

UPDATED ASSESSMENTS OF SOUTHERN HEMISPHERE HUMPBACK WHALES FROM BREEDING STOCKS D AND G

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ABSTRACT

Bayesian stock assessment methodology is used to update the stock assessments of breeding stocks D and G of the Southern Hemisphere humpback whales. These assessments take into account the recently updated historic catch series, as well as the most recent estimates of current abundance and population trend information as presented at the Southern Hemisphere humpback whale workshop held in Hobart in April 2006. These stock assessments provide estimates of current as well as past abundances. Projections under a zero harvesting strategy are also presented.

KEYWORDS: HUMPBACK WHALES, BAYESIAN ASSESSMENT

INTRODUCTION

Bayesian stock assessments of the Southern Hemisphere humpback whale breeding stocks D and G are presented in this paper. Previous assessments of these stocks have been reported in Findlay *et al.* (2000), Findlay and Johnston (2001), Johnston *et al.* (2001) and Johnston and Butterworth (2005a, b; 2006). The stock assessments presented here are based on age-aggregated production models fitted to each stock separately. Two historic catch series for each stock are used: the **core** and the **fringe** series as specified at the April 2006 workshop in Hobart (IWC 2006). These catch series can be considered to reflect two extreme options for allocating the catches south of 40° - either including the least likely amount of catch (core) or the maximum amount of catch possible (fringe). The most reliable estimates of recent stock abundance presented at this same workshop are used in fitting the model to data. There is additional information for breeding stock D in the form of trend data; assessments for three different series are explored here, one from the breeding grounds and two from the feeding grounds associated with breeding stock D.

METHODS

Data

Historic catch data

The historic catch records for Southern Hemisphere humpback whales, which have recently (May 2006) been updated by Cherry Allison (IWC) can be separated into two categories: catches taken north of 40°S and catches taken south of 40°S. 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 what is now termed the “core” model, and also for what is now termed the “fringe” model (IWC 2006).

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

Breeding Stock D: Core = 80°E - 100°E
 Fringe = 50°E - 130°E

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Breeding stock G: Core = 50⁰ W - 100⁰ W
 Fringe = 50⁰ W - 120⁰ W

Recent absolute abundance estimates

Estimates of recent absolute stock abundance for breeding stocks D and G considered here are reported in Tables 2a and b respectively, along with their associated estimated CVs. These estimates include those selected by the humpback workshop in April (IWC 2006) as being the most reliable.

Breeding stock D

The Bannister and Hedley (2001) abundance estimate for the breeding stock area in 1999 was updated by Paxton *et al.* (2006) and is now 10032 (CV=0.11), and was recommended for use by IWC (2006).

In addition, two estimates from the feeding grounds associated with breeding stock D are available and are used as sensitivity tests:

- i) the JARPA abundance estimate of 31750 (CV=0.11) for Area IV (70°-130°E) south of 60°S for 2003 provided by Matsuoka *et al.* (2006), and
- ii) the IDCR abundance estimate of 17959 (CV=0.17) for 1997 for the area south of 60°S between longitudes 60° and 120°E (corresponding to the previous “naïve” model for allocating catches) provided by Branch (2006).

Breeding stock G

For breeding stock G, the April 2006 workshop (IWC 2006) recommended stock assessments use the following two abundance estimates for breeding stock G:

- i) an estimate of 2917 (CV=0.19) from Felix *et al.* (2006), and
- ii) an estimate of 3851 (CV=0.02) from Stevick *et al.* (2006).

Trend data

Relative abundance trend data for breeding stock D are available from three sources and are reported in Table 3a:

- i) IWC (1996) for the breeding grounds; this includes five surveys spanning the period 1982-1994,
- ii) JARPA abundance estimates for the feeding grounds from Matsuoka *et al.* (2006), and
- iii) IDCR abundance estimates for the feeding grounds from Branch (2006).

CPUE data shown in Table 3b pertain to the breeding grounds for stock D; these are from Chittleborough (1965) and span the period 1950-1962.

The population dynamics models

The population model is a sex- and age-aggregated production model. The details of this model and the associated Bayesian estimation framework are reported in the Appendix. The population model for breeding stock G is fit separately to the two recent population abundance estimates only. As no trend data are available for this stock, the prior for the maximum growth rate parameter, r , needs to be informative. For this reason, the posterior distribution for this parameter from a model which has been fit for both breeding stocks D and E together (and which allows for mixing on the feeding grounds) (Johnston and Butterworth 2006) is used as a prior for the assessment of breeding stock G. Sensitivity of results to variations of this prior is explored.

For breeding stock D, the prior for r is uniform U[0, 0.126].

Projections

The populations for all breeding stocks are projected into the future under a continuation of a zero harvesting strategy.

Sensitivity analyses

For both breeding stock D and G, analyses are reported for both the core and fringe catch allocation hypotheses.

Breeding stock D

Scenarios for a number of combinations of the recent abundance level (Paxton *et al.* (2006), JARPA, IDCR) and the trend data (IWC (1996), JARPA, IDCR) are considered. Here the Paxton *et al.* (2006) recent abundance estimate is considered in conjunction with the three alternate trend series, as well as models that input either only JARPA data or only IDCR data. Future analyses will consider further combinations, as well as sensitivity to an upper bound on the r prior and a change in the carrying capacity over time.

Breeding stock G

Analyses using both the recent abundance estimates are conducted. Sensitivity to the prior specified for r is examined, where r is instead drawn from a uniform distribution $U[0, 0.126]$. Sensitivity to placing an upper bound on the prior for r of either 0.11 or 0.10 is also examined. Finally, the possibility of depensation is explored as detailed below.

Depensation

For each stock, a minimum plausible population size is determined. This is reasonably specified as 4 times the number of mitochondrial haplotypes observed for the population (J Jackson, pers. comm). For breeding stock D the number of such haplotypes is 51 (Rosenbaum *et al.* 2006) giving a minimum plausible population size of 204. For breeding stock G this number is 27 (Rosenbaum *et al.* 2006) corresponding to a minimum plausible population size of 108.

As will become evident below, for breeding stock G (though not for breeding stock D), some fits of the population model reflect minimum size distributions which extend below this genetically determined minimum. As a sensitivity therefore, some runs of the model for breeding stock G are re-computed with depensation included to an extent sufficient that none of the set of population trajectories generated show a size lower than the genetically determined minimum of 108.

Depensation is introduced into the population model through the following simple one-parameter formulation:

$$\text{Basic Model: } N_{y+1} = N_y + rN_y \left[1 - \left(\frac{N_y}{K} \right)^{2.39} \right] - C_y$$

$$\text{With depensation added: } N_{y+1} = N_y + rN_y \left[1 - \left(\frac{N_y}{K} \right)^{2.39} \right] f(N_y) - C_y$$

$$\text{where } \begin{aligned} f(N) &= 1 && \text{for } N > xK \\ f(N) &= N/(xK) && \text{for } N \leq xK \end{aligned}$$

Figure 1 illustrates how the introduction of depensation in this way alters both the net population growth and the net per capita growth functions. The (minimum) value of x was determined by increasing x slowly until no population trajectories (amongst the 5000 generated from the Bayesian analysis) contained a population level below the minimum plausible population size indicated by genetics.

For breeding stock G with the Stevick *et al.* (2006) recent abundance estimate input, this value of x was determined to be 0.026.

RESULTS AND DISCUSSION

Breeding stock D

Table 4 reports breeding stock D model results for a number of model variants. There is very little sensitivity to the historic catch series used. for the Paxton *et al.* (2006) recent abundance estimate (and the core historic catch series), sensitivity to fitting to three alternative trend data series is reported. The IWC (1996) trend data lead to

an estimate of the present status of the breeding stock of about 0.86K, whilst the JARPA and IDCR trend series produce slightly more optimistic estimates of present status – 0.90K and 0.95K respectively. Figure 2a illustrates these model fits to their respective trend data series. Note that the model is unable to match the high rate of increase indicated by both the JARPA and the IDCR series of estimates. Figure 2b compares the estimated and observed CPUE trends for the model variant which assumes the Paxton *et al.* (2006) recent abundance estimate and the IWC (1996) relative abundance trend; there is a reasonably good agreement between the two.

Model fits which input either the recent IDCR or JARPA estimate of abundance give poor results, in that they are unable to reflect the trends in these estimates of abundance (Figures 2c and 3b), and indicate minimum population sizes which are unrealistically large because they do not reflect the clearly depressed state of the stock in the 1960s (see Table 4). If breeding stock D as modeled here is indeed a closed population, an increase in carrying capacity would need to be postulated to restore some agreement between observed and modeled population trends for these cases.

Breeding stock G

Table 5a shows that for this stock there is very little sensitivity of results to the alternate historic catch series used (core versus fringe). There is far greater sensitivity to the recent abundance estimate input, with the Felix *et al.* (2006) estimate producing results which show breeding stock G to be currently around 0.39K, while the Stevick *et al.* (2006) estimate producing results which are more optimistic, with a current abundance estimate of 0.80K for the Reference case. The median N_{\min} estimate when the Felix *et al.* (2006) abundance estimate is input is 68-70, which is below the genetically indicated minimum plausible population size of 108.

The sensitivity results when using a prior for r of U[0, 0.126] for breeding stock G illustrate why an informative prior is required for this stock, for which there is no information on trend. The median of the posterior for r for this sensitivity test is simply the average of 0 and 0.126.

Reducing the upper bound on the r prior makes little difference to most of the results, except that the lowest population size (N_{\min}) increases. Including depensation to an extent sufficient to ensure that all population trajectories generated have N_{\min} values above the genetically indicated minimum plausible population size results in smaller posterior median r estimates - 0.095 compared to 0.117 in the absence of depensation.. The median N_{\min} values increase, as do the estimates of current (2006) abundance, both in absolute terms and relative to K .

Projections

Estimated population trends together with posterior probability intervals for breeding stock D are illustrated in Figures 3a and 3b, and for breeding stock G in Figure 3c. Under a zero continued future harvesting strategy, by 2020, breeding stock D is estimated to be fully recovered (effectively back at K) in median terms for all model variants examined here. For the Reference case assessments, breeding stock G is estimated, in posterior median terms, to reach 0.94K (for the Felix *et al.* (2006) current abundance estimate) and 1.00K (for the Stevick *et al.* (2006) current abundance estimate) by 2020. These results are less well founded than for breeding stock D as they are heavily dependent on the use of an informative prior for r because no trend information is available (unlike the situation for stock D).

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Table 1a

Catches taken north of 40⁰S for southern hemisphere humpback whales. Catches are reported for breeding stocks (BS) D and G (C. Allison pers. commn).

	BS D	BS G		BS D	BS G
1900	0	0	1951	1224	26
1901	0	0	1952	1187	27
1902	0	0	1953	1300	29
1903	0	0	1956	1119	10
1904	0	0	1957	1120	5
1905	0	0	1958	967	0
1906	0	0	1959	700	3
1907	0	0	1960	545	2
1908	0	16	1961	580	3
1909	0	44	1962	548.2	4
1910	0	62	1963	87	1
1911	0	92	1964	2	35
1912	234	86	1965	75.8	143
1913	993	45	1966	30	58
1914	1968	195	1967	2	0
1915	1297	30	1968	0	3
1916	388	15	1969	0	1
1917	0	15	1970	0	0
1918	0	23	TOTALS	28406	2119
1919	0	24			
1920	0	21			
1921	0	21			
1922	155	19			
1923	166	16			
1924	0	34			
1925	669	248			
1926	735	277			
1927	996	40			
1928	1035	36			
1929	0	26			
1930	0	33			
1931	0	53			
1932	0	21			
1933	0	11			
1934	0	13			
1935	0	31			
1936	3076	18			
1937	3250	28			
1938	917	6			
1939	0	7			
1940	0	0			
1941	0	0			
1942	0	0			
1943	0	0			
1944	0	0			
1945	0	0			
1946	0	15			
1947	2	19			
1948	4	5			
1949	190	6			
1950	388	5			
1954	1320	106			
1955	1126	7			

Table 1b

Catches taken south of 40°S for southern hemisphere humpback whales. Catches have been apportioned into feeding areas (C. Allison pers. commn). These catches correspond to either the **core** or the **fringe** catch allocation hypotheses (IWC, 2006). Catches allocated to breeding areas D and G are reported.

	Core Hypothesis		Fringe Hypothesis			Core Hypothesis		Fringe Hypothesis	
	BS D	BS G	BS D	BS G		BS D	BS G	BS D	BS G
1900	0	0	0	0	1942	0	0	0	0
1901	0	0	0	0	1943	0	0	0	0
1902	0	0	0	0	1944	0	0	0	0
1903	0	1	0	1	1945	0	0	0	0
1904	0	0	0	0	1946	0	0	0	0
1905	0	23	0	23	1947	0	0	1	0
1906	0	498	0	498	1948	0	0	0	0
1907	0	366	0	366	1949	564	0	784	0
1908	0	1246	217	1246	1950	950	271	1115	271
1909	0	1481	118	1481	1951	268	0	1132	0
1910	0	2527	83	2527	1952	190	0	193	0
1911	0	2039	0	2039	1953	259	0	261	0
1912	0	976	0	976	1954	20	0	27	0
1913	0	1038	0	1038	1955	436	14	1576	14
1914	0	656	0	656	1956	0	599.6	3	665.6
1915	0	219	0	219	1957	1488	59	1911	90
1916	0	21	0	21	1958	1866	52.4	4571	52.4
1917	0	69	0	69	1959	108	201	310	282.1
1918	0	81	0	81	1960	131.8	88	740	88
1919	0	181	0	181	1961	178	1167	378	1265
1920	0	149	0	149	1962	1057	278.2	1780	320.7
1921	0	0	0	0	1963	221.4	0	379	0
1922	0	189	0	189	1964	36.8	0	94	0
1923	0	96	0	96	1965	61.2	0	103	0
1924	0	102	0	102	1966	65	0	147	0
1925	0	163	0	163	1967	45	0	98	0
1926	0	88	0	88	1968	0	0	0	0
1927	0	3	0	3	1969	0	0	0	0
1928	0	16	11	16	1970	0	0	0	0
1929	0	0	11	0	1971	0	0	0	3
1930	20	1	35	1	1972	0	0	0	0
1931	52	0	161	0	1973	0	0	0	0
1932	79	0	86	0	1974	0	0	0	0
1933	500	0	620	0	1975	0	0	0	0
1934	1230	0	1351	0	TOTALS	12753.2	14959.2	22751	15280.8
1935	940	0	950	0					
1936	1352	0	1435	0					
1937	462	0	869	0					
1938	173	0	859	0					
1939	0	0	0	0					
1940	0	0	342	0					
1941	0	0	0	0					

Table 2a

Recent absolute abundance estimates considered for assessments of breeding stock D. The first entry refers to a survey on the breeding ground, and the other two to feeding ground surveys.

Year	Abundance estimate	Source
1999	10032 (CV=0.11)	Paxton <i>et al.</i> (2006)
2003	31750 (CV=0.11)	Matsuoka <i>et al.</i> (2006)
1997	17959 (CV=0.17)	Branch (2006)

Table 2b

Recent absolute abundance estimates considered for assessments of breeding stock G.

Year	Abundance estimate	Source
2003	2917 (CV=0.19)	Felix <i>et al.</i> (2006)
1997	3851 (CV=0.02)	Stevick <i>et al.</i> (2006)

Table 3a

Relative abundance estimates for breeding stock D that are used to provide information on population trend.

IWC (1996) reports estimates from breeding ground surveys. The other two series of estimates refer to feeding grounds south of 60°S, and are estimates of absolute abundance though they are treated as relative indices in the model fitting process. The JARPA estimates apply to Area IV (70°-130°E) (Matsuoka *et al.* 2006), while those from the IDCR-SOWER sightings surveys (Branch 2006) pertain to the original naïve model's specification of 60°-120°E for the feeding area for breeding stock D.

Year	IWC 1996
1982	10.2
1986	16.2
1988	12.7
1991	23.6
1994	36.0
JARPA	
1989	5230
1991	5350
1993	2740
1995	8850
1997	10874
1999	16211
2001	33010
2003	31750
IDCR	
1978	1033
1988	3869
1997	17959

Table 3b

Breeding stock D CPUE data (Chittleborough 1965).

Year	Breeding stock D
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	0.090
1960	0.062
1961	0.055
1962	0.051

Table 4

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

Historic Catch Recent abundance Trend information	Reference Case: Core Paxton <i>et al.</i> (2006) IWC (1996)	Reference Case: Fringe Paxton <i>et al.</i> (2006) IWC (1996)
r	0.101 [0.052; 0.122]	0.101 [0.055; 0.123]
K	16639 [14972; 22776]	17163 [15631; 22394]
N_{min}	563 [299; 1932]	553 [294; 1820]
N_{2006}	14209 [12550; 15439]	14494 [12647; 15729]
N_{min}/K	0.034 [0.020; 0.086]	0.032 [0.019; 0.081]
N_{2006}/K	0.858 [0.556; 0.950]	0.846 [0.567; 0.942]
N_{2020}/K	0.996 [0.844; 1.000]	0.996 [0.860; 0.999]
N_{2040}/K	1.000 [0.981; 1.000]	1.000 [0.983; 1.000]

Historic Catch Recent abundance Trend information	Core Paxton <i>et al.</i> (2006) JARPA trend	Core Paxton <i>et al.</i> (2006) IDCR trend
r	0.087 [0.021; 0.122]	0.100 [0.023; 0.124]
K	13368 [11163; 23125]	12410 [11079; 21868]
N_{min}	909 [333; 4667]	693 [307; 4227]
N_{2006}	11762 [10599; 13480]	11578 [10587; 13291]
N_{min}/K	0.068 [0.029; 0.204]	0.056 [0.027; 0.193]
N_{2006}/K	0.902 [0.454; 0.983]	0.947 [0.465; 0.991]
N_{2020}/K	0.996 [0.582; 0.999]	0.999 [0.597; 1.000]
N_{2040}/K	1.000 [0.761; 0.999]	1.000 [0.964; 1.000]

Historic Catch Recent abundance Trend information	Core JARPA JARPA trend	Core IDCR IDCR trend
r	0.056 [0.005; 0.118]	0.056 [0.007; 0.117]
K	33357 [27014; 49979]	20043 [15624; 36906]
N_{min}	26172 [17251; 34324]	10189 [5860; 17356]
N_{2006}	32856 [25479; 37939]	18795 [15480; 22421]
N_{min}/K	0.785 [0.515; 0.956]	0.409 [0.270; 0.861]
N_{2006}/K	0.998 [0.625; 1.000]	0.977 [0.489; 1.000]
N_{2020}/K	1.000 [0.653; 1.000]	0.997 [0.525; 1.000]
N_{2040}/K	1.000 [0.695; 1.000]	1.000 [0.939; 1.000]

Table 5a

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

Reference case		
<i>r</i> prior	<i>r</i> ~ posterior (D,E)	<i>r</i> ~ posterior (D,E)
Historic catch	Core	Core
Recent abundance	Felix <i>et al.</i> (2006)	Stevick <i>et al.</i> (2006)
<i>r</i>	0.117 [0.086; 0.125]	0.117 [0.086; 0.125]
<i>K</i>	9998 [9816; 10758]	10000 [9816; 10762]
<i>N</i> _{min}	68 [44; 174]	165 [133; 365]
<i>N</i> ₂₀₀₆	3937 [2896; 5272]	7970 [7064; 8265]
<i>N</i> _{min} / <i>K</i>	0.007 [0.004; 0.016]	0.017 [0.013; 0.034]
<i>N</i> ₂₀₀₆ / <i>K</i>	0.391 [0.281; 0.527]	0.798 [0.656; 0.839]
<i>N</i> ₂₀₂₀ / <i>K</i>	0.942 [0.779; 0.981]	0.997 [0.968; 0.998]
<i>N</i> ₂₀₄₀ / <i>K</i>	1.000 [0.997; 1.000]	1.000 [1.000; 1.000]
Reference case		
<i>r</i> prior	<i>r</i> ~ posterior (D,E)	<i>r</i> ~ posterior (D,E)
Historic catch	Fringe	Fringe
Recent abundance	Felix <i>et al.</i> (2006)	Stevick <i>et al.</i> (2006)
<i>r</i>	0.117 [0.086; 0.126]	0.117 [0.086; 0.125]
<i>K</i>	10000 [9816; 10764]	10001 [9817; 10767]
<i>N</i> _{min}	70 [46; 177]	167 [134; 364]
<i>N</i> ₂₀₀₆	3943 [2900; 5276]	7969 [7056; 8258]
<i>N</i> _{min} / <i>K</i>	0.007 [0.005; 0.016]	0.617 [0.014; 0.034]
<i>N</i> ₂₀₀₆ / <i>K</i>	0.391 [0.282; 0.526]	0.798 [0.655; 0.838]
<i>N</i> ₂₀₂₀ / <i>K</i>	0.942 [0.774; 0.982]	0.997 [0.968; 0.998]
<i>N</i> ₂₀₄₀ / <i>K</i>	1.000 [0.997; 1.000]	1.000 [1.000; 1.000]
<i>r</i> prior	<i>r</i> ~ U[0, 0.126]	<i>r</i> ~ U[0, 0.126]
Historic catch	Core	Core
Recent abundance	Felix <i>et al.</i> (2006)	Stevick <i>et al.</i> (2006)
<i>r</i>	0.064 [0.006; 0.120]	0.063 [0.006; 0.121]
<i>K</i>	11490 [9935; 17744]	11556 [9920; 18417]
<i>N</i> _{min}	334 [58; 2385]	680 [149; 3240]
<i>N</i> ₂₀₀₆	3471 [2446; 4830]	6226 [4060; 8068]
<i>N</i> _{min} / <i>K</i>	0.029 [0.005; 0.137]	0.059 [0.015; 0.176]
<i>N</i> ₂₀₀₆ / <i>K</i>	0.297 [0.157; 0.461]	0.539 [0.221; 0.812]
<i>N</i> ₂₀₂₀ / <i>K</i>	0.630 [0.177; 0.960]	0.871 [0.238; 0.997]
<i>N</i> ₂₀₄₀ / <i>K</i>	0.968 [0.199; 1.000]	0.994 [0.267; 1.000]

Table 5b

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

<i>r</i> prior	<i>r</i> ~ posterior (D,E) with upper bound of 0.11	<i>r</i> ~ posterior (D,E) with upper bound of 0.11
Historic catch	Core	Core
Recent abundance	Felix <i>et al.</i> (2006)	Stevick <i>et al.</i> (2006)
<i>r</i>	0.100 [0.071; 0.109]	0.100 [0.070; 0.109]
<i>K</i>	10391 [10169; 11242]	10390 [10171; 11279]
<i>N</i> _{min}	111 [70; 272]	252 [199; 555]
<i>N</i> ₂₀₀₆	3769 [2804; 5064]	7535 [6523; 7911]
<i>N</i> _{min} / <i>K</i>	0.011 [0.007; 0.024]	0.024 [0.020; 0.049]
<i>N</i> ₂₀₀₆ / <i>K</i>	0.361 [0.264; 0.487]	0.726 [0.579; 0.775]
<i>N</i> ₂₀₂₀ / <i>K</i>	0.879 [0.673; 0.955]	0.988 [0.913; 0.994]
<i>N</i> ₂₀₄₀ / <i>K</i>	0.993 [0.985; 1.000]	1.000 [0.997; 1.000]
<i>r</i> prior	<i>r</i> ~ posterior (D,E) with upper bound of 0.10	<i>r</i> ~ posterior (D,E) with upper bound of 0.10
Historic catch	Core	Core
Recent abundance	Felix <i>et al.</i> (2006)	Stevick <i>et al.</i> (2006)
<i>r</i>	0.091 [0.066; 0.099]	0.091 [0.066; 0.099]
<i>K</i>	10625 [10411; 11437]	10626 [10412; 11444]
<i>N</i> _{min}	147 [94; 350]	321 [256; 631]
<i>N</i> ₂₀₀₆	3713 [2721; 5023]	7242 [6288; 7626]
<i>N</i> _{min} / <i>K</i>	0.014 [0.009; 0.031]	0.030 [0.025; 0.055]
<i>N</i> ₂₀₀₆ / <i>K</i>	0.346 [0.249; 0.473]	0.682 [0.551; 0.729]
<i>N</i> ₂₀₂₀ / <i>K</i>	0.829 [0.605; 0.930]	0.977 [0.886; 0.988]
<i>N</i> ₂₀₄₀ / <i>K</i>	0.998 [0.969; 1.000]	1.000 [0.995; 1.000]
<i>r</i> prior	<i>r</i> ~ posterior (D,E)	<i>r</i> ~ posterior (D,E)
Historic catch	Core	Core
Recent abundance	Felix <i>et al.</i> (2006)	Stevick <i>et al.</i> (2006)
Depensation	<i>x</i> = 0.026	<i>x</i> = 0.026
<i>r</i>	0.095 [0.069; 0.111]	0.100 [0.070; 0.109]
<i>K</i>	10526 [10135; 11301]	10401 [10171; 11274]
<i>N</i> _{min}	144 [116; 283]	256 [208; 552]
<i>N</i> ₂₀₀₆	4350 [3134; 5886]	7540 [6540; 8006]
<i>N</i> _{min} / <i>K</i>	0.014 [0.011; 0.025]	0.025 [0.020; 0.049]
<i>N</i> ₂₀₀₆ / <i>K</i>	0.412 [0.282; 0.578]	0.725 [0.581; 0.786]
<i>N</i> ₂₀₂₀ / <i>K</i>	0.898 [0.655; 0.979]	0.988 [0.916; 0.995]
<i>N</i> ₂₀₄₀ / <i>K</i>	1.000 [0.979; 1.000]	1.000 [0.997; 1.000]

Figure 1

Figure to illustrate the effect of depensation. The population growth function without depensation shown in the top panel is $f(N) = N[1 - (N/K)^2]$, and the lower panel shows the corresponding per capita function $f(N)/N$. For illustrative purposes, x is set to 0.20 in these plots. See text for further details.

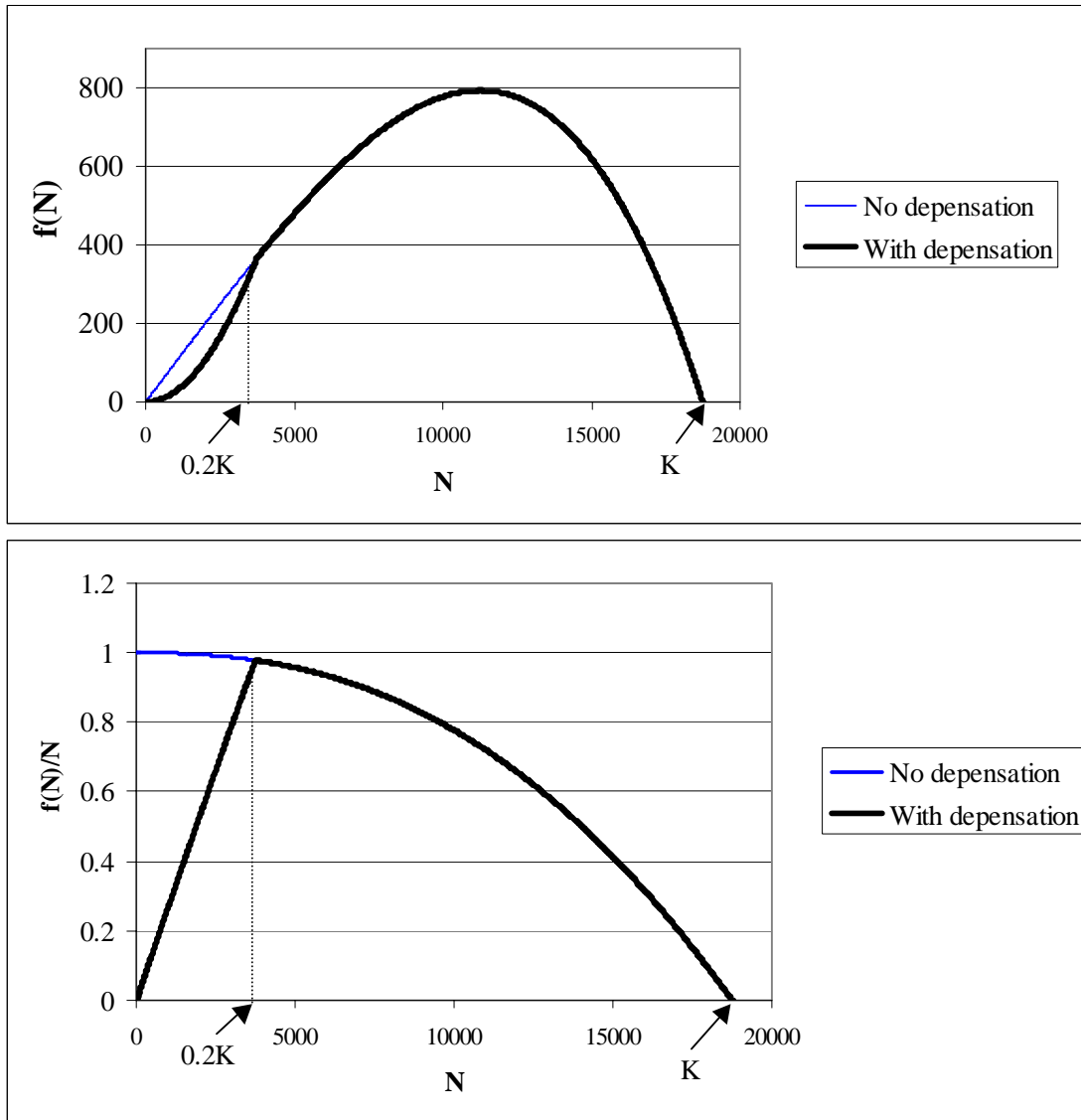


Figure 2a

Breeding stock D model fit to relative abundance data provided by i) IWC (1996), ii) JARPA and iii) IDCR surveys, where the Paxton *et al.* (2006) recent abundance estimate and the core historic catch series are used. The curves shown join the posterior medians.

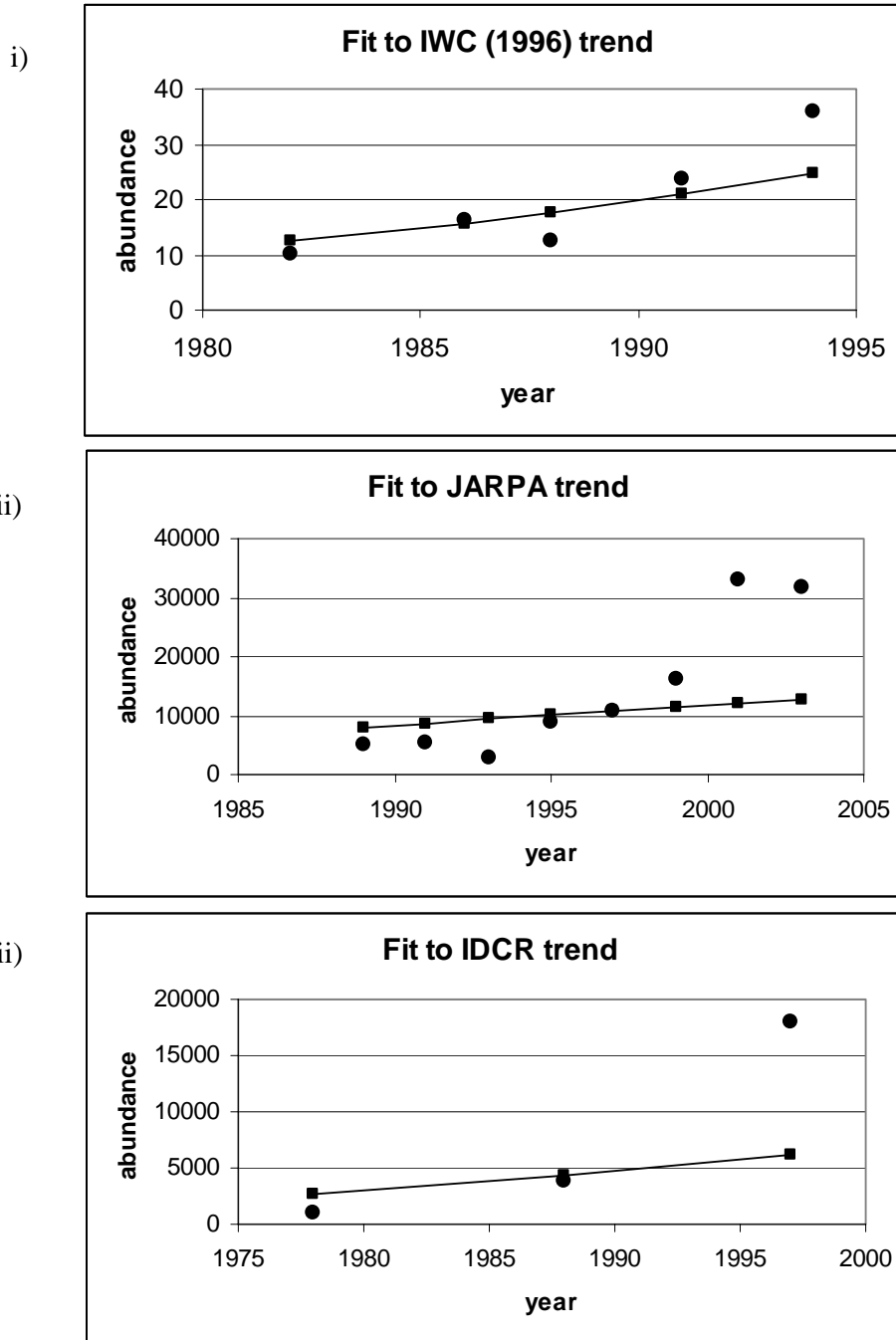


Figure 2b

Breeding stock D model fit to the CPUE data, where the Paxton *et al.* (2006) recent abundance estimate, the IWC (1996) trend data and the core historic catch series are input.. The curve shown joins the posterior medians.

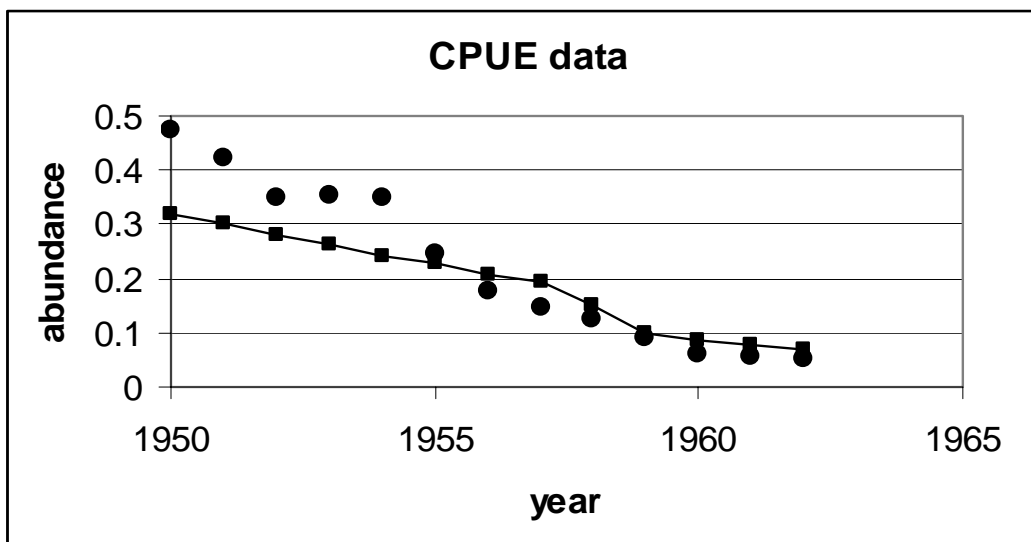
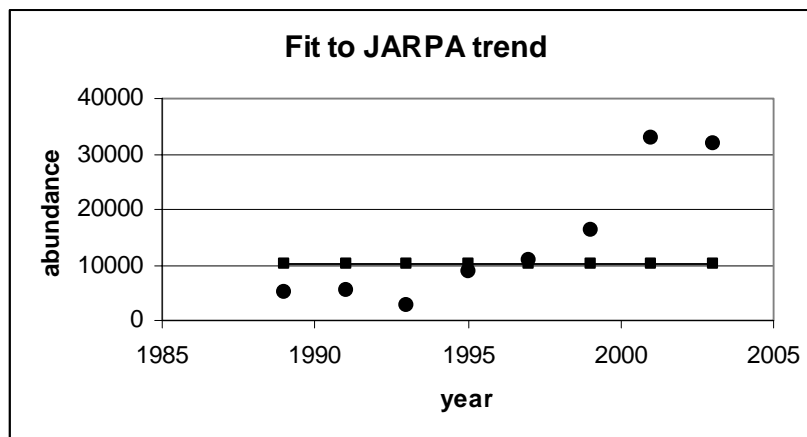


Figure 2c

Breeding stock D model fit to relative abundance data provided by i) JARPA and ii) IDCR surveys, where either the JARPA recent abundance estimate (for i) for the IDCR recent abundance estimate (for ii) are used, and the core historic catch series are used. The curves shown join the posterior medians.

i)



ii)

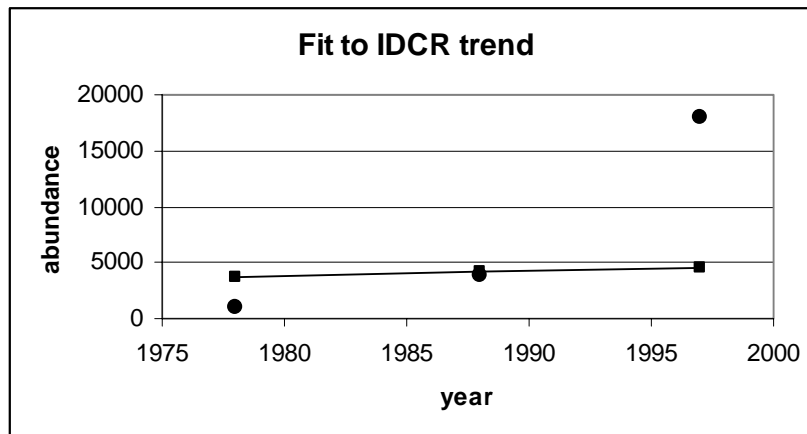


Figure 3a

Breeding stock D estimated population trends, with projected trajectories which assume a continued zero harvesting strategy. Results are for the scenarios where the Paxton *et al* (2006) recent abundance estimate is input together with relative abundance trend data from either the i) IWC (1996), ii) JARPA or iii) IDCR surveys.. The posterior medians together with 90% probability interval envelopes are illustrated. The vertical dashed lines are at 2004, after which the projections shown assume zero catch.

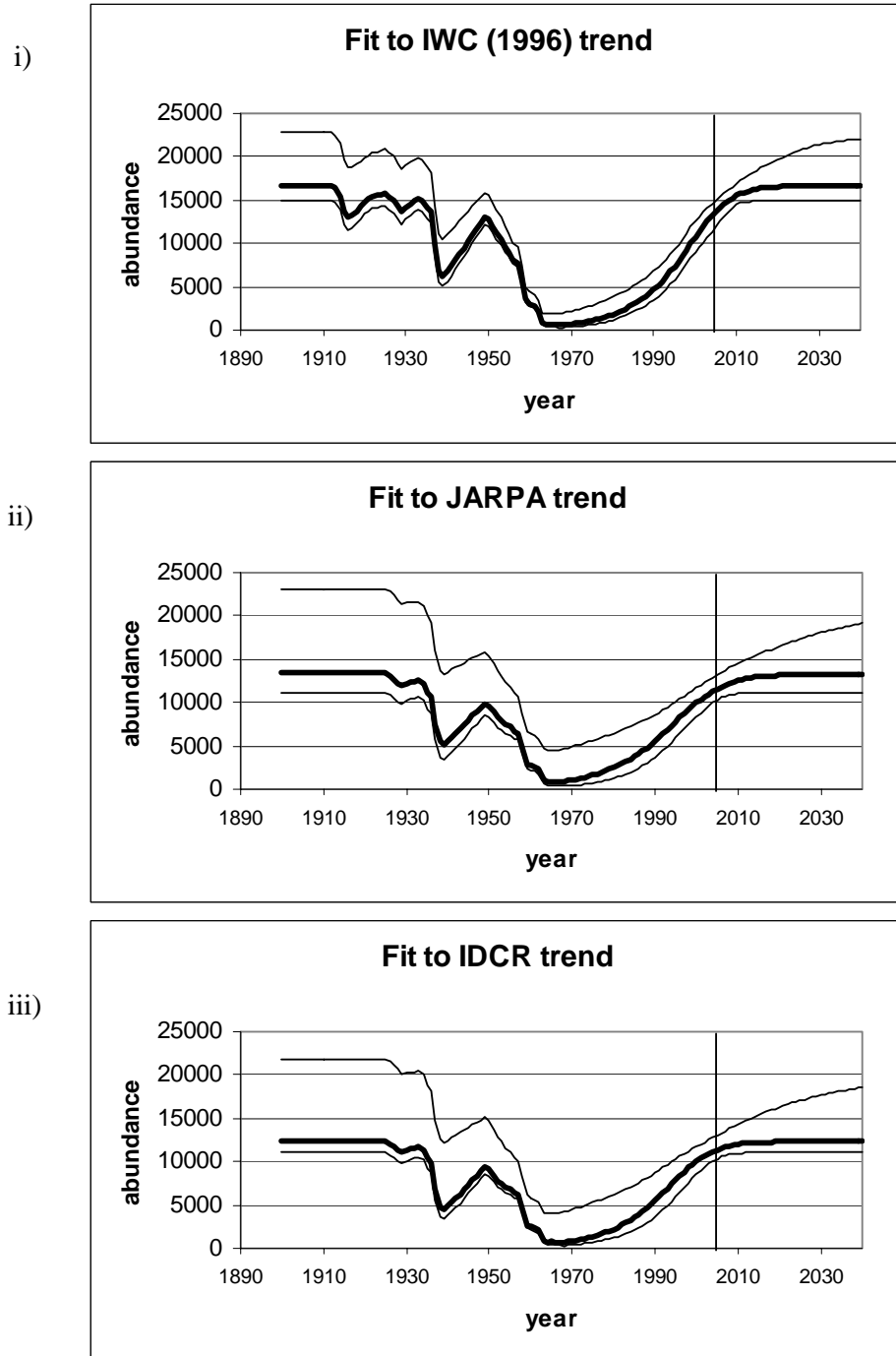
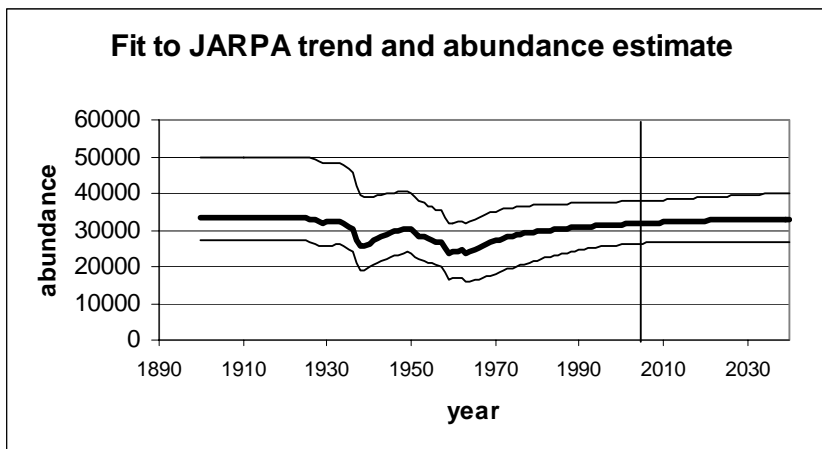


Figure 3b

Breeding stock D estimated population trends, with projected trajectories which assume a continued zero harvesting strategy. Results shown are for the scenarios where the model is fit to both the recent abundance estimate and the relative abundance data provided respectively by i) the JARPA and ii) the IDCR surveys. The posterior medians together with 90% probability interval envelopes are illustrated. The vertical dashed lines are at 2004, after which the projections shown assume zero catch.

i)



ii)

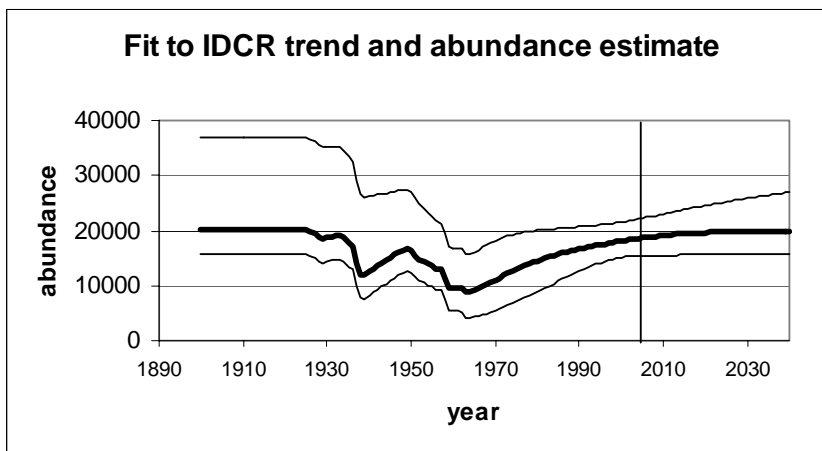
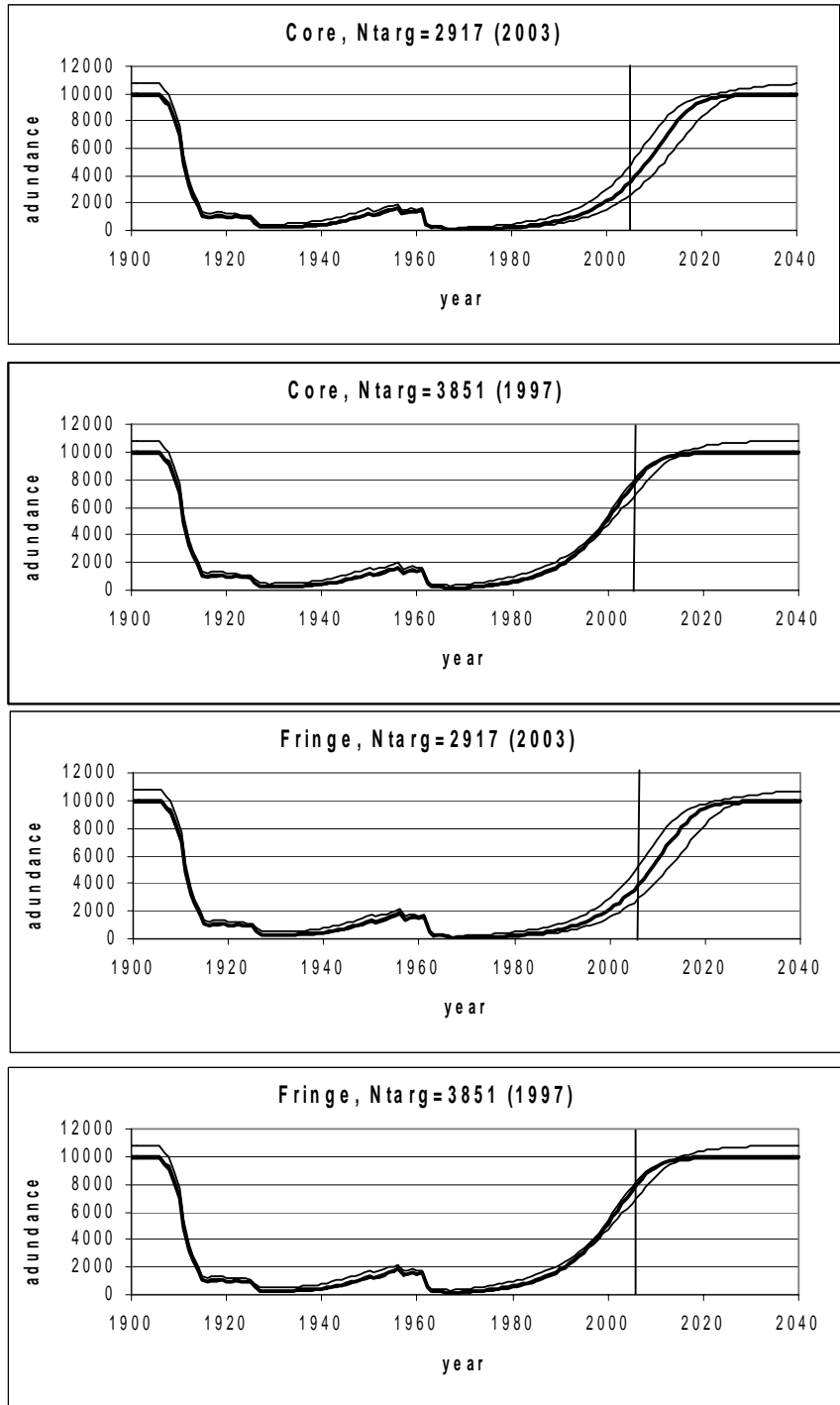


Figure 3c

Breeding stock G estimated population trends, with projected trajectories which assume a continued zero harvesting strategy. The posterior medians together with 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.



Appendix

Population model and Bayesian estimation procedure

The population dynamics models

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

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

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 IWC 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 derived from a joint assessment of stocks D and E (Johnston and Butterworth 2006), or $r \sim U[0,0.126]$
- 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 for r (based on the posteriors for 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, usually from the breeding grounds (see Table 2), and in the case of breeding stock C, also relative abundance trend data (see Table 3a). The components of the negative log likelihood are calculated as follows:

For breeding stock D:

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

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

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:

$$\begin{aligned}
 -\ln L = & \sum (n^X \ln \sigma^X + \frac{1}{2\sigma^{X^2}} \sum_y (\ln I_y^X - \ln q^X - \ln \hat{N}_y^X)^2) + \\
 & \frac{1}{2CV^2} (\ln N_Y^{X,obs} - \ln \hat{N}_Y^X)^2
 \end{aligned} \tag{3}$$

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

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

where

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

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

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

(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)).

For breeding stock G:

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

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

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:

$$w_j = \frac{L(\theta_j / data)}{\sum_{j=1}^{n_1} L(\theta_j / data)} \tag{7}$$

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.