

A Generalized Length Based Assessment Model

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Abstract

What could be better than sliced bread? Who cares!

Introduction

Statistical catch age models have several advantages over simple production type models in that age and size composition data can be used to better inform structural features such as recruitment variability, and total mortality rates. There are a number of generic age-structured models in use today, but there are very few generic size-based, or staged based models that are used in stock assessment.

In this paper we describe a generalized statistical catch-at-length model that is well suited for animals that cannot be aged, and only precise length measurements are available. The description is based on a crustaceans that undergo molting and with each subsequent molt increase in length.

Methods

The analytical details of the generalized model is summarized using tables of equations (e.g., Table 2). These tables serve two purposes: (1) to clearly provide the logical order in which calculations proceed, and (2) organization of a relatively large integrated model into a series of sub-models that represent specific components such as population dynamics, observation models, reference point calculations, fisheries dynamics, and the objective function. We first start with a description of the population dynamics under steady-state (equilibrium) conditions. Model notation and a description of symbols are provided in Table 1.

Equilibrium considerations

Parameters for the population sub model are represented by the vector Θ (T2.1 in Table 2), which consists of the natural mortality rate, average-recruitment, initial recruitment in the first year, parameters that describe the size-distribution of new recruits, and stock-recruitment parameters (see Table 1 for notation). Constraints for these model parameters

Table 1: Mathematical notation, symbols and descriptions.

Symbol	Description
<u>Index</u>	
g	group
h	sex
i	year
j	time step (years)
k	gear or fleet
l	index for length class
m	index for maturity state
o	index for shell condition.
<u>Leading Model Parameters</u>	
M	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
<u>Size schedule information</u>	
$w_{h,l}$	Mean weight-at-length l
$m_{h,l}$	Average proportion mature-at-length l

are defined in (T2.2). Assuming the molt increments are linear, growth following each molt is a parametric function with the parameters defined in Φ .

The model is based on a set of user defined size categories. We assume at any time the population consists of a vector where each component of the vector consists of a number of individuals in some size category. The size category intervals and mid points of those intervals are defined by (T2.3). Average molt increments from size category l to the next is assumed to be sex-specific, and is defined by a linear function (T2.4). The probability of transitioning from size category l to l' assumed that variation in molt increments follows a Gamma distribution (T2.5), and the size-transition matrix for each sex h is denoted as \mathbf{G}_h .

The size distribution of new recruits is assumed to follow a gamma distribution (T2.7) with the parameters α_r and β_r . The gamma distribution is scaled such that α_r is the mode of the distribution and could potentially be obtained from empirical size composition data. The vector of new recruits at each time step (T2.8) assumes a 50:50 sex ratio.

For unfished conditions that are subject only to sex-specific natural mortality M_h rates, we assume that each year members of the population grow and experience mortality. The basic assumption is that this process is a linear function of the numbers in each size category, where the categories are separated by sex to accommodate differential growth and survival rates. Survival and growth at each time step in unfished conditions is based on (T2.9), where $(\mathbf{I}_n)_{l,l'}$ is the identity matrix and M_h is a scalar. It's also possible to accommodate size-specific natural mortality rates in (T2.9) where M_h represents a vector of length-specific natural mortality rates.

Assuming a non-zero steady-state fishing mortality rate vector \mathbf{f} , the equilibrium growth and survival process is represented by (T2.10). The vector \mathbf{f}_h represents all mortality associated with fishing, including mortality associated with discards in directed and non-directed fisheries.

Assuming unit recruitment, then the growth and survivorship in unfished and fished conditions is given by the solutions to the matrix equations (T2.11) and (T2.12), respectively. The vectors \mathbf{u}_h and \mathbf{v}_h represent the unique equilibrium solution for the numbers per recruit in each size category. The total unfished numbers in each size category is defined as $R_0\mathbf{u}_h$.

The unfished spawning stock biomass is defined as the equilibrium unfished recruitment multiplied by the sum of products of survivorship per recruit, weight-at-length, and proportion mature-at-length (T2.13). The definition of spawning biomass may include only the females, or only males, or some combination thereof. To accommodate various definitions of spawning biomass the parameter λ_h , with the additional constraint $\sum_h \lambda_h = 1$, assigns the relative contribution of each sex to the spawning biomass. For example, if $\lambda = 1$ then the definition of spawning biomass is determined by a single sex. If $\lambda = 0.5$, the spawning biomass consists of an equal sex ratio.

Under steady-state conditions where the fishing mortality rate is non zero, (T2.14) defines the equilibrium spawning biomass based on the survivorship of a fished population. In this case the equilibrium recruitment \tilde{R} must be defined based on a few additional assumptions; the first of which being the form of the stock-recruitment relationship. Assuming recruitment

Table 2: Mathematical equations and notation for a steady-state length based model.

model parameters

$$\Theta = (M_h, \bar{R}, \ddot{R}, \alpha_r, \beta_r, R_0, \kappa) \quad (\text{T2.1})$$

$$M_h > 0, \bar{R} > 0, \ddot{R} > 0, \alpha_r > 0, \beta_r > 0, R_0 > 0, \kappa > 1.0 \quad (\text{T2.2})$$

$$\Phi = (\alpha_h, \beta_h, \varphi_h) \quad (\text{T2.3})$$

length-schedule information

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

$$a_{h,l} = (\alpha_h + \beta_h l) / \varphi_h \quad (\text{T2.4})$$

$$p(l, l')_h = \mathbf{G}_h = \int_l^{l+\Delta l} \frac{l^{(a_{h,l}-1)} \exp(l/\varphi_h)}{\Gamma(a_{h,l}) l^{(a_{h,l})}} dl \quad (\text{T2.5})$$

recruitment size-distribution

$$\alpha = \alpha_r / \beta_r \quad (\text{T2.6})$$

$$p(\mathbf{r}) = \int_{x-0.5\Delta x}^{x_l+0.5\Delta x} \frac{x^{(\alpha-1)} \exp(x/\beta_r)}{\Gamma(\alpha) x^\alpha} dx \quad (\text{T2.7})$$

$$\mathbf{r}_h = 0.5 p(\mathbf{r}) \ddot{R} \quad (\text{T2.8})$$

growth and survival

$$\mathbf{A}_h = \mathbf{G}_h[\exp(-M_h)(\mathbf{I}_n)_{l,\nu}] \quad (\text{T2.9})$$

$$\mathbf{B}_h = \mathbf{G}_h[\exp(-M_h - \mathbf{f}_{h,l})(\mathbf{I}_n)_{l,\nu}] \quad (\text{T2.10})$$

survivorship to length

$$\mathbf{u}_h = -(\mathbf{A}_h - (\mathbf{I}_n)_{l,\nu})^{-1} p(\mathbf{r}) \quad (\text{T2.11})$$

$$\mathbf{v}_h = -(\mathbf{B}_h - (\mathbf{I}_n)_{l,\nu})^{-1} p(\mathbf{r}) \quad (\text{T2.12})$$

steady-state conditions

$$B_0 = R_0 \sum_h \lambda_h \sum_l \mathbf{u}_{h,l} w_{h,l} m_{h,l} \quad (\text{T2.13})$$

$$\tilde{B} = \tilde{R} \sum_h \lambda_h \sum_l \mathbf{v}_{h,l} w_{h,l} m_{h,l} \quad (\text{T2.14})$$

stock-recruitment parameters

$$s_o = \kappa R_0 / B_0 \quad (\text{T2.15})$$

$$\beta = (\kappa - 1) / B_0 \quad (\text{T2.16})$$

$$\tilde{R} = \frac{s_o \phi - 1}{\beta \phi} \quad (\text{T2.17})$$

follows the familiar asymptotic function, or Beverton-Holt relationship:

$$\tilde{R} = \frac{s_o \tilde{B}}{1 + \beta \tilde{B}}, \quad (1)$$

where \tilde{B} is the equilibrium spawning biomass, s_o is the slope at the origin, and s_o/β is the asymptote of the function. The parameters of this model can be derived from the unfished recruitment R_0 and the recruitment compensation ratio κ . The slope at the origin, or s_o , is defined as (T2.16) with the additional constraint that $\kappa > 1$ for an extant population. Substituting (T2.16) into the Beverton-Holt model (1), and solving for β yields (T2.17).

Given (T2.12) is defined as the vector of individuals per recruit in a fished population, the relative reproductive potential per individual recruit is defined as the sum of products of weight-at-length, maturity-at-length and survivorship-to-length:

$$\phi = \sum_h \lambda_h \sum_l \mathbf{v}_{h,l} w_{h,l} m_{h,l}$$

The total equilibrium spawning biomass is defined as $\tilde{B} = \tilde{R}\phi$. Substituting this expression into (1) and solving for \tilde{R} results in (T2.17).

The equilibrium model defined in Table 2 is a very concise system of equations from which fisheries reference points are easily derived. The minimum amount of information that is necessary to derive SPR-based reference points is an estimate of the natural mortality rate, fisheries selectivity, the size-transition matrix (or growth based on molt increment information). These data alone are sufficient enough to calculate F_{SPR} , and the only additional requirement for B_{SPR} is to have an estimate of unfished recruitment or a specified average recruitment.

SPR-based reference points