

# Bayesian state-space modeling of age-structured data: fitting a model is just the beginning

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**Abstract:** Explicit modeling of process variability in the dynamics of fisheries is motivated by a desire to incorporate more realism into stock assessment models, and much recent research effort has been devoted to the computational features of fitting state-space models for this purpose. Here, we extend the Bayesian application of nonlinear state-space modeling to sequential population analysis of age-structured data using a model formulation that allows for unreported catches and incidental fishing mortality. It is shown that, once a familiarity with the general-purpose Bayesian software BUGS is acquired, implementing a state-space model is a relatively simple task. Indeed, this application requires just 18 lines of code in its entirety, and does not require the programmer to know the formulae for any prior density functions or likelihoods. Consequently, we suggest that this methodology may permit the implementation phase of nonlinear state-space modeling to be relegated, thereby allowing more effort to be devoted to the challenging issues of model checking, selection/averaging, sensitivity and prior specification.

## Introduction

A model provides a conceptual framework for learning about reality. It is necessarily a simplification, but must retain the ability to capture the features that are required to address questions of interest. In fisheries stock assessment the modeling considerations are manifold. In addition to the question of appropriate functional specification (e.g., Fox or Schaefer surplus production; depensation at low stock size; hyperstability of CPUE data), other vital issues include the ability of the model to cope with the frequent shortcomings of the data (e.g., mis-reported catches; ageing errors; correlation) and the effects of process randomness (e.g., variability in population dynamics).

Much recent effort has been invested in using state-space methodology to incorporate process randomness in stock assessment models (e.g., Sullivan 1992; Pella 1993; Schnute 1994; Gudmundsson 1994, 1995; Freeman and Kirkwood 1995; Kimura et al. 1996; Reed and Simons 1996). State-space models can also incorporate variability in key population parameters (e.g., carrying capacity or natural mortality) by allowing the parameter to follow a first order autoregressive process over time. In contrast, models without process error imply deterministic biomass trajectories and time invariant parameters. Under these assumptions, a surplus production model (e.g., Schaefer 1954; Hilborn and Walters 1992) predicts the exact biomass of the stock into the infinite future as a deterministic function of the current biomass and harvesting policy.

Most of the existing work on state-space modeling of fisheries dynamics has used classical likelihood-based statistical theory, as distinct from the Bayesian approach used here. Calculation of the likelihood function requires high dimensional integration because it is

necessary to integrate over the unobserved process errors (see Schnute 1994). A tractable integral is obtained when the model is linear and has normally distributed errors, whence the fit can be achieved using the Kalman filter (see Meinhold and Singpurwalla 1983). However, linearity and normality greatly restrict the realism and general applicability of the state-space methodology. In the case of nonlinear state-space models, the computational intractability results in the use of approximate fits such as that obtained using linear approximation (the extended Kalman filter). Despite considerable interest in state-space models, and indications that they *do* have superior performance compared to deterministic models (Anon 1995), they are not widely used because of these complications.

Some fisheries state-space models have been fitted using penalized likelihood (e.g., Ludwig et al. 1988; Schnute 1994; Richards and Schnute 1998) as an alternative to standard likelihood. This approach treats process errors as fixed parameters to be estimated, and hence, fitting of the model reduces to a conceptually simple maximization problem because the likelihood for the observables is an explicit function of the specified values of the model parameters and process errors. This methodology has the advantage of being very generally applicable, but the disadvantage of undesirable properties under common circumstances. For example, when using penalized likelihood to fit generalized linear mixed models, the estimates of fixed effects are not consistent when there are limited data per random effect (which is typically the case), for which asymptotic bias correction formulae have been provided by Lin and Breslow (1996).

Tractability concerns are not as relevant to fully Bayesian state-space models (e.g., Carlin et al. 1992) because the Markov Chain Monte Carlo (MCMC) techniques used for

sampling from the joint posterior are very general in their application. These are numerically intensive techniques which do not rely on algebraic simplifications being obtained from assumptions such as linearity and normality. Millar and Meyer (1999) and Meyer and Millar (1999a) implemented surplus production and delay-difference state-space models, respectively, and used C++ to perform the MCMC sampling. Recently, the use of C++ has become unnecessary due to enhancements to the BUGS (Bayesian inference Using Gibbs Sampling) software package (Gilks et al. 1994; Spiegelhalter et al. 1996). Meyer and Millar (1999b) introduced the BUGS software and showed how it provides a convenient implementation of the Bayesian state-space surplus production model of Millar and Meyer (1999).

The use of MCMC does require some care. The joint posterior distribution is the equilibrium distribution of the Markov chain. Hence, it is necessary to check that the Markov chain has been run for sufficiently long to ensure that it is sampling from its equilibrium distribution. (This is called “burning in” of the chain). In addition, it must be checked whether the chain is “mixing” well, in the sense of being able to move easily through the possibly high dimensional space of the posterior distribution. These concerns are briefly examined in the context of the example presented herein. See Meyer and Millar (1999b) for more detail.

The purposes of this manuscript are two-fold. First, the application of Bayesian state-space models is extended to age-structured data. In its entirety, the implementation requires 18 lines of BUGS code, and at no stage is there a requirement for the modeler to know the details (e.g., formulae) for density functions or likelihoods. A knowledge of

modeling at the level of Hilborn and Mangel (1997) is sufficient. Second, we consider the wider consequences of the demonstrated flexibility and expedience of implementation. In particular, we suggest that the process of stock assessment modeling should now focus on the more important issues of model checking and selection (or averaging). Of course, in the Bayesian paradigm, there is also the need to consider prior specification.

### **Age-structured state-space model**

The model presented here is developed for an example where the data are indices of numbers-at-age obtained from research vessel surveys. Reported catch-at-age numbers are also utilized, but these are treated as constants and are not modeled as response variables. (In assessments where reliable commercial effort data are available then treating reported catch as a response may be a sensible modification to the model.) Moreover, the model does not rely on the reported catches being accurate or precise and they are simply regarded as one component of the true overall fishing mortality.

Randomness in the fisheries dynamics is incorporated by dispensing with the concept of a fixed (and typically “known”) natural mortality. In fact, here, the notation  $m^+$  will be used to denote *all* mortality in addition to the reported catches. It therefore includes natural mortality, unreported catches, and unaccounted fishing mortality arising from discarding, high-grading, ghost fishing, and due to injury of fish escaping the gear (e.g., Sangster et al. 1996). (See Chopin et al. (1996) for an in depth discussion of unaccounted mortality.) Unaccounted mortality can be a major problem in some fisheries, for example, Myers et al. (1997) argued that high unaccounted mortality of juveniles was a contributing

cause of the collapse of six Canadian populations of Atlantic cod.

The data and model formulation used here differ substantively from the likelihood-based age-structured model used by Gudmundsson (1994). However, they do have in common the modeling of mortality, and consequently both are nonlinear models. Gudmundsson (1994) used the extended Kalman filter to obtain an approximate maximum likelihood fit. In the Bayesian implementation, the BUGS software is sufficiently versatile at performing MCMC sampling that the nonlinearity does not present any additional difficulties.

### Process equation

If  $N_{a,y}$  is the true number of age  $a$  fish at the start of year  $y$  and  $C_{a,y}$  is the catch taken during year  $y$ , then the cohort equation is frequently written as

$$N_{a,y} = N_{a-1,y-1} \exp(-m) - C_{a-1,y-1} \exp(-0.5 * m) \quad (1)$$

where  $m$  is natural mortality. This model is derived from assuming that fishing occurs in the middle of the year, and is known to be insensitive to this assumption (Mertz and Myers 1996).

Of course, in reality, the catches are not known exactly, natural mortality may vary, and other sources of fishing related mortality are likely. There are a variety of ways to incorporate variability in (1) (see Discussion). Here, the cohort equation was modified by putting age and year subscripts and a "+" superscript on the quantity  $m$ , giving

$$N_{a,y} = N_{a-1,y-1} \exp(-m_{a-1,y-1}^+) - C_{a-1,y-1} \exp(-0.5 * m_{a-1,y-1}^+) . \quad (2)$$

The biological interpretation of equation (2) effectively gives  $m_{a,y}^+$  the desired definition of all mortality on age  $a$  fish in year  $y$  beyond that accounted for by the reported catches.

### Observation equation

The published research vessel indices and catches of Myers and Cadigan (1995b) are used here. Their Table 1A gives relative indices of numbers-at-age,  $I_{a,y}$ , from autumn research surveys on the 2J-3KL stock of Atlantic from 1978 through 1993 and for ages 3 through 12. Table 1B of Myers and Cadigan (1995b) gives the reported catches-at-age,  $C_{a,y}$ , for age  $a$  in calendar year  $y$ . Myers and Cadigan (1995a, 1995b) assume the indices,  $I_{a,y}$ , to have lognormal distributions. However, Table 1A of Myers and Cadigan (1995b) contains five indices which, to two decimal places, were rounded down to zero. Here, these five indices were given the value of 0.001 so that they would not violate the assumption of lognormal distribution.

The autumn surveys for 2J-3KL cod take place largely in November. If the numbers-at-age at the time of the survey are denoted  $N_{a,y}^I$ , then the log of numbers-at-age at the time of the survey is well approximated by

$$\log(N_{a,y}^I) = (\log(N_{a,y}) + 11 \log(N_{a+1,y+1}))/12 . \quad (3)$$

There are a variety of choices for modeling the distribution of the relative abundance index  $I_{a,y}$ . The lognormal distribution is generally considered a sensible choice for a relative abundance index, whence

$$I_{a,y} \sim LN(\log(q_a N_{a,y}^I), \sigma^2) , \quad (4)$$



where  $\sim$  denotes “distributed as”,  $LN(\cdot, \cdot)$  denotes the lognormal distribution (with parameters being the mean and variance of the log of the variable), and the  $q_a$ 's are age dependent catchabilities. That is,

$$\log(I_{a,y}) = \log(q_a N_{a,y}^I) + \epsilon_{a,y} , \quad (5)$$

where  $\epsilon_{a,y}$  are independent  $N(0, \sigma^2)$  distributed error terms. The expected value of  $\log(I_{a,y})$  is  $\log(q_a N_{a,y}^I)$ , which (from equation (3)) can be written as

$$\log(q_a N_{a,y}^I) = \log(q_a) + (\log(N_{a,y}) + 11 \log(N_{a+1,y+1}))/12 . \quad (6)$$

## Priors

Bayesian implementation of this model requires specification of prior distributions on all unobserved quantities (these are denoted in Appendix A). The specification of some of these priors has parallels with the classical methodology for sequential population analysis where, for example, auxiliary information is used to specify various mortality rates. In particular, virtual population analyses (VPA's) of the 2J-3KL cod stock have traditionally fixed  $m$  at 0.2 and regarded this quantity as natural mortality. Recall that here this quantity is denoted  $m_{a,y}^+$  because it is permitted to vary with age (of cohort) and year, and denotes all mortality in addition to the reported catch. For example, the distribution of  $m_{a,y}^+$  can be made age-specific by use of a hierarchical prior of the form

$$\begin{aligned} m_{a,y}^+ &\sim LN(\mu_a, \tau^2) \\ \mu_a &\sim N(\nu, \sigma^2) \quad , \quad \tau^2 \sim IG(\alpha, \beta) , \end{aligned} \quad (7)$$

where  $IG$  denotes the inverse gamma distribution. Setting  $\nu = \log(0.2)$  gives each  $m_{a,y}^+$  a prior median value of 0.2. A high value of  $\sigma^2$  would then represent little prior confidence

in the presumption that  $m_{a,y}^+$ 's are close to 0.2 and age-independent. This particular prior specification does not explicitly model a year effect on the  $m_{a,y}^+$ , notwithstanding that choosing  $\alpha$  and  $\beta$  to give a highly dispersed hyperprior distribution for  $\tau^2$  corresponds to little prior belief in  $m_{a,y}^+$  being constant over time within each age class.

In a VPA it is necessary to specify terminal mortalities for age  $A$  fish in each year and for all ages in the most recent year. For the model herein the analogy of this is the requirement to place priors on recruitment (in all years) and numbers-at-age in the initial year ( $y = 1$ ). Lack of knowledge about these quantities would be represented by use of a noninformative prior or a diffuse prior.

The wider issue of specifying priors is deferred to the Discussion, where we discuss this aspect of model specification in conjunction with the issues of model selection and checking.

## Implementation

In a Bayesian example, "analysis" corresponds to determining the posterior distribution of unknowns of interest. The BUGS software is a Markov chain Monte-Carlo tool that samples numerically from the joint posterior of the unknown quantities (Gilks et al. 1996), subject to the chain being run sufficiently long to ensure burn-in. See Meyer and Millar (1999b) for details of the operation of BUGS in the context of a surplus production model.

Programs implemented in BUGS can be expressed in text form (Appendix A) or represented graphically (Fig. 1). For this catch-at-age example, the heart of the program (lines 02 to 10, Appendix A) is simply the requirement to write equations (2), (4), and

Fig. 1  
near  
here

(7) within the permitted syntax of BUGS. (For the program, the age and years have been translated such that  $a = 1$  and  $y = 1$  are the youngest age and first year for which data are available.) The latter part of the BUGS code (lines 11 to 18) is specifying prior distributions for the unobserved quantities. (BUGS does not allow improper priors to be used, and hence non-informative improper priors are approximated by diffuse proper priors.) Meyer and Millar (1999a) show how the statistical risks associated with various harvest and management scenarios can be assessed by minor addition to the BUGS program.

As an indication of the type of “results” provided by this example, density plots of 9500 samples from the posterior distribution of numbers-at-age at the start of 1983 are displayed in Fig 2. These were obtained from a run of length 100 000 in which a thinning of ten was used, that is, only every tenth sample was saved to disk. This is a useful strategy when successive samples are correlated and also keeps the output file down to a reasonable size. Convergence diagnostics were checked using CODA (Best et al. 1995) and burn-in was achieved after discarding the first 500 of the saved samples.

Fig 2  
near  
here

## Discussion

The previous section constructs and fits an age-structured model in which the state-space formulation of equation (2) permits a plausible cohort equation with a biological interpretation. However, it would be inappropriate to use the results from this model for inference about current stock status or for risk management. There are many challenging issues which must first be addressed. A non-exhaustive list is given below:

1. Alternative formulations to equation (2):

- For example, Northern cod are traditionally analysed using a VPA model which reconstructs the cohorts backwards in time and requires assumptions about terminal fishing mortalities.
- True catches could be modeled as unobservables, and reported catches used as measurements on these unobservables.

2. Use of additional data:

- Commercial effort data could be used to model reported catch.
- Further structure could be imposed upon  $m_{a,y}^+$  by using environmental data, or assuming that incidental mortality is related to fishing effort. For example, if  $E_y$  is the fishing effort in year  $y$  and  $d_a$  is a measure of instantaneous age-dependent incidental mortality, then the incidental mortality component of  $m_{a,y}^+$  could be modeled by adding a term proportional to  $d_a E_y$ .

3. Paradigm shifts, such as increased natural mortality, could be modeled by imposing temporal autoregressive structure on  $m_{a,y}^+$ . Similar consideration could be given to putting autoregressive structure on recruitment.

4. Ageing errors.

5. Correlated research survey indices,  $I_{a,y}$ , within years.

6. Specification of priors.

7. Sensitivity to priors.

The model fitting considerations in items 1 to 5 are relevant to any age-structured analysis. There are two features of the model fitting process that are particularly relevant to the Bayesian state-space approach presented here: prior specification and flexibility of implementation.

### **Prior specification**

The model formulation (Appendix A) requires prior specification of  $m_{a,y}^+$ 's,  $q_a$ 's,  $\sigma^2$  (observation variance), and of the top and left margins of the table of numbers-at-age (that is, the age-structure in the first year, and subsequent recruitments). Opponents to Bayesian methodology would argue that this daunting task is sufficient reason to dismiss this Bayesian model as unworkable. However, such an expedient dismissal overlooks the reality that classical VPA requires similar prior knowledge. For example,  $m$  is typically assumed to be *constant* and *known*, structure on catchabilities by age,  $q_a$ 's is imposed, the ratio of error variances is assumed (e.g., Richards and Schnute 1998), and terminal mortalities must be specified or derived.

When prior knowledge is not available then non-informative priors can often be derived. However, much current work is aimed at obtaining formally derived informative priors using hierarchical analysis (Myers et al. 1999; Hilborn and Liermann 1999). Finally, recommendations for construction of vaguely informative priors can be utilized (e.g., Spiegelhalter et al. 1994; Gelman et al. 1995), along with suitable sensitivity analysis.

### **Flexibility**

BUGS is a numerically intensive software package that implements general Bayesian models using “Metropolis-Hastings within Gibbs sampling” (Gilks 1996). It does not rely on simplifying assumptions (e.g. linearity, normality) for the very reason that it employs a numerical technique for sampling from the joint posterior. In addition, all commonly used (and many other) statistical distributions are recognized by BUGS and this allows a vast range of models to be implemented in BUGS without the need to specify formulae for densities or likelihoods. With few exceptions, once the model has been expressed (in the form of equations (2) and (4), for example) then it can be transcribed into a BUGS program. Thus, using BUGS for stock assessment is quite different from using pre-written computer code, spreadsheets, or specific modules, functions or procedures within statistical software packages, which typically constrain the user to a particular class of model and analysis.

Some of the above alternative models can be implemented with very little change to the BUGS code (Appendix A). For example, Myers and Cadigan (1995a) detected a significant within-year correlation in the research survey indices,  $I_{a,y}$ , and modeled this as a normally distributed random effect on the log-scale. Appendix B shows that the BUGS code required to implement this alternative differs from the BUGS code of Appendix A by just two lines.

We can not guarantee that all the above model alternatives listed above (or of interest to the reader) can be fitted with ease using BUGS. However, the potential for exploring a vast number of (possibly very complex) models is definitely immense.

## Looking ahead

The great flexibility of implementation and the possibilities for alternative prior specification combine to create a bewildering set of competing models. Model checking (e.g., Gelman et al. 1996) and sensitivity analysis will of course be vital tools, and model averaging may be a useful approach (e.g., Raftery 1996).

The issue of prior specification is receiving considerable research attention, both theoretical and applied, within the statistical and fisheries communities (e.g., Myers et al. 1999, Sun and Berger 1998). These efforts will establish guidelines for prior specification and formally derived priors will become available for certain key population parameters. Nonetheless, there will never be an “absolute” regarding the specification of priors, and many modelers therefore see the need for priors as the Achilles heel of Bayesian methodology. However, it is also the strength of the Bayesian approach - it is the only coherent statistical methodology for updating knowledge using the information contained in data (De Finetti 1974). This property enables the posterior from one analysis to be used as an induced prior in a subsequent analysis, thereby building and exploiting an accumulated base of knowledge.

There is a moderate learning curve to ascend before one can write a complete BUGS program. However, anyone who is comfortable with model formulae and has an intuitive grasp of fundamental statistical concepts should be capable of understanding, using, and modifying BUGS code that has already been written for a particular stock assessment task. For a Bayesian analysis, the required statistical knowledge includes familiarity with the Bayesian paradigm and an appreciation for the numerically intensive methods used to

sample from the posterior distribution.

Knowledge, preferably first-hand, of the stock is required for either a Bayesian or classical model. If the tribulations of model implementation are reduced then there may be an opportunity to address some of the concerns identified by Rose (1997). In particular, looking beyond the mere fitting of the model, the issues of model selection and prior specification can not be fully answered from the desktop. The modeler will have to go further afield, to obtain a greater understanding of the aquatic system that they have the responsibility of modeling.

The example herein is the most sophisticated that we have yet fitted using BUGS and is perhaps at the present limit of practical usability in terms of computational requirements. A 233 MHz laptop generates about 5000 samples per hour from the joint posterior. However, many useful models for stock assessment will be of lesser complexity, for example, the state-space surplus production model used in Meyer and Millar (1999b) generated timely results at the rate of 100 samples from the joint posterior per second. We are optimistic that the slow speed of the age-structured model presented herein will be just a transient difficulty. Continual improvements in the BUGS software are improving its performance and capabilities, and indeed, it was simply not possible to implement any of these state-space models in the 1997 versions of BUGS. Moreover, the most successful speed-ups are often obtained via minor changes to the code (such as reparameterization) and this is an area that requires further exploration.



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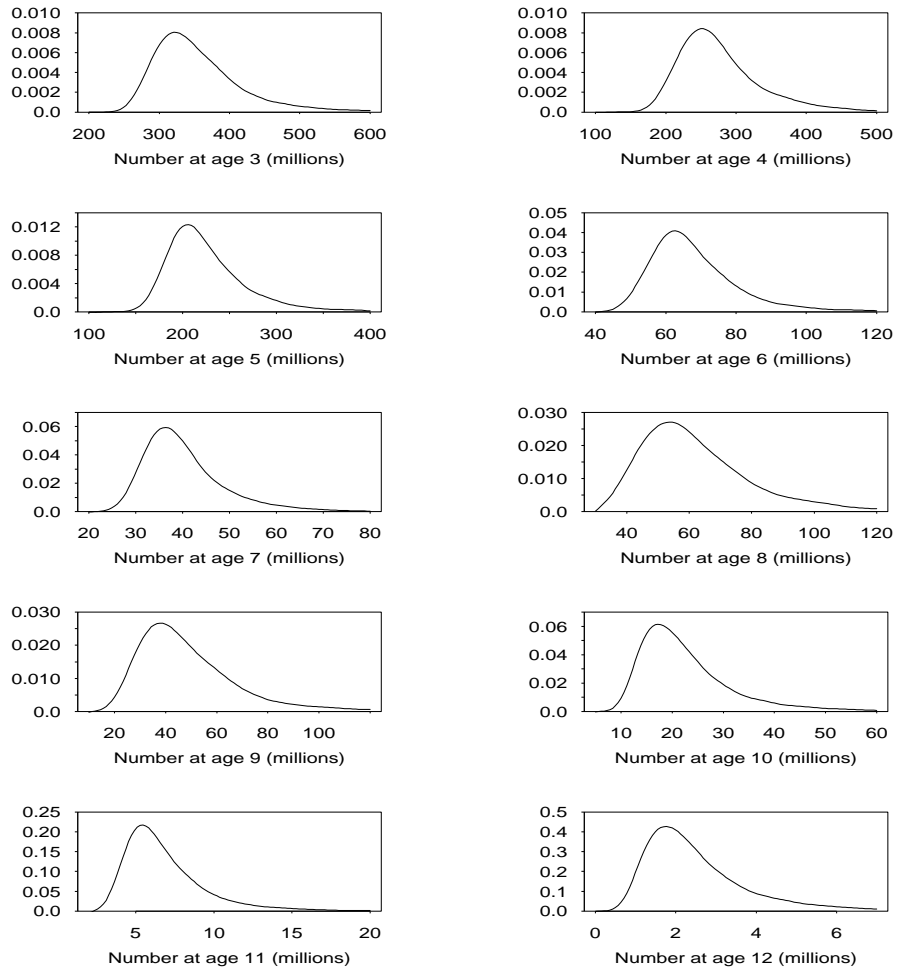
## Figure captions

Figure 1. Directed acyclic graph of the model in Appendix A. Logical links are shown using a double arrow and correspond to use of the  $\leftarrow$  symbol in Appendix 1. Stochastic links use a single arrow and correspond to the  $\sim$  symbol in Appendix 1. Catch-at-age numbers are treated as constants and hence are represented using a rectangular box.

Figure 2. Posterior distributions for numbers-at-age at the start of 1983, obtained from 100 000 iterations of the Gibbs sampler. Every tenth sample was saved, and the first 500 of the 10 000 saved samples were discarded to allow for “burn-in” (i.e., convergence of the chain). The plots used the remaining 9500 samples.

Fig. 1

Fig. 2:





## Appendix A

This appendix contains the entire WINBUGS (BUGS for Windows, version 1.1.1) program required to implement the example. The data (Tables 1a and 1b of Myers and Cadigan, 1995b) are contained in a separate data file which is loaded into WINBUGS by double clicking on the file icon. WINBUGS' menus are used to monitor and sample from the joint posterior distribution.

Notes:

1. All lines beginning with the character # are comments.
2. In this code, M is used to denote  $m^+$ .
3. BUGS follows the Bayesian tradition of using precision rather than variance when specifying the parameters of a distribution such as the normal or lognormal. Precision is the inverse of variance.
4. BUGS uses the symbol <- as the "equals" operator, and uses ~ to denote "distributed as". For example,  
  
`x~dnorm(0,0.25)`  
  
denotes that x has a normal distribution with mean and variance equal to 0 and 4, respectively. To denote the lognormal distribution, dlnorm is used.
5. Values p1 through p12 are scalar constants specifying parameters of prior distributions. Several of these constants have values that can be justified via reasonable argument or from prior belief. For example, the prior on MeanLogM could reflect the

historical value of 0.2 used for natural mortality by setting  $p_3 = \log(0.2)$ . Then, the prior for  $M[a, y]$  has median of 0.2. Other values can be chosen to reflect a lack of prior knowledge.

```
#State-space sequential population model for the age-structured 2J3KL cod
#data from Myers and Cadigan (1995b)
```

```
01  model cod; {

    #####Distribution for data, I[a,y]#####
02  for (a in 1:A) {
03    for (y in 1:Y) {
04      MeanLogI[a,y]<-Logq[a]+(LogN[a,y]+11*LogN[a+1,y+1])/12;
05      I[a,y]~dlnorm(MeanLogI[a,y],PrecLogI); } }

    #####Prior on mortalities, hierarchical#####
06  PrecLogM~dgamma(p1,p2);
07  for(a in 1:A){ MeanLogM[a]~dnorm(p3,p4);
08    for(y in 1:Y) { M[a,y]~dlnorm(MeanLogM[a],PrecLogM); } }

    #####Cohort equations#####
09  for(a in 2:(A+1)) {
10    for(y in 2:(Y+1)) {
11      LogN[a,y]<-log(exp(LogN[a-1,y-1])*exp(-mplus[a-1,y-1])-
12                C[a-1,y-1]*exp(-0.5*mplus[a-1,y-1])); } }

    #####Priors on first row and column#####
13  for(y in 1:(Y+1)) {LogRecruits[y]~dnorm(p5,p6);
14                    LogN[1,y]<-LogRecruits[y]; }
15  for(a in 2:(A+1)) {LogInitials[a-1]~dnorm(p7,p8);
16                    LogN[a,1]<-LogInitials[a-1]; }

    #####Prior on q's#####
17  for (a in 1:A){ Logq[a]~dnorm(p9,p10); }

    #####Prior on precision of log(I)#####
18  PrecLogI~dgamma(p11,p12); } }
```

## Appendix B

Myers and Cadigan (1995a, 1995b) discovered that the relative biomass indices were correlated within years. They modeled this correlation in the form

$$\log(I_{a,y}) \sim N(\log(q_a N_{a,y}^I) + \xi_y, \sigma^2)$$

where  $\xi_y$  are independent  $N(0, \phi)$ . This new specification for the distribution of  $I_{a,y}$  can be added to the model by inserting as line 19

```
for (y in 1:Y) {xi[y]~dnorm(0,p13);}
```

and changing line 04 to

```
04      MeanLogI[a,y]<-Logq[a]+(LogN[a,y]+11*LogN[a+1,y+1])/12+xi[y];
```