SC/57/SH16

A BAYESIAN ASSESSMENT OF BREEDING STOCKS B, C AND G OF SOUTHERN HEMISPHERE HUMPBACK WHALES USING A PRIOR FOR GROWTH RATE FROM ANALYSES FOR STOCKS D AND E

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ABSTRACT

Bayesian assessment of breeding stocks B, C and G of the Southern Hemisphere humpback whales are presented. These assessments incorporate a prior for the maximum growth rate r derived from similar assessments for breeding stocks D and E. This is the first time an assessment for breeding stock B has been attempted. Results show current abundance estimates for breeding stocks B and G are low (less than 0.15*K*), whilst the current abundance estimate for breeding stock C much further recovered at 0.79*K*. Projections under a zero continued harvesting strategy estimate breeding stock C to be fully recovered by 2020, whilst breeding stocks B and G will be fully recovered only by about around 2030.

WORDS: HUMPBACK WHALES, BAYESIAN ASSESSMENT

INTRODUCTION

Initial assessments of breeding populations of Southern Hemisphere humpback whales (*Megaptera novaengliae*) were presented at the 2000 IWC Scientific Committee meeting (Findlay *et al.* 2000; Findlay and Johnston 2001). These assessments were updated the following year (Johnston *et al.* 2001), and covered five of the seven distinct Southern Hemisphere breeding populations, coupled with three sets of hypotheses as to how historic catches from mixtures of these breeding populations on the high latitude feeding grounds are to be allocated to such breeding populations; results were shown to be relatively insensitive across these hypotheses. Johnston *et al.* (2001) further reported results for models for two of the breeding populations (stocks D and E) for which the models were fitted to CPUE trends as well as to relative abundance indices. Johnston and Butterworth (2004) updated assessments of breeding stocks A and C. All the assessments mentioned above were based on an age-aggregated production model approach and maximum likelihood estimates.

Bayesian stock assessments of three of the breeding stocks (stocks B – West Africa, C –East Africa and G – West South America) of Southern Hemisphere humpback whales are presented here. This is the first time a stock assessment for breeding stock B has been attempted. The estimation procedure used here has been described in Zerbini (2004), where the status of breeding stock A was assessed using a Bayesian approach. The authors of this paper have thus extended this assessment approach to several of the other breeding stocks of Southern Hemisphere humpback whales. One of the inputs required for this modelling approach is a prior for the maximum growth rate parameter *r*. The authors here use a prior for *r* given by the posterior distribution for *r* that resulted from an assessment of breeding stocks D and E (Johnston and Butterworth 2005). The assessment of the breeding stocks D and E involved fitting a population model that allows for mixing of these two populations in the feeding areas. Data available for fitting that model included absolute abundance estimates, relative abundance trends and CPUE series from the breeding stocks, as well as abundance information from the feeding grounds.

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METHODS

Data

Historic Catch data

The historic catch record for Southern Hemisphere humpback whales can be separated into two categories: catches taken north of 40^0 S and catches taken south of 40^0 S. The updated catch record of whales caught north of 40^0 S is reported in Table 1a of Johnston and Butterworth (2005). Two alternate catch records exist however, for the catches south of 40^0 S. The first is here termed the "KP" record. The second, here termed the "CA" record, includes both different data sources and new information available in 2005. These two catch series are reported in Tables 1b and c in Johnston and Butterworth (2005). Recent attempts by Allison and by Findlay have been made to update both these catch records. In particular, following the 2004 meeting of the IWC Scientific Committee, the catches from the $60\text{-}70^0$ W longitude band (including those from the South Shetland and "West Antarctica") have been assigned to breeding stock G. In this study, the "KF" series is used for the "base-case" and a sensitivity analysis for the "CA" series is run. These catches have been apportioned to each of the seven hypothesised feeding areas that are associated with breeding stocks A-G under what has previously been termed the "naïve" model (this simply means that each breeding stock is assumed to correspond to a single feeding area), although as stated above, the catches from the $60\text{-}70^0$ W longitude band have been assigned to the G stock, whereas previously they were assigned to the A stock.

Recent absolute abundance estimates

The estimates of recent absolute abundance for each of the breeding stocks examined here are reported in Table 1.

Breeding stock B

For breeding stock B, an abundance estimate of 1259 (CV=0.32) for year 2002 is provided by Rosenbaum *et al.* (2004). This estimate is based on aerial surveys, and is considered an initial estimate by the authors. Rosenbaum *et al.* (2004) also report that this estimate is an "uncorrected and conservative abundance estimate", and provide an upper range of a corrected estimate of 2798. A sensitivity test to this upper range of the corrected estimate is explored here.

Breeding stock C

For breeding stock C, the authors calculated a total abundance estimate for 2003 as follows:

- An estimate for sub-stock C1 for 2003 of 5811 (CV=0.15) is provided by Findlay *et al.* (2004). This estimate is based on a vessel-based line transect survey off Mozambique.
- An estimate for sub-stock C3 for 1994 of 2532 (CV=0.27) is provided by Best *et al.* (1996). This estimate was based on a yacht-based line transect survey in water off south Madagasgar.
- Using the trend in raw sightings per hour of observation made during shore-based surveys of the C1 migration past Cape Vidal over the period 1988-2002 (reported here in Table 2, Findlay pers. commn), a rate of increase over this period of 9.9% per annum can be calculated. Using this ROI, the C3 estimate of 2352 in 1994 is extrapolated up to 6172 in 2003. A total abundance estimate for breeding stock C in 2003 is thus calculated by adding these C1 and C3 estimates together (5811+6172), which gives a total of 11983 whales for 2003.
- A value of σ =0.20 is assumed for this estimate in the modeling analyses here (if the extrapolation of the C3 abundance estimate were to be taken as error free, a CV of 0.16 would follow; this seems unrealistically low, so has been inflated to 0.20, corresponding to a CV of 0.33 associated with the extrapolation).

Note that although there are no abundance data for what is termed C2, the number of these whales is likely to be small and they are in any case most likely a component of the C1 and/or C3 estimates. However, it should be noted that both the C1 and C3 estimates used here are probably negatively biased by incomplete survey coverage of the breeding grounds. For example, no survey has been carried out over the west coast of Madagascar.

Breeding stock G

For breeding stock G, a preliminary abundance estimate of 1922 (CV=0.43) whales for the year 1997 is provided by Felix and Haase (1999).

"Trend" data

The only stock for which any abundance trend data are available is stock C. Table 2 reports a series of densities of whales sighted (whales per hour) during shore-based surveys off Cape Vidal for years 1988-1991 and 2002 (Findlay pers. commn).

The population dynamics models

The population dynamics model used for the updated assessments of this paper is a lumped (sex- and age-structured) model. The basic population dynamics equation is:

$$N_{t+1} = N_t + rN_t\left(1-\left(N_t / K\right)^{\mu}\right) - C_t \qquad (1)$$

where N_t 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;

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 Scientific Committee; and

C_t is the total catch (in terms of number of animals) in year *t*.

Bayesian estimation framework

Priors

Prior distributions were defined for the following parameters:

i) $r \sim r$ posterior reported in Johnston and Butterworth (2005)

ii) $\ln N_Y^{X,obs} * \sim U[\ln N_Y^{X,obs} - 4CV,\ \ln N_Y^{X,obs} + 4CV]$

where $N_Y^{X,obs} *$ is the absolute abundance estimate for breeding stock *X*, in year *y*.

Note that the prior distribution on *r* (based on the posterior from breeding stocks D and E) is bounded by zero (negative rates of growth are biologically implausible) and 0.126 (this corresponds to the maximum growth rate for the species as evaluated by Clapham *et al.* 2001). The prior distribution from which target abundance estimates ($N_Y^{X,obs} *$) are drawn at random is uniform on a natural logarithmic scale. The lower and upper bounds are set by four times the CV.

For each of n_1 simulations, 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 estimate of $\hat{N}_Y^X$ is identical to the randomly drawn value $N_Y^{X,obs} *$.

For each n_1 simulation, using the *r* and calculated *K* value, a negative log likelihood is then calculated by comparing the population model to observed data - these being the target abundance estimates from the breeding grounds (see Table 1), and in the case of breeding stock C, also relative abundance trend data (see Table 2). The components of the negative log likelihood are calculated as follows:

For breeding stock C:

It is assumed that the observed abundance trend index is log-normally distributed about its expected value:

$$I_y^X = q^X \hat{N}_y^X e^{\varepsilon_y} \qquad (2)$$

where

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

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

$\hat{N}_y^X$ is the model estimate of population size at the start of year *y* for breeding stock *X*, and

ε_y is from $N(0,\sigma_X^2)$.

The contributions of the data to the negative of the log-likelihood function are then given by:

$$-\ln L = \sum \left(n^X \ln \sigma^X + \frac{1}{2{\sigma^X}^2}\sum_y \left(\ln I_y^X - \ln q^X - \ln \hat{N}_y^X\right)^2\right) + \frac{1}{2CV^2}\left(\ln N_Y^{X,obs} - \ln \hat{N}_Y^X\right)^2 \qquad (3)$$

The σ parameter is the residual standard deviation which is estimated in the fitting procedure by its maximum likelihood value:

$$\hat{\sigma}_X = \sqrt{1/n\sum_y \left(\ln I_y^X - \ln q^X - \ln \hat{N}_y^X\right)^2} \qquad (4)$$

where

n is the number of data points in the abundance series (5 in this case), and

q is the index abundance constant of proportionality, estimated by its maximum likelihood value:

$$\ln \hat{q}^X = 1/n\sum_y \left(\ln I_y^X - \ln \hat{N}_y^X\right) \qquad (5)$$

(This is a short cut to avoid integrating over priors for the *q*'s and σ^2's, and in fact corresponds to the assumption that these priors are uniform in log-space and proportional to σ^{-3} respectively (Walters and Ludwig 1994)).

<u>For breeding stocks B and G:</u>

There are no relative abundance trend data for these stocks, only single absolute abundance estimates. The negative log-likelihood is thus simply:

$$-\ln L = \frac{1}{2CV^2}\left(\ln N_Y^{X,obs} - \ln \hat{N}_Y^X\right)^2 \qquad (6)$$

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 θ_i s is generated. This sample is then resampled with replacement n_2 times with probability equal to weight w_j, where

$$w_j = \frac{L\ (\theta_j / data)}{\sum_{j=1}^{n1} L\ (\theta_j / data)} \qquad (7)$$

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 (original number of simulations) used is 500 000 and of n_2 (number of resamples) is 5000. Convergence was tested by examining results for different random number seeds, and by ensuring that no sample contributed more than 0.001% of the total weight.

Projections

The populations are projected into the future under a continuation of a zero harvesting strategy.

Sensitivity analyses

For each breeding stock, two sensitivity analyses are explored here. The first is where the "CA" historic catch series is used (instead of the "KF" series). The second relates to fitting to an "upper" bound for the absolute abundance estimate. The following values were used:

i) Breeding stock B: $N_{2002}^{obs} = 2798$ - the upper bound of the corrected estimate reported by Rosenbaum *et al*. (2004).

ii) Breeding stock C: $N_{2003}^{obs} = 14577$ - this estimate is calculated by adding the C1 2003 estimate of 5811 (Findlay *et al.* 2004), to the estimates extrapolated to 2003 (assuming ROI=9.9% pa) from both the Best *et al.* (1996) C3 1994 yacht based line transect survey off south Madagascar and the Rosenbaum *et al.* (2000) C3 1999 photographic capture-recapture estimate from Antongil Bay (NE Madagascar).

iii) Breeding stock G: $N_{1997}^{obs} = 3367$ - this corresponds to the upper 95% CI reported by Felix and Haase (1999).

RESULTS AND DISCUSSION

The results of the base case and sensitivity analyses are reported in Tables 3a, b and c for breeding stocks B, C and G respectively. For all three breeding stocks, there appears to be very little sensitivity to the alternate historic catch series. Results for the sensitivity analyses for higher observed absolute abundance estimates show more optimistic appraisals of current resource status. For example, the base case estimate for current population size (N_{2004}) for breeding stock B is 1428 (0.086K) whales. For this sensitivity test, this increases to 3167 (0.190K) whales. The trend information available for stock C allows for an update of the prior for the maximum growth rate parameter r; the lower tail is truncated, with the lower 5th percentile increased to 0.10.

Base case estimates of current population abundance for breeding stocks B and G are low (less than 0.15K), whereas the corresponding base case estimate of current population abundance for breeding stock C is far healthier, at 0.79K.

Figures 1-3 illustrate the posterior distributions for r, K, N_{2004}/K and N_{2020}/K for breeding stocks B, C and G respectively. Figure 4 shows the base case model fit (in posterior median terms) to the relative abundance data for breeding stock C..

Projections

Estimated population trends for the base case scenario are illustrated in Figure 5. Under a zero continued future harvesting strategy, by 2020, breeding stock B is estimated to reach about 0.47K and breeding stock G about 0.64K. Both populations are projected to reach K by around 2030. The situation for breeding stock C is more optimistic, with the model estimating full recovery by 2020.

Comparisons to previous analyses

No stock assessments have previously been reported for breeding stock B. A recent assessment for breeding stock C using maximum likelihood estimation (Johnston and Butterworth 2004) showed somewhat more optimistic results for this stock – the current population was estimated to be at 0.96K compared to the updated estimate of 0.79K reported in this paper. A previous assessment for breeding stock G (Johnston *et al.* 2001) estimated a far lower K (8421) compared to the estimate presented in this paper of 16725. The current estimate of abundance relative to K (N_{2004}/K = 0.14) is far less optimistic than the N_{1999}/K estimate of 0.34 reported in Johnston *et al.* (2001). The reason is a re-allocation of catches in the latest revisions from the feeding ground for breeding stock A to that for breeding stock G; thus the cumulative historic catch for breeding stock G is now 15441 ("KP" series) compared to the 14607 for the analyses of Johnston *et al.* (2001).

REFERENCES

Best, P.B., Sekiguchi, K., Rakotonirina, B. and Ventresca, G. 1996. The distribution and abundance of humpback whales off Southern Madagascar, August-September 1994. *Rep, int Whal. Commn* 46: 323-332.

Clapham, P., Robbins, J., Brown, M., Wade, P. and Findlay, K. 2001. Appendix 5, Report of the sub-committee on the Comprehensive Assessment of Whale stocks – In-depth Assessments. *J. Cet. Res. Manag.* 3 (suppl): 196-197.

Felix, F. and Haase, B. 1999. Preliminary estimation of the south eastern Pacific humpback whale stock. Document SC/51/CAWS2.

Findlay, K.P., Cunningham, C.L. and D.S. Butterworth. 2000. A first step towards a preliminary assessment of Southern Hemisphere Humpback whales. Document SC/52/IA5 submitted to the IWC Scientific Committee, 23pp.

Findlay, K.P. and S.J. Johnston. 2001. Further steps towards a preliminary assessment of Southern Hemisphere humpback whales (breeding populations A and G). J. Cetacean Res. Manage. 3(Suppl.) 193-194.

Findlay, K.P., Meyer, M., Elwen, S., Kotze, D., Johnson, R., Truter, P., Uamusse, C., Sitoe, S., Wilke, C., Kerwath, S., Swanson, S., Staverees, L. and van der Westhuizen, J. 2004. Distribution and abundance of humpback whales, *Megaptera novaengliae*, off the coast of Mozambique, 2003. Document SC/56/SH12 submitted to the IWC Scientific Committee, Sorrento, Italy.

Johnston, S.J., Butterworth, D.S. and K.P. Findlay. 2001. Further results from a preliminary assessment of Southern Hemisphere Humpback whales. Document SC/53/IA20 submitted to the IWC Scientific Committee, 31pp.

Johnston, S.J., and Butterworth, D.S. 2004. Updated Age-aggregated production modelling assessments of the Southern Hemisphere Humpback whales breeding stocks A and C. Document SC/56/SH20 submitted to the IWC Scientific Committee, Sorrento, Italy. 20pp.

Johnston, S.J., and Butterworth, D.S. 2005. A Bayesian assessment of the west and east Australia breeding populations (stocks D and E) of Southern Hemisphere humpback whales. Document SC/57/SH15 submitted to the IWC Scientific Committee, Ulsan, South Korea, 25pp.

Rosenbaum, H.C., Strindberg, S. and Ersts, J. 2004. Initial estimates of abundance and distribution of humpback whales on their wintering grounds of Gabon (southeastern Atlantic Ocean, Area B) based on aerial surveys. Paper SC/56/SH2 presented to the IWC Scientific Committee, Sorrento, Italy, June 2004.

Rosenbaum, H.C., Razafindrakoto, Y., Ersts, P. and Ventresca, G. 2000. A preliminary population estimate for humpback whales from the Antongil Bay, Madagascar wintering ground in the southwestern Indian Ocean. Paper SC/52/IA10 presented to the IWC Scientific Committee.

Rubin, D.B. 1988. Using the SIR algorithm to simulate posterior distributions. Pp. 395-402. In. J.M. Bernado, M.H. DeGroot, D.V. Lindlley and A.F.M Smith (eds). *Bayesian Statistics 3: Proceedings of the Third Valencia International Meeting.* June 1-5, 1987. Clarendon Press, Oxford. 805pp.

Walters, C. and Ludwig, D. 1994. Calculation of Bayes posterior probability distributions for key population parameters. *Can. J. Fish. Aquat. Sci.* 51: 713-722.

Zerbini, A.N. 2004. Status of the Southern Hemisphere humpback whale breeding stock A: preliminary results from a Bayesian assessment. Paper SC/56/SH17 presented to the IWC Scientific Committee, Sorrento, Italy, June 2004.18pp.

Table 1
Recent absolute abundance estimates used for each breeding btock.

Breeding Stock	Year	Abundance estimate	Source
B	2002	1259 (CV=0.32)	Rosenbaum *et al.* 2004.
C	2003	11983 (CV=0.20)*	Findlay pers. commn; Johnston and Butterworth (this paper)
G	1997	1922 (CV=0.43)	Felix and Haase (1999)

* CV value assumed by authors – see text

Table 2
Breeding stock C: Relative abundance trend (Findlay pers. commn).

Year	Whales per hour
1988	0.97
1989	0.56
1990	1.06
1991	1.13
2002	3.47

Table 3a

Breeding stock **B** model parameter estimates. Posterior medians with the 5th and 95th percentiles (in parentheses) are reported.

	Base Case: “KF” historic catch series	Sensitivity: “CA” historic catch series	Sensitivity to recent abundance estimate: N_{2002}= 2798
r	0.117 [0.086, 0.125]	0.117 [0.086, 0.125]	0.117 [0.086, 0.125]
K	16455 [16105, 18135]	16466 [16116, 18201]	16453 [16104, 18177]
N_{2004}	1428 [1158, 1718]	1427 [1156, 1718]	3167 [2569, 3809]
N_{2004}/K	0.086 [0.068, 0.105]	0.086 [0.068, 0.105]	0.190 [0.152, 0.232]
N_{2020}/K	0.466 [0.273, 0.593]	0.466 [0.272, 0.593]	0.807 [0.560, 0.898]

Table 3b

Breeding stock **C** model parameter estimates. Posterior medians with the 5th and 95th percentiles (in parentheses) are reported.

	Base Case: “KF” historic catch series	Sensitivity: “CA” historic catch series	Sensitivity to recent abundance estimate: N_{2003}= 14710
r	0.120 [0.098, 0.126]	0.120 [0.097, 0.126]	0.120 [0.097, 0.126]
K	15373 [15160, 16293]	15355 [15147, 16283]	15379 [15162, 16402]
N_{2004}	12235 [10588, 14260]	12210 [10555, 14289]	13517 [12456, 14956]
N_{2004}/K	0.790 [0.681, 0.924]	0.789 [0.679, 0.927]	0.874 [0.797, 0.964]
N_{2020}/K	0.998 [0.992, 1.000]	0.998 [0.992, 1.000]	0.999 [0.996, 1.000]

Table 3c

Breeding stock **G** model parameter estimates. Posterior medians with the 5th and 95th percentiles (in parentheses) are reported.

	Base Case: “KF” historic catch series	Sensitivity: “CA” historic catch series	Sensitivity to recent abundance estimate: N_{1997}= 3367
r	0.111 [0.070, 0.125]	0.111 [0.07, 0.125]	0.112 [0.074, 0.125]
K	16725 [16119, 19516]	16716 [16133, 19485]	16674 [16118, 19075]
N_{2004}	2365 [1754, 2644]	2364 [1742, 2644]	4160 [3254, 4623]
N_{2004}/K	0.139 [0.098, 0.162]	0.139 [0.098, 0.162]	0.245 [0.185, 0.283]
N_{2020}/K	0.636 [0.314, 0.785]	0.638 [0.321, 0.784]	0.870 [0.563, 0.941]

Figure 1
Breeding stock **B** base case posterior probability distributions of various parameters and management related quantities.

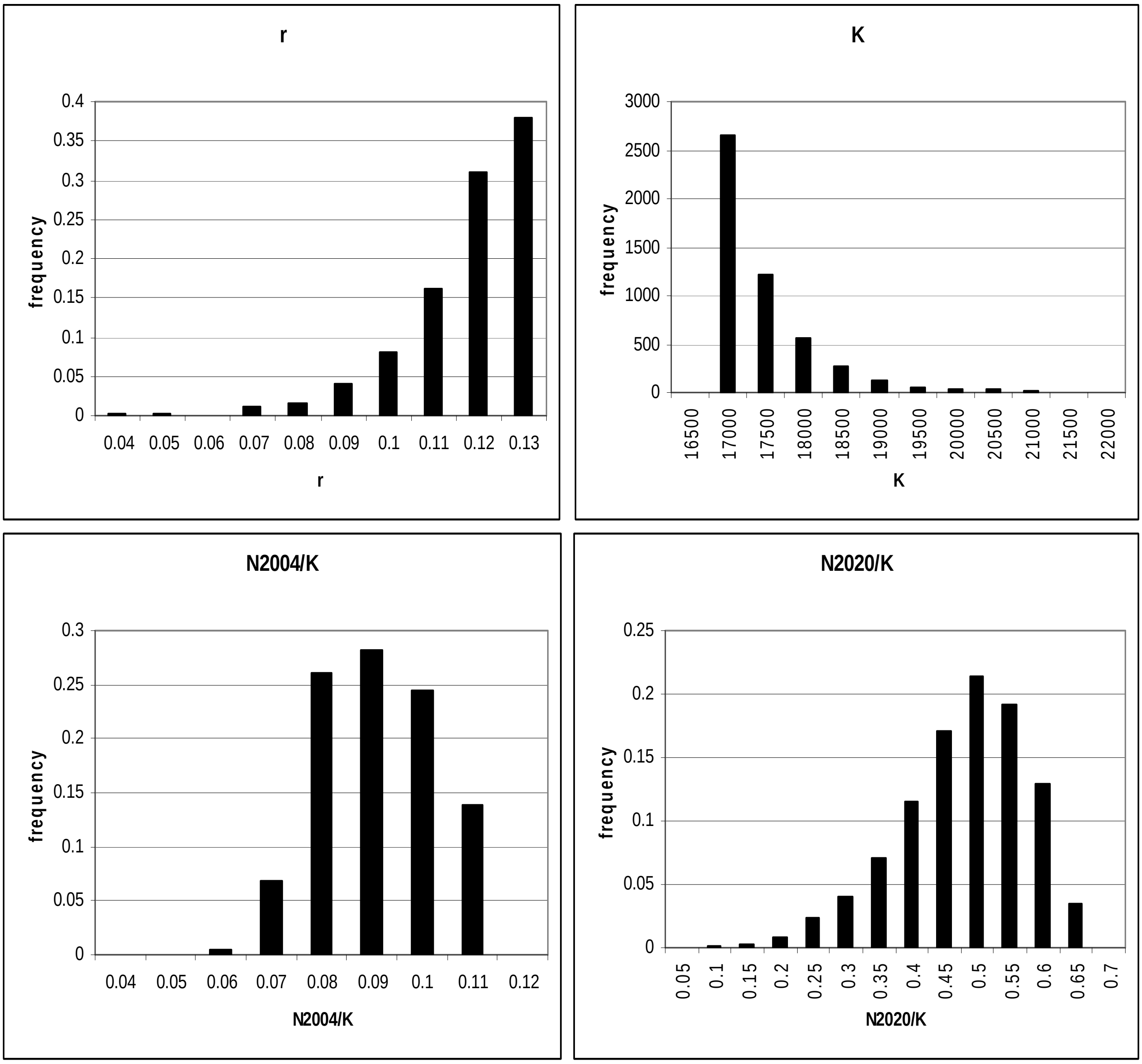

Figure 2
Breeding stock **C** base case posterior probability distributions of various parameters and management related quantities.

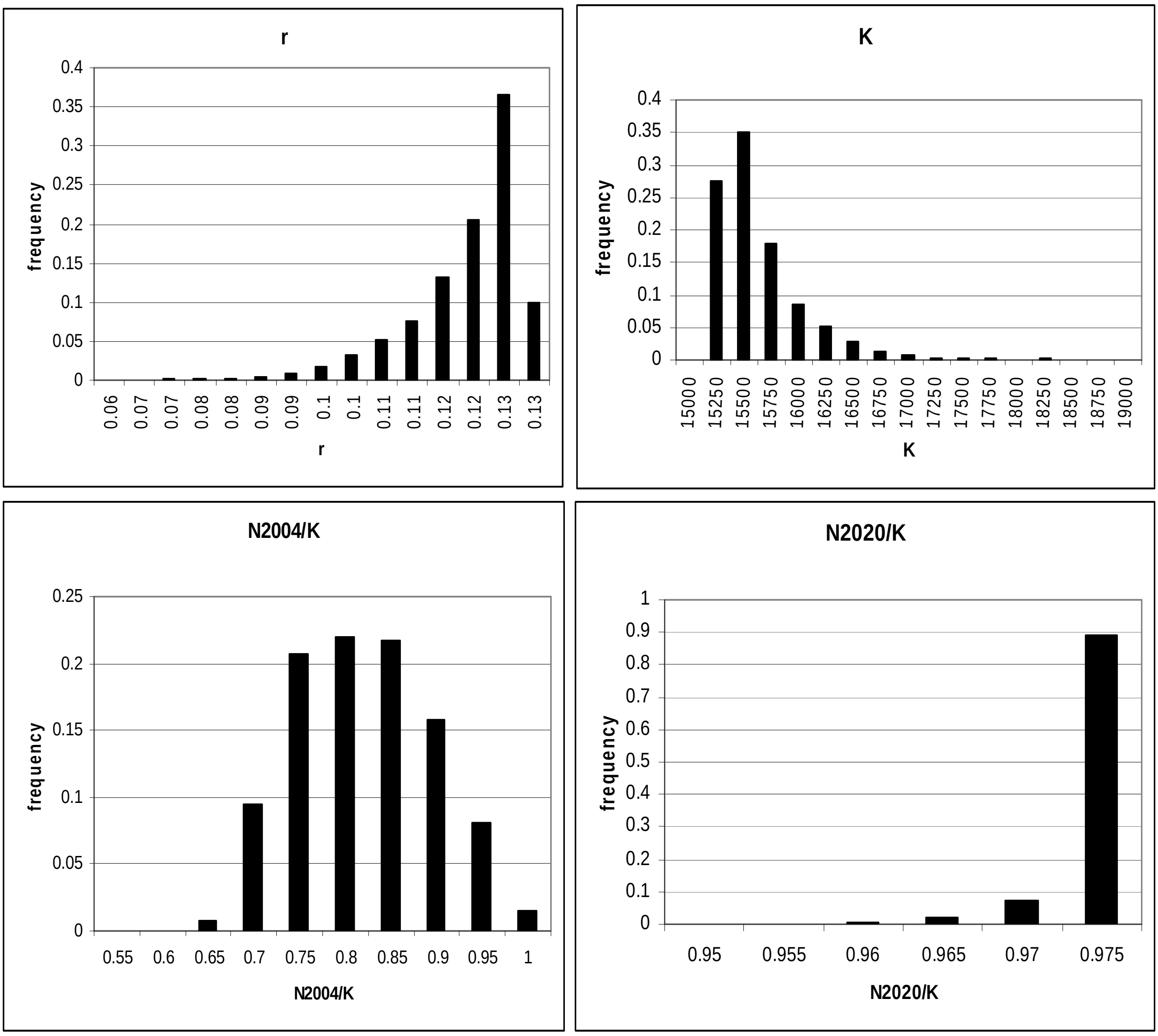

Figure 3
Breeding stock **G** base case posterior probability distributions of various parameters and management related quantities.

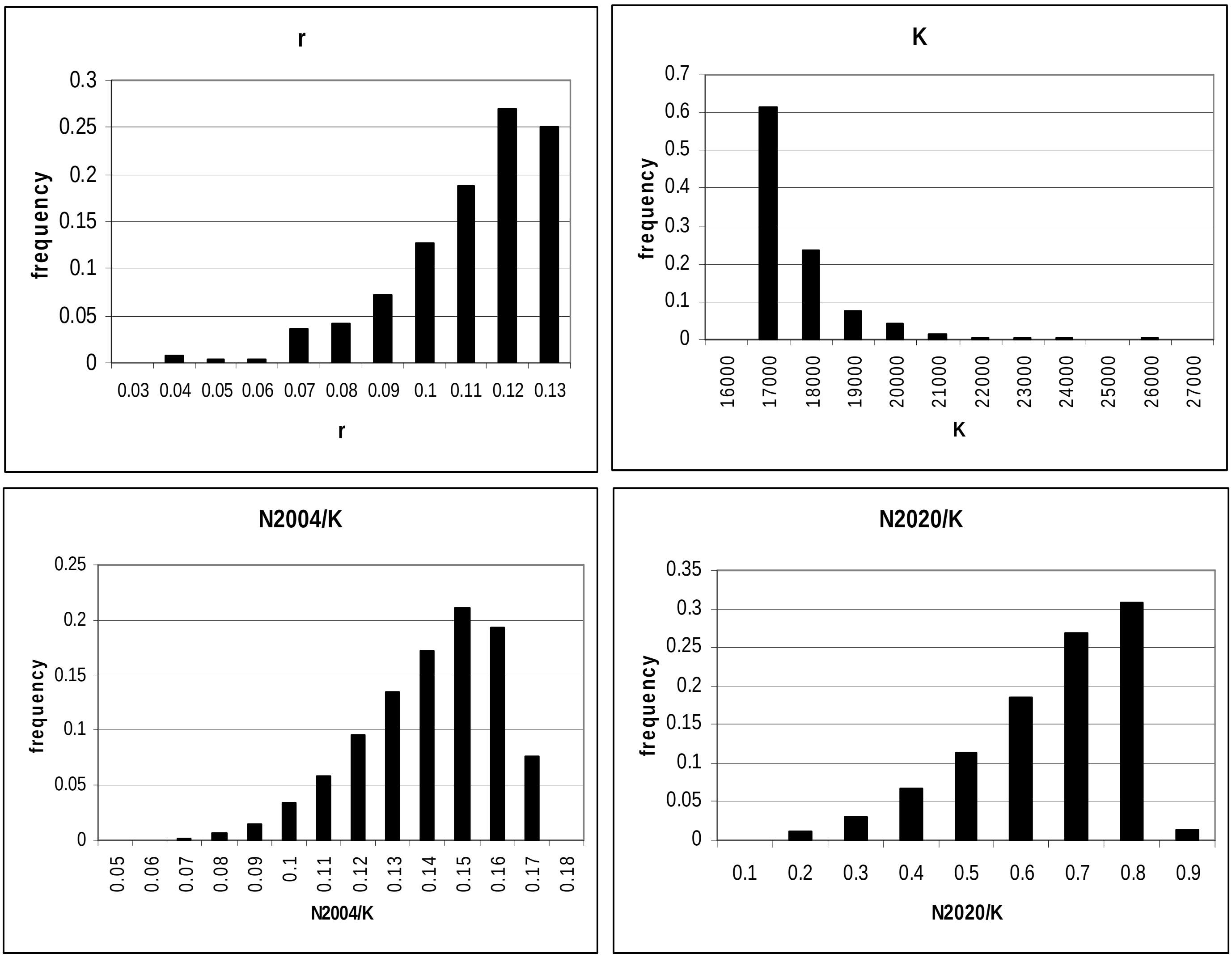

Figure 4

Breeding stock **C** model fit to the relative abundance data. Posterior medians are plotted to reflect the model results.

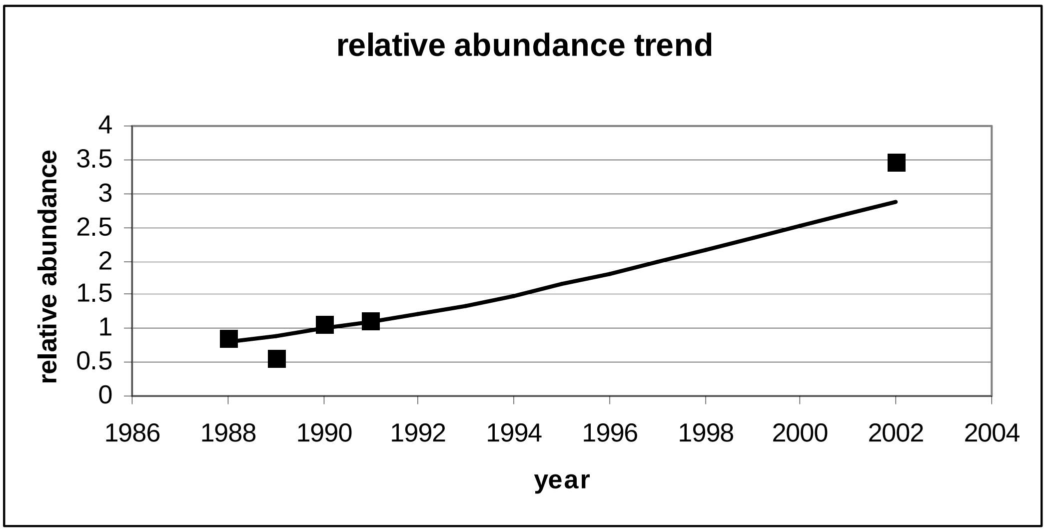

Figure 5

Base case model estimated population trends, with projected trajectories assuming a continued zero harvesting strategy. The posterior medians with the 90% probability intervals are illustrated (note that the lower percentile is sometimes not evident as it is very close to the median.) The vertical dashed lines are at 2004, after which the projections assume zero catch.