

**Not to be cited without permission of the author(s)**

*New Zealand Fisheries Assessment Research Document 93/12*

**The accuracy of an estimate of natural mortality for orange roughy**

**I. J. Doonan  
MAF Fisheries Greta Point  
P.O. Box 297  
Wellington**

**August 1993**

**MAF Fisheries, N.Z. Ministry of Agriculture and Fisheries**

**This series documents the scientific basis for stock assessments and fisheries management advice in New Zealand. It addresses the issues of the day in the current legislative context and in the time frames required. The documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.**

## The accuracy of an estimate of natural mortality for orange roughy

I.J. Doonan

### EXECUTIVE SUMMARY

1. Punt proposed a method to correct the estimate of natural mortality made last year because it used data that was sampled non-randomly. He reported a corrected value of 0.045, an increase of 0.005.
2. This corrected estimate was insensitive to changes in the value of a single parameter, but was sensitive to setting two or three parameters simultaneously to values that were more consistent with the data.
3. Natural mortality was re-estimated using parameter values that both MAF Fisheries and FIB consultants agreed on. However, the analysis shows that natural mortality is somewhere between 0.030 and 0.055; it cannot be chosen any more exactly. Hence, the status quo estimate, 0.04, is as valid as any.
4. The data suggest that natural mortality is not constant for all ages. An extension that covers this is proposed and is estimated for a restricted case.

### 1. INTRODUCTION

In last year's stock assessment of orange roughy for ORH 3B, natural mortality ( $M$ ) was assumed to be 0.04 (Francis et al. 1992). The data on which this figure was based came from an unfished Australian stock (Smith & Robertson 1991) which, unfortunately, was not sampled randomly.

Punt (MS) showed that, in general, the way that they sampled this stock caused bias. The simulation method he proposed to correct it gave a corrected  $M$  of about 0.045, an increase of 0.005.

The obvious question is: is Punt's method sufficiently accurate to pick a difference of 0.005? Punt knew some of the parameters roughly, and assigned them probability distributions instead of just one value. While this acknowledges the uncertainty of the parameters, the distributions are largely subjective. How would small changes to them alter the estimate of  $M$ ? Other parameters had values inconsistent with the data, e.g., he used known growth parameters from New Zealand instead of those estimated from the (Australian) data. This was investigated with a sensitivity analysis.

Re-estimation of  $M$  using Punt's method, but with parameter values agreed to by both MAF Fisheries and the FIB consultants, showed an inconsistency between the corrected values of  $M$  obtained from different estimators, i.e., between estimators based on the tail of the age distribution and an estimator based on the whole distribution. This inconsistency was resolved by including an extra source of mortality for older fish, which was estimated for a restricted case.

## 2. DATA AND METHODS

The data, lengths and counts of sectioned otoliths of Australian orange roughy, are shown in the bottom graph of figure 2 in Smith & Robertson (1991) (Figure 1). For this study, I digitised the points on this graph for lengths greater than about 25 cm (Figure 2) as these were generally well separated, whereas those below 25 cm were crowded, with many points overlapping.

The estimation method follows that of Punt (MS). Briefly, a model is specified which mimics the interaction of the non-random sampling on the age distribution in the sample. The parameters used are given in Table 1. Some parameters were made into random variables and for each simulation their values were drawn at random. This incorporates uncertainty about the parameter values into the analysis. To correct for the non-randomness, a sample of lengths was drawn from a distribution (LDistn) that reflected the non-random way sampling took place. Punt used a uniform distribution for LDistn as, by eye, this approximated the distribution of lengths in figure 2 of Smith & Robertson (1991) (Figure 1).

In a single simulation, a trial  $M$  is specified, then a series of parameter values is simulated, which, in turn, are used to generate a population age structure and a set of age distributions for each length class. A length sample is then drawn from the distribution, LDistn. Ages are drawn for these lengths from the appropriate age-for-length distribution, after which reading errors are added on. These ages are used to estimate a raw  $M$  which is the simulated equivalent of the original (biased) estimate. The latter is based on the real sample data and is referred to in this report as the "sample raw  $M$ ". By repeating the simulation hundreds of times, an approximate likelihood value is built up for the sample raw  $M$  if the trial  $M$  is the true one. The more simulations that are done, the closer this gets to the true likelihood.

The sample raw  $M$  is, in general, biased, but it can be corrected by finding the trial  $M$  with the maximum likelihood, which then becomes the corrected  $M$  estimate. The likelihoods were not found directly. Instead, a value proportional to it was calculated, i.e., the fraction of runs in a simulation that estimated a raw  $M$  to be 'close' to the sample raw  $M$ . A simulated estimate was 'close' if it was within 0.004 of the sample raw  $M$ .

### 2.1 Sensitivity

The base case for the sensitivity analysis is the set of parameter values (Table 1) that Punt used to estimate his corrected  $M$ . The software was also checked by reproducing, approximately, Punt's results (Figure 3).

Punt used three estimators for raw  $M$ , but I use only one, H&L, the estimator of Hoenig & Lawing (1983) which uses the sample size and the three largest ages in the sample.

Changes in parameter values (Table 1) tested the sensitivity of the method (e.g., for the distribution of the coefficient of variation in the reading error,  $\sigma_e$ , the upper bound was decreased from 0.20 to 0.10) and the effect of using values more consistent with the data (e.g., the growth estimated from the Australian rather than the New Zealand growth data).

Software limitations reduced the number of simulations for each trial  $M$  to 200; Punt used 500. This reduction was undesirable because repeating the procedure for a few cases gave one in which the corrected  $M$  estimates were 0.007 apart. In some simulations,  $\sigma_r = 1.2$ , the estimated value that is used in assessments by MAF Fisheries, instead of it being drawn from the distribution  $U[0,4]$

for each simulation run as Punt did. This made little difference to the base case.

Table 1: Parameter values for the base and for the alternative cases. An alternative case replaces one or more of the parameter values in the base case with those in the 'Alternative' column.  $L_\infty$ ,  $K$ , and  $t_0$  are the von Bertalanffy growth parameters,  $\sigma_r$  is the standard deviation of the log of the recruitment,  $\sigma_L$  is the standard deviation of the log of the lengths-at-age,  $\lambda$  is the "between agency" bias in reading,  $\sigma_\varepsilon$  is the coefficient of variation for the reading error, and "LDistn" is the length distribution that reflects the way sampling was non-random. U[0.8, 1.2] indicates a uniform distribution from 0.8 to 1.2.

Parameter	Base case	Alternative	Comment
$L_\infty$	42.5	39.06	Growth for this data set (Australian growth)
$K$	0.059	0.06	
$t_0$	-0.3	-3.2	
$\sigma_r$	U[0,4]		
$\sigma_L$	0.15	0.03 0.05	
$\lambda$	U[0.8,1.2]		Sensitivity
$\sigma_\varepsilon$	U[0.05,0.2]	U[0.05,0.10]	
LDistn	U[15,45]	U[15,14] U[35,41] "bootstrap"	
Ageing sample size	323	125 if LDistn U[35,41] or "bootstrap"	Sample size for fish 35 cm or larger

For the bootstrap version of LDistn, the length distribution that reflects the non-random sampling, a sample was obtained by resampling from the digitised lengths that were greater than 35 cm (really  $35 - 0.125 = 34.875$  cm, as the lengths were grouped into 0.25 cm classes). There were 125 samples with length greater than 35 cm.

## 2.2 Re-estimation of $M$ using the agreed parameter values

MAF Fisheries and the FIB consultants agreed on the parameter values in Table 2, and also agreed to accept the corrected  $M$  estimate provided it was between 0.035 and 0.055. The criteria for selecting the parameter values were consistency with the data collected, and representing the likely errors in ageing and the uncertainty in recruitment.

Table 2: Re-estimation of natural mortality: agreed parameter values

Parameter	Value
$L_{\infty}$	39.06
$K$	0.06
$t_0$	-3.2
$\sigma_r$	Punt's posterior distribution for $\sigma_r$
$\sigma_L$	0.05
$\lambda$	U[0.8, 1.2]
$\sigma_{\epsilon}$	U[0.05, 0.2]
LDistn	"bootstrap"
Ageing sample size	323

Two further changes were also agreed upon. Firstly, another estimator ( $ML^1$ ) was used which is based on the mean age for fish larger than 35 cm. The mean age uses all fish over 35 cm and  $ML$  is the preferred estimator for a simple random sample where all fish are aged. In contrast, the H&L estimator is based on the tail of the age distribution, and uses only the oldest three fish in the sample.

Secondly, the size of the length sample was allowed to vary instead of being fixed at 125. The sample size was first drawn from a binomial distribution with  $n = 323$  and  $p = 125/323$ , mimicking the original sample of 323 fish that had 125 fish of 35 cm or more. A length sample was drawn by re-sampling the digitised lengths, as described above.

### 3. RESULTS

#### 3.1 Sensitivity

The bias in the sample raw  $M$  from the H&L estimator can be considerable and changes systematically as  $M$  changes, becoming unbiased at one specific  $M$ . While the bias at a trial  $M$  depends on the values of all parameters, changes in LDistn gave the largest differences (Table 1). The sample raw  $M$  was 0.042 (H&L estimator) if the lower length sampled was 15 cm, but dropped to 0.034 when the length limit was 35 cm.

<sup>1</sup>  $\hat{M} = \log(1 + \bar{t}/\bar{l})$ , where  $n$  is the sample size and  $\bar{t}$  is the average age.

Table 3: Relative biomass (percentage of  $M$ ) for different values of  $M$  using the H&L estimator for various values of  $\sigma_\epsilon$ , growth, and LDistn (based on 200 simulations with a sample size ( $n$ ) of 323 unless otherwise stated).  $\sigma_r = 1.2$  instead of being drawn from the distribution  $U[0,4]$ . "Repeated" in the first column signifies that the case on the previous line was simulated again, i.e., two results for the same case.

Alternative value(s) substituted in base case	$M$				
	0.03	0.04	0.05	0.06	0.07
Base	6.7	5.0	0	-3.3	-10.0
Repeated	6.7	5.0	0	-6.7	-11.4
Australian growth	3.3	-2.5	-8	-10.0	-17.1
$\sigma_\epsilon \sim U[5\%,10\%]$	13.3	7.5	4	-3.3	-7.1
LDistn $\sim U[15,41]$	20.0	15.0	8	5.0	1.4
LDistn $\sim U[35,41]$ , $n = 118$	-13.3	-15.0	-20	-23.3	-27.1
LDistn $\sim$ "bootstrap", $n = 125$	-13.3	-17.5	-22	-21.7	-27.1
LDistn $\sim$ "bootstrap", $n = 125$ , and with Australian growth	-16.7	-20.0	-24	-28.3	-31.4

When a single parameter only has been changed (rows 3–8 of Table 4),  $\hat{M}_c$  stays between 0.040 and 0.043; the base case has values in the same range. These eight cases are not statistically significant at the 5% level using a variance ( $0.0031^2$ ), which was derived from the difference in  $\hat{M}_c$  when a case was repeated ("Repeated" in Table 4, i.e., 0.003, 0.000, and 0.007). Admittedly this variance is not particularly good as it was based on three degrees of freedom, but the  $\hat{M}_c$  are in an interval of length 0.003. Hence, on the scale of interest (0.005), the new procedure is insensitive to changes of a single parameter.

As the above cases were not significantly different, they can be aggregated to provide a new mean of 0.0415 for the base case, and an improved standard deviation of 0.0016 which is based on seven degrees of freedom.

When two or more parameter values are changed simultaneously, the corrected  $M$  estimates may change significantly. For the case using the Australian growth and a bootstrap LDistn, there is a significant difference at the 5% level from the new mean of the base case. Lowering this case's standard deviation of the log of the lengths-at-age ( $\sigma_L$ ) to 0.05 increases  $\hat{M}_c$  from 0.0415 to 0.06 or 0.053, an even more significant difference. These cases involve changes in parameter values to those more consistent with the data. Thus changes in some combinations of parameter values can affect  $M$  by as little as 0.005 (the range under discussion).

Table 4: Corrected estimates of natural mortality,  $\hat{M}_c$ , using the H & L estimator for different assumptions of  $\sigma_\epsilon$ , growth, and LDistn (based on 200 simulations with a sample size ( $n$ ) of 323 unless otherwise stated). "Repeated" in the first column signifies that the case on the previous line was simulated again, i.e., two results for the same case.

Alternative value(s) substituted in base case	$\hat{M}_c, \sigma_r = 1.2$
Base	0.043
Repeated	0.040
LDistn ~ U[15,41]	0.040
Australian growth	0.043
$\sigma_r = 3\%$	0.040
$\sigma_\epsilon \sim U[5\%,10\%]$	0.040
LDistn ~ U[35,41], $n = 118$	0.043
LDistn ~ "bootstrap", $n = 125$	0.043
LDistn ~ "bootstrap", $n = 125$ , and with Australian growth	0.047
Repeated	0.047
LDistn ~ "bootstrap", $n = 125$ , Australian growth, and $\sigma_L = 5\%$	0.060
Repeated	0.053

### 3.2 Re-estimation of $M$ using the agreed parameter values

The ML estimator gave 0.038 for the sample raw  $M$  and a corrected  $M$  of 0.035 (based on 1000 simulations for each trial  $M$ ). The corrected estimate is the  $M$  which has the maximum likelihood (Figure 4). However, the likelihood about this maximum was relatively constant from 0.03 to 0.045, and so it may be inappropriate to fix the estimate at exactly 0.035.

This likelihood is only an approximation as it is constructed from the fraction of simulated raw  $M$  values that are close to the sample raw  $M$ , 0.038. A raw  $M$  is close if it is within  $\pm dM$  of 0.038, where  $dM$  was set to 0.004. But when  $dM$  was varied from 0.001 to 0.008 the maximum of the likelihood changed, thereby shifting the corrected  $M$  from 0.045 to 0.032 (Figure 5).  $dM = 0.008$  is probably too coarse to approximate the curve, as up to 40% of the simulated raw  $M$  values were close to 0.038. Fixing the value of  $dM$  was not considered, as Punt found that the corrected estimate was insensitive to changes in  $dM$ .

The choice of a value for  $dM$  is subjective, so although the analysis shows that  $M$  is somewhere between 0.03 and 0.045, it cannot be more exact. Hence, the status quo estimate, 0.04, is as valid as any.

Another problem with this analysis lies in the underlying model for the age structure, i.e., that natural mortality is constant for all ages. If this were so, then estimates based on the extreme tail of the age distribution (i.e., the oldest fish) should be consistent with the estimate obtained here. This does not seem to hold as the estimators based on the three greatest ages in a sample (H&L) and the greatest age (Hoenig 1983, coded MaxAge) give corrected estimates of 0.055 and something greater than 0.06, respectively.

The statistical significance of these differences can be expressed as the chance of seeing simulated raw  $M$  estimates greater than or equal to the sample raw  $M$ , if the true  $M$  were 0.035. For the MaxAge estimator, this chance is 1.5%, but if the true  $M$  is 0.045, it is 10.2%. Unfortunately, the simulations were not kept for the H&L estimator and so its significance is unresolved. A similar calculation for the ML sample raw  $M$  (0.038) gives a chance of 3.1% of seeing simulated  $M$  estimates less than or equal to 0.038 if the true  $M$  were 0.06. This suggests that  $M$  is not constant for all ages, resulting in a further uncertainty with the method and, hence, of the corrected estimate of  $M$ .

### 3.3 Extending the model of natural mortality

If  $M$  is not constant, then it is likely to be higher for older fish because of factors such as the cumulative stress from several spawnings or senescence. This would upwardly bias the ML estimator the least and the MaxAge estimator the most, which agrees with the results of the last section.

This can be modelled by letting natural mortality depend on age as follows;

$$M(\text{age}) = \begin{cases} M & , \text{age} < t_{sen} \\ M e^{M_a(\text{age} - t_{sen})} & , \text{age} \geq t_{sen} \end{cases}$$

where  $M$  and  $M_a$  are positive constants, and  $t_{sen}$  is the cutoff age.

To estimate all three parameters requires too much computer time, so I have restricted it to  $M_a$ , setting  $M = 0.038$  and  $t_{sen} = 80$ . This is to illustrate the extension, and is not definitive.

For the H&L and MaxAge estimators, which are both directly affected by a senescent phase, the estimate of  $M_a$  is 0.03 (Figure 6). For this estimate of  $M_a$ , mortality is 0.15 for the greatest age (125) seen in the data. With the ML estimator,  $M_a$  is estimated at about 0.01, its likelihood function is almost flat from 0 to 0.02, and the maximum likelihood is about half that for the other two estimators. The ML estimator appears to be uninformative about  $M_a$ , which might be expected as it is the least affected by senescent mortality.

This demonstrates a source of bias that Punt's method cannot account for — bias from a failure of one or more of the assumptions in the model. In this case, it really affects only the H&L and MaxAge estimators, suggesting that these estimators are unsuitable.

Alternatively, the inconsistency between the data and the mortality model may arise because the older fish are less available to sampling (this occurs in other species). This has the same effect on the model as senescent mortality. If both effects operate, they cannot be distinguished from each other using this data set alone. Whatever the cause, however, the conclusion in the previous paragraph still holds.

#### 4. SUMMARY

Punt's corrected  $M$  estimate was insensitive to changes in a single parameter, but was sensitive to changing two or three parameters simultaneously to their more realistic values.

$M$  was re-estimated using Punt's method after MAF Fisheries and the FIB consultants had agreed on the parameter values to use, and to accept the resulting corrected  $M$  estimate provided it fell between 0.035 and 0.055.

This corrected estimate was 0.035, but varied between 0.03 and 0.045 depending on the value used for the incidental parameter,  $dM$ , which controls how close a simulated estimate of  $M$  must be before it is considered close to the sample raw  $M$ . This is a practical way to calculate the likelihood. Usually, the value of  $dM$  is unimportant, but not here.

The choice of a value for  $dM$  is subjective with no obvious way to choose one value of it over another, so although the analysis shows that  $M$  is between 0.03 and 0.045, it cannot be more exact. Hence, the status quo estimate, 0.04, is as valid as any.

Finally, the data were inconsistent with the model used to mimic natural mortality, which assumed a constant mortality for all ages. Thus, although the method corrects for bias, this depends on its model being correct. To remedy this, I included a senescent component into mortality and estimated it in a simple case. This suggested a positive bias in the corrected  $M$  estimate if the raw  $M$  estimator uses only the tail of the age distribution (i.e., the greatest ages). This in turn suggests that Punt's analysis was also biased as he used, at most, the three greatest ages in the sample.

#### 5. REFERENCES

- Francis, R.I.C.C., Robertson, D.A., Clark, M.R., & R.P. Coburn 1992: *N.Z. Fisheries Assessment Research Document 92/4*.
- Hoenig, J.M. 1983: Empirical use of longevity data to estimate mortality rates. *Fishery Bulletin* 82(1): 898-902.
- Hoenig, J.M. & Lawing, W.D. 1983: Using the K oldest ages in a sample to estimate the total mortality rate. *International Council for the Exploration of the Sea CM. 1983/D: 22*. 14 p (Cited with permission).
- Punt, A.E. (MS). Specifying prior distributions for use in Bayesian stock assessments. Unpublished MS submitted to *Canadian Journal of Fisheries and Aquatic Sciences* in February 1993.
- Smith, D. & Robertson, S. 1991: Age determination studies of orange roughy. Unpublished report to Demersal and Pelagic Fisheries Research Group 32.3.4. 8 p. (Copy held Fisheries Research Institute, Cronulla, NSW, Australia.)

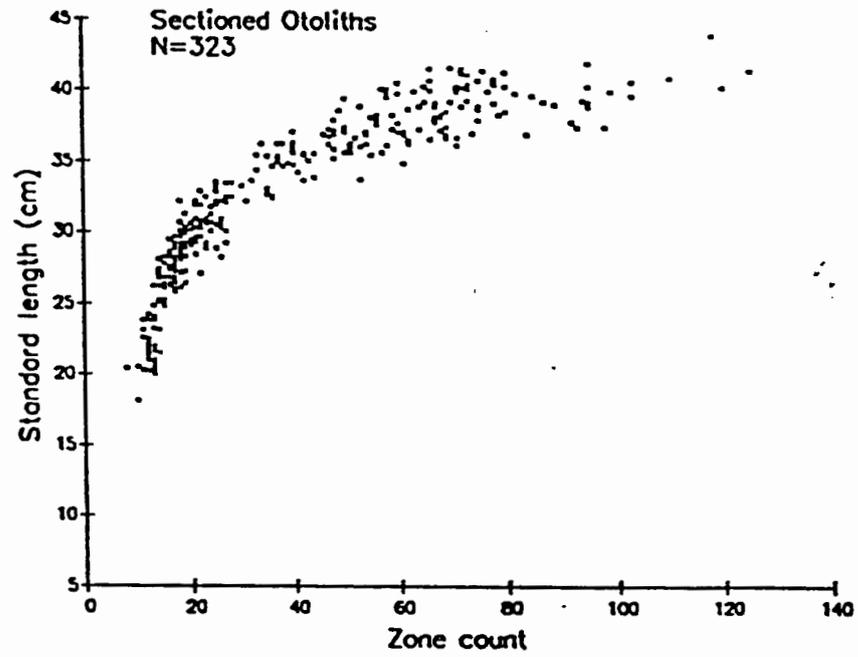


Figure 1: Reproduction (with permission) of figure 2 from Smith & Robertson (1991): age vs fish length.

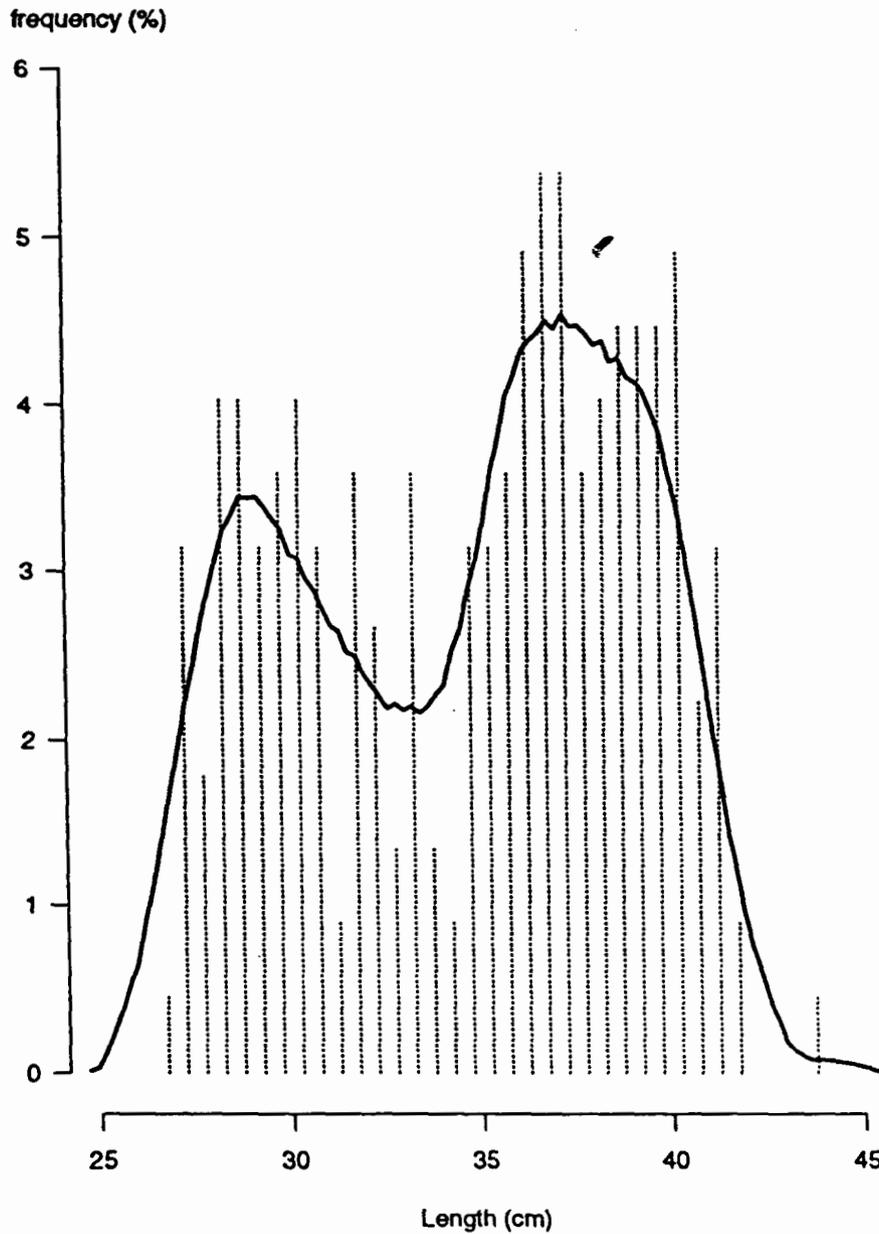


Figure 2: Length frequency of the digitised data from Smith & Robertson's (1991) figure 2. Lengths are in bins of 0.5 cm. The solid line is a smoothed representation.

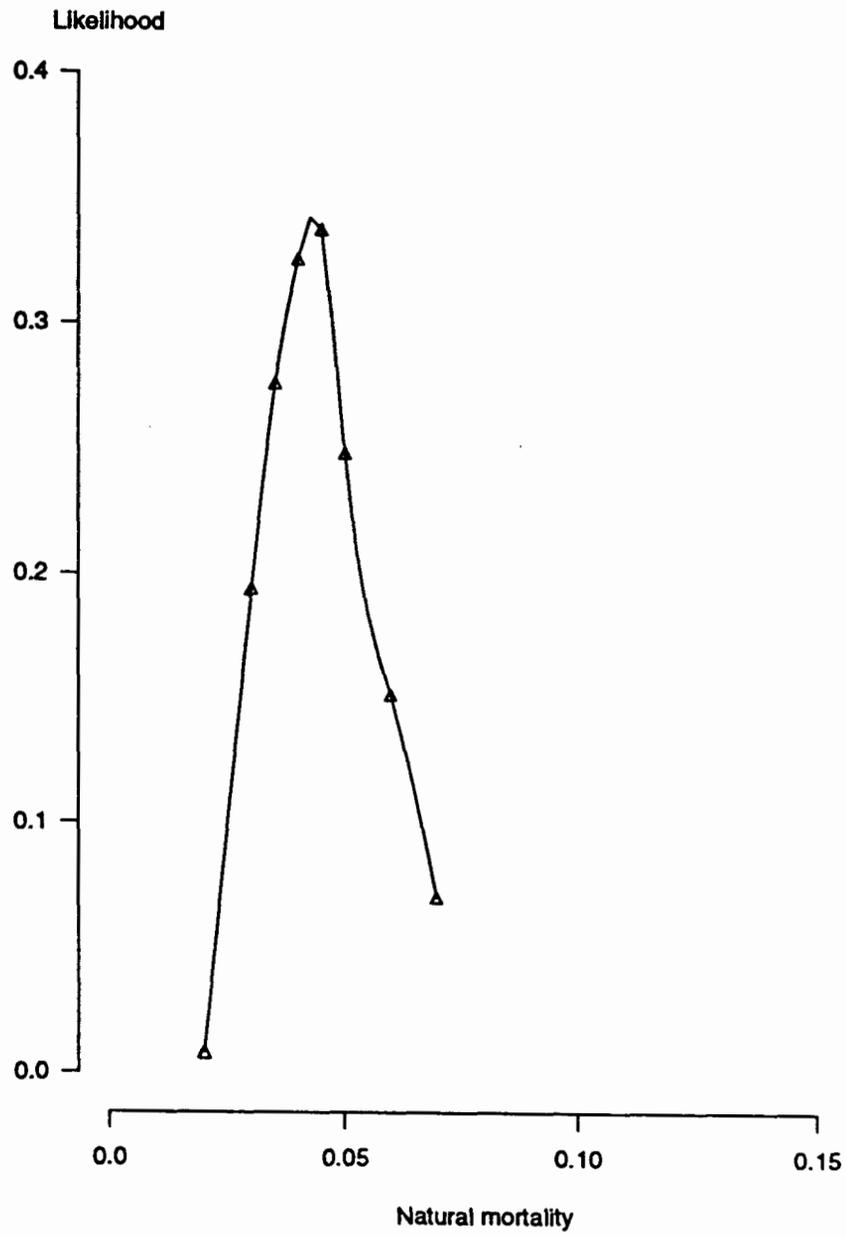


Figure 3: Likelihood function for the base case.

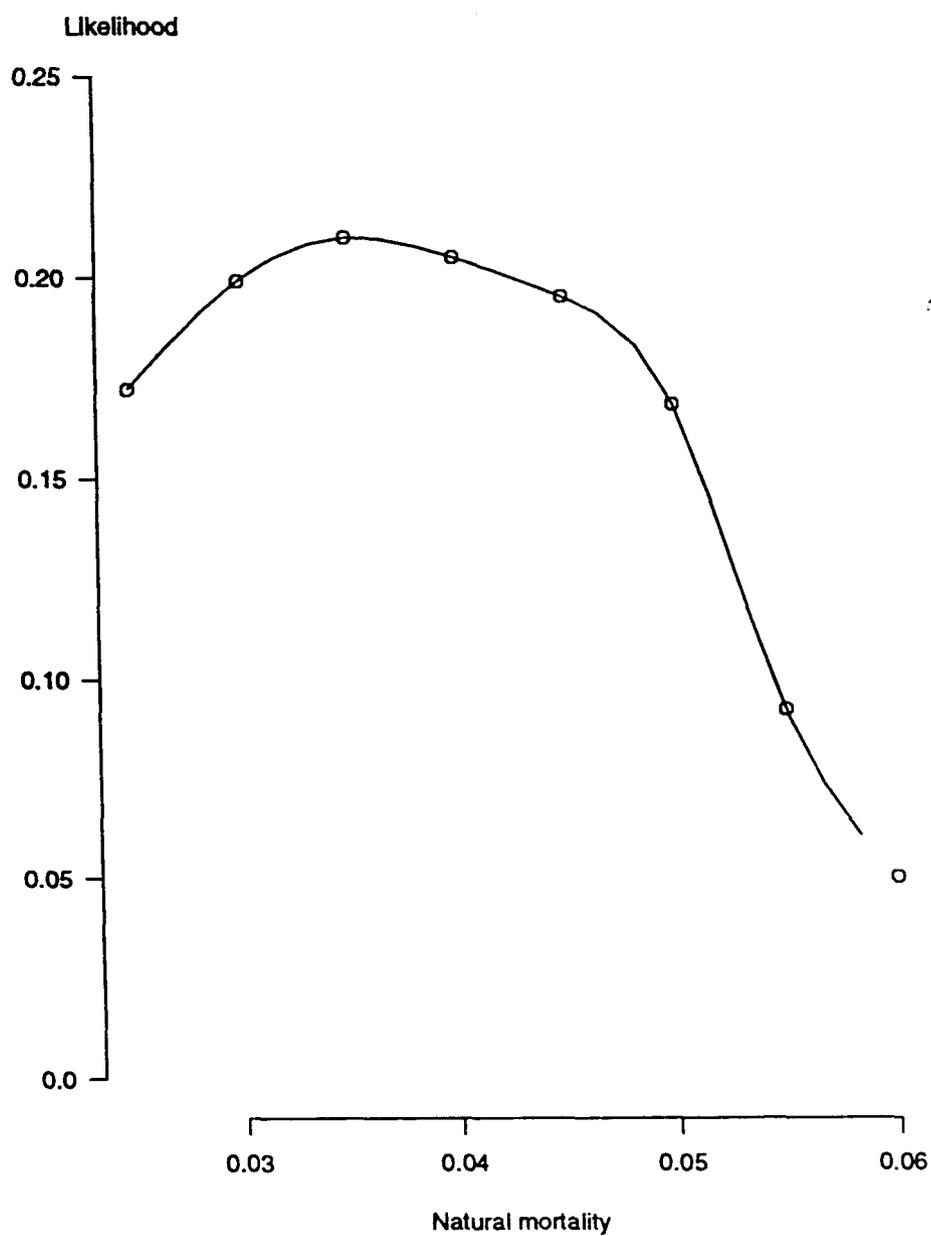


Figure 4: Re-estimation of natural mortality: likelihood function from using the agreed parameter values. The corrected  $M$  estimate is the  $M$  which has the maximum likelihood, i.e., 0.035.

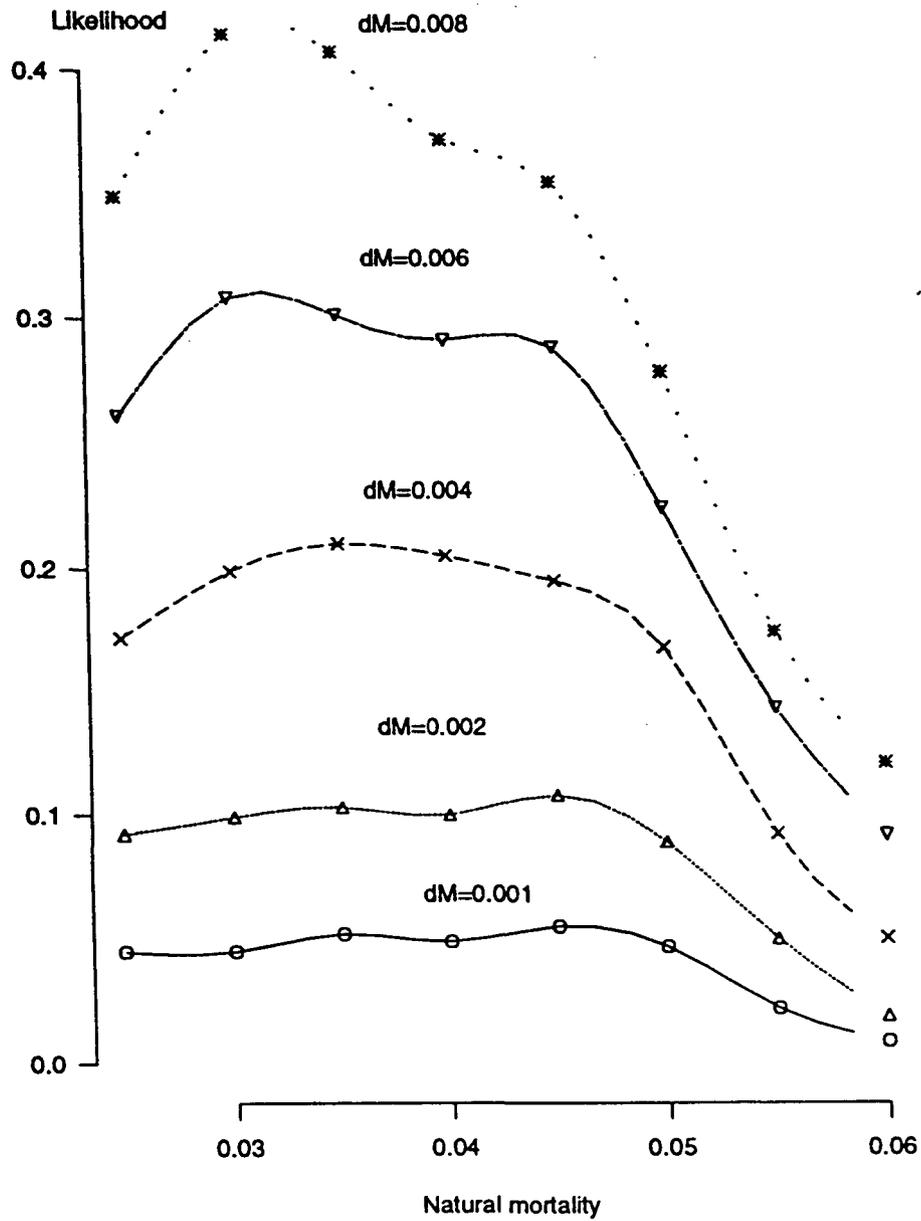


Figure 5: Re-estimation of natural mortality: likelihood function for different values of the "closeness" parameter,  $dM$ : 0.001, 0.002, 0.004, 0.006, and 0.008. The corrected  $M$  estimate shifts within the interval [0.03, 0.045] as  $dM$  is changed.

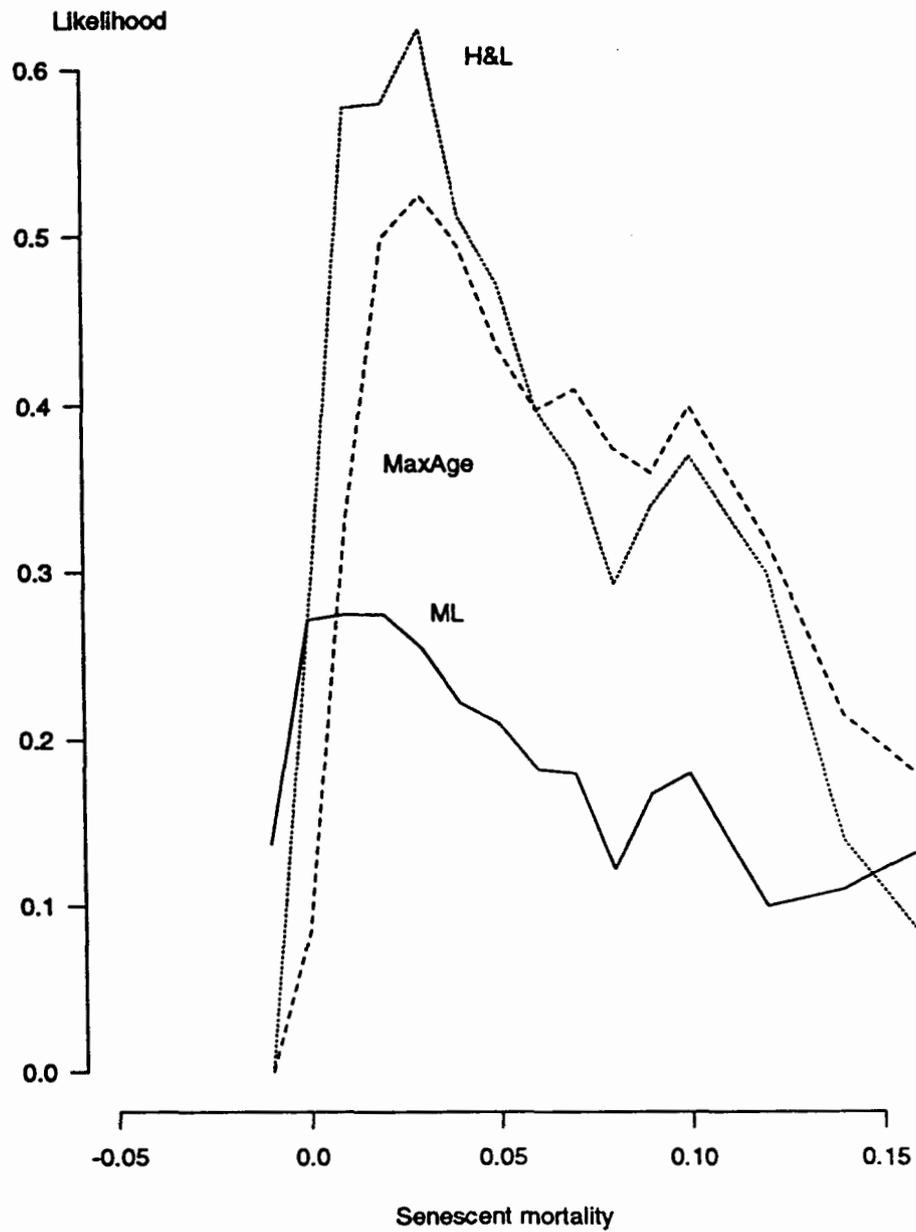


Figure 6: Senescent mortality ( $M_a$ ): likelihood functions by the estimators ML, H&L, and MaxAge, given that  $M$  is set to 0.038 and  $t_{sen}$  is set to 80 years.