

**Abstract.**—Recently, J. J. Pella showed how the Kalman filter could be applied to production modeling to estimate the size and productivity of fish stocks from a time series of catches and relative abundance indices. We apply these methods to the Deriso-Schnute delay-difference equation. The Kalman filter approach incorporates process and measurement error naturally in the model description. When the production model is the delay-difference equation, the error structure is particularly attractive because process error can be interpreted as simply the variance of recruitment, and measurement error as the variance of the relative abundance estimates. We derived prior distributions of initial biomass in order to begin the Kalman filter calculations. Reanalysis of the data from the eastern tropical Pacific for yellowfin tuna, *Thunnus albacares*, shows that modeling results can differ greatly depending on whether error is interpreted to be process error or measurement error. Simulation results show that nonlinear least squares and Kalman filter estimates agree well if data contain only measurement error. In contrast, the Kalman filter was clearly superior if simulated data contained significant amounts of process error. The presence of process error positively biased biomass estimates from both the nonlinear least-squares and Kalman filter methods. The Kalman filter performed well with Schnute's form of the delay-difference equation, even though this model violates the assumption of independent process error vectors. The Kalman filter also performed well when the variance ratio  $r$  was assumed known and individual variances were estimated from the data. However, it appeared difficult to estimate  $r$  as a parameter in the maximum-likelihood estimation.

## Kalman filtering the delay-difference equation: practical approaches and simulations

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Fishery production models are used to model fishery population dynamics when only catch (measured in biomass units) and relative abundance data are available. Originally, only fishery catch-per-unit-of-effort data (Schaefer, 1954; Pella and Tomlinson, 1969) were used as relative abundance indices for fish populations, but surveys often provide less biased abundance measures. Therefore, both time series of fishery CPUE and survey abundance indices are commonly used estimates of relative abundance.

Production models contrast with age-structured models, such as ADAPT (Gavaris, 1988) and Stock Synthesis (Methot, 1989), that model the population cohort in numbers at age and typically require catch-at-age data. Age-structured models allow for variation in recruitment which has given this class of model greater credence among stock assessment scientists. However, age data are technically difficult to obtain, expensive, and contain biases and variability that can be difficult to interpret. In addition, age-structured models often contain a large number of parameters, and sifting through possible solutions when fitting multiple sources of data can be subjective.

Because of these data requirements and technical problems, production models have remained of

interest to stock assessment scientists. Recent production model offerings have included statistical refinements such as bootstrapping (Prager, 1994), Bayesian analysis (Hoenig et al., 1994), and the treatment of statistical error (Polachek et al., 1993). Two of the earliest papers to consider both process and measurement error in population dynamics modeling were those of Ludwig and Walters (1981) followed by Collie and Sissenwine (1983). The Kalman filter approach, which allows the consideration of both process and measurement error, now appears to be becoming standard for assessments by either production or age-structured models (Mendelsohn, 1988; Sullivan, 1992; Pella, 1993; Schnute, 1991, 1994).

The methods described in this paper meld two distinct pieces of technology: the delay-difference equation (Deriso, 1980; Schnute, 1985), and the Kalman filter (Kalman, 1960; Harvey, 1990; Pella, 1993). Collie and Walters (1991) used the Kalman filter to predict and update biomass estimates on the basis of the delay-difference equation but did not use the Kalman filter for parameter estimation. The delay-difference equation has deep roots in fishery modeling. In fact, to a remarkable extent it can encompass the fundamental paradigms of age structure, exponential

survival, and von Bertalanffy growth. The Kalman filter (Kalman, 1960), on the other hand, originated in engineering where it has been widely used in control theory and quality control. The basic idea of Kalman recursive filtering (Meinhold and Singpurwalla, 1983) is that the current state of the system (i.e. the current fish biomass) can be estimated from the system's past (biomass) estimates in two steps: a forecast step and an update step. The forecast estimate is made prior to the current observation of relative abundance; the updated estimate is made following the current observation of relative abundance. The updated estimate of biomass is the modeler's best estimate of the "true" biomass and is, roughly speaking, a weighted average between the forecast and observed abundance values. The updated biomass estimate is used to forecast the next biomass estimate, which then is updated with the next observed value. The absolute and relative magnitude of process and measurement error, which are assumed normal and whose values are generally assumed by the filter, largely determine the result of the update step. If there is little process error assumed by the filter, updating will not substantially change the forecast biomass estimate.

For fishery modeling, the most salient feature of the Kalman filter is its allowance for both process and measurement error. In the implementation of the delay-difference equation with the Kalman filter, process error can be interpreted as the variance of recruitment,<sup>1</sup> and measurement error as the variance of the estimate of relative abundance. Thus the Kalman filter method allows for variation in recruitment, a property that heretofore seemed to be exclusive to age-structured models.

The implementation of the Kalman filter presented here is due to Pella (1993), who applied the method to a simple recruitment model ascribed to Schnute (1991) and to the generalized production model of Pella and Tomlinson (1969). For comparative purposes, we also fitted the delay-difference equation with ordinary nonlinear least squares, which in this case assumes that data contain only measurement error.

## The delay-difference population dynamics model

The delay-difference equation is a simple biomass-based model that contains the core dynamics of age-

structured models (Deriso, 1980; Schnute, 1985). Thus under many conditions the population dynamics described by the delay-difference equation should agree with that of age-structured models (e.g. virtual population analysis). The applications of the delay-difference equation we propose require the following parameter values and information:

- 1 The instantaneous natural mortality rate  $M$ .
- 2 Brody<sup>2</sup> growth parameters  $\rho$  and  $\omega$ .
- 3 Annual catches in biomass  $c_t$ ,  $t=1, \dots, n$ .
- 4 Annual survey biomass estimates  $y_t$ , either relative (catchability unknown) or absolute (catchability known) abundance indices, with a few missing values allowed.

The natural mortality rate,  $M$ , is always difficult to know but estimates or educated guesses are usually available. The Brody growth parameters can be estimated with nonlinear least squares on relatively small aged samples that provide weight-at-age data (Schnute, 1985):

$$W_{k+j} = \omega_{k-1} + (\omega_k - \omega_{k-1})(1 - \rho^{1+j}) / (1 - \rho) \quad \text{for } j \geq 0. \quad (1)$$

Here,  $W_{k+j}$  is the observed weight of a  $k+j$  yr-old fish,  $\omega_{k-1}$ ,  $\omega_k$ , and  $\rho$  are parameters to be estimated, and  $k$  is the age at recruitment. Our application of the delay-difference equation requires  $\omega = \omega_{k-1} / \omega_k$  so that  $\hat{\omega} = \hat{\omega}_{k-1} / \hat{\omega}_k$ . The difference between Deriso's and Schnute's forms of growth (and hence their delay-difference equations) is that Deriso's original equation requires unrealistically that  $\omega_{k-1} = 0$  so that  $\omega = 0$ . A simple substitution in Schnute's more general formulations of growth and delay-difference equation results in Deriso's forms of growth and delay-difference equation.

Catches and fishing effort are usually among the first statistics collected from a fishery. Survey estimates of stock biomass sometimes come later through significant cost and effort by fisheries management agencies (Gunderson, 1993). If insufficient numbers of survey estimates are available, fishery CPUE can provide the biomass indices. However, fishery CPUE data may bias model estimates because catchability often changes over time. Survey data provide either relative (catchability unknown) or absolute (catchability known) biomass abundance indices. Absolute abundance estimates for a few years will typically

<sup>1</sup> A reviewer noted that process error can also arise from other factors, such as variability in growth and survival, and other sources that make the deterministic delay-difference population dynamics incorrect.

<sup>2</sup> A reviewer pointed out that "Ford" may be a better name for these growth parameters (Ricker, 1975).

constrain an analysis more accurately than will many years of relative abundance indices.

Population dynamics are described by Schnute's (1985,  $\omega > 0$ ) or Deriso's (1980,  $\omega = 0$ ) delay-difference equation:

$$B_t = (1 + \rho)s_{t-1}B_{t-1} - \rho s_{t-1}s_{t-2}B_{t-2} + R_t - \rho\omega s_{t-1}R_{t-1}. \quad (2)$$

For the case when  $t=2$ ,

$$B_2 = (1 + \rho)s_1B_1 - \rho s_1s_0B_0 + R_2 - \rho\omega s_1R_1. \quad (3)$$

$B_t$  and  $R_t$  are the population biomass and recruitment biomass at the beginning of year  $t$ , and  $s_t$  is total survival during year  $t$  (note  $B_t$  includes  $R_t$ ).

The delay-difference equations allow for variable recruitment. In the data analysis and simulations performed in this paper the recruitment process is assumed to have constant mean, i.e.  $E(R_t) = R_1$  for all  $t$ . The delay-difference Kalman filter method allows for variable recruitment by considering variable recruitment to be process error about the mean recruitment. The nonlinear least-squares estimation method allows only for measurement error, therefore the recruitment process is assumed to be strictly constant with  $R_t = R_1$  for all  $t$ .

However, both the nonlinear least-squares and Kalman filter methods can be easily generalized to have mean recruitment as a function of stock biomass in earlier years. In this case  $E(R_t) = f(B_{t-k})$ , where  $k \geq 1$  (Kimura, 1988).

## Estimating parameters with nonlinear least squares

To fit the delay-difference equation with nonlinear least squares, we must provide biomass projections  $\{B_t\}$ , from Equations 2 and 3, using as parameters to be estimated, initial values ( $B_1, R_1$ ). If  $B_1$  is assumed to be virgin biomass and  $R_1$  is in equilibrium with  $B_1$ , the expected (i.e. equilibrium) recruitment line (ERL) follows from Equation 2 (Kimura, 1985):

$$R_1 = B_1 \left\{ [1 - \rho \exp(-M)] [1 - \exp(-M)] / [1 - \rho\omega \exp(-M)] \right\}. \quad (4)$$

The ERL is a straight line through the origin of the ( $B_1, R_1$ ) plane.

The initial parameters ( $B_1, R_1$ ) may be parameterized by either of two assumptions: 1)  $B_1$  is virgin biomass or 2)  $B_1$  is not virgin biomass. If  $B_1$  is virgin

biomass,  $R_1$  is determined from Equation 4 (or conversely,  $B_1$  can be determined from  $R_1$ ).  $B_2$  can then be projected from Equation 3, with  $B_0 = B_1$  and  $s_0 = \exp(-M)$ . Projections of biomass for  $t > 1$  requires  $\{s_t, t = 1, \dots, n\}$ . These survivals  $s_t = \exp(-M - F_t)$ , are obtained by iteratively solving the catch equations for  $F_t$  (Kimura and Tagart, 1982):

$$c_t = B_t F_t (1 - \exp(-M - F_t)) / (M + F_t) \quad (5)$$

in a sequential manner (relative to  $t$ ). If  $B_1$  is not virgin biomass,  $B_1$  and  $R_1$  are independent parameters to be estimated. The initial projection value  $B_0 = B_1$  will be used, but with  $s_0 = \exp(-M - F_0)$  if information concerning  $F_0$  is available. In either case, further projections of biomass can be made by using Equation 2.

In the simulations to be presented, we assume that the initial population is a virgin biomass (i.e. Equation 4 holds). This allows us to initiate the biomass time series using the results in Appendix 1 and to fit the simulated data without substantial model bias. However, the fits to the simulated data with both nonlinear least squares and the Kalman filter will *not* assume virgin biomass. Instead, the delay-difference equation is fit to a time series of relative abundance data by varying three parameters:  $B_1, R_1$ , and a catchability coefficient  $\lambda$ . We assume the catchability coefficient scales the biomass projections from the delay-difference equation ( $B_t$ ) to the expected values of observed relative abundance indices  $\{y_t\}$  (i.e.  $E(y_t) = \lambda B_t$ ). For nonlinear least squares, if abundance indices  $y_t$  have coefficient of variation  $cv_t$ , parameters can be estimated by minimizing

$$SS = \sum [\ln(y_t) - \ln(\lambda B_t)]^2 / cv_t^2. \quad (6)$$

We used a lognormal formulation because of its superior numerical stability in quasi-Newton estimation algorithms. Parameters were estimated in two stages: initial estimates were found by a direct search over a grid of values for  $B_1, R_1$ , then refined by using quasi-Newton methods.

The survey catchability  $\lambda$  can be either estimated or fixed depending on whether  $y_t$  is thought to be a relative or absolute index of abundance. Differentiating Equation 6 with respect to  $\lambda$  and solving the normal equation shows that  $\lambda$  can be estimated by

$$\hat{\lambda} = \exp \left\{ \frac{\sum [\ln(y_t / \hat{B}_t) / cv_t^2]}{\sum [1 / cv_t^2]} \right\} \quad (7)$$

so that at this stage searches for  $\lambda$  are not necessary. However, the final minimization of Equation 6 with quasi-Newton methods should be based on all three

parameters  $\Psi = (\ln(B_1), \ln(R_1), \ln(\lambda))$ , because the estimates by using Equation 7 may be suboptimal. If the coefficient of variation is the same for all  $y_t$ , then all  $cv_t$  can be set equal to one.

We also briefly examined the possibility of estimating nonlinear least-squares parameters by modeling both measurement and process error:

$$SS = \sum [(y_t - \hat{\lambda} \hat{B}_t)^2 / \sigma_m^2 + (R_t - \hat{R}_t)^2 / \sigma_p^2]. \quad (8)$$

Here,  $\hat{R}_t$  is the estimated mean recruitment as before, but  $R_t$ ,  $t > 1$ , are allowed to vary. For Deriso's form of the delay difference equation, differentiating Equation 8 with respect to  $R_t$  and setting the result equal to zero yields

$$\hat{R}_t = [(R_1/r) + \lambda(y_t - \lambda P_t)] / [(1/r) + \lambda^2], \quad (9)$$

where  $r = \sigma_p^2 / \sigma_m^2$ , and  $P_t$  is the delay-difference projection of biomass to year  $t$  prior to adding recruitment. Estimating parameters by minimizing Equation 8 appeared unstable and was not pursued further. This may be because mean recruitment  $R_1$ , and the individual recruitments  $R_t$ , both were estimated from the data. With additional constraints, or if recruitment indices were available, such an approach might be useful.

## Maximum-likelihood estimation for the Kalman filter

We also applied the Kalman filter as described by Pella (1993) to the delay-difference equation. Pella (1993) credits Harvey (1990) for his own presentation, but we found Pella's presentation to be quite adequate for applying the method. As described earlier, the main reason for using the Kalman filter is that it allows for process error in addition to measurement error. The nonlinear least-squares estimates of the previous section assume constant recruitment and allow only for measurement error.

The state transition equation of the Kalman filter views the delay-difference equation (Eq. 2) as being composed of both deterministic and stochastic components. The deterministic component of the process assumes that the expected values of  $R_t$  and  $R_{t-1}$  are constant, say equal to  $R_1$ . If desired, we can also assume virgin biomass when applying the Kalman filter, i.e. we can estimate  $R_1$  by using Equation 4. This is analogous to the constant nonrandom recruitment model fit by nonlinear least squares. The biomass prediction given by Equation 2 is in error owing to variability in recruitment. This variability is defined to be process error. Now, even though  $B_t$  and

$\lambda$  have definite though unknown values, the abundance index  $y_t$  is observed only with error, which we define as measurement error. The Kalman filter method provides maximum-likelihood estimates of  $B_0$ ,  $R_1$ , and  $\lambda$ , almost the same parameters as for the nonlinear least-squares method but for the process and measurement error model we have just described. Note that we estimate  $B_0$  (see below) instead of  $B_1$  because  $B_0$  cannot simply be defined to be equal to  $B_1$  in the equations which initialize the Kalman filter method. For consistency, when comparing parameter estimates for nonlinear least-squares and the Kalman filter methods, we shall compare only estimates of  $B_1$  (i.e. the one year projection of  $B_0$ ).

Modeling and assumptions in addition to those of nonlinear least squares are needed by the Kalman filter. Because the Kalman filter is essentially a Bayesian procedure (Meinhold and Singpurwalla, 1983), it requires a prior joint distribution for  $B_0$  and  $B_{-1}$ . In addition, in order to partition process and measurement error, either the magnitude of process or measurement error (or both) or their ratio must be known or estimated. Nearly all of our simulations will assume that process and measurement error variances are known. Kalman filter estimation without prior information concerning error variances appears to be generally difficult.

## Simulating datasets satisfying Kalman filter assumptions

In this section we describe simulation of relative abundance indices that satisfy the assumptions of the delay-difference equation and the Kalman filter. As stated earlier, these simulations assume virgin biomass (i.e. Equation 4 holds with  $B_0$  substituted for  $B_1$ ). This is the easiest way to avoid an initial modeling bias in the simulation and model fits. Data simulated in this manner will be fitted by using nonlinear least-squares and the delay-difference Kalman filter methods *without* the assumption of virgin biomass. To a large extent we followed the notation of Pella (1993). Note that the "state space" of the system is simply jargon for the unobservable true biomass of the system.

**Initial conditions and assumptions** The initial state of the system is defined to be

$$\alpha_0 = \begin{pmatrix} B_0 \\ B_{-1} \end{pmatrix}.$$

We assume that  $\alpha_0$  is unknown but has prior distribution with mean

$$\alpha_0 = E(\alpha_0) = \begin{pmatrix} B_0 \\ B_0 \end{pmatrix}$$

and with covariance matrix

$$P_0 = \Sigma(\alpha_0) = \begin{pmatrix} \gamma_0 & \gamma_1 \\ \gamma_1 & \gamma_0 \end{pmatrix}.$$

Estimators for  $\gamma_0$  and  $\gamma_1$  are provided in Appendix 1 and only require prior estimates of  $\rho, \omega, \sigma_p^2$  and  $s_0$ . To predict  $\alpha_1$ , we assumed

$$T_0 = \begin{pmatrix} (1+\rho)s_0 & -\rho s_0 s_0 \\ 1 & 0 \end{pmatrix}, C_0 = \begin{pmatrix} R_1(1-\rho\omega s_0) \\ 0 \end{pmatrix}, \\ \tilde{R}_0 = \begin{pmatrix} 1 & -\rho\omega s_0 \\ 0 & 0 \end{pmatrix}, \text{ and } \eta_0 = \begin{pmatrix} n_1 \\ n_0 \end{pmatrix}.$$

The state of the system at time  $t=1$  is then  $\alpha_1 = T_0\alpha_0 + C_0 + \tilde{R}_0\eta_0$ , where  $n_1$  is assumed to be a normal random variable with mean zero and variance  $\sigma_p^2$ . For Deriso's form of the delay-difference equation,  $\omega = 0$ , so that the value of  $n_0$  is irrelevant. However, for Schnute's form of the delay-difference equation we used  $n_0 = 0$  because the data contained no information concerning  $n_0$ .

**Projecting the state space** Given the initial conditions (above), and a catch sequence  $\{c_t\}$ , the state space variable  $\alpha_t$  can be projected indefinitely:

$$\alpha_t = \begin{pmatrix} B_t \\ B_{t-1} \end{pmatrix}, T_t = \begin{pmatrix} (1+\rho)s_t & -\rho s_t s_{t-1} \\ 1 & 0 \end{pmatrix}, C_t = \begin{pmatrix} R_1(1-\rho\omega s_t) \\ 0 \end{pmatrix} \\ \tilde{R}_t = \begin{pmatrix} 1 & -\rho\omega s_t \\ 0 & 0 \end{pmatrix}, \eta_t = \begin{pmatrix} n_{t+1} \\ n_t \end{pmatrix}$$

so that

$$\alpha_{t+1} = T_t\alpha_t + C_t + \tilde{R}_t\eta_t.$$

The process error vectors  $\eta_t$  are assumed to be independent with

$$E(\eta_t) = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$

and with covariance matrix

$$Q = \begin{pmatrix} \sigma_p^2 & 0 \\ 0 & \sigma_p^2 \end{pmatrix}.$$

Recall that  $T_t$  requires a value for  $s_t$  by first solving Equation 5 for  $F_t$ .

**Addition of measurement error** Given a catchability coefficient  $\lambda$ , the observed variables can be de-

scribed as  $y_t = Z\alpha_t + \varepsilon_t$ , where  $Z = (\lambda \ 0)$ ,  $\varepsilon_t = e_t$ , and  $e_t$  is assumed to be normally distributed with mean zero and variance  $h = \sigma_m^2$ .

If expected recruitment is to be a function of stock biomass in earlier years, the state space project vector  $C_t$  must become a function of  $\alpha_t$  so that

$$C_t(\alpha_t) = \begin{pmatrix} E(R_{t+1}) - \rho\omega s_t E(R_t) \\ 0 \end{pmatrix}.$$

If the delay between hatching and recruitment is to be many years, then the dimension of  $\alpha_t$  must be increased, so that the earlier biomass will be available to calculate recruitment.

So far we have described a statistical model which includes process and measurement error and which can be used to compute a realization of relative abundance indices, say  $\{\tilde{y}_t\}$ . In the implementation of the Kalman filter given here, Deriso's form ( $\omega = 0$ ) of the delay-difference equation fully satisfies the assumptions of the model, but Schnute's ( $\omega > 0$ ) more realistic form does not. This difference is due to the process error vectors

$$\eta_t = \begin{pmatrix} n_{t+1} \\ n_t \end{pmatrix},$$

which represent variability in recruitment and which are assumed to be independent by the Kalman filter. Because  $\eta_t$  and  $\eta_{t+1}$  both contain  $n_{t+1}$ , this assumption is clearly violated for Schnute's form of the delay-difference equation. This trade-off between realism in the delay-difference equation and statistical independence required of process error will be examined further with simulation.

**Kalman filter estimates**

If values of variance for process and measurement error are assumed, parameters  $\Psi = \{\ln(B_0), \ln(R_t), \ln(\lambda)\}$  can be estimated by the method of maximum likelihood. In principle, the method is very similar to that described for calculating nonlinear least-squares estimates. Given a value for  $\Psi$ , initial values for  $\alpha_0, P_0$  can be specified as in the simulations; estimates of biomass and its covariance matrix can then be forecast  $\{\alpha_{it-1}, P_{it-1}\}$ . The value of  $\Psi$ , whose forecasts maximize the log-likelihood, is taken as the estimate.

Because the Kalman filter incorporates process as well as measurement error, estimation of biomass occurs in two steps.

- 1 Initial projections  $\alpha_{t|t-1} = T_{t-1}\alpha_{t-1} + C_{t-1}$  and  $P_{it-1} = T_{t-1}P_{t-1}T_{t-1}' + \tilde{R}_{t-1}Q\tilde{R}_{t-1}'$  are calculated on the

basis of the value of  $\Psi$ , initial conditions, and the data ( $c_1, \dots, c_{t-1}$ ) and ( $y_1, \dots, y_{t-1}$ ). Recall again that  $T_{t-1}$  requires a value for  $s_{t-1}$  that can be estimated by first solving the catch equation (Eq. 5) for  $F_{t-1}$ . As described earlier, if expected recruitment is to be a function of earlier biomass estimates, then  $C_{t-1}$  must be a function of  $a_{t-1}$ .

2 If an observation of  $y_t$  exists, the initial projections  $a_{t|t-1}$  and  $P_{t|t-1}$  are updated on the basis of  $a_t = a_{t|t-1} + P_{t|t-1}Z'f_t^{-1}(y_t - Za_{t|t-1})$  and  $P_t = P_{t|t-1} - P_{t|t-1}Z'f_t^{-1}ZP_{t|t-1}$ , where  $f_t = ZP_{t|t-1}Z' + h$ . If an observation of  $y_t$  does not exist, further projections can be made by using Equation 1, with  $a_{t|t-1}$  and  $P_{t|t-1}$  used in place of  $a_t$  and  $P_t$ . Therefore, Kalman filter estimation can accommodate missing relative abundance indices provided they are few in number.

3 The log-likelihood is calculated to be

$$\ln(L(y, \Psi)) = -\left(\frac{n}{2}\right)\ln(2\pi) - \frac{1}{2}\sum_{t=1}^n \ln(f_t) - \frac{1}{2}\sum_{t=1}^n \frac{v_t^2}{f_t},$$

where  $v_t = y_t - Za_{t|t-1}$ , and  $f_t = ZP_{t|t-1}Z' + h$ .

As with the nonlinear least-squares method, the Kalman filter estimate of  $\Psi$  was also calculated in two stages. First, we searched a grid of possible initial  $\lambda_0$  values, say from 0.5 to 1.5 at 0.1 intervals. For each fixed  $\lambda_0$  value, we then estimated the conditional maximum-likelihood estimate  $\Psi^* = [\ln(B_0^*), \ln(R_1^*)]$  by a quasi-Newton method. We then picked the  $\lambda_0^*$  and  $\Psi^*$  having the largest conditional likelihood, and used that as an initial estimate for finding the unconditional maximum likelihood estimate  $\hat{\Psi} = [\ln(\hat{B}_0), \ln(\hat{R}_1), \ln(\hat{\lambda})]$ , again by using a quasi-Newton method. The asymptotic covariance matrix of the maximum-likelihood estimates can be estimated from the inverse Hessian of minus the log-likelihood.

Generally, our Kalman filter estimates were made with the assumption that process and measurement error variances were known. However, under the Kalman filter, if  $r = \sigma_p^2 / \sigma_m^2$  is known, then all model parameters, including  $\sigma_m^2$  and hence  $\sigma_p^2$ , can be estimated from the data. Following Pella (1993), we reparameterized  $h = 1$  and

$$Q = \begin{pmatrix} r & 0 \\ 0 & r \end{pmatrix}.$$

It can be noted that

$$P_0^* = P_0 / \sigma_m^2 = \frac{1}{\sigma_m^2} \begin{pmatrix} \gamma_0 & \gamma_1 \\ \gamma_1 & \gamma_0 \end{pmatrix} = rA,$$

where  $A = P_0 / \sigma_p^2$  is dependent only on  $\rho$ ,  $\omega$ , and  $s_0$ . The Kalman recursions are then carried forward just as would have been done if no reparametrization had been performed. However, the covariance matrices  $\{P_{t|t-1}$  and  $P_t\}$  are now automatically scaled versions  $\{P_{t|t-1}^* = P_{t|t-1} / \sigma_m^2$  and  $P_t^* = P_t / \sigma_m^2\}$ , and  $f_t^* = f_t / \sigma_m^2$ . The vectors  $a_{t|t-1}$  and  $a_t$  are unaffected by the scaling which cancels in their equations. The parameter estimates are dependent only on the value of  $r$ , not the variance components  $\sigma_p^2$  and  $\sigma_m^2$ . However,  $\sigma_m^2$  can be estimated from

$$\hat{\sigma}_m^2 = \sum (v_t^2 / f_t^*) / n,$$

where  $n$  is the number of  $y_t$  observed (also  $\hat{\sigma}_p^2 = r\hat{\sigma}_m^2$ ). The log-likelihood to be maximized (see Appendix 2) then becomes

$$\ln(L_c(y, \Psi)) = -\frac{n}{2}[\ln(2\pi) + 1] - \frac{1}{2}\sum_{t=1}^n \ln(f_t^*) - \frac{n}{2}\ln(\hat{\sigma}_m^2). \tag{10}$$

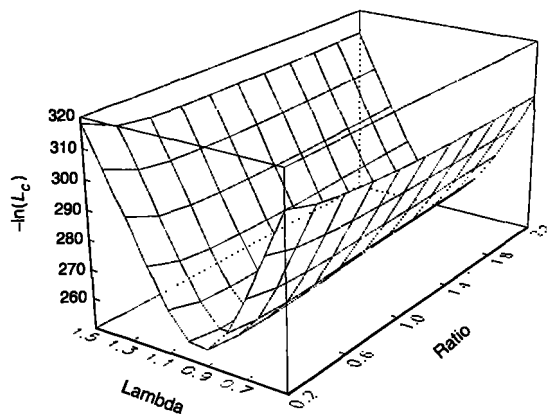
The question arises whether  $r$  can be estimated as just another parameter by using the method of maximum likelihood? Although estimation of  $r$  appears possible in theory, our experience suggests that this will be impractical for many data sets. The reason is that the likelihood function appears to be insensitive to  $r$  (Fig. 1).

### Data analysis and simulations

We reanalyzed the data set for yellowfin tuna, *Thunnus albacares* (Table 1), taken from Pella and Tomlinson (1969) by using methods described in this paper. Ages read from otoliths of yellowfin tuna (Wild, 1986) indicate that length at age is nearly linear. This implies exponential growth in weight at age, but we shall assume linear growth in weight at age (i.e.  $\rho = 1.0$ ,  $\omega = 0.0$ ). Because fish rapidly disappear from the population at age 4 yr, we assume  $M = 0.60$ . Therefore, we assume constant growth with a large natural mortality rate. Analysis by Pella (1993) indicates a biomass range of from 600 to 1,400 million pounds and an annual sustainable yield of 193 million pounds.

Our data analyses (i.e. fits to the data in Table 1) assume

**D1**  $\sigma_m^2 = 46, \sigma_p^2 = 32,775$  as reported by Pella (1993). These values suggest that most of the error



**Figure 1**

The likelihood profile (minus  $\ln(L_c)$ ) for estimating Kalman filter parameters as a function of the variance ratio ( $r = \sigma_p^2 / \sigma_m^2$ ) and lambda ( $\lambda$ ), showing that the likelihood profile appeared insensitive to the value of variance ratio. The assumed parameters were  $R_1 = 250$ ,  $\lambda = 1$ ,  $\rho = 1$ ,  $\omega = 0$ ,  $M = 0.60$ ,  $s_0 = \exp(-0.60)$ ,  $r = 1.0$ , variances assumed to be  $\sigma_m^2 = 100$ ,  $\sigma_p^2 = 100$ , with  $n = 100$  yr of simulated data.

is process error (i.e. variance of recruitment) as opposed to measurement error (i.e. error in measuring the relative abundance index).

**D2**  $\sigma_m^2 = 5,000$ ,  $\sigma_p^2 = 1,000$ . These values suggest that most of the error is measurement error as opposed to process error.

Under the heading "Simulating datasets satisfying Kalman filter assumptions," we describe a detailed model for simulating data that satisfy the Kalman filter assumptions. In this paper all simulations are roughly related to the yellowfin tuna dataset (i.e. 34 yr of simulated data with similar model parameter values). To do this we specified values for natural mortality,  $M$ , Brody growth parameters  $\rho$  and  $\omega$ , expected recruitment  $R_1$ , catchability  $\lambda$ , and variances  $\sigma_p^2$  and  $\sigma_m^2$ . Assuming virgin biomass (Eq. 4), values for  $(M, \rho, \omega, \sigma_p^2, R_1)$  provide us with the mean virgin biomass and its covariance matrix over neighboring years  $(a_0, P_0)$ . The simulation is initialized by generating biomass estimates, i.e. bivariate normal random deviates having the prior expectation  $a_0$  and covariance matrix  $P_0$ . These initializations assumed  $s_0 = \exp(-M)$ . Because trends in the catch data can affect modeling results, we also simulated the catch data by assuming that catches were lognormal (see Kimura, 1989),  $\ln(c_t) \sim N(\mu, \sigma^2)$ , with  $E(c_t) = \bar{c}$ , and  $\text{var}(c_t) = cv^2 \bar{c}^2$ , with  $\bar{c} = 141.8$  (average from Table 1), and  $cv = 0.2$ .

**Table 1**

Catch ( $c_t$  in million pounds) and relative abundance ( $y_t$  in pounds per boat day) for yellowfin tuna, *Thunnus albacares*, in the eastern Pacific Ocean (Pella and Tomlinson, 1969).

Year	Catch	Relative abundance
1934	60.9	10,361
1935	72.3	11,484
1936	78.4	11,571
1937	91.5	11,116
1938	78.3	11,463
1939	110.4	10,528
1940	114.6	10,609
1941	76.8	8,018
1942	42.0	7,040
1943	50.1	8,441
1944	64.9	10,019
1945	89.2	9,512
1946	129.7	9,292
1947	160.2	7,857
1948	207.0	8,353
1949	200.1	8,363
1950	224.8	7,057
1951	186.0	10,108
1952	195.3	5,606
1953	140.0	3,852
1954	140.0	5,339
1955	140.9	8,191
1956	177.0	6,507
1957	163.0	6,090
1958	148.5	4,768
1959	140.5	4,982
1960	244.3	6,817
1961	230.9	5,544
1962	174.1	4,120
1963	145.5	4,368
1964	203.9	4,844
1965	180.1	4,166
1966	182.3	4,513
1967	178.9	5,292

Three simulations were replicated 100 times so that we could examine the bias, variance, and root mean square error (i.e. the square root of mean square error) of Kalman filter and nonlinear least-squares parameter estimates when the true parameter values were known. For these simulations we assumed that the stock was initially a virgin biomass ( $R_1 = 250$ ,  $\lambda = 1$ ,  $\rho = 1$ ,  $\omega = 0$ ,  $M = 0.60$ ), and the catch data were generated as lognormal random deviates  $LN(\bar{c} = 141.8, cv = 0.2)$ . We assumed that data sets had only measurement error, only process error, or a mixture of both.

**S1**  $\sigma_m^2 = 1,000$ ,  $\sigma_p^2 = 1$ . Measurement error only.

**S2**  $\sigma_m^2 = 1$ ,  $\sigma_p^2 = 1,000$ . Process error only.

**S3**  $\sigma_m^2 = 500$ ,  $\sigma_p^2 = 500$ . Measurement and process error.

In order to understand the distribution of bias in the estimated biomass trends, we made histograms of the residuals  $Z_t = \hat{B}_t - B_t$  (true) for years  $t=1, 17,$  and  $34,$  for both the Kalman filter and nonlinear least-squares estimates.

Finally, two specialized simulations were replicated 100 times:

**SP1**

$\omega > 0:$

$$R_1 = 250, \lambda = 1, \rho = 0.75, \omega = 0.75,$$

$$M = 0.3, \sigma_m^2 = 1, \sigma_p^2 = 1,000$$

**SP2**

$r$  fixed:

$$R_1 = 250, \lambda = 1, \rho = 1, \omega = 0,$$

$$M = 0.6, \sigma_m^2 = 500, \sigma_p^2 = 500.$$

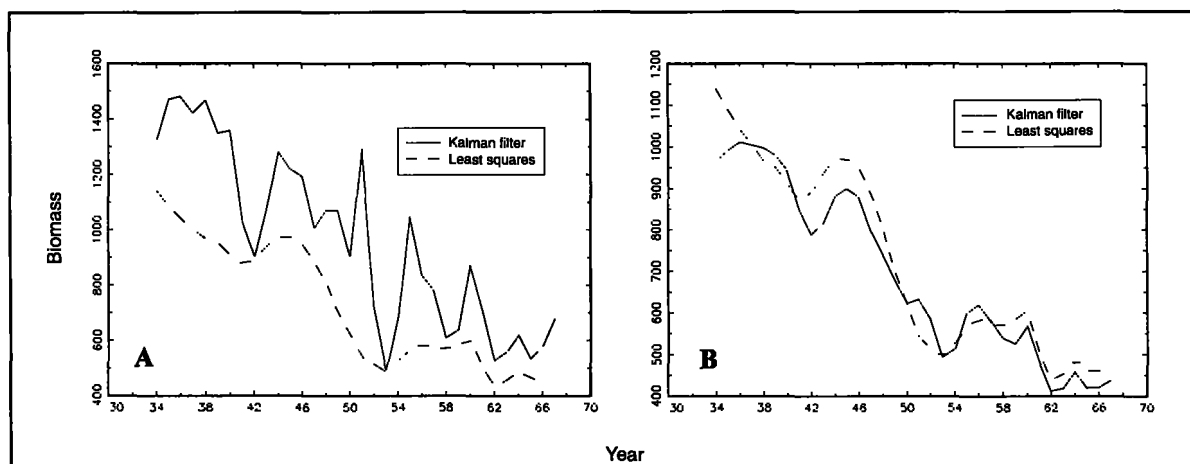
With these simulations the stock was assumed to be initially a virgin biomass. The purpose of simulation SP1 was to examine how severely the correlation in process error ( $\eta_t$ ) induced by Schnute’s form of the delay-difference equation ( $\omega > 0$ ) degrades the parameter estimates from the Kalman filter. The purpose of SP2 was to examine whether estimating parameters by assuming only  $r = \sigma_p^2 / \sigma_m^2 = 1.0$  was known (i.e. by maximizing Equation 10), would degrade the Kalman filter estimates.

**Results**

Our results from reanalyzing the data set in Table 1 with variance assumptions described as D1 and D2

are shown in Figure 2. The variance assumption D1, that of Pella (1993), is close to assuming only process error. The result is estimated biomass trends that are scaled but that exactly trace the relative abundance indices (Fig. 2A). Our model fit is very similar to that reported by Pella (1993) and indicates that, despite great differences in the underlying state transition models (delay-difference versus generalized production), the Kalman filter method, with large process error, can provide quite similar estimates of biomass trends. The nonlinear least-squares fit assumes only measurement error and differs considerably from the Kalman filter fit. In the analysis with variance assumed to be D2, the Kalman filter assumes that error is predominantly measurement error but also contains a realistic component of process error. The result is Kalman filter estimates of relative abundance that are very similar to nonlinear least-squares estimates (Fig. 2B).

Results from replicated simulations based on assumptions S1–S3 are shown in Table 2. Under the variance assumption S1, we have only measurement error. Under this assumption, the Kalman filter and nonlinear least-squares methods performed similarly. Root mean square error (RMSE) estimates, compared with sample standard deviations of parameter estimates, show that both methods have little bias but that the inverse Hessian of minus the log-likelihood appears to give estimates of the uncertainty of parameter estimates that are biased low (i.e. are more similar to standard deviation than RMSE). Residual plots (Fig. 3) indicate biomass traces have symmetrical error.



**Figure 2**

Fits to yellowfin tuna, *Thunnus albacares*, assuming  $\rho = 1, \omega = 0, M = 0.60, s_0 = \exp(-0.60),$  and data from the eastern Pacific Ocean (Table1). (A) Kalman filter fit assuming  $\sigma_m^2 = 46, \sigma_p^2 = 32,775$  as in Pella (1993). (B) Kalman filter by assuming predominantly measurement error  $\sigma_m^2 = 5,000, \sigma_p^2 = 1,000.$  Nonlinear least-squares estimates are the same in both (A) and (B); biomass is in millions of pounds.



Table 2

Simulation result from 100 replications of the simulations described below. Time series were simulated by assuming virgin biomass with ( $R_1=250$ ,  $\lambda=1$ ), growth parameters ( $\rho=1$ ,  $\omega=0$ ),  $s_0=\exp(-0.60)$ ,  $\sigma_m^2, \sigma_p^2$  values given below, and relationships described in Appendix 1. Catches were simulated as lognormal random variables with  $\bar{c}=141.8$ ,  $cv=0.2$ ). Because the true  $B_1$  value varies in each replication, an average value for each simulation is presented below. Standard errors for Kalman filter (KF) estimates were calculated from the inverse of the Hessian of minus the log-likelihood. RMSE = root mean square error; NLS = nonlinear least squares.

	$B_1$	$R_1$	$\lambda$
<b>Simulation S1: <math>\sigma_m^2 = 1,000</math> <math>\sigma_p^2 = 1</math></b>			
Average true $B_1$	1,228		
Average of Kalman filter estimates	1,237	250.9	1.004
Standard deviation of KF estimates	135	13.3	0.098
Average standard error of KF estimates	175	16.4	0.120
RMSE of KF estimates	232	23.0	0.169
Average NLS estimates	1,235	250.7	1.007
Standard deviation of NLS estimates	140	14.1	0.106
RMSE of NLS estimates	240	24.3	0.183
<b>Simulation S2: <math>\sigma_m^2 = 1</math> <math>\sigma_p^2 = 1,000</math></b>			
Average true $B_1$	1,222		
Average of Kalman filter estimates	1,282	256.9	0.963
Standard deviation of KF estimates	139	15.5	0.095
Average standard error of KF estimates	154	14.8	0.094
RMSE of KF estimates	244	29.2	0.176
Average NLS estimates	1,332	263.7	1.082
Standard deviation of NLS estimates	618	67.6	0.431
RMSE of NLS estimates	1,072	118.9	0.756
<b>Simulation S3: <math>\sigma_m^2 = 500</math> <math>\sigma_p^2 = 500</math></b>			
Average true $B_1$	1,230		
Average of Kalman filter estimates	1,287	257.0	0.979
Standard deviation of KF estimates	232	24.5	0.153
Average standard error of KF estimates	228	22.0	0.145
RMSE of KF estimates	400	44.0	0.266
Average NLS estimates	1,304	259.4	1.026
Standard deviation of NLS estimates	481	52.8	0.263
RMSE of NLS estimates	831	92.4	0.455

With variance assumption S2, we have only process error. With this assumption both the Kalman filter and nonlinear least-squares biomass estimates are biased high (Table 2; Fig. 4). However, root mean square errors show that the Kalman filter performance is clearly superior to nonlinear least squares for this case. It is interesting that simulation S2 also shows that nonlinear least-squares estimates are not necessarily more biased under process error but that parameter estimates have larger variances.

Variance assumption S3 represents a combination of process and measurement error. Results from S3 are similar to those from S2, with biomass estimates appearing to be biased high for both the Kalman filter and nonlinear least-squares methods (Table 2; Fig. 5), but with RMSE clearly favoring the Kalman filter method over the nonlinear least-squares method. It should be noted that in simulation S2 and S3, 1 or 2 of

the nonlinear least-squares fits failed to converge probably owing to the inclusion of process error. These simulations were thrown out and the runs were repeated.

Results from simulation SP1 (Table 3) indicate that Schnute's form of the delay-difference equation can be used with the Kalman filter, despite the violation of the assumption that process error vectors are independent. And finally, results from simulation SP2 (Table 4) indicate that the Kalman filter parameter estimates have smaller RMSE compared with nonlinear least-squares parameter estimates when only the value of  $r = \sigma_p^2 / \sigma_m^2$  is assumed in the model fit.

## Conclusions

Simulations show that with the fit of the delay-difference equation, the Kalman filter and nonlinear least-

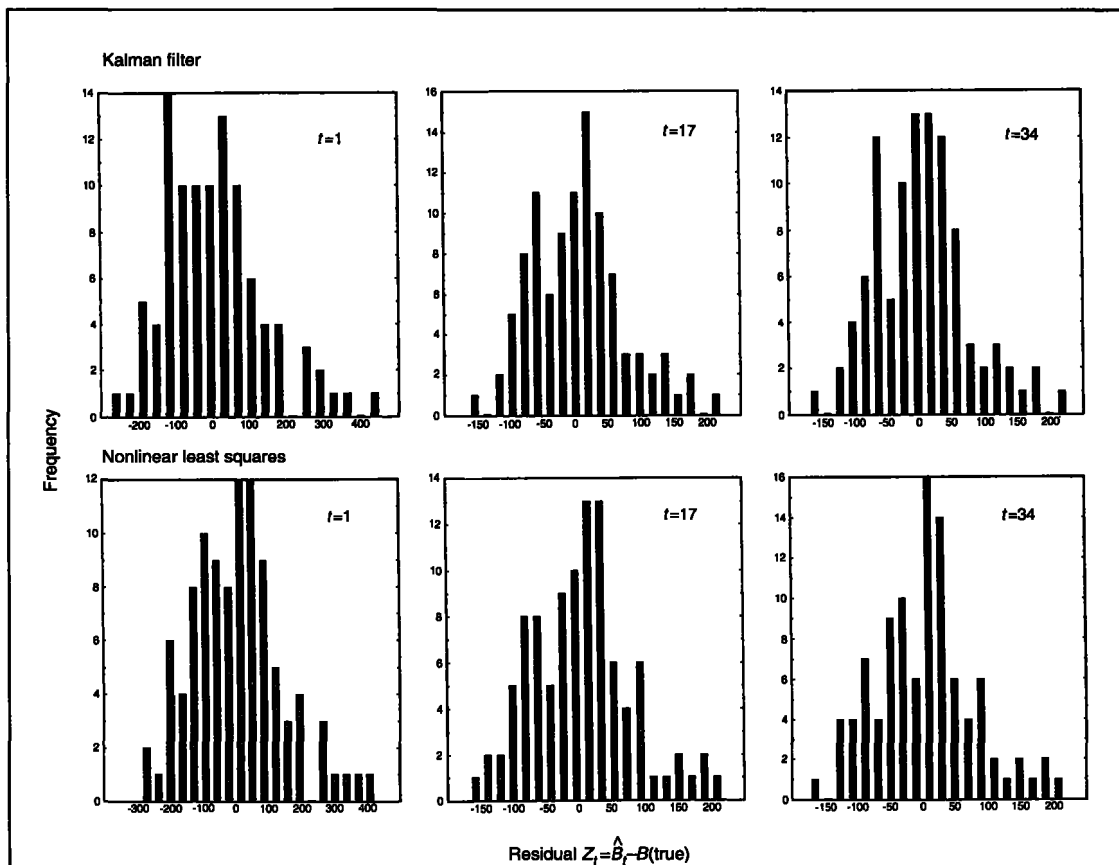
squares methods give similar results if there is only measurement error. Bias in parameter estimates for both methods tend to be small in this case. The Kalman filter was superior to nonlinear least squares, as mea-

sured by RMSE, if there is only process error. Both methods tended to give biomass estimates that were positively biased, and nonlinear least-squares estimates were dramatically skewed to the right. A similar result

**Table 3**

Simulation result from 100 replications of the simulation described as SP1 in the text. Time series were simulated by assuming virgin biomass ( $R_1=250, \lambda=1$ ), growth parameters ( $\rho=0.75, \omega=0.75$ ),  $s_0=\exp(-0.30)$ , ( $\sigma_m^2=1, \sigma_p^2=1,000$ ), and relationships described in Appendix 1. Catches were simulated as lognormal random variables with ( $\bar{c}=141.8, cv=0.2$ ). Because the true  $B_1$  value varies in each replication, an average value for each simulation is presented below. Standard errors for Kalman filter (KF) estimates were calculated from the inverse of the Hessian of minus the log-likelihood. RMSE = root mean square error.

	$B_1$	$R_1$	$\lambda$
<b>Simulation SP1: <math>\sigma_m^2 = 1, \sigma_p^2 = 1,000</math></b>			
Average true $B_1$	1,262		
Average of Kalman filter estimates	1,287	252.1	0.993
Standard deviation of KF estimates	155	16.4	0.113
Average standard error of KF estimates	159	16.2	0.105
RMSE of KF estimates	257	28.5	0.195



**Figure 3**

Histograms of the residual between estimated and true biomass,  $Z_t = \hat{B}_t - B(\text{true})$ , for simulation S1, with  $\sigma_m^2 = 1,000$ , and  $\sigma_p^2 = 1.0$ . Top row is for the Kalman filter method; bottom row is for the nonlinear least-squares method; columns are for years  $t=1, 17$ , and  $34$ .

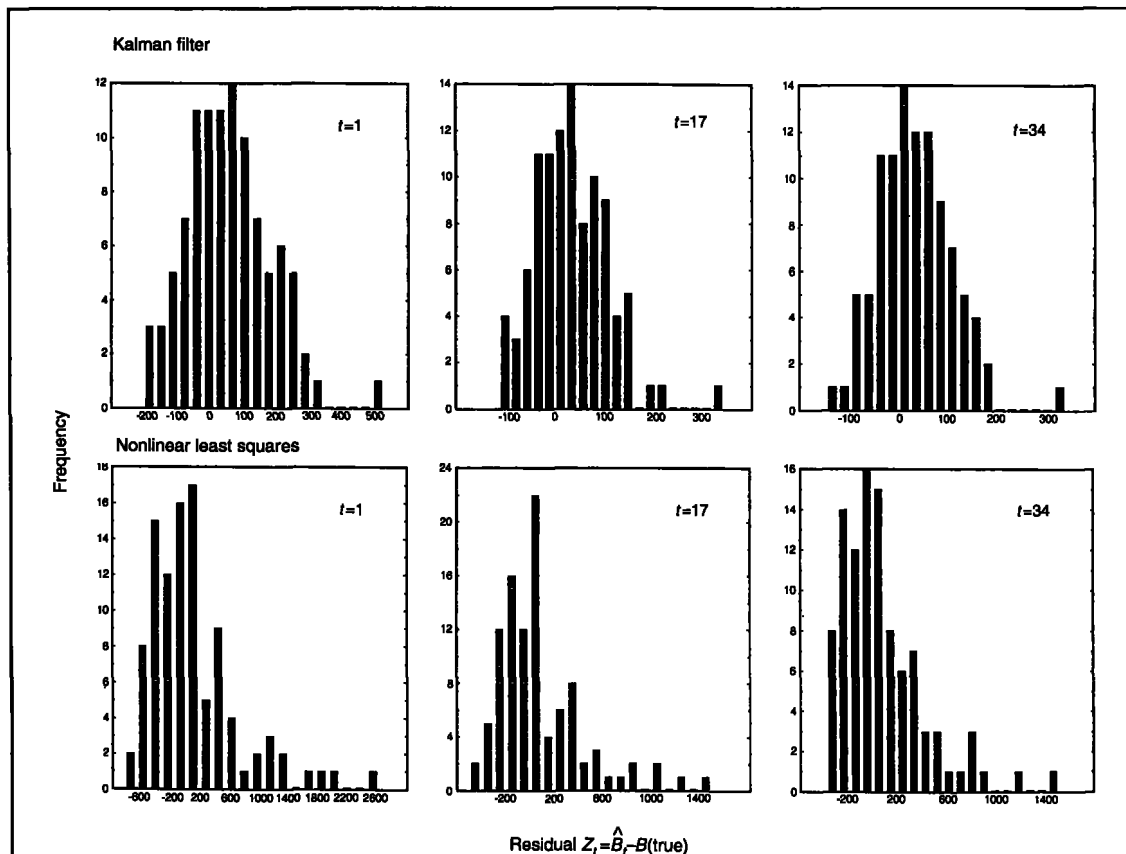
occurred when measurement and process error were included in the simulations, the Kalman filter and nonlinear least-squares biomass estimates were positively biased and appeared positively skewed.

We interpret these results to mean that the Kalman filter method provides superior performance in terms of RMSE but provides biased biomass estimates. This is a serious problem for a stock assess-

**Table 4**

Simulation result from 100 replications of the simulation described as SP2 in the text. Time series were simulated by assuming virgin biomass ( $R_1=250$ ,  $\lambda=1$ ), growth parameters ( $\rho=1$ ,  $\omega=0$ ),  $s_0=\exp(-0.60)$ ,  $\sigma_m^2=500$ ,  $\sigma_p^2=500$ , and relationships described in Appendix 1. Catches were simulated as lognormal random variables with ( $\bar{c}=141.8$ ,  $cv=0.2$ ). Because the true  $B_1$  value varies in each replication, an average value for each simulation is presented below. KF = Kalman filter; RMSE = root mean square of error; NLS = nonlinear least squares.

	$B_1$	$R_1$	$\lambda$
<b>Simulation SP2: <math>\sigma_m^2=500</math> <math>\sigma_p^2=500</math></b>			
Average true $B_1$	1,226		
Average of Kalman filter estimates	1318	259.9	0.967
Standard deviation of KF estimates	291	28.6	0.173
RMSE of KF estimates	502	55.6	0.313
Average NLS estimates	1310	260.3	1.035
Standard deviation of NLS estimates	565	61.7	0.290
RMSE of NLS estimates	982	107.8	0.503



**Figure 4**

Histograms of the residual between estimated and true biomass,  $Z_t = \hat{B}_t - B_t(\text{true})$ , for simulation S2, with  $\sigma_m^2 = 1.0$ , and  $\sigma_p^2 = 1,000$ . Top row is for the Kalman filter method; bottom row is for the nonlinear least-squares method; columns are for years  $t=1, 17$ , and  $34$ .

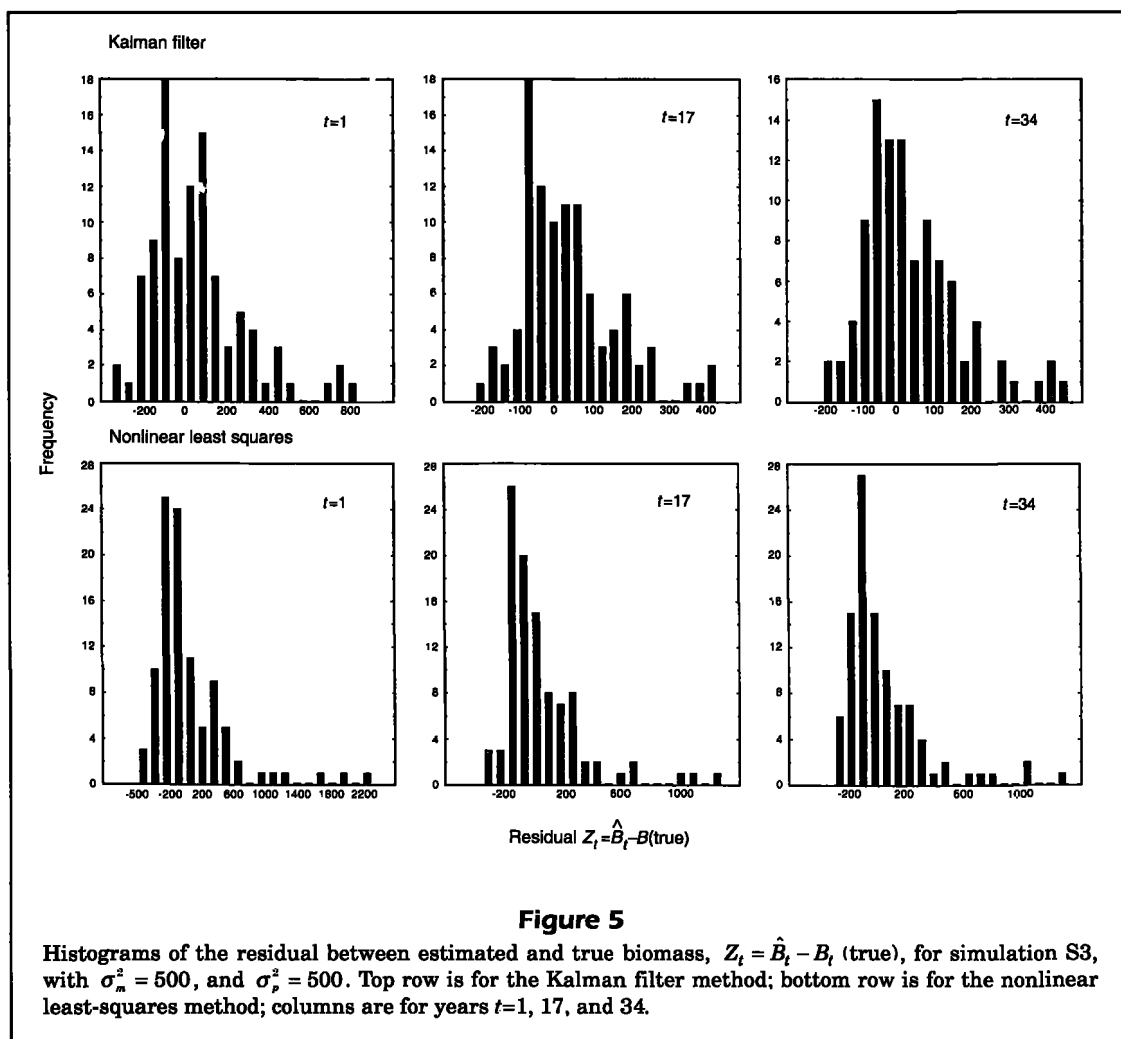
ment model because it can lead to overfishing. However, simulation results also indicate that under the presence of process error, nonlinear least-squares methods provide biomass estimates with comparable bias, and have much poorer RMSE properties. We therefore conclude that the Kalman filter method provides superior parameter estimates in the face of process error.

Simulation results indicate that Schnute’s form of the delay-difference equation can be used with the Kalman filter despite violation of the independent process error assumption. Although it appears difficult to estimate  $r$  directly with maximum-likelihood estimation, simulation results indicate that the Kalman filter can be used to estimate biomass when only  $r = \sigma_p^2 / \sigma_m^2$  is known, rather than the individual variances.

It is important to acknowledge that simulation results will differ if natural mortality, catch levels, growth parameters, biomass, and recruitment, or error variances, are changed. We believe that custom-

ized simulation studies should be a routine part of production modeling. The simulations performed in this paper favored the Kalman filter in that the true measurement and process error variances were assumed to be known to the Kalman filter fitting algorithm. Under these circumstances, the performance of the Kalman filter method might be described as less than fully satisfactory.

There appears to be few published simulation studies describing the performance of production models in the presence of process error. Process error is particularly troublesome because errors are propagated through the years rather than being quickly forgotten as is measurement error. Our results, and those of Polacheck et al. (1993), indicate that parameter estimation in the presence of process error is inherently difficult for production models. However, the process error method of Polacheck et al. (1993) is regression-based and may not provide fully efficient parameter estimates. Because real data contain process error, we feel process error must be dealt with,



**Figure 5**

Histograms of the residual between estimated and true biomass,  $Z_t = \hat{B}_t - B_t(\text{true})$ , for simulation S3, with  $\sigma_m^2 = 500$ , and  $\sigma_p^2 = 500$ . Top row is for the Kalman filter method; bottom row is for the nonlinear least-squares method; columns are for years  $t=1, 17$ , and  $34$ .

at least to the extent of investigating the effects of such errors on modeling results.

One final note. In this paper we have not emphasized model output beyond biomass traces and basic parameter estimates. For example, annual estimates of fishing mortality rates and exploitation rates were obvious byproducts of the model fits we presented. The models presented here can be thought of as extensions to what we earlier called Stock Reduction Analysis (Kimura and Tagart, 1982; Kimura et al., 1984; Kimura 1985, 1988). These papers contain various methods of analysis that are useful for providing fishery management advice. For example, output from both the Kalman filter and nonlinear least-squares models can be treated as a constant recruitment model, and target ABC's (allowable biological catches) or target biomass levels can be made on the basis of this assumption.

## Acknowledgments

This paper was inspired by J. J. Pella's lucid application of the Kalman filter method (Pella, 1993). We thank J. J. Pella for reviewing the manuscript, and providing numerous corrections, clarifications, and improvements. Also, we thank two anonymous reviewers for helpful comments and corrections.

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**Appendix 1: Time series properties of the delay-difference equation**

If recruitments  $\{R_t\}$  are assumed to be uncorrelated with  $E(R_t) = R_1$  and  $V(R_t) = \sigma_p^2$ , then the delay-difference equation (Eq. 2) is close to being a standard ARMA time series model (Box and Jenkins, 1970). Let  $\phi_1 = (1 + \rho)s_0$ ,  $\phi_2 = -\rho s_0^2$ , and  $\theta = \rho \omega s_0$ . Then Equation 2 can be written as

$$B_t = \phi_1 B_{t-1} + \phi_2 B_{t-2} + R_t - \theta R_{t-1}. \tag{1'}$$

Defining  $B_t = (R_t - \theta R_{t-1}) / (1 - \phi_1 - \phi_2)$ , and substituting  $R_t = n_t + R_1$  and  $B_t = \tilde{B}_t + B_1$  into Equation 1', yields the process

$$\tilde{B}_t = \phi_1 \tilde{B}_{t-1} + \phi_2 \tilde{B}_{t-2} + n_t - \theta n_{t-1}, \tag{2'}$$

where  $n_t$  the are now white noise. Thus under the assumption of constant growth parameters ( $\rho$ ,  $\omega$ ), constant survival  $s_0$ , and random recruitment ( $R_t$ ), the displaced process  $\{\tilde{B}_t\}$  is an ARMA time series model with the same statistical properties of  $\{B_t\}$ .

The stationarity and invertibility of this time series can easily be established by considering the roots of the characteristic polynomials (see Box and Jenkins, 1970):

$$1 - \phi_1 X - \phi_2 X^2 = 0, \text{ and} \tag{3'}$$

$$1 - \theta X = 0. \tag{4'}$$

The stationarity and invertibility of  $\{\tilde{B}_t\}$  follows from the observation that the roots  $1/s_0$  and  $1/(\rho s_0)$  of Equation 3' and  $1/(\rho \omega s_0)$  of Equation 4' are all almost surely greater than unity.

Let  $c_0 = (1 - \theta\phi_1 + \theta^2)\sigma_p^2$ , and  $c_1 = -\theta\sigma_p^2$ . The autocovariance terms (i.e. the  $\gamma_k$  in standard notation) of the process  $\{B_t\}$  can then be shown to be

$$\begin{aligned} \gamma_0 &= [c_0 + (1 + \phi_2)\phi_1 c_1 / (1 - \phi_2)] / [(1 - \phi_2^2) - (1 + \phi_2)\phi_1^2 / (1 - \phi_2)], \\ \gamma_1 &= (c_1 + \phi_1 \gamma_0) / (1 - \phi_2), \\ \gamma_2 &= \phi_1 \gamma_1 + \phi_2 \gamma_0, \text{ and} \\ \gamma_k &= \phi_1 \gamma_{k-1} + \phi_2 \gamma_{k-2}, \text{ for } k \geq 3. \end{aligned}$$

Two interesting correlation coefficients that can be estimated using the  $\gamma_k$  are

$$\rho(B_t, R_t) = \sqrt{\sigma_p^2 / \gamma_0} \text{ and } \rho(B_{t-k}, B_t) = \gamma_k / \gamma_0.$$

**Appendix 2: Derivation of the log-likelihood when only the variance ratio  $r = \sigma_p^2 / \sigma_m^2$  is known.**

Source: Pella, J. J. 1995. Auke Bay Laboratory, National Marine Fisheries Service, NOAA, 11305 Glacier Highway, Juneau, AK 99801. Personal communication.

We start with the usual log-likelihood when variances are assumed known

$$\ln(L(y, \Psi)) = -\frac{n}{2} \ln(2\pi) - \frac{1}{2} \sum_{t=1}^n \ln(f_t) - \frac{1}{2} \sum_{t=1}^n \frac{v_t^2}{f_t}. \tag{1''}$$

Substituting  $f_t = \sigma_m^2 f_t^*$  into (1''), we have

$$\begin{aligned} \ln(L(y, \Psi)) &= -\frac{n}{2} \ln(2\pi) - \frac{n}{2} \ln(\sigma_m^2) - \\ &\frac{1}{2} \sum_{t=1}^n \ln(f_t^*) - \frac{1}{2\sigma_m^2} \sum_{t=1}^n \frac{v_t^2}{f_t^*}. \end{aligned} \tag{2''}$$

By differentiating with respect to  $\sigma_m^2$ , and by setting this result equal to zero, we obtain the estimator

$$\hat{\sigma}_m^2 = \frac{1}{n} \sum_{t=1}^n \frac{v_t^2}{f_t^*},$$

which we substitute into Equation 2'' to arrive at the function to be maximized

$$\begin{aligned} \ln(L_t(y, \Psi)) &= -\frac{n}{2} [\ln(2\pi) + 1] - \\ &\frac{1}{2} \sum_{t=1}^n \ln(f_t^*) - \frac{n}{2} \ln(\hat{\sigma}_m^2). \end{aligned} \tag{3''}$$