GMACS: A Generalized Size-Structured Model and Stock Reduction Analysis

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Abstract

Stock reduction analysis (SRA) is a data-poor technique that typically just uses historical catch information to estimate recruitment rates needed to explain those historical catches. The method is easily extended to accommodate sparse information on trends in abundance, composition information, and tagging data. Estimation of model parameters using maximum likelihood or Bayesian methods is possible. GMACS is a generalized framework for size-structured models suitable for data-poor to data-rich assessments. Reference points are derived from steady-state conditions by solving matrix equations that represent size-dependent mortality and growth. Our results show how the scalability of GMACS can be used as an integrated data-poor assessment method. Next steps include the evaluation of such "simple" methods testing simulated data generated from within GMACS (or from a separate R package) but configured to have greater complexity of underlying dynamics (e.g., time-varying natural mortality)

General Size-structured Equilibrium Model

Given a vector $\boldsymbol{n} = (n_1, n_2, \ldots, n_m)$ that represents the number of individuals in discrete size bins in a given year. Each year the numbers in each size bin are subject to growth and survival $\boldsymbol{A}$ and the addition of recruits $\boldsymbol{r}$. Assuming growth and survival is a linear function of the number of individuals in each size bin, then the following matrix equation represents the steady-state or equilibrium conditions:

$$\boldsymbol{n} = \boldsymbol{A}\boldsymbol{n} + \boldsymbol{r}$$

with the equilibrium solution for the numbers-at-size given by

$$\boldsymbol{n} = -(\boldsymbol{A} - \boldsymbol{I})^{-1}(\boldsymbol{r})$$

where $\boldsymbol{I}$ is the m x m identity matrix. In practical terms, the challenge is in developing the matrix $\boldsymbol{A}$ and the vector of new recruitment $\boldsymbol{r}$.

GMACS is based on this simple matrix equation equation for modeling the dynamics of molting probabilities, size-transition or growth, and also jointly models various life-history stages, such as, new- and old-shell crab.

Model Features

Table 1: Data inputs and dimensions implemented in GMACS, required elements in **bold**

Data Type	Dimensions	Symbol	Implemented
Catch	year, fleet, sex	C_t	✓
Discards	year, fleet, sex	D_t	✓
Effort	year, fleet	E_t	✗
CPUE	year, fleet, sex, shell	I_t	✓
Composition	year, fleet, sex, shell, type	$Q_{i,h,o}$	✓
Composition	maturity status		✗
Molt Increment	sex	g_l	✓
Tagging data	sex		✗

Generalized Model Notation (equilibrium conditions)

model parameters

$$\Theta = (M, \alpha_r, \beta_r, R_0, \kappa) \quad (1)$$

$$M > 0, \alpha_r > 0, \beta_r > 0, R_0 > 0, \kappa > 1.0, \quad \text{constraints} \quad (2)$$

$$\Phi = (\alpha, \beta, \varphi), \quad \text{Size-transition parameters} \quad (3)$$

size-transition matrix $\boldsymbol{G}$

$\vec{l}, \vec{x}$ vector of size intervals and midpoints, respectively

$$a_l = (\alpha + \beta l)/\varphi \quad (4)$$

$$p(l, l') = \boldsymbol{G} = \int_l^{l+\Delta l} \frac{l^{(a_l - 1)} \exp(l/\varphi)}{\Gamma(a_l) l^{(a_l)}} dl \quad (5)$$

recruitment size-distribution

$$\alpha = \alpha_r/\beta_r \quad (6)$$

$$p[\boldsymbol{r}] = \int_{x_l - 0.5\Delta x}^{x_l + 0.5\Delta x} \frac{x^{(\alpha-1)} \exp(-x/\beta_r)}{\Gamma(\alpha)\beta_r^{\alpha}} dx \quad (7)$$

$$\boldsymbol{r} = 0.5 p[\boldsymbol{r}] \ddot{R} \quad (8)$$

growth and survival

$$\boldsymbol{A} = \boldsymbol{G}[\exp(-M)(\boldsymbol{I}_n)_{l,l'}] \quad \text{unfished} \quad (9)$$

$$\boldsymbol{B} = \boldsymbol{G}[\exp(-M - \boldsymbol{f}_l)(\boldsymbol{I}_n)_{l,l'}] \quad \text{fished} \quad (10)$$

survivorship to size-interval

$$\boldsymbol{u} = -(\boldsymbol{A} - (\boldsymbol{I}_n)_{l,l'})^{-1}(p[\boldsymbol{r}]) \quad \text{unfished} \quad (11)$$

$$\boldsymbol{v} = -(\boldsymbol{B} - (\boldsymbol{I}_n)_{l,l'})^{-1}(p[\boldsymbol{r}]) \quad \text{fished} \quad (12)$$

steady-state conditions

$$B_0 = R_0 \phi_B, \quad \text{where} \quad \phi_B = \sum_l \boldsymbol{u}_l w_l m_l \quad (13)$$

$$\tilde{B} = \tilde{R}\tilde{\phi}_B \quad \text{where} \quad \tilde{\phi}_B = \sum_l \boldsymbol{v}_l w_l m_l \quad (14)$$

stock-recruitment parameters

$$s_o = \kappa R_0 / B_0 \quad (15)$$

$$\beta = (\kappa - 1)/B_0 \quad (16)$$

$$\tilde{R} = \frac{s_o \tilde{\phi}_B - 1}{\beta \tilde{\phi}_B} \quad (17)$$

Size-based selectivity, retention, and fishing mortality

Parameters

$$\ln(f), a, \sigma_s, \lambda, \sigma_y, \xi \qquad \xi = \text{Discard mortality} \quad (18)$$

Selectivity & retention

$$s_l = (1 + \exp(-(l - a)/\sigma_s))^{-1} \qquad \text{Capture probability} \quad (19)$$

$$y_l = (1 + \exp(-(\lambda - l)/\sigma_y))^{-1} \qquad \text{Retention probability} \quad (20)$$

$$\nu_l = s_l[y_l + (1 - y_l)\xi] \qquad \text{Joint probability of dying from fishing} \quad (21)$$

Fishing mortality

$$F = \exp(\ln(f)) \qquad \text{Instantaneous fishing mortality} \quad (22)$$

$$\boldsymbol{f}_l = F\nu_l \qquad \text{Size-based fishing mortality} \quad (23)$$

Reference Points (SPR-based)

The Spawning Potential Ratio (SPR) is the ratio of spawning stock biomass in fished:unfished conditions. Or,

$$SPR = \frac{\tilde{\phi}_B}{\phi_B}$$

Fishing mortality that achieves SPR values in the range of 0.3-0.4 are often considered a proxy for rates associated with Maximum Sustainable Yield.

GMACS uses an interative solution based on solving equations (13) and (14) to find the fishing mortality rate (F_{SPR}) that corresponds to a specified SPR value.

Methods

Model descriptions

- Data from the Bristol Bay red king crab fishery (BBRKC).
- Four Alternative Models (Table 2).

Table 2: Alternative model configurations where ✓ option is turned on, and ✗ is off and the number of estimated parameters.

Model	Fit to Data C_t	I_t	$\boldsymbol{Q}$	Initial States	No. Parameters
M1	✓	✗	✗	✗	184
M2	✓	✓	✗	✗	188
M3	✓	✓	✓	✗	189
M4	✓	✓	✓	✓	190

Results

- The joint probability model (21) attempts to simultaneously estimate retained and discarded catch (Fig. 1).
- Catch only method requires prior information on one of the following:
  - Average fishing mortality rates, or
  - an estimate of current depletion level, or
  - an estimate of absolute fishing mortality for one or more gears.
- Estimates of $F_{\text{SPR}=35\%}$ are consistent across models because same natural mortality and selectivity are assumed (Table 3).

Figure 1: Observed and predicted catch.

Table 3: SPR-based reference points from each model

Model	$F_{\text{SPR}=35\%}$	$B_{\text{SPR}=35\%}$	F_{OFL}	OFL	$R_{\text{SPR}=35\%}$
M1	0.26	22.17	0.07	0.31	5.95
M2	0.25	33.46	0.25	3.33	7.36
M3	0.25	25.04	0.24	1.80	5.52
M4	0.28	28.06	0.28	2.63	7.15

Results cont.

Figure 2: Fits to relative abundance data (left) and estimates of mature male biomass. Shaded regions approximate 95% confidence intervals.

Figure 3: Observed and predicted size composition of newshell crabs in NMFS trawl survey.

Discussion

- Size- or stage-structured models contain additional confounding between estimates of recruitment, size-transition, and size-based mortality in contrast to age-structured models.
- It is possible to conduct Stock Reduction Analysis (using only catch data) and additional assumptions about natural mortality, growth, and the size-distribution of new recruits.
- The generalized size-structured equilibrium model also extends to additional classes such as sex, new and old-shell, immature and mature animals.

Acknowledgements

Financial support for this project was provided by the Bering Sea Fisheries Research Foundation, NOAA, the North Pacific Fisheries Management Council, International Pacific Halibut Commission, and the ADMB Foundation. We are grateful for the contributions from the following people: Jack Turnock, Jie Zheng, Hamachan Hamazaki, Athol Whitten, André Punt, Darcy Webber and John Levitt.

No crabs were eaten during the production of this poster.