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# The Ensemble Kalman Filter for Multidimensional Bioeconomic Models

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### Abstract

To integrate economic considerations into management decisions in ecosystem frameworks, we need to build models that capture observed system dynamics and incorporate existing knowledge of ecosystems, while at the same time accommodating economic analysis. The main constraint for models to serve in economic analysis is dimensionality. In addition, to apply in long-term management analysis, models should be stable in terms of adjustments to new observations. We use the ensemble Kalman filter to fit relatively simple models to ecosystem or foodweb data and estimate parameters that are stable over the observed variability in the data. The filter also provides a lower bound on the noise terms that a stochastic analysis requires. In the present article, we apply the filter to model the main interactions in the Barents Sea ecosystem. In a comparison, our method outperforms a regression-based approach.

Keywords: Barents Sea, Bioeconomics, Ecosystem-Based Management, Ensemble Kalman Filter, Multidimensional Models, State Space Model

# 1 Introduction

The ecosystem approach to fisheries management has been broadly embraced at both the political and scientific levels (UN 2002, Olsen *et al.* 2007, Holland *et al.* 2010, Link 2010), but adoption in real world situations is limited (Vert-pre *et al.* 2013, Skern-Mauritzen *et al.* 2015). While both empirical and theoretical evidence demonstrate the insufficiency of management regimes based on single species models (see Link 2010 and Skern-Mauritzen *et al.* 2015 and references therein), single species models remain at the center of attention for a number of reasons. Two central reasons are (i) the limited (in most cases) knowledge of the extent and importance of ecological and economic interactions and (ii) the complexity that arises in models with such interactions. Notwithstanding, the future lies in co-management and multidimensional analysis, and we need methods and techniques to harness multispecies models for use in fisheries management (Link 2010, Peck *et al.* 2014).

Multispecies models provide insights into how a group of populations responds to a process; such models are critical for better management and evaluation of multispecies tradeoffs and tradeoffs between different user sectors (Link 2010, p. 100). Multispecies models can also address dynamics that are hard to deal with consistently in single species models. Examples are interaction-induced critical depensation, effective carrying capacity (which depends on interactions and on the state of the system), dynamic interactions, and consistent system responses. Sandal and Steinshamn (2010) is a case in point, where highly nonlinear harvest profiles are derived for a multispecies model. The harvest profiles have features hardly imaginable in a single species model, such as a declining harvest rate with increasing stock level in parts of the state space.

To construct tractable multispecies fisheries models, we need estimation techniques that deal with parameter and model uncertainty. In our view, relevant models should submit to dynamic decision analysis, which implies a limitation in the number of dynamic variables

(that is, dimensionality). At the same time, we want models to capture as much as possible of the system structure and dynamics, including nonlinear and chaotic behavior. We suggest applying the ensemble Kalman filter (Burgers *et al.* 1998, Evensen 2003), a data assimilation method that has seen wide application in meteorology, oceanography, and other fields that are concerned with chaotic, nonlinear, and stochastic dynamic systems (Evensen 2009).

We use the ensemble Kalman filter to fit a marine ecosystem model to data. Evensen (2003, 2009) reviews both theoretical developments and applications of the ensemble Kalman filter and related methods. This literature extends the Kalman filter to a large class of nonlinear models. The fundamental idea is to use a Markov Chain Monte Carlo approach to solve the Fokker-Planck equation that governs the time evolution of the model. The model is formulated as a stochastic differential equation, and both the model and observations are assumed to have error. The method facilitates simultaneous model fitting and parameter estimation. Simultaneity is consistent with viewing the problem as a combined state and parameter estimation problem, which differs from traditional approaches that essentially ignore model error (typically, parameters are first estimated and then model predictions are calculated in a deterministic fashion; for further details and discussion, see Evensen 2009, pp. 95–ff.). With the ensemble Kalman filter, relatively simple models can capture much of the complexity observed in marine ecosystems. We briefly describe the ensemble Kalman filter and apply it to a three-species model of the Barents Sea ecosystem. We compare our results with those of a regression-based approach.

Several different data assimilation methods, usually variational adjoint methods, have been suggested to fit aggregated biomass models to data (see Ussif *et al.* 2003, and references therein). Grønnevik and Evensen (2001) applied different ensemble-based data assimilation techniques to age-structured fish stock assessment models, the ensemble Kalman filter among them. An advantage of the ensemble Kalman filter when

compared to variational adjoint methods is that it does not rely on direct optimization, and all observations are not processed simultaneously, which reduces computational demand. Instead, variable and parameter estimates are updated sequentially according to the filtering procedure. The ensemble Kalman filter also facilitates flow-dependent noise attribution; flow-dependent (or rather, state-dependent) noise processes, it turns out, are fundamental in capturing the dynamics of marine ecosystems.

If, as in Ussif *et al.* (2003), there is a known or easily identified functional relationship between biological variables and the exploitation strategy, the filter can also estimate economic parameters (for example, the exploitation rate). Another feature of the ensemble Kalman filter is that it readily applies to both continuous and discrete time formulations. This is a useful feature, because, while much bioeconomic modeling uses discrete time models, a substantial share of related work in optimization relies on continuous time. The difference in models of time may seem innocuous, but the corresponding discrete time model of a nonlinear model in continuous time is rather complex, while the corresponding continuous time model of a nonlinear model in discrete time time cannot be uniquely determined because of missing information about the dynamic behavior between discrete observation times.

The ensemble Kalman filter fits, in an efficient manner, nonlinear aggregated biomass ecosystem models to data. It also estimates the model error, which can be translated into uncertainty in model predictions. Combined with developments in highdimensional, stochastic optimization, the filter can make bioeconomic analysis relevant for real-world fisheries management decisions. Perhaps the main critique of bioeconomics, the over-simplification of biological models, loses much of its force when the explanatory power of the fitted biomass models matches, and even competes with, that of agestructured and synthetic models. The potential of the ensemble Kalman filter reaches

further. It has the ability to process large amounts of data in high-dimensional systems with large numbers of poorly known parameters (see Evensen 2003 and references therein) and it should be of interest to researchers working with large and volatile systems.

### 2 The Ensemble Kalman Filter

Our theoretical presentation of the ensemble Kalman filter is based upon Evensen (2003, 2009). Our point of departure is the continuous time state space model:

$$dx = f(x) dt + \sigma(x) dB \tag{1}$$

$$y = M(x) + v \tag{2}$$

An incremental change dx in the state variable (or n-vector) x is the sum of the drift term f(x) dt and the stochastic diffusion term  $\sigma(x) dB$ . The diffusion term represents model error, which is composed of inadequacy in f(x), potential parameter uncertainty, and stochastic drivers. When x is an aggregated biomass vector, f(x) is the multidimensional growth function  $(f: \mathbb{R}^n \to \mathbb{R}^n)$ .  $\sigma(x)$  is generally a matrix  $(\mathbb{R}^r \to \mathbb{R}^n;$ elements may depend on x) and the r-dimensional stochastic, Brownian increments in dBare independent, identical, and normally distributed with mean zero and variance dt. That is, stochastic drivers in equation (1) are Gaussian white noise. The measurement functional M(x) relates the state vector to the observations y. When the state vector is directly observed, the measurement functional is the identity operator. v is a normally distributed error term with mean zero and covariance R. Equation (1) is called the state equation; equation (2) is called the measurement or observation equation.

The ensemble Kalman filter is a sequential method and works as follows. The model is integrated forward in time until measurements become available. Measurements are used to update the model. The updated model is then further

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integrated until the next measurement time. In the theoretical literature, the updating step is called the analysis, thus the notation  $x^a$  for the updated state vector. The forward integrated model (the forecast) is denoted  $x^f \cdot C^f$  is the covariance of the model forecast;  $C^a$  is the covariance of the model analysis.

The ensemble Kalman filter uses, as the name suggests, an ensemble of model states: a cloud of points in state space, to represent the probability density function at any given time. Each ensemble member represents a realization of the state vector from the underlying distribution, and, with a large enough ensemble, it conveys distributional properties. With a Markov Chain Monte Carlo method (meaning that the model can be formulated as a Markov Chain and that a large number of simulated solutions are considered; see Evensen 2009), each ensemble member is integrated forward in time according to (1). Errors are simulated. The integrated ensemble represents a forecast of the probability density and the only approximation is the limited number of ensemble members (Evensen 2009, p. 47). The Markov Chain Monte Carlo method is the backbone of the ensemble Kalman filter and is equivalent to solving the Fokker-Planck equation for the time evolution of the probability density; see Evensen (2003, p. 348) for further details.

When measurements are available, each ensemble member is updated as a linear weighting between the forecast and the measurements:

$$x^a = x^f + K(y - M x^f) \tag{3}$$

The weight K is called the Kalman gain. Assuming M is the identity operator, we see that, with K = 0, no weight is put on the observation y; with K = I (the identity operator), no weight is put on the forecast  $x^{f}$ . The Kalman gain is given by:

$$K = C^{f} M^{T} (MC^{f} M^{T} + R)^{-1}$$
(4)

where we assume that M is a linear operator (a matrix);  $M^T$  denotes its transpose. It is crucial that observations are treated as uncertain (R > 0), and, therefore, in the

ensemble Kalman filter, the observation probability density is represented by an ensemble; in other words, observations are perturbed (Burgers *et al.* 1998, pp. 1720-1721). It is convenient to let the number of ensemble members in the observation ensemble, denoted *Y*, equal the number of ensemble members in the state space ensemble, denoted *X*.

In the standard Kalman filter, both the forecast and analysis covariance  $(C^f \text{ and } C^a)$  are in principle unknown; they are defined in terms of the unknown true state (see Evensen 2003, p. 347). In the ensemble Kalman filter, they are defined in terms of the ensemble means (*E* denotes the mean or expected value):

$$C_e^f = \boldsymbol{E}[(X^f - \boldsymbol{E}[X^f])(X^f - \boldsymbol{E}[X^f])^T]$$
(5)

$$C_e^a = \boldsymbol{E}[(X^a - \boldsymbol{E}[X^a])(X^a - \boldsymbol{E}[X^a])^T]$$
<sup>(6)</sup>

That is, covariances are represented by the ensemble moments that carry the subscript e. The observation covariance is also represented by the ensemble moment:

$$R_e = \boldsymbol{E}[(Y - y)(Y - y)^T]$$
(7)

The observation ensemble is defined such that it has the true (given) observation as its mean: E[Y] = y. The ensemble Kalman gain is defined as

$$K_e = C_e^f M^T (M C_e^f M^T + R_e)^{-1}$$
(8)

We assume that the ensemble is large enough that  $MC_e^f M^T$  and  $R_e$  are nonsingular; see Evensen (2003, p. 349). The analysis step (3) for ensemble member *j* is given by:

$$X^{a}(j) = X^{f}(j) + K_{e}(Y(j) - M X^{f}(j))$$
(9)

It can be shown that, by updating the ensemble with the perturbed observations Y, the updated ensemble  $X^a$  has the correct error statistics (Evensen 2003, p. 349). The analysis covariance can be written as

$$C_e^a = (I - K_e M) C_e^f \tag{10}$$

which is equivalent to the standard Kalman filter expression for the covariance matrix. See Evensen (2003) for derivations and further discussion. Page 9 of 38

The filter can estimate parameters by adding the parameters to the state vector – in essence, by adding dimensions to the state space. Parameters are treated as unobserved, constant model states, which implies they are assumed to have zero drift and diffusion terms (Hansen and Penland 2007, Kivman 2003). With parameters in the state space, involved operators must adapt to make them compatible with the extended state vector. The distribution of the ensemble members in the relevant dimension of the state space represents the conditional probability density function of the parameter. We interpret the mean of the ensemble as the estimate and the spreading of the ensemble as a measure of the estimate uncertainty.

The ensemble Kalman filter estimates state variables and parameters simultaneously. As Evensen (2009, pp. 95-97) points out, the approach represents an improvement to more traditional approaches that ignore model error and stochastic, dynamic noise. The sequential nature of the approach yields, for each observation time t, parameter estimates conditional upon observations up until t; estimates for the last observation are conditional upon all observations and are usually the estimates of interest. In situations where regime shifts or similar situations occur, one should inspect the behavior of the sequential parameter estimates.

While the filter does not directly estimate the scaling of the diffusion term in (1), the estimated  $C_e^a$  can be used to infer the appropriate noise scaling.  $C_e^a$  estimates the second moment of the density of the state vector at a given moment in time (at, say, t).  $C_e^a$  will vary with time (it is dynamic or flow-dependent; dynamic covariance is an advantage with the ensemble Kalman filter over variational methods). The second moment of the state vector density can be interpreted as the uncertainty in the estimated state conditional upon the state at t - 1 and the uncertainty, observational t. The uncertainty in the state estimate accounts for parameter uncertainty, observational

uncertainty, and model inadequacy; the latter is what the diffusion term in (1) represents. Thus, if the covariance is stable over time, or if it is stable after controlling for some assumed functional form of the scaling term, such as  $\sigma(x) = \sigma_0 \cdot x$ ,  $C_e^a$  can be interpreted as an estimate of  $\sigma(x)$  (or  $\sigma_0$ ). How  $C_e^a$  varies over time maps out the distribution of  $\sigma_0$ ; that is, we essentially follow Hansen and Penland (2007).

The initial ensemble should reflect beliefs about the initial state of the system (Evensen 2003, p. 350). The filter can be initialized by specifying means and standard deviations that characterize the initial ensemble. In the case of unknown parameters, initialization is not necessarily straightforward. Our experience is that, with large enough standard deviations, such that the initial ensemble covers all eventualities, and with enough ensemble members, it is possible to find reasonable traits of the initial ensemble. Often, theory and earlier results are available to guide this process.

For a given time t, the ensemble Kalman filter provides an estimate of the state of the system and its parameters conditional upon observations up until t. By smoothing the filter estimates, we obtain estimates conditional upon all observations (Evensen and van Leeuwen 2000). The filter and smoother estimates for the final observation are identical, and the smoothed parameter estimates are constant through time. The ensemble Kalman smoother can be formulated as a sequential method and in terms of the filter analysis; see Evensen (2003, p.360) for details. That smoother parameter estimates are constant and identical to the final filter estimates follows from the explicit modeling of parameters as deterministic but unknown constants (see Hansen and Penland 2007 and Kivman 2003) and is straightforward from the formulation in terms of the filter estimates; see Evensen (2009) for details. The ensemble Kalman smoother is particularly useful in problems involving unknown parameters, as it provides estimates of the state variables, conditional upon all

observations, and upon parameter estimates, also conditional upon all observations. In contrast, the filter provides, for a given t, state estimates conditional upon observations up until t and upon parameter estimates conditional upon observations up until t; these estimates clearly are poor before the parameter estimates converge.

To summarize, the ensemble Kalman filter can be interpreted as a statistical Monte Carlo method where the ensemble evolves in state space with the mean as the best estimate and the spreading of the ensemble as the error variance (Burgers *et al.* 1998, p. 1720). For many problems, the sequential processing of observations proves to be a better approach than the simultaneous processing that is typical in variational methods (Evensen 2009, p. 101).

# 3 The Barents Sea Model

The Barents Sea is one of the most productive ocean areas in the world, and is subject to extensive research (Gjøsæter *et al.* 2009, Huse *et al.* 2004, Durant *et al.* 2008; see also further references therein). The commercially most important stocks are cod (*Gadus morhua*) and capelin (*Mallotus villosus*); cod is highly valued as human food and capelin is an important part of the cod diet. Capelin is also caught for fishmeal and oil production. Juvenile herring (*Clupea harengus L.*) enters the Barents Sea when large year-classes arise in the Norwegian Sea. Herring has an important influence on the ecosystem; it is preyed on by cod while it preys on capelin larvae. We limit our model to these three fish stocks for two main reasons. First, our model captures the dynamics of the cod stock to a high degree, and the cod fishery, as the most important fishery in the region, is our main interest. Second, for the model to be relevant for bioeconomic analysis, we have to limit its complexity and dimensionality. We have in mind the type of analysis carried out in Sandal and Steinshamn (2010) and Poudel *et al.* (2012); see also Kugarajh *et al.* (2006).

To limit complexity, we use simple growth functions and interaction terms common in traditional bioeconomic analysis. While dimensionality is based upon technical limitations, we find comfort in the view promoted by Holling and Meffe (1996, p. 333) that the driving forces of an ecosystem are confined to a relatively small subset of variables and relationships. While our choice of variables and relationships does not contain all driving forces of the Barents Sea ecosystem, we observe that our model captures much of the variation detected in stock assessments.

### 3.1 The State Space Model

The biomass of the three stocks are the state variables; cod is denoted  $x_1$ , capelin is denoted  $x_2$ , and herring is denoted  $x_3$ . Both cod and capelin are harvested in the Barents Sea;  $h_1$  and  $h_2$  denote harvest rates of cod and capelin. Herring is not harvested in the Barents Sea, but eggs and larvae flow in from the Norwegian Sea. The best model would feature a lagged inflow variable (see discussion below), but a lagged variable would mean that the model is not autonomous; to accommodate dynamic analysis, the model should be autonomous. Thus, we use  $x_3$  as a proxy for the herring inflow; again, see discussion below. Finally, we denote parameters  $c_i$  and vectors in boldface. The dynamic model for the system is written in differential form:

$$dx_1 = (f_1(x_1, c_1, c_2) + g_1(x_1, x_2, c_3) + g_2(\mathbf{x}, c_4) - h_1)dt + \sigma_1(\mathbf{x})dB_1$$
(11)

$$dx_2 = (f_2(x_2, c_5, c_6) - g_1(x_1, x_2, c_7) - g_1(x_2, x_3, c_8) - h_2)dt + \sigma_2(\mathbf{x})dB_2$$
(12)

$$dx_3 = (f_2(x_3, c_9, c_{10}) + g_1(x_2, x_3, c_{11}) - g_2(\mathbf{x}, c_{12}) + c_{13}x_3)dt + \sigma_3(\mathbf{x})dB_3$$
(13)

where growth functions are denoted  $f_i$  and interaction terms are denoted  $g_i$ . Table 1 reports functional forms that we discuss further below. The stochastic increments  $dB_i$  are independent, with mean zero and variance dt. The scaling term  $\sigma_i(x)$  reflect correlations in the noise processes. Two principal models of the scaling term were tried: white noise

 $(\sigma_i(x) = \sigma_{0i})$  and state-dependent white noise  $(\sigma_i(x) = \sigma_{0i} \cdot x = \sigma_{0i1}x_1 + \sigma_{0i2}x_2 + \sigma_{0i3}x_3)$ .

The first terms in each model equation are the growth functions. The growth functions model the growth that does not happen through the modelled interactions. For cod (11), we use the logistic growth function; for the pelagic stocks capelin (12) and herring (13), we use the modified logistic growth function (see Table 1 for specifications). The related parameters ( $c_1$ ,  $c_2$ ,  $c_5$ ,  $c_6$ ,  $c_9$ , and  $c_{10}$ ) are interpreted accordingly. (The idea of carrying capacity, that is, the standard interpretation of the second parameter in the logistic and modified logistic, becomes unclear in an ecosystem setting. The capacity of the ecosystem to harbor any one species depends on the state of the entire system. Hence, intrinsic single species notions such as carrying capacity must be treated with caution in our multispecies approach.) While the logistic is the standard assumption, we found that the modified logistic better captures the tendency of the pelagic stocks to remain at low stock levels for extended periods before rapidly growing to high levels.

All species interactions in the system are predator-prey relationships. Cod preys upon both herring and capelin, while herring preys upon the capelin stock. (A competitive, mutually destructive interaction between the pelagic species is an interesting alternative model that was estimated, together with a few other specifications. The model reported here provided the best overall fit to the data. Brief descriptions of, and results from, alternative models are available from the authors.) The interaction terms are per definition positive, and corresponding terms (cod-capelin corresponding to capelin-cod, for example) have opposite signs. The capelin-cod and capelin-herring interaction terms ( $g_1(\cdot)$ ) are inspired by the crude Lotka-Volterra form of predator-prey interaction (May *et al.* 1979, p. 268), where the product of the stock levels is adjusted by an intensity parameter. The functional form of, for example, the capelin-cod interaction is  $g_1(x_1, x_2, c_7) = c_7 x_1 x_2$ , where  $c_7$  is the

intensity parameter. We will discuss the interpretation of the interaction intensity parameter further below.

While cod preys upon both capelin and herring, it has a tendency to prefer capelin when both types of prey are available (Durant *et al.* 2008, Gjøsæter *et al.* 2009). That is, the predation pressure on herring from cod is reduced when capelin is abundant. Thus, we modify the cod-herring interaction term to reflect cod's preference for capelin, and have  $g_2(x, c_{12}) = c_{12}x_1x_3\frac{x_3}{x_2+x_3}$ . The fraction  $\frac{x_3}{x_2+x_3}$  yields a model of preference such that, in the extreme case with no capelin  $(x_2 = 0)$ , the fraction equals one and the interaction term is unmodified. When capelin is present  $(x_2 > 0)$ , the fraction takes a value between zero and one and the interaction (cod predation) is weaker.

As is evident from the model equations (11 - 13), the interaction terms  $g_1$  and  $g_2$  represent a biomass loss for the prey species and a biomass gain for the predator species. The intensity parameters scale the product of biomass for each species in the terms to account for the rate of biomass loss in the prey species. Biomass is not conserved in the interactions, and the additional interaction parameters ( $c_3$ ,  $c_4$ , and  $c_{11}$ ) reflect the loss of biomass in the interactions. The loss in the cod-capelin interaction, for example, is given by  $\frac{c_3}{c_7}$ , and this and corresponding fractions are expected to take values between zero and one. Because most of the biomass is lost, these values are expected to lie closer to zero than one. We can think of these fractions as biomass conversion rates. While known or assumed interaction relationships would be helpful in reducing the number of parameters in the model, biologists reject the idea of stable relationships (S. Tjelmeland, personal communication). Thus, we refrain from prescribing fixed conversion rates.

The final parameter,  $c_{13}$ , measures the influence of the inflow of herring on the herring stock growth. Most of the time, the amount of herring biomass that enters the Barents Sea is relatively small. Over a few years, however, the herring biomass grows substantially. Thus, we could lag the inflow variable two years and multiply it with the scaling parameter  $c_{13}$ . The idea is that three-year-old (and older) herring make up most of the herring biomass in the Barents Sea, and the biomass influx two years earlier better explains the change in the herring stock. As mentioned above, a lagged variable would go against the need for an autonomous model. Thus, we use  $x_3$  as a proxy for the inflow. The correlation coefficient of  $x_3$  and inflow lagged two years is 0.811 and is nonzero with a *p*-value of  $5.5 \cdot 10^{-14}$ ; therefore, we find  $x_3$  to be a reasonable proxy. The assimilation run with the lagged inflow yields only minor alterations to our results; these results are available from the authors. (After three or four years in the Barents Sea, the juvenile herring returns to its main habitat in the Norwegian Sea to mature and eventually spawn; the herring growth rate in our model reflects the migration behavior.)

To avoid negative parameters, parameters are all assumed to be log-normally distributed. (Formally, they are treated as  $c_i = \exp(\alpha_i)$ , where each  $\alpha_i$  is a stochastic constant that is normally distributed.)

We treat estimates from stock assessments as measurements of the state variables, and the measurement operator is thus the identity operator. Note that parameters are added to the state vector as described above. We denote the extended state vector  $\Psi$ . The measurement operator must thus be adjusted to be compatible with the state vector by adding zeros. Parameters are treated as unobserved states. The observation equation becomes

$$\mathbf{y} = M\Psi + \mathbf{v} \tag{14}$$

where

$$\Psi = \begin{bmatrix} x_i \\ c_j \end{bmatrix}, \ i = [1 \cdots 3], \ j = [1 \cdots 13], \ \text{and} \ M = [I \ \mathbf{0}]$$
(15)

*I* is a three by three identity matrix and **0** is a three by thirteen null matrix. y is a three-element vector of observations, and v is the error term vector, which is normal, independent, and identically distributed with mean zero and variance *R*.

### 3.2 An Alternative Model

For comparison, we set up a simple, alternative model in the spirit of much of the work in bioeconomic analysis. The crude idea is to fit the individual stock equations with ordinary least squares. The independent variables  $z_t$  are defined as observed changes in stock levels from year to year, controlling for harvest in the case of cod and capelin. We have  $z_{i,t} = y_{i,t+1} - y_{i,t} + h_{i,t}$  for cod and capelin (i = 1,2); for herring (not harvested), we have  $z_{3,t} = y_{3,t+1} - y_{3,t}$ . The regression equations are as follows:

$$z_{1,t} = \gamma_1 + \beta_1 y_{1,t} + \beta_2 y_{1,t}^2 + \beta_3 y_{1,t} y_{2,t} + \beta_4 y_{1,t} y_{3,t} \frac{y_{3,t}}{y_{2,t} + y_{3,t}} + \epsilon_{1,t}$$
(16)

$$z_{2,t} = \gamma_2 + \beta_5 y_{2,t}^2 + \beta_6 \gamma y_{2,t}^3 + \beta_7 y_{1,t} y_{2,t} + \beta_8 y_{2,t} y_{3,t} + \epsilon_{2,t}$$
(17)

$$z_{3,t} = \gamma_3 + \beta_9 y_{3,t}^2 + \beta_{10} \gamma y_{3,t}^3 + \beta_{11} y_{2,t} y_{3,t} + \beta_{12} y_{1,t} y_{3,t} \frac{y_{3,t}}{y_{2,t} + y_{3,t}} + \beta_{13} x_{3,t} + \epsilon_{3,t}$$
(18)

The parameters denoted  $\gamma_i$  are the intercepts and are added to the otherwise unchanged equations for the main model. Thus, the parameters  $\beta_i$  refer to the same terms as do the parameters  $c_i$  above.

The model in equations (16-18) is formulated in discrete time, and the model in general and the parameters in particular are not directly comparable to those in the continuous time formulation (11-13). The comparison is nevertheless not completely irrelevant; as discussed above, fitting of continuous time model formulations in discrete time frameworks is widespread in the bioeconomic literature.

### 3.3 Data

The fish stocks in the Barents Sea cannot be observed directly. However, the Institute of Marine Research in Bergen and the Knipovich Polar Research Institute of Marine Fisheries and Oceanography in Murmansk carry out extensive, yearly ecosystem surveys. Based upon these surveys, they provide yearly estimates of the stock levels of all the important species in the Barents Sea. The stock estimates are published by the International Council for the Exploration of the Sea (ICES), and most of our data are collected from the ICES online database. We treat the stock estimates as observations. Notably, Ekerhovd and Gordon (2013) raise issues with stock estimates from virtual population models. We share their concern about the consistency in the stock estimates, but find it beyond our scope to apply the (Ekerhovd and Gordon 2013) adjustment here. Uncertainty in stock assessments is unfortunately not reported, and we are left to speculate. The herring inflow data was provided by S. Tjelmeland (personal communication).

We have stock estimates, catch data and herring inflow estimates from 1950 to 2007. However, the ICES database does not contain data on capelin prior to 1972. For the period prior to 1972, we collected catch data from Røttingen and Tjelmeland (2008, see Figure 2). Capelin stock estimates were collected from Marshall *et al.* (2000, see Figure 1, p. 2435). The early capelin stock estimates are more uncertain than later estimates, and we assume a 50% increased observation uncertainty on the capelin stock data prior to 1972.

All data are visually presented in Figure 1, with error bars showing assumed observation uncertainty. All numbers are given in tonnes.

3.4 Estimation Strategy and the Initial Ensemble

While the success of our approach hinges to some degree on reasonable characteristics of the initial ensemble, it is not immediately clear what constitutes reasonable characteristics. While we can rely on external, empirical evidence for a few of the parameters in the interaction terms, we must produce reasonable initial ensemble characteristics for most parameters in a heuristic fashion. The parameter subspace has thirteen dimensions (one for each parameter), and, while it is not impossible to search, via trial and error, the parameter subspace for an appropriate, initial ensemble, the high dimensionality makes the approach unlikely to succeed. (Our main metrics of appropriateness are whether the state estimates resemble the stock assessment data and to what degree the spread of the ensemble in the parameter dimensions contracts over time. In addition, we have used the Bayesian Information Criterion (BIC), but carefully, since the criterion is not unique because of the Monte Carlo element of the filter (see Ekerhovd and Kvamsdal 2014). We have also considered the distribution of the Kalman gain over time and stability of parameter.)

By first assimilating each equation individually, we reduce the dimensionality of the relevant parameter subspace substantially. When we assimilate the cod equation (11), for example, the state space consists of the cod stock level as the only state variable and the four parameters in the equation  $(c_1 - c_4)$  as parameter variables. The variables  $x_2$  and  $x_3$  are treated as control variables.

We have good ideas about reasonable ensemble initializations of the biomass conversion rates (limited support) and the interaction intensity parameters for the cod-capelin and cod-herring interaction terms (empirical evidence). The capelinherring interaction intensity is assumed to be an order smaller than the cod-capelin interaction intensity. Thus, when searching for reasonable initial ensemble characteristics in the single equation assimilations, we need mostly to be concerned

with the parameters of the growth functions. What we have called the capacity parameters are characterized by an ensemble mean higher than observed historic levels (exploited fisheries usually have stock levels below their full capacity). To find reasonable characteristics for the ensembles along the growth rate dimensions, we consider a range of levels and compare, as mentioned above, model fit, ensemble contraction, the Bayesian Information Criterion, and the distribution of the Kalman gain. To demonstrate, we briefly discuss an example of the procedure in Appendix A.2. Means and spreads of the initial ensemble for the parameter dimensions in the single equation assimilations are listed in Table A2 in the appendix.

The estimates from the single equation assimilations are used to characterize the mean of the normal distributions from which we draw the initial ensemble for assimilation of the full model. Exceptions are those parameters for which we have empirical support for the initial ensemble characteristics. Ensemble spreads (standard deviations of distributions from which initial ensembles are drawn) are also inherited from the single equation assimilations, with the same exceptions.

The initial ensemble is drawn randomly from a multivariate normal distribution. For the three state variables, we use the first observations as the mean of the initial ensemble and 30% of the first observations as the standard deviation.

The initial ensemble for the interaction intensity parameters  $c_7$ ,  $c_8$ , and  $c_{12}$  were characterized based upon empirical evidence. The term  $g_1(x, c) = c_7 x_1 x_2$  in (12) reflects the loss of capelin biomass from the interaction with cod. Gjøsæter *et al.* (2009, see figure 5, p. 45) estimated, from stomach content data, the amount of capelin consumed by the Barents Sea cod for the years 1984-2006. The consumption varies over time, as do the cod and capelin stock levels. To get a reasonable initial measure of  $c_7$ , we regressed the total consumption of capelin on the product  $x_1x_2$  (without intercept; we also ran the regression

with the intercept, and with and without two outliers; slope estimates varied somewhat but the distribution finally used for the initial ensemble spanned all estimates). Notably, Gjøsæter *et al.* (2009) provided us with data for 1984-2007 (that is, one more year of data than what they based their original analysis upon). The estimated coefficient was  $3.46 \cdot 10^{-10}$  (standard error  $5.1 \cdot 10^{-11}$ ,  $R_{adj}^2$  0.63). Similar data for the capelinherring interaction are not available. Herring is, however, thought to have a smaller predation rate on capelin than does cod; we set the implied mean for  $c_8$  at 10% of the implied mean of  $c_7$ . For the herring-cod interaction intensity parameter  $c_{12}$ , data are available. Gjøsæter *et al.* (2009) also estimated the amount of herring consumed by the Barents Sea cod. Regressing the consumed amount of herring on the term  $x_1x_3\frac{x_3}{x_2+x_3}$ yielded a coefficient of  $3.03 \cdot 10^{-11}$  (standard error  $6.46 \cdot 10^{-12}$ ,  $R_{adj}^2$  0.44). As with  $c_7$ , we set the mean of the initial shadow parameter ( $\alpha_{12}$ ) ensemble to correspond to the estimated coefficient. In comparison, regressing on the term  $x_1x_3$  produces the coefficient  $2.49 \cdot 10^{-11}$  (standard error  $3.76 \cdot 10^{-12}$ ,  $R_{adj}^2$  0.61).

The additional interaction parameters  $c_3$ ,  $c_4$ , and  $c_{11}$  (reflecting biomass conversion rates) cannot be larger than the corresponding parameters  $c_7$ ,  $c_8$ , and  $c_{12}$ , as it is assumed that some biomass is lost in the interactions. The biomass loss assumption is not explicitly enforced, but initial implied ensemble means for the three additional interaction parameters were set to 25% of  $c_7$  for  $c_3$ , 10% of  $c_{12}$  for  $c_4$  and 10% of  $c_8$ for  $c_{11}$ . Typically, one assumes that 90% of the biomass is lost between trophic levels, but cod is particularly adapted to catching capelin and thus we specified a higher biomass conversion rate for the cod-capelin interaction.

We discuss further implementation details in Appendix A.1.

### 4 Results

Table 2 reports parameter estimates, with standard errors in parentheses, for the single equation assimilations. Table A2 in the appendix reports the prior characterizations for comparison. The third column ('Contraction') in Table 2 reports the standard error of the estimates as a fraction of the standard deviation of the prior distribution. The ensemble Kalman filter will mechanically contract parameter ensembles, but the amount of contraction depends on the amount of information the filter retains. Assessing the contraction is equivalent to comparing the width of the parameter confidence intervals at the beginning and end of the assimilation. Both tables and also subsequent tables report estimates of the shadow parameters  $\alpha_i$ . However, our interest lies with the parameters  $c_i = \exp(\alpha_i)$ , and Table 2 reports what we call the *c*-interval, which is the two standard error interval around the mean estimate of the underlying parameter  $c_i$ .

We also calculate an estimate and standard error of the parameters in the diffusion terms. We denote the parameters  $\sigma_{i,i}$ , where the subscripts denote the relevant state variable. Table 2 reports the results.

Further, Table 2 reports the BIC-scores, the average root mean squared innovations, the difference R-squared ( $R_D^2$ , appropriate for time series data, see Harvey 1984), the Lilliefors *k*-statistic and the Ljung-Box *q*-statistic (with 15 lags) for each equation. A few comments on these statistics are in order. The BIC-scores, both here and later, are evaluated with a bandwidth of 200.000 (tonnes); see Ekerhovd and Kvamsdal (2014) for details. The innovation is the distance between the observations and the estimated state variables. In our model, with the state-dependent noise scaling  $\sigma \cdot x$ , it is useful to normalize the root mean squared innovations with the estimated state. Thus, what we report as the average root mean squared innovation is the time-average of the following expression

$$RMSI = \frac{\sqrt{E[(y - M\Psi_s^a)^2]}}{E[M\Psi_s^a]}$$
(19)

The subscript *s* denotes that it is the smoothed estimate which goes into the expression. The lower the average root mean squared innovation, the better is the model fit. Note that, in the absence of the normalization issue, the average root mean squared innovation is the average distance between the ensemble members and the observation; if the observation and the ensemble mean are close, the average root mean squared innovation will be close to the estimate of the noise scaling term, which is derived from the second moment of the ensemble.

The Lilliefors *k*-statistic tests normality of error terms; the Ljung-Box *q*-statistic tests autocorrelation in errors. There are no signs of autocorrelation in any of the assimilations. Errors in the capelin equation deviate from normality to some degree (the *p*-value is slightly below the conventional 5% level). A density error plot shows that the deviation consists of an overrepresentation of large, negative errors. A scatterplot of the errors shows that large negative errors occur mainly at low stock levels and likely reflect that the model cannot predict exactly when the stock escapes near zero states.

To discuss the actual estimates in Table 2 is of limited interest; their main function is to serve as priors for the full model. We do note, however, that while the contraction rate is substantial for most other parameters, the interaction parameters (parameters 3, 4, 7, 8, 11, and 12) have not contracted much. As the full model results will show, contraction is somewhat better when we assimilate all equations simultaneously. The small contraction rates for the interaction parameters underline the need for informative priors.

The cod equation has the smallest average root mean squared innovation and has a similar BIC-score as that for the capelin equation.  $R_D^2$  is much lower for the cod

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equation than for the other equations, however. The high  $R_D^2$  in the other equations likely derives from relatively high gain values, which leads to state variable estimates close to the observations. Comparing with results from the alternative (regression-based) model (see Table 4), they all have lower  $R^2$ -statistics. (We will discuss the results in Table 4 in more detail below.) Finally, the estimated noise scaling parameters in Table 2 are highly significant for all equations and underline the importance of the state-dependent noise processes.

Table 3 reports results for the full model assimilation. The BIC-score for the entire model is 269.70, while  $R_D^2$  is 0.9548. To properly test multivariate normality would require more observations than are available here. The multivariate Ljung-Box *q*-statistic (Hosking 1980), with 15 lags, is 125.47 (*p*-value is 1.000; no signs of autocorrelation). Notably, the prior for the full model assimilation is based upon the results reported in Table 2 for all parameters, apart from the two parameters for which we have empirical evidence ( $c_7$  and  $c_{12}$ ). For those parameters, we kept the original prior information as given in Table A2.

If we compare the contraction rates reported in Tables 2 and 3, we observe that, overall, contraction is better in the full model assimilation for the capelin and herring equation. In the cod equation, the interaction parameters have better contraction rates in the full model assimilation, while the growth parameters contract better in the single equation assimilation. That some growth parameters do not contract as much in the full model assimilation is likely because most of the signal in the data about these parameters is picked up in the single equation assimilation that was run prior to the full model assimilation.

In Table 3, the average root mean squared innovations have improved considerably for all state variables compared to the values in the single equation assimilations (Table 2). As discussed above, the average root mean squared innovations can be close to the  $\sigma_0$  estimate if the ensemble mean is close to the observations. Further, significant cross-correlations

in  $\sigma_0$  (the off-diagonal terms) may be challenging in model applications; as we report below, estimated cross-correlations are close to zero.

Below, we report estimates and standard errors of the noise scaling term  $\sigma_0$  (20). All off-diagonal elements are statistically indifferent from zero, which suggests that there is little correlation in the different stochastic processes of the system. The diagonal elements are also relatively small, at least when compared to hypothetical scenarios studied in theoretical work (Poudel *et al.* 2012). The standard errors do not give a correct measure of the significance of the diagonal elements, as the elements are positive by definition, but nevertheless show that the system is stochastic. If one wishes to carry out studies of worst-case scenarios, it could be of interest to investigate whether high or low levels are correlated in time across equations.

$$\sigma_0 = \begin{bmatrix} 0.0802 & 0.0004 & 0.0008 \\ (0.0098) & (0.0034) & (0.0035) \\ 0 & 0.1113 & -0.0010 \\ 0 & (0.0250) & (0.0030) \\ 0 & 0 & 0.0948 \\ 0 & 0 & (0.0047) \end{bmatrix}$$

Figure 1 shows the smoothed stock level estimates (solid curves) with two standard errors to each side (shaded areas) for all three state variables (top panel: cod; middle panel: capelin; bottom panel: herring). The figure also shows the observed stock levels (circles) with assumed observation uncertainty (the error bars show two standard deviations around the observations). Most observations lie within the four standard error band and the model captures most of the system dynamics. The smoothed parameter estimates are constant over time, and we interpret the smoothed estimates as model fit with uncertain but stable parameters (that is, as reported in Table 3).

Capelin stock data is more uncertain prior to 1972. As expected, the stock estimates have larger standard errors prior to 1972. Compare, for example, the width of the standard error band in Figure 1 (middle panel) in the years before and after 1972, or at

(20)

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the peaks around 1970 and 1980, which are at roughly the same level. After 1972, the capelin stock estimates, in addition to being more precise, lie closer to the measurements.

If we compare our estimates in the cod equation to those of Ussif *et al.* (2003), there are considerable differences. (Our estimates are based on some ten years more of data, but there is nothing spectacular about the last ten years of our data, perhaps apart from considerable levels of herring.) Our central estimate for the carrying capacity is 6.5 million tonnes; their estimate is 5.2 million tonnes. As mentioned above, the carrying capacity parameter in our model does not reflect the full capacity because interaction terms may contribute. Thus, our estimate is a lower bound (perhaps the lower end of the *c*-interval should be considered: 5.4 million tonnes). We estimate the logistic growth rate in the cod equation at 0.55; Ussif *et al.* estimate it at 0.34. Our estimate is larger and suggests that much larger harvest quotas can be sustainable. The maximum of our estimated growth curve, interaction terms aside, is at 899 thousand tonnes, while that of Ussif *et al.* (2013) is 460 thousand tonnes. In comparison, quotas in recent years have exceeded our maximum. Thus, our estimates in the cod equation seem to better align with reality. Published estimates of the remaining parameters were not available to us.

### 4.1 Alternative Model Results

Ordinary least squares parameters estimates and related *t*-statistics, root mean squared errors,  $R^2$ -statistics, Lillifors *k*-statistics, and Ljung-Box *q*-statistics, for the individual equations (16 – 18), are reported in Table 4. The overall impression is a poor fit, with  $R^2$  statistics barely acceptable. There are no signs of autocorrelation, but errors are not normally distributed in the cod (16) and herring (18) equations. Plots show that deviations are minor for the cod equation, but severe deviations are present in the herring equation. Few parameter estimates are

statistically significant at the conventional 95% level. Most parameters are of the expected sign in the cod and capelin equations (16 – 17), except for the insignificant capelin-cod interaction parameter  $\beta_7$ . The intercepts ( $\gamma_1$  and  $\gamma_2$ ) should be close to zero if the classical growth model were to hold water, but they are not. The herring equation (18) seems entirely driven by the inflow ( $\beta_{13}$ ), with the rest of the equation seemingly representing noise. The interaction parameters ( $\beta_{11}$  and  $\beta_{12}$ ) are of the expected sign and somewhat removed from zero; the growth parameters are essentially zero.

The root mean squared errors in Table 4 are reported in levels and do not, as such, compare to the average root mean squared innovations reported in Table 3. More relevant is the root mean squared error relative to the mean of the left-hand side variables (for equation *i*:  $RMSE_i/\overline{z_{i,t}}$ ), which evaluates to 0.4015, 2.673, and 52.44 in the three equations. Only the first is similar to any of the average root mean squared innovations reported in Tables 2 and 3, but is still higher than all of them. That  $RMSE_i/\overline{z_{i,t}}$  evaluates as a static concept (all points matter) while the average root mean squared innovations evaluates in a dynamic sense (measured locally in time) reflect the larger point that, while ordinary least squares fits all points simultaneously without regard for their order, the ensemble Kalman filter operates sequentially and fits paths in the state space.

The carrying capacity in the cod equation in the alternative model (16) is estimated at 4.8 million tonnes; the growth rate at 0.35. The implied maximum of the growth curve, again when interaction terms are ignored, is 436 thousand tonnes. As discussed above, the ensemble Kalman filter estimates from the model (11 - 13) seem more realistic.

### 5 Conclusions

The ensemble Kalman filter relates structurally to the standard Kalman filter and the extended Kalman filter in the sense that they minimize the variance of the state estimates.

However, the ensemble Kalman filter has some advantages. Unlike the extended Kalman filter, it requires no linearization. It solves rank problems that may occur with large numbers of observed variables. Unlike variational adjoint methods, it requires no adjoint operator and is thereby simpler to implement, and it has flow-dependent (non-constant) covariance. Further, the ensemble Kalman filter is well suited to large-scale problems, as it extends to asynchronous and missing observations and other issues (Evensen 2009). On the other hand, the ensemble integration (in the forecast step) can be computationally costly and, with strongly nonlinear systems, iterative procedures called multiple data assimilations hold better promise (Emerick and Reynolds 2012). As such, the ensemble Kalman filter is just the tip of the iceberg of a range of related methods that apply to a large range of problems (Evensen 2003).

In applying the ensemble Kalman filter, we have shown how relatively simple aggregated biomass models, typical in bioeconomic analysis, can capture much of the dynamics of ecosystems. When compared to earlier efforts of applying data assimilation methods to bioeconomic models (Ussif *et al.* 2003), our model seems a better fit and agrees better with stylized facts. The model presented here shows the most promise from among a number of different specifications. (Among the specifications we tried were: capelin and herring with common carrying capacity, that is, competitive, mutually destructive interaction, notably with fewer parameters; pure, white – not level dependent – noise in the error term; assumed perfect observations of the control variables; herring inflow as a state variable; and herring inflow as white noise around a non-zero mean.) In the interest of space, we cannot go into full details, but the alternative models have a number of undesirable properties that, when added together, wipe out the advantage of, for example, fewer parameters.

A prominent modeling possibility that could be explored is data timing. In our current approach, we assume a constant harvest rate throughout each year. The harvesting is more concentrated in winter and spring, however. Further, the stock assessments are usually carried out in the fall. These nuances of timing could influence the dynamics of the system were they taken into account. We have chosen not to go into this in our current approach for two reasons. One is a need to limit the scope of our present work. Second and more important, our current approach better serves the model needs in a bioeconomic framework for decision and management analysis.

The main model does of course have room for other improvements. The *c*-intervals for several of the parameters are not particularly tight, for example, and the estimates of elements in the  $\sigma_0$  matrix are not very precise. Based upon our experience, we conclude that the best source of improvements would be more data. While some of the series we use here extend further than what we utilize, herring inflow estimates are not further available. Notwithstanding, estimates of parameters in chaotic systems are not likely to be very precise, and management models should be flexible and adaptive (Holling and Meffe 1996, p. 332). It is important that management models take the uncertainty of the dynamics into account (Hill *et al.* 2007). Adaptive management models such as feedback models are already well understood in the bioeconomic literature (Sandal and Steinshamn 1997). The challenge is to solve models of higher dimensionality that must underlie ecosystem-based management (Fulton *et al.* 2011). We believe the ensemble Kalman filter has an important role to play in both theoretical and operational management research, particularly in light of calls for ecosystem-based management (Pew Oceans Commission 2003).

When we compare the ensemble Kalman filter to the standard approach that relies on ordinary least squares, two major points emerge. First, the discrete time equivalent of a

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model formulated in continuous time does not, in general, have the same functional form, but this is nevertheless often assumed. If, as with certain discretization schemes, the discrete time equivalent cannot be efficiently written in one equation, how to apply ordinary least squares is unclear. If, on the other hand, one formulates the model in discrete time in order to apply ordinary least squares, there is no unique representation of the discrete time model in continuous time and, therefore, optimization schemes in continuous time, for example, cannot be applied. Second, the ensemble Kalman filter fits the dynamics of the model in the sense that it forces paths in the state space to track the observations. Ordinary least squares, at least in the standard formulation, differentiates away the dynamics and is left with a cloud of points where the order is no longer essential. Further, we have the flow-dependent covariance (model error) that can be used to fit dynamic noise models and the explicit incorporation of observational uncertainty; these features of the ensemble Kalman filter have no equivalent in ordinary least squares, to our knowledge. In the final analysis, with the ensemble Kalman filter, we obtain a model that represents the continuous time dynamics of key species in the Barents Sea. Our adaptation of the standard approach is admittedly naïve, but discrete time estimation methods based on ordinary least squares cannot provide anything similar.

In a broader scope, we aim to answer calls for 'flexible, adaptive, and experimental' management models (Holling and Meffe 1996, p. 332), who further write that 'effective natural resource management that promotes long-term system viability must be based on an understanding of the key processes that structure and drive ecosystems, and on acceptance of both the natural ranges of ecosystems variation and the constraints of that variation for long-term success and sustainability' (p. 335). We think that, when models are simplified and reduced down to the key driving phenomena, the ensemble Kalman filter can capture both variation and stability in ecosystems and can serve in tractable management models.

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Table 1: Functional forms used in the model equations.

Term	Functional Form
Logistic Growth	$f_1(x_i, c_p, c_q) = c_p x_i \left(1 - \frac{x_i}{c_q}\right)$
Modified Logistic Growth	$f_2(x_i, c_p, c_q) = c_p x_i^2 \left(1 - \frac{x_i}{c_q}\right)$
Modified Logistic Growth with Common Capacity	$f_3(x_i, x_j, c_p, c_q) = c_p x_i^2 \left(1 - \frac{x_i + x_j}{c_q}\right)$
Lotka-Volterra Interaction	$g_1(x_i, x_j, c_p) = c_p x_i x_j$
Modified Lotka-Volterra Interaction	$g_2(x_i, x_j, x_k, c_p) = c_p x_i x_k^{-x_k} / x_j + x_k$

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Table 2: Parameter estimates with standard errors in parentheses for the single equation assimilations (the horizontal lines separate the different assimilations). The table also reports contraction rates and the *c*-interval for each parameter, noise-scale estimates ( $\sigma_{i,i}$ ), and BICscores, the average root mean squared innovation,  $R_D^2$ , the Lilliefors *k*-statistic, and the Ljung-Box *q*-statistic (with 15 lags) for each equation (*p*-values in parentheses).

	Estimate	Contraction	<i>c</i> -interval
Cod, equation (12), BIC: 91.63, Avg. RMSI: 0.1518, R <sup>2</sup> <sub>D</sub> : 0.2724, k: 0.1026 (0.1366), q: 22.60 (0.0928)			
$\alpha_1$	-0.5694	0.114	(0.5039, 0.6354)
1	(0.1159)		
$\alpha_2$	15.64	0.544	(4.780 e6, 8.158 e6)
-	(0.2672)		
$\alpha_3$	-23.12	0.986	(0.4540 e-10, 1.472 e-10)
	(0.4886)		
$lpha_4$	-26.46	0.982	(1.959 e-12, 5.240 e-12)
	(0.4917)		
$\sigma_{1,1}$	0.1248		
	(0.0115)		
Capelin, e	equation (13), BIC: 17	7.63, Avg. RMSI: 0.2300, $R_D^2$ : 0.9938, k: 0.118	82 (0.0450), <i>q</i> : 10.18 (0.8079)
$\alpha_5$	-12.58	0.3780	(2.335 e-6, 5.024 e-6)
	(0.3831)		
$\alpha_6$	16.45	0.710	(11.35 e6, 17.26 e6)
	(0.2094)		
$\alpha_7$	-21.74	0.978	(2.206  e-10, 5.815  e-10)
	(0.4845)		
$\alpha_8$	-24.10	0.970	(2.095  e-11, 5.533  e-11)
	(0.485)		
$\sigma_{2,2}$	0.2289		
	(0.0430)		
Herring, e	equation (14), BIC: 89	.13, Avg. RMSI 0.1956, $R_D^2$ : 0.9972, k: 0.0929	(0.2488), <i>q</i> : 11.07 (0.7472)
α9	-11.58	0.693	(0.4633  e-5, 1.859  e-5)
	(0.6948)		
$\alpha_{10}$	15.70	0.690	(4.647 e6, 9.330 e6)
	(0.3484)		
$\alpha_{11}$	-26.36	0.976	(2.206 e-12, 5.714 e-12)
	(0.4757)		
$\alpha_{12}$	-24.24	0.978	(1.136  e-11, 7.631  e-11)
	(0.9523)		/ · - · · · - · ·
$\alpha_{13}$	-0.1432	0.929	(0.5471, 1.372)
	(0.4597)		
$\sigma_{3,3}$	0.1953		
	(0.0092)		

Table 3: Parameter estimates with standard errors in parentheses for the full model assimilation. The table also reports contraction rates and the *c*-interval for each parameter, and the average root mean squared innovation for each state variable.

	Estimate	Contraction	c-interval	
Cod, equat	Cod, equation (12), Avg. RMSI: 0.09445			
$\alpha_1$	-0.5829	0.623	(0.5186, 0.6008)	
-	(0.0735)			
$\alpha_2$	15.69	0.704	(5.403 e6, 7.937 e6)	
	(0.1922)	0.014		
$\alpha_3$	-23.16	0.914	$(0.5660 \text{ e}{-}10, 1.347 \text{ e}{-}10)$	
0	(0.4337)	0.020	(2,033,0,12,5,000,0,12)	
$a_4$	(0.4508)	0.929	(2.055 e-12,5.009 e-12)	
Capelin, ed	nuation (13). Avg. RMSI: 0.1202			
α <sub>5</sub>	-12.81	0.169	(2.548 e-6, 2.899 e-6)	
5	(0.0643)			
$\alpha_6$	16.56	0.372	(1.445 e7, 1.692 e7)	
	(0.0788)			
$\alpha_7$	-21.86	0.931	$(2.034 \text{ e}{-}10, 4.994 \text{ e}{-}10)$	
	(0.4490)	0.022	$(1.770 \circ 11 - 4.202 \circ 11)$	
$\alpha_8$	-24.31 (0.4415)	0.922	(1.779  e-11, 4.302  e-11)	
Herring e	(0.4413) mation (14) Avg RMSI 0 1013			
α <sub>o</sub>	-11.53	0.270	(0.8099 e-5, 1.171 e-5)	
	(0.1844)		()	
$\alpha_{10}$	15.18	0.490	(3.327 e6, 4.614 e6)	
	(0.1634)			
$\alpha_{11}$	-26.13	0.937	(2.847 e-12,6.951 e-12)	
	(0.4463)	0.024	(1.0.(5	
$\alpha_{12}$	-24.36	0.934	(1.065  e-11, 6.4/2  e-11)	
a	0.1168	0.879	(0.7673, 1.646)	
<i>u</i> <sub>13</sub>	(0.3817)	0.077	(0.7075, 1.040)	
	(0.5017)			

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Table 4: Parameter estimates with standard errors in parentheses for regressions of the individual equations in the alternative model. The table also reports *t*-statistics, the root mean squared errors  $R^2$ , the Lilliefors *k*-statistic, and the Ljung-Box *q*-statistic (with 15 lags) for each equation (*p*-values in parentheses).

	Estimate	<i>t</i> -stat	
Cod, equation (16), RMSE: 2.52 e5, R <sup>2</sup> : 0.258, k: 0.1583 (0.0013), q: 16.08 (0.3762)			
$\gamma_1$	1.147 e5	0.56	
• 1	(2.02 e5)		
$\beta_1$	0.357	1.69	
	(0.211)		
$\beta_2$	-7.29 e-8	-1.59	
	(4.57 e-8)		
$\beta_3$	1.49 e-8	1.95	
	(7.64 e-9)		
$\beta_4$	1.88 e-8	1.52	
	(1.23 e-8)		
Capelin, ec	juation (17), RMSE: 1.4.	3 e6, <i>R</i> <sup>2</sup> : 0.331, <i>k</i> : 0.0668 (>0.500), <i>q</i> : 13.96 (0.5278)	
$\gamma_{2}$	6.63 e5	1.96	
- 2	(3.37 e5)		
$\beta_5$	1.11 e-7	1.85	
	(5.96 e-8)		
$\beta_6$	-1.44 e-5	-2.14	
	(6.76 e-6)		
$\beta_7$	2.03 e-8	0.326	
	(6.21 e-8)		
$\beta_8$	-1.53 e-7	-4.66	
	(3.29 e-8)		
Herring, ec	uation (18), RMSE: 1.1	7 e6, $R^2$ : 0.252, k: 0.1968 (<0.001), q: 21.76 (0.1141)	
$\gamma_{2}$	-1.01 e5	-0.31	
- 3	(3.15 e5)		
$\beta_9$	-3.07 e-7	-1.04	
	(2.95 e-7)		
$\beta_{10}$	2.71 e-5	0.90	
	(2.98 e-5)		
$\beta_{11}$	3.88 e-8	1.27	
	(3.05 e-8)		
$\beta_{12}$	-2.13 e-7	-1.33	
-	(1.60 e-7)		
$\beta_{13}$	0.83	1.28	
-	(0.65)		





Figure 1: Smoothed stock level estimates (solid curves) with two standard errors to each side (shaded areas). Stock level observations with observation uncertainty (circles and error bars) and harvest (squares) and inflow (triangles) levels. Top panel: Cod. Middle panel: Capelin. Bottom panel: Herring.