Gmacs

A generalized size-structured stock assessment model

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Outline

Notation

Generally

- a bold capital symbol $\mathbf{A}$ refers to a matrix
- a bold lowercase symbol $\mathbf{a}$ refers to a vector
- an unbolded italic symbol a refers to a scalar
- $\{a_i\}_{i=1}^{n}$ is an ordered n-tuple
- the terms $p(\cdot)$ or $\pi(\cdot)$ represent probability distributions
- $a|b$ means event a conditional on event b having occurred
- the symbol $\forall$ means for all values, usually referring to all of the values within an ordered tuple.
- we use red to indicate an estimable parameter
- we use blue to represent covariates and fixed parameters
- we use green to represent data

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

Notice no area index.

Leading model parameters

Symbol	Support	Description
M_0	$0 < M_0 < \infty$	Initial instantaneous natural mortality rate
R_0	$0 < R_0 < \infty$	Unfished average recruitment
$\ddot{R}$	$0 < \ddot{R} < \infty$	Initial recruitment
$\bar{R}$	$0 < \bar{R} < \infty$	Average recruitment
α_r	$0 < \alpha_r < \infty$	Mode of size-at-recruitment
β_r	$0 < \beta_r < \infty$	Shape parameter for size-at-recruitment
κ	$1 < \kappa < \infty$	Recruitment compensation ratio
ρ	$-\infty < \rho < \infty$	Recruitment autocorrelation

We group the leading model parameters into the vector

$$\boldsymbol{\theta} = \{M_0, R_0, \ddot{R}, \bar{R}, \alpha_r, \beta_r, \kappa, \rho\}.$$

Cubic splines

A spline is a numeric function that is piecewise-defined by polynomial functions, and which possesses a sufficiently high degree of smoothness at the places where the polynomial pieces connect (which are known as knots). A cubic spline is constructed of piecewise third-order polynomials. Cubic splines can be defined by a simple tridiagonal system which can be solved easily to give the coefficients of the polynomials.

Growth parameters

Symbol	Support	Description
α_h	$\alpha_h > 0$	Growth intercept
β_h	$\beta_h > 0$	Growth slope
φ_h	$\varphi_h > 0$	Growth scale
μ_h	$\mu_h > 0$	Length at 50% molting probability
c_h	$c_h > 0$	Coefficient of variation of molting probability

We group the growth parameters into the vector

$$\boldsymbol{\psi} = \{\alpha_h, \beta_h, \varphi_h, \mu_h, c_h\}.$$

Growth involves:

- average molt increment from size class ℓ to ℓ'
- probability of transitioning from size class ℓ to ℓ'
- molting probability
- size transition probability

Growth matrix

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

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

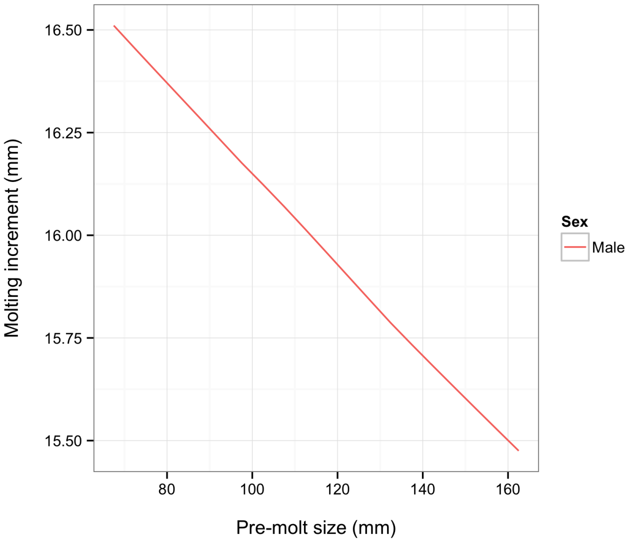
The probability of transitioning from size class ℓ to ℓ' assumes that variation in molt increments follows a gamma distribution

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

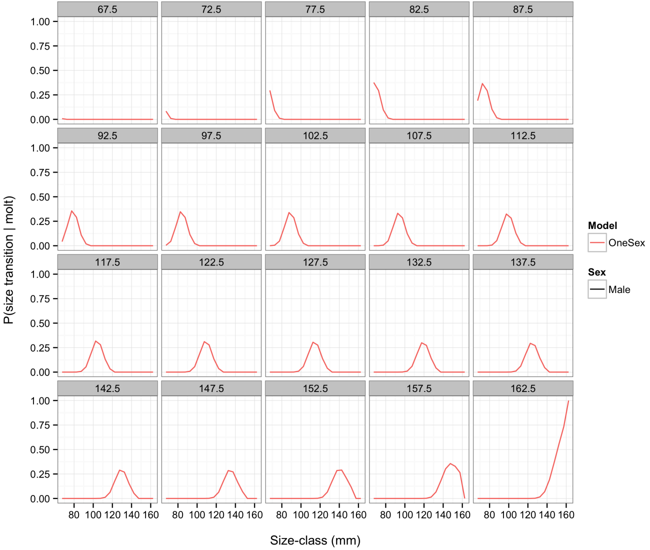
Specifically

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

Growth increments ($a_{h,\ell}$)



Growth transitions ($\boldsymbol{G}_h$)



Molting probability ($\boldsymbol{P}_h$)

The standard deviation of molting probability (σ_h) is calculated from the length at 50% molting probability (μ_h) coefficient of variation of molting probability (c_h) as

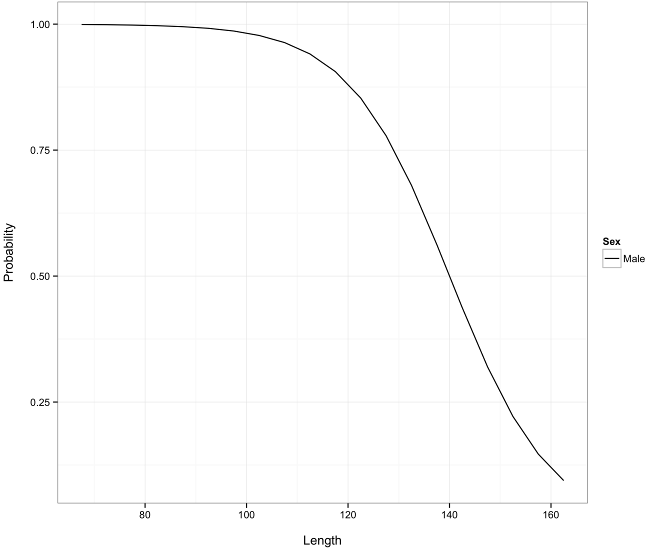
$$\sigma_h = \mu_h c_h.$$

The molting probability ($\boldsymbol{P}_h$) is calculated as

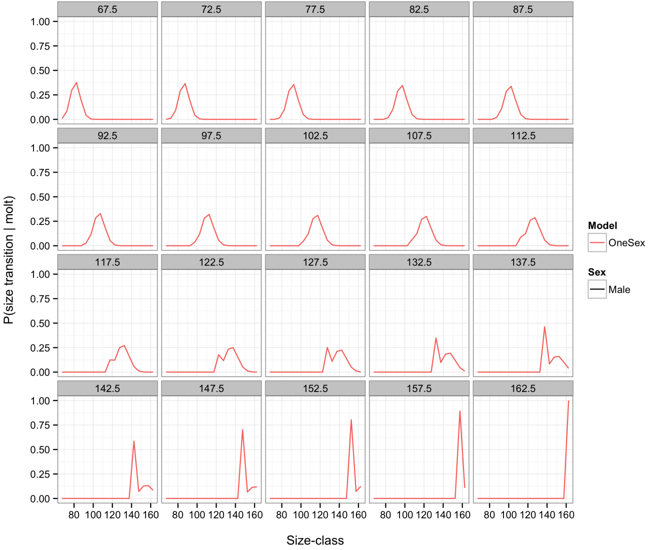
$$\boldsymbol{P}_h = 1 + (-1 - \exp(\mu_h - \ell)/\sigma_h)^{-1}.$$

The molting probability ($\boldsymbol{P}_h$) and the growth probability ($\boldsymbol{G}_h$) are combined to yield the size transition matrix ($\boldsymbol{P}_h \boldsymbol{G}_h$).

Molting probability ($\boldsymbol{P}_h$)



Size transitions ($\boldsymbol{P}_h \boldsymbol{G}_h$)



Natural mortality variables

Symbol	Description
$M_{0,h}$	Initial instantaneous natural mortality rate
σ_M	Standard deviation of natural mortality
δ_i	Natural mortality deviate
$M_{h,i}$	Natural mortality by sex h and year i

Natural mortality options

Natural mortality (M) is assumed to be sex-specific (h), size-independent (ℓ), and may or may not be constant over time (i). The options currently available in Gmacs include:

1. Constant natural mortality ($M_{h,i} = M_{0,h}$)
2. Random walk (deviates constrained by variance σ_M^2)
3. Cubic Spline (deviates constrained by nodes and node placement)
4. Blocked changes (deviates constrained by variance in specified blocks $\iota \in i$)

Natural mortality: option 2

If time-varying natural mortality is specified using the **random walk** option, the model constrains $M_{h,i}$ to be a random-walk process with variance σ_M^2

$$M_{h,i+1} = \begin{cases} M_{0,h} & \text{for} \quad i = 1 \\ M_{h,i} e^{\delta_i} & \text{for} \quad i > 1 \end{cases},$$

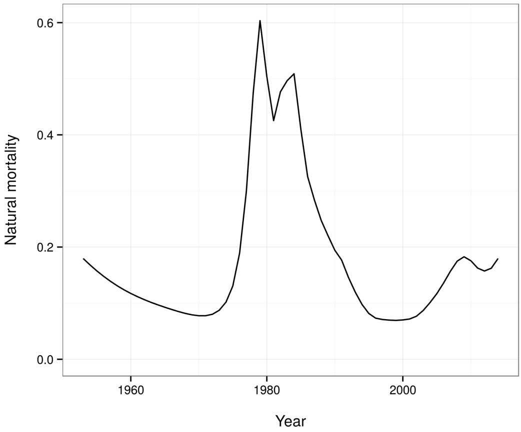
where

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

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

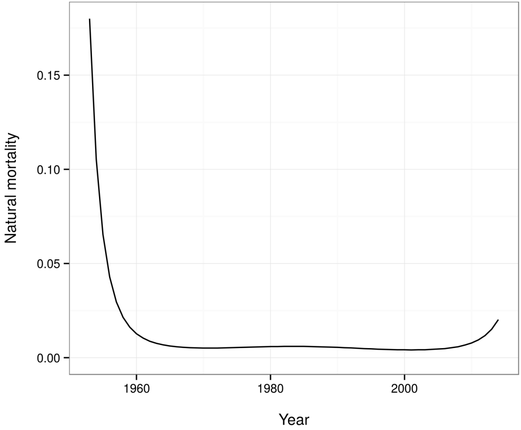
Natural mortality: option 2

Below we present an example in which time-varying natural mortality is estimated as a **random walk** process for all years (i)



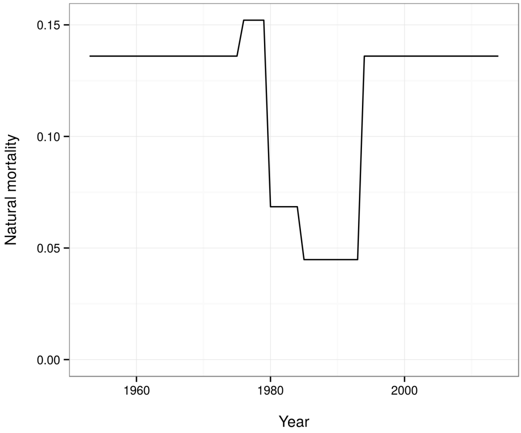
Natural mortality: option 3

If time-varying natural mortality is specified using the **cubic spline** option, the model constrains $M_{h,i}$ to be a cubic spline process at specified knots. For example



Natural mortality: option 4

If time-varying natural mortality is specified using the **blocked changes** option, the model constrains $M_{h,i}$ by the variance (σ_M^2). For example, setting $\sigma_M^2 = 0.04$ and four specific years (1976, 1980, 1985, 1994) we get



Selectivity, retention and fishing mortality

Symbol	Dimensions	Description
$a_{h,i,k}$	1	Length at 50% selectivity
$\sigma^s_{h,i,k}$	1	Standard deviation in length at selectivity
$\boldsymbol{s}_{h,i,k}$	$\ell \times 1$	Length at 50% selectivity in length interval ℓ
$r_{h,i,k}$	1	Length at 50%
$\sigma^y_{h,i,k}$	1	Standard deviation in length at retention
$\boldsymbol{y}_{h,i,k}$	$\ell \times 1$	Length at 50% retention in length interval ℓ
$\xi_{i,k}$	1	Discard mortality rate for gear k in year i
$\boldsymbol{\nu}_{h,i,k}$	$\ell \times 1$	Vulnerability due to fishing mortality for sex h
$\bar{\boldsymbol{f}}_k$	$i \times 1$	Average fishing mortality rate for gear k
$\boldsymbol{\Psi}_{i,k}$	1	Fishing mortality deviate for gear k in year i
$\boldsymbol{F}_{i,k}$	1	Annual fishing mortality rate for gear k in year i

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

$$\boldsymbol{s}_{h,i,k} = \left(1 + \exp\left(-(\ell - a_{h,i,k})/\sigma^{s}_{h,i,k}\right)\right)^{-1}.$$

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

$$\boldsymbol{y}_{h,i,k} = \left(1 + \exp\left(-(r_{h,i,k} - \ell)\,/\sigma^{y}_{h,i,k})\right)\right)^{-1}.$$

Selectivity, retention and fishing mortality

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

$$\boldsymbol{\nu}_{h,i,k} = \boldsymbol{s}_{h,i,k}\left[\boldsymbol{y}_{h,i,k} + (1 - \boldsymbol{y}_{h,i,k})\xi_{i,k}\right],$$

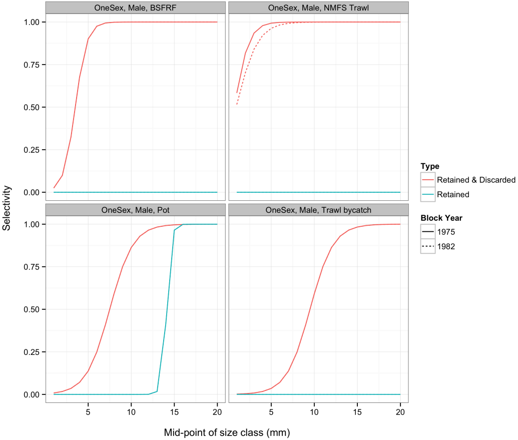
where $\xi_{i,k}$ is the discard mortality rate for fishery k in year i. Finally the fishing mortality is calculated as

$$\boldsymbol{F}_{h,i} = \sum_{k} \exp\left(\bar{\boldsymbol{f}}_k + \boldsymbol{\Psi}_{i,k}\right)\boldsymbol{\nu}_{h,i,k},$$

The vector $\boldsymbol{F}_{h,i}$ represents all mortality associated with fishing, including discards in directed and non-directed fisheries.

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 $\boldsymbol{y}_{h,i,k} = \boldsymbol{y}_{h,k}$

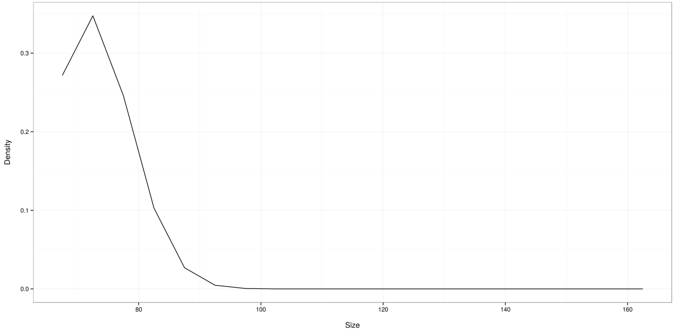


Recruitment

Recruitment size-distribution

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

$$p[x_\ell - 0.5\Delta x \leq x \leq x_\ell + 0.5\Delta x] = p[x] = \int_{x_\ell - 0.5\Delta x}^{x_\ell + 0.5\Delta x} \frac{x^{\alpha - 1} \exp\left(\frac{x}{\beta_r}\right)}{\Gamma(\alpha) x^{\alpha}} dx.$$



Recruitment

Initial recruitment

$$\boldsymbol{r}_{h,i} = 0.5p[x]\ddot{R} \quad \text{for} \quad i = 1.$$

Recruitment

$$\boldsymbol{r}_{h,i} = 0.5p[x]\bar{R}e^{\delta_i} \quad \text{for} \quad i > 1,$$

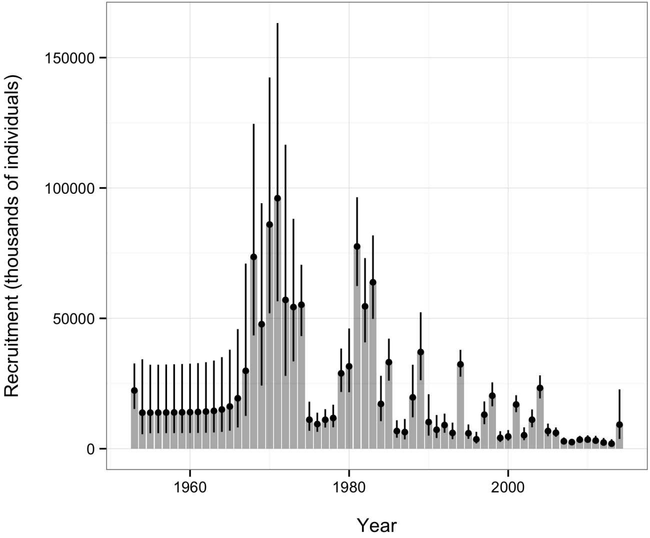
where

$$\delta_i = \log(r_i) - (1-\rho)\log(\bar{R}) - \rho\log(r_{i-1}) + 0.5\sigma_R^2$$

and

$$r_i = \sum_h r_{h,i}.$$

Recruitment



Growth and survival

Growth and survival process are combined, represented by

$$\boldsymbol{A}_{h,i} = \begin{cases} \boldsymbol{G}_h\left[\exp(-M_{h,i})\boldsymbol{I}\right] & \text{for} \quad i = 1 \\ \boldsymbol{G}_h\left[\exp(-\boldsymbol{Z}_{h,i})\boldsymbol{I}\right] & \text{for} \quad i > 1 \end{cases}.$$

where

$$\boldsymbol{Z}_{h,i} = M_{h,i} + \boldsymbol{F}_{h,i}.$$

Growth and survivorship in unfished and fished conditions is given by the solution to the equation

$$\boldsymbol{u}_{h,i} = -(\boldsymbol{A}_{h,i} - \boldsymbol{I})^{-1}(p[x]) \quad \forall i.$$

The vector $\boldsymbol{u}_{h,i}$ represent the unique equilibrium solution for the numbers per recruit in each size category.

Initial population

The mean weight at length (ℓ) by sex (h) is represented by the $\ell \times 1$ vector $\boldsymbol{w}_h$ and can take any form the user wishes

$$\boldsymbol{w}_h = f_w(\ell, \theta)$$

Similarly, the average proportion mature at length (ℓ) by sex (h) is represented by the $\ell \times 1$ vector $\boldsymbol{w}_h$ and can take any form the user wishes

$$\boldsymbol{m}_h = f_m(\ell, \theta)$$

Steady-state conditions

$$B_0 = R_0 \sum_h \lambda_h \sum_\ell \boldsymbol{u}_{h,i} \boldsymbol{w}_h \boldsymbol{m}_h \quad \text{for} \quad i = 1,$$

$$\tilde{B} = \tilde{R} \sum_h \lambda_h \sum_\ell \boldsymbol{u}_{h,i} \boldsymbol{w}_h \boldsymbol{m}_h \quad \text{for} \quad i > 1.$$

Population evolution

The total unfished numbers in each size category is defined as $R_0 \boldsymbol{u}_{h,i=1}$. Initial numbers at length

$$\boldsymbol{n}_{h,i} = \left[-\left(\boldsymbol{A}_h - \boldsymbol{I} \right)^{-1} \boldsymbol{r}_{h,i} \right] e^{\boldsymbol{\varepsilon}} \quad \text{for} \quad i = 1,$$

where $\boldsymbol{\varepsilon}$ is an $\ell \times 1$ vector of initial recruitment deviates. The numbers in each size-class in the following time-step ($\boldsymbol{n}_{h,i+1}$) is the product of the numbers in each size-class in the previous time-step ($\boldsymbol{n}_{h,i}$), size-specific growth and survival ($\boldsymbol{A}_{h,i}$), plus new recruits ($\boldsymbol{r}_{h,i}$)

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

Likelihoods and penalties

Likelihoods

- likelihood of catch (log-normal)
- likelihood of relative abundance (weighted log-normal)
- likelihood of size compositions (multinomial, robust multinomial, Dirichlet)
- likelihood of recruitment deviations (log-normal)
- likelihood of growth increment data (log-normal)

Penalties

- constrain $\log(\Psi_{i,k})$ to ensure they sum to zero
- constrain mean $\bar{\boldsymbol{f}}_k$ to regularize the solution
- constrain $M_{h,i}$ in random walk (log-normal)

Log-likelihood: catch

The standard deviation of the catch ($\sigma_{i,k}$) is calculated from the CV as

$$\sigma_{i,k} = \sqrt{\log\left(1 + {c_{i,k}}^2\right)}.$$

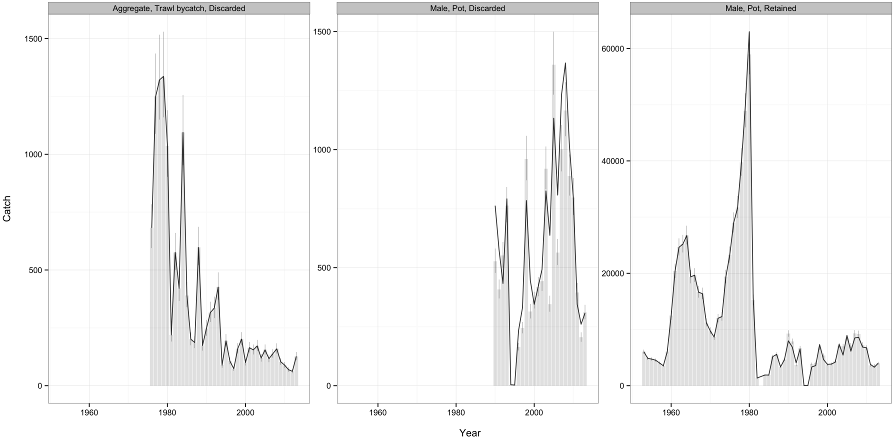
The expected catch is calculated using the Baranov catch equation

$$\hat{C}_{i,k} = \sum_{\ell} \left[\boldsymbol{n}_{h,i} \boldsymbol{w}_h \frac{\boldsymbol{F}_{h,i}}{\boldsymbol{Z}_{h,i}} \left(1 - e^{-\boldsymbol{Z}_{h,i}}\right) \right] \quad \text{where} \quad \boldsymbol{Z}_{h,i} = M_{h,i} + \boldsymbol{F}_{h,i}.$$

The log-likelihood is

$$\ell(C_{i,k}) = 0.5\log(2\pi) + \log(\sigma_{i,k}) - \frac{1}{2{\sigma_{i,k}}^2}\left(\log(C_{i,k}) - \log(\hat{C}_{i,k})\right)^2.$$

Log-likelihood: catch



Log-likelihoods: relative abundance

The catchability coefficient q is treated as a nuisance parameter and integrated out of the model (Walters & Ludwig 1994).

$$q = \exp\left(\frac{1}{n}\sum_i \log\left(\frac{I_i}{V_i}\right)\right).$$

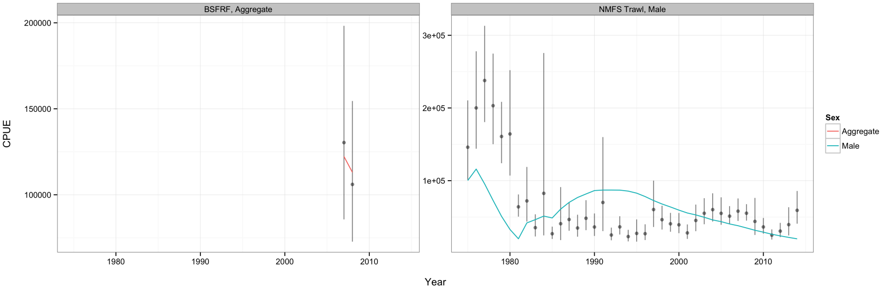
The standard deviation ($\sigma_{i,k}$) is calculated from the CV as

$$\sigma_{i,k} = \sqrt{\log\left(1 + {c_{i,k}}^2\right)}.$$

The log-likelihood is

$$\ell(I_{i,k}) = \lambda\left(0.5\log(2\pi) + \log(\sigma_{i,k}) + \frac{1}{2\sigma_{i,k}^2}(\log(I_{i,k}) - \log(qV_{i,k}))^2\right).$$

Log-likelihood: relative abundance



Log-likelihoods: size composition

Size composition data is assumed to be multinomial distributed

$$\boldsymbol{P}_{h,i} = (P_\ell)_{h,i} = \mathcal{M}\text{ultinomial}\left(n_{h,i}, \boldsymbol{Q}_{h,i}\right)$$

Alternatively we could use

$$\boldsymbol{P}_{h,i} = (P_\ell)_{h,i} = \mathcal{D}\text{irichlet}\left(\lambda_0 n_{h,i} \boldsymbol{Q}_{h,i}\right).$$

In this context, λ_0 can be thought of as the data weight (which may be estimated in the model) and $n_{h,i}$ is the relative sample size between years.

Penalties

Natural mortality

$$\ell(M_{h,i}) = 0.5 \log(2\pi) + \log(\sigma_M) + 0.5 \frac{1}{\sigma_M^2} \sum_i \delta_i^2.$$

Random thoughts

- Include environmental indices via $a_f(E_f - \bar{E}_f)$ where a_f is the shift factor and E_f the exogenous variable
- the alternative is a more statistical approach whereby selectivity is estimated as a latent state

References

Walters, C. & Ludwig, D. (1994), 'Calculation of Bayes posterior probability distributions for key parameters', *Canadian Journal of Fisheries and Aquatic Science* **51**, 713–722.