

# Recent GMACS Updates: 2026-05

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Updates to GMACS since the September 2025 Crab Plan Team (CPT) meeting are listed in the following tables. Text highlighted in red indicates a change in input model format or other important information.

Table A. Updates to GMACS 2025-12-30 to 2026-03-19. Versions 2.20.32 - 2.20.35.

Date	Author	Version	Changes	Branch
2025-12-30	AEP	2.20.32	Allowed for more general environmental drivers for mean recruitment. Incremented version to 2.20.32. <b>NOTE: THIS CHANGES the specification for the "MAIN PARS"/recruitment section of the ctl file: "phase" is specified in the column after Prior_2 and additional columns Block, Block_fn Env_L, Env_vr, RW, RW_Blk, and RW_Sigma are now required. NOTE: you will also need to add a line to the ctl file after the Block_Groups specification to specify the number of environmental treatments.</b>	devel_20250402
2026-01-05	AEP		Found a print out bug	devel_20250402
2026-01-14	AEP	2.20.32a	Incremented version to 2.20.32a.	devel_20250402
2026-01-14	TJ	2.02.32b	Allowed for spr_lambda to be equal to 1 for full contribution of both sexes when ctl input is negative. Incremented version to 2.20.32b.	devel_20250402
2026-01-14	AEP		<b>Added the isTyler flag as model_controls(19) which forces female growth to match that for males</b>	devel_20250402
2026-01-15	WTS	2.20.33	Updated version to 2.20.33.	devel_202601
2026-01-15	WTS	2.20.33a	Added output for isTyler/model_controls(19) to gmacs_ctl, echoinput, and OutinpFile1. Incremented version to 2.20.33a.	devel_202601
2026-01-15	AEP	2.20.34	Correct selectivity deviance parameter pointer. Revised the jitter function so that the jittered value is centered from a value from a PIN file. Incremented version to 2.20.34.	devel_202601
2026-01-15	WTS	2.20.34a	Several int variables were not initialized prior to use. This caused a crash when compiled using the MacOSX SDK but not the Windows compiler. These are now initialized to 0 prior to use. Version incremented to 2.20.34a.	devel_202601
2026-03-09	WTS	2.20.34b	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. Only affected this output. Corrected unitstype entry from "biomass" 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. Incremented version to 2.20.34b.	devel_202601
2026-03-10	WTS	2.20.34c	Removed M_out(syr,nyrRetro,1,nclass), 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. Incremented version to 2.20.34c.	devel_202601
2026-03-13	WTS	2.20.35	<b>Added Term_molt = 2 flag and associated logic to implement Tanner crab growth</b> , 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 now be used to update the population numbers. Incremented version to 2.20.35.	devel_202603
2026-03-16	WTS		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, consistent with the recruits being new shell, immature crab (even if model categories are less precise). Results are output to gmacs.rep1 as dataframes CohortProgression1 and CohortProgression2. Revised update_population_numbers_at_length_season to simplify the code flow (broke up if statements with 4 or 5 terms into smaller, nested code fragments). 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 nmatue=2, nshellcon=2, and Term_molt=0.	devel_202603
2026-03-17	WTS		<b>Added alternative multinomial likelihood as option to fit size comps (option 7) to match TCSAM02 calculation.</b> This just changes the the overall constant (so exact fit results in nll = 0).	devel_202603
2026-03-18	WTS		Changed name of input effective sample size parameters array from log_vn_pars to vn_pars to avoid confusion because the input values are on the arithmetic scale, not on the ln scale--the values are converted to the ln-scale. Revised dirichlet_alt function in dirichlet_alt class so that all elements of `obsp` and `modp` vectors are non-zero by adding a small constant to each element of `o` and `p` during normalization to `obsp` and `modp`: this avoids generating nan's where `o` or `p` were zero.	devel_202603
2026-03-19	WTS		<b>Added male maturity data section to data file. Requires older data files to add "0" on a line just before the environmental data section.</b>	devel_202603

Table B. Updates to GMACS 2026-03-23 to 2026-05-05. Versions 2.20.35 - 2.20.37.

Date	Author	Version	Changes	Branch
2026-03-23	WTS	2.20.35a	Completed adding male maturity ogive data as a component in the likelihood as <code>nloglike(7)</code> , which is a vector with the unweighted NLL for each model year ( <code>syr-&gt;nyrRetro+1</code> ). Likelihood calculation occurs in function <code>"mmos_likelihoood"</code> ; currently, only a binomial likelihood option is implemented. Data quantities begin with <code>"mmod"</code> , model quantities are <code>d3_PrdMMOs</code> (annual model-predicted male maturity ogives by model size bins) and <code>d3_PrdMMOsp</code> (annual model-predicted male maturity ogives by observed size bins). Total and annual values for the nll are reported in the <code>Likelihood_summary</code> dataframe of the <code>gmacs.rep1</code> file. The ivector <code>"like_vector"</code> was modified to an imatrix ( <code>"like_matrix"</code> ) to facilitate dimensioning the ragged array <code>"nloglike"</code> correctly. Version incremented to 2.20.35a. Commented out <code>"calc_predicted_catch_out"</code> and associated results arrays ( <code>obs_catch_out_pre_catch_out</code> ) because these were never used for anything constructive (the function was called, but nothing was done with the results).	devel_202603
2026-03-25	WTS	2.20.35b	Added <code>"doTCSAM02EffExp"</code> flag to dat file (right after flag to read catch data in new format). Setting <code>doTCSAM02EffExp=0</code> ("off") results in the original method of effort extrapolation for missing catch based on <code>"log_q_catch"</code> being used (see <code>"calc_predicted_catch"</code> ). If <code>"on"</code> (1), effort extrapolation for missing catch is based on average catch divided by average effort for years specified by new <code>"avg_eff"</code> column in new-format <code>CatchDFs</code> . Functions <code>"calc_fishing_mortality"</code> and <code>"calc_predicted_catch"</code> have been modified. If <code>"off"</code> , the number of <code>log_fdevs</code> and <code>log_fdovs</code> for each catch dataframe depends on the number of rows of catch data given (whether catch was observed or not). If <code>"on"</code> , the number of <code>log_fdevs</code> and <code>log_fdovs</code> depends only on the number of rows which contain non-missing catch data. Thus, the required number of estimated fishing mortality parameters may be different between the two options and different <code>par</code> files would be required to switch between options if initializing model runs with a <code>par</code> file. Incremented version to 2.20.35b.	devel_202603
2026-03-27	WTS		Added growth transition options 9 and 10 to provide same functionality as TCSAM02, mainly for direct comparisons with results from that code.	devel_202603
2026-04-06	WTS		Increased required verbose level to > 4 on fishing mortality devs. Added function <code>writeRepPar</code> to write parameters and prior values to <code>gmacs_rep_last.par</code> on a function call basis if <code>verbose &gt; 2</code> . Increased precision and width of output to <code>RepFile1</code> .	devel_202603
2026-04-08	WTS	2.20.35c	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 <code>includeFs</code> option to project cohort numbers at length. Revised <code>nmatue=2</code> , <code>nshell=2</code> section of <code>update_population_numbers_at_length_season_new</code> to clarify original, updated, and final numbers during update using <code>o_</code> , <code>u_</code> , and <code>f_</code> to indicate such. The version number was incremented to 2.20.35c.	devel_202603
2026-04-09	WTS		Added alternative 4-parameter double normal selectivity option ( <code>SELEX_DOUBLENORM4a = 15</code> ) to match TCSAM02. The plateau is determined from a scale parameter and the distance between the max possible size and the size at the ascending limb. See <code>selex.hpp</code> and search here for <code>SELEX_DOUBLENORM4a</code> for details. Extracted repeated code (three times!) for construction of "anystring" labels for <code>SELEX</code> functions as a function <code>addToAnystring</code> defined in the <code>GLOBALS</code> section. The function is now called in the three sections where the previous code has been commented out (pending deletion).	devel_202603
2026-04-10	WTS		Added export of population abundance by year, season, group, size class to <code>"gmacs_popprog.csv"</code> file to facilitate comparison with TCSAM02 results. TODO: apply verbose check to this export.	devel_202603
2026-04-11	WTS		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. Old function <code>mmos_likelihoood</code> is now <code>mmos_likelihoood_pop</code> and the new function is <code>mmos_likelihoood_survey</code> . <code>mmos_likelihoood_pop</code> is not called and associated model output to <code>RepFile1</code> is now based on <code>mmos_likelihoood_survey</code> .	devel_202603
2026-04-13	WTS	2.20.36	Version 2.20.36. Added <code>"fit_id"</code> 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 <code>RepFile1</code> output that provide dataframes for verifying maturity ogive calculations and comparisons with TCSAM02 (getting "exact" agreement for maturity ogive dataset from 2025 assessment).	devel_202603
2026-04-15	WTS		Revised output to "Derived quantities" section of <code>Gmacs.all.out</code> and <code>RepFile1</code> to output management quantities <code>ParsOut(NRefPars+1:6)</code> when running under <code>-nohess</code> . Also added output of <code>spr_cofl</code> and <code>Bmsy</code> as vectors using <code>REPVEC</code> to those files.	devel_202603
2026-04-28	WTS		Added <code>NO_PRIOR</code> (= -1) as possible prior for parameters. Sets the <code>prior_pdf = 0</code> for the term in question (perhaps simpler than using <code>UNIFORM_PRIOR</code> (= 0)).	devel_202603
2026-05-05	WTS	2.20.37	Added new options for calculating/extending size comps and modified output/input files to reflect new options. Added <code>CATCH_COMP_NOSCL</code> (= -1) and renamed <code>CATCH_COMP</code> (=1) to <code>CATCH_COMP_DOSCL</code> to provide sample size scaling/no scaling options for input fishery size comps. Added <code>SURVEY_COMP_NOSCL</code> (= -2) and renamed <code>SURVEY_COMP</code> (=2) to <code>SURVEY_COMP_DOSCL</code> to provide sample size scaling/no scaling options for input survey size comps. Fixed calculation of predicted fishery size comps in <code>calc_predicted_composition</code> by including fully-selected F's ( <code>ft(k,h,i,j)</code> ) in the calculations. Calculation of predicted survey size comps in <code>calc_predicted_composition</code> *should* be correct because the calculations apply appropriate q's to the predicted comps. Reformatted some sections of code for better(?) readability.	devel_202605