PRELIMINARY RESULTS FOR A COMBINED ASSESSMENT OF ALL SEVEN SOUTHERN HEMISPHERE HUMPBACK WHALE BREEDING STOCKS

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ABSTRACT

This paper reports preliminary results from the development of an assessment process that aims to include all seven Southern Hemisphere humpback whale breeding stocks in a single joint assessment, with the purpose of allowing high-latitude historic catches (i.e. catches taken south of 40˚S, where mixing amongst the populations occurs), to be allocated to breeding stocks in proportion to abundance, rather than on set ratios. The approach can be broadened to allow for uncertainties in the placement of the boundaries assumed to link high latitude catches to breeding stocks. Because of the interaction between populations arising from the procedure to allocate high latitude catches amongst breeding stocks, the conventional SIR-based Bayesian approach proved impractical to expand. Instead uniform priors on the various pre-exploitation level (K) parameters were assumed with the intent to later iteratively adjust these to account for their being informative about the values of the intrinsic growth rate (r) parameters. Initial results (which will need later refinement) are presented purely for the purposes of illustrating the application of the approach.

KEYWORDS: HUMPBACK WHALES, MAXIMUM LIKELIHOOD, BAYESIAN, MCMC

INTRODUCTION

The Southern Hemisphere humpback whale populations have been divided into seven breeding stocks for managerial purposes (Findlay *et al.*, 2009):

Breeding stock **A**: 70˚W-20˚W (linked to Brazil)

Breeding stock **B**: 20˚W-10˚E (linked to Angola, Gabon)

Breeding stock **C**: 10˚E-60˚E (linked to Mozambique, Comores, Madagascar)

Breeding stock **D**: 60˚E-120˚E (linked to Western Australia)

Breeding stock **E**: 120˚E-170˚W (linked to Eastern Australia, Tonga, New Zealand)

Breeding stock **F**: 170˚W-120˚W (linked to Oceana)

Breeding stock **G**: 120˚W-70˚W (linked to Oceana)

The regions above refer to the breeding areas (north of 40˚S).

Over the years various assessments have been conducted for the respective individual stocks. One recurring problem throughout these assessments has been the question of catch allocation. Catch records give historic catches by position. In the low latitude areas it is fairly straightforward to allocate the catches to the various breeding stocks because of their linkages to areas close to the coast. The high latitude catches in and near the Antarctic are however more problematic. The populations are known to migrate to the Antarctic for feeding purposes, where mixing between the various breeding populations occurs. Over the years various hypotheses have been proposed to deal with the catch allocation for these high latitude catches (Findlay *et al.*, 2009). The latest of these, referred to as Hypothesis 1 (IWC, 2009), divides the high-latitude waters into nucleus and margin regions, the former being associated with single breeding stocks and the latter with two neighbouring stocks (see Figure 1), and was recommended as a reference case by the Sub-Committee on Southern Hemisphere Humpback Whales. Catches in the margin areas are split 50-50 between neighbouring stocks in this hypothesis.

This assessment aims to combine all breeding stocks into one assessment, thus allowing catches in margin regions to be split in proportion to the abundances of the respective neighbouring populations, rather than by set ratios. This approach, within the Bayesian paradigm, is intended as a first step in a process that can take account of the uncertainty in the placement of the boundaries between these nucleus and margin regions through specifying priors for each, while also avoiding the "double-counting" that effectively takes place in current

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assessment practice when sensitivities explore widening the range from which the high latitude catches from a particular breeding stock might have been taken. It also allows account to be taken of the intrinsic growth rates r for each of the breeding stocks, while not being identical, nevertheless being likely to be somewhat similar to each other.

DATA

Historic Catch data
There are two sources of historic catch data.

i) Catches north of 40°S, given by region and easily allocated to the respective breeding stocks (see Table 1). Records of a series of Russian catches are also available by 10 degree longitude and latitude bands and these catches have been incorporated into Table 1.

ii) Catches south of 40°S, which are given according to assumed nucleus and margin regions (see Figure 1) and are shown in Table 2.

Abundance and trend data
These include absolute abundance estimates, relative abundance estimates and tag-recapture information and are all given in Appendix 2.

METHODS
Each population's dynamics is modeled by the Pella-Tomlinson equation, given in Appendix 1. For catch allocation purposes for regions where more than one stock/sub-stock of whales is present, complete mixing is assumed with catches each year allocated amongst the stocks in proportion to their relative abundances.

Maximum likelihood procedure

The initial idea was to use the standard Bayesian approach adopted in the past for assessments of individual breeding stocks, where for each such population i ($i \in \{A, B, C1, C3, D, E, F, G\}$) values of r^i and $\ln \tilde{N}_{t\,\mathrm{arg}\,et}^{i,obs}$ are randomly drawn from prior distributions and a downhill simplex method of minimisation is used to calculate K^i such that the model estimate of $N_{t\,\mathrm{arg}\,et}^i$ is identical to $\tilde{N}_{t\,\mathrm{arg}\,et}^{i,obs}$ (for an example of one such assessments see Johnston *et al.*, 2009). However the complexity of the problem owing to the interaction amongst the populations (arising because catches are split in proportion to the population abundances) led to time-intensive processes and poor ability to find solutions necessary to be able to implement the conventional SIR approach to effect the Bayesian integration over priors.

An alternative approach was sought, leading to this assessment using a Markov chain Monte Carlo (MCMC) approach to achieve the Bayesian integration. Here uniform priors are assumed on r^i and K^i, and AD Model Builder is used to obtain a maximum (penalised) likelihood estimate (the penalty corresponding to the log of the joint priors), i.e. a combination of r^i and K^i values that is the most likely given the abundance and trend data (equations for the likelihood function are given in Appendix 1). Once this maximum likelihood solution has been obtained, the MCMC approach is used to obtain a set of equally likely values of r^i and K^i, thus allowing posterior distributions to be computed.

The exercise reported here intends only to produce some initial results, and these results should be considered as preliminary only. There are problems associated with specifying a uniform prior on K – the model dynamics are such that a uniform prior on K is in fact informative regarding the intrinsic growth rate parameter r given the catch series and prior for recent abundance, and future adjustments will aim to address this issue by varying the priors for K in a way that sees them correspond more closely to post-model pre-data posteriors for recent abundances that are near uniform..

This approach also takes account of the fact that the intrinsic growth rates r for each of the breeding stocks, while not being identical, are nevertheless likely to be somewhat similar to each other. This is done by including a prior that assumes the r values for each population to be "generated" from an underlying normal distribution.

The prior distributions used in this initial illustrative assessment were:

$r^i \sim U[0, 0.106]$ (i.e. the same uniform prior for all populations)

$K^A \sim U[0, 35000]$

$K^B \sim U[0, 40000]$

$K^{C1} \sim U[0, 25000]$

$K^{C3} \sim U[0, 25000]$

$K^D \sim U[0, 50000]$

$K^E \sim U[0, 45000]$

$K^F \sim U[0, 25000]$

$K^G \sim U[0, 25000]$

The uninformative r prior is bounded by zero (negative rates of growth are biologically implausible) and 0.106 (this corresponds to the maximum growth rate for the species as agreed by the IWC Scientific Committee (IWC, 2007)). Then further prior information was added by assuming the different r^i values to be realisations of a normal distribution of standard deviation 0.02 (see equation A1.16 of Appendix 1). Based on what is known about the respective populations, a large interval was placed around feasible K values to obtain the distribution bounds given above.

Nmin constraints

Rosenbaum *et al.* (2006) provides the minimum number of haplotypes for the respective breeding stocks. These values, multiplied by a factor of four, give a lower bound for minimum population numbers, and these constraints will be implemented in future implementations of this assessment as lower bounds.

RESULTS

Tables 3a and b report the MCMC results for a chain of 10 million, with the initial 1 million discarded for burn in and every 1000th value sampled, to give the median values as well as the 5th and 95th percentiles of r, K and other values of interest for each breeding population. The MCMC appears reasonably close to, but not yet having achieved full convergence. The median population trajectories for the respective models, along with the 90% probability interval envelopes, are shown in Figures 2a and b. No plots showing fits to data have been included at this stage.

DISCUSSION

Given the preliminary nature of this exercise whose purpose is primarily an illustration of the approach, an in-depth discussion of said results is not entirely warranted, also as the lack of complete convergence of the MCMC may have affected the results. The results seem to favour fairly high r values, with the posterior for breeding stock E concentrated effectively entirely at the upper bound of 0.106 (a result that merits further checking).

The assumption that the r values are normally distributed about some mean value results in populations for which more data are available being a driving component behind the r estimation. This is an added advantage in attempting a combined assessment: that populations for which less data are available can be informed in an internally consistent way by data for the other populations.

Looking forward, convergence is an issue that needs to be addressed. With eight interacting breeding populations, the initial minimisation process is sensitive to the parameter vector used to initiate the minimisation process. Manual exploration of the likelihood profile will hopefully give a better idea as to what the "solution" is; this may in turn assist resolve MCMC convergence difficulties. Following this, the iterative procedure mentioned above that is intended to remove the informative aspects of the uniform priors on K for the r parameters will be pursued, followed by extension of the implementation to allow for priors on the placement of the Antarctic boundaries governing the allocation of high latitude catches amongst breeding stocks.

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Table 1: Historic catch series for all stocks for the breeding areas, north of 40˚S (Allison, pers. commn).

Year	A	B	C1	C3	D	E	F	G
1900	0	0	0	0	0	8	0	0
1901	0	0	0	0	0	8	0	0
1902	0	0	0	0	0	8	0	0
1903	0	0	0	0	0	8	0	0
1904	0	0	0	0	0	8	0	0
1905	0	0	0	0	0	8	0	0
1906	0	0	0	0	0	8	0	0
1907	0	0	0	0	0	8	0	0
1908	0	0	104	0	0	8	0	16
1909	0	576	149	0	0	16	0	44
1910	0	962	632	0	0	77	0	62
1911	102	2603	1580	0	0	77	0	92
1912	342	4692	2313	25	234	224	0	86
1913	352	5962	1805	0	993	440	0	45
1914	317	2873	830	0	1968	93	0	195
1915	82	169	334	0	1297	106	0	30
1916	68	70	94	0	388	82	0	15
1917	62	10	7	0	0	94	0	15
1918	62	10	9	0	0	90	0	23
1919	29	17	91	0	0	119	0	24
1920	0	40	148	0	0	107	0	21
1921	0	0	251	0	0	89	0	21
1922	0	626	285	0	155	57	0	19
1923	0	899	183	0	166	79	0	16
1924	0	662	187	0	0	107	0	34
1925	0	842	372	0	669	96	0	248
1926	0	442	124	0	735	78	0	277
1927	0	47	86	0	996	127	0	40
1928	0	68	62	0	1035	105	0	36
1929	0	50	99	0	0	102	0	26
1930	0	614	134	0	0	78	0	33
1931	0	0	72	0	0	109	0	53
1932	0	0	307	0	0	18	0	21
1933	0	0	162	0	0	44	0	11
1934	0	723	514	0	0	52	0	13
1935	0	1238	418	0	0	57	0	31
1936	0	869	300	0	3076	69	0	18
1937	0	327	242	1223	3250	55	0	28
1938	0	0	177	1752	917	75	0	6
1939	0	0	200	1240	0	80	0	7
1940	0	0	176	0	0	107	0	0
1941	0	0	79	0	0	86	0	0
1942	0	0	156	0	0	71	0	0
1943	0	0	80	0	0	90	0	0
1944	0	0	115	0	0	88	0	0
1945	0	0	116	0	0	107	0	0
1946	0	0	93	0	0	110	0	15
1947	11	5	89	0	2	101	0	19
1948	23	14	182	0	4	92	0	5
1949	17	1371	190	1333	190	144	0	6
1950	26	1411	151	714	388	79	0	5

1951	28	1114	103	0	1224	111	0	26
1952	9	280	111	0	1187	721	0	27
1953	8	9	89	0	1300	809	0	29
1954	18	0	28	0	1320	898	0	106
1955	9	0	49	0	1126	832	0	7
1956	17	0	36	0	1119	1013	0	10
1957	3	3	34	0	1120	1025	16	5
1958	5	2	39	0	967	1023	16	0
1959	8	168	38	0	700	1278	16	3
1960	13	4	36	0	545	1341	16	2
1961	13	23	36	0	580	981	16	3
1962	11	15	38	1	548.2	209	0	4
1963	12	9	39.6	1.6	87	9	0	1
1964	0	1	4	4	2	0	0	35
1965	0	1	4.5	4.5	75.8	2.5	0	143
1966	0	9	119	119	30	0	0	58
1967	189	3	33.5	33.5	12	0	0	0
1968	0	0	0	0	0	0	0	3
1969	0	0	0	0	0	0	0	1
1970	0	0	0	0	0	0	0	0
1971	0	0	0	0	0	0	0	0
1972	0	0	0	0	0	0	0	0
1973	0	0	1	0	0	0	3	0
1974	0	0	0	0	0	0	4	0
1975	0	0	0	0	0	0	8	0
1976	0	0	0	0	0	0	4	0
1977	0	0	0	0	0	0	4	0
1978	0	0	0	0	0	0	11	0
1979-2009	0	0	0	0	0	0	0	0

Table 2: Historic catch series for all stocks for the feeding areas, south of 40˚S (Allison, pers. commn). The columns with grey shading are those corresponding to catches taken in the nucleus regions; the columns in white show the catches taken in marginal regions.

Year	A	A/B	B	B/C	C	C/D	D	D/E	E	E/F	F	F/G	G	G/A
1900	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1901	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1902	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1903	0	0	0	0	0	0	0	0	0	0	0	0	1	0
1904	180	0	0	0	0	0	0	0	0	0	0	0	0	0
1905	288	0	0	0	0	0	0	0	0	0	0	0	23	0
1906	240	0	0	0	0	0	0	0	0	0	0	0	498	0
1907	1261	0	0	0	0	0	0	0	0	0	0	0	366	0
1908	1849	0	0	0	0	217	0	0	0	0	0	0	1246	9
1909	3391	0	0	0	0	118	0	0	0	0	0	0	1481	94
1910	6468	0	0	0	0	83	0	0	0	0	0	0	2527	70
1911	5730	0	0	0	0	0	0	0	0	0	0	0	2039	17
1912	2539	0	0	0	0	0	0	0	0	0	0	0	976	8
1913	647	0	0	0	0	0	0	0	0	0	0	0	1038	7
1914	838	0	0	0	0	0	0	0	0	0	0	0	656	12
1915	1615	0	0	0	0	0	0	0	0	0	0	0	219	0
1916	379	0	0	0	0	0	0	0	0	0	0	0	21	0
1917	59	0	0	0	0	0	0	0	0	0	0	0	69	0
1918	67	0	0	0	0	0	0	0	0	0	0	0	81	0
1919	82	0	0	0	0	0	0	0	0	0	0	0	181	0
1920	102	0	0	0	0	0	0	0	0	0	0	0	149	0
1921	9	0	0	0	0	0	0	0	0	0	0	0	0	0
1922	364	0	0	0	0	0	0	0	0	0	0	0	189	0
1923	133	0	0	0	0	0	0	0	0	0	0	0	96	0
1924	266	0	0	0	0	0	0	0	0	0	0	0	102	0
1925	254	0	0	0	0	0	0	0	0	0	0	0	163	0
1926	7	0	0	0	0	0	0	0	0	82	0	0	0	0
1927	0	0	0	0	0	0	0	0	0	16	0	0	0	2
1928	18	0	0	0	0	11	0	0	0	17	0	0	0	0
1929	50	9	8	4	0	11	0	0	0	775	0	0	0	0
1930	107	26	37	111	38	4	23	1	81	58	96	0	0	0
1931	18	1	2	0	2	109	52	0	0	0	0	0	0	0
1932	23	2	16	9	28	3	79	0	0	0	0	0	0	0
1933	132	38	47	9	45	101	500	0	0	0	0	0	0	0
1934	57	14	24	265	277	92	1252	0	0	0	0	0	0	0
1935	48	201	99	1518	351	1	940	0	4	0	0	0	0	0
1936	105	88	162	2390	293	15	1420	0	0	0	0	0	1	0
1937	242	65	123	498	281	57	650	161	0	0	0	0	0	0
1938	0	0	0	0	0	0	655	204	24	0	0	0	0	0
1939	2	0	0	4	0	0	0	0	0	0	0	0	0	0
1940	36	111	131	0	0	0	0	342	1026	684	342	0	1	0
1941	13	0	0	0	0	0	0	0	0	0	0	0	0	0
1942	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1943	4	0	0	0	0	0	0	0	0	0	0	0	0	0
1944	60	0	0	0	0	0	0	0	0	0	0	0	0	0
1945	238	0	0	0	0	0	0	0	0	0	0	0	0	0
1946	30	1	0	0	0	0	0	0	0	0	0	0	0	0
1947	24	1	0	0	0	1	0	0	0	0	0	0	0	0
1948	25.3	38.1	45.4	33.2	1	0	0	0	0	0	0	0	0	0
1949	66	257.5	207.8	350.7	44	0	665	119	908	0	0	0	0	0
1950	672.6	27.9	201	69.9	3	5	1110	0	0	85	403	0	271.8	0
1951	17.6	114.9	313	209.6	1	104	626	402	1	169	227	0	0	0

1952	24.6	33.4	168.1	193.9	14	3	190	0	0	382	148	0	0	0
1953	132.2	31.2	69.8	51.7	14	0	259	0	0	0	150	0	0	0
1954	25.1	52.1	265.4	42.3	7	0	26	0	751	22	507	0	0	0
1955	87.3	83.2	60.2	22.4	6	111	546	919	1962	0	334	0	14	0
1956	150.2	65.2	30.5	0	3	0	0	0	0	0	10	66	626.2	2.8
1957	57.5	32.4	28	55.3	11	70.3	1828	12	87	133	167	31	59	0
1958	10.9	6.5	80.6	55.3	63.6	297.3	2106	2158	447.5	735.2	0	0	0	52.4
1959	7.7	7.7	53	130	21.8	11.6	205.7	85.8	8774	3227	757	81.1	19	0
1960	14.2	4	113.2	27	44.2	51.6	427.3	242.3	2090	6334	3498	0	81	5.8
1961	0	0	18	25	3	2	241	134	511	923	2401	98	1166	1
1962	12.6	4	10	19	55	120	1474	176.4	93.3	311.4	294.9	42.5	255.1	49.4
1963	0	0	2	0	38.8	79.2	256.2	23.7	45.7	238	0	0	0	0
1964	0	0	0	0	48	16	55.8	17.9	40.3	45	0	0	0	0
1965	52	34	880	64	11	6.5	76.4	17.6	82.8	177.1	562.2	0	0	0
1966	0	0	147	137	59	6	90	33	8	25	253	0	0	0
1967	0	6	359	35	31	11	66	12	12	14	111	0	0	0
1968	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1969	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1970	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1971	0	0	0	0	0	0	0	0	0	0	0	3	0	0
1972	2	0	1	0	0	0	0	0	0	2	0	0	0	0
1973-2009	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 3a: Assessment results for breeding stocks A to C3

	BS A	BS B	BS C1	BS C2+3
Recent abundance	**6251 (2005)**	**7196 (2003)**	**5965 (2003)**	**none**
Trend information	**- Breeding ground index of abundance** **- IDCR/SOWER feeding ground index of abundance**	**- IDCR/SOWER index of abundance** **- Photographic mark-recapture data for all regions combined**	**- Cape Vidal relative abundance estimates** **- Photographic mark-recapture data**	**- Photographic mark recapture data**
r	0.096 [0.092;0.104]	0.092 [0.089;0.099]	0.097 [0.089;0.104]	0.088 [0.068;0.104]
K	23282 [22920;23509]	18749 [18339;18957]	7515 [7175;7843]	8372 [7600;9448]
N_{min}	214 [143;306]	285 [217;360]	442 [234;1380]	974 [322;2174]
N_{2010}	9960 [7579;12846]	10585 [9087;12273]	7307 [6718;7654]	8229 [7366;9377]
N_{min}/K	0.009 [0.006;0.013]	0.015 [0.012;0.019]	0.058 [0.032;0.184]	0.116 [0.042;0.237]
N_{2010}/K	0.429 [0.325;0.555]	0.566 [0.484;0.659]	0.978 [0.897;1.000]	0.998 [0.912;1.000]
N_{2040}/K	0.999 [0.995;1.000]	0.999 [0.998;1.000]	1.000 [1.000;1.000]	1.000 [1.000;1.000]

Table 3b: Assessment results for breeding stocks D to G

	BS D	BS E	BS F	BS G
Recent abundance	**21750 (2008)**	**7090 (2004)**	**3827 (2002)**	**6504 (2006)**
Trend information	**- IWC 1996 estimates** **- JARPA estimates** **- IDCR/SOWER estimates**	**- Estimates from Noad *et al.*** **- JARPA estimates** **- IDCR/SOWER estimates**	**- IDCR/SOWER estimates**	**- IDCR/SOWER estimates**
r	0.100 [0.095;0.106]	0.106 [0.106;0.106]	0.064 [0.039;0.095]	0.069 [0.054;0.098]
K	19644 [18984;20227]	27187 [26897;27441]	15362 [14113;17037]	11351 [10501;11948]
N_{min}	885 [452;1713]	129 [119;139]	498 [198;1087]	627 [369;960]
N_{2010}	18918 [16813;19927]	8614 [7995;9275]	6167 [4682;7976]	9161 [6355;10970]
N_{min}/K	0.045 [0.023;0.087]	0.005 [0.004;0.005]	0.032 [0.014;0.064]	0.055 [0.033;0.081]
N_{2010}/K	0.971 [0.863;0.997]	0.317 [0.294;0.341]	0.400 [0.283;0.554]	0.802 [0.547;0.998]
N_{2040}/K	1.000 [1.000;1.000]	0.998 [0.998;0.999]	0.972 [0.735;0.999]	0.999 [0.984;1.000]

Figure 1: Southern Hemisphere humpback whale catch allocation reference case showing Nucleus and Margin Areas in the feeding grounds associated with breeding stocks A-G (IWC 2009).
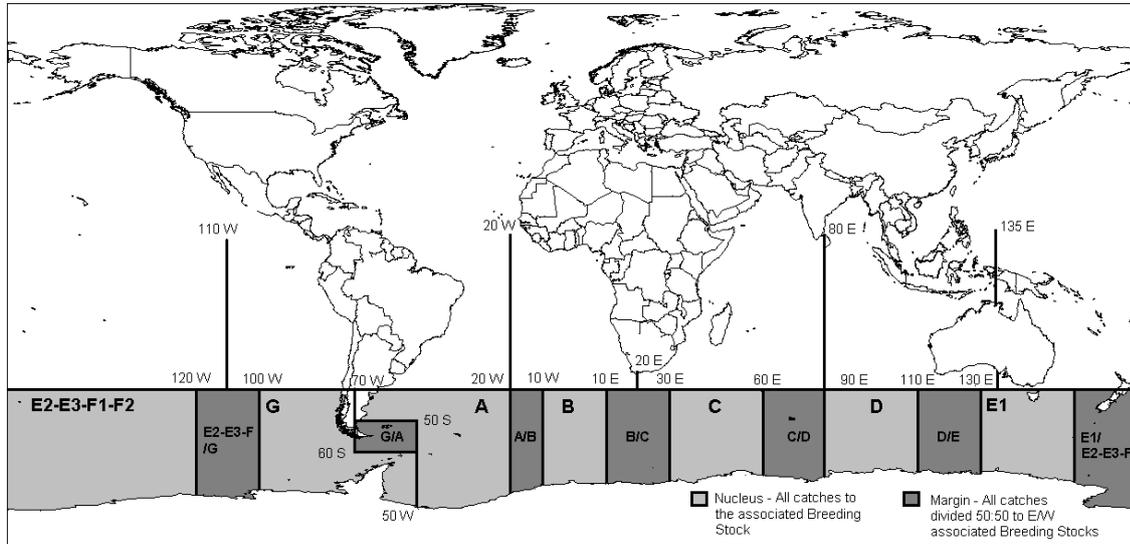
Figure 2a: Population trajectories for breeding stocks A to C3. The posterior medians and 90% probability interval envelopes are shown. Results for years to the right of the vertical dashed line are projections under zero future catch.
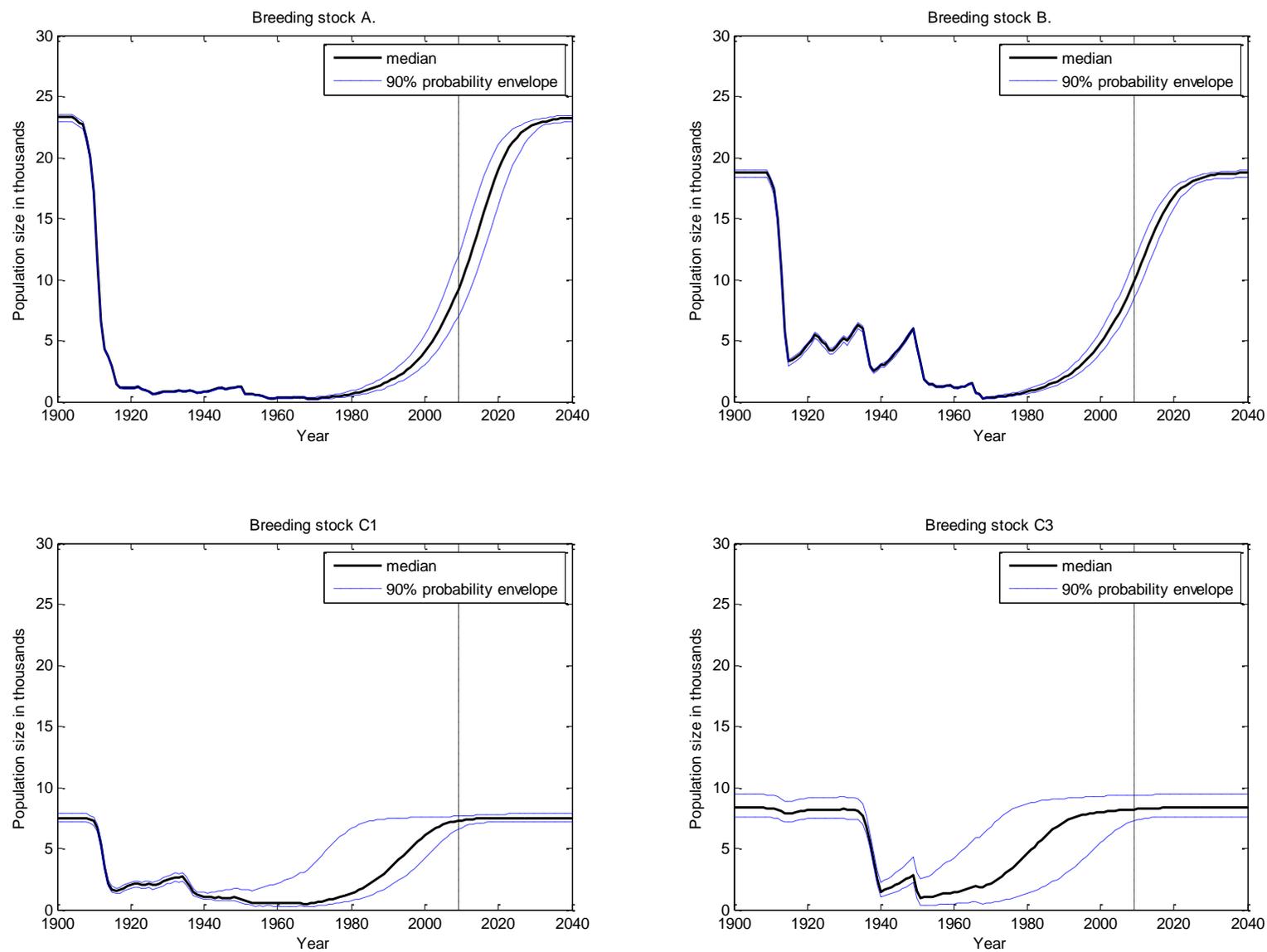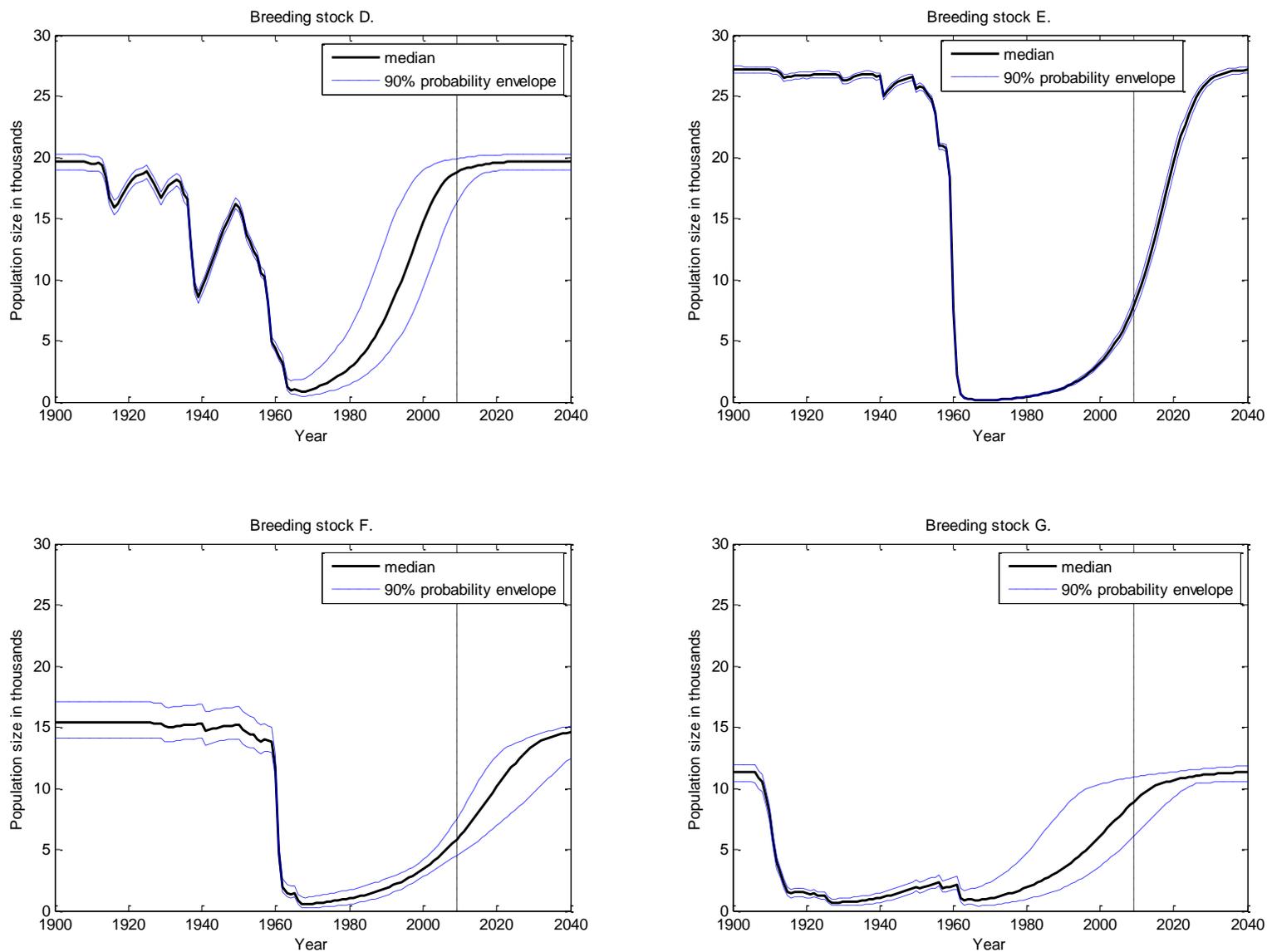
Figure 2b: Population trajectories for breeding stocks D to G. The posterior medians and 90% probability interval envelopes are shown. Results for years to the right of the vertical dashed line are projections under zero future catch.

APPENDIX 1 - Model dynamics and Likelihood function

Breeding stock population dynamics

$$N_{y+1}^i = N_y^i + r^i N_y^i \left(1 - (\frac{N_y^i}{K^i})^\mu \right) - C_y^i \qquad i \in \{\text{A, B, C1, C3, D, E, F, G}\} \quad \text{(A1.1)}$$

where

N_y^i is the number of whales in the breeding population i at the start of year y,

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

K^i is the carrying capacity for population i,

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

C_y^i is the total catch (in terms of animals) for breeding population i in year y.

C1 and C3 are sub-stocks of breeding stock C, which is assumed to follow the sabbatical model (Johnston *et al.* 2009). Every year there is a probability α^{C1} that an animal from sub-stock C1 travels to the C3 region instead of C1 and similarly a probability α^{C3} that an animal from sub-stock C3 travels to the C1 region instead of C3. The observed numbers in regions C1 and C3 each year are then given by η^{C1} and η^{C3} respectively, and these are the variables to which observations apply (both capture-recapture and survey data). The observed populations are given by:

$$\eta_y^i = (1-\alpha^i)N_y^i + \alpha^j N_y^j \qquad \begin{Bmatrix} i \\ j \end{Bmatrix} = \begin{Bmatrix} C1 \\ C3 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C1 \end{Bmatrix} \qquad \text{(A1.2)}$$

Note that for simplicity reasons, this assessment uses $\alpha^{C1} = 0.01$ and $\alpha^{C3} = 0.05$. Future assessments will allow these values to be estimated.

Catch Allocation

Catches north of 40˚S are available by area and thus easily allocated to the respective breeding stocks (see Table 1). The feeding ground regions south of 40˚S are split into nucleus and margin regions (see Figure 1). Catches taken in any of the nucleus regions are allocated to the corresponding breeding stock. Catches taken in a marginal region are allocated to the neighbouring stocks in proportion to the population abundances. For example, if 1, 2 and 3 are three neighbouring populations, the feeding ground catch allocated to population 2 is given by:

$$C_y^{feed,2} = C_y^{nucleus,2} + C_y^{margin,12} \frac{N_y^2}{N_y^1 + N_y^2} + C_y^{margin,23} \frac{N_y^2}{N_y^2 + N_y^3} \qquad \text{(A1.3)}$$

where

$C_y^{feed,2}$ is the total feeding ground catch in year y from breeding population 2,

$C_y^{nucleus,2}$ is the catch in year y taken from the nucleus region associated with breeding stock 2,

$C_y^{margin,12}$ is the catch year y taken from the marginal area shared between stocks 1 and 2, and

$C_y^{margin,23}$ is the catch year y taken from the marginal area shared between stocks 2 and 3.

The total catch for breeding stock i is given by:

$$C_y^i = C_y^{breed,i} + C_y^{feed,i} \qquad i \in \{A, B, C, D, E, F, G\} \tag{A1.4}$$

Note that (A1.4) applies for the combined breeding stock C. The feeding ground catches for stock C are further split in proportion to the respective C1 and C3 population sizes. The breeding ground catches, which are given for regions C1 and C3, need to be adjusted to take into account the movement within the stocks. The C1 and C3 catches are thus given by:

$$C_y^{Ci} = C_y^{breed,Ci} + C_y^{feed,C} \frac{N_y^{Ci}}{\left(N_y^{C1} + N_y^{C3}\right)}, \qquad \begin{Bmatrix} i \\ j \end{Bmatrix} = \begin{Bmatrix} C1 \\ C3 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C1 \end{Bmatrix} \tag{A1.5}$$

where

$$C_y^{breed,Ci} = C_y^{Ci,reported} \frac{(1-\alpha^{Ci})N_y^{Ci}}{\left(1-\alpha^{Ci}\right)N_y^{Ci} + \alpha^{Ci}N_y^{Cj}} + C_y^{Cj,reported} \frac{\alpha^{Ci}N_y^{Ci}}{\left(\alpha^{Ci}N_y^{Ci} + (1-\alpha^{Cj})N_y^{Cj}\right)}$$

and $C_y^{Ci,reported}$ is breeding ground catch allocated to sub-stock Ci.

Likelihood Function

Given a combination of r^i and K^i values, the abundance and trend data are used to assign a likelihood component corresponding to that particular stock. The components of the negative log likelihood are calculated as follows:

Absolute abundance estimates

Each breeding population has an absolute abundance estimate, $N_{target}^{i,obs}$, with an associated CV (see Appendix 2). Given this estimate, the contribution to the negative of the log-likelihood is:

$$-\ln L = \frac{1}{2CV^2} \left(\ln N_{target}^{i,obs} - \ln N_{target}^i\right)^2 \tag{A1.6}$$

where N_{target}^i is the model-estimated abundance for the target year for population i.

Relative abundance indices

Appendix 2 gives the series of indices that are available for the respective breeding populations. Given one such series, it is assumed that the observed relative abundance index is log-normally distributed about its expected value:

$$I_y^i = q^i N_y^i e^{\varepsilon_y} \tag{A1.7}$$

I_y^i is the relative abundance for year y for breeding sub-stock i,

q^i is the catchability coefficient/constant of proportionality for the particular index in question,

N_y^i is the model estimate of observed population size at the start of year y for breeding stock i, and

ε_y is from $N\left(0, \left(\sigma^i\right)^2\right)$ (see equation A.1.8 below)

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

$$\hat{\sigma}^i = \sqrt{1/\overline{n}^i \sum_y \left(\ln I_y^i - \ln q^i - \ln N^i\right)^2} \qquad \text{(A1.8)}$$

where

$\overline{n}^i$ is the number of data points in the particular series in question, and

q^i is the multiplicative bias, estimated by its maximum likelihood value:

$$\ln \hat{q}^i = 1/\overline{n}^i \sum_y \left(\ln I_y^i - \ln N_y^i\right) \qquad \text{(A1.9)}$$

The final contribution to the negative of the log-likelihood is given by:

$$-\ln L = \overline{n}^i \ln \sigma^i + \frac{1}{2(\sigma^i)^2} \sum_y \left(\ln I_y^i - \ln q^i - \ln N_y^i\right)^2 \qquad \text{(A1.10)}$$

Capture-recapture data

Capture-recapture information is available for breeding stocks B and C. These are incorporated into the likelihood as follows:

Captures: $n_y^i = p_y^i N_y^i$ $i = $ B, C1, C3   (A1.11)

Recaptures: $m_{y,y'}^{i,j}$

where: n_y^i is the number of animals captured in breeding region i in year y,

                   $m_{y,y'}^{i,j}$ is the number of animals captured in i in year y that were

                         recaptured in j in year y',

                   p_y^i is the probability that an animal is captured in i year y.

Inter-region recaptures apply only to breeding stock C, which has two sub-stocks. Since B is treated as a single stock, $i=j=B$ and $m_{y,y'}^{B,B}$ is estimated by:

$$\hat{m}^B_{y,y'} = p^B_y p^B_{y'} N^B_y e^{-M(y'-y)} \tag{A1.12}$$

where:

$\hat{m}^B_{y,y'}$ is the model-predicted number of animals in B captured in year y that were recaptured in year y', and

M is the natural mortality rate (set here to equal 0.03).

For breeding stock C, there are data for within-region recaptures, and the model predicted number of animals in i captured in year y that were recaptured in j in year y' is given by:

$$\hat{m}^{i,j}_{y,y'} = p^i_y [(1-\alpha^i)N^i_y e^{-M(y'-y)}\alpha^i + \alpha^j N^j_y e^{-M(y'-y)}(1-\alpha^j)]p^j_{y'} \tag{A1.13}$$

$$\hat{m}^{i,i}_{y,y'} = p^i_y [(1-\alpha^i)N^i_y e^{-M(y'-y)}(1-\alpha^i) + \alpha^j N^j_y e^{-M(y'-y)}\alpha^j]p^i_{y'} \tag{A1.14}$$

where:

$$\begin{Bmatrix} i \\ j \end{Bmatrix} = \begin{Bmatrix} C1 \\ C3 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C1 \end{Bmatrix} ; \begin{Bmatrix} i \\ i \end{Bmatrix} = \begin{Bmatrix} C1 \\ C1 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C3 \end{Bmatrix}$$

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

$$-\ln L = \sum_i \sum_j \sum_{y=y_o}^{y_t-1} \sum_{y'=y+1}^{y_t} [-m^{i,j}_{y,y'} \ln \hat{m}^{i,j}_{y,y'} + \hat{m}^{i,j}_{y,y'}] \tag{A1.15}$$

Prior on variation of r amongst breeding stocks:

The last term in the likelihood is introduced to favour solutions for which the variance amongst the eight r values is not too high:

$$-\ln L = \sum_{i=A}^{G} \frac{(r^i - \bar{r})^2}{2\sigma^2} \tag{A1.16}$$

where

$\bar{r}$ is the mean of the r^i values, and

σ is a variance term, taken to be 0.02 in this assessment.

Thus each r^i value is assumed to be normally distributed about some mean, with a standard deviation of 0.02.

APPENDIX 2 – Abundance and trend data

The data used in this assessment for the respective breeding populations are reported here.

There are three basic forms of abundance and trend data.

1. Absolute abundance estimates
2. Relative abundance estimates
3. Capture-recapture data

The minimum number of haplotypes for each population is also given. These numbers are used as an indication of what the minimum size of the populations may have been, and (when multiplied by 4) could be incorporated into the model as lower bounds.

Breeding Stock A

Absolute abundance estimate

From Andriolo et al. (2006).

Estimate from a fixed-wing aircraft survey off Brazil

Year	N	CV
2005	6251	0.17

Relative abundance estimates

Breeding ground index of abundance:

From Andriolo et al. (2006).

These are from line transect surveys using ship and aerial surveys. Ship surveys were conducted off the northeastern coast of Brazil (5-12˚S) (Zerbini *et al.,* 2004) and aerial surveys were conducted from 2001-2005. Estimates of abundance from the aerial surveys conducted from 2002-2004 were obtained using comparable methodology (Andriolo *et al.*, 2006), but covered only a portion of the range of the stock (12-21˚S). Therefore these estimates are used as an index of relative abundance (Zerbini *et al.,* in press).

Year	N	CV
2002	2305	0.2
2003	2539	0.19
2004	3615	0.19

Feeding ground index of abundance:

From Branch (in press).

IDCR/SOWER estimates

Year	Mid year	N	CV
1981/82	81/82	45	0.88
1986/87	86/87	259	0.62
1996-1998	97/98	200	0.64

Minimum number of haplotypes

62 (Rosenbaum *et al.*, 2006)

Breeding Stock B

Absolute abundance estimate

From Collins et al. (2008).

The estimates given below are for the year 2003 and result from the MARK program estimates when fitted to the photo-ID capture-recapture data from Iguela only (lower estimate of 6342 in 2003) and the genetic data from Iguela only (upper estimate of 7196 in 2003).

lower	6432	CV	0.18
upper	7196	CV	0.15

Relative abundance estimates

From Branch (in press)

IDCR/SOWER estimates for the breeding grounds over 20˚W-10˚E for breeding stock B.

Year	Mid year	N	CV
1980	80/81	692	0.84
1986	86/87	70	0.63
1995	95/96	595	0.51

Mark-recapture

From Collins et al. (2008)

Photographs and biopsies were collected from the coastal waters of Gabon during the austral winter (July-October) in each year between 2001 and 2006. Data analysed were from two field sites: Iguela (1˚51'S, 9˚20'E) and Mayumba (3˚22'S, 10˚38'E).

Photo-ID (total sample from all sites)

N	2000	2001	2002	2003	2004	2005	2006
	24	111	233	161	138	216	199

M	2000	2001	2002	2003	2004	2005	2006
2000	X	0	1	0	0	0	0
2001		X	5	6	5	2	1
2002			X	12	2	2	4
2003				X	7	2	1
2004					X	2	2
2005						X	6
2006							X

Photo-ID (Iguela only)

N		2001	2002	2003	2004	2005
		111	143	161	138	123

M		2001	2002	2003	2004	2005
2001		X	4	6	5	1
2002			X	6	6	1
2003				X	7	1
2004					X	0
2005						X

Genotypes (total samples from all sites) (secondary data)

N	2000	2001	2002	2003	2004	2005	2006
	82	155	257	270	188	296	207

M	2000	2001	2002	2003	2004	2005	2006
2000	X	1	1	4	2	3	0
2001		X	6	8	6	3	2
2002			X	6	6	6	4
2003				X	8	7	1
2004					X	3	3
2005						X	11
2006							X

Genotypes (Iguela only) (secondary data)

N		2001	2002	2003	2004	2005
		155	170	270	188	137

M		2001	2002	2003	2004	2005
2001		X	6	8	6	0
2002			X	4	2	6
2003				X	8	4
2004					X	6
2005						X

Note: In line with the methods of analysis used, these Tables are structured such that if a whale is recaptured twice, say, the second recapture is linked only to the first recapture treated as a new capture.

Note that in this assessment only the photographic capture-recapture information for all regions combined was used.

<u>**Minimum number of haplotypes**</u> (Rosenbaum *et al*., 2006)

Total: 147

Gabon (B1): 92

Angola & West South Africa: 55

Breeding Stock C

<u>**Absolute abundance estimate**</u>

C1 estimate provided by Findlay *et al.* (in press)

C3 estimates obtained using the MARK program applied to capture-recapture data from both photo-ID and genotypic data (lower est 6737, CV=0.31, upper est 7715, CV=0.24) (Cerchio *et al.,* 2008a)

	Year	Estimate	CV
C1	2003	5965	0.17
C3	2005	7715	0.24

<u>**Relative abundance estimates**</u>

Cape Vidal sightings per unit effort data for the 1988-2002 period (Findlay and Best, 2006). These are obtained form shore-based surveys of northwards-migrating humpback whales at Cape Vidal, north KZN.

Year	Estimate
1988	358
1989	249
1990	359
1991	587
2002	1673

IDCR/SOWER estimates for the breeding grounds (10˚E-60˚E). *(*Branch, in press)

Year	Mid year	N	CV
1979	79/80	1043	0.62
1987	87/88	926	0.57
1993	93/94	2391	0.41

<u>**Mark-recapture**</u>

Reported in Cerchio *et al.* (2008a and b) except for the addition of C1 data for 2007 provided by Findlay (pers. commn). These consist of photo-ID 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 years 2000 and 2004 for C1 and the year 2002 for C3 are excluded in the assessment due to poor temporal coverage of capture effort.

Seen in C1 and re-seen in C1

n	2000	2001	2002	2003	2004	2005	2006	2007
	3	24	49	115	21	134	112	167

m	2000	2001	2002	2003	2004	2005	2006	2007
2000	X	0	0	0	0	0	0	0
2001		X	1	0	0	0	0	0
2002			X	1	1	0	0	1
2003				X	0	0	0	1
2004					X	1	0	0
2005						X	2	3
2006							X	1

Seen in C3 and re-seen in C3

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

Between C1 and C3

n	2000	2001	2002	2003	2004	2005	2006
C1	89	159	16	126	151	144	158
C3	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	0	0	0	0	0
2002			X	0	0	0	0
2003				X	0	0	0
2004					X	0	0
2005						X	0
2006							X

Minimum number of haplotypes (Rosenbaum *et al*. ,2006)

Total: 188

C1: 62

C2: 38

C3: 88

Updated C2&C3: 93 (Rosenbaum, pers. commn)

Breeding Stock D

Absolute abundance estimate

From Hedley et al. (2008)

Single platform aerial line transect and land-based surveys:

Estimated abundance of northward-migrating whales during that time (2 June-7 Sep 2008) is **21750 (95% CI: 17550-43000)**. This estimate is based on an estimate of relative abundance of surface whales of 11850 (9550-23450) and an estimated $g(0)$ of 0.54 (+-0.21). Note the numbers in parenthesis are 95% percentile intervals and these do not include variance in $g(0)$.

Relative abundance estimates

From Bannister and Hedley (2001)

IWC 1996: Aerial survey estimate for 1999 is 3441 (95%CI 2757, 4294)

Year	Estimate
1982	10.2
1986	16.2
1988	12.7
1991	23.6
1994	36

From Matsuoka et al. (in press)

JARPA surveys conducted during 1989/90-2004/05 austral summer seasons (January and February) alternating survey areas between Area IV (70˚E-130˚E) and Area V (130˚E-170˚W), all south of 60˚S. Areas IV and V were divided into 2 sectors, western and eastern. Each sector was divided into northern (60˚S to 45 n. miles from ice-edge) and southern (from ice-edge to 45 n. miles away). BSD corresponds to Area IV.

Year	Estimate	CV
1989	5325	0.302
1991	5408	0.188
1993	2747	0.153
1995	8066	0.142
1997	10657	0.166
1999	16751	0.143
2001	31134	0.123
2003	27783	0.115

IDCR/SOWER estimates come from Branch (in press) (60˚E-120˚E).

Year	Estimate	CV
1978	1219	0.46
1988	4202	0.52
1997	17959	0.17

CPUE data from Chittleborough (1965)

Area IV (70˚E-130˚E)

Year	Estimate
1950	0.475
1951	0.424
1952	0.347
1953	0.353
1954	0.351
1955	0.244
1956	0.178
1957	0.146

1958	0.123
1959	0.09
1960	0.062
1961	0.055
1962	0.051

Minimum number of haplotypes (Rosenbaum *et al*., 2006)

51

Breeding Stock E

Absolute abundance estimate

From Noad et al. (2006)

In 2004 a land-based survey was conducted at Pt Lookout on the east coast of Australia over 14 weeks from 25 May to 27 August. The Hermite polynomial method was used to arrive at an absolute abundance estimate of **7090 ± 660 (95% CI)** for 2004.

Relative abundance estimates

Values provided by M. Noad (pers. commn), used for assessment in Noad et al. (2008).

Estimates from land-based surveys conducted at Pt Lookout and two other locations. The values give the number of whales passing per 10h during 4 weeks of the peak migration.

Year	Estimate
1984	6.1175
1985	5.92
1986	8.245
1987	8.5272
1988	9.1475
1989	10.22
1990	11.5815
1991	12.9275
1992	14.3575
1994	17.7525
1996	20.9075
1998	28.445
1999	27.454
2001	34.666
2002	37.34
2004	47.11
2007	70.73

CPUE (Chittleborough, 1965)

Area V (130˚E-170˚W)

Year	Estimate
1953	0.972
1954	0.755
1955	0.779
1956	0.704
1957	0.714
1958	0.75
1959	0.74
1960	0.522
1961	0.23
1962	0.69

Feeding area (JARPA)

From Matsuoka et al. (in press)

Surveys conducted during 1989/90-2004/05 austral summer seasons (January and February) alternating survey areas between Area IV (70˚E-130˚E) and Area V (130˚E-170˚W), all south of 60˚S. Areas IV and V were divided into 2 sectors, western and eastern. Each sector was divided into northern (60˚S to 45 n. miles from ice-edge) and southern (from ice-edge to 45 n. miles away). BSE corresponds to Area V.

Year	Estimate	CV
1990	602	0.343
1992	4388	0.623
1994	3678	0.307
1996	1474	0.274
1998	3831	0.430
2000	5128	0.215
2002	2873	0.157
2004	9342	0.337

IDCR/SOWER estimates for the breeding grounds (Branch, in press)

Here breeding stock E estimates corresponds to south of 60˚S and between 120˚E-170˚W.

Year	Mid year	N	CV
1978-1981	80/81	995	0.58
1985-1989	85/86	622	0.50
1991-1999	92/93	3484	0.33
1998-2004	01/02	13300	0.22

<u>Minimum number of haplotypes</u> (Rosenbaum *et al.*,2006)

Total: 108

E2: 60

E3: 48

From Olavarria *et al.*(2006): E1: 42

Breeding Stock F

Absolute abundance estimate

From Baker et al. (2006)

The estimate arises from a sighting-resighting analysis of individual identification photos collected from 1999 to 2004. Survey areas were New Caledonia and Tonga (E2 and E3), Cook Islands and French Polynesia (F).

Year	N	CV
2002	3827	0.12

Relative abundance estimates

IDCR/SOWER estimates for the breeding grounds. (Branch, in press)

In Branch (in press) BSF corresponds to the area south of 60˚S and between 170˚W-110˚W, where the naïve model is assumed.

Year	Mid year	N	CV
1982-1984	83/84	3240	0.47
1989-1991	90/91	2976	0.51
1995-2001	97/98	3852	0.22

<u>Minimum number of haplotypes</u> (Rosenbaum *et al.*, 2006)

Total: 230

F1: 131

F2: 99

Breeding Stock G

Absolute abundance estimate

From Felix et al. (in press)

Breeding ground estimate is from a photographic mark-recapture study in Ecuador, and is based on Chapman modified-Peterson estimator.

Year	N	CV
2006	6504	0.21

Relative abundance estimates

IDCR/SOWER estimates for the breeding grounds (Branch, in press)

Area for G: 110˚W-50˚W, south of 60˚S

1982	1452	0.65
1989	2817	0.38
1996	3310	0.21

Minimum number of haplotypes (Rosenbaum *et al*., 2006)

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