

Production model based estimates of lower confidence limits for the abundance of West Greenland minke whales

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ABSTRACT

The methodology advanced by Brandão and Butterworth (2007) for simulating catch sex sampling data in the process of computing lower confidence bounds for the abundance of the West Greenland minke whale population is applied to the new modelling scenarios developed at the March 2008 IWC Workshop on Greenlandic Fisheries. To date calculations have extended only to $MSYR = 2\%$, and been implemented for Models 3, 4b and 5 for a production model of resource dynamics, and to Model 4b for the age-structured population model of Witting and Schweder (2008). For Model 5 for the SW stratum treated as an independent stock, the MLE of pre-exploitation abundance K is finite, so that standard likelihood profile estimates of lower confidence bounds for abundance are provided. For the production model, lower bounds for Model 4b (the “influx” model) are higher than for Model 3 (the “redistribution” model); however these Model 4b bounds decrease when an age-structured population model is used instead of a production model. A concern, however, is indications of non-convergence of some of the model fits required to compute the deviance distributions which are used to determine the confidence bounds; this matter is being investigated further.

INTRODUCTION

This paper reports applications of the methodology set out in IWC (2008) for the computation of lower confidence limits for the abundance of minke whales using an assessment model based upon imbalanced catch sex-ratio data and under the procedures of Brandão and Butterworth (2007) for simulating such catch sex sampling data. The scenarios postulated in Models 3, 4b and 5 of IWC (2008) are investigated using an underlying production model for the resource dynamics, with sensitivity to replacing this by an age structured model examined for the Model 4b scenario.

DATA

The data used for these analyses are generally identical to those used by Witting and Schweder (2008). For Model 5 the prescriptions of IWC (2008) were used; those were incomplete in one respect (the specification for the split of the unsampled whales by stratum and sex for the early Greenlandic period of whaling; the procedures used to specify these splits are set out in the Appendix.

METHODS

The basic methodology used is the same as that of Brandão and Butterworth (2007), and is repeated immediately below and in the Appendix. Evaluations to deal with new scenarios specified by IWC (2008) are detailed further below; the basic approach to compute deviance distributions has followed that set out in IWC (2008), and is not repeated in detail here.

Population dynamics

A sex-structured age-aggregated (or production) model is used:

$$N_{y+1}^m = N_y^m + rN_y^f \left(1 - \left(\frac{N_y}{K} \right)^{2.39} \right) - C_y^m \quad (1)$$

$$N_{y+1}^f = N_y^f + rN_y^f \left(1 - \left(\frac{N_y}{K} \right)^{2.39} \right) - C_y^f \quad (2)$$

where:

N_y is the total number of minke whales in year y , which is given by:

$$N_y = N_y^m + N_y^f,$$

N_y^m is the total number of male minke whales in year y ,

N_y^f is the total number of female minke whales in year y ,

K is the carrying capacity,

C_y^m is the number of male West Greenland minke whales caught in year y ,

C_y^f is the number of female West Greenland minke whales caught in year y , and

r is the intrinsic population growth rate, which is linked to the assumption of a 50:50 sex ratio at birth; to correspond to MSYR values of 1, 2 and 4%, r is set respectively to 0.0142, 0.0284 and 0.0567.

The number of male and female minke whales is assumed to be the same before exploitation so that $N_{1948}^m = N_{1948}^f = K/2$.

The total number of minke whales caught in the whaling period i in year y is given by:

$$C_y^i = C_y^{m(i)} + C_y^{f(i)} \quad (3)$$

where:

$C_y^{m(i)}$ is the number of male minke whales caught in period i by the fishery concerned,

where the period/fishery i represents:

$$i = \begin{cases} I & \text{the period 1955 – 1978 by Greenlanic whalers} \\ II & \text{the period 1968 – 1985 by Norwegian whalers, and} \\ III & \text{the period 1987 – 2006 by Greenlanic whalers} \end{cases}$$

$C_y^{f(i)}$ is the corresponding number of female minke whales caught in period/fishery i .

For the simplest form of the model, the expected number of female minke whales caught by each period/fishery i in year y is given by:

$$\hat{C}_y^{f(i)} = C_y^i \frac{N_y^f}{N_y^f + \lambda^i N_y^m}, \quad (4)$$

where:

λ^i is the selectivity of males relative to females for the period and fishery concerned, and is assumed to remain constant over that period, with equation (4) following from the associated assumptions that:

$$\hat{C}_y^{f(i)} = F_y^{(i)} N_y^f; \quad \hat{C}_y^{m(i)} = \lambda^i F_y^{(i)} N_y^m. \quad (5)$$

Age-structured model

For some scenarios, results are also provided for an age-structured population model. This model is identical to that described in Witting and Schweder (2008).

The likelihood function

The likelihood is calculated assuming that the observed female catches are distributed about their expected value according to an overdispersed Poisson model. The negative of the approximate log-likelihood (ignoring constants) which is minimised in the fitting procedure is thus given by:

$$-\ln L = \sum_{i=I}^{III} \sum_{y=y_i^1}^{y_i^2} \left\{ \frac{1}{\sigma_i^2} \frac{(C_y^{f(i)} - \hat{C}_y^{f(i)})^2}{(2\hat{C}_y^{f(i)})} + \ln \sigma_i + \ln \sqrt{\hat{C}_y^{f(i)}} \right\} \quad (6)$$

where

- y_i^1 is the first year of catches for period i ,
- y_i^* is the last year of catches for period i ,
- σ_i measures overdispersion of the distribution of catches compared to a Poisson distribution for which the variance is equal to the expected catch for the period and fishery concerned, whose maximum likelihood estimate is given by:

$$\hat{\sigma}_i = \sqrt{\frac{1}{n_i} \sum_{i=1}^{III} \sum_{y=y_i^1}^{y_i^*} \left\{ \frac{(C_y^{f(i)} - \hat{C}_y^{f(i)})^2}{\hat{C}_y^{f(i)}} \right\}} \quad (7)$$

n_i is the total number of years in the summation of each whaling period.

Note that the formulation of equation (6) assumes that the Poisson-like catch distribution can be approximated by a normal distribution of the same variance. The estimable parameters of this basic model are λ^I , λ^{II} , λ^{III} , σ_I , σ_{II} , σ_{III} and K .

Recent refinements

The approach above is applied to three scenarios set out in IWC (2008):

Model 3: A closed population model with time dependence of the fractions of females and of males distributed in the NW + CW and SW strata in the later period of Greenlandic whaling commencing in 1987. To reflect this variation, the proportions of males and of females in the NW + CW stratum (relative to the NW+CW and SW strata combined) are assumed to change with time during the recent period of Greenlandic whaling as:

$$r_t^{m/f} = e^{\alpha^{m/f} + \beta^{m/f} t} / [1 + e^{\alpha^{m/f} + \beta^{m/f} t}]$$

with a complementary change in the SW stratum. The time t is specified by the standard calendar year.

Model 4b: An “influx” model where the number of male whales in the SW stratum is assumed to be influenced by whales moving in from other areas in recent years. To effect this, the λ parameter is assumed to vary linearly from 1987 (λ_{37}) to 2006 (λ_{06}) when these Greenlandic catches were sampled for sex.

Model 5: The animals in the NW + CW and SW strata are assumed to exhibit site fidelity, and so (*in extremis*) are treated as separate populations with different values of λ for each period and stratum which do not change within those periods.

In other changes from earlier analyses, catch data from the Norwegian fishery period II are not taken into account in the likelihood (except for Model 5 for the NW + CW stratum), but are included amongst the catches taken into account in the population dynamics equations.

RESULTS

The core results obtained for lower confidence bounds (for N_{2006} , K and their ratio) are reported in Table 1, with the best estimates of the λ , α , β and σ parameters listed in Table 2, and the process used to determine the bounds from the deviances quartiles illustrated in Figs 1-4. Note that restrictions on time have precluded applications for other than the $MSYR = 2\%$ case, and that only Model 4b has been run for the age-structured as well as for the age-aggregated production model of the dynamics.

In the case of Model 5 for the SW stratum treated as if it were an isolated stock, a finite MLE of K results, so that the simulation approach is not needed to determine lower confidence bounds, and these are instead reported using the standard likelihood profile approach.

Comparing the different scenarios, production model results yield lower values for lower bounds on K (and for N_{2006}) for Model 3 (“redistribution”) than for Model 4b (“influx”). If results for Model 5 for the two strata are added, they are intermediate between those for Models 3 and 4b.

Of some importance is the fact that when age-aggregated and age-structured models are compared for Model 4b, the former gives appreciably lower values for $K(0+)$ than does the latter for K .

CONCLUDING REMARKS

The results provided in this paper should be seen as initial. It became evident during the process of developing the deviance distributions that there were instances when the minimisation to obtain the best value of the likelihood had not converged (as indicated by negative values for deviance). This was a problem for Model 4b at low K values and for Model 3 at all K values, and likely relates to the likelihood being fairly flat in some of the parameters being estimated. Replicates with such negative values were omitted when computing deviance distributions, but this decreased sample size so that the lower quantiles in particular of these distributions are subject to Monte Carlo error. In these cases therefore, more simulations were carried out so that the first 500 non-negative deviances were used in calculating the quantiles.

Runs with greater numbers of replicates to further reduce Monte Carlo error will be pursued in due course (though a concern does arise that the elimination process applied may introduce bias). A further problem associated with such non-convergence is that the diagnostic of negative deviance will not detect all such cases. This matter is being pursued further by considering the convergence diagnostics for each replicate.

In Brandão and Butterworth (2007), it was found that for some series, the procedure in the Appendix used to generate the sex-sampled catch yielded results with less variability (in median terms) than the original data, and autocorrelation was introduced into the resampling process to correct for that. This matter is being investigated further for the new scenarios; in the meantime, results reported in this document all correspond to setting that autocorrelation to zero.

ACKNOWLEDGMENTS

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REFERENCES

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- International Whaling Commission. 2008. Report of the Workshop on Greenlandic Fisheries. Report submitted to this meeting.
- Witting, L. and Schweder, T. 2008. Lower bound on population status from catch sex ratio: applied to minke whales off West Greenland. IWC document SC/60/AWMP1.

Table 1. Lower 5%, 10% and 50% quantiles for the population abundance in 2006 (N_{2006}), the carrying capacity (K) and the current depletion (N_{2006}/K) at the start of 2006 for various models for a MSYR value of 2%. For Model 5 (SW) results are for the likelihood profile method and hence are shown in italics (the values in the 50% columns are then the MLEs). The methods are applied to provide the quantiles for K , and then the corresponding values of N_{2006} (and N_{2006}/K) follow from the MSYR value assumed and the actual catches made. For the age-structured population model, values given are for the 0+ (total) population.

| | N_{2006} | | | K | | | N_{2006}/K | | |
|--|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | 5% | 10% | 50% | 5% | 10% | 50% | 5% | 10% | 50% |
| Model 3 | 10 140 | 14 002 | 144 242 | 16 000 | 19 000 | 147 000 | 0.634 | 0.737 | 0.981 |
| Model 4b | 21 954 | 34 558 | 180 279 | 26 000 | 38 000 | 183 000 | 0.844 | 0.909 | 0.985 |
| Model 4b (age structured) | 7 348 | 17 163 | 129 201 | 18 000 | 25 000 | 134 000 | 0.408 | 0.687 | 0.964 |
| Model 5 (NW+CW) | 18 283 | 24 554 | 163 121 | 21 000 | 27 000 | 165 000 | 0.871 | 0.909 | 0.989 |
| Model 5 (SW) | <i>2 011</i> | <i>2 044</i> | <i>2 294</i> | <i>3 856</i> | <i>3 879</i> | <i>4 049</i> | <i>0.522</i> | <i>0.527</i> | <i>0.566</i> |

Table 2. Parameter estimates for overdispersion and male selectivity relative to females for the case of $K \rightarrow \infty$ (approximated numerically here by $K = 200\,000$) for various models for a MSYR value of 2%. Model 5 (SW) results correspond to genuine MLEs and hence are shown in italics.

| Parameter | Model 3 | Model 4b | Model 4b (age structured) | Model 5 (NW+CW) | Model 5 (SW) |
|--|---------|----------|---------------------------|-----------------|--------------|
| λ^I (Greenland 1955-1978) | 0.356 | 0.356 | 0.356 | 0.394 | <i>0.235</i> |
| λ^{II} (Norwegian) | — | — | — | 0.372 | — |
| λ^{II} (Greenland NW+CW 1987-2006) | 0.698 | 0.352 | 0.363 | 0.357 | — |
| λ^{III} (Greenland SW 1987-2006) | 0.001 | — | — | — | <i>0.070</i> |
| λ_{87} (Greenland SW 1987-2006) | — | 0.118 | 0.120 | — | — |
| λ_{06} (Greenland SW 1987-2006) | — | 0.365 | 0.379 | — | — |
| α^f | -82.24 | — | — | — | — |
| α^m | 52.89 | — | — | — | — |
| β^f | 0.044 | — | — | — | — |
| β^m | -0.026 | — | — | — | — |
| σ_I (Greenland 1955-1978) | 0.814 | 0.814 | 0.814 | 0.738 | <i>0.433</i> |
| σ_{II} (Norwegian) | — | — | — | 1.694 | — |
| σ_{II} (Greenland NW+CW 1987-2006) | 0.661 | 0.675 | 0.673 | 0.674 | — |
| σ_{III} (Greenland SW 1987-2006) | 0.366 | 0.378 | 0.378 | — | <i>0.352</i> |

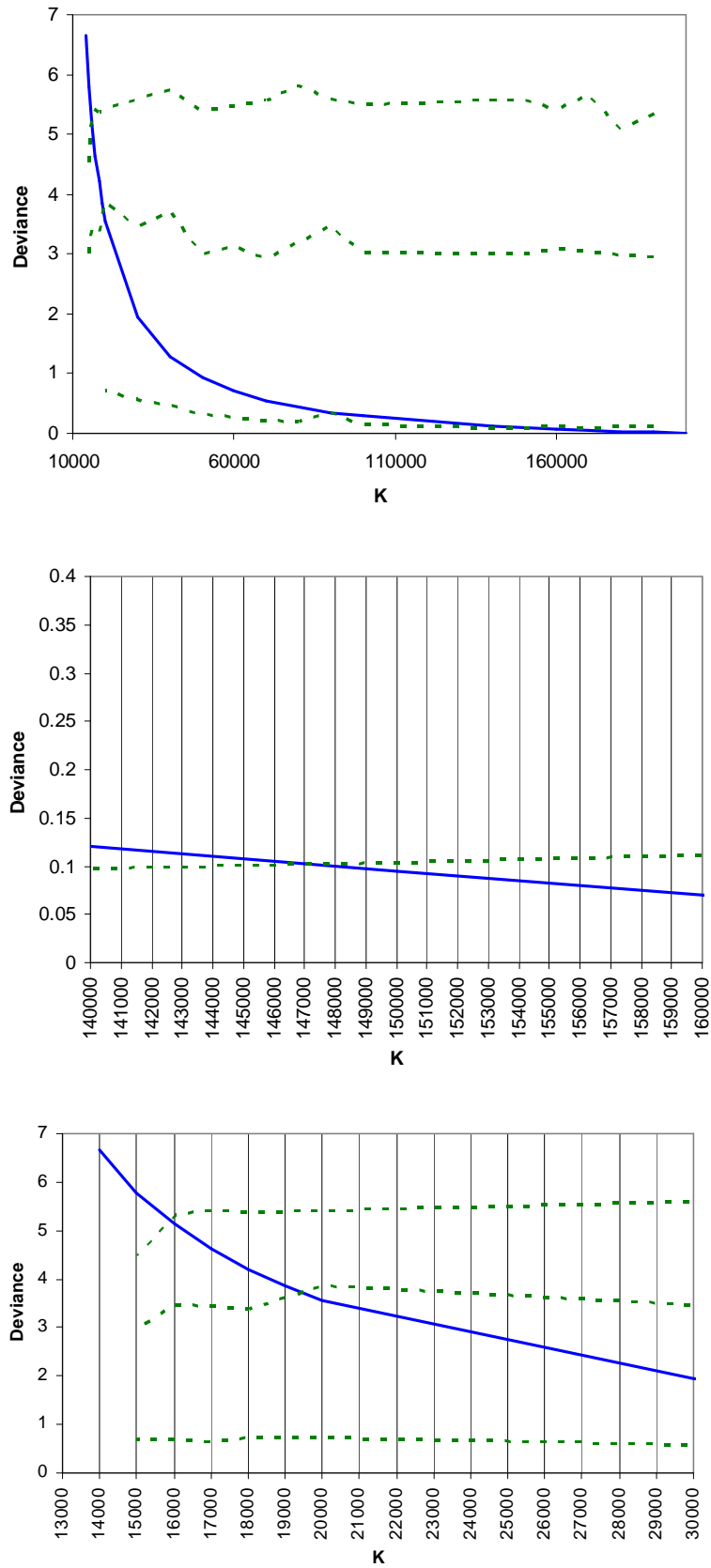


Figure 1. Observed deviance (solid line) and 5%, 10% and 50% quantiles (dashed lines) based on 500 simulations, together with close ups of the intersections of the quantiles and the observed deviance curve, for **Model 3** with MSYR = 2%.

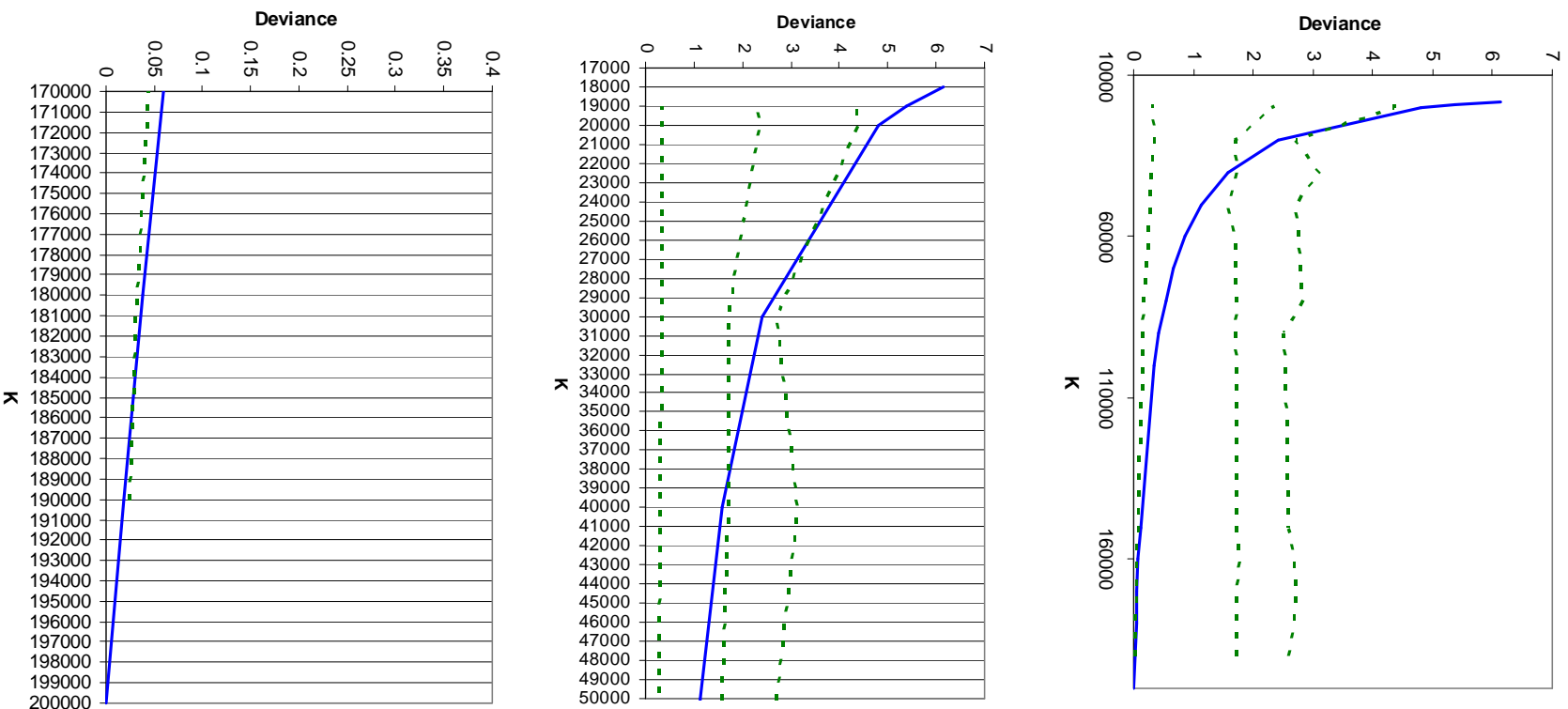


Figure 2. Observed deviance (solid line) and 5%, 10% and 50% quantiles (dashed lines) based on 500 simulations, together with close ups of the intersections of the quantiles and the observed deviance curve, for **Model 4b** with $MSYR = 2\%$.

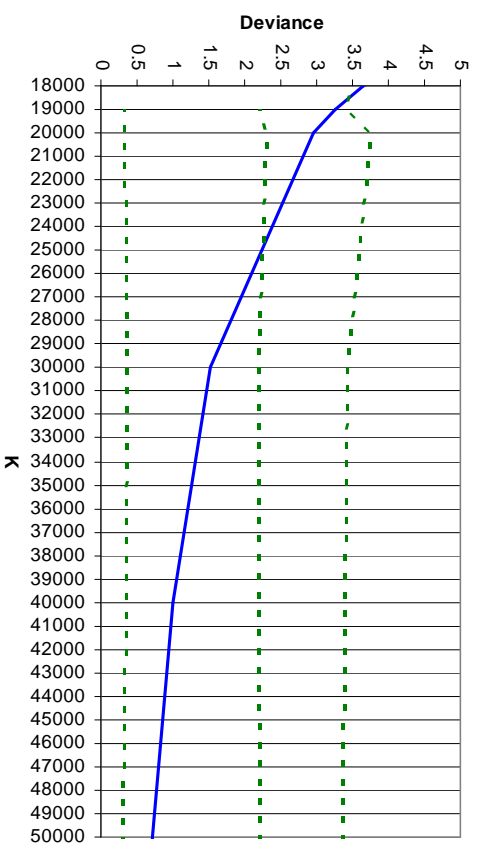
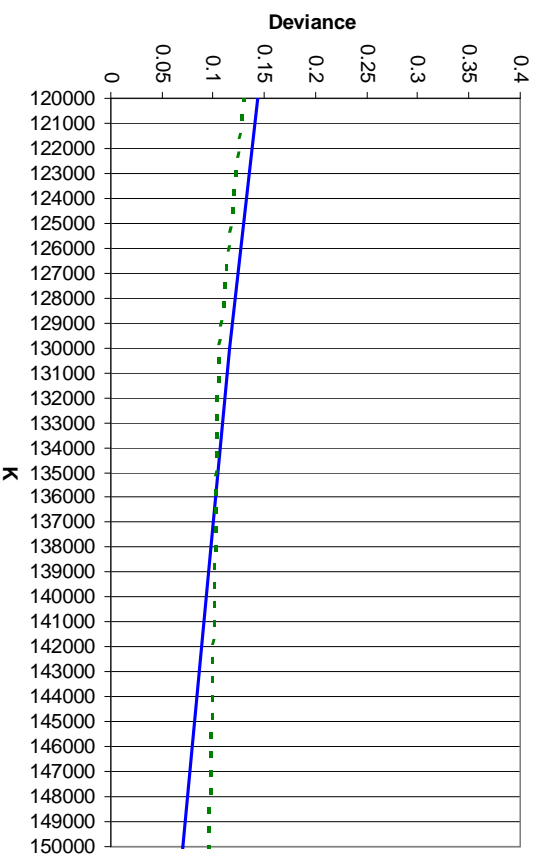
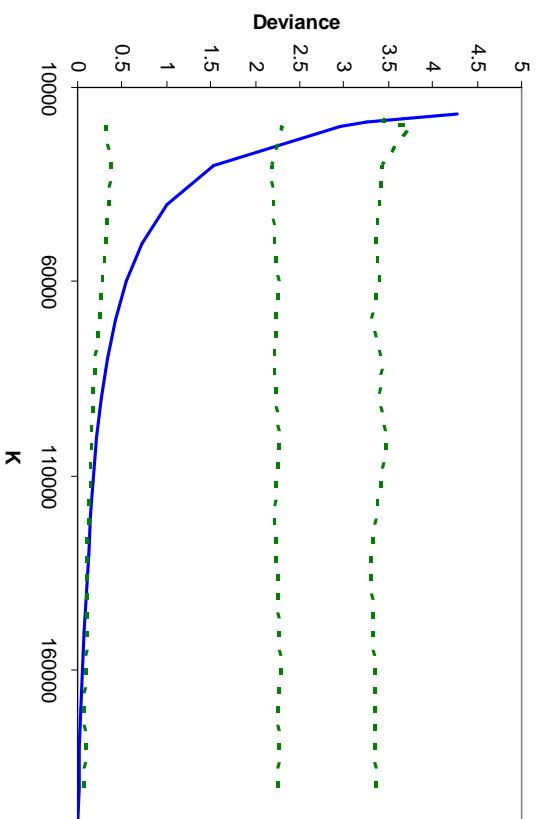


Figure 3. Observed deviance (solid line) and 5%, 10% and 50% quantiles (dashed lines) based on 500 simulations, together with close ups of the intersections of the quantiles and the observed deviance curve, for **Model 4b (with age structure)** for $MSYR = 2\%$.

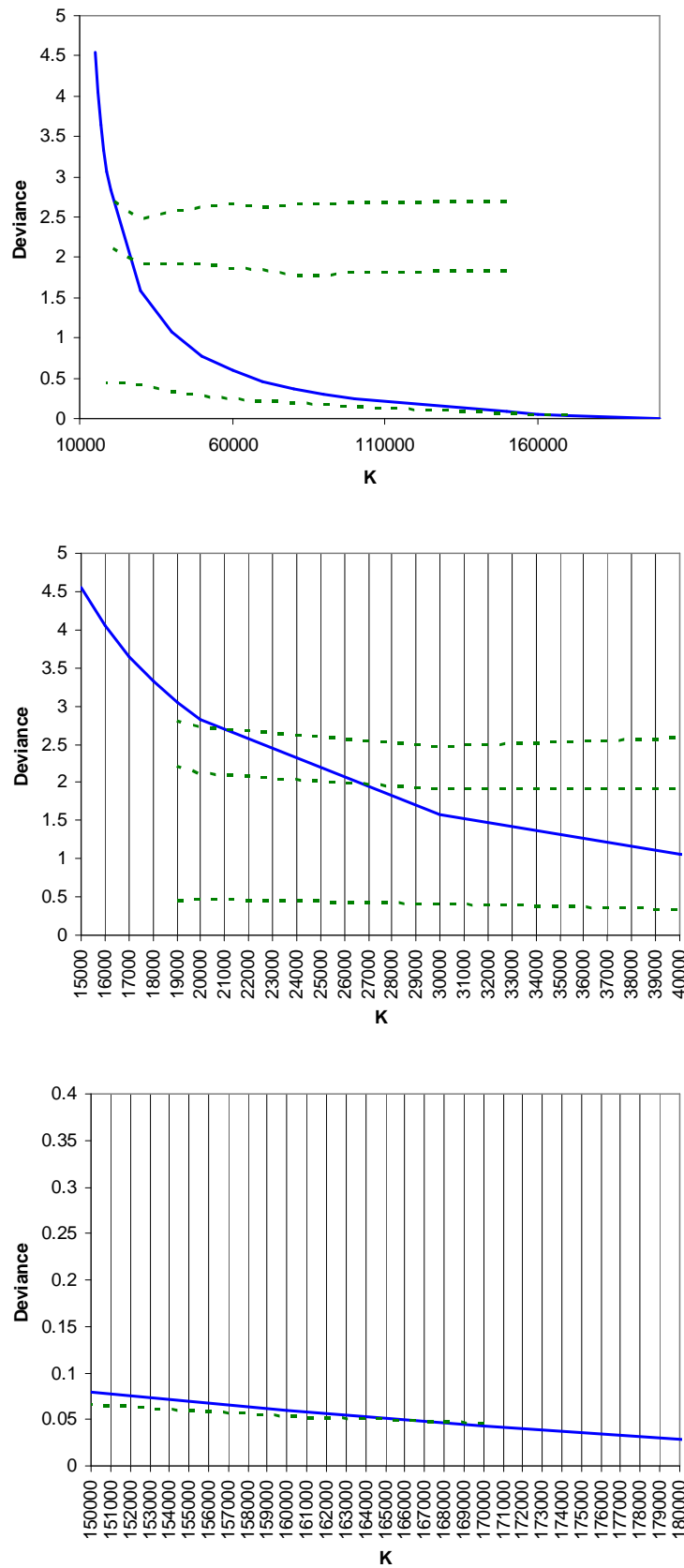


Figure 4. Observed deviance (solid line) and 5%, 10% and 50% quantiles (dashed lines) based on 500 simulations, together with close ups of the intersections of the quantiles and the observed deviance curve, for **Model 5 (NW+CW)** with MSYR = 2%.

APPENDIX

Simulation algorithm

For the best estimate of virgin biomass (K) (here taken to be 200 000 as a surrogate for infinity), the models described in the text are fitted to the original data to obtain estimates for the overdispersion (σ) and the selectivity of males relative to females (λ s) parameters for the period and whalers concerned. For the age-aggregated production model, a fixed intrinsic population growth rate (r) of 0.0284, corresponding to an MSYR of 2%, has been set for all simulations conducted to date. Then for a given value of the true virgin biomass (K), and the overdispersion as estimated for $K = 200\ 000$, the models are fitted to the original data to obtain estimates of the λ s. For each model the deviance as a function of K is obtained for the original data.

For each set of values of K , r , and λ_i , the total annual catches ($C_y = C_y^m + C_y^f$) and the annual reported total catches (C_y^i), the following steps are taken:

1. Set $N_{1948} = K = N_{1948}^f + N_{1948}^m$.
2. Generate C_y^f , C_y^m , $C_y^{f(i)}$ and $C_y^{m(i)}$.
3. From C_y , project N_y^f and N_y^m forward one year (using equations (1) and (2)).
4. Repeat steps (2) and (3) until the end of the time period (i.e. 2006).
5. Fit models to the generated data in which K is fixed and for the case when K is estimated to get the deviance value for the generated data.
6. Repeat steps (1) to (5) 500 times to get the distribution of the deviance values.

Data generation

The data generation has to take into account that not all whales are sampled for sex, and that there is a period over which both Norwegian and Greenlandic catches occurred. The assumption has been made that the Norwegian catch was always fully sampled, so that the sampled Greenland catch has to be generated from the total Greenland catch each year.

1] Period 1948–1954 and 1986 (no sampling):

- Generate C_y^f from the normal distribution given by:

$$\mathbf{N}\left(\frac{N_y^f}{N_y^f + \lambda^l N_y^m} C_y, \sigma_i^2 \frac{N_y^f}{N_y^f + \lambda^l N_y^m} C_y\right), \quad (\text{A.1})$$

i.e. the λ_i and σ_i correspond to the Greenlandic (1955-1978) period.

- The total number of males is then given by $C_y^m = C_y - C_y^f$.

2] Period 1955–1967 (only Greenland catch, which is sampled):

- Generate C_y^f and C_y^m as in 1] above.
- Sample C_y^l without replacement and with autocorrelation ρ from C_y with sex split given by C_y^f and C_y^m , to get sampled numbers $C_y^{f(l)}$ and $C_y^{m(l)}$.

3] Period 1968–1978 (both Greenland and Norwegian catches, both sampled):

- Generate the Norwegian catch $C_y^{f(II)}$ from the normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda^{II} N_y^m} C_y^{II}, \sigma_{II}^2 \frac{N_y^f}{N_y^f + \lambda^{II} N_y^m} C_y^{II}\right)$$

- The total number of males caught by the Norwegians is then given by $C_y^{m(II)} = C_y^{II} - C_y^{f(II)}$.
- Note that the Greenland catch is $C_y - C_y^{II}$, to be comprised of $C_y^{f(l)*}$ females and $C_y^{m(l)*}$ males.
- Generate $C_y^{f(l)*}$ from the normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda^I N_y^m} (C_y - C_y^{II}), \sigma_I^2 \frac{N_y^f}{N_y^f + \lambda^I N_y^m} (C_y - C_y^{II})\right)$$

- The total number of males caught by Greenland is then given by $C_y^{m(l)*} = (C_y - C_y^{II}) - C_y^{f(l)*}$.
- Sample without replacement and with autocorrelation from $C_y - C_y^{II}$ with sex split given by $C_y^{f(l)*}$ and $C_y^{m(l)*}$, to give the whales caught and sampled by Greenland $C_y^{f(l)}$ and $C_y^{m(l)}$.
- Add the $C_y^{f(l)*}$ and $C_y^{m(l)*}$ to the Norwegian generated catches to get the total catches by sex (e.g. $C_y^f = C_y^{f(II)} + C_y^{f(l)*}$).

4] Period 1979–1985 (both Greenland and Norwegian catches; the former is not sampled, but is assumed to be governed by the parameters for the first (1955–1978) period of sampled Greenland catches):

- Generate the Norwegian catch $C_y^{f(II)}$ from the normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda^{II} N_y^m} C_y^{II}, \sigma_{II}^2 \frac{N_y^f}{N_y^f + \lambda^{II} N_y^m} C_y^{II}\right)$$

- The total number of males caught by the Norwegians is then given by $C_y^{m(II)} = C_y^{II} - C_y^{f(II)}$.
- Note that the Greenland catch is $C_y - C_y^{II}$, to be comprised of $C_y^{f(I)*}$ females and $C_y^{m(I)*}$ males.
- Generate $C_y^{f(I)*}$ from the normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda' N_y^m}(C_y - C_y^{II}), \sigma_I^2 \frac{N_y^f}{N_y^f + \lambda' N_y^m}(C_y - C_y^{II})\right)$$

- The total number of males caught by Greenland is then given by $C_y^{m(I)*} = (C_y - C_y^{II}) - C_y^{f(I)*}$.
- Add the $C_y^{f(I)*}$ and $C_y^{m(I)*}$ to the Norwegian generated catches to get the total catches by sex (e.g. $C_y^f = C_y^{f(II)} + C_y^{f(I)*}$).

5] Period 1987–2006 (only Greenland catch, which is sampled):

- Generate C_y^f from normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda^{III} N_y^m} C_y, \sigma_{III}^2 \frac{N_y^f}{N_y^f + \lambda^{III} N_y^m} C_y\right).$$

- The total number of males is then given by $C_y^m = C_y - C_y^f$.
- Sample C_y^{III} randomly without replacement from C_y with sex split given by C_y^f and C_y^m , to get sampled numbers $C_y^{f(III)}$ and $C_y^{m(III)}$.

In the data generation algorithm described above, in instances in which a negative catch was generated for one of the sexes, the catch for that sex was set to zero and consequently the catch for the opposite sex was set to the total number being sampled (as otherwise in this case, a catch greater than the number being sampled would have been generated to compensate for the negative generated catch).

Modifications for new applications of this paper

The data generation algorithm described above applies to Model 5, where the total catches and the reported catches refer to those in the NW+CW strata. All the Norwegian catches are assumed to come from the NW+CW population. The catches in the earlier Greenlandic period are split by area by taking males and females separately, calculating the average ratio of the total Greenlandic catch of NW+CW to SW over the years of the later Greenlandic period, and then applying this ratio

to the earlier period for which this split is not known. In other respects, the specification of Model 5 follows the prescription given in IWC (2008).

For the other models considered in this paper, the following alterations to the data generation algorithm were made:

Model 4b: In Step 3 and in Step 4, the Norwegian catches are not generated but the observed Norwegian data is used (assuming that all Norwegian catches were sampled). Therefore the following changes are made:

$$\begin{aligned} C_y^{II} &\rightarrow C_y^{\text{Norwegian}} \\ C_y^{f(II)} &\rightarrow C_y^{f(\text{Norwegian})} \\ C_y^{m(II)} &\rightarrow C_y^{m(\text{Norwegian})} \end{aligned}$$

In Step 5, the total Greenland catches (C_y) have to be split into the NW+CW and SW strata (C_y^{NW+CW} and C_y^{SW}), where these are taken to be the observed data as used for Model 5(NW+CW) and Model 5 (SW). Step 5 is thus changed into:

- Generate $C_y^{f(NW+CW)}$ from normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda^{II(NW+CW)} N_y^m} C_y^{NW+CW}, \sigma_{II(NW+CW)}^2 \frac{N_y^f}{N_y^f + \lambda^{II(NW+CW)} N_y^m} C_y^{NW+CW}\right), \text{ where}$$

- The total number of males is then given by $C_y^{m(NW+CW)} = C_y^{NW+CW} - C_y^{f(NW+CW)}$.
- Sample $C_y^{II(NW+CW)}$ randomly without replacement from C_y^{NW+CW} with sex split given by $C_y^{f(NW+CW)}$ and $C_y^{m(NW+CW)}$, to get sampled numbers $C_y^{f(II(NW+CW))}$ and $C_y^{m(II(NW+CW))}$.
- Generate $C_y^{f(SW)}$ from normal distribution given by:

$$N\left(\frac{N_y^f}{N_y^f + \lambda^{III(SW)} N_y^m} C_y^{SW}, \sigma_{III(SW)}^2 \frac{N_y^f}{N_y^f + \lambda^{III(SW)} N_y^m} C_y^{SW}\right), \text{ where}$$

$$\lambda^{III(SW)} = \lambda_{87} (2006 - y)/19 + \lambda_{06} (y - 1987)/19,$$

i.e. λ is assumed to change linearly over time during this period.

- The total number of males is then given by $C_y^{m(SW)} = C_y^{SW} - C_y^{f(SW)}$.
- Sample $C_y^{II(SW)}$ randomly without replacement from C_y^{SW} with sex split given by $C_y^{f(SW)}$ and $C_y^{m(SW)}$, to get sampled numbers $C_y^{f(III(SW))}$ and $C_y^{m(III(SW))}$.

- Get total catches by sex by adding the catches by sex from each strata (e.g.

$$C_y^f = C_y^{f(III(NW+CW))} + C_y^{f(III(SW))}$$

Model 4b (age structured): The data generation algorithm remains the same as for Model 4b except that the following changes are made to the number of whales:

$$N_y^f \rightarrow \sum_a N_{y,a}^f \cdot G_a$$

$$N_y^m \rightarrow \sum_a N_{y,a}^m \cdot G_a$$

where G_a is the selectivity at age as specified in Witting and Schweder (2008).

Model 3: The data generation algorithm remains essentially the same as for Model 4b, but with the following changes:

- When generating data for the NW+CW strata:

$$N_y^f \rightarrow N_y^f(A^f)$$

$$N_y^m \rightarrow N_y^m(A^m), \text{ where}$$

$$A^f = \frac{e^{(\alpha^f + \beta^f y)}}{1 - e^{(\alpha^f + \beta^f y)}}$$

$$A^m = \frac{e^{(\alpha^m + \beta^m y)}}{1 - e^{(\alpha^m + \beta^m y)}}$$

- When generating data for the SW strata:

$$N_y^f \rightarrow N_y^f(1 - A^f)$$

$$N_y^m \rightarrow N_y^m(1 - A^m)$$