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# Up the Ante on Bioeconomic Submodels of Marine Foodwebs: A Data Assimilation-based Approach

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## Abstract

While economists have discussed ecosystem-based management and similar concepts, little attention has been devoted to the art of modeling. Models of ecosystems or foodwebs that make economic analysis viable should capture as much as possible of system structure and dynamics while balancing biological and ecological detail against dimensionality and model complexity. Relevant models need a strong, empirical content, but data availability may inhibit modeling efforts. Models are bound to be nonlinear, and model and observational uncertainty should be observed. We suggest the data assimilation method ensemble Kalman filtering to improve modeling of ecosystems or foodwebs. To illustrate the method, we model the dynamics of the main, pelagic species in the Norwegian Sea. In order to reduce the parameter dimensionality, the species are modeled to rely on a common carrying capacity. We also take further methodological steps to deal with a still high number of parameters. Our best model captures much of the observed dynamics in the fish stocks, but the estimated model error is moderate.

**Keywords:** Ecosystem Management, Pelagic Fisheries, Norwegian Sea, Ensemble Kalman Filter, Bioeconomics

# 1 Introduction

Resource economists should be concerned with building models of marine foodwebs and ecosystems that readily integrate with frameworks for economic decision analysis. Ecosystem-based fisheries has been on the agenda for decades, but fisheries management is still largely based on single-species approaches (May et al., 1979; Edwards et al., 2004; Link, 2010). The need to incorporate ecological and economic interactions and tradeoffs is pressing, however (Mangel and Levin, 2005; Scheffer et al., 2005; Tschirhart, 2009, and references therein). Further, to provide operationally relevant management advice that is ‘straightforward, succinct, and on-point’ (Link, 2010, p. 54), we need a unified approach to the decision problem that acknowledges inherent uncertainty and reflects the conflicting societal needs for resources and longevity.

When modeling foodwebs or ecosystems such that dynamic decision analysis is feasible, we are forced to balance biological and ecological detail against dimensionality and, to some degree, model complexity. The art of modeling thus relies on our ability to capture as much as possible of the system structure and observed dynamics while limiting dimensionality to a handful of dynamic variables (Link, 2010; Crépin et al., 2011; Levin et al., 2012). Not only do we need to choose our variables with great care, we also need to model their dynamics appropriately. Even though we limit ourselves to just a few variables, the model should still capture key ecological tradeoffs and is bound to become nonlinear, possibly non-convex (Dasgupta and Mäler, 2003), and certainly stochastic. Finally, we need to fit the model to relevant data with methods appropriate for the nonlinearity, stochasticity, and the inherent model and observational uncertainty.

As pointed out by many, the complexity and nonlinearity inherent in ecosystem-based fisheries management makes it impossible to provide general analyses and results; each specific case and scenarios require a specific and empirically based analysis (Link, 2010; Crépin et al., 2011; Levin et al., 2012). Of general interest, then, is the methods and conceptual approaches that is found to yield valuable insights in special cases and

accordingly has potential when applied to new scenarios. Thus, our present effort to model the Norwegian Sea pelagic complex, while aiming at relevancy for bioeconomic decision analysis, has interest both in the special setting of the Norwegian Sea and in a methodological and conceptual sense.

Our analysis has two elements of particular methodological interest. The first concerns data. Our model is formulated in terms of aggregated biomasses, and relevant ‘observations’ are then output from stock assessments. The stock level data are maintained and published by the International Council for the Exploration of the Sea (ICES, [www.ices.dk](http://www.ices.dk)), who also publishes annual harvest levels. The stock level data are based on stock assessments via virtual population analyses, and recent work shows that the generated data have potential problems with endogeneity (Ekerhovd and Gordon, 2013). Taking care of the problem yields alternative observations that are more statistically coherent, but the method require age-structured data and the resulting time series are shorter than the ICES stock level series (Ekerhovd and Gordon, 2013). When we model the Norwegian Sea pelagic complex (limiting ourselves to Norwegian spring spawning herring, Northeast Atlantic mackerel, and Northeast Atlantic blue whiting; see Skjoldal et al. 2004), length of the available time series becomes a pressing issue. In some sense, models are only as good as the data used to parameterize them (Mangel and Levin, 2005), and in applying the Ekerhovd-Gordon approach, we face a tradeoff between time series length and data quality.

The second methodological element of interest is our application of the ensemble Kalman filter (EnKF) to fit the aggregated biomass dynamic model to data on stock and harvest levels. The EnKF treats nonlinear models more rigourously than alternatives like the extended Kalman filter (Evensen, 2003); application to nonlinear models is the main motivation for using the EnKF. The method has further advantages; it fits the model in an adaptive way and thereby allowing relatively simple models to capture complex dynamics and it provides a measure of model error. The latter is of particular interest in our context, where the model is intended to serve in further stochastic decision analysis.

The Norwegian Sea harbours some of the world's largest stocks of herring, mackerel, and blue whiting, often collectively referred to as the pelagic complex of the Norwegian Sea (Huse et al., 2012). The related fisheries are of considerable, commercial interest and hence leads to conflict of interest among neighboring fishing nations (Bjørndal and Ekerhovd, 2014). Further, because the Norwegian Sea is very deep, with an average depth of more than 5,500 feet, there are no (significant) demersal predators like cod present. Thus, at least from a commercial perspective, there are no species at higher trophic levels of interest. Similarly, at lower trophic levels, the main species is the zooplankton species *Calanus finmarchicus*, also of limited commercial interest. *Calanus* is, however, the main food source for the pelagic complex for large parts of the year (Utne et al., 2012). In other words, the particular geographical and ecological structure of the Norwegian Sea gives rise to a rather simple foodweb where the pelagic complex relies, to a large extent, on a common food base. In an admittedly simplified perspective, we model the Norwegian Sea pelagic complex as three species at the same trophic level that compete for food and, in model speak, share a common carrying capacity. Modeling of competition in ecological models has seen little use in practice (Link, 2010, p. 100), but we find the approach appropriate and useful for the Norwegian Sea pelagic complex. Thus, establishing models for economic analysis in the Norwegian Sea setting should be of both scientific and industrial interest.

We think there is a need for an explicit focus on modeling of biology and ecology that provides relevant structures for further, economic analysis (*sensu* Sandal and Steinshamn, 2010; Poudel et al., 2012). In our experience, biologists and ecologists have limited inherent interest in providing the necessary models, data, and structures. Furthermore, the existing understanding of ecological-economic interactions in marine foodwebs is far from complete (Peck et al., 2014), something that underlines the the need for research into ecological-economic models. As we commit to such modeling, we gain a broader focus on the interdisciplinary nature of our work and it provides us with a more unified perspective on ecosystem-based management. We also think such modeling is necessary



to support better economic decisions because decision makers need good measures of how the underlying, interconnected systems responds to different management regimes.

## 2 Data and Method

Figure 1 displays the aggregated stock level estimates and annual harvest levels for Norwegian spring spawning herring, Northeast Atlantic mackerel, and Northeast Atlantic blue whiting that are published by ICES. The time series for herring and mackerel go back to 1972 (39 observations until 2010), while the blue whiting series go back to 1977 (34 observations). As discussed in great detail by Ekerhovd and Gordon (2013), the ICES stock level estimates are likely biased because of endogeneity between stock and catch variables (see Gordon 2013 for a comprehensive review of the endogeneity problem and related issues in fisheries). Ekerhovd and Gordon (2013) find a valid instrument for the catch variable in a lagged catch variable. We implement the Ekerhovd-Gordon approach to obtain statistically coherent stock estimates for the stocks of interest. Some details on the procedure are provided in the appendix; see Ekerhovd and Gordon (2013) for the full account.

The Ekerhovd-Gordon approach leads to improved stock estimates presented in Figure 2. Since the approach relies on lagged variables and the availability of age-structured data, improved estimates are only available from 1988 for herring, 1982 for mackerel, and 1981 for blue whiting. When we fit a model to the stock levels in figure 2, we only use observations for the years where all stocks are observed (1988-2011). It is technically feasible to fit a model with missing observations, but the fitted model is hard to interpret when the missing observations are at the beginning of the time series. Another alternative is to use the observations in Figure 1, with increased observation error, when Ekerhovd-Gordon estimates are missing. For the balance of this work, however, we limit ourselves to the observations in Figure 2 with 10 percent observation uncertainty.

To fit our model of the Norwegian Sea pelagic complex to data, we use the ensemble

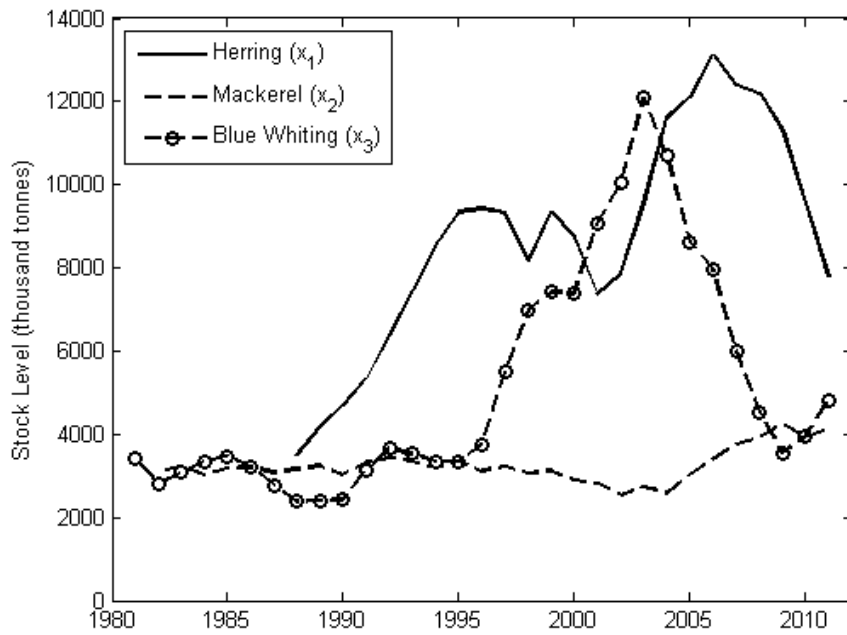


Figure 1: Stock estimates from ICES.

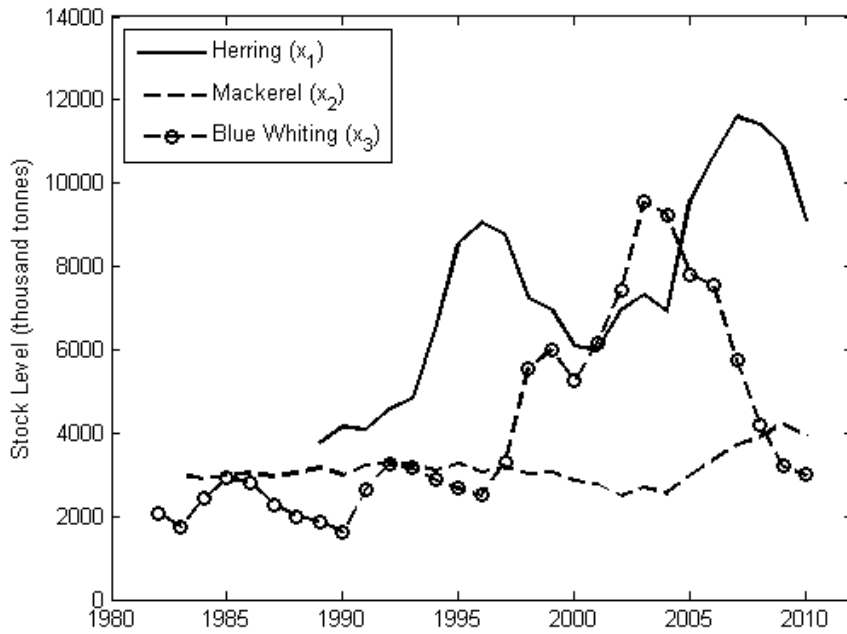


Figure 2: Stock estimates from the Ekerhovd-Gordon approach.

Kalman filter (Evensen, 2003, 2009). Kvamsdal and Sandal (2014) applies the ensemble Kalman filter to a similar model of species in the Barents Sea and discuss motivations for using the method and yield a relatively comprehensive discussion of some of the technical details. In the interest of space, we hereby provide a relatively compact description of the ensemble Kalman filter and its application to the Norwegian Sea pelagic complex.

First, we need to describe the state space representation of our model. The state space representation has two sets of equations, the state equations and the observation or measurement equations. The state equation describes the time evolution of the state vector  $x$ , and consist of a drift term and a stochastic diffusion term. The drift term is the key element to model. We formulate the model in continuous time such that the state equation describes an incremental change  $dx$  to the state vector over the incremental time step  $dt$ . The measurement equations relates the state vector to the data  $d$  via the measurement functional  $M(x)$  that maps the state vector to the ‘observation space.’ In our case, we treat the stock levels as directly observed and the measurement functional is then the identity operator. (When we estimate parameters, they become parts of the state vector, and the measurement functional and further operators need to be modified accordingly; see Evensen, 2009 for details.)

The continuous time state space model is written

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

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

Equation (1) is the state equation, where  $f(x)dt$  is the drift term and  $\sigma dB$  is the stochastic diffusion term. The stochastic, Brownian increments  $dB$  are independent, identical, and normal distributed with mean zero and variance  $dt$ . Equation (2) is the measurement equation, where  $v$  is a normal distributed error term with mean zero and covariance  $R$ .

The filtering procedure consist of two steps; the forward integration step and the update or analysis step. The first step integrates the state vector forward in time,

generally between observation times, according to the state equation. The second step updates the state vector as a weighted mean of the observation vector and the integrated (forecasted) state vector. The weights are constructed to minimize the variance of the state estimate. Often, a smoothing step is also carried out, after each or only the final update step. Ultimately, we want to describe a probability density function in the state space.

In order to avoid approximations in the integration step, the ensemble Kalman filter uses a Markov Chain Monte Carlo approach. An ensemble of state vectors, a cloud of points in the state space, represents the probability density function. Each individual vector in the ensemble is integrated according to the state vector. The diffusion term is simulated. When the state equation (1) is formulated as a Markov Chain, the integration of individual ensemble members amounts to evaluation of the drift term and simulation of the diffusion term. The integration step is equivalent to solving the Fokker-Planck equation for the time evolution of the probability density of the state, which is inconvenient in practical settings with for example a nonlinear drift term. But the Monte Carlo integration of an ensemble of states approximates the solution of the Fokker-Planck equation. The only approximation is the limited number of ensemble members (Evensen, 2009, p. 47).

After the integration step, the state vectors in the ensemble are updated through a weighting against observations. The weights are determined by the Kalman gain  $K$ . Observations are perturbed to form an ensemble of observations that accounts for observation uncertainty. By perturbing the observations, the updated ensemble of state vectors retain the proper covariance structure (Burgers et al., 1998). Perturbations are drawn from the distribution that describes the observation uncertainty. We denote the updated ensemble  $X^a$  (in the technical literature, the update step is called the analysis, which explains the superscript  $a$ ). For a given ensemble member  $i$ , the update is written

$$X^a(i) = X^f(i) + K (D(i) - MX^f(i)) \quad (3)$$

where  $X^f$  is the forward integrated ensemble,  $D$  is the observation ensemble, and  $M$  is the observation operator that here is assumed to be linear. (See Evensen 2009 for a more general treatment.) The Kalman gain is given by

$$K = C^f M' (M C^f M' + R)^{-1} \quad (4)$$

where  $C^f$  is the covariance of the forecast ensemble  $X^f$ . The apostrophe denotes the transpose. The ensemble has to be of sufficient size such that inverted matrices are nonsingular (Evensen, 2009).

The ensemble Kalman filter accommodates parameter estimation, essentially by adding dimensions to the state space and thus the state vector. Parameters are treated as unobserved, constant model states, which implies that they have zero drift and diffusion terms (Hansen and Penland, 2007; Kivman, 2003). The distribution of the ensemble members in the relevant dimension of the state space represents the conditional probability density function of the parameter.

The ensemble represents the probability density function of the state vector. At any given time, the estimate of the state is the mean of the state ensemble, with the ensemble covariance representing uncertainty in the estimate. The initial ensemble should reflect belief about the initial state of the system. An advantage with the approach outlined above is that state and parameter variables are estimated simultaneously, taking model error into account (Evensen, 2009, pp. 95-97). The filter produces estimates conditional upon observations up until and including a given time. When estimates conditional upon the full information set is relevant, the estimates should be smoothed with the ensemble Kalman smoother. The ensemble Kalman smoother can be formulated sequentially in terms of the filtered estimates; see Evensen (2003, p. 360) for details.

As an aid to compare goodness of fit of models and between models, we consider different measures. The technical literature (see Evensen, 2003, and references therein) often considers root mean squared errors and root mean squared innovations. (The term

innovation is used for the distance between observed and estimated states and reflect the idea that filtering improves the knowledge about the state.) Errors in the parameter ensembles decline over time by construction, but should stabilize before the end of the time series in the ideal case with a long enough time series and an appropriate model. Innovations does not decline by construction, but are also expected to stabilize in the ideal case. Weak or nonexistent signs of stabilization of either errors or innovations means either that the model has not converged (inappropriate initialization or simply too few observations) or that the model is poor. While useful, errors and innovations have limited ability to inform about model choice between alternative models.

To compare between models, we consider the Akaike (AIC) and the Bayesian (or Schwarz) Information Criteria (BIC). Both measures require likelihood evaluations, which essentially means that we must consider the estimated density of the observations. With the ensemble Kalman filter, the estimated density is represented by a discrete cloud of points in the state-space. While it is possible to make distributional assumptions and carry out calculations of the criteria, we apply a more rudimentary approach where distributional assumptions are avoided. First of all, to make distributional assumptions with an involved covariance structure in a high-dimensional space can be cumbersome. Second, distributional assumptions lead to heavy calculations as the entire distribution has to be considered. In our rudimentary approach, which simply consider a local density relative to the observation, any kind of covariance is accommodated and the calculations are comparatively simple.

Our approach to evaluate the information criteria considers a given neighborhood in the state-space around each observation where the density is given by the relative weight of the neighborhood compared to the remainder of the state-space. Weights are decided by the distribution of ensemble members within and outside the neighborhood. The neighborhood, or bandwidth, which is kept constant over the time series, should be as small as possible without being empty. Models should be compared at the same bandwidth. Given that the exact distribution of the ensemble members vary for different,

independent runs of the filter, criteria calculations from more than one run should be compared. Each run provide equally representative information criteria scores. When comparing different models, the basis for comparison grows exponentially with the number of runs, such that relatively few runs could form solid ground for comparisons. For example, two models that both are run five times provide us with twenty five independent comparisons of information criteria scores. However, comparisons between individual runs becomes cumbersome when models are run many times. Thus, we consider mean criteria scores over multiple runs. (The exact ensemble distribution depends on the Markov Chain Monte Carlo mechanism, which has a strong, random element. In the limit where the ensemble size goes to infinity, the random element is cancelled out and the criteria calculations are unique.) Finally, we refer to the discussion in Kass and Raftery (1995) for what constitutes significant differences in criteria values.

### 3 Modeling the Norwegian Sea Pelagic Complex

The Northeast Atlantic sustains a number of pelagic fish stocks, the most important of which are Norwegian Spring Spawning (NSS) herring, Northeast Atlantic blue whiting and Northeast Atlantic mackerel (Skjoldal et al. 2004). All these stocks are classified as straddling in the sense that they not only cross boundaries between the exclusive economic zones of coastal states, but also traverse the high seas areas between those boundaries (Bjørndal and Munro 2003).

NSS herring mainly inhabit Norwegian waters throughout the life cycle, but can migrate into Russian waters during the juvenile phase, and into Faroese, Icelandic and international waters as adults during the summer feeding period (Holst et al. 2004). The feeding migration pattern, especially for large herring, has changed several times over the last 60 years (Holst et al. 2002; Utne et al. 2012), varying with the size of spawning stock biomass and possibly ocean conditions as well. Mackerel spend most of the year in EU waters, but a large part of the stock migrates into the eastern part of the Norwegian Sea

and the North Sea from June to October (Belikov et al. 1998; Iversen 2004). In recent years Icelandic waters have also been inhabited by mackerel (Nøttestad and Jacobsen 2009) possibly due to changing water temperatures. Blue whiting is mainly found in the Norwegian Sea throughout the year, but spawns west of the British Isles in February-May (Bailey 1982). The stock is located in Norwegian, Icelandic, Faroese and EU waters, but the large scale distribution pattern varies and is related to total stock size and water temperature (Utne et al. 2012).

In order to make headway with our modeling effort, we need to introduce a number of simplifications to the relatively complicated picture that arises from the situation in the Norwegian Sea. First, we need to decide what are the relevant state variables. As juvenile individuals the NSS herring spend their time in the coastal waters of northern Norway or in the Barents Sea, and only appear in the Norwegian Sea along with the mature part of the stock at the age of 3 - 4 years old. Therefore, and since the overlap and interactions with the two other stocks mainly takes place in the Norwegian Sea, we could use the spawning stock biomass as the state variable for herring. However, total biomass is more likely to capture the stock dynamics. Moreover, the ICES present the total stock biomass following each cohort as different age classes over time. We can use this information when we implement the Ekerhovd-Gordon approach to obtain statistically coherent stock estimates. For mackerel and blue whiting the choice of state variable is not so clear cut. Both juvenile and adult blue whiting spend time in the Norwegian Sea, while the mature individuals migrate west of the British Isles to spawn, (some of) the juveniles remains in the Norwegian Seas. This is for a large part the case with mackerel; a large part of the stock, both young and adult individuals, spend time in the Norwegian Sea. Thus, we use the total stock biomasses for mackerel and blue whiting as state variables in our model.

We denote our state variables  $x_1$  (herring),  $x_2$  (mackerel), and  $x_3$  (blue whiting). The harvest rates are denoted  $h_1$ ,  $h_2$ , and  $h_3$ , while we denote parameters  $c_j$ . In addition, we consider parameters  $m_j$  that modify the functional form (or structural characteristics) of



the growth functions. Using aggregated biomass growth functions modified to reflect a common foodbase, we can write a dynamic model, on differential form, as follows:

$$dx_1 = \left( c_1 x_1^{m_1} \left[ 1 - \frac{x_1 + x_2 + x_3}{c_4} \right] - h_1 \right) dt + \sigma_1(x) dB_1 \quad (5)$$

$$dx_2 = \left( c_2 x_2^{m_2} \left[ 1 - \frac{x_1 + x_2 + x_3}{c_4} \right] - h_2 \right) dt + \sigma_2(x) dB_2 \quad (6)$$

$$dx_3 = \left( c_3 x_3^{m_3} \left[ 1 - \frac{x_1 + x_2 + x_3}{c_4} \right] - h_3 \right) dt + \sigma_3(x) dB_3 \quad (7)$$

The growth functions, which in general can be written  $f(x_i) = c_i x_i^{m_i} \left( 1 - \sum_j x_j / c_4 \right)$ , derive from the classic logistic growth function, but are modified in the following ways. The positive term has an additional exponent  $m_i$  that allow a band of low stock levels with near zero growth and a right-skewed growth profile. Essentially,  $m_i$  modifies the growth function such that growth has a degree of depensation. Pelagic stocks often display violent dynamics that to some degree can be accounted for with depensated growth functions. For example, in a model of the Barents Sea foodweb, depensated growth was found crucial to capture the dynamics in the pelagic species (Kvamsdal and Sandal, 2014). The negative term, which in the classic logistic measures the biomass relative to the the carrying capacity, measures the total biomass in the system relative to a common carrying capacity. The parameter  $c_4$  is the common carrying capacity.

In our model, all species carry the same weight in the balance against the common carrying capacity, which implies that a unit of the capacity supports the same amount of each specie. If lower trophic levels were included in the model, we would have to assume that all species had identical biomass conversion factors with respect to the lower levels in order to maintain our assumption. Equal weighting is clearly a simplification, but a useful assumption in that it reduces the parameter space considerably. Further, previous experience with modeling and estimation of biomass conversion factors is mixed (Kvamsdal and Sandal, 2014).

Equations (5 - 7) serve as state equations (1) in our state space model. The stochastic

Table 1: Initial ensemble parameters and standard deviations

Parameter	Implied Mean ( $\exp \bar{\alpha}_k$ )	Ensemble Mean ( $\bar{\alpha}_k$ )	Ensemble St. Dev.
$c_1 - c_3$	1/1000	-6.69078	1.0
$c_4$	30000 <sup>a</sup>	10.30895	0.2
	20000	9.90349	
$m_1 - m_3$	1.5	0.4054	0.2

<sup>a</sup> Thousand tonnes

increments  $dB_i$  are independent, with mean zero and variance  $dt$ . Correlations in the noise processes are reflected in the scaling term  $\sigma_i(x)$ . The scaling term is state-dependent in that  $\sigma_i(x)$  is the  $i$ 'th row in  $\Sigma \cdot x$ , where off-diagonal elements in the upper triangular matrix  $\Sigma$  reflect covariation (see Kvamsdal and Sandal, 2014 for further details).

All parameters are log-normal distributed, and are thus always positive. That the stocks share carrying capacity essentially means that they compete for resources, and thus signs of the interactions are negative. For example, the herring stock is negatively affected by its own stock size as well as the size of the mackerel and blue whiting stocks.

The initial ensemble (the prior) is drawn from a multivariate normal distribution. For the three state variables, we use the first observations as the mean of the initial ensemble and 20% of the first observation as standard deviation. As parameters enter the model equations as  $c_k = \exp(\alpha_k)$ , the parameter variable ensembles are defined in terms of the  $\alpha_k$ 's, which may be called shadow parameters. Means and variances for the shadow parameter variable ensembles are listed in Table 1. The table also lists the implied parameter mean  $\exp(\bar{\alpha}_k)$ . Since it is intuitively much easier to relate to the actual parameters  $c_k$  rather than the shadow parameters  $\alpha_k$ , we refer to the actual parameters in the discussion that follows. Table 1 also lists prior characteristics for the modification parameters that are necessary in some specifications (further details on the different specifications are discussed in the results section below).

For mackerel and blue whiting the single species intrinsic growth rates are estimated to lie between 0.3 to 0.4 (Ekerhovd 2003; Hannesson 2013), and for herring the rate is estimated in the range 0.4 to 0.5 (Arnason et al., 2000). However, here the growth

equations are modified logistic functions, and the intrinsic growth rates must be scaled accordingly. Hence, the initial means for the growth parameters for herring, mackerel and blue whiting,  $c_1 - c_3$ , were set to 1/1000.

Utne et al. (2012) calculated the consumption of zooplankton by herring, mackerel and blue whiting in 1997, which was estimated to be 82 million tonnes. This gives a consumption/biomass ratio in the range 5.2 - 6.3. The total biomass of the pelagic fish stocks was estimated to be between 13 and 16 million tonnes. However, the pelagic fish stock is subject to substantial commercial fisheries and the question remains what would the pelagic fish biomass be if there was no fisheries? Is the total ‘carrying capacity’ biomass of the pelagic fish stocks substantially larger than the biomass we observe in the current situation? Moreover, all three fish stocks spend a substantial amount of time in waters where they do not interact with each other. This indicates that the  $c_4$  parameter could be substantially larger than the observed biomass. We try two different priors for the  $c_4$ -parameter; one with mean 20 million tonnes and one with mean 30 million tonnes.

## 4 Results

The first specification (model 1) estimates all parameters in equations (5) - (7), that is,  $c_1 - c_4$  and  $m_1 - m_3$ , with the first of the two alternative priors for  $c_4$  (implied mean 30 000 thousand tonnes). Table 2, column 1, lists parameter estimates with standard errors in parenthesis. (Note that the table lists estimated values for the shadow parameters  $\alpha_i$ . Table A1 in the appendix lists corresponding confidence intervals for the  $c_i$  and  $m_i$  parameters.) Table 2 also lists information criteria (bandwidth: 500) and the average root mean squared innovation, which is the root mean squared distance between the smoothed state estimate (mean of smoothed ensemble) and the observation vector. The average is taken over the time series. To overcome the inherent randomness in the calculation of the information criteria, the results in table 2 and all other subsequent results are means over fifty independent runs of the filter. Repeated filtering runs also improves

Table 2: Parameter estimates and statistics for four different models: Model 1 (column 1), model 1R (column 2), model 2 (column 3), and model 2R (column 4).

Column	1	2	3	4
Model	Model 1	Model 1R	Model 2	Model 2R
Parameters				
$c_1$	-6.9268 (0.95399)	-4.9667 (0.22051)	-6.9470 (0.95471)	-4.6612 (0.25398)
$c_1$	-6.8263 (0.95374)	-4.7296 (0.21386)	-6.7976 (0.95631)	-4.5016 (0.23985)
$c_1$	-6.8199 (0.94459)	-4.8335 (0.17825)	-6.7751 (0.94420)	-4.6067 (0.21194)
$c_1$	10.328 (0.19174)	10.340 (0.13893)	10.056 (0.18158)	10.262 (0.12333)
$m_1$	0.36124 (0.16777)		0.34555 (0.16608)	
$m_2$	0.40546 (0.16926)		0.39639 (0.16962)	
$m_3$	0.40526 (0.16072)		0.39718 (0.15691)	
Statistics				
AIC	74.382	115.36	76.763	125.01
BIC	82.019	119.72	84.400	129.38
Avg. RMSI	911.45	1014.2	908.39	1051.1

estimates, and in particular error statistics (Sætrum and Omre, 2013). Each run uses one thousand ensemble members. The standard errors for  $c_1$  to  $c_4$ , which are similar to the prior spreads, suggest that model 1 fitted to the data provides little information about the parameters (there is little convergence in the parameter ensembles; see Kvamsdal and Sandal, 2014 for further discussion).

Model 2, which uses the second of the two alternative priors for  $c_4$  (implied mean 20 000 thousand tonnes), similarly provides little information about the parameters  $c_1$  -  $c_4$ . Results are listed in column 3 of table 2. Model 1 scores decisively better on the information criteria (a decisive difference is two or larger, see Kass and Raftery 1995), while model 2 has a slightly better average RMSI.

The problem in model 1 and 2 is likely that to estimate seven parameters in a nonlinear model with only 22 observations is difficult, in particular with all the uncertainty

presented by priors and observational noise. A further worry is the effect of the modification parameters  $m_i$  on the structure of the growth function. Emerick and Reynolds (2012) present a scheme where the filtering procedure is run repeatedly on each data point and that improves estimates in nonlinear models (estimates are equivalent in linear models). Inspired by Emerick and Reynolds (2012), we decided to run the filter twice, but where we in the second run used a reduced form of the model. The reduced model has only the  $c_i$  parameters to be estimated. The modification parameters  $m_i$  are set to their estimated values in the model 1 (or 2, respectively) and are treated as known constants in the second run. That is, model 1 and 2 serve as the initial run for the dual filter reduced models 1R and 2R. To be clear, we use the results from the initial run to inform priors for the second run. The attempt to estimate  $c_i$  in a second run is a consequence of the little information about these parameters provided in model 1 and 2.

The results from a secondary filtering with reduced models are presented in table 2. Column 2 holds the results for model 1R that uses model 1 (column 1) as initial run. The standard errors show that the model provides much more informed estimates of parameters  $c_i$  (see table A1 in the appendix for parameter confidence intervals). The information criteria, and the average RMSI, however, clearly suggest that model 1 is better. When we turn to model 2R in column 4, table 2, we observe a similar effect on the standard errors from the second run, and parameter estimates are better than in model 2. The information criteria and average RMSI is better for model 2, and we note that the information criteria deteriorates more when we move from model 2 to 2R than from model 1 to 1R. We also note that parameter estimates in models 1R and 2R are relatively close, but removed from the priors (that is, model 1 and 2). The  $c_4$  estimates, which prior was what discerned model 1 and 2, are more similar than in model 1 and 2. Further, the  $c_4$  estimates are closer to the model 1 prior. Thus, in our subsequent efforts to improve parameter estimates and model fit, we depart from the high  $c_4$  prior.

While model 1 and 2 give decent model fit, they provide little in terms of parameter estimates. Estimates are close the priors, and standard errors are little improved. On

the other hand, model 1R and 2R yield sharper parameter estimates, but the model fit declines. In particular, we are not confident in our estimates of  $m_i$ , which are treated as known constants in models 1R and 2R. Thus, we pursue an alternative approach that require substantial computations, but let us indirectly identify more appropriate values for the modification parameters  $m_i$ .

The idea is simply to lay out a grid in the  $m_i$  parameters and estimate the reduced model (with only the  $c_i$  parameters to estimate) on each node in the grid. Then, we simply compare information criteria scores and subsequently the average RMSI to decide which node yields the best values for  $m_i$ . To reduce the computational requirements somewhat, we first estimate the reduced model on a rather coarse grid, and then establish a finer grid covering the most promising nodes in a second round of estimates. The initial coarse grid has 216 nodes ( $6 \times 6 \times 6$ ), with nodes at  $m_i = [1.0, 1.2, 1.4, 1.6, 1.8, 2.0]$  for  $i = 1 \dots 3$ . As before, we run the filter fifty times (independent runs with one thousand ensemble members) to deal with the inherent randomness in the calculation of the information criteria. Thus, over the initial grid we run the filter 10 800 times at an average of 65 seconds per run, so the computational burden is significant.

Table 3 lists the top 20 nodes ranked according to BIC score. BIC score is listed in the first column, while the three next columns specify the node values of  $m_i$ . Next are estimated values for  $c_i$  with standard errors in parenthesis. The last column lists the average RMSI. Parameter estimates vary with node values for  $m_i$ , as expected. Note that the estimates for  $m_i$  from model 1, which are used in model 1R and are  $[1.43, 1.50, 1.49]$ , are not spanned by the top twenty nodes in table 3. Neither the model 2 estimates for  $m_i$  are spanned by the top nodes. This observation further fuels our suspicion that the results in table 2 are subpar. In addition, we observe that the BIC score is significantly improved. The top three nodes are within what Kass and Raftery (1995) describes as indistinguishable in terms of BIC scores. We also note that while the BIC score increases gradually between the top seven nodes, there is a large jump to node eight. Thus, based on the top seven nodes we establish a finer grid with nodes at 0.05 steps in the following

intervals: For  $m_1$ , [1.65, 2.10], for  $m_2$ , [1.25, 1.95], and for  $m_3$ , [1.85, 2.10]. The fine grid has 900 nodes (15 x 10 x 6); with fifty independent runs on each node, we run the filter 45 000 times in total.

Table 4 lists the top 20 nodes in the fine grid, ranked according to BIC score. The table is organized in the same way as the previous table, with  $m_i$  grid values, parameter estimates with standard errors in parenthesis, and the average RMSI. In the fine grid, the entire top 20 list is within 2 score units of the best node (24 nodes are within 2 score units). The average RMSI is also similar for all nodes (it varies with approximately five percent in the top 20 list), but the top node also has the best RMSI score. Nevertheless, we find the BIC score the most important measure as it consider the estimated state distribution in relation to the observations, while the average RMSI only considers the ensemble mean. We consider the top node listed in table 4, with  $m = [1.85, 1.60, 1.90]$ , as our best model, and observe that it lies close to the top node in table 3. Table A2 in the appendix lists parameter confidence intervals for the top five nodes.

Figure 3 shows error bars for parameter estimates from all fifty runs on the top node (table 4), and there are no signs of filter divergence (ensemble collapse, see Evensen, 2009; signs of trouble would be runs with significantly different estimates). The figure also shows that not only does the precision in the BIC score increase with repeated filter runs; in nonlinear models like ours, different realizations of noise in the Monte Carlo step lead to different parameter estimates that are all equally representative, and the estimates improve with repeated runs. In particular, the standard errors are improved (Sætrom and Omre, 2013). Figure 4 shows how the best model fits the observations in the state space. The shaded areas illustrate how the estimated density varies; errorbars illustrate observational uncertainty.

Finally, (8) reports the top node estimate (mean over all runs) of  $\Sigma$ , which forms the basis for the stochastic terms in equations (5 - 7); standard errors in parenthesis. We note that while diagonal terms are relatively small but statistically significant, off-diagonal terms are small and insignificant. Thus, covariate noise can safely be disregarded

Table 3: Top 20 nodes in the coarse grid (216 nodes) ranked according to BIC score.

BIC	$m_1$	$m_2$	$m_3$	$c_1$	$c_2$	$c_3$	$c_4$	Avg. RMSI
71.1991	1.8	1.6	2.0	-8.1854 (0.39391)	-5.4753 (0.33863)	-6.9873 (0.68812)	10.444 (0.13964)	843.1165
72.213	2.0	1.6	2.0	-6.1274 (0.47188)	-5.1649 (0.35559)	-5.5738 (0.4895)	10.3725 (0.16078)	906.5269
72.7344	2.0	1.8	2.0	-5.9885 (0.47198)	-6.838 (0.46026)	-5.4636 (0.46571)	10.2631 (0.15698)	907.0614
73.3707	1.8	1.4	2.0	-8.2926 (0.36199)	-3.878 (0.32969)	-7.7961 (0.72655)	10.4316 (0.14255)	849.5203
73.3949	1.8	1.8	2.0	-7.9986 (0.39933)	-7.1184 (0.42196)	-6.2474 (0.66272)	10.3577 (0.13564)	855.8724
73.563	2.0	1.4	2.0	-6.2335 (0.4821)	-3.5737 (0.39401)	-5.7232 (0.54225)	10.4612 (0.15913)	910.0952
74.5773	2.0	2.0	2.0	-5.9617 (0.64171)	-6.5885 (0.88664)	-6.4267 (0.73301)	9.9664 (0.13361)	901.1179
80.9702	1.8	2.0	2.0	-7.3986 (0.5169)	-6.5283 (0.87446)	-6.6833 (0.73648)	10.1298 (0.13292)	892.974
82.0295	2.0	1.6	1.8	-6.3566 (0.39116)	-5.4135 (0.29244)	-7.5506 (0.34258)	10.4988 (0.14104)	929.6722
82.2414	1.6	1.8	2.0	-6.4212 (0.33517)	-7.2534 (0.42168)	-6.3797 (0.64838)	10.4466 (0.14239)	891.4135
82.4937	1.6	1.6	2.0	-6.6038 (0.30315)	-5.6184 (0.30839)	-7.4114 (0.6842)	10.5163 (0.14498)	890.1095
83.9905	2.0	1.8	1.8	-6.1957 (0.38436)	-7.2481 (0.41716)	-7.3492 (0.34758)	10.3902 (0.13639)	935.1757
84.0845	1.6	1.4	2.0	-6.6951 (0.28734)	-4.0529 (0.29232)	-8.227 (0.73805)	10.5293 (0.15004)	896.0693
84.2738	1.8	1.2	2.0	-8.1889 (0.38967)	-3.2432 (0.70791)	-7.0609 (0.64652)	10.4235 (0.14833)	885.498
84.7132	2.0	1.4	1.8	-6.3585 (0.41187)	-3.6121 (0.31606)	-7.4952 (0.31763)	10.4747 (0.13871)	936.3013
85.0385	2.0	2.0	1.8	-5.951 (0.47024)	-6.595 (0.82998)	-6.324 (0.44162)	10.1251 (0.11872)	931.3596
88.5862	2.0	1.2	2.0	-6.1452 (0.47426)	-4.1419 (0.86163)	-5.9459 (0.58491)	10.3565 (0.16763)	958.8742
88.7298	2.0	1.6	1.6	-6.3725 (0.4097)	-5.3725 (0.29015)	-5.8018 (0.28258)	10.4928 (0.14027)	951.6819
89.078	2.0	1.8	1.6	-6.2827 (0.40752)	-7.1031 (0.40493)	-5.6938 (0.30319)	10.432 (0.13748)	951.4994
89.2972	2.0	1.2	1.8	-6.3272 (0.38141)	-3.0063 (0.63812)	-7.3664 (0.34166)	10.4717 (0.13927)	952.9953



Table 4: Top 20 nodes in the fine grid (900 nodes) ranked according to BIC score.

BIC	$m_1$	$m_2$	$m_3$	$c_1$	$c_2$	$c_3$	$c_4$	Avg. RMSI
65.7026	1.85	1.6	1.9	-8.371 (0.56914)	-5.5176 (0.29561)	-7.8559 (0.65714)	10.3903 (0.1368)	803.579
65.8133	1.85	1.5	1.9	-8.3452 (0.55548)	-4.6862 (0.28596)	-7.8261 (0.66474)	10.405 (0.14129)	804.3131
66.058	1.85	1.45	1.9	-8.3092 (0.57115)	-4.261 (0.29154)	-7.8539 (0.64302)	10.4056 (0.1391)	806.2787
66.1489	1.85	1.55	1.9	-8.2867 (0.56503)	-5.0687 (0.28673)	-7.8679 (0.64953)	10.3764 (0.13618)	808.0455
66.2482	1.85	1.4	1.9	-8.316 (0.57871)	-3.8026 (0.30296)	-7.8388 (0.65676)	10.3836 (0.13986)	806.0587
66.2795	1.85	1.55	1.95	-8.3124 (0.56052)	-5.0362 (0.30557)	-8.0922 (0.72116)	10.3346 (0.13431)	812.4237
66.3121	1.85	1.5	1.95	-8.32 (0.56256)	-4.6322 (0.3082)	-8.0655 (0.72791)	10.3464 (0.13797)	812.652
66.4704	1.85	1.65	1.9	-8.3477 (0.5565)	-5.9053 (0.29184)	-7.8764 (0.65896)	10.3759 (0.13593)	807.1582
66.4986	1.85	1.45	1.95	-8.3729 (0.53915)	-4.2258 (0.30604)	-8.1455 (0.73033)	10.3586 (0.13987)	811.7163
66.7375	1.85	1.6	1.95	-8.3091 (0.56243)	-5.4547 (0.30831)	-8.1428 (0.71099)	10.3465 (0.13391)	816.6333
66.9549	1.85	1.35	1.9	-8.3164 (0.54984)	-3.3553 (0.31153)	-7.8344 (0.6634)	10.3751 (0.14072)	806.155
66.9556	1.85	1.7	1.9	-8.3395 (0.56397)	-6.349 (0.28561)	-7.9064 (0.64611)	10.3756 (0.13621)	809.9115
67.0736	1.85	1.65	1.95	-8.349 (0.54151)	-5.8675 (0.31167)	-8.1004 (0.72215)	10.3283 (0.13452)	817.3368
67.0776	1.85	1.4	1.95	-8.3354 (0.55177)	-3.7812 (0.32239)	-8.0591 (0.73644)	10.3582 (0.14112)	814.9704
67.0936	1.85	1.75	1.9	-8.3742 (0.5537)	-6.7769 (0.2915)	-7.9096 (0.62797)	10.36 (0.13393)	809.0864
67.1933	1.85	1.25	1.9	-8.0358 (0.5584)	-2.3108 (0.37313)	-7.7563 (0.65145)	10.3025 (0.13753)	806.7234
67.2725	1.85	1.3	1.9	-8.2055 (0.56775)	-2.8524 (0.33059)	-7.8245 (0.65049)	10.3568 (0.14225)	807.3225
67.3221	1.85	1.5	2.0	-8.2421 (0.57289)	-4.5593 (0.36337)	-7.385 (0.73364)	10.3897 (0.14074)	829.4626
67.3487	1.85	1.3	1.95	-8.1735 (0.54423)	-2.8 (0.35603)	-8.0965 (0.73799)	10.3243 (0.14116)	815.1889
67.3515	1.85	1.55	2.0	-8.2314 (0.54935)	-4.9624 (0.35824)	-7.46 (0.72163)	10.3732 (0.13784)	828.0434

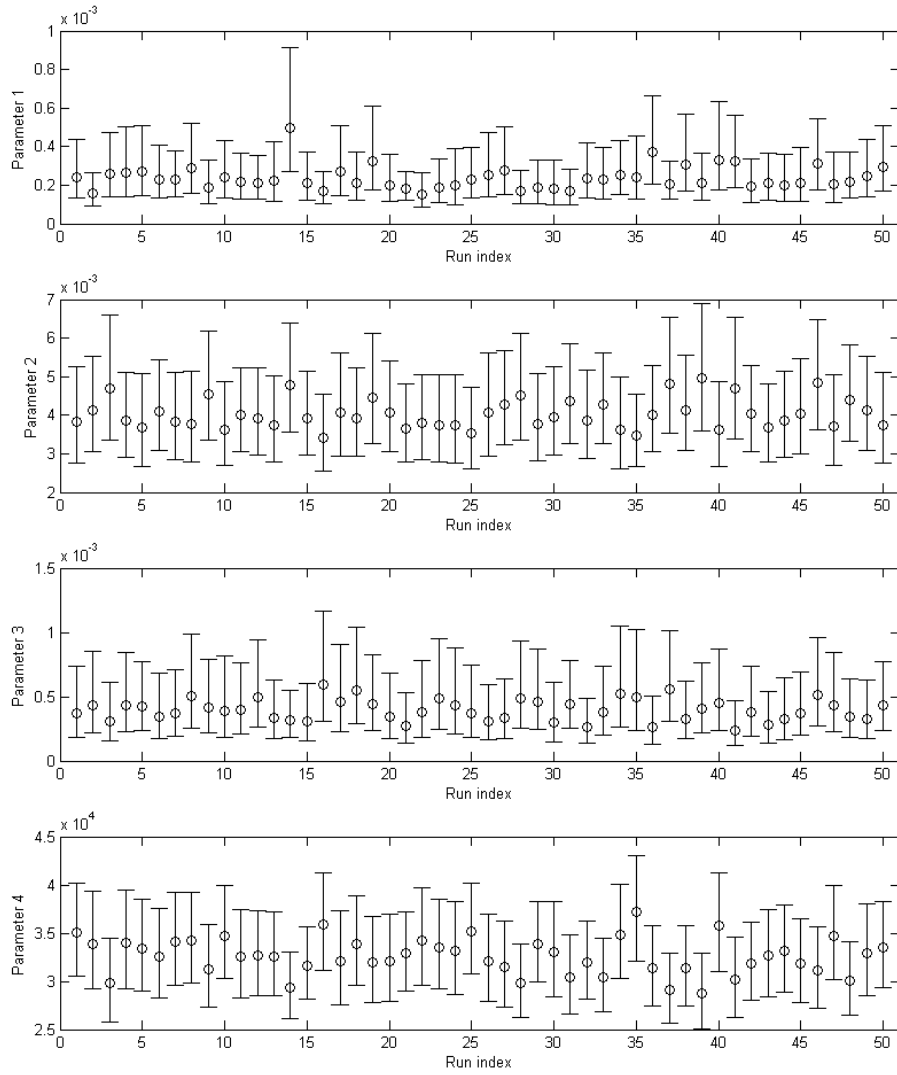


Figure 3: Parameter estimates for all runs on top node in fine grid. See table 4 for statistics.

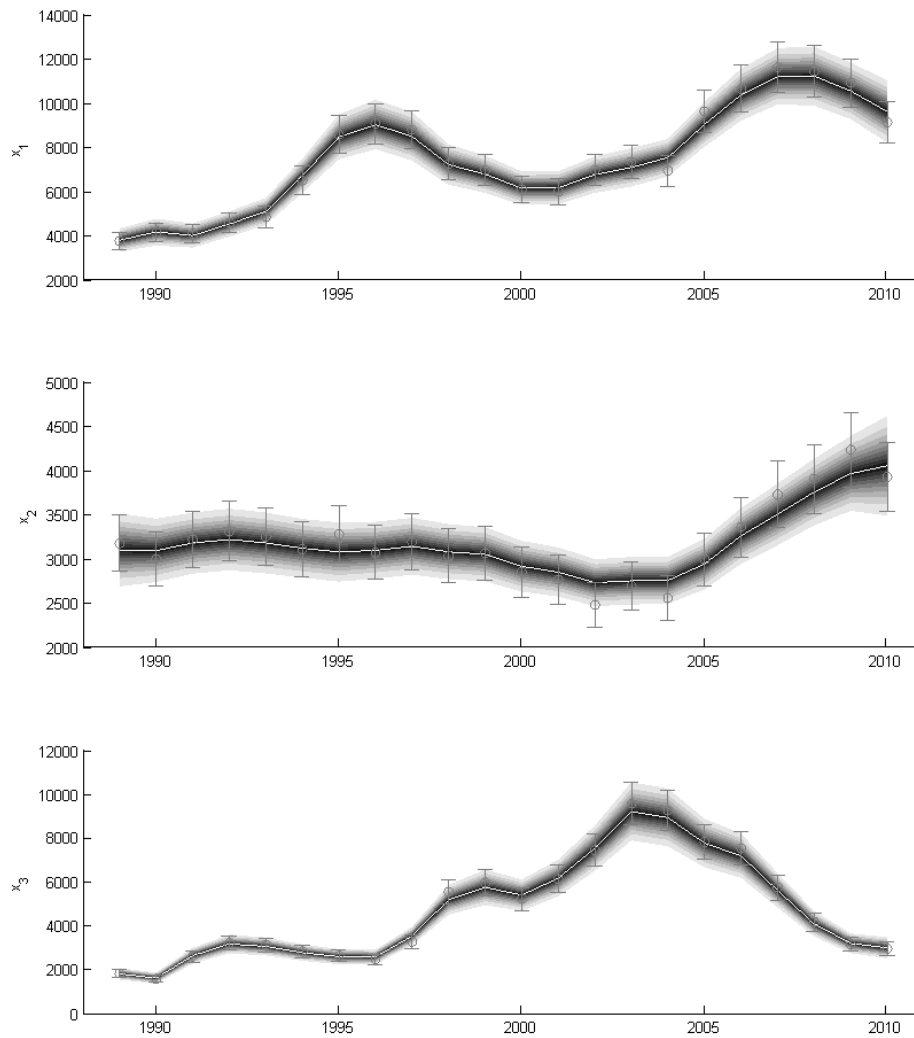


Figure 4: State estimates (white curves) for the top node in fine grid, mean over all runs. Shaded areas show the estimated state space density. Errorbars show observations with observation uncertainty. See table 4 for statistics.

in the model.

$$\Sigma = \begin{bmatrix} 0.0763 & 0.00113 & 0.000898 \\ (0.00666) & (0.00240) & (0.00356) \\ 0 & 0.0641 & 0.00183 \\ & (0.00722) & (0.00298) \\ 0 & 0 & 0.0838 \\ & & (0.00592) \end{bmatrix} \quad (8)$$

## 5 Final Remarks

In 2006-2009, there was a strong buildup of biomass of planktivorous (mostly pelagic) species in the Norwegian Sea. Biologists have observed negative relationships between length at age and stock biomass, a pronounced reduction in zooplankton abundance, and extension of the spatial distribution of populations, and suggest that planktivorous fish biomass has been above the carrying capacity (Huse et al., 2012). The populations showed signs of density-dependent length growth, and for herring and blue whiting there was also significant effects of interspecific competition. The results in Huse et al. (2012) support the hypothesis that interactions among Norwegian Sea planktivorous fish populations negatively affect growth mediated through depletion of their common zooplankton resource.

The migratory patterns of these stocks have undoubtedly made it more difficult to attain and to uphold international agreements on catch quotas. While agreements on less migratory demersal stocks (cod and haddock, for example) between Russia and Norway have remained unchanged since the early 1980s, the agreements on the pelagic stocks have sometimes broken down or taken a long time to establish (Bjørndal and Ekerhovd 2014). Although the literature on straddling fish stocks is extensive, with several contributions in recent years, no study addresses these issues in a multispecies context (Bailey et al. 2010; Hannesson 2011; Bjørndal and Munro 2012). The present work will be a step

toward closing this gap by developing a useful framework for game theoretic analysis of such systems.

We present a model of the Norwegian Sea pelagic complex that incorporates species interspecific competition and a common carrying capacity while maintaining a low dimensionality. The model is nonlinear, non-convex, and stochastic. The model captures much of the observed dynamics in the modelled populations, also in forecasting (an earlier study of the model that calculated two-year-ahead forecasts found that the main, dynamic features were picked up, but that forecasts tended to be low; see Ekerhovd and Kvamsdal, 2013). The low dimensionality is a key feature in that it makes economic analysis (that is, dynamic decision analysis; see Sandal and Steinshamn, 2010; Poudel et al., 2012) feasible, see Kvamsdal and Sandal (2014) for further discussion. Our efforts to model and estimate the Norwegian Sea pelagic complex combines a biological and ecological familiarity and understanding, the use of recent advances in data improvement (Ekerhovd and Gordon, 2013), and application of data assimilation methods (Evensen, 2003) that have seen little use in our field.

The procedure in Ekerhovd and Gordon (2013) obtains statistically coherent stock estimates and points out problems that seem previously overlooked. In light of the debate about the use and importance of fisheries data (Pauly et al., 2013), the Ekerhovd-Gordon approach points forward to better models and better informed decisions. Again, good models require good data (Mangel and Levin, 2005). We also think data assimilation methods like the ensemble Kalman filter points to better models that serve towards economic decision analysis. Ultimately and in the broader scope of things, we need to develop methods and frameworks that are appropriate for the dimensionality, nonlinearity and stochasticity inherent in ecosystem-based fisheries management, all in a holistic view (Hill et al., 2007; Link, 2010; Fulton et al., 2011). In this perspective, our work may be a small step, but nevertheless a step in the right direction.

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## A Appendix

The data generated using Virtual Population Analysis (VPA) is interesting in that it is rich in its coverage of catch, mortality, and stock size information, but mortality and stock size are generated variables based on biological assumptions, actual catch levels, and assumed decay functions. Moreover, the generated regressors are endogenous and a least squares estimator produces inconsistent and inefficient estimates. To address this issue we use a predicted instrumental variable for stock size (Ekerhovd and Gordon, 2013).

Ekerhovd and Gordon (2013) identified a valid exogenous instrument in the past cohort catch  $C_{a-1,i}^{t-1}$  that is structurally correlated with current stock, impacts current catch only through its influence on current stock and subject to independent shocks. Following Ekerhovd and Gordon, for each stock estimate we instrument out  $C_{a,i}^t$  using  $C_{a-1,i}^{t-1}$ . However, if the endogeneity problem is viewed as measurement error, an additional instrument is available. The VPA procedure for generating stock is an approximation and subject to measurement error; thus correlation between stock and the regression error term. It is common in empirical practice to use the rank order ( $RO_{a,i}^t$ ) of the stock variable as an instrument to avoid the correlation problem. The argument is that the rank order is correlated with stock but not correlated with measurement error. This is true as long as the measurement error is not strong enough to change the rank order. Accepting the rank order as an exogenous instrument, we proceed to estimation using both  $C_{a-1,i}^{t-1}$  and  $RO_{a,i}^t$  in the first-stage regression for predicting the instrumental variable for generated stock. To be complete, the instrumental variable (IV) for stock is the predicted values from the first-stage regression written generally as  $S_{a,i}^t = \delta_1^{IV} C_{a-1,i}^{t-1} + \delta_2^{IV} RO_{a,i}^t + \delta_3^{IV} C_{a+1,i}^{t+1} + \alpha_{a,i} + \beta_i t + \vartheta_{a,i}^t$ , where  $\alpha_{a,i}$  is the age-class fixed

effect,  $t$  dummy outs time shocks, and  $\vartheta_{a,i}^t$  is a random error term.

Our strategy, following Ekerhovd and Gordon, is to use both lagged cohort catch and rank order of the stock variable as exogenous variables to build the IV. However, with both past and forward lags in the IV regression, we lose degrees of freedom and the youngest age classes.

We apply a within estimator with fixed time effects corrected for heteroskedasticity and autocorrelation within the panels to estimated the IV equation. A test of the strength of the correlation of the assumed exogenous variables, lagged catch, and rank order on current stock can be tested with a joint F-test. We test the null that  $H_0 : \delta_1^{IV} = 0$  and  $\delta_2^{IV} = 0$  with generated F-statistics of 15.56 (0.00), 27.98 (0.00), and 6.55 (0.03) for herring, mackerel, and blue whiting, respectively (p-values in parentheses). These tests provide some statistical validation for using the exogenous instruments in the IV equation.

Table A1: Parameter confidence intervals (two standard errors): Model 1 (column 1), model 1R (column 2), model 2 (column 3), and model 2R (column 4). See table 2 for shadow parameter estimates and statistics.

Column	1	2	3	4
Model	Model 1	Model 1R	Model 2	Model 2R
Parameters				
$c_1$	(0.000380, 0.00256)	(0.00560, 0.00870)	(0.000377, 0.00254)	(0.00736, 0.0122)
$c_2$	(0.000422, 0.00283)	(0.00715, 0.0109)	(0.000434, 0.00294)	(0.00876, 0.0141)
$c_3$	(0.000427, 0.00282)	(0.00668, 0.00954)	(0.000450, 0.00298)	(0.00811, 0.0123)
$c_4$	(25255, 37059)	(26962, 35625)	(19425, 27934)	(25325, 32429)
$m_1$	(1.21, 1.69)		(1.19, 1.66)	
$m_2$	(1.26, 1.77)		(1.25, 1.76)	
$m_3$	(1.27, 1.76)		(1.27, 1.74)	

Table A2: Parameter confidence intervals (two standard errors) for top five nodes in fine grid. See table 4 for shadow parameter estimates and statistics.

Column	1	2	3	4	5
<i>m</i> -values	[1.85, 1.60, 1.90]	[1.85, 1.50, 1.90]	[1.85, 1.45, 1.90]	[1.85, 1.55, 1.90]	[1.85, 1.40, 1.90]
Parameters					
$c_1$	(0.000134,0.000423)	(0.000138,0.000423)	(0.000141,0.000445)	(0.000145,0.000456)	(0.000140,0.000449)
$c_2$	(0.00300,0.00542)	(0.00695,0.0123)	(0.0105,0.0190)	(0.00474,0.00843)	(0.0166,0.0305)
$c_3$	(0.000205,0.000764)	(0.000210,0.000801)	(0.000208,0.000759)	(0.000204,0.000754)	(0.000207,0.000778)
$c_4$	(28423.4431,37383)	(28723,38118)	(28820,38096)	(28070,36880)	(28193,37349)

While economists have discussed ecosystem-based management and similar concepts, little attention has been devoted to the art modeling. Models of ecosystems or foodwebs that make economic analysis viable should capture as much as possible of system structure and dynamics while balancing biological and ecological detail against dimensionality and model complexity. Relevant models need a strong, empirical content, but data availability may inhibit modeling efforts. Models are bound to be nonlinear, and model and observational uncertainty should be observed. We suggest the data assimilation method ensemble Kalman filtering to improve modeling of ecosystems or foodwebs. To illustrate the method, we model the dynamics of the main, pelagic species in the Norwegian Sea. In order to reduce the parameter dimensionality, the species are modeled to rely on a common carrying capacity. We also take further methodological steps to deal with a still high number of parameters. Our best model captures much of the observed dynamics in the fish stocks, but the estimated model error is moderate.

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