

Stock Reduction Analysis using catch at length data

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Abstract

Last thing to be written

1 Introduction

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 (e.g. Shirippa and Goodyear, ref.). 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 (ref) 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 estimation

25 of numbers at age over time. The suggested approach may have two key advantages over statistical catch at age
26 and/or catch at length models: (1) it does not require estimation of age or size vulnerability schedules, and (2)
27 catch at length data are commonly available for every year, even when age composition sampling has not been
28 conducted.

29 We demonstrate the performance of this model with a simulation-evaluation analysis and apply it to real
30 fisheries data from the Chilean jack mackerel and Pacific Hake fisheries.

31 **2 Methods**

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

35 **2.1 Stock reduction analysis with catch at length data**

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

41 The proportions of length at age is used to convert the length based quantities into age based quantities
42 which are used to propagate the age structured population dynamics forward. We assume that recruitment
43 follows a Beverton and Holt type recruitment curve, that harvesting occurs over a short, discrete season in each
44 time step (year or shorter time period) and that natural survival rate is stable over time (Table 2)

45 The model estimates three main parameters: the average unexploited recruitment R_0 , the recruitment com-
46 pensation ratio k_{rec} and the recruitment in the initial year R_{init} . In addition, the recruitment deviations are
47 estimated for all cohorts observed in the model, that is, the number of recruitment deviations is equal to the
48 number of years in the time series plus the number of ages classes greater than recruitment age. The parameters
49 of the model are estimated with two likelihood components: Index of abundance and Recruitment deviations

Table 1: Age at Length

Variable definition	
$P_{l a}$	Matrix of proportions of length at age
$z1_{a,l}$	Normalized Z score for lower limit length bins
$z2_{a,l}$	Normalized Z score for upper limit length bins
$b1_l$	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 length at age
L_{inf}	Maximum average length
k	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	
$P_{l a} = \int_{z1_{a,l}}^{z2_{a,l}} \mathcal{N}(0, 1)$	(T1.2)
$z1_{a,l} = \frac{b1_l - \bar{L}_a}{\sigma_{L_a}}$	(T1.3)
$z2_{a,l} = \frac{b2_l - \bar{L}_a}{\sigma_{L_a}}$	(T1.4)
$\bar{L}_a = L_{inf} \cdot (1 - \exp^{(-k \cdot (a - t_o))})$	(T1.5)
$\sigma_{L_a} = \bar{L}_a \cdot cvL$	(T1.6)

Table 2: Population dynamics

Variable definition	
$N_{a,t}$ = Numbers of fish at age and time	
Age-schedule information	
$N_{a,t} = \begin{cases} \frac{a \cdot SB_{t-1}}{1+b \cdot SB_{t-1}} \cdot \exp(wt), & a = 1 \\ N_{a-1,t-1} \cdot S_a \cdot (1 - U_{a-1,t-1}), & 1 < a < A \\ \frac{N_{a-1,t-1} \cdot S_a \cdot (1 - U_{a-1,t-1})}{1 - S_a \cdot 1 - U_{a,t}}, & a = A \end{cases} \quad (\text{T2.1})$	
$U_{a,t} = \sum_a (P_{l a} \cdot U_{l,t})$	(T2.2)
$U_{l,t} = \frac{C_{l,t}}{N_{l,t}}$	(T2.3)
$N_{l,t} = \sum_a (P_{l a} \cdot N_{a,t})$	(T2.4)

50 **2.2 Simulation routines and scenarios**

51 We tested the model performance under three exploitation rates trajectories. The first exploitation rate
52 trajectory is the contrast trajectory. U is

53 In order to test the performance of the model under a known Three In order to test the performance of the
54 model under a range of known scenarios three exploitation rates trajectories and two selectivity scenarios

55 30 years of data and 200 simulation runs for each scenario.

56 **2.3 Real data examples**

57 Two species were chosen to illustrate the application of the model to real datasets: Chilean jack mackerel
58 and Pacific Hake

59 **3 Results**

60 **3.1 Simulation-evaluation**

61 and simulated data

62 **3.2 Real data examples**

63 show figures with real

64 **4 Discussion**

65 Does the model work?

66 assumption regarding U_{msy} changes with selectivity

References

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