

APPLICATION OF A SIZE-STRUCTURED VPA TO BLUEFIN TUNA (*THUNNUS THYNNUS*)

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SUMMARY

A size-structured version of virtual population analysis for use with bluefin tuna (*Thunnus thynnus*) is described, and some advantages and disadvantages relative to the age-structured approach are discussed. A formulation is provided for using catch rate indices to tune the size-structured VPA.

RESUMÉ

Une version structurée par taille de la VPA destinée à être utilisée pour le thon rouge (*Thunnus thynnus*) est décrite ici, et quelques avantages et inconvénients concernant l'approche structurée par âge sont soupesés. Une formule est fournie pour utiliser les indices du taux de capture pour ajuster la VPA structurée par taille.

RESUMEN

Se describe una versión estructurada por talla del Análisis de Población Virtual, para su aplicación al atún rojo (*Thunnus thynnus*), y se discuten algunas de las ventajas e inconvenientes del enfoque de estructuración por edad. Se facilita una fórmula para usar índices de tasa de capturas en el ajuste del VPA estructurado por edad.

INTRODUCTION

Age-structured VPA's have been the main basis for SCRS assessment of the bluefin tuna in recent years. Records of catches by size are converted to estimates of catch by age using techniques such as age-slicing. In this paper, a formulation is proposed for a size-structured VPA which is able to make use of catch data by size directly, without pre-converting it to age. The approach taken is that developed for the size-structured simulation of sperm whale populations (Cooke de la Mare and Beddington, 1983). This paper outlines an adaptation for application to bluefin tuna.

METHODS

Stock simulation by size

The stock simulation is structured in three dimensions: time (by year), age (by year), and size. The choice of resolution for the size class structure depends both on the growth curve of the species and on the resolution of the catch at size data. If the catch at size data are grouped into length classes, it is appropriate to use these same classes for the simulation model. Otherwise, about 20-30 classes can be defined. The size classes should be contiguous and non-overlapping, but need not represent equal length increments. The highest size class should be a plus group (sink class).

In the absence of mortality, there is assumed to be an underlying distribution of size within each age class: U_{ij} is the proportion of age class i that falls within size class j . In the absence of more specific information, the following simple model for the U_{ij} is suggested: the mean size at each age is given by a von Bertalanffy curve, while the distribution of size in each age class is normal with constant variance. The entries in each U_{ij} cell are then calculated by taking the appropriate slice of the normal distribution:

$$\begin{aligned} U_{ij} &= \Phi((s_{j+1} - \mu_i)/\sigma) - \Phi((s_j - \mu_i)/\sigma) \\ U_{ij} &= 1 - \Phi((s_j - \mu_i)/\sigma) \end{aligned} \quad (1)$$

where Φ is the cumulative Normal function, s_j is the size at the boundary of size classes $j-1$ and j , μ_i is the mean size at age i given by the growth curve, and σ is the standard deviation of size at age. s_0 is the minimum size of fish included in the model. J is the index of the maximum size class (the sink class). If part of an age class is below this size, then the U_{ij} for that age class will sum to less than unity.

We need to calculate the array G_{ijk} which gives the proportion of fish in age-size cell (i,j) which will grow into size class k at age $i+1$. For this purpose, an additional assumption is required. We assume that for an two fish of the same age, the larger fish of the two will remain the larger in the following year: no crossovers in individual growth curves are allowed. This implies the following recursive formulae for the G_{ijk} :

$$G_{ijk} = \min \left\{ 1 - \sum_{l=k+1}^J G_{ijl}, \left[U_{i+1,k} - \sum_{l=j+1}^J U_{il} G_{ilk} \right] / U_{ij} \right\}$$

(For the sink age class, i_{\max} , the $i+1$ in the second term is replaced by i .) For each i , the G_{ijk} can be calculated recursively in descending order of J , and, within each J , in descending order of k .

Let N_{ijt} be the beginning-of-year number of fish in the stock of age i in size class j in year t . For the zeroth age class, the numbers are given by:

$$N_{0,j,t} = R_t U_{0,j}$$

where R_t is the recruitment (at age zero) in year t . For the zeroth length class, the numbers are given by:

$$N_{1,0,t} = R_{t-1} \exp(-iM_0) U_{1,0}$$

where M_0 is the natural mortality rate for fish below size s_0 .

The remaining cells of the N_{ijt} array are calculated as follows:

$$N_{i+1,k,t+1} = \sum_j G_{jkk} [N_{ijt} \exp(-M_j) - C_{ijt} \exp(-\frac{1}{2}M_j)]$$

where M_j is the natural mortality rate for size class j , and C_{ijt} is the catch of age/size class i,j in year t . The formula assigns half the natural mortality to the pre-catch period and half to the post catch period, which approximates quite closely to the continuous-time version. The obvious adjustment to the formula is made for the sink age class.

For full generality, natural mortality could have been expressed as M_{ijt} , but in practice either a single value of M will be used, or possibly a few size-specific values, based on tagging or predation information.

The catches C_{ijt} are calculated from the recorded catch at size on the assumption that, within a size class, the fishing mortality rate is independent of age:

$$C_{ijt} = C_{jt} N_{ijt} / \sum_l N_{ljt}$$

where C_{jt} is the recorded catch of size class j .

Usually the model will be employed in cases where the stock simulation is repeated many times as part of an automatic search to find a simulation which gives the best fit to a set of abundance data. In this case it is not appropriate to abort a simulation completely when a single size class becomes extinct in the simulation. In practice the best results are obtained by reallocating the catches that could not be removed to other size classes, and attaching a penalty for this to the residual function. Such reallocations should not normally be necessary in the final simulation that is found by the parameter search.

Linkage to abundance indices

If an abundance index is deemed to refer to a particular set of size classes, then the abundance in those classes can be summed during the simulation for calculation of the predicted abundance for that index in each year which is then used to calculate the contribution of that index to the overall residual function (see, for example, SCRS/95/77).

If the abundance index is the catch rate for a fishery which takes a range of sizes according to a size-specific selectivity pattern which is unknown but assumed constant over time, then the predicted abundance for that fishery can be calculated in the stock simulation context as follows.

Let c_{jt} be the catch of size class j from that fishery in year t . (We use a small c to indicate that it is not the total catch from the stock). For each stock simulation, the selectivity pattern, conditional on that simulation is estimated. Let S_j be the size-specific selectivity for size class j . The exact formula depends on the assumptions made about the probability distribution of catches by size. With a Poisson distribution, the maximum likelihood estimates of S_j are those which match the expected total catch in each size class with the observed:

$$\begin{aligned} \sum_t c_{jt} &= \sum_t S_j f_t A_{jt} && \text{for each } j \\ \sum_j c_{jt} &= \sum_j S_j f_t A_{jt} && \text{for each } t \end{aligned}$$

where A_{jt} is the mid-year abundance of size class j in year t in the simulation, and the f_t are nuisance parameters representing the fishing mortality for that fishery by year. These equations are solved typically in 3-5 iterations. A_{jt} is given by:

$$A_{jt} = \sum_i [N_{ijt} \exp(-\frac{1}{2}M_j) - \frac{1}{2}C_{ijt}]$$

The predicted abundance for the fishery in year t is then given by:

$$P_t = \sum_j S_j A_{jt}$$

Alternatively, the analysis of the fishery data can include a size/year interaction term, to yield an array of standardised catch rates by size and year. This can be compared with the N_{jt} directly, using the information matrix of the abundance array.

DISCUSSION

The size-structured simulation model is one step nearer to the original data than the usual age-structured approach, which may be of benefit. It takes account of individual variability in size by age. In its current formulation, the model does not allow growth rates to vary over time, although this could be included in principle.

A consequence of the model structure is that fishing is predicted to change not only the size structure of the population but also the size distribution within each age class. The apparent mean size at age is therefore predicted to change, although not necessarily by much. To be fully consistent, one should not use an estimate of the growth curve from recent data directly as input to the size-based simulation. Instead, the parameters of the size distribution model should be chosen which give the best-fitting predictions for the apparent growth curve in the years in which the growth curve data were collected. If the predicted change in apparent growth curve is small, this issue can be neglected.

REFERENCES

Cooke, J.G., de la Mare, W.K. and Beddington, J.R. 1983. An extension of the sperm whale models for the simulation of the male population by length and age. *Rep. int. Whal. Commn* 33:731-3.