UPDATED ASSESSMENTS OF SOUTHERN HEMISPHERE HUMPBACK WHALE BREEDING STOCK C AND ITS COMPONENT SUB-STOCKS

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ABSTRACT

Bayesian stock assessment results for a mixed model breeding sub-stocks C1 and C2+3 are presented. The modelling approach allows mixing on the feeding grounds and fits to various data sources, including capture-recapture data from both sub-stocks. A baseline case which inputs all capture-recapture data directly suggests posterior median 2006 abundances for each sub-stock of a little more than 7000, with C1 at about 85% and C2+3 at about 55% of their pristine levels. These results are intended to be illustrative only, and the variety of choices available for the various model inputs require further discussion by the IWC Scientific Committee.

KEYWORDS: HUMPBACK WHALES, BAYESIAN ASSESSMENT

INTRODUCTION

This document reports updated stock assessment results for breeding stock C, which consists of two sub-stocks:

C1: east coast of South Africa and Mozambique

C2+3: C2 refers to whales wintering around the Comoros Islands, whereas C3 refers to whales wintering in the coastal waters of Madagascar.

There are several sources of trend data available for sub-stock C1, whereas no direct measurements of trend from the breeding area for sub-stock C2+3 are available. Trend data (from the IDCR/SOWER surveys) from the combined feeding area for both sub-stocks are available. Although historic catches from the breeding grounds are available for each sub-stock, the historic catches from the feeding grounds (south of 40°S) are for both sub-stocks combined. The mixed modelling approach reported here allows for mixing of the C1 and C2+3 sub-stocks on the feeding grounds, but no mixing between the breeding grounds. Further analyses could be performed which would allow for mixing between the sub-stocks on the breeding grounds.

The two sub-stocks are assessed jointly, with r^{C1}, r^{C2+3}, K^{C1} and K^{C2+3} the estimable parameters of the model fit to various data sources from both the sub-stocks.

DATA

Historic Catch data

There are two sources of historic catch data that relate to breeding sub-stocks C1 and C2+3.

i) Catches north of 40°S

C1 — those from "SCape", "Natal", and "Mozamb" from Allisons's database (Allison pers. commn) [note the total for each category is SCape =68, Natal=10330 and Mozamb=3995]

C2+3 — those from "W Indian Ocean" from Allisons's database.

ii) Catches south of 40°S

This series refers to catches recorded for 10°E-60°E and thus includes both C1 and C2+3 whales. Table 1a and Figure 1 show these three historic catch series.

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Absolute abundance data
The absolute abundance data used in these analyses are presented in Table 1b. For breeding stock C1, an estimate of 5965 (CV = 0.17) for the 2003 season has been provided by Findlay *et al.* (in press). For breeding stock C2+3, upper and lower abundance estimates are suggested in Cerchio *et al.* (2008); these were obtained using the MARK program applied to capture-recapture data from both photo-ID and genotypic data. These estimates are 6737 (CV=0.31) and 7715 (CV=0.24) for the year 2002. These estimates are for sub-stock C3 – primarily for Antongil Bay in the northeast of Madagascar.

Trend information
Several sources of direct information on trend are available for sub-stock C1. These are reported in Table 2, and include:

i) Cape Vidal sightings per unit effort data for the 1988-2002 period (Findlay and Best 2006). These are obtained from shore-based surveys of northwards-migrating humpback whales at Cape Vidal, South Africa each year between 1988 and 1991, and in 2002.
ii) Four sets of relative abundance trend data from the Durban whaling ground (reported in Best 2003); these are:
   - Catch per unit effort 1920-1928
   - Catch per unit effort 1954 – 1963 (i.e. until protection)
   - Catcher sightings per unit effort 1969-1975
   - Aircraft sightings per unit effort 1954-1975.
iii) CPUE data from Durban for 1910-12 (Olsen 1914).

IDCR/SOWER survey estimates (adjusted for areal comparability) provided by Branch (2006) are available for feeding ground III (10ºE-60ºE) for 1978, 1987 and 1993. These trend data clearly relate to both C1 and C2+3 animals, and are also shown in Table 2.

Capture-recapture data
The capture-recapture data used here are reported in Cerchio *et al*. (2008a and b). These consist of both photo-ID and genotypic mark-recapture data from Antongil Bay (C3) (Cerchio *et al.* 2008a), as well as photo-ID mark-recapture data for C1 (Cerchio *et al.* 2008b). The data span the period 2000-2006 and are reproduced in Appendix 1. Only the data for which the recapture site is the same as the capture site are used in these analyses, as no mixing between the feeding grounds is taken into account.

General
In previous assessments (e.g. Johnston and Butterworth 2007) of sub-stock C1, it became apparent that it was not possible that the impact of humpback catches alone could account for the large drop in Durban CPUE for the 1920-28 period. Best (pers. commn) suggests that there was a switch to other species during this period, so that more of the effort was devoted to the offshore whaling ground at the end of this time series than the beginning. The authors therefore essentially gave this series no weight in the analyses that follow, estimating only an effective catchability coefficient to facilitate plots showing trend comparisons.

METHODS

Mixed modelling approach

Breeding stock population dynamics

$$N_{y+1}^{B,C1} = N_y^{B,C1} + r^{C1} N_y^{B,C1}\left(1-(\frac{N_y^{B,C1}}{K^{C1}})^{\mu}\right) - C_y^{C1} \quad (1)$$

$$N_{y+1}^{B,C2+3} = N_y^{B,C2+3} + r^{C2+3} N_y^{B,C2+3}\left(1-(\frac{N_y^{B,C2+3}}{K^{C2+3}})^{\mu}\right) - C_y^{C2+3} \quad (2)$$

where

$N_y^{B,C1}$ is the number of whales in the breeding population C1 at the start of year *y*,

$N_y^{B,C2+3}$ is the number of whales in the breeding population C2+3 at the start of year *y*,

r^{C1} is the intrinsic growth rate (the maximum per capita the population can achieve, when its size is very low) for breeding population C1,

r^{C2+3} is the intrinsic growth rate for breeding population C2+3,

K^{C1} is the carrying capacity of breeding population C1,

K^{C2+3} is the carrying capacity of breeding population C2+3,

μ is the "degree of compensation" parameter; this is set at 2.39, which fixes the MSY level to MSYL = 0.6*K*, as conventionally assumed by the IWC Scientific Committee,

C_y^{C1} is the total catch (in terms of animals) in year *y* from breeding population C1, and

C_y^{C2+3} is the total catch (in terms of animals) in year *y* from breeding population C2+3.

Feeding stocks

Mixing of the breeding populations in the feeding area (defined by 10ºE – 60ºE) yields:

$$N_y^F = N_y^{B,C1} + N_y^{B,C2} \tag{3}$$

which we take to reflect complete mixing of sub-stocks C1 and C2+3 in the feeding area.

Catches

$$C_y^{C1} = C_y^{C1,B} + C_y^{C1,F} \tag{4}$$

$$C_y^{C2+3} = C_y^{C2+3,B} + C_y^{C2+3,F} \tag{5}$$

where

$C_y^{C1,B}$ are the catches of animals in year *y* in the C1 breeding area,

$C_y^{C1,F}$ are the catches of animals in year *y* from the C1 sub-stock in the feeding area,

$C_y^{C2+3,B}$ are the catches of animals in year *y* in the C2+3 breeding area, and

$C_y^{C2+3,F}$ are the catches of animals in year *y* from the C2+3 sub-stock in the feeding area.

Table 1a provides the $C_y^{C1,B}$ and $C_y^{C2+3,B}$ breeding area catches, but only the combined catch ($C_y^F = C_y^{C1,F} + C_y^{C2+3,F}$) for the feeding area. To split this feeding ground catch, it is assumed that the catches each year are proportional to their relative abundances in the feeding area (given that complete mixing is assumed). Thus the breakdown of feeding ground catches is calculated as follows:

$$C_y^{C1,F} = C_y^F \frac{N_y^{C1,B}}{\left(N_y^{C1,B} + N_y^{C2,B}\right)} \quad \text{and} \tag{6}$$

$$C_y^{C2+3,F} = C_y^F \frac{N_y^{C2+3,B}}{\left(N_y^{C1,B} + N_y^{C2+3,B}\right)} \quad (7)$$

Bayesian estimation framework

Priors

Prior distributions are defined for the following parameters:

i) r^{C1} and $r^{C2+3} \sim U[0, 0.106]$ (as there are appreciable trend data to inform on r)

ii) $\ln \tilde{\tilde{N}}_{target}^{C1,obs} * \sim U[\ln N_{target}^{C1,obs} - 4CV,\ \ln N_{target}^{C1,obs} + 4CV]$ and

iii) $\ln \tilde{\tilde{N}}_{target}^{C2+3,obs} * \sim U[\ln N_{target}^{C2+3,obs} - 4CV,\ \ln N_{target}^{C2+3,obs} + 4CV]$.

The uninformative r^{C1} and r^{C2+3} priors were bounded by zero (negative rates of growth are biologically implausible) and 0.106 (this corresponds to the maximum growth rate for the species agreed by the IWC Scientific Committee (IWC, 2007)). The prior distributions from which target abundance estimates ($\tilde{\tilde{N}}_{target}^{C1,obs} *$, $\tilde{\tilde{N}}_{target}^{C2+3,obs} *$) are drawn at random are uniform on a natural logarithmic scale. The lower and upper bounds are set by four times the CV. For these *N* targets, the Findlay *et al.* (in press) estimate is used for C1, and the lower Cerchio *et al.* (2008a) estimate is used for C2+3.

Using the randomly drawn vector of values of $\tilde{\tilde{N}}_{target}^{C1,obs} *$, $\tilde{\tilde{N}}_{target}^{C2+3,obs} *$, r^{C1} , and r^{C2+3}, a downhill simplex method of minimization is used to calculate K^{C1} and K^{C2} such that the model estimates of $\hat{\tilde{N}}_{target}^{C1}$ and $\hat{\tilde{N}}_{target}^{C2+3}$ are identical to the randomly drawn values $\tilde{\tilde{N}}_{target}^{C1,obs} *$ and $\tilde{\tilde{N}}_{target}^{C2+3,obs} *$.

For each simulation, using the r^{C1} , r^{C2+3} and calculated K^{C1} and K^{C2+3} values, a negative log likelihood is then computed by comparing the population model to observed data - CPUE data from the breeding grounds for C1, aircraft SPUE data for C1, relative abundance trend data from the breeding grounds for C1 (Cape Vidal data), IDCR/SOWER relative abundance trend data from the combined feeding area, and the capture-recapture data (photo-ID for C1 and photo-ID and genotypic for C3). For some sensitivity scenarios, the capture-recapture data are omitted for C3, and the upper or lower abundance estimates as suggested by Cerchio *et al.* (2008a) are used instead. The components of the negative log likelihood are calculated as follows.

The model treats the CPUE estimates as relative indices of abundance. It is assumed that the observed relative abundance index is log-normally distributed about its expected value:

$$I_y^{C1} = q^A \hat{\tilde{N}}_y^{B,C1} e^{\varepsilon_y} \quad (8)$$

where

I_y^{C1} is either the survey-based relative abundance or CPUE index for year *y* for breeding sub-stock C1,

q^{C1} is the catchability coefficient for that index for breeding sub-stock C1,

$\hat{\tilde{N}}_y^{B,C1}$ is the model estimate of observed population size at the start of year *y* for breeding sub-stock C1, and

ε_y is from $N(0, \sigma_{B,C1}^2)$.

The model also treats the IDCR/SOWER abundance estimates as relative indices as follows. It is assumed that the observed abundance index is log-normally distributed about its expected value:

$$I_y = q_{IDCR}\hat{N}_y^F e^{\eta_y} \quad (9)$$

where

I_y is the IDCR/SOWER abundance estimate for year *y* and the combined feeding area,

q_{IDCR} it the multiplicative bias of the IDCR/SOWER abundance estimate for the combined feeding stock,

$\hat{N}_y^F$ is the model estimate of population size at the start of year *y* in the combined feeding stock, and

η_y is from $N(0,(\sigma_{IDCR})^2)$.

The model treats the aircraft SPUE abundance estimates slightly differently as follows, in particular to take proper account of zero sightings in some years. A Poisson distribution is assumed. The expected number of sightings in year *y* is:

$$\hat{n}_y = q_{SPUE}\hat{\tilde{N}}_y^{B,C1}E_y \quad (10)$$

where

$\hat{\tilde{N}}_y^{B,C1}$ is the model estimate of observed population size at the start of year *y* for breeding sub-stock C1, and

E_y is the aircraft searching effort in year *y*.

The associated "catchability" coefficient is calculated as follows:

$$q_{SPUE} = \frac{\sum_y n_y}{\sum_y \hat{\tilde{N}}_y^{B,C1}.E_y} \quad (11)$$

where

n_y is the observed number of whale sightings in year *y*.

Capture-recapture

$$\tilde{n}_y^A = p_y^A \hat{\tilde{N}}_y^{B,A} \quad (12)$$

$$\hat{m}_{y',y}^A = p_{y'}^A p_y^A \hat{\tilde{N}}_y^A e^{-M(y'-y)} \quad (13)$$

where:

$\tilde{n}_y^A$ = number of animals captured in *A* year *y*

$m_{y',y}^A$ = number of animals captured in *A* in year *y* that were recaptured in *A* in year y'

$\hat{m}_{y',y}^A$ = model predicted number of animals in *A* captured in year *y* that were recaptured in *A* in year y'

M = natural mortality rate (set here to equal 0.03)

p_y^A = probability animal is seen in *A* year *y*

$\hat{\tilde{N}}_y^A$ = estimated observed breeding population size in *A* in year *y*

A = breeding sub-stock C1 or C3

The contributions of the various data to the negative of the log-likelihood function are then given by equation (14) below, where the absolute abundance estimate for C1 ($\tilde{N}_Y^{C1,obs}$) refers to that of Findlay *et al.* (in press):

$$-\ln L = \sum_S \{w_{cpue,S}[n_{CPUE,S}^{C1} \ln \sigma_{CPUE,S}^{C1} + \frac{1}{2\sigma_{CPUE,S}^{C1\ 2}} \sum_y \left(\ln I_{CPUE,S,y}^{C1} - \ln q_{CPUE,S}^{C1} - \ln \hat{\tilde{N}}_y^{B,C1} \right)^2]\} +$$

$$w_{IDCR}[n_{IDCR} \ln \sigma_{IDCR} + \frac{1}{2\sigma_{IDCR}^{\ 2}} \sum_y \left(\ln I_{IDCR,y} - \ln q_{IDCR} - \ln \hat{N}_y^F\right)^2] +$$

$$w_{SPUE}\left[\sum_y \{q_{SPUE} \hat{N} *_y^{B,C1} E_y - n_y \ln(q_{SPUE} \hat{\tilde{N}}_y^{B,C1} E_y)\}\right] +$$

$$[\frac{1}{2CV^2}\left(\ln \tilde{N}_Y^{C1,obs} - \ln \hat{\tilde{N}}_Y^{B,C1}\right)^2] + \sum_{y=y_0}^{y_f-1} \sum_{y'=y+1}^{y_f} [-m_{y',y}^{C1,pho} \ln \hat{m}_{y',y}^{C1,pho} + \hat{m}_{y',y}^{C1,pho}] \quad (14)$$

To this $-ln$L, the following is added:

i) Baseline (where the photo-ID and genotypic capture-recapture data from C3 are both added)

$$+ \sum_{y=y_0}^{y_f-1} \sum_{y'=y+1}^{y_f} [-m_{y',y}^{C3,pho} \ln \hat{m}_{y',y}^{C3,pho} + \hat{m}_{y',y}^{C3,pho}]$$

$$+ \sum_{y=y_0}^{y_f-1} \sum_{y'=y+1}^{y_f} [-m_{y',y}^{C3,gen} \ln \hat{m}_{y',y}^{C3,gen} + \hat{m}_{y',y}^{C3,gen}] \quad (15)$$

or

ii) $$+ [\frac{1}{2CV^2}(\ln \tilde{N}_Y^{C3,obs} - \ln \hat{\tilde{N}}_Y^{B,C3})^2] \quad (16)$$

where this includes (as $\tilde{N}_Y^{C3,obs}$ for Y=2005) either Cerchio *et al's* (2008) suggested upper (7715, CV=0.24) or lower (6737, CV=0.31) abundance estimate obtained from the capture-recapture data.

where

$w_{cpue,S}$ is the weight given to the CPUE data series S,

w_{SPUE} is the weight given to the SPUE data series (for C1),

w_{IDCR} is the weight given to the IDCR/SOWER survey data.

In these analyses all data receive equal weight, except for the 1920-28 Durban CPUE series, which receives a weight of 0.001 (for reasons discussed above).

The σ parameters are the residual standard deviations which are estimated in the fitting procedure by their maximum likelihood values:

$$\hat{\sigma}_{CPUE}^{C1} = \sqrt{1/n \sum_{y} \left(\ln I_{CPUE,y}^{C1} - \ln q_{CPUE}^{C1} - \ln \hat{\tilde{N}}_{y}^{B,C1} \right)^2} \quad \text{for CPUE data} \qquad (12)$$

and

$$\hat{\sigma}_{IDCR} = \sqrt{1/n \sum_{y} \left(\ln I_{IDCR,y} - \ln q_{IDCR} - \ln \hat{N}_{y}^{F} \right)^2} \quad \text{for feeding ground IDCR/SOWER survey data}$$

where

n is the number of data points in the CPUE/survey series, and

q is the multiplicative bias/catchability coefficient, estimated by its maximum likelihood value:

$$\ln \hat{q}^{C1} = 1/n \sum_{y} \left(\ln I_{y}^{C1} - \ln \hat{\tilde{N}}_{y}^{B/F,C1} \right) \qquad (13)$$

(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).)

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 essentially 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 (importance function modified) 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_is is generated. This sample is then resampled with replacement n_2 times with probability equal to weight w_j, where:

$$w_j = \frac{L\ (\theta_j / data)}{\sum_{j=1}^{n1} L\ (\theta_j / data)} \qquad (14)$$

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

Values of n_1 (original number of simulations) are 100 000 and the value of n_2 (number of resamples) is 1000. Tests showed that no sample contributed more than 0.05% of the total weight, and that at least 94% of the resamples were unique values.

Nmin constraints

N_{min} constraints of 248 and 496 whales are imposed for sub-stocks C1 and C2+3 respectively. These values are 4 times the number of haplotypes estimated by Rosenbaum *et al.* (2006) for these sub-stocks.

RESULTS AND DISCUSSION

The model was implemented with the various weights *w* in the log likelihood of equation (14) set to 1, except for the Durban CPUE from 1920 to 1928 which is ignored for the reasons given above. Results for the baseline case are listed in Table 3a, with corresponding population trajectories shown in Figs 2 and 3. These indicate posterior median 2006 abundances for each sub-stock of a little more than 7000, with C1 at about 85% and C2+3 at about 55% of their pristine levels. Results for the sensitivity of replacing the C3 capture-recapture data by the Cerchio *et al.* (2008a) lower estimate are listed in Table 3b, and show

somewhat less optimistic results from those for the baseline case, estimating the posterior median 2006 abundances at around 60% and 70% or their pristine levels for sub-stocks C1 and C2+3 respectively. Pressures of time prevented a further run for Cerchio *et al.*'s preferred upper estimate.

Clearly alternative combinations of inputs are possible; what is shown here is intended to be illustrative, and aid further discussion in the Scientific Committee. This might include consideration of further extensions to the model, such as incorporating photo-ID data on interchange between the two sub-stocks in a similar manner to the approach in Johnston and Butterworth (2008).

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Table 1a: Historic catch series for sub-stocks C1 and C2+3 (Allison, pers. commn).

Season	C1 Breeding grounds	C2+3 Breeding grounds	C1+2+3 Feeding grounds	Season	C1 Breeding grounds	C2+3 Breeding grounds	C1+2+3 Feeding grounds	Season	C1 Breeding grounds	C2+3 Breeding grounds	C1+2+3 Feeding grounds
1900	0	0	0	1926	124	0	0	1952	111	0	208
1901	0	0	0	1927	86	0	0	1953	89	0	66
1902	0	0	0	1928	62	0	0	1954	28	0	50
1903	0	0	0	1929	99	0	4	1955	49	0	28
1904	0	0	0	1930	134	0	150	1956	36	0	4
1905	0	0	0	1931	72	0	2	1957	34	0	66
1906	0	0	0	1932	307	0	38	1958	39	0	120
1907	0	0	0	1933	162	0	54	1959	38	0	152
1908	104	0	0	1934	514	0	554	1960	36	0	72
1909	149	0	0	1935	418	0	1870	1961	40	4	28
1910	632	0	0	1936	300	0	2684	1962	38	1	74
1911	1580	0	0	1937	242	1223	780	1963	38	0	40
1912	2313	25	0	1938	177	1752	0	1964	3	3	48
1913	1805	0	0	1939	200	1240	4	1965	2	1	76
1914	830	0	0	1940	176	0	0	1966	0	0	196
1915	334	0	0	1941	79	0	0	1967	8	8	66
1916	94	0	0	1942	156	0	0	1968	0	0	0
1917	7	0	0	1943	80	0	0	1969	0	0	0
1918	9	0	0	1944	115	0	0	1970	0	0	0
1919	91	0	0	1945	116	0	0	1971	0	0	0
1920	148	0	0	1946	93	0	0	1972	0	0	0
1921	251	0	0	1947	89	0	0	1973	1	0	0
1922	285	0	0	1948	182	0	34	1974	0	0	0
1923	183	0	0	1949	190	1333	396	1975	0	0	0
1924	187	0	0	1950	151	714	74				
1925	372	0	0	1951	103	0	212				

Table 1b

Absolute abundance estimates used in analyses for sub-stocks C1 and C2+3

Breeding sub-stock	**Abundance estimate**	**Year applicable**	**Source**
C1	5965 (CV = 0.17)	2003	Findlay *et al.* (in press)
C2+3 lower	6737 (CV = 0.31)	2005	Cerchio *et al.* (2008a)
C2+3 upper	7715 (CV = 0.24)	2005	Cerchio *et al.* (2008a)

Table 2: Relative abundance trend data for sub-stock C1. [Note that the IDCR/SOWER data relate to the combined feeding area for C1+2+3, and have been adjusted to correspond to the same northern boundary for comparability.]

Year	**Cape Vidal (Findlay and Best 2006)**	**Year**	**IDCR/ Sower**	**Year**	**Olsen (1914)**	**Year**	**CPUE from Durban 1920-28**	**Year**	**CPUE from Durban 1954-63**	**Year**	**CPUE from Durban 1969-75**	**Year**	**Aircraft SPUE and effort from Durban 1954-75**		
													SPUE	**N**	**Effort**
1988	358	**1979**	1043	**1910**	0.9057	**1920**	1.772	**1954**	0.404	**1969**	0.404	**1954**	2.868	5	174.35
1989	249	**1987**	926	**1911**	0.8499	**1922**	3.333	**1955**	0.564	**1970**	0.564	**1957**	0	0	325.49
1990	359	**1993**	2391	**1912**	0.4884	**1923**	1.377	**1956**	0.406	**1971**	0.406	**1958**	0	0	423.40
1991	587					**1924**	1.655	**1957**	0.437	**1972**	0.437	**1959**	0.223	1	448.58
2002	1673					**1925**	1.151	**1958**	0.439	**1973**	0.439	**1960**	0	0	585.00
						1926	0.895	**1959**	0.406	**1974**	0.406	**1961**	1.289	9	698.22
						1927	0.553	**1960**	0.381	**1975**	0.381	**1962**	0.257	2	779.71
						1928	0.459	**1961**	0.408			**1963**	0.180	2	1119.99
								1962	0.377			**1964**	0.197	2	1016.33
								1963	0.343			**1965**	0	0	1102.26
												1966	1.336	13	972.86
												1967	0.710	6	844.95
												1968	0.294	2	681.36
												1969	1.254	9	717.87
												1970	0.536	4	745.83
												1971	0.426	3	704.31
												1972	0.966	7	724.51
												1973	1.720	11	639.23
												1974	1.514	8	528.32
												1975	1.871	10	534.35

Table 3a: **Baseline** mixed sub-stock modelling assessment results (posterior medians with 5th and 95th percentiles in parenthesis). Model includes fitting to all capture-recapture data for both sub-stocks. Results assume r^{C2+3} and r^{C1} are estimated separately, each with a prior of U[0, 0.106].

	BS C1		**BS C2+3**
***r* prior**	**U[0, 0.106]**		**U[0, 0.106]**
Historic catch	**Feeding grounds split proportional to abundance**		**Feeding grounds split proportional to abundance**
Recent abundance	**5965 (2003)**		**None**
Trend information	**5 trends from breeding grounds (Durban 1920-28 excluded**	**IDCR/SOWER trend for combined feeding ground**	
Capture-recapture data	**All photo-ID data**		**All photo-ID and genotypic data**
r	0.088 [0.074; 0.103]		0.026 [0.003; 0.057]
K	8,421 [8,068; 9,092]		13,149 [10,060; 20,225]
N_{min}	316 [257; 544]		3,017 [1,139; 7,069]
N_{2006}	7,120 [6,276; 7,703]		7,450 [6,363; 9,218]
N_{min}/K	0.038 [0.031; 0.060]		0.227 [0.112; 0.354]
N_{2006}/K	0.844 [0.699; 0.942]		0.559 [0.380; 0.820]
N_{2020}/K	0.992 [0.996; 0.998]		0.703 [0.391; 0.965]
N_{2040}/K	1.000 [0.999; 1.000]		0.874 [0.424; 0.998]

Table 3b: Mixed sub-stock modelling assessment results (posterior medians with 5th and 95th percentiles in parenthesis) for which the model includes fitting to all capture-recapture data from C1 only, and the mid-range (best) abundance estimate for C3 obtained from capture-recapture data by Cerchio *et al.* (2008a). Results assume r^{C2+3} and r^{C1} are estimated separately, each with a prior of U[0, 0.106].

	BS C1		**BS C2+3**
***r* prior**	**U[0, 0.106]**		**U[0, 0.106]**
Historic catch	**Feeding grounds split proportional to abundance**		**Feeding grounds split proportional to abundance**
Recent abundance	**5965 (2003)**		**6737 (2006)**
Trend information	**5 trends from breeding grounds (Durban 1920-28 excluded**	**IDCR/SOWER trend for combined feeding ground**	
Capture-recapture data	**All photo-ID data**		**None**
r	0.091 [0.074; 0.103]		0.024 [0.002; 0.096]
K	8,388 [8,030; 9,068]		13,845; 20,358]
N_{min}	307 [252; 483]		3,706 [1,415; 8,033]
N_{2006}	7,174 [6,211; 7,679]		8,234 [4,838; 13,291]
N_{min}/K	0.037 [0.031; 0.055]		0.262 [0.126; 0.431]
N_{2006}/K	0.856 [0.698; 0.943]		0.562 [0.300; 1.000]
N_{2020}/K	0.993 [0.963; 0.999]		0.708 [0.322; 1.000]
N_{2040}/K	1.000 [0.999; 1.000]		0.880 [0.345; 1.000]

Figure 1: Historic catch series for sub-stocks C1 and C2+3.

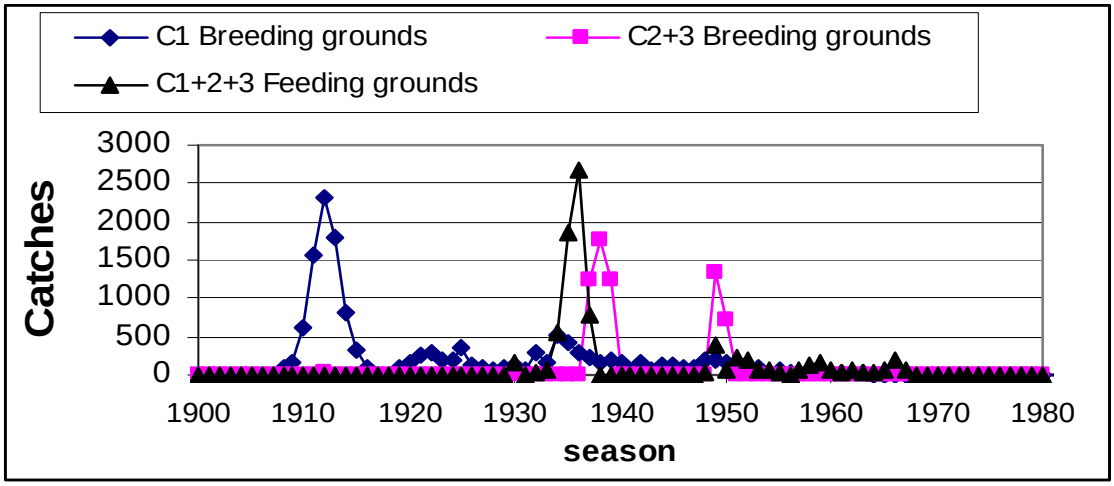


Figure 2a: Mixed model fit to C1 trend information, where the model trajectory is the Bayesian posterior median. The CPUE1, CPUE2 and CPUE3 trends here refer to the Durban CPUE trends for 1920-1928, 1954-1963 and 1969-1975 respectively, reported in Table 1b, as are the other relative abundance indices tabulated below. Note that the IDCR trend information is applied to both sub-stocks in combination. The vertical line shows 2006.

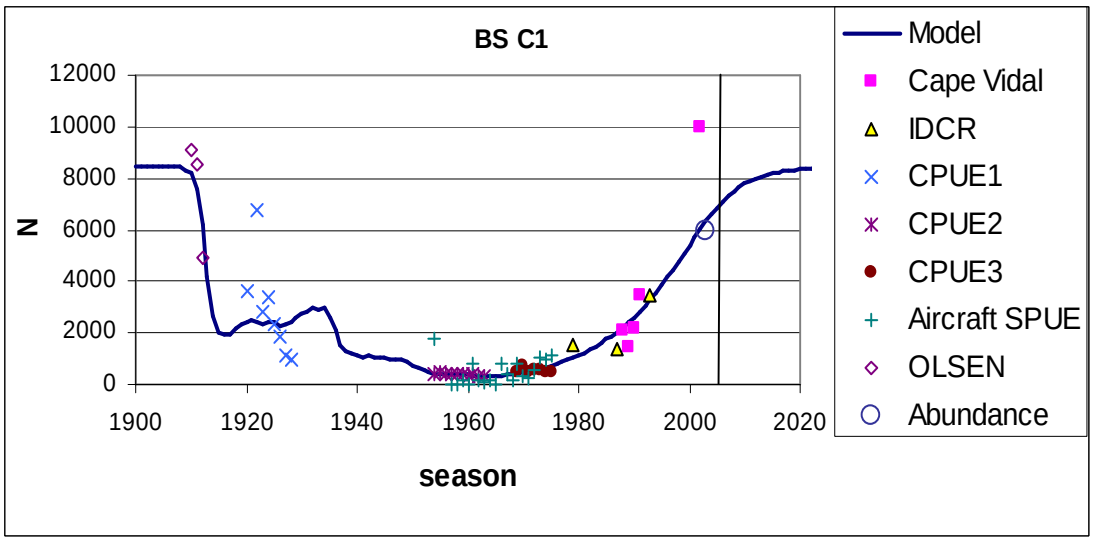


Figure 2b: Baseline mixed model stock assessment C1 population trajectories, showing the median and 95% probability envelopes. The vertical line shows 2006.

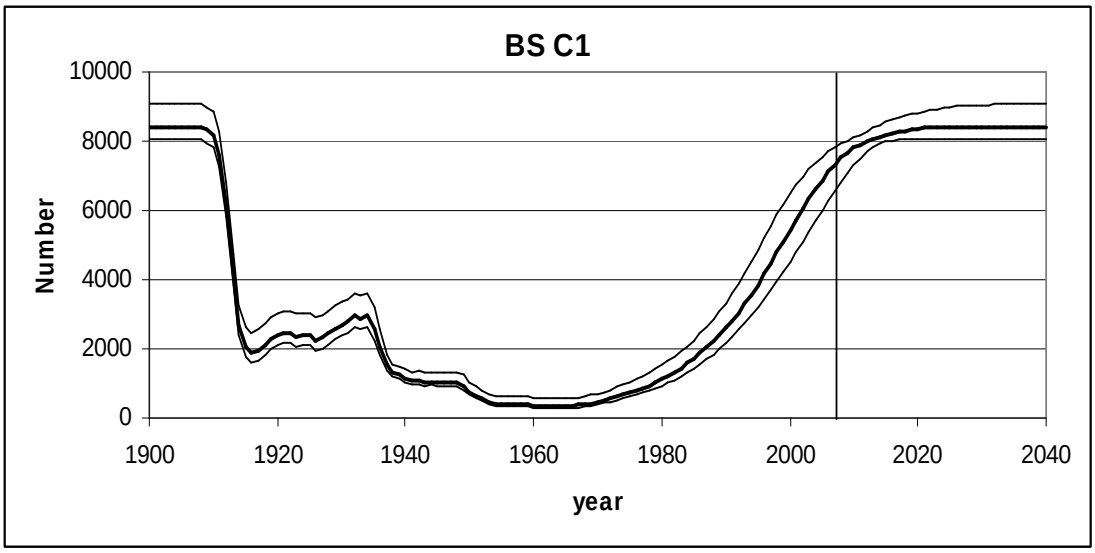


Figure 3a: Baseline mixed model assessment of sub-stock C2+3 population fit to IDCR data, where the trajectory shown is the posterior median. The upper and lower abundance estimates reported in Cerchio *et al.* (2008a) are also indicated (although not amongst the data fitted in this case). The vertical line shows 2006.

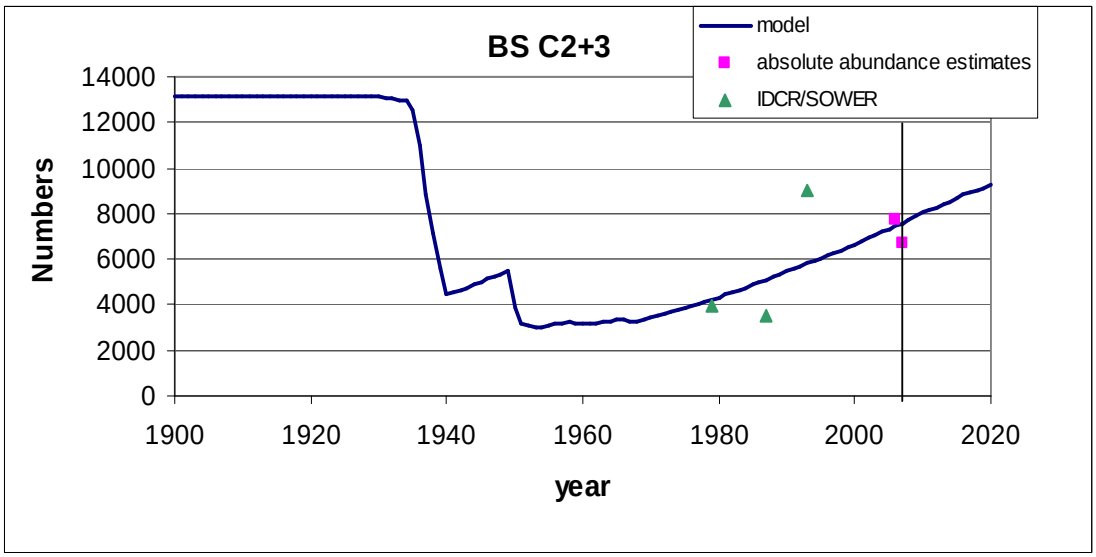
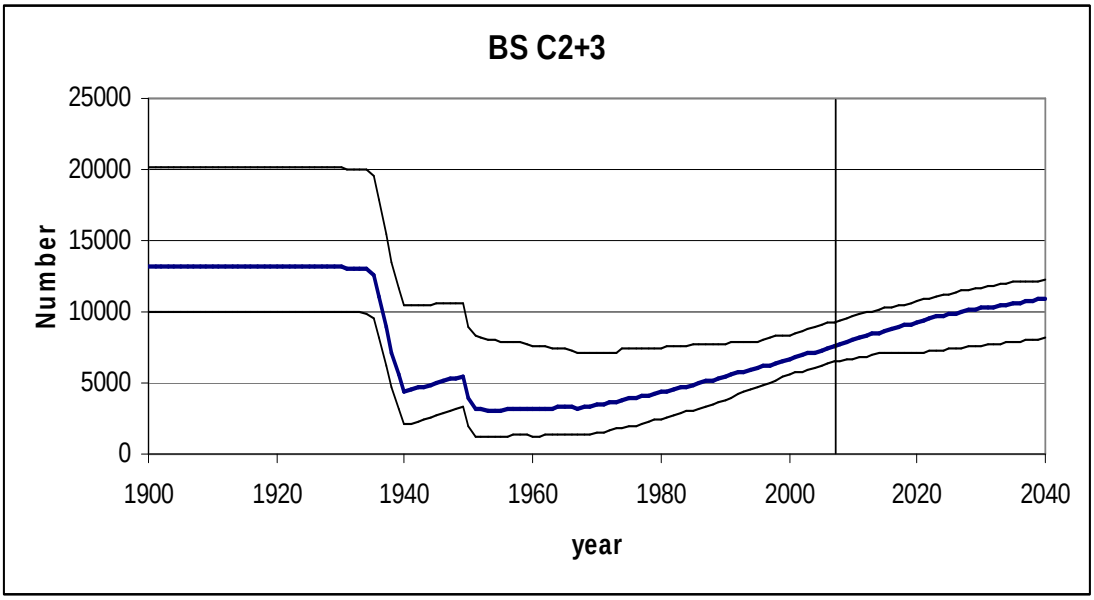


Figure 3b: Baseline mixed model stock assessment C2+3 population trajectories showing the median and 95% probability envelopes. The vertical line shows 2006.



Appendix 1: Data from Cerchio *et al.* (2008a and b) used in these analyses

Table A1.1: Photographic capture-recapture data from BS C1 – from SC/60/SH33 (Cerchio *et al.* 2008b)

[*n* = number of different individuals sighted each year, *m* = total recaptures between pairs of years]

n							
	2000	2001	2002	2003	2004	2005	2006
	3	24	49	115	21	134	112

m							
	2000	2001	2002	2003	2004	2005	2006
2000	X	0	0	0	0	0	0
2001		X	1	0	0	0	0
2002			X	1	1	0	1
2003				X	0	0	0
2004					X	1	0
2005						X	2
2006							X

Table A1.2 Photographic capture-recapture data from C3 – from SC/60/SH33 (Cerchio *et al.* 2008a)

[*n* = number of different individuals sighted each year, *m* = total recaptures between pairs of years]

n							
	2000	2001	2002	2003	2004	2005	2006
	89	159	16	126	151	144	158

m							
	2000	2001	2002	2003	2004	2005	2006
2000	X	2	1	3	1	0	1
2001		X	1	3	3	3	2
2002			X	3	0	0	0
2003				X	2	1	3
2004					X	4	3
2005						X	4
2006							X

Table A1.3: Genotypic "capture-recapture" data from C3 – from SC/60/SH33 (Cerchio *et al.* 2008a)

[*n* = number of different individuals sighted each year, *m* = total recaptures between pairs of years]

n							
	2000	2001	2002	2003	2004	2005	2006
	114	161	28	185	163	161	153

m							
	2000	2001	2002	2003	2004	2005	2006
2000	X	4	1	2	2	0	0
2001		X	2	6	2	1	2
2002			X	6	1	1	1
2003				X	2	2	3
2004					X	2	4
2005						X	3
2006							X