Untitled

Grant Adams

January 3, 2019

CEATTLE is short for Climate-Enhanced, Age-based model with Temperature-specific Trophic Linkages and Energetics, which is a multi-species age-structured assessment model developed for groundfish in the Bering Sea, USA by Holsman et al. (2015). To incorporate the impacts of climate, the model includes temperature-dependent von Bertalanffy weight-at-age functions (VBGF) and temperature-specific, bioenergetics-based predation interactions. Inputs of the model include U.S. National Marine Fisheries Service Alaska Fisheries Science Center (AFSC) survey and fishery data. Outputs include historical estimates of predation mortality, fishing mortality, biomass, recruitment, etc.

Rceattle is an R package designed to implement the CEATTLE model using Template Model Builder (TMB; Kristensen et al. (2015)). Rceattle is structured similar to the original manuscript in terms of modularization. Seperate functions (i.e. modules) estimate retrospective temperature- and size-specific predator rations, prey preference, and weight-at- age. These are then used as inputs to the CEATTLE model to evaluate how predation mortality, recruitment, and survival of three target species change under historical climate conditions and harvest rates. Estimates from CEATTLE in Rceattle can then be forward projected to derive estimates of unfished biomass and fishing mortality under future climate conditions and various harvest scenarios.

Currently RCeattle takes CEATTLE ADMB based inputs and estimates them in TMB. To run Rceattle a user selects a control file located in a data directory with .dat files used in ADMB. The model will then initialize assuming for all parameters unless a parameter list is provided or "ceattle.par" or "ceattle\_par.std" is selected. In the later case, a .par or .std file provided from a previously estimated ADMB model must by included in the folder prior to the data directory. Currently, .dat files and ADMB outputs are included in the \data folder.

# Example

For example, to run the 2017 single species assessment for the Bering Sea, a data file must first be created:

data\_list\_ss <- build\_dat(ctlFilename = "asmnt2017\_0A\_corrected", TMBfilename = "ceattle\_v01\_02", dat\_dir = "data/BSAI/BS\_SS\_Files/dat files/", nspp = 3)

Then the model can be fit by setting msmMode = 0 using the Rceattle function:

ss\_run <- Rceattle(TMBfilename = "ceattle\_v01\_02",   
 data\_list = data\_list\_ss,  
 inits = NULL, # Initial parameters = 0  
 file\_name = NULL, # Don't save  
 debug = 0, # Estimate  
 random\_rec = FALSE, # No random recruitment  
 msmMode = 0, # Single species mode  
 avgnMode = 0,  
 silent = FALSE)

The you can plot the model results using using

plot\_biomass(ceattle\_list = list(ss\_run))  
plot\_recruitment(ceattle\_list = list(ss\_run))

For the 2017 multispecies model starting from the single species parameters, the following can be specified:

data\_list\_ms <- build\_dat(ctlFilename = "asmnt2017\_2A\_corrected", TMBfilename = "ceattle\_v01\_02", dat\_dir = "data/BSAI/BS\_MS\_Files/dat files/", nspp = 3)  
  
ms\_run <- Rceattle(TMBfilename = "ceattle\_v01\_02",   
 data\_list = data\_list\_ms,  
 inits = ss\_run$estimated\_params, # Initial parameters from ss run  
 file\_name = NULL, # Don't save  
 debug = 1, # Estimate  
 random\_rec = FALSE, # No random recruitment  
 niter = 10, # Number of iterations around predation/pop dy functions  
 msmMode = 1, # Multi-species holsman mode  
 avgnMode = 0)  
  
plot\_biomass(ceattle\_list = list(ms\_run))  
plot\_recruitment(ceattle\_list = list(ms\_run))

# Equations

**Table 1.** Population dynamics equations for species and age in each simulation year . BT indicates the AFSC bottom trawl survey and EIT represents the echo-integrated acoustic- trawl survey. For all parameter definititions see Table 3.

|  |  |  |
| --- | --- | --- |
| Definition | Equation |  |
| Recruitment |  | T1.1 |
| Initial abundance |  | T1.2 |
| Numbers at age |  | T1.3 |
| … |  | … |
| Catch |  | T1.4 |
| Total yield (kg) |  | T1.5 |
| Biomass at age (kg) |  | T1.6 |
| Spawning biomass at age (kg) |  | T1.7 |
| Total mortality at age |  | T1.8 |
| Fishing mortality at age |  | T1.9 |
| Weight at age (kg) |  | T1.10a |
| … |  | T1.10b |
| … |  | T1.10c |
| BT survey biomass (kg) |  | T1.11 |
| EIT survey biomass (kg) |  | T1.12 |
| Fishery age composition |  | T1.13 |
| BT survey age composition |  | T1.14 |
| EIT survey age composition |  | T1.15 |
| BT selectivity |  | T1.16 |
| Fishery selectivity |  | T1.17 |
| Proportion females |  | T1.18 |
| Proportion of mature females |  | T1.19 |
| Weight at age (kg) |  | T1.20 |
| Residual natural mortality |  | T1.21 |

**Table 2.** Predation mortality equations for predators of age , and prey of age

|  |  |  |
| --- | --- | --- |
| Definition | Equation |  |
| Predation mortality |  | T2.1 |
| Predator-prey suitability |  | T2.2 |
| Mean gravimetric diet proportion |  | T2.3 |
| Individual specific ration () |  | T2.4 |
| Temperature scaling algorithim |  | T2.5 |
| … |  | T2.5a |
| … |  | T2.5b |
| … |  | T2.5c |
| … |  | T2.5d |

**Table 3.** Parameter definitions.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Definition | Type | Model Object |
| Year |  | M | i |
| Predator |  | M |  |
| Predator age (years) |  | M |  |
| Prey |  | M | k |
| Prey age (years) |  | M |  |
| Number of prey species |  | I | nspp |
| Number of predator species |  | I |  |
| Number of prey ages |  | I | nages |
| Number of predator ages |  | I |  |
| Number of simulation years |  | I | nyrs |
| Start year |  | I | styr |
| Annual relative foraging rate () |  | I |  |
| Intercept of the allometic maximum consumption function () |  | I | aLW |
| Allometric slope of maximum consumption |  | I | bLW |
| Consumption maximum physiological temperature (°C) |  | I | Tcm |
| Consumption optimum physiological temperature (°C) |  | I | Tco |
| Max consumption parameter |  | I | Qc |
| Mean recruitment |  | E |  |
| Annual recruitment deviation |  | E | rec\_dev |
| Initial abundance |  | E |  |
| Mean fishing mortality |  | E |  |
| Anuual fishing mortality deviation |  | E |  |
| Fishery age selectivity coefficient |  | E |  |
| Survey age selectivity slope |  | E |  |
| Survey age selectivity limit |  | E |  |
| VBGF allometric slope of consumption |  | P | d |
| VBGF max asymptotic weight (kg) |  | P | Winf |
| Proportion of mature females at age |  | P |  |
| Residual natural mortality |  | F | M1\_base |
| Intercept for VBGF parameter |  | F |  |
| Annual intercept for VBGF parameter |  | F | log\_mean\_d |
| Temperature covariate for VBGF parameter |  | F | Tcoef |
| VBGF energy loss constant () |  | F | logK |
| VBGF assimilation constant () |  | F | logH |
| VBGF age when (years) |  | F | t0 |
| EIT survey selectivity |  | F |  |
| Female natural mortality |  | F |  |
| Male natural mortality |  | F |  |
| Female proportion of population |  | F |  |
| Age-specific maturity proportions |  | F | pmature |
| Observed total yield () |  | D | tc\_biom\_obs |
| Observed fishery age comp. |  | D | fsh\_age\_obs |
| Observed BT age comp. |  | D | srv\_age\_obs |
| Observed EIT age comp. |  | D | obs\_eit\_age |
| Observed BT survey biomass (kg) |  | D | srv\_bio |
| Observed EIT survey biomass (kg) |  | D | obs\_eit |
| Bottom temperature (°C) |  | D | TempC |
| Gravimetric proportion of prey in predator stomach |  | D |  |
| Biomass of other prey (kg) |  | D | other\_food |
| **Not in table 3** |  |  |  |
| Annual survey biomass error |  | F | srv\_Mean\_CV |
| Number of years with total observed catch |  | M | nyrs\_tc\_biom\_obs |
| Years with total observed catch |  | I | yrs\_tc\_biom\_obs |
| Number of years in the fishery sp\_age composition data |  | E | nyrs\_fsh\_comp |
| Number of estimation years |  | I | nyrs\_est |
| End year |  | I | endyr |
| Number of years in the fishery age composition data |  | I | nyrs\_fsh\_comp |
| Years in the fishery age composition data |  | I | yrs\_fsh\_comp |
| Method of calculating fishery age |  | I | fsh\_age\_type |
| Number of fishery age bins |  | I | fsh\_age\_bins |
| Number of years with weight-at-age data |  | I | nyrs\_wt\_at\_age |
| Years with weight-at-age data |  | I | yrs\_wt\_at\_age |
| Weight-at-age data |  | D | wt |
| Number of years in the BT survey data |  | I | nyrs\_srv\_biom |
| Years in the BT survey data |  | I | yrs\_srv\_biom |
| BT survey standard error |  | F | srv\_biom\_se |
| Number of years in the BT survey age or length composition data |  | I | nyrs\_srv\_age |
| Years in the BT survey age composition data |  | I | yrs\_srv\_age |
| Method of calculating BT survey age type (age or length) |  | I | srv\_age\_type |
| Number of BT survey age bins |  | I | srv\_age\_bins |
| Sample size for BT survey age composition multinomial |  | I | srv\_age\_n |
| Observed survey BT size compositions |  | I | srv\_age\_sizes |
| Age transition matrix |  | I | age\_trans\_matrix |
| Number of years in the EIT survey data |  | I | n\_eit |
| Years in the BT survey data |  | I | yrs\_eit |
| Sample size for EIT survey age composition multinomial |  | I | eit\_age\_n |
| Number of years in the EIT selectivtiy data |  | I | nyrs\_eit\_sel |
| Years in the BT selectivity data |  | I | yrs\_eit\_sel |
| Sample size for EIT survey age composition multinomial |  | I | eit\_sel |
| Sex specific mortality and weight-at-age: 1 for combined, 2: for seperate |  | I | mf\_type |
| Proportion |  | I | propMorF |
| Observed catch-at-age |  | I | obs\_catch |
| Estimated catch-at-age |  | E | obs\_catch\_hat |
| Observed total catch |  | D | tc\_obs |
| Estimated total catch |  | D | tc\_hat |
| Estimated total yield |  | E | tc\_obs |
| Observed fishery age composition |  | I | fsh\_age\_obs |
| Estimated fishery age composition |  | E | fsh\_age\_hat |

**Table 4.** Components of the likelihood function for each species of age in year .

|  |  |  |  |
| --- | --- | --- | --- |
| Description | Equation | Data source |  |
| **Data components** |  |  |  |
| BT survey biomass |  | NMFS annual EBS BT survey | T4.1 |
| BT survey age composition |  | NMFS annual EBS BT survey | T4.2 |
| EIT survey biomass |  | Pollock acoustic trawl survey | T4.3 |
| EIT survey age composition |  | Pollock acoustic trawl survey | T4.4 |
| Total catch |  | Fishery observer data | T4.5 |
| Fishery age composition |  | Fishery observer data | T4.6 |
| **Penalties** |  |  |  |
| Fishery selectivity |  |  | T4.7 |
| **Priors** |  |  |  |
|  |  |  | T4.8 |
|  |  |  | T4.9 |
|  |  |  | T4.10 |
|  |  |  |  |

# References

Holsman, K.K., Ianelli, J., Aydin, K., Punt, A.E., Moffitt, E.A., 2015. A comparison of fisheries biological reference points estimated from temperature-specific multi-species and single-species climate-enhanced stock assessment models. Deep-Sea Research Part II: Topical Studies in Oceanography 134, 360–378. <https://doi.org/10.1016/j.dsr2.2015.08.001>

Kristensen, K., Nielsen, A., Berg, C.W., Skaug, H., Bell, B., 2015. TMB: Automatic Differentiation and Laplace Approximation. arXiv 70, 1–21. <https://doi.org/10.18637/jss.v070.i05>