

Bayesian biomass dynamic model for fisheries stock assessment

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1 Brief introduction to biomass dynamic models

Biomass dynamic models in fisheries have a long history of application. Because fisheries data are generally collected over discrete timesteps, the models themselves are also usually written in discrete form, with a production function $g(B_t)$, which combines recruitment, growth and natural mortality elements of the dynamics, written in terms of the current depletion x_t relative to the biomass at unexploited equilibrium K .

$$x_{t+1} = x_t + g(x_t) - H_t \quad (1)$$

where $H_t = C_t/K$ is the harvest rate. This type of model was first applied within a fisheries context by Schaefer [1, 2], who implemented a logistic production function.

$$g(x_t) = rx_t(1 - x_t) \quad (2)$$

This has two estimable parameters, usually referred to as the intrinsic rate of population growth r and the carrying capacity K . The logistic model has a number of useful reference points associated with it, which can be obtained directly from parameter estimates. These correspond to a maximum sustainable yield $MSY = rK/4$ and the associated biomass $B^{MSY} = K/2$ and harvest rate $H^{MSY} = r/2$. If we define the ratio $\phi = B^{MSY}/K = x^{MSY}$, then the logistic model specifically assumes that $\phi = 0.5$. However this is usually inconsistent with predictions made by age structured models, which are based on a stock-recruitment function that often predicts $\phi < 0.5$. It is therefore desirable to implement a biomass dynamic model that has reference points consistent with an age-structured analogue. The logistic model was first gearalised by Pella and Tomlinson [3] to allow $\phi \neq 0.5K$ by introducing a shape parameter p , and was subsequently re-paramaterised by Fletcher [4] in terms of the shape parameter n and $m = MSY$. However, both formulations of this gearalised production model have the anomalous property of predicting excessively high per capita production at low biomass levels. For the logistic model, the parameter r is consistent with the definition of intrinsic growth as defined in ecological theory [5], as the maximum rate of

increase as the biomass converges on zero (equation 3). However, for the Pella-Tomlinson-Fletcher model this is not the case.

$$r = \lim_{b \rightarrow 0} \frac{1}{b} \frac{db}{dt} \quad (3)$$

Two alternative solutions have been proposed to rectify this problem. A combined Fletcher-Schaefer hybrid model was derived by McAllister [6] to allow $\phi < 0.5$. It has a discontinuous inflection point at x^{MSY} with dynamics for values of $x < x^{MSY}$ governed by the logistic (Schaefer) model, and dynamics at higher biomass levels governed by the generalised (Fletcher) production model. This has the notable advantage of an ecologically consistent interpretation of r .

$$g(x_t) = \begin{cases} r.x_t. \left(1 - \frac{x_t}{2\phi}\right) & \text{if } x \leq \phi \\ \gamma.m.(x_t - x_t^n) & \text{if } x > \phi \end{cases} \quad (4)$$

$$\phi = \left(\frac{1}{n}\right)^{(1/(n-1))} \quad (5a)$$

$$\gamma = \frac{n^{n/(n-1)}}{n-1} \quad (5b)$$

$$m = \frac{r\phi}{4} \quad (5c)$$

An alternative model that utilises a Beverton-Holt production function was proposed by Mangel et al. [7] (equation 6).

$$g(B_t) = \frac{\alpha.B_t}{1 + \beta.B_t} - M.B_t \quad (6)$$

This model is parameterised by M and $\phi < 0.5$. Given these two inputs α can be estimated numerically as the solution to the relationship in equation 7a, and the β parameter is then obtained from equation 7b.

$$\phi = \frac{\sqrt{\frac{\alpha}{M}} - 1}{\frac{\alpha}{M} - 1} \quad (7a)$$

$$\beta = \frac{1}{K} \left(\frac{\alpha}{M} - 1 \right) \quad (7b)$$

This model predicts a similar replacement yield to the Fletcher-Schaefer hybrid model across a range of ϕ values. However the productivity per unit biomass is a different shape, being higher at low biomass levels. This difference becomes even more exaggerated at lower ϕ values.

It is informative to compare all potentially useful models at $\phi = 0.4$ (figures 1 and 2). The Fletcher model notably exaggerates the productivity at low biomass levels. The Fletcher-Schaefer hybrid model and Beverton-Holt model are similar, but only the former includes a term that can be interpreted as the intrinsic growth. This is an important consideration, since it is possible to develop informative priors for r which can greatly facilitate parameter estimation [8]. The Fletcher-Schaefer model is therefore preferred here, and implemented in the **bdm** package.

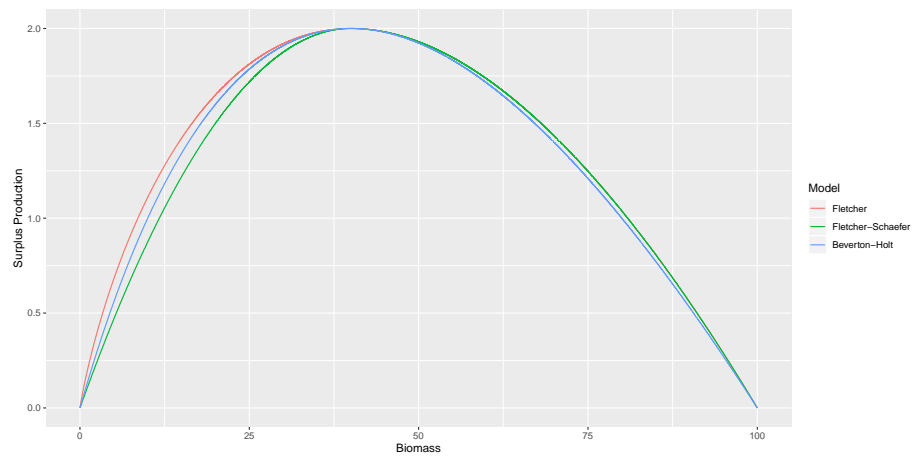


Figure 1: Production functions for different models assuming $\phi = 0.4$

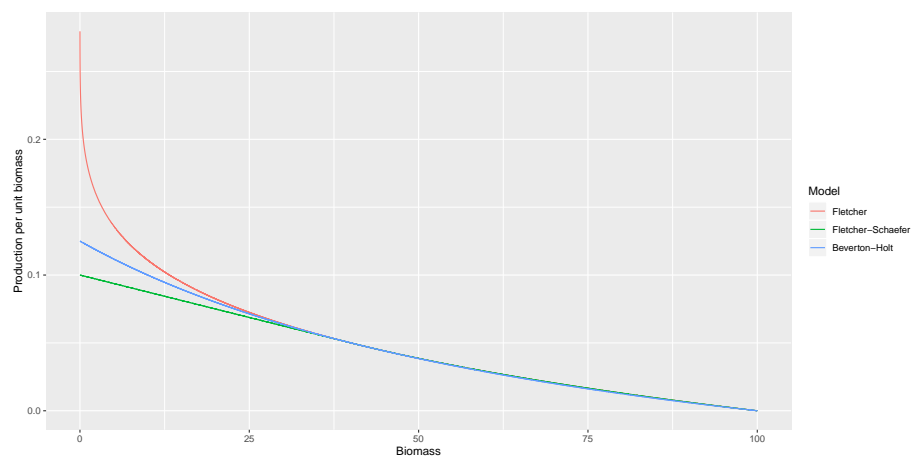


Figure 2: Growth rate per capita as a function of biomass

2 The **bdm** package

The package fits a state space biomass dynamic model using Bayesian methods, specifically the Hamiltonian MCMC implemented in the package **rstan**. To a large extent, the package is an external wrapper for **rstan**, providing functionality relevant to the intended application. The package is generalisable, meaning that any number of model formulations can be specified by the user. The default implements the Fletcher-Schaefer hybrid model mentioned above, with ϕ specified as an input value. As a default, $\phi = 0.5$ (i.e. $n = 2$), making it equivalent to the logistic model.

2.1 Estimation framework

Parameters are estimated within a Bayesian state-space framework. This re-formulates the process equation to include a time-dependent error term (the process error, ϵ^p) and a parallel observation process that relates an abundance index I to the unobserved biomass state with some degree of error (the observation error, ϵ^o), according to an estimated catchability scalar q .

$$x_{t+1} = [x_t + g(x_t) - H_t] \cdot \epsilon_t^p \quad (8a)$$

$$I_{it} = [q_i x_t] \cdot \epsilon_{it}^o \quad (8b)$$

The advantage of this class of models is that they allow both process and observation error to be represented simultaneously, which is important for effective precautionary or risk based management [9].

Parameters to be estimated in the model are therefore: r , K , q for each index, and the error terms. The large number of parameters necessitates a Bayesian approach with appropriate priors. Parametric distributional assumptions for ϵ^p and ϵ^o are required, which unfortunately cannot be estimated in an hierarchical manner with fisheries data. We assume them to follow a log-normal distribution with an expectation of one, and therefore fix values of σ_p and σ_o on input, based on a subjective measure of model fit to the data, with minimum bounds $\sigma_p \geq 0.05$ and $\sigma_o \geq 0.15$.

$$r \sim LN(\mu_r, \sigma_r^2) \quad (9a)$$

$$\ln(K) \sim U(.,.) \quad (9b)$$

$$\epsilon^p \sim LN(-\sigma_p^2/2, \sigma_p^2) \quad (9c)$$

$$\epsilon^o \sim LN(-\sigma_o^2/2, \sigma_o^2) \quad (9d)$$

The r and K parameters of the logistic model are highly correlated, and their estimation is helped through the use of an informative prior or priors. We assumed an uninformative log-uniform prior for K , but an informative log-normal prior for r . The expectation and variance for the prior on intrinsic growth, with $E[r] = \exp(\mu_r + \sigma_r^2/2)$ can be constructed from available life-history data using the function `bdm:rcalc`, which implements methods described by McAllister et al. [8].

Log-normal prior distributions for the error terms are specified to have an expectation of one, which gives an intuitive interpretation of the expected quantities.

$$E[x_{t+1}] = x_t + g(x_t) - H_t \quad (10a)$$

$$E[I_{it}] = q_i x_t \quad (10b)$$

The catchability q is estimated analytically from its maximum posterior density estimate assuming an uninformative uniform prior (i.e. $q \sim U(.,.)$).

$$\hat{q}_i = \exp \left[\frac{1}{n_t} \sum_t \{ \ln(I_{it}) - \ln(B_t) \} + \frac{\sigma_o^2}{2} \right] \quad (11)$$

If we assume that the biomass is exactly known for purposes of the estimation of \hat{q} , then $E[\ln(B_t)] = \ln(B_t)$. Since $E[\ln(I_{it})] = \ln(q_i \cdot B_t) - \sigma_o^2/2$, then $E[\ln(\hat{q}_i)] = E[\ln(q_i)]$ and $E[\hat{q}_i] = E[q_i]$ as required.

$$\begin{aligned} E[\ln(\hat{q}_i)] &= \left[\frac{1}{n_t} \sum \{ E[\ln(I_{it})] - E[\ln(B_t)] \} + \frac{\sigma_o^2}{2} \right] \\ &= \left[\frac{1}{n_t} \sum \left\{ \ln(q_i \cdot B_t) - \frac{\sigma_o^2}{2} - \ln(B_t) \right\} + \frac{\sigma_o^2}{2} \right] \\ &= \ln(q_i) \end{aligned} \quad (12)$$

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