Stock Reduction Analysis using catch at length data

Catarina Wor, Roberto Licandeo, Brett van Poorten, Carl Walters

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4 Abstract

Last thing to be written

6 1 Introduction

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Modern stock assessments typically attempt to fit population dynamics models to catch at age and catch at length data, in hopes of extracting information from these data about age/size vulnerability and fishing mortality patterns (Methot and Wetzel, 2013; Hilborn and Walters, 1992). In cases where age data are lacking, softwares like MULTIFAN-CL attempt to obtain estimates of vulnerability and fishing mortality only from size distribution data (Fournier et al., 1998). Combined with a few assumptions regarding the structure and variability in length at age, this procedure can even be used to attempt to recover information about changes in body growth patterns if there is a strong age-class signal in the length frequency data (Fournier et al., 1998). Some older assessment methods attempt to put aside the length frequency data, by converting these data to age compositions using age-from-length tables, perhaps using iterative methods to estimate proportions of fish at age for each length interval (Kimura and Chikuni, 1987). It is typical for assessment results from length-based assessment models to show substantial deviations between predicted and observed length distributions of catches, reflecting both sampling variation in the length composition data and incorrect assumptions about stability of both growth and vulnerability patterns.

Here we suggest an alternative approach to assessment modeling that begins by assuming that the assessment model should exactly reproduce the observed catch at length distribution. This is similar to the classical assumption in virtual population analysis that reconstructed numbers at age should exactly match observed catch at age data, or the suggestion by Schnute (1994) that statistical catch at age models might best be run in a "conditioned on catch" format by subtracting observed catches at age from modeled numbers at age in estima-

- tion of numbers at age over time. The suggested approach may have two key advantages over statistical catch at age and/or catch at length models: (1) it does not require estimation of age or size vulnerability schedules, and (2) catch at length data are commonly available for every year, even when age composition sampling has not been conducted.
- We demonstrate the performance of this model with a simulation-evaluation analysis and apply it to real fisheries data from the Chilean jack mackerel and Pacific Hake fisheries.

¹ 2 Methods

In this section we describe the stock reduction analysis with catch at length data, describe the simulation analysis and scenarios used to test the model and provide a description of the real data used to illustrate the model applicability.

2.1 Stock reduction analysis with catch at length data

The stock reduction analysis described here starts by calculating, the proportions of individual at length for each age class (Table 1. The calculation of such proportions relies on three main assumptions regarding the distribution of length at age: (1) The mean length at age follows a von Bertalanffy growth curve (eq.T1.5), (2)
The length at age is normally distributed (eqs. T1.2-T1.4) and (3) The standard deviations of the length at age distributions is given by the product of the mean length at age and a constant CV (eq.T1.6).

The proportions of length at age is used to convert the length based quantities into age based quantities which are used to propagate the age structured population dynamics forward (Table 2). We assume that recruitment follows a Beverton & Holt type recruitment curve (eq. T2.1), that harvesting occurs over a short, discrete season in each time step (year or shorter time period) and that natural survival rate is stable over time (eqs. T2.1-T2.5). Differences in the population dynamics equations in the initial year as well as incidence functions are shown in Table 3.

The model estimates three main parameters: the average unexploited recruitment R_0 , the recruitment compensation ratio k_{rec} and the recruitment in the initial year R_{init} . In addition, the recruitment deviations are estimated for all cohorts observed in the model, that is, the number of recruitment deviations is equal to the number of years in the time series plus the number of age classes greater that recruitment age. The parameters of the model are estimated with two likelihood components: Index of abundance and Recruitment deviations, both are assumed to be lognormally distributed with fixed variances.

 $P_{l|a}$ = Matrix of proportions of lengh at age

 $z1_{a,l}$ = Normalized Z score for lower limit length bins

 $z2_{a,l}$ = Normalized Z score for upper limit length bins

 $b1_I$ = Lower limit of length bins

 $b2_l$ = upper limit of length bins

 \bar{L}_a = Mean length at age

 σ_{L_a} = Standard deviation of lengh at age

 L_{inf} = Maximum average length

 $k = \text{rate of approach to } L_{inf}$

 t_o = Theoretical time in which length of individuals is zero

cvL = Coefficient of variation for length curve (T1.1)

Age-schedule information

$$P_{l|a} = \int_{z1_{al}}^{z2_{a,l}} \mathcal{N}(0,1) \tag{T1.2}$$

$$z1_{a,l} = \frac{b1_l - \bar{L}_a}{\sigma_{L_a}} \tag{T1.3}$$

$$z2_{a,l} = \frac{b2_l - \bar{L}_a}{\sigma_{L_a}} \tag{T1.4}$$

$$\bar{L}_a = L_{inf} \cdot (1 - \exp^{(-k \cdot (a - t_o))})$$
(T1.5)

$$\sigma_{L_a} = \bar{L}_a \cdot cvL \tag{T1.6}$$

 $N_{a,t}$ = Numbers of fish at age and time

 SB_t = Spawning biomass at time t

 a_{rec}, b_{rec} = Beverton & Holt stock recruitment parameters

wt = Normally distributed recruitment deviations

 S_a = Survival rate at age

 $U_{a,t}$ = Exploitation rate at age and time

 $U_{l,t}$ = Exploitation rate at length and time

 $C_{l,t}$ = Catch at length and time

 $N_{l,t}$ = Numbers at length and time

syr = Initial year of data

 a_o = Age of recruitment

Age-schedule information

$$N_{a,t>syr} = \begin{cases} \frac{a_{rec} \cdot SB_{t-1}}{1+b_{rec} \cdot SB_{t-1}} \cdot e^{wt}, & a = a_o \\ N_{a-1,t-1} \cdot S_{a-1} \cdot (1 - U_{a-1,t-1}), & 1 < a < A \\ \frac{N_{a-1,t-1} \cdot S_{a-1} \cdot (1 - U_{a-1,t-1})}{1 - S_A \cdot 1 - Ua,t}, & a = A \end{cases}$$
 (T2.1)

$$U_{a,t} = \sum_{a} \left(P_{l|a} \cdot U_{l,t} \right) \tag{T2.2}$$

$$U_{l,t} = \frac{C_{l,t}}{N_{l,t}}$$
 (T2.3)

$$N_{l,t} = \sum_{a} (P_{l|a} \cdot N_{a,t}) \tag{T2.4}$$

$$SB_t = \sum_{a} (fec_a \cdot w_a \cdot N_{a,t})$$
 (T2.5)

Table 3: Population dynamics: initial year and incidence functions

 $N_{a,t}$ = Numbers of fish at age and time

syr = Initial year of data

 a_o = Age of recruitment

 a_{rec}, b_{rec} = Beverton & Holt stock recruitment parameters

 ϕ_e = Unfished average spawning biomass per recruit

Initial year

$$N_{a=a_o,t=syr} = R_{init} * \cdot e^{wt}$$
 (T3.1)

$$a_{rec} = \frac{k_{rec}}{\phi_e} \tag{T3.2}$$

$$b_{rec} = \frac{k_{rec} - 1}{R_o \cdot \phi_e} \tag{T3.3}$$

$$\phi_e = \sum_a lx_a \tag{T3.4}$$

$$lx_{a} = \begin{cases} 1, & a = a_{o} \\ lx_{a-1} \cdot S_{a-1}, & 1 < a < A \\ \frac{lx_{a-1} \cdot S_{a-1}}{1 - S_{A}}, & a = A \end{cases}$$
 (T3.5)

Table 4: Population dynamics: changes in operating model

 $U_{l,t}$ = Exploitation rate at length and time

 $sel_{l,t}$ = fishing selectivity at length and time

 U_t = annual maximum exploitation rate

 $C_{l,t}$ = Catch at length and time

 $N_{l,t}$ = Numbers at length and time

Operating model

$$U_{l,t} = U_t \cdot sel_{l,t} \tag{T4.1}$$

$$C_{l,t} = N_{l,t} \cdot U_{l,t} \cdot P_{l|a} \tag{T4.2}$$

$$sel_{l,t} = \frac{1}{1-g} \cdot \left(\frac{1-g}{g}\right)^g \cdot \frac{e^{a \cdot g \cdot (b-l)}}{1+e^{a \cdot (b-l)}}$$
(T4.3)

In order to perform a simulation evaluation of the length-SRA under various scenarios we used the same model dynamics described in Table 2 as an operating model. However we modified the model population dynamics to include time varying selectivity and a maximum annual exploitation rate (eq. T4.1) as well as observation and process errors. Selectivity in the operating model was computed with the three parameter selectivity equation described by Thompson (1994) (eq. T4.3). The observation error in the operating model included lognormal error in the index of abundance and logistic multivariate error in the catch numbers at length. Recruitment deviations were assumed to be lognormally distributed.

2.2 Simulation evaluation scenarios

We tested a total of six different scenarios in the simulation evaluation runs. We tested three different historical exploitation rate trajectories: contrast, one way trip and U ramp. In the contrast scenario the exploitation rate(U) starts low and increases up to $U > U_{msy}$ and then decreases until $U = U_{msy}$. In the one way trip scenario U increased through time until $U = 2 \cdot U_{msy}$. In the U ramp scenario, U increases steadily until $U = U_{msy}$ and remains constant. In addition to the exploitation rate scenarios, we considered two selectivity scenarios: constant and time varying selectivity. In the constant selectivity scenario, selectivity was assumed to follow a

- sigmoid shape. In the time varying selectivity scenario, the selectivity curve was assumed to vary every year,
- progressively changing form a dome shaped curve to sigmoid and back to dome shaped.
- All simulation runs had 30 years of data and we used 200 simulation runs for each scenario.

70 2.3 Real data examples

- Two species were chosen to illustrate the application of the model to real datasets: Chilean jack mackerel and Pacific hake.
- Have to come up with good justification for these species. Pacific hake is migratory and shows spasmodic recruitment episodes

75 **Results**

3.1 Simulation-evaluation

and simulated data

78 3.2 Real data examples

show figures with real

80 4 Discussion

- Does the model work?
- assumption regarding Umsy -; changes with selectivity

33 References

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