

Gmacs

A generalized size-structured stock assessment model

The Gmacs Development Team

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Outline

1 Notation and symbols

- Indices
- Key parameters
- Growth parameters
- Stuff

2 Growth and survival

- Growth
- Natural mortality
- Growth and survival

3 Steady-state conditions

- Survivorship to length

Indices

Symbol	Description
g	group
h	sex
i	year
j	time step (years)
k	gear or fleet
ℓ	index for size class
m	index for maturity state
o	index for shell condition

Estimated parameters

Symbol	Description
M_0	Instantaneous natural mortality rate
\bar{R}	Average recruitment
\ddot{R}	Initial recruitment
α_r	Mode of size-at-recruitment
β_r	Shape parameter for size-at-recruitment
R_0	Unfished average recruitment
κ	Recruitment compensation ratio

$$M_{0,h} > 0, \bar{R} > 0, \ddot{R} > 0, \alpha_r > 0, \beta_r > 0, R_0 > 0, \kappa > 1.0$$

$$\Theta = \{M_0, \bar{R}, \ddot{R}, \alpha_r, \beta_r, R_0, \kappa, \alpha_h, \beta_h, \varphi_h, \nu, \xi\}.$$

Growth parameters

Symbol	Description
α_h	Mode of size-at-recruitment
β_h	Shape parameter for size-at-recruitment
φ_h	Instantaneous natural mortality rate

$$\Phi = \{\alpha_h, \beta_h, \varphi_h\}.$$

Stuff

Symbol	Description
$w_{h,\ell}$	Mean weight at length
$m_{h,\ell}$	Average proportion mature at length

Growth

The average molt increment from size class ℓ to ℓ' is assumed to be sex-specific and is defined by the linear function

$$a_{h,\ell} = \frac{\alpha_h + \beta_h \ell}{\varphi_h}.$$

The probability of transitioning from size class ℓ to ℓ' assumes that variation in molt increments follows a gamma distribution

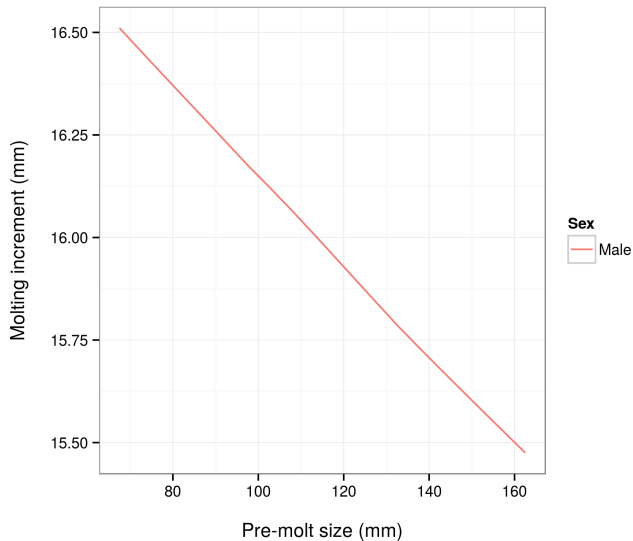
$$p(\ell, \ell')_h = \mathbf{G}_h = \int_{\ell}^{\ell+\Delta\ell} \frac{\ell^{a_{h,\ell}-1} \exp\left(-\frac{\ell}{\varphi_h}\right)}{\Gamma(a_{h,\ell}) \ell^{a_{h,\ell}}} \quad \text{where} \quad \Delta\ell = \ell' - \ell.$$

Specifically

$$\mathbf{G} = G_{\ell,\ell'} = \begin{pmatrix} G_{1,1} & G_{1,2} & \dots & G_{1,n} \\ G_{2,1} & G_{2,2} & \dots & G_{2,n} \\ \vdots & \vdots & \ddots & \vdots \\ G_{n,1} & G_{n,2} & \dots & G_{n,n} \end{pmatrix} \quad \text{where} \quad \sum_{\ell'} G_{\ell,\ell'} = 1 \quad \forall \ell.$$

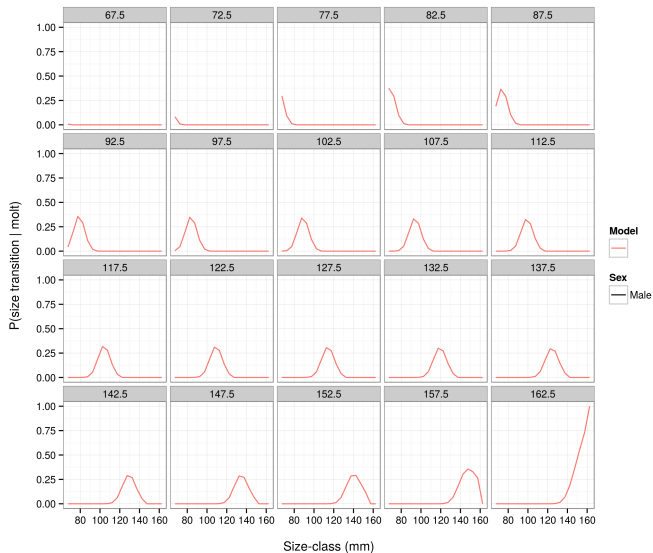
Growth

Growth increment



Growth

Growth transition



Natural mortality

Natural mortality (M) is assumed to be sex-specific (h), size-independent (ℓ), and may or may not be constant over time (i). If time-varying natural mortality is used, the model constrains $M_{h,i}$ to be a random-walk process with variance σ_M^2

$$M_{h,i+1} = \begin{cases} \bar{M}_h \\ M_{h,i}e^{\delta_i} \end{cases} ,$$

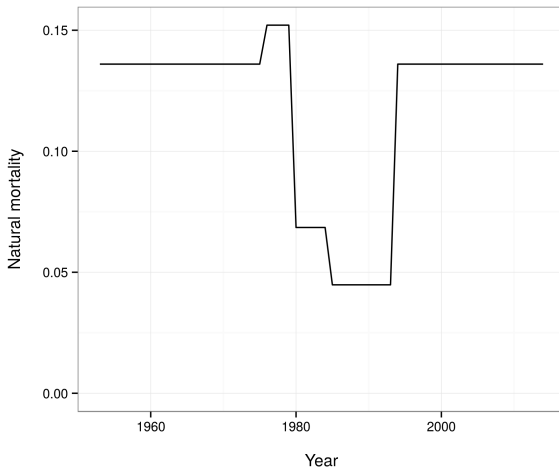
where

$$\delta_i \sim \mathcal{N}(0, \sigma_M^2) .$$

A time-varying natural mortality can be estimated for all years (i), or for specified blocks of years ($\iota \in i$).

Natural mortality

Assuming natural mortality is time-varying constrained by variance ($\sigma_M^2 = 0.04$) at four specific knots (1976, 1980, 1985, 1994)



Selectivity and retention

The probability of catching an animal of sex h , in year i , in fishery k , of length ℓ (i.e. selectivity) is

$$s_{h,i,k,\ell} = (1 + \exp(-(\ell - a_{h,i,k})/\sigma_{h,i,k}^s))^{-1}.$$

The probability of an animal of sex h , in year i , in fishery k , of length ℓ being retained is

$$y_{h,i,k,\ell} = (1 + \exp(-(r_{h,i,k} - \ell)/\sigma_{h,i,k}^y))^{-1}.$$

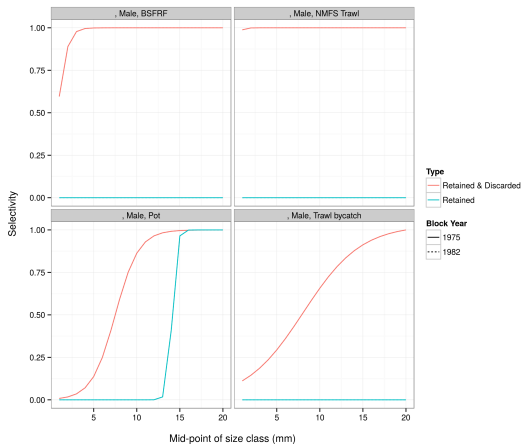
The joint probability of vulnerability due to fishing mortality and discarding is

$$\nu_{h,i,k,\ell} = s_{h,i,k,\ell} [y_{h,i,k,\ell} + (1 - y_{h,i,k,\ell})\xi_{h,k}],$$

where $\xi_{h,k}$ is the discard mortality rate for sex h in fishery k .

Selectivity and retention

Assuming that selectivity for the NMFS trawl fishery is split into two blocks (1975-1981 and 1982-2014) and that retention is constant with time $y_{h,i,k,\ell} = y_{h,k,\ell}$



Fishing mortality

$$\begin{aligned} F_{k,i} &= \exp \left(\bar{f}_k + \Psi_{k,i} \right), \\ f_{h,i} &= \sum_k F_{k,i} \nu_{h,i,k,\ell}, \end{aligned}$$

Growth and survival

Growth and survival

$$\mathbf{A}_h = \mathbf{G}_h \left[\exp(-\bar{M}_h) \mathbf{I} \right] .$$

Growth and survival including fishing mortality

$$\mathbf{B}_{h,i} = \mathbf{G}_h \left[\exp(-M_{h,i} - \mathbf{f}_{h,i}) \mathbf{I} \right] .$$

Survivorship to length

Survivorship to length

$$\mathbf{u}_h = -(\mathbf{A}_h - \mathbf{I})^{-1}(p(\mathbf{r})),$$

$$\mathbf{v}_h = -(\mathbf{B}_h - \mathbf{I})^{-1}(p(\mathbf{r})).$$

Steady-state conditions

$$B_0 = R_0 \sum_h \lambda_h \sum_{\ell} \mathbf{u}_h w_{h,\ell} m_{h,\ell},$$

$$\tilde{B} = \tilde{R} \sum_h \lambda_h \sum_{\ell} \mathbf{v}_h w_{h,\ell} m_{h,\ell}.$$

Recruitment

Recruitment size-distribution

$$\alpha = \frac{\alpha_r}{\beta_r},$$

$$p(\mathbf{r}_i) = \int_{x_\ell - 0.5\Delta x}^{x_\ell + 0.5\Delta x} \frac{x^{\alpha-1} \exp\left(\frac{x}{\beta_r}\right)}{\Gamma(\alpha)x^\alpha} dx,$$

$$\mathbf{r}_{h,i} = 0.5p(\mathbf{r}_i)\ddot{R}.$$

Population dynamics

Initial numbers at length

$$\mathbf{n}_{h,i} = \left[-(\mathbf{A}_h - \mathbf{I})^{-1} \mathbf{r}_{h,i} \right] e^{\nu} \quad \text{where } i = 1.$$

The numbers in each size-class in the following time-step ($\mathbf{n}_{h,i+1}$) is the product of the numbers in each size-class in the previous time-step ($\mathbf{n}_{h,i}$), size-specific growth and survival ($\mathbf{A}_{h,i}$), plus new recruits ($\mathbf{r}_{h,i}$)

$$\mathbf{n}_{h,i+1} = \mathbf{n}_{h,i} \mathbf{A}_{h,i} + \mathbf{r}_{h,i} \quad \text{where } i > 1.$$

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Data weighting

Log-likelihood, likelihood, distribution

$$\ell(\mu, \sigma^2, \lambda; x) = \lambda \left(-\frac{1}{2} \log(2\pi) - \frac{1}{2} \log(\sigma^2) - \frac{1}{2\sigma^2} (x - \mu)^2 \right)$$

$$p(x|\mu, \sigma^2, \lambda) = \exp(\lambda) (2\pi\sigma^2)^{-\frac{1}{2}} \exp \left[-\frac{1}{2\sigma^2} (x - \mu)^2 \right]$$

$$x|\mu, \sigma^2, \lambda \sim \mathcal{N}(\mu, \lambda\sigma^2)$$