A Bayesian Analysis of NSW Eastern King Prawn Stocks (*Melicertus plebejus*)

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EXTENDED ABSTRACT

Eastern king prawns (*Melicertus plebejus*) are the primary species for significant commercial fisheries in New South Wales (NSW) and Queensland. There is assumed to be a single stock of eastern king prawns that is shared between these jurisdictions with a large migration of both larval and adult prawns across the state borders. The two states manage their exploitation of this species separately. Considerable assessment work has been undertaken on the Queensland fishery and the stock assessment of eastern king prawns has been identified as priority research in NSW.

A Bayesian framework was selected to calibrate a delay-difference model of eastern king prawn stocks in NSW. This allowed the more extensive Queensland research to be incorporated whilst allowing for any unique circumstances in the southern part of the stock to be captured. This methodology enabled the quantification of the uncertainties in the dynamics of the fishery, which was reflected in the subsequent analysis.

There are two primary goals of this analysis (or preliminary stock assessment). The first is to determine the current state and productivity of the stock. The second is to analyse the consequences of various management strategies for the stock. The Bayesian Approach is well suited to both these aims, particularly when there is significant uncertainty about the true population dynamics of the stock; gaps in the data; and multiple sources of information that are relevant.

The Bayesian approach involves comparing the data from various population dynamics models with actual observed data to produce probability distributions of model parameters (posterior probability distribution functions or pdf(s)). This study applied the sampling/importance re-sampling (SIR) method, which was numerically robust and straightforward to implement.

The results of each model run were evaluated by the following criteria: spread of the posterior probability distribution functions and derived statistics; comparison of priors with the associated marginal posteriors; analysis of sensitivity of results to alternative priors; the performance of the model against simulated data; an analysis of residuals and correlation between fitted parameter values; information criteria; a consideration of the strength of the underlying science and a comparison against observable biological indicators.

Various types of uncertainty were considered in this analysis including: process and observation error; uncertainty in model structure and uncertainty associated with the parameter values used in the prior probability distribution functions. Four alternative model structures were considered in this analysis and results indicated that the largest source of uncertainty is the structure of the model.

For all models, the comparison of the parameter priors to their marginal posteriors indicated that the catch rate (catch/effort) data was not a particularly valuable source of information on the dynamics of the stock. This was caused by the lack of contrast in the catch and effort data and the natural variability in the system.

One of the unavoidable consequences of this low contrast in the catch rate data was that it was not possible for any of the four models to determine absolute population levels or stock biomass. This is a common problem for most fish stocks and has led to a number of scientists cautioning against decisions based on absolute biomass levels. Fortunately, results show that the level of uncertainty in the relative biomass levels (such as the depletion ratio over the last 20 years) is much smaller than the uncertainty associated with an estimate of absolute biomass.

1 INTRODUCTION

Eastern king prawns (*Melicertus plebejus*) are the primary species for significant commercial fisheries in New South Wales (NSW) and Queensland. The combined value of the landed catch in both states is over AUD$100 million per year (Queensland DPI 2005; DPI 2001; DPI 2004) with the majority caught in Queensland waters. A small recreational fishery in both states also harvests this species. The commercial and ecological importance of eastern king prawns has seen the development of a number of population models including Lucas 1974; Glaister et al. 1990; Gordon et al. 1995 and O'Neill et al. 2003.

Both industry and fishery managers in NSW have identified the stock assessment of eastern king prawns as research priority (DPI 2001; DPI 2004). A dynamic model of population is an important component of such an assessment and is the motivation for the research presented here. An earlier model on the NSW component of the stock published by Gordon et al. 1995 was a spatial extension to a yield-per-recruit analysis. This deterministic model provided important insight into the trade-offs operating between individual growth, mortality and migration for the fishery along the NSW coast. In contrast, the modelling frameworks developed by O'Neill et al. (2005) used the more standard structures of a delay-difference and length-structured models. Although O'Neill et al. (2005) considered examples from both the NSW and Queensland the emphasis of their study was the Queensland fishery.

The biology and the life-history of eastern king prawns has been considered by Ruello (1975) and Glaister (1983) (amongst others). Such studies have shown that, although the morphology of the species varies little along the east coast of Australia, the demography of the species is very difficult to generalise. The growth, mortality and recruitment of this species appear to vary greatly in time and space.

Data from the commercial fisheries in NSW are not as extensive as those available from Queensland, where the catch and effort information are better resolved. Furthermore, the extensive research into the efficiency or catchability of the fleet (O'Neill et al. 2003) has not been repeated in NSW. The dynamic models developed in NSW need to utilise the information available from Queensland but also re-orient the models toward the management of the fishery in NSW. This requirement suggested that a Bayesian framework would be appropriate to study the dynamics of this fishery in NSW. Although Queensland catch and effort data were not used, much of the research drawn upon to develop the informative prior probability distributions was derived from research conducted on the Queensland fishery.

There are two primary goals of a stock assessment: (1) to determine the current state and productivity of a stock; (2) to analyse the consequences of various management strategies on the stock. The Bayesian approach is well suited to both these aims, particularly when there is significant uncertainty about the true population dynamics of the stock and there are multiple sources of information that are relevant. Only the first aspect of a stock assessment is presented here.

2 METHODS

The Bayesian approach involves comparing the output from various population dynamics models with actual observed data to produce posterior probability distribution functions (pdf). Conceptually the posterior pdf can be regarded as the combination of prior information and observed information. The relative density of a value in the posterior pdf provides the probability that the observed data was produced by the particular model and parameter set (incorporating the prior information) (Walters and Ludwig 1994).

This study applied the sampling/importance re-sampling (SIR) method to all the models. The SIR method is numerically robust and fairly straightforward to implement. Firstly, model parameter values are generated according to their probability within each parameter's prior pdf and the model is run using these values to generate estimated catch rates for each year. These estimated catch rate values are then compared to the actual values using a log likelihood function. This process is done many times (15 million in our case) storing the parameter values of each run along with the results. The final posterior pdf is then fashioned by "re-sampling" (with replacement) from this large sample of runs based on an importance function. In our case the joint prior pdf was used as the importance function which meant that the re-sampling was determined by each run's likelihood value. In this case, the higher the relative likelihood of a run, the better the run's results matched the actual catch rate data, and the more frequently this run would be re-sampled to become part of the posterior. For a more detailed explanation of these steps in the Bayesian SIR model fitting process see McAllister et al. (1994).

A delay difference model was used in this analysis. In terms of complexity, the delay-difference model lies between the simpler surplus production models and the more complex age- or length-structured models. Delay difference models are able to provide some of the advantages of both of these alternatives types of models. Like an age-structured model, the delay-difference model has a sound biological background (such as life history), allowing many parameters of biological significance to be estimated from direct observation. The delay-difference model also retains the simpler data requirements of the surplus production model but allows for the representation of time-lags in growth and recruitment. The model also enables predictions of average body weight (and therefore size), which is an important management indicator when age composition data are not available (Walters and Ludwig 1994). Delay-difference models are also numerically efficient; this aids their application within Bayesian analyses that usually require many millions of iterations.

Delay-difference models are based on a general equation for population biomass that incorporates processes for survival, growth and recruitment. Equations 1 and 2 show the coupled difference equations for biomass and prawn numbers used in this study are:

$$B_t = s_{t-1}\alpha N_{t-1} + s_{t-1}\rho B_{t-1} + w_k R_t \qquad \textbf{(1)}$$

$$N_t = s_t N_{t-1} + R_t \qquad \textbf{(2)}$$

where B_t is the total prawn stock biomass at the beginning of month *t* for prawns that are aged *k+1* months and older; $N_{,t}$ is the total number of prawns in this stock at month *t*; w_k is the average weight of prawns at age *k*; and R_t is the count of new recruit prawns entering the fishable stock at the month *t*. Parameters α and ρ are discussed below.

Survival rate s_t at month *t* is determined by the instantaneous natural mortality rate (*M*) and emigration rate (*G*) to Queensland, as well as the harvest rate h_t using Equation 3:

$$s_t = e^{-(M+G)}(1-h_t) \qquad \textbf{(3)}$$

The harvest rate h_t was calculated as $h_t=C_t/B_t$ (4), where C_t is the observed landed catch in NSW from all commercial fisheries.

Growth of individuals is modelled using the recursive equation:

$$w_a = \alpha + \rho w_{a-1} \qquad \textbf{(5)}$$

where α and ρ are the intercept and slope of the Ford-Walford plot for the prawn species and w_a is the weight of a prawn at month *a* (see Hilborn and Walters 1992 for more details). The growth parameter α is not estimated by the Bayesian analysis but is instead derived from available empirical data on the prawn species including length-at-age plots and weight-length relationships found in Glaister (1983).

In equations (1) to (5) no assumptions have been made about recruitment. A number of alternative representations of recruitment resulted in the creation of multiple model structures. Equations (1)-(5) are common to all four models developed in this study.

For the "Base Model" the stock-recruitment relationship is based upon the Beverton-Holt model (see Haddon 2001). The stock-recruitment relationship is as follows:

$$A^{sr} = w_k\left(1 - \frac{z-0.2}{0.8z}\right) \qquad \textbf{(6)}$$

$$B^{sr} = w_k\left(\frac{z-0.2}{0.8zB_0}\right) \qquad \textbf{(7)}$$

$$R_{t+k} = \frac{(B_t - C_t)}{A^{sr} + B^{sr}(B_t - C_t)} \qquad \textbf{(8)}$$

The parameter *z* represents the steepness of the stock-recruitment relationship, and A^{sr} and B^{sr} are the parameters of the Beverton-Holt stock-recruitment relationship. The parameter *k* represents the number of months between spawning and recruitment into the fishable population.

Bayesian analysis requires the use of the likelihood function to determine the "goodness of fit" of the model to the observation data. The use of the likelihood function thus requires a relationship between the indices of abundance from the model and the actual observed abundance from the observation data. It is assumed that the observed abundance index (in this study the Ocean Trawl Fishery catch per unit effort, CPUE or U_t) is directly proportional to the stock biomass, and is log-normally and independently distributed:

$$U_t \sim Lognormal\,(q_t B_t, \sigma^2) \qquad \textbf{(9)}$$

where B_t is the absolute biomass by weight at time *t*, q_t is the catchability coefficient at time *t*, and σ is the standard deviation of the log-transformed catch rates.

The base model also added seasonal variability to catchability term in the model to reflect the periodicity in the data. This seasonality was approximated with a sine wave:

$$q_t = q_{\min}(1 + [\cos(t / f - p)]^c) \quad \textbf{(10)}$$

where t is the numeric time period in months, f and p are the frequency and phase of the sine wave, and c is the pitch of the sine wave function. The frequency f was set to 12/π in all cases, spreading one full wave over 12 months reflecting the annual catch rate cycles. The pitch parameter, c, provides a mechanism for altering the width of the sine wave that was set to 2 in all cases. This seasonality function parallels the recruitment pattern function used by O'Neill et al. (2005).

Catchability is affected by changes in fishing power, such as gear and vessel changes and technological improvements. An extensive study on the changes in fishing power in the east coast prawn fisheries was conducted by O'Neill et al. 2003. This study relied primarily on Queensland catch and effort data and database of technological changes but has been used here as a means of calibrating our NSW CPUE data. Accordingly a monthly growth in fishing power of 0.00041 month^{-1} was applied over the last 20 years of observations.

Three additional models were also considered in this study. Each model contained the same underlying delay-difference model (described above) but with different representations of recruitment. These alternative models were justified because of the serial autocorrelation identified in the CPUE time series. The presence of autocorrelation in the data violates the assumptions required for the use of the likelihood function. This autocorrelation was likely caused by process error, or a misrepresentation of the relationship specified to link consecutive time-steps. Replacing, or amending, the stock recruitment relationship is the simplest way to improve this representation.

The first derived model is the delay-difference with recruitment error model (RE model) which contains an additional 20 recruitment error parameters, one for each year of the observations. Each process error term is an exponent value applied to the estimated recruitment for each month in one year. Thus, re_y is applied to each estimated recruitment value for month m, in year y.

$$R_{m,y} = \hat{R}_{m,y} e^{re_y} \quad \textbf{(11)}$$

The second model assumes (as per Glaister (1983), Schnute (1985) and Walters and Ludwig (1994)) that recruitment for prawns is primarily driven by the environment. This second derived model replaces the stock recruitment function associated with a constant recruitment with a stochastic term (the recruitment error exponents). We have termed this model the delay-difference with stochastic recruitment (SR) model and have replaced Equation 8 with the stochastic recruitment function given in Equation 12

$$R_{m,y} = (R_0)^{re_y} \quad \textbf{(12)}$$

where R_0 is regarded as the virgin recruitment levels and re_y is the exponent term applied to the estimated recruitment for each month in a year.

The final derived model is the delay-difference with 2 Cycles (2C) model. This model is based on an analysis of the process error terms in the RE model which exhibit a long run cyclic pattern. Thus, this model contains both the short run seasonal catchability cycle as well as an additional long run recruitment cycle. This model is the same as the SR model except that the 20 recruitment error parameters are replaced with the cyclic recruitment function given in Equation 13.

$$R_t = R_0.(1 + \tfrac{1}{2}[\cos(t / LRf - LRp)]^2) \quad \textbf{(13)}$$

where t is the numeric time period in months (1 to 240), LRf and LRp are the frequency and phase of the long-run recruitment sine wave. The ½ term was employed to constrain the amplitude of the function. This equation replaces equation 12 in the SR model.

Simulated catch rates are compared with observations from Jul-1984 to Jun-2004 (20 × 12 = 240 months). Due to transient effects in the model, an iterative burn-in process was used to stabilize the simulation before comparisons with observations were made. The first year of compared data was therefore B_1 (1984/85) not B_0 (which was only used to initialise the simulation).

3 RESULTS

A summary of the results from the assessment are shown below in Table 1. The table includes: the priors and marginal posteriors for the five main estimated parameters for which prior pdfs were used; the estimated biomass at the completion of the run (B_{now} or the biomass in financial year 2003/04); the biomass depletion ratio (B_{now}/B_1); the Average Stock Weight (avg.w) in the final year and two information criteria AIC (Akaike Information Criteria) and BIC (Bayes Information Criteria) (Kass and Raftery 1995). For these information criteria lower values indicate a better model.

Table 1 Results from running each model against the observed data using informative priors.

Parameter	Prior pdf Value		Base Model Est Value	RE Model Est Value	SR Model Est Value	2C Model Est Value
q	5.6E-07	Q1	1.7E-06	1.6E-06	1.9E-06	1.4E-06
	1.4E-05	Mean	2.6E-06	3.0E-06	3.7E-06	2.5E-06
	3.1E-06	Med	2.2E-06	2.3E-06	2.9E-06	2.0E-06
	1.8E-05	Q3	3.1E-06	4.0E-06	4.9E-06	3.1E-06
z	0.81	Q1	0.81	0.81	1.00	1.00
	0.87	Mean	0.88	0.87	1.00	1.00
	0.87	Med	0.88	0.87	1.00	1.00
	0.94	Q3	0.94	0.93	1.00	1.00
M+G (month^{-1})	0.34	Q1	0.36	0.29	0.32	0.46
	0.45	Mean	0.46	0.37	0.40	0.54
	0.45	Med	0.46	0.34	0.39	0.54
	0.57	Q3	0.56	0.44	0.46	0.61
rho (month^{-1})	0.99	Q1	0.95	1.00	0.99	0.98
	1.02	Mean	1.00	1.03	1.03	1.02
	1.02	Med	1.00	1.04	1.03	1.02
	1.06	Q3	1.05	1.08	1.07	1.05
B_0 (tonnes)	5,740	Q1	9,988	6,697	5,852	8,432
	10,456	Mean	13,254	10,905	10,230	12,000
	10,460	Med	13,677	10,832	9,571	12,090
	15,263	Q3	16,801	15,152	14,400	16,293
Bnow (tonnes)		Q1	9,375	6,509	5,127	9,548
		Mean	14,095	12,332	9,309	14,414
		Med	13,056	11,053	8,462	13,926
		Q3	17,188	16,678	12,829	18,847
Bnow/B1		Q1	1.00	0.86	0.88	1.12
		Mean	1.00	0.87	0.89	1.14
		Med	1.00	0.87	0.89	1.14
		Q3	1.00	0.88	0.90	1.16
avg.w (kgs)		Q1	0.04	0.05	0.04	0.05
		Mean	0.05	0.05	0.05	0.05
		Med	0.05	0.05	0.05	0.05
		Q3	0.06	0.06	0.06	0.06
AIC		Q1	-17	-96	-108	-77
BIC		Q1	7	-2	-18	-49
MIR			**0.00**	**0.02**	**0.01**	**0.01**
CV(AIW)			**0.00**	**0.00**	**0.01**	**0.01**
MaxLL Bnow/B1			**1.00**	**0.88**	**0.90**	**1.15**

The last three rows of Table 1 give diagnostic variables that are used to test the quality of the posterior. They are the maximum importance ratio, MIR (McAllister and Ianelli 1997), the coefficient of variation of the average importance weight, CV(AIW) (McAllister et al. 2001). A value of less than 0.05 for each of these variables indicates that the posterior contains an acceptable diversity of parameter sets. The final variable is the value of the Bnow/B1 for the run that achieved the maximum log likelihood, MaxLL B_{now}/B_1. This last posterior diagnostic is compared to the median and the first and third quartiles of the Bnow/B1 posterior pdf to ensure that the maximum log likelihood does not occur on the edges of the posterior (Oh and Berger 1992).

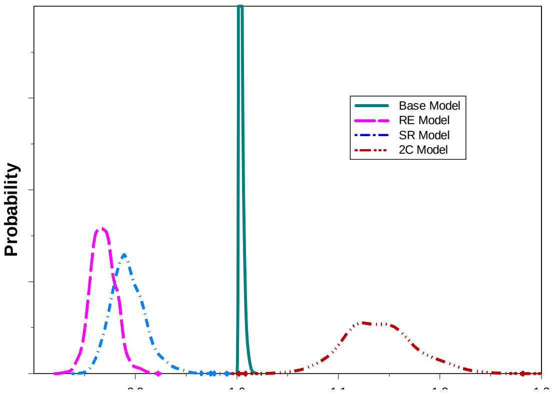

Figure 1 Illustration of the posterior probability distributions of B_{now}/B_1 for the four models.

Figure 1 illustrates the marginal posterior probability distributions of B_{now}/B_1 of the four models using the prior pdfs given in Table 1. Note how the differing representations of recruitment cause a far greater divergence in the biomass ratios than the variability in the parameters estimates within a particular model.

The small variability of the posterior for the Base model was consequence of the poor model fit (note the relatively large AIC and BIC values for this model). Only the RE, SR and 2C models gave a satisfactory fit to the data.

4 DISCUSSION

The Bayesian Sampling Importance/Resampling (SIR) algorithm applied here is a relatively simple and versatile Monte Carlo method for use in fisheries assessment. The method allows the use of prior pdfs for any number of model parameters enabling existing research on the species to be incorporated into the model fitting exercise. Such information not only provides information on parameter values but also levels of uncertainty or variability in these parameter values. Bayesian methods also provide us with a framework in which to compare multiple model structures allowing us to deal with the important problem of model uncertainty (Hilborn and Punt 2001).

Comparing the model against simulated and actual data exposed a number of weaknesses in our Bayesian SIR approach. None of the models could be fitted to the data satisfactorily if completely uninformative priors were used. Solutions were found for each of our models using informative priors although we were required to fix a number of parameters (i.e. set completely informative priors) despite our knowledge of these parameters being imperfect. Finally, for the SR and RE models we also had to provide the recruitment error terms with partially informative priors.

In short, the lack of contrast in the catch and effort observations meant that we had to point our Bayesian model in the right direction using informative priors. Increasing the number of iterations used in the SIR algorithm could ameliorate this issue. However, computational limitations prevented us from exceeding 15 million iterations despite our use of a method for reducing memory requirements by storing only each run's random number seed instead of their complete parameter vectors (McAllister and Ianelli 1997).

This analysis of the NSW eastern king prawn stocks illustrates the large degree of model structure uncertainty possible in such stock assessments. Each of the four models provides a very different posterior pdf of the management indicator B_{now}/B_1 (Figure 1). However, despite this uncertainty, none of the model structures suggest that the stock is in a severely overfished condition.

One of the unavoidable issues resulting from the low contrast in the catch and effort data was that it was not possible for any of our models to credibly determine absolute biomass. This is a problem for many fish stocks; even those rich with observational data, and has led to a number of scientists cautioning against decisions or decision-making frameworks that require absolute estimates of biomass (Hilborn 2002). These results have shown that the level of uncertainty surrounding management indicators based on relative biomass levels, such as the depletion ratio, is much smaller than that associated with an estimate of the absolute exploitable biomass.

This research has a range of possible future directions. The Bayesian approach could be refined by improving the importance function or applying an alternative sampling methodology, such as adaptive importance sampling (Oh and Berger 1992). Including spatial processes and a length structure for the prawn population would increase the biological resolution of the models, but at the expense of an increase in the number of parameters. Incorporating the Queensland fishery would eliminate the need for an emigration term and may enable easier specification of a stock recruitment relationship (if it exists).

There are also a number of avenues for further research into the consequences of alternative management of this stock. For example, simulation modelling could be utilised to evaluate the most efficient avenues for further research, such as whether research in biological parameters would bear more fruit than conducting independent surveys. The model could also be expanded to include socio-economic components to consider the possible consequences of alternative management strategies on the individuals and industries dependent on the prawn stock. The recently published work of Holland et al. (2005) demonstrated the values of coupling an economic component to a Bayesian stock assessment model

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