

Empirical weighting of multiple stock-abundance indices for parameter estimation and stock assessment in a multi-zone or multi-species fishery

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In order to make use of all available information, fishery stock assessment researchers often use several indices of stock abundance. These indices are derived from commercial, as well as fishery-independent sources. Since the indices all relate to the same fishery but may differ in the degree of accuracy with which they reflect stock size, appropriate weights must be chosen for each. This paper contains an outline of an empirical approach to assigning index weights via the likelihood function that underpins both classical and Bayesian statistical methods. The approach is demonstrated for a stimulated three-zone paua (*Haliotis iris*) fishery, and can be used readily for multi-species fisheries and/or for assessment of multiple-use management of marine resources.

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Introduction

Stock assessments may involve the use of several indices of stock abundance derived from commercial fisheries data, observer data from fisheries, and scientific surveys. It is non-trivial to determine how much weight should be assigned to each index in practice because of both model and measurement uncertainty. In the best of circumstances the system of links among the indices could be derived from scientific principles and included explicitly in the model dynamics. Such a model would address both deterministic and stochastic aspects of the fishery concerned. Unfortunately this is not an option for most, if any, fisheries. A straightforward empirical solution to this problem is available via the likelihood function. The likelihood function underpins both maximum likelihood and Bayesian methods widely used in fisheries stock assessments and management strategy evaluation. Convenient index weights are implied by relaxing the commonly-used assumption of statistical independence among measured indices of abundance and by specifying

a joint likelihood function that accounts for possible correlation among the index errors.¹

In addition to addressing more than one index of abundance for stock assessment, the methods outlined here are readily applicable to stock assessment for management of multi-zone or multi-species fisheries, as well as to multiple-use management of marine resources. In applying this approach to our example fishery, we take explicit account of any correlation among indices of abundance for a particular management zone, as well as similar correlation across zones. In a multi-species fishery, correlation within and between constituent species, rather than between geographical regions, might just as readily be the focus of the work. The hypotheses that we test are, therefore, concerned with restrictions on the likelihood function covariance matrix that arise from

¹See McAllister *et al.* (1994) and Punt and Hilborn (1997), for example, where more than one index of abundance is used and index prediction errors are assumed to be independent.

Table 3. Restricted covariance matrix for H_2 ; indices correlated within zone. The shaded off-diagonals are covariances ($\times 1000$) between different indices within the same zone. The upper triangle of the matrix is a reflection of the lower triangle.

		Zone 1			Zone 2			Zone 3		
		cpue	ML	IS	cpue	ML	IS	cpue	ML	IS
Zone 1	cpue	122.15	-4.06	157.85	0	0	0	0	0	0
	ML	-4.06	0.16	-6.39	0	0	0	0	0	0
	IS	157.85	-6.39	339.55	0	0	0	0	0	0
Zone 2	cpue	0	0	0	152.12	4.91	-63.86	0	0	0
	ML	0	0	0	4.91	0.22	-2.93	0	0	0
	IS	0	0	0	-63.86	-2.93	42.98	0	0	0
Zone 3	cpue	0	0	0	0	0	0	24.44	-2.38	-16.49
	ML	0	0	0	0	0	0	-2.38	0.27	1.91
	IS	0	0	0	0	0	0	-16.49	1.91	13.54

Table 4. Unrestricted covariance for H_0 ; all index-zone combinations correlated. The shaded off-diagonals are covariances ($\times 1000$) between different indices across zones.

		Zone 1			Zone 2			Zone 3		
		cpue	ML	IS	cpue	ML	IS	cpue	ML	IS
Zone 1	cpue	122.28	-4.10	156.23	-96.77	-4.20	60.47	-41.76	4.39	31.57
	ML	-4.10	0.16	-6.42	3.57	0.15	-2.06	1.50	-0.15	-1.09
	IS	156.23	-6.42	337.32	-90.84	-3.90	49.69	-40.02	3.48	24.93
Zone 2	cpue	-96.77	3.57	-90.84	152.79	4.99	-66.00	56.07	-5.31	-36.12
	ML	-4.20	0.15	-3.90	4.99	0.22	-2.99	2.14	-0.24	-1.67
	IS	60.47	-2.06	49.69	-66.00	-2.99	44.05	-27.81	3.28	23.25
Zone 3	cpue	-41.76	1.50	-40.02	56.07	2.14	-27.81	24.18	-2.33	-16.08
	ML	4.39	-0.15	3.48	-5.31	-0.24	3.28	-2.33	0.26	1.85
	IS	31.57	-1.09	24.93	-36.12	-1.67	23.25	-16.08	1.85	13.06

periods than the observed fishery indices such as cpue, and research data (surveys and length frequencies) may exist for even shorter periods. Thus the time-series length varies among the three indices.

Parameters of the model are: R_0 , the recruitment to the population at the unexploited (virgin) biomass; M , the instantaneous rate of natural mortality; h , the “steepness” of the Beverton–Holt stock-recruit relation (Francis, 1992); q_1 , the catchability coefficient relating cpue to abundance; and q_2 , the catchability coefficient relating the research survey index to abundance.

Initial conditions for simulation

Initial conditions are determined by the parameter R_0 . The model is “burnt in” for 30 years by running it with no fishing to allow numbers-at-length to approach an equilibrium. Males and females are not modelled separately. In year $i=1$, the number of paua in length class $j=1$ is

$$N_{1,2}=R_0 \tag{1}$$

A growth transition matrix, \mathbf{G} , was determined outside the model, as described by Andrew *et al.* (1996). From the von Bertalanffy growth parameters L_∞ and K , an expected yearly growth increment Δl_j was calculated for the j th length class:

$$\Delta l_j=(L_\infty - L_j)(1 - e^{-K}) \tag{2}$$

Using these growth increments and an assumed standard deviation of increments, the distribution of increments for length class j was calculated from the gamma distribution. The distribution of increments was then translated into the vector of probabilities of transition from length class j to other length classes, and this was done for all length classes to form the matrix \mathbf{G} . Negative increments were not permitted, so the transition probabilities for abalone moving from a larger size to a smaller one were set to zero. Zero growth was permitted. The largest size group was treated as a “plus group”, so that abalone in this group had a probability of one of remaining in this size group.

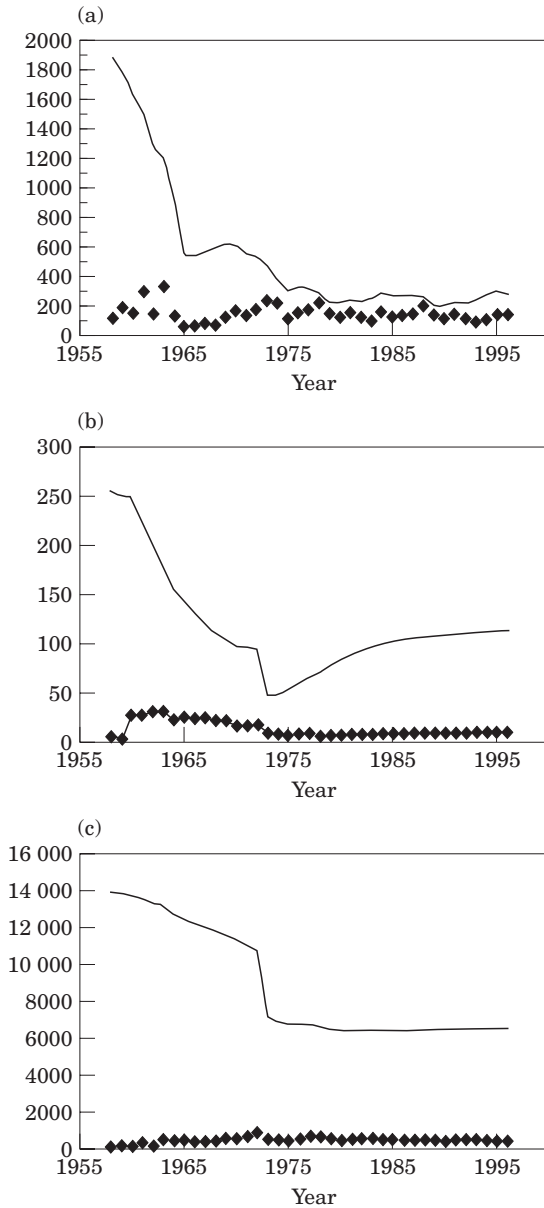


Figure 1. Recruited biomass (lines) and commercial catch (points) for each of the three simulated paua populations in the example fishery. (a) Zone 1; (b) zone 2; (c) zone 3.

Simulation

The model contains 22 length groups, each of 5-mm interval width, from 20 mm length at the lower limit to 130 mm at the upper limit. In the “burn-in” period, the vector N_t of numbers-at-length for each year t is determined from the numbers in the previous year, survival, G and R_0 :

$$N'_t = N'_{t-1} G \cdot \exp(-M) \tag{3}$$

where the prime (') denotes vector transposition and the dot (·) denotes matrix multiplication. In this model, we assume that all recruitment enters the first length class, which is appropriate for one-year-old paua:

$$N_{t,1} = R_0 \tag{4}$$

Total biomass is given by the sum total of the product of numbers and weight:

$$B_t^{\text{total}} = N'_t \text{weight} \tag{5}$$

where **weight** is the vector of weight-at-length. A vector **P** incorporates the effect of minimum legal size (MLS): it is zero for all length groups for which the centre is less than the MLS, and 1 for all groups with mid-point equal to or greater than the MLS. A vector **vuln** describes vulnerability-at-length, which is related to the visibility of paua to divers; smaller paua tend to be cryptic. The biomass of legal-sized paua is given by the sum total of the element-by-element product of the four vectors for numbers, weight, legality and vulnerability:

$$B_t^{\text{legal}} = \text{one}'(N_t \times \cdot \text{weight} \times \cdot \mathbf{P} \times \cdot \text{vuln}) \tag{6}$$

where $\times \cdot$ denotes element-by-element multiplication and one is a column vector of ones. The dynamics of the model, once an equilibrium has been approached, incorporate the observed catch and a selectivity function. Exploitation rate U_t is calculated from observed catch and model biomass:

$$U_t = \min(\text{catch}_t / B_t^{\text{legal}}, 0.80) \tag{7}$$

The arbitrary constraint of 0.80 prevents exploitation rate from reaching unrealistically high levels. The survival-from-fishing vector is calculated as:

$$SF_t = 1 - (\mathbf{P} \times \cdot \text{vuln} \times \cdot U_t) \tag{8}$$

Numbers in the following year are then calculated from the vectors of numbers, percentage survival from natural mortality, S , and survival from fishing:

$$N_{t+1} = N_t \times \cdot S \times \cdot SF_t \tag{9}$$

The model incorporates a Beverton–Holt stock-recruit function using the parameter “steepness” (Francis, 1992) to calculate α and β from the egg production and recruitment in the virgin state. Spawning biomass is calculated from the vectors of numbers-at-length, weight-at-length, and the proportion mature-at-length:

$$B_t^{\text{spawn}} = N_t \times \cdot \text{maturity} \times \cdot \text{weight} \tag{10}$$

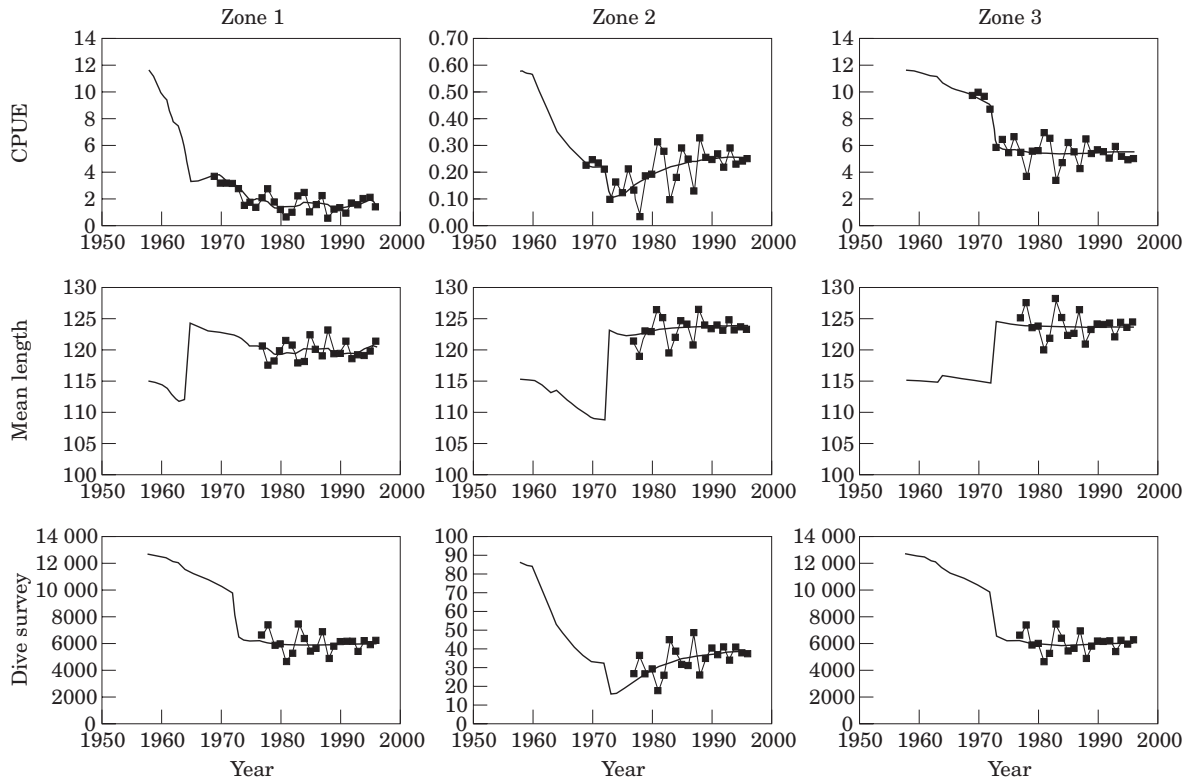


Figure 2. Predicted indices for simulated populations of example fishery (lines) and indices with observation error added (points).

Weight-at-length is based on the morphometric relation of Schiel & Breen (1991). Recruitment to the population is then calculated as:

$$R \cdot {}_tB_{t-1}^{\text{spawn}} / (\alpha + \beta B_{t-1}^{\text{spawn}}) \quad (11)$$

Predictions

Predicted cpue is determined from legal biomass and the catchability coefficient q_1 :

$$\text{cpue}_t^{\text{pred}} = q_1 B_t^{\text{legal}} \quad (12)$$

Similarly the independent survey index IS is determined with a second catchability coefficient:

$$\text{IS}_t^{\text{pred}} = q_2 B_t^{\text{legal}} \quad (13)$$

Predicted mean length for each year is calculated from the vectors of length, numbers-at-length, legality and vulnerability:

$$\text{ML}_t^{\text{pred}} = \frac{\text{sum}(\text{length} \times \cdot \mathbf{N}_t \times \cdot \mathbf{P} \times \cdot \text{vuln})}{\text{sum}(\mathbf{N}_t \times \cdot \mathbf{P} \times \cdot \text{vuln})} \quad (14)$$

For each of these model-based predictions there are equivalent observed values for the fishery. The differences between the observed values and the predictions yields prediction errors, the magnitude of which depends on the values of the model parameters. The prediction errors may be modified, therefore, by changing some or all of the model parameter values.

Indicator variables

These are variables calculated from model parameters to help assess the state of the stock and include current biomass as a proportion of initial biomass (B_{curr}/B_0), referred to here as depletion.

Likelihood function

A generalisation of selecting model parameter values to minimise the sum of squared errors is to find the parameter values that maximise the likelihood function. The likelihood function may also be used to obtain Bayesian distribution estimates for parameters. In the case of fish stock assessment it is common to use the Gaussian (or normal) likelihood function

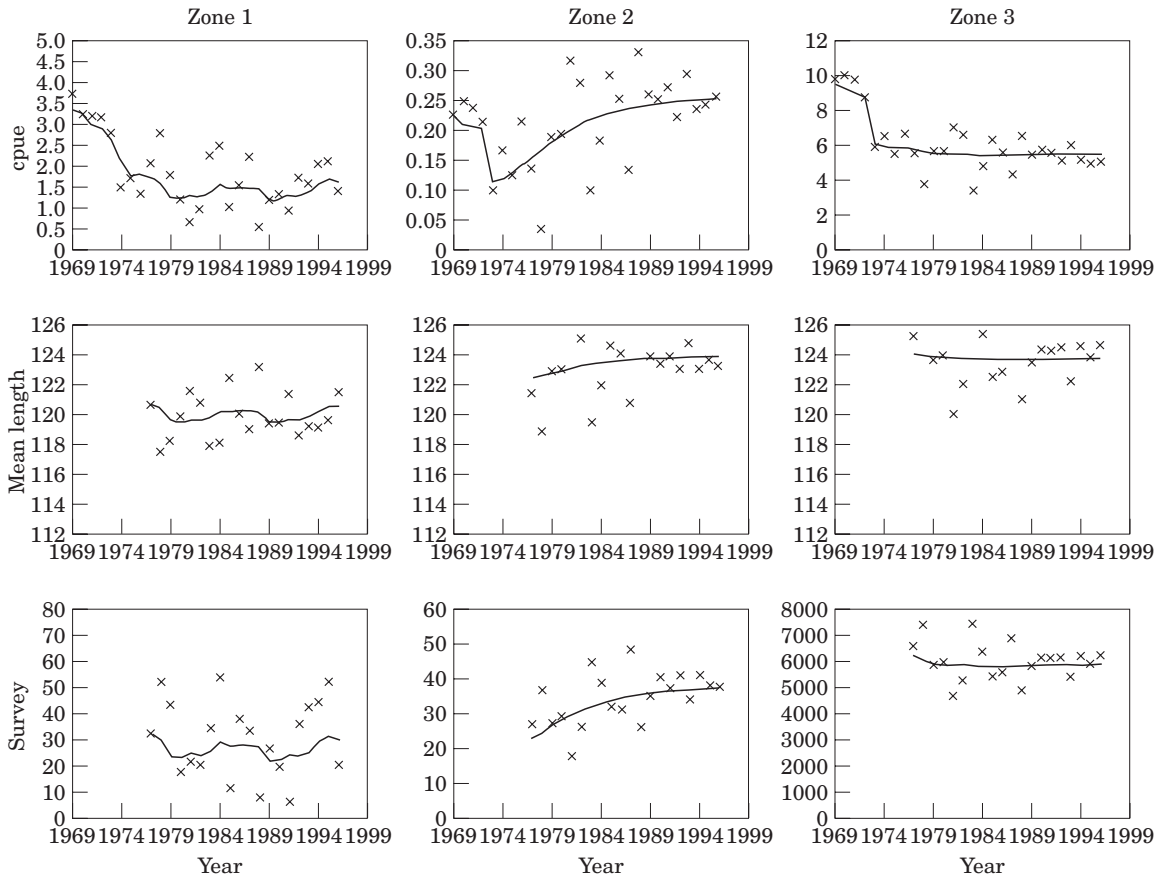


Figure 3. Model fits under H_0 , cpue, mean-length and independent surveys, for three neighbouring zones. Model fits under the alternative covariance hypotheses were not very different, and for clarity are not plotted.

for the parameters of the biological model, given the available data for the fish stock. Available data are observed from the fishery and/or from scientific surveys. These data are used for enumerating the errors produced by the biological model in evaluating fish stock size. The joint probability distribution of these errors is interpreted as the likelihood function of the population parameters in the model, given the observed data.

The indices of abundance for pua in the present paper are catch per unit effort (cpue), mean length (ML) and the index obtained from the scientific surveys (IS). The errors in model predictions of these three indices are assumed to be jointly Gaussian and not necessarily uncorrelated.

Regardless of the number of indices observed and evaluated by the biological model, the individual likelihood function for each observation period (year) can be expressed in matrix form as:

$$L(\theta) = (2\pi)^{-\frac{n}{2}} |\Sigma|^{-\frac{1}{2}} e^{-\frac{1}{2} E' \Sigma^{-1} E} \tag{15}$$

or in logarithm form:

$$L(\theta) = -\frac{1}{2} [n \ln(2\pi) + \ln |\Sigma| + E' \Sigma^{-1} E] \tag{16}$$

where θ is the vector of parameters in the model, E is the vector of index errors and Σ is the covariance matrix of the index errors.

Covariance matrix

The covariance matrix has column and row dimension given by the product of number of indices and zones. The diagonal elements are variances for each of the indices and are calculated respectively as the sum of squared prediction errors divided by the number of observations in the data set on the appropriate index. The off-diagonal elements are covariances between two indices. Depending on the hypothesis regarding the covariance matrix being tested, covariances are either set to zero or calculated as the sum of the products of one

Table 5. Maximum likelihood parameter estimates and standard errors under H_1 : each index and zone independent and therefore uncorrelated; H_2 : indices correlated within zone; and H_0 : all index-zone combinations correlated.

Parameter	Zone	"Actual" simulated values	H_1 : No covariance		H_2 : Covariance within zones		H_0 : Full covariance	
			Model estimate	s.d.	Model estimate	s.d.	Model estimate	s.d.
Recruitment [$\ln(R_0)$]	1	14.00	13.88	0.143	13.92	0.061	13.81	0.019
	2	12.00	11.91	0.154	11.96	0.057	11.84	0.023
	3	16.00	15.80	0.230	15.91	0.091	15.74	0.044
M	All	0.150	0.132	0.014	0.138	0.006	0.125	0.002
	All	0.750	0.797	0.091	0.800	0.036	0.851	0.017
Commercial catchability [$\ln(q_1)$]	1	-12.00	-12.24	0.079	-12.24	0.066	-12.27	0.044
	2	-13.00	-13.21	0.136	-13.24	0.044	-13.21	0.030
	3	-14.00	-13.99	0.181	-14.06	0.081	-14.02	0.046
Survey catchability [$\ln(q_2)$]	1	-9.00	-9.31	0.117	-9.34	0.092	-9.34	0.077
	2	-8.00	-8.15	0.119	-8.17	0.061	-8.21	0.025
	3	-7.00	-6.96	0.190	-7.08	0.074	-7.02	0.042
Starting biomass	1	1 394 551	2 079 200	44 995	2 057 400	17 557	2 080 900	12 770
	2	188 732	289 040	14 378	288 930	5 646	289 850	2 573
	3	10 304 415	14 200 000	1 674 200	15 062 000	746 250	14 412 000	397 090
Starting recruitment (R_0)	1	1 202 604	1 068 600	152 810	1 113 200	67 483	992 440	18 943
	2	162 755	148 550	22 840	156 330	8 898	138 230	3 211
	3	8 886 111	7 297 900	1 675 300	8 149 400	745 190	6 873 300	303 860
Depletion	1	0.21	0.16	0.014	0.17	0.006	0.16	0.005
	2	0.61	0.46	0.025	0.46	0.011	0.47	0.004
Log likelihood	3	0.64	0.45	0.034	0.46	0.014	0.46	0.008
			-691.789		-999.372		-1 212.74	

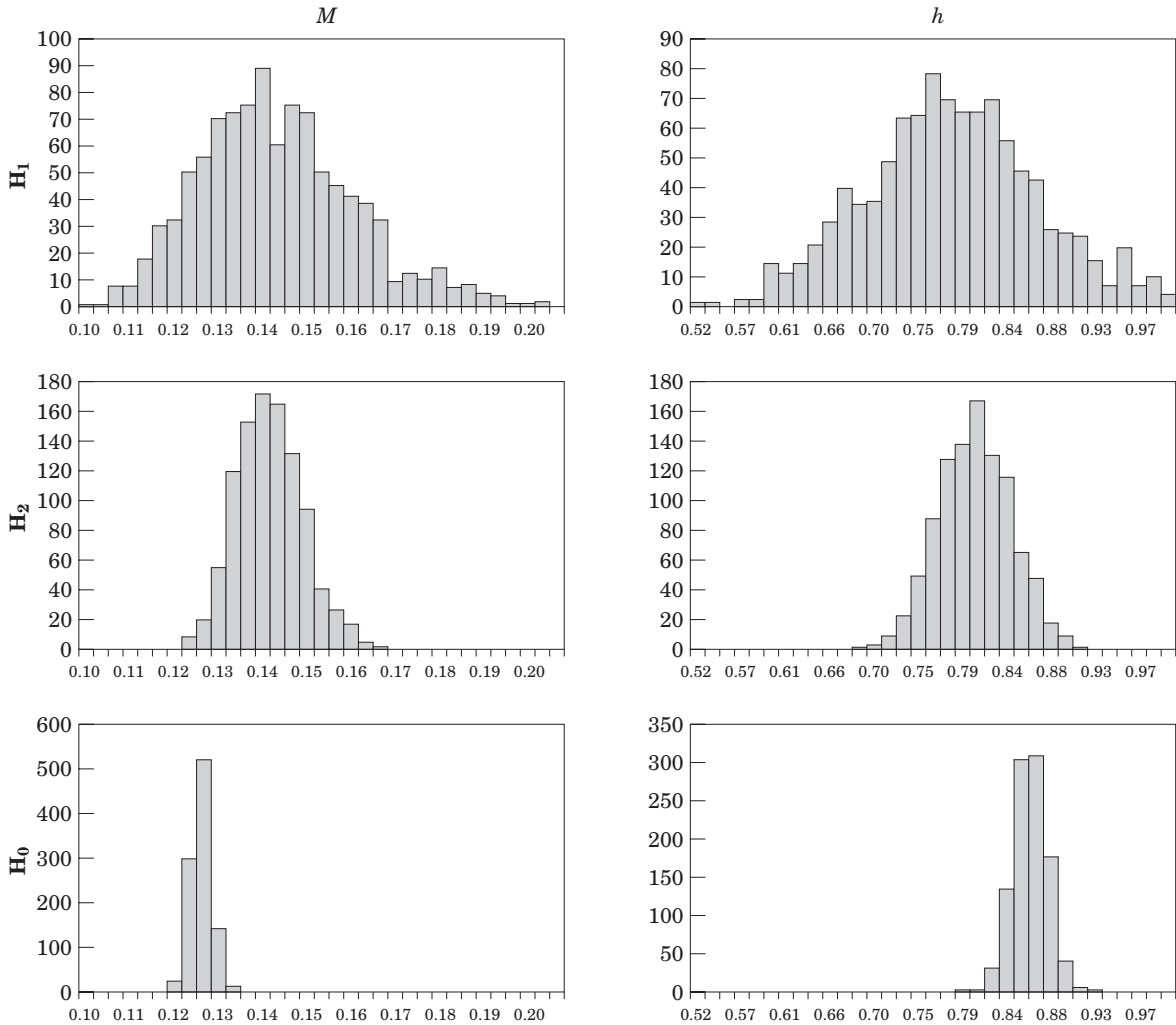


Figure 4. Bayesian posteriors for mortality (M) and for steepness (h) with uniform priors under alternative covariance hypotheses. The parameter M (mortality) was restricted to values less than 0.3. The parameter h (steepness) was restricted to values greater than or equal to 0.5.

index prediction error for a particular year and another index prediction error in the same year, divided by the square root of the product of the number of observations available for each index (Greene, 1990).

Consider a two-index case, for example. Ignoring the constant term, let:

$$\begin{aligned}
 -2L(\theta) &= \ln \left| \begin{matrix} a & c \\ d & b \end{matrix} \right| + [e_1 e_2] \begin{bmatrix} a & c \\ d & b \end{bmatrix}^{-1} \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \\
 &= \ln(ab - cd) + (be_1^2 + ae_2^2 - (c+d)e_1e_2)/(ab - cd) \quad (17)
 \end{aligned}$$

so, when Σ is diagonal ($c=d=0$), the usual assumption of uncorrelated indices holds and the “weights” for the likelihood function are straightforward:

$$-2L(\theta) = \ln(ab) + e_1^2/a + e_2^2/b \quad (18)$$

where a is the variance of the error for index 1, e_1 , b is the variance of the error for index 2, e_2 , and $c=d$ is the covariance between the errors for indices one and two.

When Σ is non-diagonal the weights for the various components of the likelihood function are clearly more complicated and involve both the variances of, and the covariances among, index errors. In order to determine the weights on each of the indices we specify a testable hypothesis for each of three objectives: (1) To evaluate the fishery under H_1 : that the indices and specified management zones are statistically independent (and therefore uncorrelated); we restrict Σ (the covariance matrix) to a diagonal matrix where only variances for each index in each management zone, are included in the overall likelihood function (Table 2). (2) To

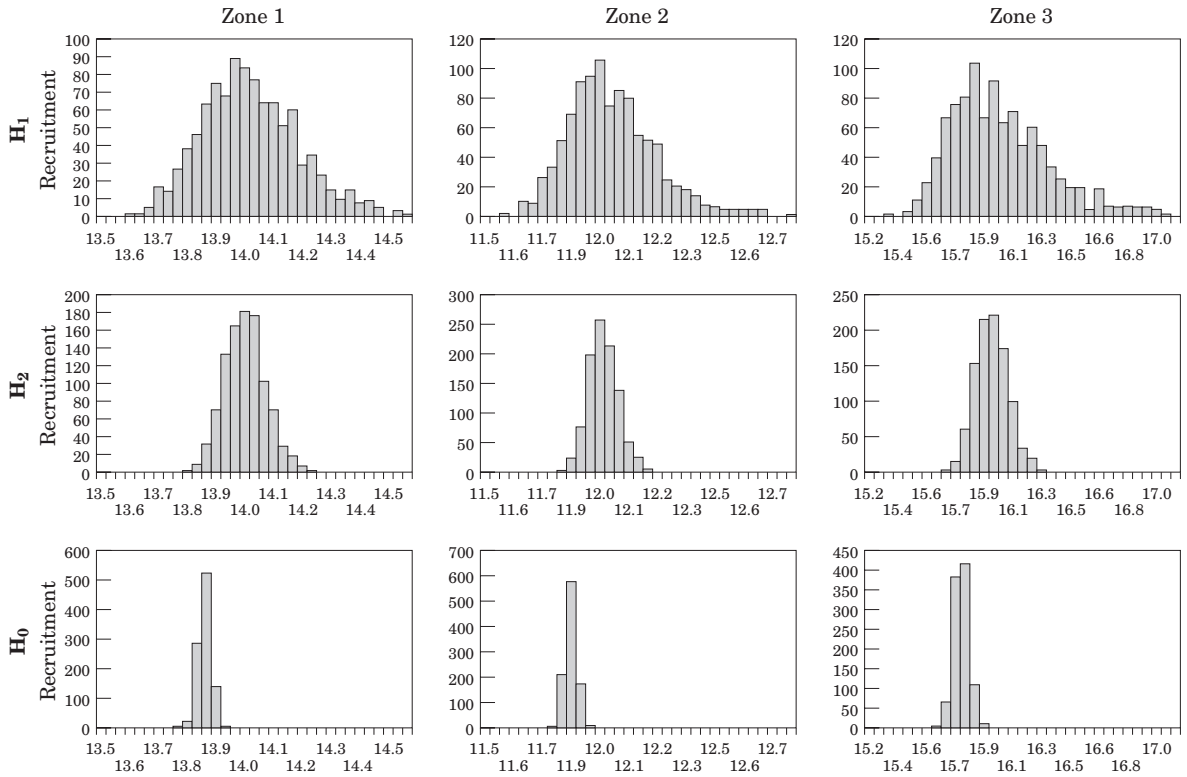


Figure 5. Bayesian posteriors for recruitment [$\ln(R_0)$] among zones and among covariance hypotheses.

evaluate the fishery under H_2 : that the indices of abundance within each management zone are correlated; the covariance matrix includes those off-diagonal components that are calculated between indices within each zone (Table 3). (3) To evaluate the fishery under H_0 : that all indices are correlated, both within and across management zones; the covariance matrix is unrestricted and includes all off-diagonal components (Table 4).

The likelihood function for a particular year, then, is constructed from the appropriate prediction errors and the corresponding elements of the covariance matrix. In the case of our example fishery, this means that the likelihood function for some years involves only cpue and its prediction error variance, for other years it involves both cpue and IS, or cpue and ML (and their respective variances and covariances) and for the remaining years it involves all three indices, along with all calculated variances and covariances.

Parameter estimation

Maximum likelihood estimation involves searching for parameter values that maximise the likelihood function. The likelihood function displayed above yields the same parameter values as weighted least squares. Alternative

likelihood functions may be specified in order to reflect the distribution of index errors better, and these yield different parameter estimates. In addition to giving point estimates of the biological parameters, a measure of their sampling variation is indicated by their standard deviations (which are a function of the covariance matrix in the likelihood function).

The Bayesian perspective differs from maximum likelihood estimation which reflects the view that the biological parameters and initial conditions (or values) are fixed points and their estimates vary across samples of data. By comparison, the Bayesian view is that there is a distribution of parameter values and initial conditions, and what is sought from the data is guidance on both their extreme values and their central tendency. Bayesian estimates, therefore, are based on repeated sampling from a supposed distribution of parameter values and on using available data to modify that distribution.²

²In the Bayesian case covariance among the indices is not fully accounted for by the covariance matrix in the likelihood function because of the additional variation contributed by randomness in the parameters.

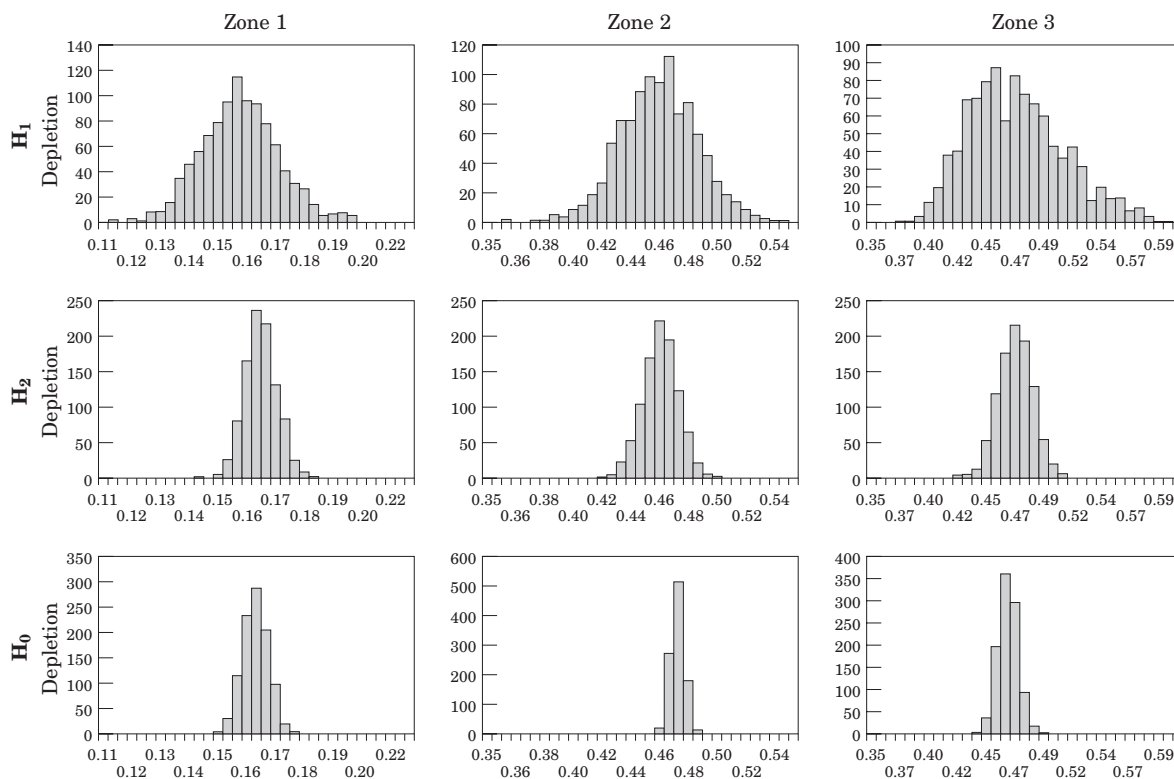


Figure 6. Bayesian posteriors for depletion (B_{curr}/B_0) across zones, under alternative covariance hypotheses.

Simulated data sets for example fishery

The data used are simulated catch, cpue, length-distribution and diving-survey indices generated for three neighbouring management zones or stocks of New Zealand blackfoot paua. We emphasise that we did not evaluate the model for stock assessment of paua; we used the data only to demonstrate a method of accounting for correlation among indices and to appropriately weight them in the joint likelihood function.

Three populations were generated by reversing the dynamics of the model described above. For each zone the parameters R_0 , q_1 and q_2 were defined, and a time series of effort, f , was supplied from which catch was calculated:

$$\text{catch}_t = q_1 f_t B_t^{\text{legal}} \quad (19)$$

The historical minimum legal length (MLL) also varied with zone. The three simulated zones of the example fishery therefore demonstrate quite different patterns of exploitation. Figure 1 shows the biomass and catch trajectories for the three simulated paua populations, and Table 1 gives parameters that characterise each of the populations.

Zone 1 represents a heavily exploited population of paua with no input controls and consequently a very low

catch rate. The large decrease in available biomass in 1965 is due to an increased MLS from 50 mm to 115 mm. Zone 2 shows a very small stock which declined rapidly under fishing pressure but subsequently recovered after effort was controlled as a constant value. MLS increased twice; from 50 to 80 mm in 1964 and to 115 mm in 1973. Zone 3 had a large stock and a stable fishery with a very high catch rate. This zone was managed with the same MLS as was Zone 2. Mortality, steepness and growth were common to all three zones, as was the number of years of data available: 28, 20 and 20 years of cpue, mean length and survey indices respectively.

Correlated error terms were generated using a known covariance matrix, and added as observation error to the predicted indices. Some scaling of these errors was necessary, and the magnitude of their variation was chosen to match the magnitude of the model predictions by zone and index (Figure 2).

Empirical results

For our chosen example we fit the population model to the three generated indices of abundance; catch per unit effort, length frequency and dive survey observations from three neighbouring coastal zones. This zonal

structure offers possibilities for a choice of management options depending on the relationships between populations in the zones and the activities of fishers within and among the zones. The three covariance hypotheses are differentiated by the Σ (covariance matrix component of the likelihood function) specified in each case. These are demonstrated in Tables 2–4 by outlining or shading each additional portion of the covariance matrix as it is included into the likelihood function. In a stock assessment application, the correlation coefficients or coefficients of variation might be more informative to the reader, but for this study, the structure of the covariance matrix and of the components included the joint likelihood are of most interest.

Likelihood ratio tests determine the goodness of fit of the model to the simulated data under each covariance hypothesis, and thus test the ability of the model to detect and account for the correlation among indices. Model fits to the three indices, for each zone, and for each covariance hypothesis examined, are shown in Figure 3.

The population parameters estimated for each of the three zones were R_0 , mortality, M , steepness, h , catchability for commercial fishing, q_1 , and catchability for dive surveys, q_2 . In addition, the initial recruitment, initial vulnerable biomass and depletion (current biomass as a proportion of initial biomass) were estimated, as was the covariance matrix specified in the likelihood function. Posterior distributions were obtained from the evaluation of every 500th set of parameters from 500000 Markov–Chain Monte Carlo (MCMC) samples.

Table 5 compares the “actual” simulated values of population and model parameters with maximum likelihood estimates and standard errors under each of the three hypotheses. Our Bayesian estimates under alternative covariance hypotheses (using uniform priors) are presented in Figures 4–6. The posterior modes conform closely to the maximum likelihood estimates with respect to biological parameter values, both among zones and across covariance hypotheses. The dispersion of the posteriors is also consistent with the maximum likelihood standard-deviation estimates.

Likelihood ratio tests can be used to test the hypotheses related to the covariance matrix Σ , thus determining the weights used in the joint likelihood function. Likelihood ratio tests for the example fishery are demonstrated below.

$$\mathbf{H}_2 \text{ vs. } \mathbf{H}_0 \quad 1212.74 - 999.372 = 213.36 \quad \chi^2_{(0.95, 54)} = 70.50$$

$$\mathbf{H}_1 \text{ vs. } \mathbf{H}_0 \quad 1212.74 - 691.789 = 520.95 \quad \chi^2_{(0.95, 72)} = 94.80$$

$$\mathbf{H}_1 \text{ vs. } \mathbf{H}_2 \quad 999.372 - 691.789 = 307.58 \quad \chi^2_{(0.95, 18)} = 28.87$$

Therefore we reject \mathbf{H}_1 in favour of \mathbf{H}_2 , we reject \mathbf{H}_1 in favour of \mathbf{H}_0 , we reject \mathbf{H}_2 in favour of \mathbf{H}_0 and conclude

that the desirable weights for the components of the likelihood function are obtained when the covariance matrix is unrestricted.

Other trials of the model included applying observation errors to the simulated abundance indices that were completely random. In that case, the likelihood ratio test correctly reflected no improvement when the covariance restrictions were removed. In the case of errors that reflected within-zone correlation only, likelihood ratio tests confirmed a significant improvement between \mathbf{H}_1 and \mathbf{H}_2 but not between \mathbf{H}_1 or \mathbf{H}_2 and \mathbf{H}_0 . This demonstrates the ability of the method to effectively detect and account for correlation among indices.

Table 5 also contains evidence of how well the biological model mimics the true data-generating process. The precision of parameter estimation is clearly better for Zones 1 and 2 than for Zone 3, as indicated by the standard-error estimates. This is true for all three covariance–matrix hypotheses. In addition, the precision of estimates for Zone 3 is markedly worse for \mathbf{H}_2 and \mathbf{H}_3 than for \mathbf{H}_0 . The abundance index plots depicted in Figure 3 reinforce these observations.

While the model fits to the observed data are not noticeably improved (Figure 3), all parameters are estimated more tightly when the assumption of independence is relaxed and the covariance matrix is unrestricted. This can be seen in the standard errors of the estimates (Table 5) and in the shape of the posteriors in Figures 4–6. For some parameters, notably h , M and R_0 , the estimates or mode of the posterior distributions actually shift away from the “true” value, however the entire range of estimates still lies well within the range under the other hypotheses. The model overestimates depletion, but this is probably a function of the “one-way trip” and lack of contrast in the data available. This bias does not alter noticeably across covariance hypotheses.

These patterns of improvement and bias can be seen just as clearly in the point and variation statistics of the maximum likelihood results as they can in the Bayesian posterior distribution.

Discussion

We have introduced an approach to using multiple indices of stock abundance and obtaining empirical weights for each of them when assessing fish stocks. The example presented indicates that, where indices are correlated within or across zones or species, simply adding univariate likelihoods for parameter estimation must be rejected in favour of the weighted sum imposed by the multivariate likelihood function. Alternative weighting schemes may be used, of course, but the one that we adopt follows directly from the dynamic model

and likelihood function specified, making its application straightforward and readily computed.

A major implication of testing hypotheses related to the likelihood weights in applied work is that it may become clear whether particular indices are providing inadequate, duplicated or redundant signals. In such circumstances, a review of the need to collect particular data may be warranted. Also of importance is the application of the approach to management of a fishery itself. Because of the clarity of the formal procedure for weighting the abundance indices, interpretation of the resulting stock assessments over time is likely to be less contentious than when arbitrary weights are chosen in a less-structured manner. Furthermore, the structure of our computer program allows relatively easy modification of the biological model to account for direct linkages among species, zones or marine resource uses. Such modification would permit examination of the strength of both deterministic and stochastic linkages within the system supporting marine fisheries.

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