

Progress on GMACS and its application to Bristol Bay red king crab (with comments on the Bristol Bay red king crab assessment)

André E. Punt

School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA 98195

Abstract

GMACS (Generic size-structured stock assessment model) is compared to the model (and software) currently used as the basis for the assessment of red king crab in Bristol Bay, Alaska. Several coding errors have been detected (and corrected) in the current assessment approach. In addition, GMACS needed to be modified to allow it to fully mimic the calculation of numbers-at-size and the likelihood function for Bristol Bay red king crab. However, the process is not complete as the models differ in terms of how retention is modelled and how bycatch in the Tanner fishery is determined given effort in that fishery. This is a “policy call” that needs to be made by the CPT / SSC. Given the same parameter values, the revised GMACS can replicate the current approach in terms of the numbers-at-size matrix and closely for the likelihood. However, estimates differ when GMACS is allowed to estimate parameters. Also, GMACS currently leads to a non-positive definite Hessian matrix.

Introduction

GMACS (Generic size-structured stock assessment model) is a generalized and flexible size-structured modeling framework consisting of four major components: 1) Assessment model; 2) R-packages and Scripts (R & Shell Scripts); 3) Code repository (<https://github.com/seacode/gmacs>) and 4) Documentation (including example assessments based on reproducible methods, i.e., Rmarkdown). It has been under development for several years and has been used as the basis for the assessment of St Matthews Blue king crab (Ianelli et al., 2017). It has been applied to data for Bristol Bay red king crab and the results compared to the official assessment (Zheng and Siddeek, 2017). To date, GMACS has not been used as the basis for the assessment of Bristol Bay red king crab *inter alia* owing to unexpected differences in results.

To better understand the differences between the actual assessment for Bristol Bay red king crab (henceforth ‘*orig*’; Jie Zheng, ASFG, pers comm) and GMACS, the code for both models has been checked line by line, with a focus on the estimation of the time series of the mature male biomass and the numbers-at-size matrix (the code to compute reference points and to apply harvest control rules will be addressed later – see discussion). In addition, versions of *orig* that more closely mimic GMACS have been developed and features added to GMACS to allow it to better mimic *orig*. The checking process led to changes / corrections to the code for both pieces of software as well as extension of GMACS to include features in *orig* – this document outlines the modifications to both sets of code and some of the consequences of those changes to the estimates of MMB.

In addition, this document compares ‘corrected’ estimates from *orig* with various configurations of GMACS. It should be noted that slightly different codings of *orig* led to different estimates even though the objective function was the same given common values for the parameters, and some runs of GMACS led to *NaNs*. This suggests that *orig* (at least) is non-differentiable somewhat (likely in the way selectivity and retention are modelled), but it is beyond the scope of this work to assess the reasons, and to propose an improved version of *orig*.

Modifications to *orig*

The following modifications were made to *orig* based on the code review (and confirmed with Jie Zheng):

- The size-transition matrix and the distribution of recruits to size-class are gamma-distributed. *Orig* implemented this using a numerical integral with a step size of 1mm. However, AD Model Builder has a cumulative gamma function which is more accurate (and is used in GMACS). The numerical algorithm in *orig* was replaced by the `cumd_gamma` function to create *orig-rev*.
- Some of the length-frequencies (in particular for the NMFS survey), are fitted as sex-combined (i.e. a single vector of males and females), but the sample sizes were by sex. This was corrected so that the “N” in the robust normal was the sum of the number of male and female size-classes.
- The likelihood for the NMFS survey was incorrectly computed, with the length frequency data for small animals were overweighted.
- The equation implementing the CVs for the BSFRF surveys was not correctly implemented.

All subsequent versions of *orig* include these corrections. Figure 1(a) compares the time-trajectories of MMB from *orig* and *orig-rev*.

Modifications to GMACS and its implementation for Bristol Bay red king crab

The review of the code identified the following problems with the-then current version of the code for GMACS and its implementation for Bristol Bay red king crab:

- In *orig*, the discard mortality (by sex) in the directed fishery for the years for which there are no data on discards was based on the annual deviations in fishing mortality multiplied by the median of the ratio of the discard mortality divided by the fully-selected mortality on males in the directed fishery (note that medians are non-differentiable). GMACS failed to include discard for years for which there were no data. This has been corrected and *orig* modified to work on mean ratios, which should be better behaved computationally.
- GMACS only included the GMACS catch equation, but the current assessment of Bristol Bay red king crab assumes that the fisheries are instantaneous. The GMACS catch equation is not appropriate for this situation. The code was consequently modified to allow for both instantaneous and continuous fisheries (with a check that the duration of the time-step within which there are instantaneous fisheries is zero).
- The number of seasons in GMACS was increased from 4 to 7 so that GMACS could match the time-steps in *orig* exactly (surveys in season 1, natural mortality in season 2, the directed fishery in season 3, natural mortality in season 4, the trawl, fixed-gear and Tanner crab fisheries in season 5, natural mortality in season 6, and spawning (MMB calculation) at the start of season 7).
- The discard mortality rate for the fixed gear fishery was corrected from 0.2 to 0.5.
- The size distribution for recruitment can now differ between the sexes (as is the case in *orig*).
- The size-composition in the first year can be estimated by sex and shell condition (as is the case in *orig*).
- The model of growth in GMACS has been extended to allow the annual expected growth increments to be parameters, and for the parameter that determines the variance in the growth increment to be estimated (in *orig*, the expected growth increments are pre-specified while the variances of the growth increments [by sex] are estimated).

- GMACS now allows for different numbers of size-classes for males and females when computing the growth matrices (which automatically guarantees that the size-classes with non-zero abundance will differ between males and females). In addition, to mimic *orig*, GMACS now allows the size-transition matrix to change over time (with the possibility of different numbers of size-transition matrices by sex). Finally, to ease parameterization, the parameter that determines the variance of the growth increment can be parameterized as an offset (0 implying that the variance in growth increment is the same for more than one size-transition matrix).
- The ability for selectivity for one gear to be nested within that of another gear has been added (so that the selectivity for the NMFS survey can be nested within that of the BSFRF survey, as is the case for *orig* – and the assessment of eastern Bering Sea snow crab).
- A new option to parameterize selectivity in terms of the length-at-50%-selection and the slope of the selection ogive has been added because that parameterization seems more stable than the current version, and matches *orig* better.
- A new retention ogive which forces retention to be zero has been added to GMACS (the old approach in GMACS was to specify a logistic function with a very high length-at-50%-retention). Also, all selectivity functions now have maxima of 1. *Orig* allowed retention to be less than 1 since 2005. GMACS has been modified to include this option (for example, asymptotic retention is only 0.72 for 2005).
- The prior for NMFS catchability has been updated to match that in *orig*. In addition, the extra CV associated with the BSFRF survey is now estimated by default (it may have been estimated in some of the sensitivity tests presented previously to the CPT).
- The initial values for the offset of fishing mortality between males and females can be now be specified in the CTL file as well as the phase for the female offsets.
- A new option to specify time-dependent natural mortality as knife-edged changes has been added to better mimic *orig*. In addition, initial values, bounds and phases for changes in *M* can be specified in the CTL file. Finally, the ability to mirror natural mortality (i.e. the natural mortality rate parameter for one period can be set to that for another period) has been added, which allows for non-contiguous blocks for natural mortality (an option in *orig*).
- The years for which recruitment deviations are to be estimated can now be specified in the CTL file.
- Emphasis factors can be specified for the catch by fleet as well as each of the penalties. The values in the CTL are set to best match how *orig* is currently configured.
- The sample sizes for the length-frequency data were incorrect in the GMACS input files, but have been updated to match those used by *orig*.

Other key differences between *orig* and GMACS

The following other changes had to be implemented to allow comparisons to be made:

- Zero catches were included in the input file for GMACS for some years to increase comparability to between GMACS and *orig*.
- *Orig* includes dev penalties for the female discard and trawl deviations from mean fishing mortality, but not for other fleets. GMACS includes penalties on all deviations. No change made.
- *Orig* treats the deviations in fishing mortality about median fishing mortality as a bounded_dev, but this can lead to cases when some of the devs fall outside of the bounds. GMACS imposes a (hard) sum to zero penalty.

- *Orig* involved fitting to bycatch in the directed fishery in mass, calculated by multiplying the total numbers by sex by the average mass (1990-present). However, the 1994 and 1995 bycatches are pre-specified. It is unclear if this is the mass landed or the mass landed multiplied by the discard mortality rate (I took this to be pre-mortality numbers).
- *Orig* involved fitting to trawl bycatch in mass, calculated by multiplying the total numbers by sex by the average mass (1976-present). However, the 1993 value is pre-specified.
- *Orig* and GMACS computed the retained catch differently, with total selectivity in *orig* being the sum of the retained selectivity plus the discarded selectivity (constrained so the sum is 1 or less). In contrast, GMACS (and *orig-rev2*) defines the retained selectivity as a total selectivity multiplied by a retention ogive.

Example comparison runs

A small number of runs of *orig-rev* and GMACS have been conducted to evaluate the potential for GMACS (once finalized) to replace *orig* for the September 2019 assessment. Given that not all potential changes to the GMACS code have been made (or may need to be made), the analyses are based on:

- Effort in the Tanner crab fisheries is 1 for all years and the fishing mortalities for the Tanner crab fishery are not estimated.
- Retention in in the directed fishery is pre-specified and set to a pattern with a length-at-50%-selectivity of 150mm and the width of 10mm.

The first set of analyses pre-specify natural mortality over time and do not estimate the variance in growth increment. Figure 1(b) show the estimated time-trajectory of MMB from GMACS and *orig-rev*. Both models estimate 275 estimated parameters (Table 1). The estimates of MMB are nearly identical (except for the last (i.e. projection) year, which is treated differently in the two models) if the estimates from *orig-rev* are given to GMACS and the model projected forward. The negative log-likelihood excluding penalties (i.e. for the data) for *orig-rev* is -15832 while that for GMACS given the same parameters is -15587 (differences likely due to rounding errors and that *orig-rev* does not normalize compositions but GMACS does). Allowing GMACS to estimate 275 parameters leads to a lower negative log-likelihood (-16004), but it must be noted that *orig-rev* and GMACS differ in terms of penalties.

Estimating the variance parameters and the changes in natural mortality (in phases 7 and 8 respectively) (Table 1) leads, as expected, to lower negative log-likelihoods and somewhat changed trajectories of mature male biomass (Figure 1c). The negative log-likelihood for GMACS is again lower and GMACS again did not lead to a positive definitive Hessian matrix.

Outstanding issues / next steps

The comparison of results has been focused on estimation of numbers-at-size and not in terms of reference points such as B_{MSY} and hence catch limits based on agreed harvest control rules. Such comparison needs to occur before the May 2019 CPT meeting if GMACS is to form the basis for the 2020 stock assessment for Bristol Bay red king crab.

GMACS and *orig* treat bycatch in the Tanner crab fishery for the years for which there are no observer data differently. There are data on effort by the Tanner crab fishery for these years but no bycatch data (except for 1991-3 and 2013-5). *Orig* computes the fishing mortality by multiplying effort by average catchability over 1991-93 where annual catchability is computed by dividing fully-selected fishing mortality by effort. The average is an arithmetic average, and implies (implicitly) that catchability for red king crab in the Tanner crab fishery changed after

1993. In contrast to *orig*, GMACS estimates fully-selected fishing mortality for red king crab in the Tanner crab fishery for all years with either catch or effort, predicts the catch for all years, and has a likelihood component for the catches where the “observed catch” for years with no data on bycatch is based on the observed effort and a maximum likelihood estimate for catchability based on all years (and not just 1991-3). The question arises whether the *orig*-like formulation should be implemented in GMACS.

GMACS and *orig* still differ somewhat in terms of penalties. This is partially a consequence of how the models are parameterized (e.g., how sex-specific annual deviations in recruitment are modelled).

Orig still has many hard-wired numbers (e.g., the asymptotic retentions by year). This makes evaluating the code more challenging than should be the case. An attempt has been made to move all parameters to the GMACS DAT and CTL files.

The modifications to the GMACS code mean that (a) the code repository is out of the date, and (b) the plotting routines no longer work as expected (or at all).

Finally, the fact that the Hessian matrix for GMACS is not positive definite suggests that either some bounds are in error (or there is an unyet-resolved programming error).

References

- Zheng, J. and M.S.M. Siddeek. 2017. Bristol Bay red king crab stock assessment in fall 2017. pg 159-308 in 2017 Final Crab SAFE.
- Ianelli, J., Webber, D., Zheng, J. and A. Letaw. 2017. Saint Matthew Island blue king crab stock assessment 2017. pg 1103-1184 in 2017 Final Crab SAFE.

Table 1. Parameters estimated by the various models. The number in round parenthesis after each variable indicates the number variables of the associated type, while the numbers in square parenthesis are phases.

Parameter	First set of runs	Second set of runs
N(1968) [3]	Est (1)	Est (1)
Mean_log_rec [1]	Est (1)	Est (1)
Log Mean Fdev (Direct) [1]	Est (1)	Est (1)
Fdev (Direct) [1]	Est (42)	Est (42)
Female F offset [1]	Est (1)	Est (1)
Fdev (Female Direct) [1]	Est (27)	Est (27)
Log Mean Fdev (Trawl) [1]	Est (1)	Est (1)
Fdev (Trawl) [1]	Est (41)	Est (41)
Log Mean Fdev (Fixed) [1]	Est (1)	Est (1)
Fdev (Fixed) [1]	Est (8)	Est (8)
Extra CV (BSFRF) [1]	Est (1)	Est (1)
Male rec_devs [2]	Est (42)	Est (42)
Female rec_devs [2]	Est (42)	Est (42)
First year devs [3]	Est (35)	Est (35)
Recruitment distribution [3]	Est (2)	Est (2)
Molt probability [3]	Est (4)	Est (4)
Fishery Selectivity [4]	Est (12)	Est (12)
Survey Selectivity [5]	Est (12)	Est (12)
Male NMFS catchability [6]	Est (1)	Est (1)
Growth variance [7]		Est (2)
M-devs [8]		Est (3)
Total	275	280

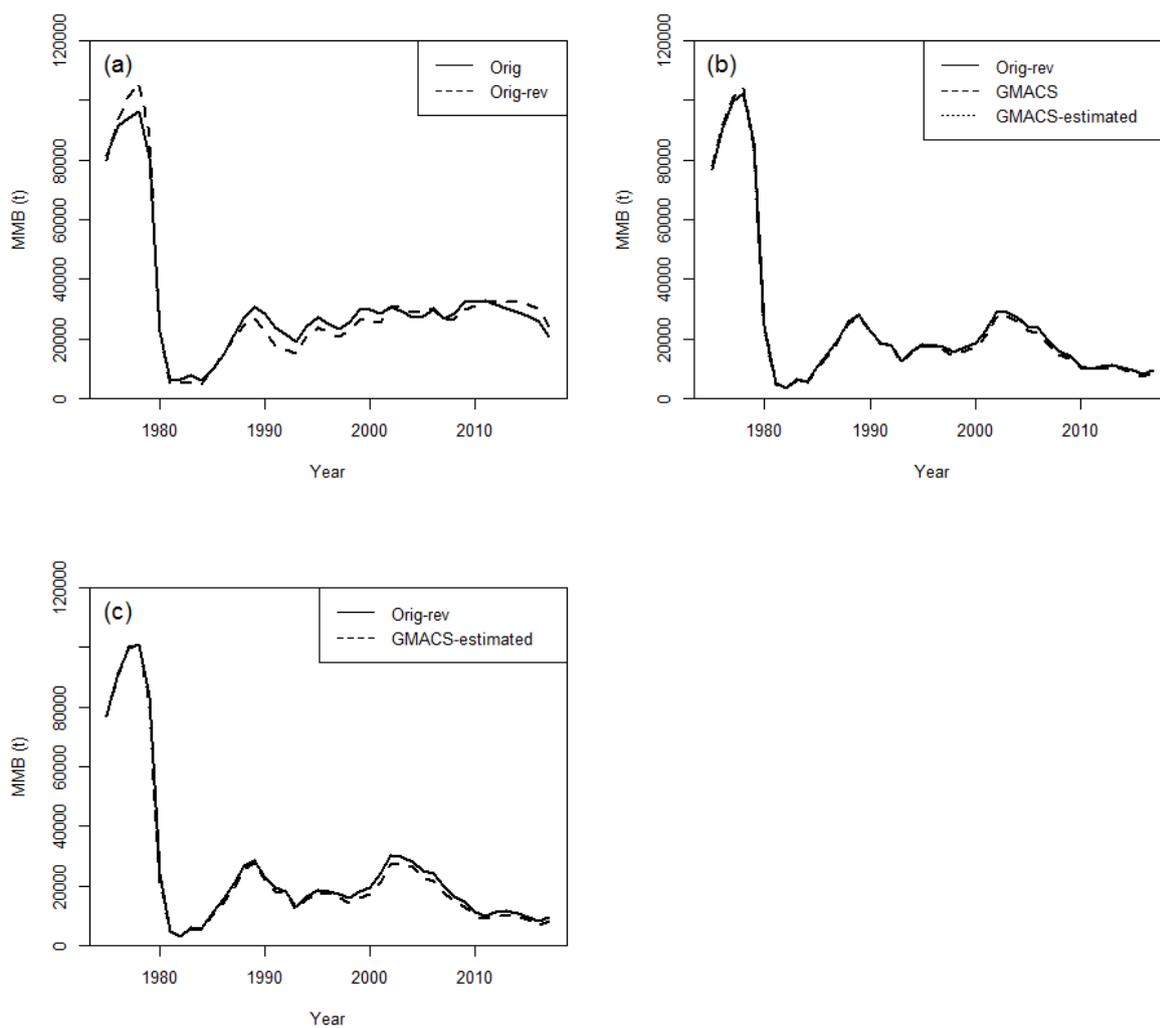


Figure 1. Comparison of mature male biomass from various assessments of Bristol Bay red king crab. The difference between panels (b) and (c) is that the runs in panel (b) are based on estimating 275 parameters, while the runs in panel (c) are based on estimating 280 parameters.