A Bayesian approach to assess the status of Southern Hemipshere humpback whales (*Megaptera novaeangliae*) with an application to Breeding Stock G

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ABSTRACT

The Bayesian stock assessment methodology presently being applied in the Comprehensive Assessment of the Southern Hemisphere humpback whales, which uses a sex- and age-aggregated population model, is detailed. This methodology is applied to Breeding Stock G, which winters off the west coast of South America. This application takes into account the recently updated historic catch series, as well as the most recent estimates of absolute abundance and population trend information.

KEYWORDS: HUMPBACK WHALE; BAYESIAN ASSESSMENT; SOUTHERN HEMISPHERE; MODELLING

INTRODUCTION

Humpback whales (*Megaptera novaeangliae*) were heavily exploited by commercial whaling in the Southern Hemisphere (Tønnessen and Johnsen, 1982). It is estimated that nearly 200,000 whales were captured in both wintering and feeding grounds (Findlay, 2000). Currently, seven Southern Hemisphere humpback whale breeding stocks are recognised by the International Whaling Commission (IWC, 1998; 2011). Breeding Stock G corresponds to whales wintering off the eastern coast of Central and South America, between Peru and Costa Rica (Acevedo-Gutiérrez and Smultea, 1995; Félix and Haase, 2001; Flórez-González *et al.*, 1998; Rasmussen *et al.*, 2007; Scheidat *et al.*, 2000). Whales from this population migrate to two likely discrete feeding grounds in the Magellan Strait, Chile (Acevedo *et al.*, 2007), and near the Antarctic Peninsula (Rasmussen *et al.*, 2007; Stevick *et al.*, 2004; Stone *et al.*, 1990).

The history of exploitation of Breeding Stock G is poorly known before the beginning of modern whaling (post-1900). During this period, whales were taken only in wintering grounds and migratory routes off Panama, Colombia, Ecuador, Peru, Chile and near the Archipelagos of Galapagos and Juan Fernandez (Townsend, 1935). The total pre-1900 catch is unknown, but estimated to be at least 4,000 whales in the 1800s (Smith *et al.*, 2006). Modern whaling catches in the wintering grounds totaled nearly 2,300 whales (Allison, 2006). Most catches were taken from land bases on the coast of Chile, but about 330 whales were taken by a factory ship that followed migrating whales to Peru, Ecuador and Colombia (Findlay, 2000). These catches were of relatively small scale (an annual average of 37 whales from 1908–68 and no more than 270 catches in a single year). Whaling in the feeding grounds was of greater magnitude, with nearly 15,000 whales taken between 1905 and 1961 (Findlay, 2000). The peak of catches occurred between 1905 and 1915, when over 11,000 whales were captured (Allison, 2006).

During the Comprehensive Assessment of Southern Hemisphere humpback whales, it has been customary to use a sex- and age-aggregated dynamic production model, with a surplus production function of the Pella-Tomlinson form, to assess population status. The reason more complex population models have not been employed is the relatively coarse nature of much of the available data, and in particular the methods used to allocate catches on the feeding grounds in the far south to stocks which breed in lower latitudes (fig. 1 in IWC, 2011). Earlier applications of this approach estimated the two parameters of the population model (the intrinsic growth rate *r* and pre-exploitation abundance *K*) by having the population trajectory hit a recent survey estimate of absolute abundance, and also replicate the trend shown by some time series of population estimates (for example from coastal surveys) or alternatively fixing *r* at a value estimated for another breeding stock. Examples of this approach may be found in Findlay *et al.* (2000), Findlay and Johnston (2001) and Johnston *et al.* (2001).

The approach was subsequently refined and cast in a Bayesian framework to provide improved indications of the precision of the estimates obtained (Zerbini, 2004, in an application to Breeding Stock A). This refinement has since been applied to assessments of other breeding stocks, making allowance also in some cases for the use of abundance estimates from surveys of the feeding grounds, and also mixing of breeding stocks on these grounds (Johnston and Butterworth, 2005a; 2005b; Johnston and Butterworth, 2006).

This paper documents this Bayesian methodology, as recently adapted and agreed (IWC, 2011), and then applies it to Breeding Stock G.

Due to the difficulty in allocating past catches to breeding stocks, applications of this assessment methodology generally considers sensitivity of results to three different options for this allocation of catches south of 40°S (allocation of catches north of 40°S being straightforward by comparison). The 'core' and the 'fringe' options can be

considered as two extremes, the former reflects the smallest longitudinal range (and hence lowest catches) considered certain to correspond to the breeding stock under consideration, while the latter covers the greatest range considered plausible. The 'overlap' option defines longitudinal ranges for the stock under consideration and the two on either side. Eighty percent of the catch from the central of these three ranges and 10% of the catches from the ranges on either side, are assumed to reflect removals from the stock being assessed.

DATA AND METHODS

The data related to Breeding Stock G
Historic catch data
The historic catch records for Southern Hemisphere humpback whales, which have recently (May 2006) been updated by Cherry Allison (IWC Secretariat) can be conveniently separated into catches taken north of 40°S and those taken south of that latitude. The updated catch records for whales caught north of 40°S are reported in Table 1a. Catches south of 40°S are reported in Table 1b for the 'core', 'fringe' and 'overlap' models as recently re-defined (IWC, 2011). The fringe catch series, together with the differences in the core and overlap catches compared to the fringe model catches are shown in Fig. 1. Table 1b also reports catches taken off the Falkland Islands which are used in a sensitivity test.

The longitudinal boundaries that correspond to the hypotheses above for apportionment of the catch are as follows for Breeding Stock G:

Core: 50°W–100°W
Fringe: 50°W–100°W + 50% of catches from 100°W–120°W

The overlap series consists of 80% of the catch from the range of 60°W–110°W associated with the original naïve catch allocation model (as described in IWC, 1998) for Breeding Stock G, and 10% from each of the ranges associated with the naïve catch allocation models for Breeding Stocks A and F (the two stocks to the east and west of Breeding Stock G) which are taken to be 20°W–60°W and 110°W–170°W respectively (see fig. 8 of IWC, 2011).

Absolute abundance data
The estimates of recent absolute stock abundance for Breeding Stock G which are considered here are reported in Table 2a, along with their associated estimated CVs. The estimate of 6,504 provided by Felix *et al.* (2011) for 2006, which relates to the breeding area, was selected by the recent humpback workshop (IWC, 2011) as being the most reliable, and is used here for the Reference Case (RC). This estimate is based on the Petersen estimator. A test of sensitivity to using the Felix *et al.* (2011) Jolly-Seber abundance estimate of 5,456 for 2006 is also conducted. The other two abundance estimates are for the feeding areas – these being the most recent IDCR/SOWER estimate of 3,310 whales (in 1996) provided by Branch (2011) from the third circumpolar set of IDCR/SOWER surveys, and 6,991 whales (in 2000) provided by Hedley *et al.* (2001) from a joint CCAMLR-IWC survey that year. These estimates are used under the assumption that each is unbiased and representative of the complete population.

Trend information
Abundance estimates which can be used to provide information on trends for Breeding Stock G are available

Table 1a

Catches taken north of 40°S for Southern Hemisphere humpback whales for BS G (C. Allison, pers. comm.). There are no catches after 1973.

Year	Catch	Year	Catch
1900	0	1937	28
1901	0	1938	6
1902	0	1939	7
1903	0	1940	0
1904	0	1941	0
1905	0	1942	0
1906	0	1943	0
1907	0	1944	0
1908	16	1945	0
1909	44	1946	15
1910	62	1947	19
1911	92	1948	5
1912	86	1949	6
1913	45	1950	5
1914	195	1951	26
1915	30	1952	27
1916	15	1953	29
1917	15	1954	106
1918	23	1955	7
1919	24	1956	10
1920	21	1957	5
1921	21	1958	0
1922	19	1959	3
1923	16	1960	2
1924	34	1961	3
1925	248	1962	4
1926	277	1963	1
1927	40	1964	35
1928	36	1965	143
1929	26	1966	58
1930	33	1967	0
1931	53	1968	3
1932	21	1969	1
1933	11	1970	0
1934	13	1971	0
1935	31	1972	0
1936	18	1973	0

from IDCR/SOWER sightings surveys in the feeding grounds, as reported by Branch (2011). Those of Branch's estimates which have been corrected to represent comparable areas for the three circumpolar sets of surveys are used. These are listed in Table 2b.

The population dynamics model and Bayesian estimation framework
The population dynamics model described here is an aggregated (over both sex and age) model. The basic population dynamics equation is:

$$N_{y+1} = N_y + rN_y\left(1 - \left(N_y / K\right)^\mu\right) - C_y \tag{1}$$

where

N_y is the total population size at the start of year y, and is set equal to K in years prior to the onset of exploitation;

K is the pre-exploitation population size;

r is the intrinsic or maximum growth rate (i.e. the maximum per capita rate the population can achieve when its size is very low);

μ is set at 2.39, which fixes the MSY level, MSYL = 0.6K, as conventionally assumed by the IWC Scientific Committee; and

C_y is the total catch (in terms of number of animals) in year y.

Table 1b

Catches taken south of 40°S for Southern Hemisphere humpback whales for Breeding Stock G. Catches have been apportioned from feeding area catches advised by C. Allison (pers. comm.). These catches correspond to either the core, fringe or overlap catch allocation hypotheses (IWC, 2011). Catches off the Falkland Islands used in sensitivity 8 are also given. There are no catches after 1973.

Year	Core	Fringe	Overlap	Falklands	Year	Core	Fringe	Overlap	Falklands
1900	0	0	0	0	1937	0	0	24	0
1901	0	0	0	0	1938	0	0	0	0
1902	0	0	0	0	1939	0	0	0	0
1903	1	1	1	0	1940	0	0	4	0
1904	0	0	18	0	1941	0	0	1	0
1905	23	23	47	0	1942	0	0	0	0
1906	498	498	422	0	1943	0	0	0	0
1907	366	366	419	0	1944	0	0	6	0
1908	1,246	1,246	1,182	9	1945	0	0	24	0
1909	1,481	1,481	1,524	94	1946	0	0	3	0
1910	2,527	2,527	2,668	70	1947	0	0	2	0
1911	2,039	2,039	2,204	17	1948	0	0	3	0
1912	976	976	1,035	8	1949	0	0	7	0
1913	1,038	1,038	895	7	1950	271	271	317	0
1914	656	656	609	12	1951	0	0	6	0
1915	219	219	337	0	1952	0	0	4	0
1916	21	21	55	0	1953	0	0	27	0
1917	69	69	61	0	1954	0	0	37	0
1918	81	81	72	0	1955	14	14	53	0
1919	181	181	153	0	1956	600	666	551	3
1920	149	149	129	0	1957	59	90	73	0
1921	0	0	1	0	1958	52	52	1	52
1922	189	189	188	0	1959	201	282	218	0
1923	96	96	90	0	1960	88	88	348	6
1924	102	102	108	0	1961	1,167	1,265	1,201	1
1925	163	163	156	0	1962	278	321	269	32
1926	88	88	82	0	1963	0	0	0	0
1927	3	3	2	2	1964	0	0	0	0
1928	16	16	14	0	1965	0	0	53	0
1929	0	0	5	0	1966	0	0	24	0
1930	1	1	12	0	1967	0	0	11	0
1931	0	0	2	0	1968	0	0	0	0
1932	0	0	2	0	1969	0	0	0	0
1933	0	0	13	0	1970	0	0	0	0
1934	0	0	6	0	1971	0	3	0	0
1935	0	0	5	0	1972	0	0	0	0
1936	0	0	11	0	1973	0	0	0	0

The following prior distributions for r and an estimate of absolute abundance are considered:

(i) If the assessment model is fit to data with information on trend (from the IDCR/SOWER surveys) then $r \sim U[0, 0.106]$. If no such trend data are used in the model fit, then $r \sim$ posterior derived from an assessment of Breeding Stock A (Zerbini *et al.*, 2011). The upper boundary of 0.106 corresponds to the maximum growth rate given a range of life history parameters observed for several humpback whale populations (Clapham *et al.*, 2006).

(ii) $\ln N_Y^{X,obs} \sim U[\ln \hat{N}_Y^{X,obs} - 4CV_Y, \ln \hat{N}_Y^{X,obs} + 4CV_Y]$

where $N_Y^{X,obs}$ refers to the absolute abundance estimate for a humpback breeding stock X in year Y.

Note that the prior distribution from which target absolute abundance estimates ($N_Y^{X,obs}$) are drawn at random is uniform on a natural logarithmic scale, corresponding to the conventional approach in the IWC Scientific Committee to make distributional assumptions for abundance estimates transformed in this way. The upper and lower bounds are set by adding and subtracting four times the CV of the survey estimate.

For each of n_1 replicates, values of $N_Y^{X,obs}$ and r are drawn from their prior distributions. A bisection method is used to calculate K such that the model value of N_Y^X is identical to the randomly drawn value $N_Y^{X,obs}$.

For each of the n_1 replicates, using the generated r and calculated K values, a negative log likelihood is then computed by comparing the population model output to observed data – these including the recent absolute abundance estimate, preferably from the breeding grounds (see Table 2a). The components of the negative log likelihood are calculated as follows for Breeding Stock G.

For the absolute abundance estimate, the negative log-likelihood component is:

$$-\ln L = \frac{1}{2CV_Y^2}\left(\ln \hat{N}_Y^{X,obs} - \ln N_Y^X\right)^2 \qquad (2)$$

where

$\hat{N}_Y^{X,obs}$ and CV_Y are the survey estimate of population size at the start of year Y for breeding stock X and the associated survey-sampling based coefficient of variation, and
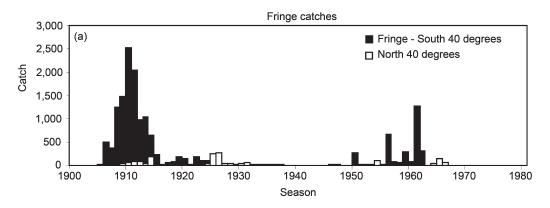
N_Y^X is the model value for population size at the start of year Y for this breeding stock.
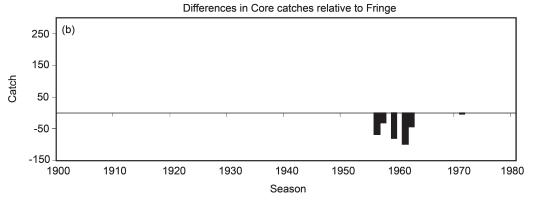
It is assumed that the abundance estimates used to provide trend information are log-normally distributed about their model values:

$$I_y^X = q^X N_y^X e^{\varepsilon_y} \qquad (3)$$
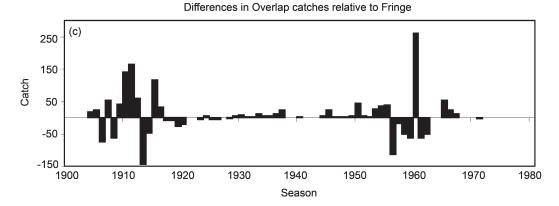
where

I_y^X is the survey-based abundance index for year y,

Fig. 1. The fringe catch series together including the catches North of 40° is shown in (a), with the differences in the core and overlap catches compared to the fringe model catches shown in (b) and (c) respectively.

q^X is the constant of proportionality between that index and the absolute abundance of breeding stock X,

N_y^X is the model value for population size at the start of year y for breeding stock X, and

ε_y is from $N(0,\sigma_X^2)$.

The contribution of these data to the negative of the log-likelihood function is then given by:

$$-\ln L = n^X \ln \sigma_x + \frac{1}{2\sigma_x^2} \sum_y \left(\ln I_y^x - \ln q^x - \ln N_y^x \right)^2 \qquad (4)$$

with the total negative log-likelihood thus being:

$$-\ln L = n^X \ln \sigma_x + \frac{1}{2\sigma_x^2} \sum_y \left(\ln I_y^x - \ln q^x - \ln N_y^x \right)^2$$

$$+ \frac{1}{2CV_Y^2} \left(\ln \hat{N}_Y^{X,obs} - \ln N_Y^x \right)^2 \qquad (5)$$

The Bayesian approach applied also requires integration over priors for σ_X, the standard deviation of the residuals about the data used for trend information, and the constant of proportionality q^X. Taking these priors to be respectively

Table 2a

Recent absolute abundance estimate considered for assessments of Breeding Stock G.

Year	Abundance estimate	Area	Source
2006	6,504 (CV=0.21)	Breeding	Felix *et al.* (2011): Petersen[#]
2006	5,456 (CV=0.21)[@]	Breeding	Felix *et al.* (2011): Jolly-Seber[#]
1996	3,310 (CV=0.21)	Feeding	Branch (2011)[*]
2000	6,991 (CV=0.32)	Feeding	Hedley *et al.* (2001)[+]

[@]As no CV was provided for the Jolly-Seber estimate, the same CV is assumed as for the Petersen estimate. [#]Survey areas covered the wintering grounds off the coast of Ecuador, varying slightly amongst years but ranging approximately 01°26'S, 80°50'W to 02°10'S, 81°05'W. [*]Survey area south of 60° and between 110° W-50°W. [+]Survey area around the Antarctic Peninsular of approximately between 60°S-65°S and between 70°W-50°W.

Table 2b

Abundance estimates for Breeding Stock G from the IDCR-SOWER sighting surveys for comparable areas (Branch, 2011) that are used to provide information on population trend.

Year	Abundance estimate
1982	1,452 (CV=0.65)
1989	2,817 (CV=0.38)
1996	3,310 (CV=0.21)

proportional to σ_X^{-3} and uniform in log-space allows the integration over these parameters to be performed analytically, with the resultant negative logarithm of the marginal likelihood of the same form as equation (5) with σ_X and q^X each substituted by their maximum likelihood estimates for the values of r and under consideration [see proof in Geromont and Butterworth (1995) from a generalisation of the results of Walters and Ludwig (1994)]:

$$\hat{\sigma}_X = \sqrt{1/n\sum_y\left(\ln I_y^X - \ln q_y^X - \ln \hat{N}_y^X\right)^2} \qquad (6)$$

where

n is the number of data points in the abundance series, and

q^X is the constant of proportionality for the index of abundance which is substituted by its maximum likelihood estimate:

$$\ln \hat{q}^X = 1/n\sum_y\left(\ln I_y^x - \ln N_y^x\right) \qquad (7)$$

The negative log likelihood is then converted into a likelihood value (L). The integration of the prior distributions of the parameters and the likelihood function then follows the Sampling-Importance-Resampling (SIR) algorithm presented by Rubin (1988) as described in Zerbini (2004). For a vector of parameter values θ_i, the likelihood of the data associated with this vector of parameters (L) as described above is calculated and stored. This process is repeated until an initial sample of n_1 $\theta_i s$ is generated. This sample is then re-sampled with replacement n_2 times with probability equal to weight w_j, where:

$$w_j = \frac{L\left(\theta_j / data\right)}{\sum_{k=1}^{n_1} L\left(\theta_k / data\right)} \qquad (8)$$

The resample is thus a random sample of size n_2 from the joint posterior distribution of the parameters (Rubin, 1988).

The value of n_1 (the original number of replicates) used is 500,000 and of n_2 (number of re-samples) is 5,000. Convergence is checked by examining results for different random number seeds, and ensuring that no sample contributes more than 0.001% of the total weight.

N_{min} constraint

It has been suggested (Jackson *et al.*, 2006) that genetic constraints be used in the assessment of humpback whale populations, given the observed genetic diversity. This idea had previously been discussed by Baker and Clapham (2004), who advocated that demographic and genetic approaches should be integrated to better describe whale population dynamics. In the application of this assessment

methodology to Breeding Stock G, this approach has been used to determine how low the minimum population size of the humpback whales from Breeding Stock G could have been, given their observed genetic diversity. Baker and Clapham (2004) suggested that the number of extant haplotypes sampled in a population which has undergone a recent bottleneck provides an absolute minimum bound on the number of mature females in the population at the time of the bottleneck. Jackson *et al.* (2006) suggested a correction factor of four to scale the number of sampled haplotypes (minimum number of mature females) to the total (1+) population size when the population was at its minimum. The rationale behind this correction factor is that the number of haplotypes must be multiplied by two to account for the male population (assuming an even sex ratio) and also by a further two to correct the minimum effective population size to a lower estimate of total population size [as described by Nunney (1993) and used in Roman and Palumbi (2003)]. Jackson *et al.* (2006) point out that this correction factor is normally too small, but nevertheless remains useful to provide a minimum population number.

In the application to Breeding Stock G, the minimum population size () of 108 whales (in any year) is set as such a constraint. This is four times the total number of mtDNA haplotypes (27) observed for this breeding stock (Rosenbaum *et al.*, 2006).

The methodology as currently agreed and applied in the Scientific Committee then excludes any population trajectory which violates this constraint (see also comments in the final section of this paper). Generally this has the effect of excluding some of the trajectories with higher r values.

Reference case and sensitivity tests

The Reference Case (RC) assessment uses inputs and makes assumptions as follows:

(a) The fringe catch allocation hypothesis is assumed for the historic catch.
(b) The Felix *et al.* (2011) Petersen estimate of 6,504 in 2006 (from the breeding grounds) is used as the absolute abundance estimate.
(c) The trend information from IDCR/SOWER surveys as reported in Branch (2011) is used.
(d) The prior for r is $r \sim U[0, 0.106]$.

The following sensitivities are explored:

Sensitivity 1: The most recent abundance estimate from the IDCR/SOWER information (3,310 in 1996, Branch, 2011) is used in place of the Felix *et al.* (2011) Petersen estimate for the recent absolute abundance estimate (though note that the Branch estimate corresponds to a slightly different longitudinal range to that which the fringe catch allocation prescription applies).

Sensitivity 2: The abundance estimate from Hedley *et al.* (2001) is used in place of the Felix *et al.* (2011) Petersen estimate for the recent absolute abundance estimate.

Sensitivity 3: The Petersen estimate for abundance is replaced by the open population estimate of 5,456 for 2006 provided by Felix *et al.* (2011). This estimate is based on a Jolly-Seber analysis with a survival rate adjusted to be the same for transient and non-transient animals.

Sensitivity 4: The model fits to the RC breeding ground abundance estimate as well as to the two abundance estimates from the feeding grounds in Table 2a. This involves adding further terms to equation (2).

Sensitivity 5: The model fits to the Felix *et al.* (2011) Petersen estimate only, and replaces data with trend information by an informative *r* prior taken from the *r* posterior for Breeding Stock A (as estimated by Zerbini *et al.*, 2011).

Sensitivity 6: The core catch allocation hypothesis replaces the fringe hypothesis.

Sensitivity 7: The overlap catch allocation hypothesis replaces the fringe hypothesis.

Sensitivity 8: The catches made off the Falkland Islands (reported in Table 1b) are included in the total catch history.

Note that the purpose of many of these sensitivities is to provide a broad indication of how dependent key outputs are to certain inputs. Thus, for example, sensitivities 1 and 2 are intended to provide only some sense of the possible range for recent abundance, rather that to suggest that these abundance estimates from the feeding grounds correspond exactly to the breeding stock being modelled.
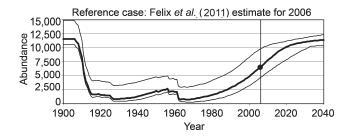
Projections
In this study, the population is projected into the future (to 2040) assuming that no future catches are taken.

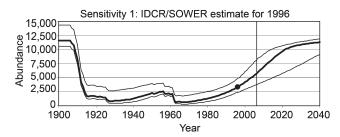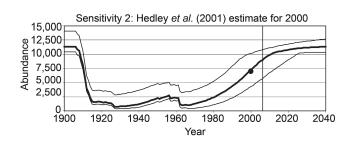## RESULTS AND DISCUSSION

Table 3 reports results for the RC and eight sensitivity tests. Posterior medians with the 5th and 95th percentiles (in parentheses) are reported. These results show that for Breeding Stock G there is very little sensitivity of results to the alternate historic catch series used (sensitivity tests 6–8). There is far greater sensitivity to the estimates of current abundance selected, with the Felix *et al.* (2011) Petersen estimate producing results which show Breeding Stock G to be currently around $0.56K$, while the use of the IDCR/SOWER current abundance estimate for the feeding grounds (sensitivity 1) produces results which are less optimistic, with a current abundance estimate of $0.49K$. The use of the Hedley *et al.* (2001) estimate (sensitivity 2) from the feeding grounds produces a more optimistic result however, with a current abundance estimate of $0.78K$. When all three recent estimates of abundance are fit instead of only one (sensitivity 4), precision is improved with the width of the 90% PI on current depletion reduced by about one third. Excluding the trend data, and using a prior for *r* from the posterior from Breeding Stock A (sensitivity 5) produces similar results to those for the RC. For all nine models explored here, the lowest population size N_{min} does not drop below the bound deduced from genetics data of 108 for any of the trajectories simulated.

Table 3

Breeding Stock G model parameter estimates. Posterior medians with the 5th and 95th percentiles (in parentheses) are reported. An N_{min} constraint >108 is imposed for all models. Headers in *italics* reflect choices differing from those for the Reference Case.

	Reference Case	Sensitivity 1	Sensitivity 2
r prior	$r\sim$ U[0, 0.106]	$r\sim$ U[0, 0.106]	$r\sim$ U[0, 0.106]
Historic catch	Fringe	Fringe	Fringe
Recent abundance	Felix *et al.* (2011): Petersen	*IDCR/SOWER*	*Hedley et al. (2001)*
Trend information	IDCR/SOWER	IDCR/SOWER	IDCR/SOWER
r	0.063 [0.023; 0.093]	0.062 [0.024; 0.092]	0.068 [0.029; 0.099
K	11,584 [10,590; 14,878]	11,617 [10,610; 14,363]	11,382 [10,424; 14,123]
N_{min}	731 [238; 2959]	608 [266; 1758]	760 [414; 2843]
N_{2006}	6,579 [4,698; 9,817]	5,736 [3,757; 8,135]	9,004 [5,699; 10,798]
N_{min}/K	0.063 [0.022; 0.198]	0.052 [0.028; 0.125]	0.067 [0.040; 0.200]
N_{2006}/K	0.561 [0.376; 0.833]	0.493 [0.281; 0.723]	0.783 [0.450; 0.987]
N_{2020}/K	0.885 [0.575; 0.988]	0.829 [0.422; 0.979]	0.972 [0.692; 1.000]
N_{2040}/K	0.994 [0.818; 1.000]	0.990 [0.660; 1.000]	0.999 [0.913; 1.000]

	Sensitivity 3	Sensitivity 4	Sensitivity 5
r prior	$r\sim$ U[0, 0.106]	$r\sim$ U[0, 0.106]	*r~ post (A)*
Historic catch	Fringe	Fringe	Fringe
Recent abundance	*Felix et al. (2011): Jolly-Seber*	*RC + Sen 1 + Sen2*	Felix *et al.* (2011): Petersen
Trend information	IDCR/SOWER	IDCR/SOWER	*None*
r	0.062 [0.023; 0.090]	0.065 [0.036; 0.093]	0.066 [0.025; 0.089]
K	11,619 [10,655; 14,813]	11,500 [10,594; 13,162]	11,480 [10,695; 14,457]
N_{min}	586 [204; 2334]	647 [283; 1615]	655 [244; 3150]
N_{2006}	5,504 [3,885; 7,970]	6,557 [5,210; 8,162]	6,539 [4,634; 9,361]
N_{min}/K	0.051 [0.019; 0.163]	0.056 [0.026; 0.123]	0.057 [0.023; 0.211]
N_{2006}/K	0.468 [0.317; 0.695]	0.568 [0.419; 0.742]	0.557 [0.375; 0.813]
N_{2020}/K	0.820 [0.496; 0.961]	0.893 [0.660; 0.981]	0.891 [0.570; 0.984]
N_{2040}/K	0.989 [0.734; 1.000]	0.995 [0.991; 1.000]	0.996 [0.784; 1.000]

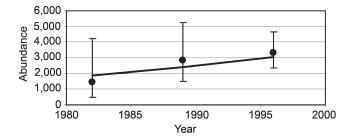|	Sensitivity 6	Sensitivity 7	Sensitivity 8
r prior	$r\sim$ U[0, 0.106]	$r\sim$U[0, 0.106]	$r\sim$U[0, 0.106]
Historic catch	*Core*	*Overlap*	*Fringe+Falklands*
Recent abundance	Felix *et al.* (2011): Petersen	Felix *et al.* (2011): Petersen	Felix *et al.* (2011): Petersen
Trend information	IDCR/SOWER	IDCR/SOWER	IDCR/SOWER
r	0.063 [0.024; 0.092]	0.062 [0.025; 0.092]	0.063 [0.027; 0.092]
K	11,569 [10,601; 14,589]	11,887 [10,866; 14,956]	11,785 [10,804; 14,475]
N_{min}	719 [242; 2922]	749 [252; 2831]	720 [246; 2662]
N_{2006}	6,573 [4,630; 9,694]	6,620 [4,678; 9,742]	6,634 [4,723; 9,579]
N_{min}/K	0.062 [0.023; 0.197]	0.062 [0.023; 0.189]	0.061 [0.023; 0.185]
N_{2006}/K	0.561 [0.376; 0.824]	0.550 [0.370; 0.808]	0.554 [0.378; 0.810]
N_{2020}/K	0.887 [0.585; 0.986]	0.877 [0.575; 0.985]	0.881 [0.593; 0.985]
N_{2040}/K	0.994 [0.820; 1.000]	0.994 [0.820; 1.000]	0.994 [0.832; 1.000]

Fig. 3. The RC model fit to the abundance data used to provide trend information, as obtained from the IDCR/SOWER sightings surveys. The dots show the abundance estimates from the surveys, together with their 90% confidence intervals, and the curve shows the model posterior medians. Note that the model estimates reflect the population abundance estimates adjusted by the estimated constant of proportionality q.

$0.97K$ by 2030. Slightly less optimistic projection estimates are obtained for sensitivity 1 (fitting to the IDCR/SOWER recent abundance estimate) for which the stock is estimated to reach $0.83K$ by 2020 and $0.95K$ by 2030, and more optimistic estimates for sensitivity 2 (fitting to the Hedley *et al.*, 2001 estimate) which reflects near full recovery ($0.97K$) by 2020.

POSSIBLE FURTHER DEVELOPMENTS

This paper has documented the Bayesian methodology currently agreed for use in the Scientific Committee for Southern Hemisphere humpback stock status evaluation, and applied that to data for Breeding Stock G. There are some ways in which the method could be technically improved and/or further sensitivities explored, some specific to the Breeding Stock G case:

(a) when using feeding ground estimates of abundance, evaluate abundance for longitudinal ranges which correspond to the basis used to develop the historical catch series for higher latitudes;

(b) take account of the CVs for the abundance estimates in Table 2b used to provide information on trend, rather than assume these to be the same (the σ_X parameter);

(c) integrate over a prior distribution for the μ parameter (or equivalently MSYL) rather than fix this at a single value;

(d) apply alternative Bayesian population model approaches (note that the approach applied here corresponds to the 'Backwards' variant of the various approaches that have been applied in assessment of the Bering-Chukchi-Beaufort bowhead whale population – see for example Punt and Butterworth (1999)); and

(e) change to a population model which disaggregates by sex and age.

A number of these would require considerably extra work, e.g. the further survey abundance estimates required under (a), or the incorporation of additional variance and more complex integration over q^X and σ_X needed for (b). Thus given the relatively coarse nature of the abundance and trend information available, and that it seems unlikely that these factors listed would greatly impact results, such additional analyses do not seem an immediate priority, and reflect a level of sophistication perhaps more appropriate to the stage when the population model is refined to incorporate age- and sex-structure as suggested in (e). A higher priority is further information on trend, as the data available do not update the prior used for r appreciably (see Fig. 4).

In the longer term a multi-stock procedure will be need, in particular so that proper account is taken of the co-

Fig. 2. Estimated population trends for Breeding Stock G, with projected trajectories which assume a continued zero catch. The posterior medians with 90% probability interval envelopes are illustrated. The vertical lines at 2006 separate assessments from projections. The scenarios shown are the Reference Case and Sensitivities 1, 2 and 5 (which explore fitting to the IDCR/SOWER recent estimate as the recent abundance data and to the Hedley *et al.*(2001)) estimate from the feeding grounds, and then omitting the IDCR/SOWER trend data by using an informative prior for the intrinsic growth rate parameter r obtained from the assessment of Breeding Stock A (Zerbini *et al.*, 2011). The single dots show the recent abundance estimate fitted by each model which replaces the Felix *et al.* (2011) Petersen estimate of recent abundance by those from the IDCR/SOWER surveys or from Hedley *et al.* (2001) for the feeding grounds for sensitivities 1–2.

Fig. 2 shows the population abundance trends for the RC and for sensitivities 1, 2 and 5. These plots also show projected trajectories which assume a continued zero catch. The posterior medians together with the 90% PI envelopes are illustrated. Fig. 3 shows the RC model fit to the abundance data provided by the IDCR/SOWER sightings estimates to inform on trend. It is evident that the model is able to fit adequately to both the Felix *et al.* (2011) recent Petersen abundance estimate (Fig. 2), as well as to the abundance data series from the feeding grounds provided by the IDCR/SOWER survey sightings (Fig. 3).

Assuming future zero catches, the RC estimates the breeding stock (in median terms) to reach $0.89K$ by 2020 and
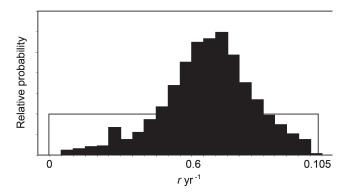
Fig. 4. Comparison of the uniform prior distribution (horizontal line) used for the intrinsic growth rate parameter *r* and the associated posterior (histogram) for the RC model for Breeding Stock G.

variances that arise for the different catch allocation hypotheses because catches taken to come from one breeding stock need then to be precluded from coming also from neighbouring breeding stock.

In the application here, the N_{min} constraint played no role. However in instances where it does so, greater care needs to be exercised as this constraint effectively modifies the independent prior distributions for *r* and absolute abundance by introducing covariance, and raises Borel's paradox difficulties (Brandon *et al.*, 2007).

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