

2026 GMACS Updates

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NOAA FISHERIES

Summary

- Principal GitHub Repo: GMACS_tpl-cpp_code - https://github.com/GMACS-project/GMACS_tpl-cpp_code
 - documentation website: https://gmacs-project.github.io/GMACS_tpl-cpp_code/
 - purpose: “code only” repository
 - Versions: 2.20.31 (Jan. 2026) -> 2.20.45d (Aug. 2026)
 - latest branch: devel_202608-45
 - recent developers: A. Punt, W. Stockhausen, T. Jackson
- Changes to
 - improve general functionality
 - expand parameterization options to all parameters
 - time-blocking
 - environmental covariates
 - random walks
 - add missing functionality for Tanner crab
 - improve code formatting and documentation

GMACS Updates

Post May 2026 CPT Meeting



Overview

2.20.37: 2026/05/05-07

- Added new options for calculating/extending size comps and modified output/input files to reflect new options.
 - sample size scaling/no scaling options for input fishery size comps
 - renamed CATCH_COMP (=1) to CATCH_COMP_DOSCL (scaling)
 - added CATCH_COMP_NOSCL (= -1) (no scaling)
 - sample size scaling/no scaling options for input survey size comps
 - renamed SURVEY_COMP (=2) to SURVEY_COMP_DOSCL (scaling)
 - added SURVEY_COMP_NOSCL (= -2) (no scaling)
- Fixed calculation of predicted fishery size comps in `calc_predicted_composition` by including fully-selected F's ($f(k,h,i,j)$) in the calculations.
- Added checks on ``hasMMOD`` for calculations and output wrto male maturity ogive data.
- Fixed error when trying to normalize a predicted size comp with all 0's.
- Added columns `origCol` and `aggCol` to `Size_fit_summary` dataframe in `gmacs.rep1`.
- Changed "Derived_quatities" to "Derived_quantities" in `gmacs.rep1`.

2.20.37a: 2026/05/14

- Added *IsJittered* checks to prevent writing out extraneous information during jitter runs



2.20.37c: 2026/05/15-06/04

- Added individual run jittering information to "jitter.csv" in function "writeJitterResults".
- Added "ssn" as first input to "calc_brute_equilibrium" function to indicate which season to extract the equilibrium numbers for (prior was equivalent to ssn=1);
 - necessary to extract equilibrium numbers and biomass at time for ssb calculation to check Bmsy calc.s.
- Added calculations and output for equilibrium numbers and biomass at the spawning season
 - *equilibrium_numbers_F0*, *equilibrium_numbers_FM*
 - *equilibrium_biomass_F0*, *equilibrium_biomass_FM*
 - output to Equilibrium_NBs dataframe in gmacs.rep1.
- Added season_type **TCSAM02_F** (=3) option to duplicate TCSAM02 OFL calculation
 - In non-projection functions, this option works the same way as **CONTINUOUS_F**.
 - In projection-related functions to determine time-averaged vulnerability,
 - **TCSAM02_F** averages selectivity, retention, discard mortality rates separately
 - **CONTINUOUS_F** averages the year-specific vulnerability.
 - modified functions
 - *project_biomass_OFL*
 - *calc_predicted_project*
 - *project_one_year*
 - *calc_brute_equilibrium*

2.20.38: 2026/06/08-20

- Corrected time-varying parameters when blocks end after last year
- extended pointer arrays to include the projections.

2.20.40: 2026-07-05

- Added F_{MEY} as an output.

2.20.41: 2026/07/07

- Revised how projection file is read depending on whether *Calc_MEY* is YES or NO.
- Corrected output to gmacs.rep1 when there is no male maturity ogive data.

2.20.42: 2026/07/28-29

- Revised output for male maturity ogives data so likelihoods and related information are not printed to files.
- revised when the *d3_PrdMMOs* and associated arrays are allocated
- Added verbose check when calling *writeToPopProg* to avoid writing extraneous information.

2.20.43: 2026/07/30

- Added small value to (0.00001) to SSB when calculating *sd_log_ssb* to avoid $\log(0)$ when SSB=0.

2.20.44: 2026/08/02-07

- Changed size composition likelihood calculations using *negativeLoglikelihood* classes.
 - "Internal" functions now return *dvar_vectors* rather than a single value for the total likelihood.
 - The total likelihood is calculated in the calling function.



2.20.45: 2026/08/03-07

- Added "emphasis" column explicitly to Likelihood_summary table in gmacs.rep1.
- Corrected calculation of Pearson's residuals calculation for *multinomial_alt* class in multinomial.cpp to match TCSAM02.
- Changed *m_sm/Val* from 0.00001 to 0.001 in multinomial_alt class to match TCSAM02.
- Revised tail compression to skip compression when observed size comp is all zeros (valid as a component of an extended comp).
- Added "growth_data" dataframe to gmacs.rep1 output to provide model-predicted growth increments for non-tagging molt increment data.
- Revised "Mean growth" to "mean_growth" dataframe name in gmacs.rep1.

2.20.45a: 2026/08/17-26

- Changed parameter 4 for DoubleNormal4a function to be on ln-scale. Like most selectivity parameters, it is defined on the arithmetic scale in the CTL file (as are the lower and upper bounds and prior parameters), but is converted to ln-scale for estimation. Note that this means the pin/par file values will not match the initial values in the CTL file.
- Increased precision of output to jitter.csv when jittering.
- Added missing "# Number of environmental treatments" to the output CTL file.
- If input allometry specified by LW relationship, output CTL now writes parameters (not LW matrix).
- Added Project_type =3 option to apply multipliers to directed Fmsy for projections.

To do

- implement smooth constraints for estimated $\text{Pr}(\text{Terminal Molt})$
- revise output CTL file so it can be used as input file
 - now includes projection information, so doesn't correspond to input file
- improve how retrospective runs can be made (e.g., initialize model to previous peel estimates)
- debug remaining Tanner-related issues
 - why are projections results scaled incorrectly?
 - why does estimating dynamic B0 invalidate sdreport variance estimates?
 - why do retrospective runs crash?
- Improve documentation
 - in-code comments
 - website
 - Veron in prep manuscript

GMACS Updates

January 2026 Modeling Workshop to May CPT Meeting



2026-01-14

- Incremented version to 2.20.32a

2.20.32b: 2026-01-14

- Allowed for *spr_lambda* to be equal to 1 for full contribution of both sexes when CTL input is negative.

2.20.33: 2026/01/14-15

- Added the *IsTyler* flag as *model_controls(19)*
 - forces female growth to match that for males

2.20.33a: 2026-01-15

- Added output for *isTyler/model_controls(19)* to *gmacs_ctl*, *echoinput*, and *OutInpFile1*.

2.20.34: 2026-01-15

- Corrected selectivity deviance parameter pointer.
- Revised the jitter function so that the jittered value is centered from a value from a PIN file.

2.20.34a: 2026-01-15

- Revised several int variables to be initialized prior to use.



2.20.34b: 2026-03-09

- Corrected order in which *unitsType*, *indexType* are written to *gmacs_data* when reading in new-format RAI data.
- Corrected scale for weight at size in *gmacs.rep1* output file. Output weights are NOW in kg.
- Corrected unitstypes entry from "biommass" to "biomass" (only affected labeling).
- Added "save_params" function to save parameter values to a par file programmatically (but no labelling). *Gmacsall.out*, *gmacs.rep1* have better format, but didn't output ALL parameters (now corrected, hopefully).
- Added parameter estimates in par file format as "gmacs_rep.par" using ofstream variable *ParFile1*. Estimates are labelled as in *Gmacsall.out* and include a couple of parameters that *Gmacsall.out* misses (F devs associated with surveys: 0's, but need to be accounted for when constructing a pin file programmatically).
- Changed labels for female *ra*, *rb* parameters in *Gmacsall.out* so they have no spaces (and can thus be captured as a single string).
- Removed log-scale conversion of *ival*, *lb*, *ub* for "Extra" theta parameters specified for a block w/out environmental or RW links.

2.20.34c: 2026-03-10

- Removed *M_out(syr,nyrRetro,1,nclass)* array, which was never used anywhere.
- Added *isexM* and *imatM* vectors to correct mirroring/indexing problem when the model includes multiple shell conditions and *M* values are mirrored.

2.20.35: 2026/03/13-19

- Added *Term_molt* = 2 flag and associated logic to implement Tanner crab growth, which assumes the probability of undergoing the terminal molt to maturity depends on pre-molt, not post-molt size. Choose *Term_molt*=2 in the CTL file by setting "Other Control 3" (Terminal molting) to 2.
 - *update_population_numbers_at_length_season_new* will update the population numbers.
- Added calculations to determine the progression of a cohort through 20 successive years based on population/fishery rates for a selected year.
 - Progressions are calculated for a single "spike" in abundance in the smallest size bin, or as per the sex-specific recruitment size structure
 - Results are output to gmacs.rep1 as dataframes *CohortProgression1* and 2.
- Revised *update_population_numbers_at_length_season* to simplify the code flow
- Corrected an error in *update_population_numbers_at_length_season* where recruitment was being added to mature new shell crab abundance as well as immature new shell crab abundance when *nmature*=2, *nshellcon*=2, and *Term_molt*=0.
- Added alternative multinomial likelihood as option to fit size comps (option 7) to match TCSAM02 calculation.
- Changed name of input effective sample size parameters array from *log_vn_pars* to *vn_pars*
- Revised *ddirichlet_alt* function in *dirchlet_alt* class so that all elements of *obsp* and *modp* vectors are non-zero
- Added male maturity data section to data file. Requires older data files to add "0" on a line just before the environmental data section.



2.20.35a: 2026-03-23

- Completed adding male maturity ogive data as a component in the likelihood as *nloglike(7)*, which is a vector with the unweighted NLL for each model year (*syr->nyrRetro+1*).
 - Likelihood calculation occurs in function "*mpos_likelihood*"; currently, only a binomial likelihood option is implemented.
 - Data quantities begin with "*mmod*";
 - predicted model quantities are
 - *d3_PrdMMOs* (by model size bins)
 - *d3_PrdMMOsP* (by observed size bins).
 - Total and annual values for the nll are reported in the *Likelihood_summary* dataframe of the *gmacs.rep1* file.
 - The ivector "*ilike_vector*" was modified to an imatrix ("*ilike_matrix*") to facilitate dimensioning the ragged array "*nloglike*" correctly.
- Commented out "*calc_predicted_catch_out*" and associated results arrays (*obs_catch_out*, *pre_catch_out*) because nothing was done with the results.

Overview

2.20.35b: 2026/03/25-04/06

- Added "doTCSAM02EffExp" flag to dat file
 - "off" (0): original method of effort extrapolation for missing catch based on "log_q_catch"
 - the number of *log_fdevs* and *log_fdovs* for each catch dataframe depends on the number of rows of catch data given (whether catch was observed or not).
 - "on" (1): effort extrapolation for missing catch is average catch divided by average effort for years specified by new "avg_eff" column in new-format CatchDFs.
 - the number of *log_fdevs* and *log_fdovs* depends only on the number of rows which contain non-missing catch data.
 - modified functions "calc_fishing_mortality", "calc_predicted_catch"
- Added growth transition options 9 and 10 to provide same functionality as TCSAM02, mainly for direct comparisons with results from that code.
- Increased required verbose level to > 4 on fishing mortality devs.
- Added function writeRepPar to write parameters and prior values to gmacs_rep_last.par on a function call basis if verbose > 2.
- Increased precision and width of output to RepFile1.

Overview

2.20.35c: 2026/04/08-11

- The growth options TCSAM02A and TCSAM02B (=9 and 10) that provide similar functionality as TCSAM02 for the growth transition matrices were reassigned and additional options TCSAM02C and TCSAM02D (11 and 12) were added. A and B apply to the case where the molt increment is assumed to be gamma-distributed while C and D apply to the case where postmolt size is gamma-distributed.
 - All of the options limit growth to a maximum number of size bins but treat probabilities from the "excluded" size bins differently: A and C drop them, then normalize the remaining probabilities to sum to 1 whereas B and D treat the max size bin as an accumulator for "raw" probabilities at larger size bins before dropping them.
- Added *includeFs* option to *project_cohort_numbers_at_length*.
- Revised *nmature=2*, *nshell=2* section of *update_population_numbers_at_length_season_new* to clarify original, updated, and final numbers during update using *o_*, *u_*, and *f_* to indicate such.
- Added alternative 5-parameter double normal selectivity option (SELEX_DOUBLENORM4a = 15) to match TCSAM02
- Extracted repeated code (three times!) for construction of "*anystring*" labels for SELEX functions as a function "*addToAnystring*"
- Added *writeToPopProg* function to export of population abundance by year, season, group, size class to "gmacs_popprog.csv" file to facilitate comparison with TCSAM02
- Revised data input, prediction, likelihood calculations for male maturity ogive data so that prediction can be based on predicted survey abundance, not population abundance in season 1.
 - new function is *mpos_likelihood_survey*.
 - model output to RepFile1 is now based on *mpos_likelihood_survey*.

Overview

2.20.36: 2026/04/13-28

- Added "*flt_id*" to input maturity ogive data table to correctly identify fleet to use correct selectivity functions when predicting MMOs based on predicted survey abundances.
- Added verbose prints to cout for maturity ogive calculations.
- Added several sections to RepFile1 output that provide dataframes for verifying maturity ogive calculations and comparisons with TCSAM02 (getting "exact" agreement for maturity ogive dataset from 2025 assessment).
- Revised output to "Derived quantities" section of Gmacsall.out and RepFile1 to output management quantities *ParsOut(NRefPars+1:6)* when running under -nohess.
 - added output of *spr_cofl* and *Bmsy* as vectors using REPVEC to those files.
- Added NO_PRIOR (= -1) as possible prior for parameters

GMACS Updates: Types



Fixes

- Correct selectivity deviance parameter pointer.
- Added isexM and imatM vectors to correct mirroring/indexing problem when the model includes multiple shell conditions and M values are mirrored.
- Fixed int variables not initialized prior to use.
- Corrected an error in update_population_numbers_at_length_season where recruitment was being added to mature new shell crab abundance as well as immature new shell crab abundance when nmature=2, nshellcon=2, and Term_molt=0.
- Fixed calculation of predicted fishery size comps in calc_predicted_composition by including fully-selected F's ($f(k,h,i,j)$) in the calculations (only affected extended size comps).
- Added "ssn" as first input to "calc_brute_equilibrium" function to indicate which season to extract the equilibrium numbers for (prior was equivalent to ssn=1); necessary to extract eq. numbers and biomass at time for ssb calculation to check Bmsy calc.s.
- corrected time-varying parameters when blocks end after final year; extended pointer arrays to include the projections.
- revised allocation of maturity ogive so they are not allocated if no data is included



Additions

- Allowed for `spr_lambda` to be equal to 1 for full contribution of both sexes when `ctl` input is negative
- Revised the jitter function so that the jittered value is centered from a value from a PIN file.
- Added individual run jittering information to "jitter.csv"
- Added parameter estimates in par file format as "gmacs_rep.par". Includes parameters that Gmacsall.out misses (F devs associated with surveys: 0's, but need to be accounted for when constructing a pin file programmatically)
- Added `Term_molt = 2` option and associated logic to base terminal molt on pre-molt size
- Added calculations to determine the progression of a cohort through 20 successive years based on population/fishery rates for a selected year.
- Added `NO_PRIOR (= -1)` as possible prior for parameters
- Added alternative multinomial likelihood as option to fit size comps (option 7) to match TCSAM02 calculation
- Added calculations and output for equilibrium numbers and biomass at the spawning season (`equilibrium_numbers_F0`, `equilibrium_numbers_FM`, `equilibrium_biomass_F0` `equilibrium_biomass_FM`); output is in the `Equilibrium_NBs` dataframe in `gmacs.rep1`.
- Added new options for calculating/extending size comps.
- Added option to do TCSAM02 F averaging for the OFL
- Added F_{MEY} as an output, if calculated
- Changed size composition likelihood calculations using `negativeLoglikelihood` classes. "Internal" functions now return `dvar_vectors` (values for each individual composition) rather than a single value for the total likelihood. The total likelihood is calculated in the calling function.

Changes to Files



New options: data file

doTCSAM02EffExp

- 0 - standard effort expansion: estimate lnQ
- 1 - TCSAM02 approach: $\ln Q = \frac{\text{sum}(\text{catch})}{\text{sum}(\text{effort})}$

```
##-----  
##--CATCH DATA  
##-----  
1 #--input format for catch data (0:old format; 1: new format)  
1 #--option for effort extrapolation (0: standard gmacs approach; 1: TCSAM02 approach)
```

Survey catchability index: Q_index; Relative abundance index: RAI_id

# row	Q_index	Year	Season	Fleet	Sex	Maturity	Obs	CV	Units	CPUE_time	RAI_id
1	1	1975	1	5	1	0	293	0.3	1	0	1
2	1	1976	1	5	1	0	157	0.1	1	0	1
3	2	1977	1	5	1	0	138	0.1	1	0	1
4	2	1978	1	5	1	0	98	0.1	1	0	1

New options: CTL file

Term_molt = 2 option

- terminal molt depends on pre-molt size

recZ_flag

- 0 - standard size-at-recruitment
- 1 - TCSAM02 size-at-recruitment

isTyler

- 0 – use standard growth declarations
- 1 – set female growth to male growth

- no prior for parameter: prior_type = -1 (NO_PRIOR)
- alternative multinomial likelihood for size comps (option 7)

```
## -----
```

```
## OTHER CONTROLS
```

```
## -----
```

```
....
```

```
1 # terminal molt (0 = off; 1 = on, post-molt; 2 = on, pre-molt).
```

```
....
```

```
1 # recruitment size distribution option (0: standard way; 1: Tanner crab approach)
```

```
0 # Set to 1 to copy growth from males to females)
```

New options: CTL file

```
#-----  
# Growth transition  
#-----  
##Type_1: Options for the growth matrix  
  
....  
# 3: Growth increment is gamma distributed (requires molt probability)  
# 4: Post-molt size is gamma distributed (requires molt probability)  
  
....  
# 9: like 3, but limits max growth and truncates at max size bin before normalizing  
# 10: like 9, but max size bin is an accumulator (no truncation)  
# 11: like 4, but limits max growth and truncates at max size bin before normalizing  
# 12: like 11 except max size bin is an accumulator  
  
  
#-----  
## Type_2: Options for the growth increment model matrix  
#-----  
  
....  
# 5: Alternative power law for mean post-molt size (5 parameters)  
## 1. reference (small) pre-molt size (constant: must have phase < 0)  
## 2. mean post-molt size corresponding to 1.  
## 3. reference (large) pre-molt size (constant: must have phase < 0)  
## 4. mean post-molt size corresponding to 3.  
## 5. gamma distribution scale parameter (on arithmetic scale)
```

growth matrix: options 9-12

mean growth type: option 5



Output

- Added calculations and output for equilibrium numbers and biomass at the spawning season (equilibrium_numbers_F0, equilibrium_numbers_FM, equilibrium_biomass_F0 equilibrium_biomass_FM)
- output management quantities ParsOut(NRefPars+1:6) when running under -nohess
- Added output for fits to growth data
- Output ctl file:
 - Added missing "# Number of environmental treatments"
 - If input allometry specified by LW relationship, the corresponding parameters are also written to the output ctl file (and not the LW matrix).
- Increased precision of output to jitter.csv



Tanner crab-specific



Tanner crab functionality

- added male maturity ogives as data:
 - optional input to “dat” file
 - added option for dependence of terminal molt: pre-molt size **or** post-molt size
 - annual prediction for model size bins
 - conversion from model size bins to input size bins
 - added binomial likelihood component
 - added fits, likelihood details to output files
- added Tanner-like growth model (options
- added Tanner-like size-at-recruitment distribution (option
- added 2-parameter ascending normal selectivity curve (option 14)
- added 5-parameter double normal function (option 15)
- added alternative multinomial likelihood as option to fit size comps (option 7) to match TCSAM02 calculation
- wrote new seasonal population dynamics code for terminal molt
- corrected “extended” size comps calculation when input comps are scaled to total abundance
- added Tanner-like fishery averaging for OFL calculation (option 3)
- projections: added option to specify multipliers on F_{MSY} in PRJ file (option 2)

```

#-----
##--MALE MATURITY OGIVES DATA-----
##-----
1      #--has male maturity data
BINOMIAL #--likelihood type
1.0    #--likelihood weight
32     #--number of size bins
##--cutpoints
25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 ...
##--observations
575#number of observations
#          fleet rai q size bin
#year season id id id bin index N prMature uncertainty
2006      1  5  1 2 27.5  1  182  0          0
2006      1  5  1 2 32.5  2  249  0          0
2006      1  5  1 2 37.5  3  197  0          0
2006      1  5  1 2 42.5  4  458  0          0
2006      1  5  1 2 47.5  5  534  0          0
2006      1  5  1 2 52.5  6   49  0          0
2006      1  5  1 2 57.5  7 1024 0.024    0.004
2006      1  5  1 2 62.5  8 1287 0.034    0.006
  
```

