

where 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 (generally Feb. 15). The numbers surviving at in year *y* are then given by:

|  |  |
| --- | --- |
|  | 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:

|  |  |
| --- | --- |
|  | A1.4a |
|  | A1.4b |
|  | A1.4c |

where is the probability that an immature (new shell) crab of sex x and size z will undergo its terminal molt to maturity and is the growth transition matrix from size *z’* to *z* for that crab, which may depend on whether (*m*=*MAT*; eq. A1.3a) or not (*m*=*IMM*; eq. A1.3b) 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 (A1.3c). 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 recruitment of immature new shell crab at the end of year *y* (*ry,x,z*) and natural mortality on crab from the time of molting in year *y* until the end of the model year (June 30) are given by:

|  |  |
| --- | --- |
|  | A1.5a |
|  | A1.5b |

## A2. Calculation sequence when

### 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 (generally Feb. 15). The numbers surviving at in year *y* are given by:

|  |  |
| --- | --- |
|  | 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:

|  |  |
| --- | --- |
|  | A2.2a |
|  | A2.2b |
|  | A2.2c |

where is the probability that an immature (new shell) crab of sex x and size z will undergo its terminal molt to maturity and 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 ). The numbers surviving at in year *y* are then given by:

|  |  |
| --- | --- |
|  | 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 in year *y*. The numbers that remain after the fisheries are prosecuted are given by:

|  |  |
| --- | --- |
|  | A2.4 |

where 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 recruitment of immature new shell crab at the end of year *y* (*ry,x,z*) and natural mortality on crab from just after prosecution of the fisheries in year *y* until the end of the model year (June 30) are given by:

|  |  |
| --- | --- |
|  | A2.5a |
|  | A2.5b |

## B. Model processes: natural mortality

At its most general, natural mortality is parameterized as a time-varying (in blocks of years) function of sex, maturity state, and size using the following functional form:

|  |  |
| --- | --- |
|  | B.1 |
|  | B.2a  B.2b |

where *y* falls into time block *t*, the ’s are (potentially) estimable parameters on the ln-scale, , is 1 if *i=j* and 0 otherwise. represents the baseline (ln-scale) natural mortality rate on mature males, while is the offset in time block *t*, is the offset for immature crab in time block *t*, is the offset for females in time block *t*, and 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 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. Additionally, TCSAM2013 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 would require modifying and recompiling the code for every alternative time block considered. A similar study using TCSAM2014 would not require modifying the model code because time blocks can be defined for any model process (e.g., natural mortality) in the model input files.

## C. Model processes: growth

Annual growth of immature crab in TCSAM2014 is based on the same approach used in TCSAM2013, except that growth can vary by time block. As such, growth is expressed by sex-specific transition matrices that specify the probability that crab in pre-molt size bin *z* grow to post-molt size bin during time block *t*. The sex-specific growth matrix is given by

|  |  |  |
| --- | --- | --- |
|  | Sex-specific (*x*) transition matrix for growth from pre-molt *z* to post-molt , with | C.1 |
|  | Normalization constant so | C.2 |
|  | Actual growth increment | C.3 |
|  | Mean molt increment, scaled by | C.4 |
|  | Mean size after molt, given pre-molt size *z* | C.5 |

where the *at,x*, *bt,x*, and (parameters in TCSAM2013) are arithmetic-scale versions of the ln-scale model parameters , , and :

|  |  |  |
| --- | --- | --- |
|  |  | C.6 |
|  |  | C.7 |
|  |  | C.8 |

Again, because *at,x*, *bt,x*, and must be non-negative, the associated parameters in TCSAM2014 are estimated on the ln-scale and transformed to the arithmetic scale.

is used to update the numbers-at-size for immature crab, , from pre-molt size *z* to post-molt size using:

|  |  |  |
| --- | --- | --- |
|  |  | C.9 |

where *y* falls within time block *t*.

Priors using normal distributions are imposed on *at,x* and *bt,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 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 TCSAM2014 is based on a similar approach to that taken in TCSAM2013, except that the sex- and size-specific probabilities of maturation, (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, , and those maturing, , at pre-molt size *z* are given by:

|  |  |  |
| --- | --- | --- |
|  |  | D.1a  D.1b |

where *y* falls in time block *t* and is the number of immature, new shell crab of sex *x* at pre-molt size *z*.

The sex- and size-specific probabilities of maturing, , are related to the logit-scale model parameters by:

|  |  |  |
| --- | --- | --- |
|  | female probabilities of maturing at pre-molt size *z* | D.2a |
|  | male probabilities of maturing at pre-molt size *z* | D.2b |

where the are constants specifying the minimum pre-molt size at which to assume all immature crab will mature upon molting. The 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 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 not explicitly included in TCSAM2014, but can be included by the user through specifying an appropriate prior on the parameters.

## E. Model processes: recruitment

Recruitment of immature (new shell) crab in TCSAM2014 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

|  |  |  |
| --- | --- | --- |
|  | recruitment of immature, new shell crab | E.1 |

where represents total recruitment in year *y* and represents the fraction of sex x crab recruiting, and is the size distribution of recruits, which is assumed identical for males and females.

Total recruitment in year *y*, , is parameterized as

|  |  |  |
| --- | --- | --- |
|  | total recruitment | E.2 |

where *y* falls within time block *t*, is the ln-scale mean recruitment parameter for *t*, and 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

|  |  |  |
| --- | --- | --- |
|  | sex-specific fraction recruiting | E.3 |

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

The size distribution for recruits in time block *t*, , is based on a gamma-type distribution and is parameterized as

|  |  |  |
| --- | --- | --- |
|  | size distribution of recruiting crab | E.4 |
|  | normalization constant so that | E.5 |
|  | offset from minimum size bin | E.6 |
|  | gamma distribution location parameter | E.7 |
|  | gamma distribution shape parameter | E.8 |

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

A final time-blocked parameter, *pLnRCVt*, 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 TCSAM2014 are specified independently from fisheries and surveys in TCSAM2014, but subsequently assigned to them. This allows a single selectivity function to be “shared” among multiple fisheries and/or surveys, and among time blocks and sexes, if so desired.

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

|  |  |  |
| --- | --- | --- |
|  | standard logistic | F.1 |
|  | logistic w/ alternative parameterization | F.2 |
|  | logistic w/ alternative parameterization | F.3 |
|  | double logistic | F.4 |
|  | double logistic w/ alternative parameterization | F.5 |

A double normal selectivity function (requiring 6 parameters to specify) will also be implemented as an alternative to the double logistic functions. In the above functions, all symbols (e.g., , ) represent parameter values, except “*z*” which represents crab size. Parameter values are specified as

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, in eq. F1 is actually expressed as in terms of model parameters *pS1* and *pDevsS1y*, where is the mean size-at-50%-selected over the time period and is the annual deviation*.* To accommodate the 6-parameter double normal equation, six “mean” parameter sets (*pS1*, *pS2*,…*pS6*) and six associated sets of “devs” parameter vectors (*pDevsS1*, *pDevsS2*,…*pDevsS6*) are defined in the model to specify the parameterization of individual selectivity/retention functions.

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

## G. Fisheries

Unlike TCSAM2013, which explicitly models 4 fisheries that catch Tanner crab (one as a directed fishery, three as bycatch), there is no constraint in TCSAM2014 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 have a corresponding data component from which parameters can be estimated.

TCSAM2014 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, , 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 by

|  |  |  |
| --- | --- | --- |
|  | fishing mortality rate | G.1 |

where is the handling (discard) mortality for fishery *f* in time block t (which includes year *y*) and 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 *ny,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

|  |  |  |
| --- | --- | --- |
|  | number of crab captured | G.2 |

is the number of crab classified in that state that were *captured* by fishery *f*, where 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

|  |  |  |
| --- | --- | --- |
|  | number of retained crab | G.3 |

while the number of discarded crab, , is given by

|  |  |  |
| --- | --- | --- |
|  | number of discarded crab | G.4 |

and the discard mortality, , is

|  |  |  |
| --- | --- | --- |
|  | discard mortality (numbers) | G.5 |

The biomass associated with the above components is obtained by multiplying each by , the associated individual crab weight (estimated outside the model).

The capture rate (*not* the fishing mortality rate ) is modeled in the usual fashion as a function separable into separate year and size components such that

|  |  |  |
| --- | --- | --- |
|  | fishing capture rate | G.6 |

where is the fully-selected capture rate in year *y* and is the size-specific selectivity.

The fully-selected capture rate for *y* in time block *t* is parameterized in the following manner:

|  |  |
| --- | --- |
|  | G.7 |

where the 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 . The latter is expressed in terms of model parameters as

|  |  |
| --- | --- |
|  | G.8 |

where is the baseline ln-scale capture rate (for mature males), is an additive modifier for time block *t*, is an additive modifier for immature crab, is the additive modifier for females, and is the additive modifier for immature females.

## H. Surveys

If *ny,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, , and biomass, , for crab classified in that state by survey *v* is given by

|  |  |  |
| --- | --- | --- |
|  | survey abundance | H.1 |
|  | survey biomass | H.2 |

where is the size-specific survey catchability on this component of the population and is the associated individual crab weight (estimated outside the model).

The survey catchability is decomposed in the usual fashion into separate time block and size components such that, for *y* in time block *t*:

|  |  |  |
| --- | --- | --- |
|  | survey catchability | H.3 |

where is the fully-selected catchability in time block *t* and is the size-specific survey selectivity.

The fully-selected catchability 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:

|  |  |
| --- | --- |
|  | H.4 |

where is the baseline ln-scale capture rate (for mature males), is an additive modifier for time block *t*, is an additive modifier for immature crab, is an additive ln-scale modifier for females, and is an additive modifier for immature females.

## I. Model fitting: objective function equations

The TCSAM2014 model is fit by minimizing an objective function, , 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:

|  |  |  |
| --- | --- | --- |
|  | model objective function | I.1 |

where represents the *p*th prior probability function, represents the *l*th likelihood function, and the ’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:

|  |  |  |
| --- | --- | --- |
|  | multinomial log-likelihood | I.2 |

where the *y*’s are years for which data exists, “*c*” indicates the population component classifiers (i.e., sex, maturity state, shell condition) the size frequency refers to, is the classifier-specific effective sample size for year y, 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), is the corresponding model-estimated size composition, and 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

|  |  |  |
| --- | --- | --- |
|  | normal log-likelihood | I.3 |

where is the observed abundance/biomass value in year *y* for sex *x*, is the associated model estimate, and is the variance associated with the observation.

The ln-scale lognormal likelihood function is

|  |  |  |
| --- | --- | --- |
|  | lognormal log-likelihood | I.4 |

where is the observed abundance/biomass value in year *y* for sex *x*, is the associated model estimate, and is the ln-scale variance associated with the observation.

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

|  |  |  |
| --- | --- | --- |
|  | “norm2” log-likelihood | I.5 |

This is equivalent to specifying a normal log-likelihood with . This is the likelihood function applied tin TCSAM2013 to fishery catch time series.

## K. Parameter specification for model processes

Parameter specification in TCSAM2014 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 TCSAM2014, “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 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 1. Example parameter specification for recruitment in TCSAM2014. Input values are in black text, comments are in green. Line numbers (text in blue) are shown for reference purposes.