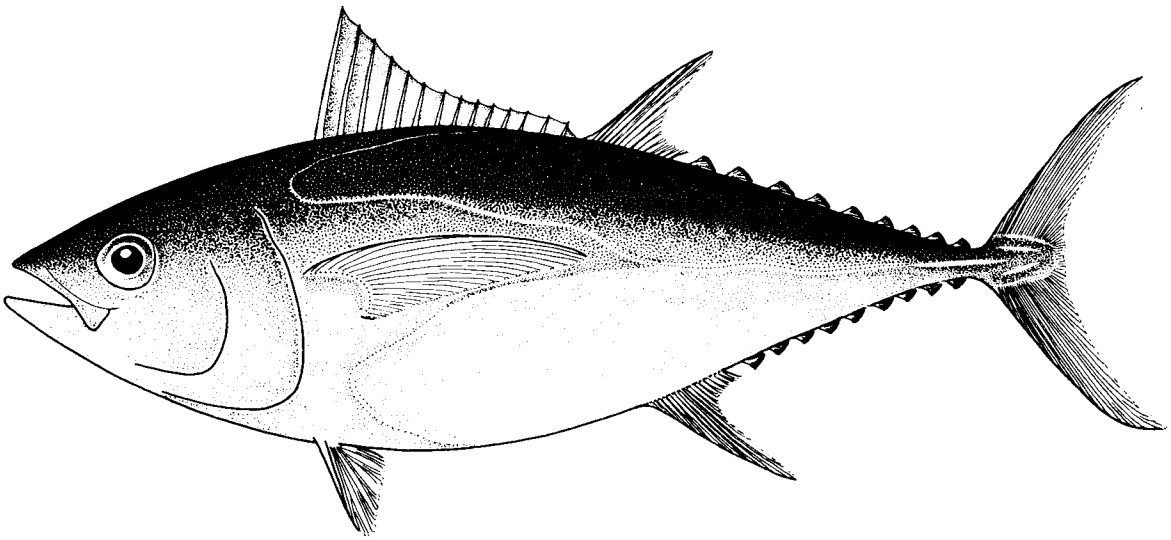
SCTB15 Working Paper

MWG-2

Recent Enhancements to the MULTIFAN-CL Software



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1 Introduction

The length-based, age-structured stock assessment known as MULTIFAN-CL is currently used for tuna and other pelagic stock assessments by the SPC Oceanic Fisheries Programme (skipjack, yellowfin, bigeye and South Pacific albacore tunas in the western and central Pacific), the National Marine Fisheries Service (NMFS) Honolulu Laboratory (blue shark, blue marlin and swordfish), the NMFS La Jolla Laboratory (North Pacific albacore) and the Japan National Research Institute of Far Seas Fisheries (what). Technical documentation of most of the model features is provided in Hampton and Fournier (2001a). Some additional information on recent developments to the software were provided at the MWG session at SCTB14 (Hampton and Fournier 2001b). This paper briefly outlines developments to the software since SCTB14.

2 MULTIFAN-CL developments since SCTB14

2.1 Reference point analysis

A reference point analysis has been added to the yield analysis section of the model. The reference points that have been chosen are the total equilibrium biomass at MSY (B_{MSY}^{total}), the adult equilibrium biomass at MSY (B_{MSY}^{adult}) and the aggregate fishing mortality MSY (F_{MSY}). To summarise, the series of steps involved is as follows:

1. Estimate population model parameters, including the parameters of a Beverton and Holt stock-recruitment relationship (SRR). Assume that the estimated parameters of the SRR (a and b) can be used to describe the relationship between equilibrium recruitment ($\tilde{R}$) and equilibrium spawning biomass ($\tilde{B}^s$):

$$\tilde{R} = \frac{a\tilde{B}^s}{b + \tilde{B}^s} \tag{1}$$

2. Compute a "base" age-specific fishing mortality vector, $\overline{F}_a$, various multiples of which are assumed to be maintained into the future; normally, the base is computed as the average over some recent period of time.

3. For various multipliers (x) of $\overline{F}_a$ compute the equilibrium total biomass ($\tilde{B}^t$) and equilibrium spawning biomass. Let

$$\tilde{B}^s(x) = \tilde{R}(x) f^s(x) \tag{2}$$

where

$$f^s(x) = \sum_{a=1}^{\infty} \exp\left[-\sum_{a'=1}^{a-1} \left(M_{a'} + x\overline{F}_{a'} \right) \right] w_a m_a \ , \tag{3}$$

M_a is the natural mortality rate at age a, w_a is mean weight at age a and m_a is the proportion spawning at age a. With all other parameters fixed, a value of $f^s(x)$ can be determined for any value of x. From substitution of (2) into (1), we can then obtain

$$\tilde{B}^s(x) = a f^s(x) - b \tag{4}$$

which specifies the equilibrium spawning biomass associated with any fishing mortality multiplier x. $\tilde{R}(x)$ may then be determined from a rearrangement of terms in (2). Similarly, the

total equilibrium biomass associated with the fishing mortality multiplier x may then be determined by:

$$\tilde{B}^t(x) = \tilde{R}(x) f^t(x) \tag{5}$$

where

$$f^t(x) = \sum_{a=1}^{\infty} \exp\left[-\sum_{a'=1}^{a-1} \left(M_{a'} + x\bar{F}_{a'} \right) \right] w_a \ . \tag{6}$$

4. Compute the equilibrium yield, $\tilde{Y}(x)$ as a function of the fishing mortality multiplier x:

$$\tilde{Y}(x) = \tilde{R}(x) \sum_{a=1}^{\infty} \left\{ \frac{x\bar{F}_a}{x\bar{F}_a + M} \left(1 - e^{-x\bar{F}_a - M_a} \right) \exp\left[-\sum_{a'=1}^{a-1} \left(M_{a'} + x\bar{F}_{a'} \right) \right] w_a \right\} \tag{7}$$

Let z be the value of x that maximizes $\tilde{Y}(x)$. The MSY is then given by $\tilde{Y}(z)$.

5. The reference points of interest are:

$$B_{MSY}^{adult} = \tilde{B}^s(z)$$

$$B_{MSY}^{total} = \tilde{B}^t(z)$$

$$F_{MSY} = \frac{\tilde{Y}(z)}{\tilde{B}^t(z)}$$

6. Compare the actual estimated biomass and fishing mortality levels at time t with these reference points. This is done by computing the ratios $B_t^{total} / B_{MSY}^{total}$, $B_t^{adult} / B_{MSY}^{adult}$, F_t / F_{MSY} and their 95% confidence intervals and comparing them with 1.0. Values of F_t / F_{MSY} significantly greater than 1.0 would indicate overfishing, while values of $B_t^{total} / B_{MSY}^{total}$ and/or $B_t^{adult} / B_{MSY}^{adult}$ of less than 1.0 would indicate an overfished state.

2.2 Incorporation of weight-frequency data

At SCTB14, weight-frequency data from the longline fishery unloading in Guam were presented by Kikkawa and Cushing (2001). These data appeared to be extremely informative with respect to age structure and growth. A search of OFP databases and consultations with various national agencies revealed that there are substantial weight-frequency data available for longline fisheries for yellowfin and bigeye tuna. These data appeared to be similarly informative as the Guam data and in many cases the sample sizes represented a very large proportion of the total catch (approaching 100% in the case of the Australian east-coast longline fishery). It was therefore decided to incorporate weight-frequency data into MULTIFAN-CL to take advantage of the availability of these data. This required the following changes/additions to the software:

1. The input data file ("frq" file) structure was changed to allow the specification of the structure of the weight-frequency data and to include a weight-frequency data record, if available, for each fishery record.
2. The MULTIFAN-CL model is age-structured at the computational level but the probability distribution of lengths for each age class is also computed to allow the model to be fit to the length-frequency data. We opted to specify the probability distribution of weight-at-age as a deterministic function of the length-at-age. The addition of weight-frequency data to the model therefore did not involve the estimation of additional parameters. The integration of the weight

distribution was done using the same intervals specified in the weight-frequency data. A weight-length relationship ($W = aL^b$) was used to compute the weight distribution from the length distribution. The weight-length parameters a and b must be specified.

3. The likelihood function for the weight data is identical to that for the length data. However, we added some flexibility in specifying the "effective" sample size for both the length and weight data. Previously, the "effective" sample size (which influences the variance term in the likelihood function) was the actual sample size up to a maximum of 1,000 divided by 10. This was done to acknowledge the likelihood that real size samples are unlikely to be truly random as assumed by the statistical model. However, some of the weight samples represent a very high proportion of the total catch, resulting in an increased likelihood of the sample being random (or representative). In these cases, it would be appropriate for the actual sample size to more accurately reflect the effective sample size. We have therefore added more flexibility to both the weight and length likelihood functions by allowing the relationship between actual and effective sample size to be specified on a fishery by fishery basis.

4. The Java-based MULTIFAN-CL viewer was updated to generate observed and predicted weight frequencies. A capability to read the data file (to display the observed length and weight data only) was also added to the viewer.

2.3 Cobb-Douglass catchability models

As part of a bioeconomic modelling project, we were asked to test the hypotheses that:

(a) catchability is independent of the level of effort, against the alternative that the level of effort impacts catchability through, for example, information sharing (positive impact) or crowding (negative impact)

(b) catchability is independent of stock size, against the alternative that stock size impacts catchability (the notion of an underlying population that "feeds" surface schools which would enable purse seine CPUE to remain relatively constant as the total population declined)

This was done as follows:

(a) $\ln(F) = \ln(s) + \ln(q) + a\ \ln(e)$, where F is fishing mortality, s is selectivity, q is catchability, e is fishing effort and a is the parameter. This effect can be grouped across fisheries, in which case an index of relative grouped effort is used. Estimates of a significantly different to 1 would provide evidence for the alternative hypothesis over the null hypothesis.

(b) $\ln(F) = \ln(s) + \ln(q) + \ln(e) + b\ \ln(B)$, where B is the biomass index and b is the parameter. This effect can also be grouped across fisheries if desired. Estimates of b significantly different to 0 would provide evidence for the alternative hypothesis over the null hypothesis.

2.4 Seasonal and time-series movement

Currently, movement coefficients are constant over time. We are currently (at the time of writing) incorporating structure to allow seasonal variation in movement for each set of coefficients. There is some indication in the data for South Pacific albacore that such seasonality could be important.

Various analyses have suggested that large-scale ENSO-type oceanographic variation influences the distribution and movement of tunas. We therefore plan to introduce structure into the model to allow movement coefficients to vary over time according to an environmental correlate.

3 References

Hampton, J., and Fournier, D.A. 2001a. A spatially-disaggregated, length-based, age-structured population model of yellowfin tuna (*Thunnus albacares*) in the western and central Pacific Ocean. *Mar. Freshw. Res.* **52**:937–963.

Hampton, J., and Fournier, D.A. 2001b. Recent enhancements to the MULTIFAN-CL software. Working Paper MWG-1, SCTB 14, 9–16 August 2001, Noumea, New Caledonia.

Kikkawa, B., and Cushing, J. 2001. Variations in growth and mortality of bigeye tuna (*Thunnus obesus*) in the equatorial western Pacific Ocean. Working Paper BET-2, SCTB 14, 9-16 August 2001, Noumea, New Caledonia.