



Random effect estimation of time-varying factors in Stock Synthesis

Journal:	<i>ICES Journal of Marine Science</i>
Manuscript ID:	Draft
Manuscript Types:	Symposium Article
Date Submitted by the Author:	n/a
Complete List of Authors:	Thorson, James; Northwest Fisheries Science Center, NMFS, NOAA, Fisheries Resource Assessment and Monitoring Division Hicks, Allan; Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Fishery Resource Analysis and Monitoring Division Methot Jr., Richard; NOAA Fisheries, Office of Asst. Administrator
Keyword:	random effect, Bayesian, maximum likelihood, hierarchical model, time-varying parameter, mixed effect, Laplace approximation, stock assessment, penalized likelihood, recruitment

SCHOLARONE™
Manuscripts

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Random effect estimation of time-varying factors in Stock Synthesis

James T. Thorson*, Allan C. Hicks, Richard D. Methot, Jr.

Fisheries Resource Assessment and Monitoring Division

Northwest Fisheries Science Center

National Marine Fisheries Service

National Oceanic and Atmospheric Administration

2725 Montlake Blvd. East

Seattle, WA 98112

* Corresponding author

Abstract

There is increasing recognition that biological processes such as fishery selectivity, natural mortality, and somatic growth vary over time, and that time-varying processes are important to include in marine population dynamics models. However, previous penalized-likelihood estimation approaches provide little guidance regarding the variance of time-varying processes, and random-effect approaches are computationally infeasible or not implemented for many models and software packages. We therefore show that existing stock assessment models and software can be used to calculate the Laplace approximation to the marginal likelihood of parameters representing variability over time, and use Stock Synthesis to show how this can be used to select an appropriate value for variation over time in stock assessment models. Using North Sea cod and Pacific hake models as case studies, we show that this method has little bias in estimating variances for simulated data. It also provides a similar estimate of hake recruitment ($\log\text{-SD} = 1.43$) to Markov chain Monte Carlo (MCMC) methods ($\log\text{-SD} = 1.68$), and estimates a non-trivial magnitude ($\log\text{-SD} = 0.07$) of variation in growth for North Sea cod. We conclude by discussing the generality of the proposed method and by recommending future research regarding its performance relative to MCMC, particularly when estimating multiple variances simultaneously.

Keywords: random effect; Bayesian; maximum likelihood; hierarchical model; time-varying parameter; mixed effect; Laplace approximation; stock assessment; penalized likelihood; recruitment

Introduction

Population dynamics models that include the effects of human-caused mortality (called stock assessment models) are an important tool in the management of aquatic and terrestrial species. These models are routinely used to assess whether population abundance and harvest rates are respectively above and below sustainable targets, as well as to forecast population responses given different proposed management actions (Hilborn and Walters 1992). They are also increasingly used for ecological purposes, e.g., to estimate life history relationships (Thorson et al. In press), evaluate environmental impacts on populations (Schirripa et al. 2009, Thorson et al. 2013), and to explore trophic interactions among species (Plagyani et al. In press.).

Integrated stock assessment models account for measurement processes (i.e. the process by which data are generated) in increasingly realistic ways (Maunder and Punt 2013). Most of these models account for stochastic processes in the dynamics (e.g., growth, productivity, or availability to harvest) through a time series of fixed effects that are penalized towards zero, and where the strength of this penalty is selected by the user *a priori*. State-space population models (Gudmundsson and Gunnlaugsson 2012, Mäntyniemi et al. 2013) expand on this capability by allowing estimation of the variance of stochastic processes such as recruitment, selectivity, natural mortality, immigration/emigration, and other demographic processes. State-space models accomplish this by using random effects, where stochasticity in one or more dynamical processes is ‘integrated out’ of the marginal likelihood (de Valpine 2002), and hence avoids statistical limitations of parameter confounding and asymptotic biases in standard ‘fixed effect’ models.

Recent research has demonstrated that random effects can be used to approximate many population processes, e.g., variability in fishing gear efficiency (Wilberg et al. 2010), and to approximate unknown functional forms in population dynamics (Thorson and Taylor In review, What would be a functional form in population dynamics?)

Thorson et al. in press). Penalized likelihood methods are often used to estimate time-varying parameters such as juvenile survival (recruitment, Maunder and Deriso 2003), but this will often result in biased parameter estimates (De Valpine and Hilborn 2005). Methot and Taylor (2011) developed a bias correction procedure to estimate recruitment variability, but it is unclear how to generalize their method to other time-varying parameters. Need to read Methot and Taylor to see how this works, also I wasn't aware the bias correction procedure was estimating sigmaR

Random effect and state-space models require integration (or its approximation, e.g., the Kalman filter comparison in Gudmundsson and Gunnlaugsson 2012) when fitting a model to a data set. Existing computation approaches to random effect estimation include Markov chain Monte Carlo (MCMC) in either a maximum likelihood (De Valpine 2004) or Bayesian framework (Meyer and Millar 1999) or the Laplace approximation as implemented in ADMB-RE (Skaug and Fournier 2006). This integral may be high-dimensional, rendering simple integration methods computationally infeasible. For example, MCMC sampling may be computationally impractical for many population dynamics models due to irregularly shaped likelihood or posterior distributions (Polansky et al. 2009, Stewart et al. 2013). Similarly, implementing a model in ADMB-RE requires a large overhead of time and expertise due to the practical necessity of finding a 'separable' formulation of the population model (Bolker et al. 2013) and still may take a considerable amount of time during optimization.

In this study, we demonstrate a novel approach to estimating random effects in existing stock assessment software that implement stochastic processes as a sequence of fixed effects. Specifically, we show that the Laplace approximation can be applied to the penalized likelihood of estimated parameters in combination with the matrix of second derivatives (i.e., the model Hessian) to estimate the variance of random effects. This approach is demonstrated specifically for the widely used Stock Synthesis software (Methot and Wetzel 2013) written in the AD Model

Hessian = matrix of second derivatives

1
2
3 82 Builder optimization software (ADMB, Fournier et al. 2012) and is distributed using the *r4ss*
4
5 83 package (Taylor et al. 2012) in R (R Core Development Team 2012). *Is the approximation in r4ss?*
6 *How difficult would it be to use the*
7 *approximation code with another*
8 *framework?*
9 84 **Methods**

10
11 85 We first review the estimation of random-effect models. Parameters in maximum-likelihood
12
13 86 models that contain both random and fixed-effects (“mixed-effects models”) are estimated by
14
15 87 maximizing the marginal likelihood that is obtained when integrating across random effects.

16
17
18
19 88
$$\hat{\theta}, \hat{\tau} = \max_{\theta, \tau} [L(\theta, \tau | D)] = \max_{\theta, \tau} \left[\int_{\epsilon} L(\theta, \epsilon | D) \cdot \pi(\epsilon | \tau) \cdot d\epsilon \right] \quad (1)$$

20
21
22 89 where $L(\theta, \tau | D)$ is the marginal likelihood that is maximized to identify values of the fixed-effect
23
24 90 parameters θ and hyper-parameters τ given data D , $L(\theta, \epsilon | D)$ is the joint likelihood of fixed-effect
25
26 91 θ and random-effect parameters ϵ , and $\pi(\epsilon | \tau)$ is the probability of random effects given
27
28 92 hyperparameters. We will call the product of the joint likelihood and the probability of random
29
30 93 effects ($L(\theta, \epsilon | D) \pi(\epsilon | \tau)$) the 'penalized likelihood'. If the penalized likelihood is maximized
31
32 94 directly (rather than integrating across random effects), this generally results in biased estimates
33
34 95 of model parameters (De Valpine and Hilborn 2005).

35
36
37
38
39 96 Notably, Eq. 1 includes a multivariate integral of the 'penalized likelihood' across random
40
41 97 effects, and this integral is the main computational impediment to the wide adoption of mixed-
42
43 98 effect models in ecology (de Valpine 2009). By contrast, Bayesian estimation of mixed-effect
44
45 99 models are estimated by approximating the integral across all coefficients:

46
47
48
49 100
$$\theta_i, \tau_i, \epsilon_i \approx \int_{\theta, \tau, \epsilon} L(\theta, \epsilon | D) \cdot \pi(\epsilon | \tau) \cdot p(\theta, \tau) \cdot d\epsilon \cdot d\theta \cdot d\tau \quad (2)$$

50
51
52 101 where samples $\theta_i, \tau_i, \epsilon_i$ from the integral are obtained using MCMC, and $p(\theta, \tau)$ is the prior
53
54 102 probability of parameters θ and τ . Thus, maximum likelihood and Bayesian estimates differ in
55
56 103 what is ‘integrated across’: Maximum likelihood integrates across random effects only, while

Bayesian integrates across all model coefficients. Bayesian methods also require a prior $p(\theta, \tau)$ on fixed effects θ and hyper-parameters τ , while this prior is not necessary in maximum likelihood models. However, many ‘maximum likelihood’ assessment models already include a penalty on these parameters, so the distinction is somewhat blurred in this regard.

We instead propose a third option for estimating the variance of random effects. Specifically, we propose to integrate across all coefficients except the hyperparameters τ . This results in the following optimization problem:

$$\hat{\tau} = \max_{\tau} [L(\tau | D)] = \max_{\tau} \left[\int_{\theta, \varepsilon} L(\theta, \varepsilon | D) \cdot \pi(\varepsilon | \tau) \cdot p(\theta) \cdot d\varepsilon \cdot d\theta \right] \quad (3)$$

where $p(\theta)$ is the prior probability of parameters θ . This third option essentially sets hyperparameters τ to the value that maximizes the marginal likelihood of all other model parameters. We subsequently show that this optimization problem can be solved using most stock assessment models and their existing software implementations, by means of the Laplace approximation.

The Laplace approximation is derived from a Taylor’s series expansion of a distribution:

$$f(z) \approx f(\hat{z}) + f'(\hat{z})(z - \hat{z}) + \frac{1}{2} f''(\hat{z})(z - \hat{z})^2 \quad (4)$$

where $f(z)$ is a distribution, i.e. the logarithm of the penalized likelihood, \hat{z} is a point, i.e., the vector of parameters z that maximizes the log-penalized likelihood, and f' and f'' are the first and second derivatives of f . At the maximum penalized likelihood estimate \hat{z} , the first derivatives of the log-penalized likelihood are 0 so the second term of the right-hand side drops out, and the second derivatives are all negative. Therefore:

$$e^{f(z)} \approx e^{f(\hat{z}) - \frac{1}{2} |f''(\hat{z})| (z - \hat{z})^2} \quad (5)$$

This approximation is useful while taking the integral of the penalized likelihood $e^{f(z)}$:

$$\int e^{f(z)} dz \approx e^{f(\hat{z})} \int e^{-\frac{1}{2} f''(\hat{z})(z-\hat{z})^2} dz \quad (6)$$

where the second-derivatives of the log-penalized likelihood $f''(\hat{z})$ is also known as the Hessian, and is routinely reported by most maximum likelihood optimization software. The term $e^{-\frac{1}{2} f''(\hat{z})(z-\hat{z})^2}$ resembles a multivariate normal likelihood (although without its normalization constant). Therefore, the Laplace approximation can be interpreted as approximating the penalized likelihood with a multivariate normal distribution, and integrating across this approximation (by calculating the area under this multivariate normal distribution; Skaug and Fournier 2006).

We now apply the Laplace approximation to our specific problem. Given the vector of coefficients $\tilde{\theta}, \tilde{\epsilon}$ that maximizes the penalized likelihood (given data \mathbf{D} and proposed values of the hyperparameters τ) and its Hessian matrix (the matrix of second derivatives of the log-penalized likelihood):

$$H(\tilde{\theta}, \tilde{\epsilon} | \tau, \mathbf{D}) = \begin{bmatrix} \frac{\delta^2 (\ln(L(\tilde{\theta}, \tilde{\epsilon} | \mathbf{D}) \cdot \pi(\tilde{\epsilon} | \tau))}{\delta \tilde{\theta}_1^2} & \dots & \frac{\delta^2 (\ln(L(\tilde{\theta}, \tilde{\epsilon} | \mathbf{D}) \cdot \pi(\tilde{\epsilon} | \tau))}{\delta \tilde{\theta}_1 \delta \tilde{\epsilon}_n} \\ \dots & \dots & \dots \\ \frac{\delta^2 (\ln(L(\tilde{\theta}, \tilde{\epsilon} | \mathbf{D}) \cdot \pi(\tilde{\epsilon} | \tau))}{\delta \tilde{\theta}_1 \delta \tilde{\epsilon}_n} & \dots & \frac{\delta^2 (\ln(L(\tilde{\theta}, \tilde{\epsilon} | \mathbf{D}) \cdot \pi(\tilde{\epsilon} | \tau))}{\delta \tilde{\epsilon}_n^2} \end{bmatrix} \quad (7)$$

the Laplace approximation is equal to the area under a multivariate normal distribution with maximum equal to the 'maximum penalized likelihood' and covariance equal to the inverse of this Hessian matrix:

$$L(\tau | \mathbf{D}) = \int_{\theta, \epsilon} L(\theta, \epsilon | \mathbf{D}) \cdot \pi(\epsilon | \tau) \cdot p(\theta) \cdot d\epsilon \cdot d\theta \approx \frac{2 \cdot L(\tilde{\theta}, \tilde{\epsilon} | \mathbf{D}) \cdot \pi(\tilde{\epsilon} | \tau)}{\sqrt{|H(\tilde{\theta}, \tilde{\epsilon} | \tau, \mathbf{D})|}} \quad (8)$$

where $\tilde{\theta}$ and $\tilde{\epsilon}$ are again the coefficients that maximize the penalized likelihood given proposed values of hyperparameters τ , and $|H(\tilde{\theta}, \tilde{\epsilon} | \tau, D)|$ is the determinant of the Hessian matrix. This approximation is exact whenever the penalized likelihood has a multivariate-normal distribution, and hence performs well given large-sample asymptotic theory, where likelihood and posterior distributions will converge on a multivariate normal distribution (Gelman et al. 2003).

Application to Stock Synthesis

We briefly summarize our implementation of this proposed approximation in Stock Synthesis. The algorithm starts with an initial value for all variance parameters, τ_0 . Given these values, Stock Synthesis is run once to obtain estimates of parameters and their standard deviations, and may optionally be run again after adjusting the recruitment bias-correction ramp following methods in Methot and Taylor (2011). The Hessian is then extracted from ADMB using auxiliary code (C. Monnahan, pers. comm.), integration constants are added where necessary to the log-penalized likelihood derived from Stock Synthesis, and these two components are used to calculate the marginal likelihood (Eq. 8). A new set of parameters is then proposed τ_1 , and this process is iterated until a local maximum is identified. Any application of this algorithm where the first 5 runs of Stock Synthesis fail to converge to a satisfactory degree (i.e. the final gradient of any Stock Synthesis optimization is greater than I) can be identified, and may not have adequately converged to the value of τ that maximizes the marginal likelihood. This algorithm is distributed as the function *NegLogInt_Fn* in the *r4ss* package.

Case study 1: Variable recruitment in Pacific hake

Pacific hake (*Merluccius productus*) is a commercially important species whose harvest is split between fisheries originating in the U.S. West Coast and Western Canada. It has recently been managed under an international treaty between these two countries, and has been assessed using

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

166 Stock Synthesis. The assessment includes fishery catches from 1966-2012, fishery age
167 composition samples from 1975-2012, an intermittent acoustic survey starting in 1995 that
168 provides an index of abundance and age-composition samples, and 'empirical' weight-at-age
169 values that are assumed to be known without error. Assessment results indicate that population
170 dynamics are driven by very high variability in early juvenile survival ("recruitment").
171 Recruitment in the hake assessment model is treated as a penalty towards a parametric stock-
172 recruit curve. For our investigations, we therefore treat the magnitude of recruitment variability
173 as a hyperparameter in the proposed Laplace approximation.

174 **Case study 2: Variable growth in North Sea cod**

175 Cod (*Gadus morhua*) supports a commercially important and iconic fishery in the North Sea.
176 The Skagerrak (northern section of Division IIIa) and eastern Channel (Division VIIId) division
177 has been assessed previously using catch, age-composition, and weight-at-age data from 1963-
178 2011, an index of adult abundance 1963-2011, and an index of juvenile abundance 1983-2011.
179 These data have been assessed using a state-space assessment model (SAM; Gudmundsson and
180 Gunnlaugsson 2012), and has been transcribed to an integrated catch-at-age model (Maunder and
181 Punt 2013) using the Stock Synthesis model software (Methot and Wetzel 2013) in preparation
182 for the World Congress on Stock Assessment Methods in 2013. Although SAM assumes that
183 weight at age are known without error, the transcribed Stock Synthesis model includes weight at
184 age as data and can estimate cohort-specific deviations in growth. These deviations are
185 penalized towards zero, so that cohort-specific growth patterns are penalized towards an average
186 growth schedule. The magnitude of this penalty cannot be estimated easily using penalized
187 likelihood, and is treated as a hyperparameter τ in the proposed Laplace approximation. For
188 simplicity, we assume that recruitment deviations have a standard deviation of 0.7 (as identified

189 using methods in Methot and Taylor 2011). We do not explore estimating the variance of both
190 processes simultaneously, although there is no reason this could not be explored in the future.

191 **Model testing and application**

192 For each case study, we apply our proposed Laplace approximation using existing Stock
193 Synthesis assessment files and record the estimated variance for the random effect. We also
194 perform a simulation study for each species, where the data sample sizes and estimated
195 parameters are used to simulate a new data set, which is then fitted again using the same Stock
196 Synthesis model where the variance of random effects is estimated using the Laplace
197 approximation. For the hake example, we additionally re-simulate recruitment deviations for all
198 years from a normal distribution with mean 0 and standard deviation of either 1.5 or 0.5
199 (depending upon simulation scenario) and compare Laplace approximation estimates of the
200 standard deviation with this known, true value. For the cod example, we re-simulate recruitment
201 deviations for all years with mean 0 and standard deviation 0.7 (i.e. the value assumed in the
202 estimation model), re-simulate growth deviations with a mean of 0 and standard deviation of
203 either 0.1 or 0.02 (depending upon simulation scenario), and re-simulate fishing mortality to
204 follow an ascending and then descending pattern.

205 Finally, we estimate the original hake case-study model using Markov chain Monte Carlo to
206 compare this estimate of recruitment variability with our Laplace approximation estimate. We
207 do not do this for the cod case study because growth variability is not programmed as a
208 ‘parameter’ in that model and hence cannot be sampled using MCMC using existing model
209 software.

210 **Results**

211 The Laplace approximation to the log-marginal likelihood is the sum of the log-penalized
212 likelihood and the log-determinant of the Hessian (Eq. 8). We therefore first show these three
213 curves as a function of random effect variability for hake (Fig. 1) and cod (Fig. 2). In the hake
214 model, the penalized likelihood is maximized by a standard deviation of approximately 0.9 for
215 recruitment variability. By contrast, the determinant of the Hessian is monotonically increasing
216 for all values from 0.5 to 2.5. Their sum has a maximum at 1.43, and represents a compromise
217 between both components. Similarly, the penalized likelihood for the cod model has maximum
218 at approximately 0.046, while the determinant of the Hessian is increasing monotonically for all
219 values 0.02 to 0.15. The Laplace approximation again indicates an intermediate value of 0.068.
220 Fig. 1-2 illustrate a general principle of this method, i.e., that the Laplace approximation estimate
221 will always be higher than maximizing the penalized likelihood by itself.

222 The simulation testing of this approximation for hake (Fig. 3) and cod (Fig. 4) shows that it
223 has little bias, and that the direction of this small bias depends upon the simulation scenario.
224 When estimating recruitment variability for Pacific hake (Fig. 3), for example, simulation testing
225 shows a negative bias when the true value is 1.5 (median converged estimate = 1.34), and a
226 positive bias when the true value is 0.5 (median estimate = 0.60). Estimating growth variability
227 in Atlantic cod shows trivial bias either when the true value is 0.10 (median converged estimate
228 = 0.099) or when the true value is 0.02 (median converged estimate = 0.022). However, the
229 algorithm has evidence of non-convergence in as many as 40% of replicates (i.e., for the case of
230 cod with 0.02 variability in growth), and generally has lower convergence rates when simulating
231 data given a low process variability. These cases of non-convergence could often be corrected
232 by applying additional user guidance (i.e. better starting values for parameters) rather than an
233 automated simulation-testing procedure.

Finally, the comparison of MCMC and Laplace approximation estimate of recruitment variability for Pacific hake (Fig. 5) illustrates a small difference in estimates between these approaches. Specifically, the mean Bayesian estimate is 1.68 , compared with the 1.43 estimated by the Laplace approximation. However, the Laplace approximation acknowledges relatively high support for the value of 1.68 ; the difference in the log-likelihood for $\sigma_R=1.43$ and $\sigma_R=1.68$ is approximately 0.90 , and $1.05 < \sigma_R < 1.95$ all have a log-likelihood within 3.0 of the maximum log-likelihood. Therefore, the Laplace approximation signals that the strength of evidence to distinguish between $\sigma_R = 1.05-1.95$ is relatively low. Similarly, the MCMC sample has a 95% credible interval ranging from $1.33-2.06$, and similarly shows little strength-of-evidence for distinguishing between MCMC and Laplace approximation estimates.

Discussion

Random-effects models are increasingly used in ecology to account for spatial and temporal variability in biological dynamics and measurement processes (Royle and Dorazio 2008, de Valpine 2009). As one example, a recent state-space model used count data in isolation to estimate site- and age-structured abundance for northern dusky salamanders (*Desomognathus fuscus*) given variability in recruitment, immigration, and natural mortality (Zipkin et al. In press). Models such as this are possible because states (i.e. local densities) and variability over time are treated as random effects, and hence avoid identifiability problems that arise when only using fixed effects or penalized likelihood (De Valpine and Hilborn 2005).

Random-effect models have also been advocated within fisheries science for many years (Maunder and Deriso 2003). These models can update expectations about the shape of species' dynamics (Thorson et al. in press) while simultaneously accounting for the many types of variability that are likely to occur for marine species (Mäntyniemi et al. 2013). However,

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

existing computational approaches to random-effect models are either slow or difficult to implement (Stewart et al. 2013), and this has prevented wide-spread application of random effects in stock assessment models (Maunder and Punt 2013).

To rectify this problem, we have shown that the Laplace approximation can be applied to existing stock assessment software to estimate the likelihood when integrating across all fixed and random effects, and that this can be used to identify an appropriate value for the variance of time-varying processes. We have also developed software to do this when using Stock Synthesis (Methot and Wetzel 2013), which is freely available using the *r4ss* package (Taylor et al. 2012). This approach performs well during simulation testing for both variability in recruitment somatic growth. This approach also performs similarly to Markov chain Monte Carlo when estimating recruitment variability, although remains a small difference in estimates between these two approaches (Laplace approximation: $\sigma_R = 1.68$; MCMC: $\sigma_R = 1.43$). This discrepancy likely arises because the Laplace approximation uses a multivariate normal distribution to approximate the posterior distribution, while MCMC samples from the distribution directly. Therefore, any divergence between the posterior and a multivariate normal distribution will likely cause the Laplace approximation and MCMC to result in different estimates in general.

We therefore conclude that our proposed approximation represents a viable approach to identifying the variance of random effects in stock assessment models. However, we recommend further case-study and simulation-modeling comparisons between MCMC, maximum marginal likelihood, and our proposed approach. These comparisons can hopefully identify when each method is fastest and can most appropriately identify the magnitude of one or more time-varying processes. We also recommend future research regarding the simultaneous estimation of multiple time-varying processes. Some assessment models can include multiple

time-varying processes (Gudmundsson and Gunnlaugsson 2012, Mäntyniemi et al. 2013), but there are few existing diagnostics for determining which are supported by the data or substantially affect model results. The proposed Laplace approximation method will in some cases be faster than MCMC estimation approaches, and also permits the use of pre-existing maximum likelihood model diagnostics (Taylor et al. 2012), so it may ease model building and evaluation given multiple time-varying processes. In other cases, however, Bayesian approaches will allow for better estimates of variance in time-varying processes. In particular, Bayesian methods can identify instances when multiple processes (e.g., time-varying selectivity or growth) can equally explain the data, i.e., by showing a ridge in the joint posterior of these variances. In these cases, maximum likelihood approaches often estimate one or the other process as having zero variance, or fail to propagate uncertainty about variances (see Gelman 2005 for details). For this reason, we advocate continued testing of models with multiple time-varying processes and comparison of computational approaches in this circumstance. Such a comparisons will be vital for stock assessment practitioners that seek to provide a biologically realistic portrayal of marine populations and processes (Kuparinen et al. 2012), where many processes will vary simultaneously over time, and may improve estimates of forecast imprecision, which is poorly estimated by existing models with parameters that are constant over time (Ralston et al. 2011).

Acknowledgements

We thank H. Skaug, whose presentation at the University of Washington on May 24, 2013 launched this project, and attendees of the ADMB developers workshop June 4-7, 2013. We also thank I. Stewart, I. Taylor, and J. Cope for early comments, C. Monnahan for providing code to extract the Hessian from ADMB, I. Taylor and I. Stewart for providing code to interface with Stock Synthesis, and H. Skaug and D. Fournier for providing ADMB and ADMB-RE.

Bibliography

Bolker, B.M., Gardner, B., Maunder, M., Berg, C.W., Brooks, M., Comita, L., Crone, E.,
Cubaynes, S., Davies, T., de Valpine, P., Ford, J., Gimenez, O., Kéry, M., Kim, E.J.,
Lennert-Cody, C., Magnusson, A., Martell, S., Nash, J., Nielsen, A., Regetz, J., Skaug,
H., and Zipkin, E. 2013. Strategies for fitting nonlinear ecological models in R, AD
Model Builder, and BUGS. *Methods Ecol. Evol.* **4**: 501–512. doi: 10.1111/2041-
210X.12044.

Fournier, D.A., Skaug, H.J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M.N., Nielsen, A.,
and Sibert, J. 2012. AD Model Builder: using automatic differentiation for statistical
inference of highly parameterized complex nonlinear models. *Optim. Methods Softw.* **27**:
1–17. doi: 10.1080/10556788.2011.597854.

Gelman, A. 2005. Analysis of variance—why it is more important than ever. *Ann. Stat.* **33**: 1–53.

Gelman, A., Carlin, J.B., Stern, H.S., and Rubin, D.B. 2003. *Bayesian Data Analysis*, Second
Edition. Chapman & Hall, Boca Raton, FL.

Gudmundsson, G., and Gunnlaugsson, T. 2012. Selection and estimation of sequential catch-at-
age models. *Can. J. Fish. Aquat. Sci.* **69**: 1760–1772. doi: 10.1139/f2012-095.

Hilborn, R., and Walters, C.J. 1992. *Quantitative Fisheries Stock Assessment - Choice,
Dynamics and Uncertainty*. In 1st edition. Springer, Norwell, Massachusetts.

Kuparinen, A., Mäntyniemi, S., Hutchings, J.A., and Kuikka, S. 2012. Increasing biological
realism of fisheries stock assessment: towards hierarchical Bayesian methods. *Environ.*
Rev. **20**: 135–151. [accessed 3 January 2013].

Mäntyniemi, S., Uusitalo, L., Peltonen, H., Haapasaari, P., and Kuikka, S. 2013. Integrated, age-
structured, length-based stock assessment model with uncertain process variances,

- 326 structural uncertainty, and environmental covariates: case of Central Baltic herring. *Can.*
327 *J. Fish. Aquat. Sci.*: 1–10. doi: 10.1139/cjfas-2012-0315.
- 328 Maunder, M.N., and Deriso, R.B. 2003. Estimation of recruitment in catch-at-age models. *Can. J.*
329 *Fish. Aquat. Sci.* **60**: 1204–1216. [accessed 15 August 2013].
- 330 Maunder, M.N., and Punt, A.E. 2013. A review of integrated analysis in fisheries stock
331 assessment. *Fish. Res.* **142**: 61–74.
- 332 Methot, R.D., and Taylor, I.G. 2011. Adjusting for bias due to variability of estimated
333 recruitments in fishery assessment models. *Can. J. Fish. Aquat. Sci.* **68**: 1744–1760.
- 334 Methot, R.D., and Wetzel, C.R. 2013. Stock synthesis: A biological and statistical framework for
335 fish stock assessment and fishery management. *Fish. Res.* **142**: 86–99.
- 336 Meyer, R., and Millar, R.B. 1999. BUGS in Bayesian stock assessments. *Can. J. Fish. Aquat.*
337 *Sci.* **56**: 1078–1087. [accessed 3 December 2012].
- 338 Plaganyi, E.E., Punt, A.E., Hillary, R., Morello, E.B., Thébaud, O., Hutton, T., Pillans, R.D.,
339 Thorson, J.T., Fulton, E.A., Smith, A.D.M., Smith, F., Bayliss, P., Haywood, M., Lyne,
340 V., and Rothlisberg, P.C. In press. Multispecies fisheries management and conservation:
341 tactical applications using models of intermediate complexity. *Fish Fish.* doi:
342 10.1111/j.1467-2979.2012.00488.x.
- 343 Polansky, L., De Valpine, P., Lloyd-Smith, J.O., and Getz, W.M. 2009. Likelihood ridges and
344 multimodality in population growth rate models. *Ecology* **90**: 2313–2320. [accessed 21
345 June 2013].
- 346 R Core Development Team. 2012. R: A Language and Environment for Statistical Computing.
347 Vienna, Austria. Available from <http://www.R-project.org/>.

1
2
3 348 Ralston, S., Punt, A.E., Hamel, O.S., DeVore, J.D., and Conser, R.J. 2011. A meta-analytic
4
5 349 approach to quantifying scientific uncertainty in stock assessments. *Fish. Bull.* **109**: 217–
6
7 350 231. [accessed 27 August 2013].
8
9
10 351 Royle, J.A., and Dorazio, R.M. 2008. Hierarchical modeling and inference in ecology: the
11
12 352 analysis of data from populations, metapopulations and communities. *In* 1st edition.
13
14 353 Academic Press, London.
15
16
17 354 Schirripa, M.J., Goodyear, C.P., and Methot, R.M. 2009. Testing different methods of
18
19 355 incorporating climate data into the assessment of US West Coast sablefish. *ICES J. Mar.*
20
21 356 *Sci.*
22
23
24 357 Skaug, H., and Fournier, D. 2006. Automatic approximation of the marginal likelihood in non-
25
26 358 Gaussian hierarchical models. *Comput. Stat. Data Anal.* **51**: 699–709.
27
28
29 359 Stewart, I.J., Hicks, A.C., Taylor, I.G., Thorson, J.T., Wetzel, C., and Kupschus, S. 2013. A
30
31 360 comparison of stock assessment uncertainty estimates using maximum likelihood and
32
33 361 Bayesian methods implemented with the same model framework. *Fish. Res.* **142**: 37–46.
34
35 362 doi: 10.1016/j.fishres.2012.07.003.
36
37
38 363 Taylor, I., Stewart, I., Hicks, A., Garrison, T., Punt, A., Wallace, J., and Wetzel, C. 2012. r4ss: R
39
40 364 code for Stock Synthesis. Available from <http://CRAN.R-project.org/package=r4ss>.
41
42
43 365 Thorson, J., Taylor, I., Stewart, I.J., and Punt, A.E. 2013. Using a recruitment-linked
44
45 366 multispecies stock assessment model to estimate common trends in recruitment for U.S.
46
47 367 West Coast groundfishes. *Mar. Ecol. Prog. Ser.* **483**: 245–256.
48
49
50 368 Thorson, J.T., Ono, K., and Munch, S. in press. A Bayesian approach to identifying and
51
52 369 compensating for model misspecification in population models. *Ecology*. doi:
53
54 370 10.1890/13-0187.1.
55
56
57
58
59
60

- 371 Thorson, J.T., Taylor, I., Stewart, I.J., and Punt, A.E. In press. Rigorous meta-analysis of life
372 history correlations by simultaneously analyzing multiple population dynamics models.
373 Ecol. Appl.
- 374 Thorson, J.T., and Taylor, I.G. In review. A comparison of parametric, semi-parametric, and
375 non-parametric approaches to selectivity in age-structured assessment models. Fish. Res.
- 376 De Valpine, P. 2002. Review of methods for fitting time-series models with process and
377 observation error and likelihood calculations for nonlinear, non-Gaussian state-space
378 models. Bull. Mar. Sci. **70**: 455–471. [accessed 21 June 2013].
- 379 De Valpine, P. 2009. Shared challenges and common ground for Bayesian and classical analysis
380 of hierarchical statistical models. Ecol. Appl. **19**: 584–588.
- 381 De Valpine, P. 2004. Monte Carlo state-space likelihoods by weighted posterior kernel density
382 estimation. J. Am. Stat. Assoc. **99**: 523–536.
- 383 De Valpine, P., and Hilborn, R. 2005. State-space likelihoods for nonlinear fisheries time-series.
384 Can. J. Fish. Aquat. Sci. **62**: 1937–1952.
- 385 Wilberg, M.J., Thorson, J.T., Linton, B.C., and Berkson, J. 2010. Incorporating time-varying
386 catchability into population dynamic stock assessment models. Rev. Fish. Sci. **18**: 7–24.
- 387 Zipkin, E.F., Thorson, J.T., See, K., Lynch, H.J., Grant, E.H.C., Kanno, Y., Chandler, R.B.,
388 Letcher, B.H., and Royle, J.A. In press. Modeling structured population dynamics using
389 data from unmarked individuals. Ecology.

Fig. 1 – Profile showing the log-penalized likelihood (dotted line), 0.5 times the log-determinant of the Hessian (dashed line), and the resulting log-marginal likelihood (solid line) arising from the proposed Laplace approximation for recruitment variability in Pacific hake

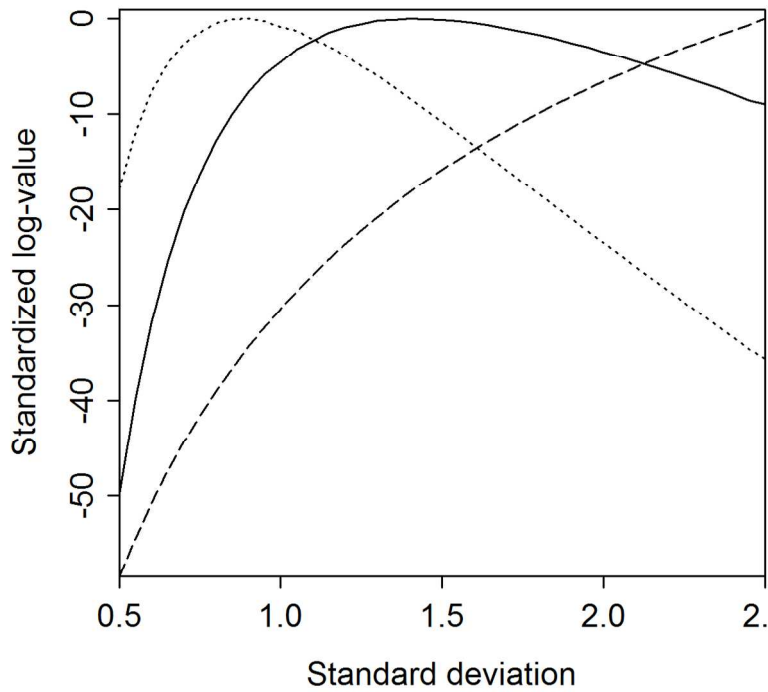


Fig. 2 – Profile showing the log-penalized likelihood (dotted line), 0.5 times the log-determinant of the Hessian (dashed line), and the resulting log-marginal likelihood (solid line) arising from the proposed Laplace approximation for variability in growth for North Sea cod

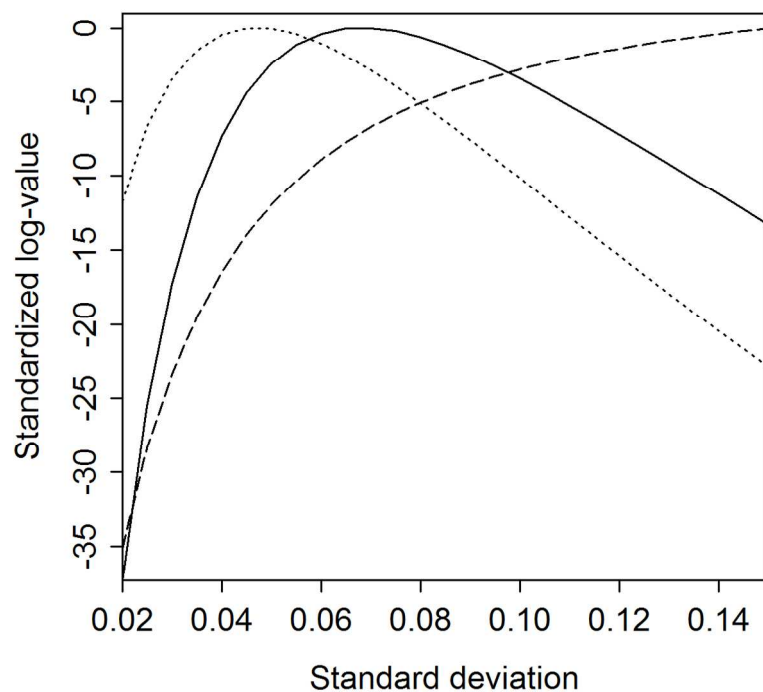


Fig. 3 – Histogram of estimated recruitment variability for Pacific hake for 200 simulated data sets, given a true value (solid vertical line) of 1.5 (panel A) or 0.5 (panel B), where the number of algorithm runs that converged (i.e. where the first 5 iterations had a final gradient less than 1) and did not converge (i.e. one of the first 5 iterations had a final gradient greater than 1) are shown in the upper right (the dark-grey area is the histogram for ‘converged’ runs, while light-grey is the additional distribution of ‘non-converged’ runs).

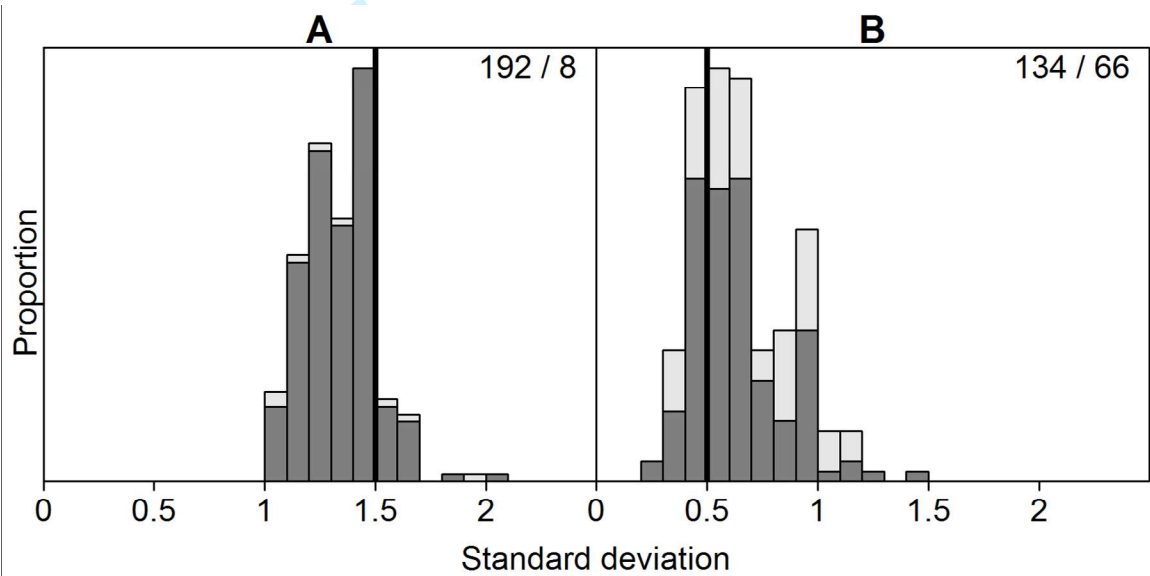


Fig. 4 – Histogram of estimated growth variability for North Sea cod for 200 simulated data sets, given a true value (solid vertical line) of 0.1 (Panel A) or 0.02 (Panel B), where the number of algorithm runs that converged (i.e. where the first 5 iterations had a final gradient less than 1) and did not converge (i.e. one of the first 5 iterations had a final gradient greater than 1) are shown in the upper right (the dark-grey area is the histogram for ‘converged’ runs, while light-grey is the additional distribution of ‘non-converged’ runs).

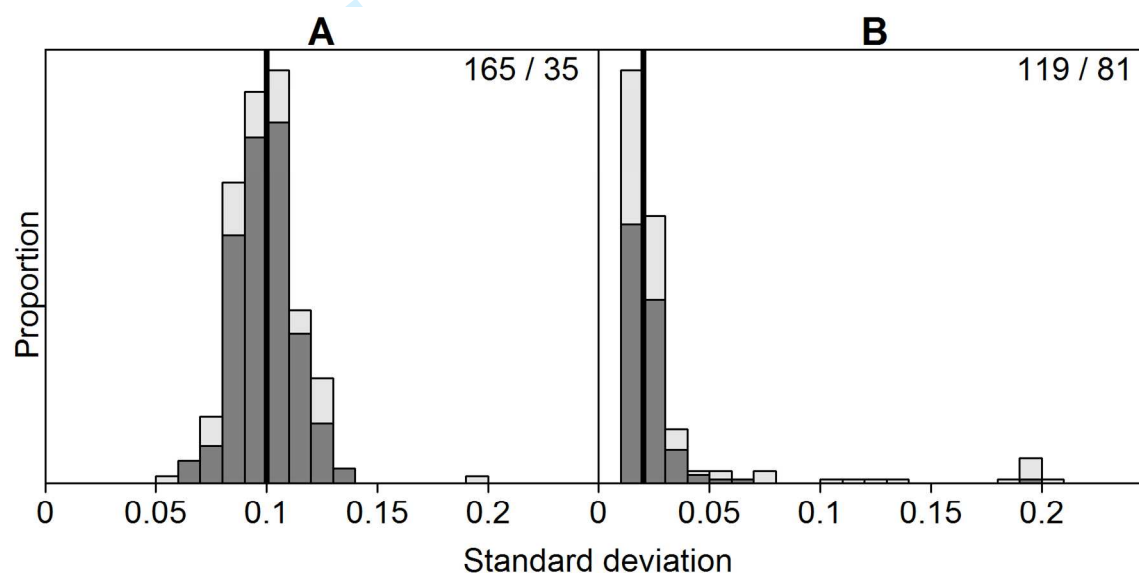


Fig. 5 – Markov chain Monte Carlo approximation of the posterior distribution for recruitment variability for Pacific hake, showing the posterior mean (solid line) and 5% and 95% quantiles (dotted lines)

