

GMACS Updates

Buck Stockhausen

GMACS updates since January 2024 (1)

- // 2024-01-29 ** AEP. (Updated GMACS to version 2.01.M.08) Fixed time-varying growth increment and added a trap for negative growth increments in fn calls 0 and 1
- // 2024-02-01 ** WTS. (Updated GMACS to version 2.01.M.09) Added alternative format for inputting size comps data.
- // 2024-02-02 ** WTS. Renamed BOTHSEX, BOTHMATURE to UNDET_SEX, UNDET_MATURE.
 - Added MALES(=1) macro. Need to refactor MALESANDCOMBINED functionality.
 - Removed MALESANDCOMBINED (duplicated MALES). Refactored selectivity assignments and recruitment (no need to loop over h, so cleaner not to).
 - Reformatted some code to add parentheses, replace tabs with spaces, and correctly indent blocks.
 - Replaced $o == 1/2$ with $o == \text{NEW_SHELL/OLD_SHELL}$, similar for m.
- // 2024-02-05 ** WTS. Reverted selectivity assignments--needed to loop over h if slx_isex(k) was 0. Added alternative input format for fishery catch data.
- // 2024-02-29 ** AEP. (Updated GMACS to version 2.01.M.10)
 - (a) corrected error wrto retrospective patterns and catch re-in,
 - (d) adding units to read-in, and (c) output selex and gradient output.

GMACS updates since January 2024 (2)

- // 2024-03-03 ** AEP. (Updated GMACS to versions 2.10) Corrected the terminal molt
- // 2024-03-04 ** AEP. (Updated GMACS to versions 2.10.01) Added immature N matrices
- // 2024-03-06 ** AEP. (Updated GMACS to versions 2.10.02) Change projections and OFL sections to use the genetic season update code and fixed a projection error for the proportional F case
- // 2024-03-07 ** AEP. (Updated GMACS to versions 2.10.03)
 - (a) Moved the read-in of the general controls to the start of the CTL file, and
 - (b) replaced the read-in of ntheta by its calculation
- // 2024-03-08 ** AEP. (Updated GMACS to versions 2.10.04)
 - (a) Improved speed for the Hessian inversion stage by making loops more efficient, and
 - (b) corrected the projection component of the code
- // 2024-03-12 ** AEP. (Updated GMACS to versions 2.10.05) Changed read-in for q and add_cv to allow for generic parameter structure
- // 2024-03-26 ** AEP. Fixed stock-recruitment bug for two sex models and models with terminal molt
- // 2024-03-28 ** WTS. Added PWRLAW_GROWTHMODEL as alternative to LINEAR_GROWTHMODEL
- // 2024-03-29 ** AEP. (Updated GMACS to version 2.20.00) Updated read-in for selectivity, M, growth, additional variance, Q and overdispersion
- // 2024-03-29 ** AEP. (Updated GMACS to version 2.20.01) Standardized how priors are handled
- // 2024-03-31 ** WTS. (Updated GMACS to version 2.20.02) Added extra info to error messages when using alternative dat file format.

GMACS updates since January 2024 (3)

- // 2024-04-01 ** WTS. For the PWRLAW_GROWTHMODEL, the input definition for the parameter corresponding to gscale is on the ln-scale, so it is exponentiated when assigning G_pars(3) to gscale. Changed format of output of block_limits to gmacs_ctl to column form.
- // 2024-04-01 ** AEP. (Updated GMACS to version 2.20.03) Tidied up output labels (GMACS_IN and GMACS_OUT).
- // 2024-04-02 ** AEP. (Updated GMACS to version 2.20.04) Tidied up penalties (added back one that was commented out)
- // 2024-04-02 ** AEP. (Updated GMACS to version 2.20.05) Added new pre-specified selectivity option (11)
- // 2024-04-03 ** AEP. (Updated GMACS to version 2.20.06) Added a smoothness penalty to spline selectivity and now output Fs and recruitent to gmacs_out.ctl
- // 2024-04-03 ** WTS. Growth transition matrix scale parameter is on l-scale when molt bUseGrowthIncrementModel2==PWRLAW_GROWTHMODEL
- // 2024-04-04 ** AEP. Added exit(1) condition when M_relative(ig==1)!=0 after flagging error condition (M specification for first group can't be relative).

GMACS updates since January 2024 (4)

- // 2024-04-04 ** WTS. Fixed issues with parameter specification when mirroring survey catchability and/or additional survey cv.
 - Cleaned up compiler warnings by changing " & " and " | " to "&& " and " || ", respectively.
 - Added missing immature crab use case for survey abundance/biomass calculations.
 - Fixed issues with prior density calculations when mirroring q's or additional cv's.
 - Added additional diagnostics for verbose>10. (Updated GMACS to version 2.20.07).
- // 2024-04-05 ** WTS. Revised Gmacsall.out formats to play nice with R.
 - Also developed R code to read and create a list object from the .out file.
- // 2024-04-08 ** WTS. Defined RepFile1 as outstream to "gmacs.rep1".
 - Changed REPORT and REPORT2 macros to REPVEC and REPVEC2 macros for vector (or scalar) quantities and added output to RepFile1. Added REPMAT and REPMAT2 macros to output matrices to OutFile1 (Gmacsall.out), OutFile2 (gmacs.rep), and RepFile1. Added FUNCTIONS to_str and strg to create an adstring representation of a space-separated vector (simplifies code to write a vector to a file).
- // 2024-04-10 ** WTS. Added more output to RepFile1.
 - Added explicit "Status" column to Summary section of Gmacsall.out to indicate whether parameter estimate was close to lower bound ("*-"), upper bound ("*+"), or neither ("ok").
 - Changed "pen_fbar", "log_pen_fbar", and "log_pen_fbar_off" to "init_fbar", "log_init_fbar", and "log_init_fbar_foff" to better clarify their purpose.

GMACS updates since January 2024 (5)

- // 2024-04-11 ** WTS. Revised size fit summary to RepFile1 (gmacs.rep1),
 - added mapInpToAggSizeComps matrix, which provides mapping from input size comps to aggregated size comps (and is used in the revised size fit summary).
 - (Updated GMACS version to 2.20.09.)
- // 2024-04-12 ** WTS. Added commandline option ("-jitter rseed") to override gmacs.dat setting. If rseed is 0, rseed is set based on the model start time.
 - The value of rseed used to initialize the random number generator is written to "jitter.txt" to allow repeating a jittered model run. (Updated GMACS version to 2.20.10.)
- // 2024-04-13 ** WTS. Added initialization of log_foff to log_init_fbar_foff in INITIALIZATION section (otherwise it initialized to 0).
 - Added likelihood penalty for ln-scale mean female offset to nlogPenalty(2) similar to ln-scale mean for males (search on '20240413').
 - Added fishing mortality parameters output to Rep1File. Updated GMACS version to 2.20.11.
- // 2024-04-22 ** AEP. ??
- // 2024-5-10 ** WTS. Added alternative format for environmental time series data in the dat file.
 - Updated GMACS version to 2.20.12.

GMACS To Do List

- 1 - Bias ramp for recruitment
- 2 - Review how female offsets are handled for fishing mortality (bounds for devs are hard-wired)?
- "log_init_fbar_foff" (column 2 of F controls) is never used anywhere. It should be removed from the ctl file.

R Code

- developed R package “wtsGMACS” (<https://github.com/wStockhausen/wtsGMACS.git>)
 - reads new gmacs.rep1 file
 - adds some additional graphics
 - runs gmacs model
 - runs gmacs jittering ensemble, selects best model
 - converts TCSAM02 input formats to GMACS format catch data, relative abundance, and size comps dataframes
 - intent is to merge into functions into gmr