Initial population model fits to the humpback breeding stocks D, E1 and Oceania

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ABSTRACT

This document provides initial results of population model fits to the Southern Hemisphere humpback whale breeding stocks D (West Australia), E1 (East Australia) and Oceania. The purpose of this document is to put preliminary results on the table to facilitate further discussion and model runs at IWC 64. The initial results indicate that breeding stock D is near to its pristine abundance, stock E1 is at an intermediate level, and Oceania is still heavily depleted. There are inconsistencies between the model and the various relative abundance indices for stock D, which need further discussion.

INTRODUCTION

The most computationally intensive aspect of the Bayesian population model presently used for assessing Southern Hemisphere humpback stocks is the development of the post-model pre-data distributions. To facilitate investigation of sensitivity of results to the different data choices for these models during IWC 64, these post-model pre-data distributions have been developed for simple separate single stock approaches to the assessment of breeding stocks D, E1 and Oceania. The paper first lists the data available, then details the analysis approach, and presents illustrative results for each of the stocks.

DATA

Historic catch data

There are two sets of historic catch data, both of which are available from Allison's database (C. Allison, *pers. comm.*):

i) Catches north of 40°S

These catches are given by location. Additionally there are some Russian catch data available by 10 degree longitude and latitude bands. The allocations of these catches to the breeding stocks considered in this assessment are described below.

Breeding stock D

Those labelled "Aust W" in the database have been allocated to BSD. Note that catches labelled "IndOcW" have been assumed to be associated with BSC. Russian catches taken between 80E and 130E have been allocated to BSD (a total of 120 catches).

Breeding Stock E1and Oceania

The catches for E1 and Oceania are given by landing station. Catches landed at LochTay, Tangalooma, Byron Bay and Rakiura have been allocated to BSE1. Catches landed at New Zealand, Kaikoura, Great Barrier Island, Whangamumu, Bay of Island, Norfolk Island, Tonga and Polynesia have been allocated to the Oceania breeding stock. Catches taken in the Cook Strait and Tory Channel are allocated according to two different catch allocation hypotheses:

   a) 100% of Cook Strait catches are allocated to BSE1 and 0% to Oceania.

   b) 0% of Cook Strait catches are allocated to BSE1 and 100% to Oceania.

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The resulting catch series are given in Table A. 1 of the Appendix.

ii) Catches south of 40°S

These catches are given in 10 degree longitude bands, and have been allocated to the breeding stocks according to Hypothesis 1 of Annex H (IWC, 2010) in the following manner:

Breeding stock D

- • 50% of catches taken between 60E and 80E (marginal C/D region)
- • 100% of catches taken between 80E and 110E (core D region)
- • 50% of catches taken between 110E and 130E (marginal D/E region)

Breeding Stock E and Oceania

- • 50% of catches taken between 110E and 130E allocated to BSE1
- • 100% of catches taken between 130E and 160E allocated to BSE1
- • Catches taken between 160E and 180E split 50:50 between BSE1 and Oceania
- • 100% of catches taken between 180E and 120W allocated to Oceania
- • 50% of catches taken between 120W and 100W allocated to Oceania

The resulting catch series are given in Table A. 2 of the Appendix.

Abundance and trend data

The data used in this assessment are listed in the Appendix. Below is a summary of which data where used for the base case and which data were used as independent consistency checks. Note that not all the data listed in the Appendix have been explored in these initial assessments.

Table 1: Summary of the assessment input data

Data	Base case	Consistency check
Breeding Stock D		
The Hedley *et al.* (2011) absolute abundance estimate	X	
The Hedley *et al.* (2011) relative abundance index	X	
The Hedley and Bannister (2001) relative abundance index	X	
The Chittleborough (1965) relative abundance index		X
The Matsuoka *et al.* (2011) relative abundance index		X
Breeding Stock E1		
The Noad *et al.* (2011) absolute abundance estimate	X	
The Noad *et al.* (2011) relative abundance index	X	
The Paton *et al.* (2011) absolute abundance index		X
The Chittleborough (1965) relative abundance index		X
The Matsuoka *et al.* (2011) relative abundance index		X
Oceania breeding stock		
The Constantine *et al.* (2011) mark recapture data	X	
The Constantine *et al.* (2011) absolute abundance estimate[2]		X

METHODS

Population dynamics

The population dynamics are given by the following equation:

$$N_{y+1}^i = N_y^i + r^i N_y^i \left(1 - (\frac{N_y^i}{K^i})^\mu \right) - C_y^i \qquad\qquad i \in \{D, E1, Oceania\} \qquad (1)$$

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[2] The absolute abundance estimate derived from the mark recapture data is used to set bounds on the uniform prior for the log target abundance estimate in the SIR process. The original mark recapture data are used in the likelihood function itself.

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 (the maximum per capita the population can achieve when its size is very low) of breeding population i,

K^i is the carrying capacity or pristine population level of breeding population i,

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

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

Bayesian estimation framework

Priors

Prior distributions are defined for the following parameters:

i) $r^i \sim U[0, 0.106]$

ii) $\ln \tilde{N}_{t\arg et}^{i,obs} \sim U[\ln N_{t\arg et}^{i,obs} - 4CV, \ln N_{t\arg et}^{i,obs} + 4CV]$

The target abundance estimate is fitted to the model-predicted number of whales for breeding population i.

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 agreed by the IWC Scientific Committee (IWC, 2007)). The prior distribution from which target abundance estimate $\tilde{N}_{t\arg et}^{i,obs}$ is drawn at random is uniform on a natural logarithmic scale. The lower and upper bounds are set by the CV of the abundance estimate multiplied by four.

Using the randomly drawn vector of values of $\tilde{N}_{t\arg et}^{i,obs}$ and r^i, a downhill simplex method of minimization is used to calculate K^i such that the model estimate of $N_{t\arg et}^i$ is identical to the randomly drawn value $\tilde{N}_{t\arg et}^{i,obs}$.

For each simulation, using the r^i and calculated K^i values, the available data are used to assign a likelihood to that particular combination. The components of the negative log likelihood are calculated as follows:

Likelihood function

Absolute abundance data

Given an absolute abundance estimate, $N_{t\arg et}^{obs}$, this is assumed to be log-normally distributed with the log of the estimate as the mean and the CV as the standard deviation[3]. Thus the negative log likelihood contribution is:

$$\frac{1}{2CV^2}\left(\ln N_{t\arg et}^{obs} - \ln N_{t\arg et}\right)^2 \tag{2}$$

where

$N_{t\arg et}^{obs}$ is the absolute abundance estimate obtained from observations,

$N_{t\arg et}$ is the model-estimated population size for the year of the abundance estimate, and

CV is the coefficient of variation of the $N_{t\arg et}^{obs}$ estimate.

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[3] If N is assumed to be log-normally distributed, then ln$N$ is normally distributed with some mean μ and standard deviation σ. The median value of N is then e^{μ} while the CV of N is given by $\sqrt{e^{\sigma^2} - 1}$. Solving backwards for μ and σ, μ is found to be the log of the median value for N and σ is simply the CV of N.

Relative abundance data

These estimates are given in a series spanning several years. Each year has a relative abundance index I_y, obtained from observations. It is assumed that this index is log-normally distributed about its expected value:

$$I_y = qN_y e^{\varepsilon_y}$$ (3)

where

I_y is the relative abundance estimate for year *y*,

q is a constant of proportionality[4],

N_y is the model estimate of observed population size at the start of year *y*, and

ε_y is from $N(0, \sigma^2)$ (see Equation (4) below).

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

$$\hat{\sigma} = \sqrt{1/\bar{n}\sum_y \left(\ln I_y - \ln q - \ln N_y\right)^2}$$ (4)

where

$\bar{n}$ is the number of data points in the series, and

q is a constant of proportionality, estimated by its maximum likelihood value:

$$\ln \hat{q} = 1/\bar{n}\sum_y \left(\ln I_y - \ln N_y\right)$$ (5)

The negative log-likelihood component for the relative abundance data is given by:

$$\bar{n}\ln\sigma + \frac{1}{2\sigma^2}\sum_y \left(\ln I_y - \ln q - \ln N_y\right)^2$$ (6)

In the Bayesian context, q and σ are "nuisance parameters, i.e. parameters that need to be estimated but are not of interest themselves (McAllister *et al.,* 1994). Walters and Ludwig (1994) show that the above approach is essentially a shortcut to avoid integrating over the prior distributions parameters and corresponds to the assumption that the *q* prior is uniformly distributed in log-space, and that the σ prior is proportional to σ^{-3}.

Mark recapture data

These data are given in the form a matrix showing counts of animals that were seen in a specific year and re-seen in a subsequent year. The method for incorporating this information into the likelihood is given below.

The capture-recapture data give:

n_y, the number of animals captured in year *y*, and

$m_{y,y'}$, the number of animals captured in year *y* that were recaptured in year *y´*.

If p_y is the probability that an animal is seen in regions *i* in year *y*, then the number of animals captured in year *y* is given by:

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[4] When plotting the relative abundance series along with the model-predicted median population values to assess how good the fit is, the relative abundance series each need to be scaled by a factor of *q*. In the SIR process, once the original sample is resampled (based on the weights calculated using the desired input data), the likelihood components for all the data sets (even those not used in the final likelihood calculation) can be computed for each of the n_2 resampled parameter combination of [*r*, lnN_{target}]. The likelihood component of each relative abundance series will have an associated *q* value, giving n_2 *q* values (representing samples from the posterior distribution of *q*), from which the median value can be computed. This value is then used to scale the relative abundance series for plotting as has been done in the figures of this document.

$$n_y = p_y N_y \tag{7}$$

where N_y is the total (1+) population. The model predicted number of animals captured in year y that were recaptured in year y' is given by:

$$\hat{m}_{y,y'} = p_y p_{y'} N_y e^{-M(y'-y)} \tag{8}$$

where M is the natural mortality rate (set here to equal 0.03 yr^{-1} as recommended by the IWC SC).

The probability of a model-predicted $\hat{m}_{y,y'}$, given the observed $m_{y,y'}$, is determined assuming a Poisson distribution[5], with the associated likelihood contribution given by:

$$\frac{\left(\hat{m}_{y,y'}\right)^{m_{y,y'}}}{\hat{m}_{y,y'}!} e^{-\hat{m}_{y,y'}} \tag{9}$$

The final component for the negative of the log-likelihood for capture-recapture data is then given by:

$$\sum_{y=y_o}^{y_f -1} \sum_{y'=y+1}^{y_f} [-m_{y,y'} \ln \hat{m}_{y,y'} + \hat{m}_{y,y'}] \tag{10}$$

where y_0 is the first year of captures and y_f is the last year of recaptures.

Note that when compiling the capture-recapture matrices, if an animal is re-seen a second time, the first resighting is treated as a new sighting that is first reseen at the second resighting.

SIR

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). 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 as $\tilde{L}$. 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:

$$w_j = \frac{\tilde{L}(\theta_j / data)}{\sum_{j=1}^{n1} \tilde{L}(\theta_j / data)} \tag{11}$$

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

N_{min} constraints

The assumption for these assessments is that given a minimum number of haplotypes, h, for a specific region, the minimum population size for that region is given by 3*h. This offers a constraint below which values the model estimated population trajectory must not go. A penalty is added to the negative log likelihood to ensure that these constraints are not violated.

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[5] The equations given here imply a multinomial distribution. However, because the annual capture probabilities are so small, the Poisson distribution is an adequate and convenient approximation.

RESULTS

Breeding Stock D

The assessment results for BSD are given in Table 2 for four different input data sets. The posterior median values for the intrinsic growth rate *r* are given, as well as the median values for the pristine population level *K*, the level of current recovery (N_{2010}/K), future recovery under the assumption of zero catch (N_{2040}/K) and the minimum level of the estimated median population trajectory[6].

Figure 1 shows the corresponding plots of the median population trajectories, along with their 90% probability envelopes. In each case, fits to all the available breeding ground input data have been shown for comparison purposes, even if the model has not been fit to every data set shown.

Figure 2a and b repeat the plots shown in Figure 1c and d, but the number of years shown are limited to 1985-2010, for the purpose of clearer illustration. The Matsuoka *et al.* (2011) relative abundance series has also been shown in these Figures.

Breeding Stock E1

The assessment results for BSE1 are given in Table 3, both for the case where the Cook Strait catches have been split 100:0 between East Australia and Oceania, and for the case where this split is 0:100. Parameters and related estimates are repeated in the same manner as for BSD in Table 2.

Figure 3a shows the posterior median population trajectory for the case where the Cook Strait catches have been allocated entirely to the East Australian stock. Since the results given in Table 3 show very little difference between the two catch allocation scenarios, the population trajectory has been shown only for case a). Figure 3b replicates Figure 3a, except that the years shown are limited to 1980-2011. The figure also includes the Paton *et al.* (2011) absolute abundance estimates along with the 95% CI given by the authors, as well as the Matsuoka *et al.* (2011) relative abundance series.

Oceania breeding stock

The assessment results for the Oceania breeding stock are given in Table 4. As for BSE1, the results are shown for both catch allocation cases of the Cook Strait catches. The parameters and related estimates are also reported as for BSD and BSE1.

Figure 4a shows the posterior median population trajectory of the Oceania whales, along with its 90% probability envelope. The Constantine *et al.* (2011) absolute abundance estimate is shown along with its 95% CI as provided by the authors. Note that this estimate is not used in the model fitting process, but instead the underlying mark recapture data from Constantine *et al.* (2011) are used. The fit to these mark recapture data is shown in Figure 4b.

DISCUSSION

Breeding Stock D

The fits to the various combinations of data sets shown in Figure 1 suggest that there is some level of inconsistency. A comparison between Figure 1a and b (along with the values given in Table 2) suggest that the Bannister and Hedley (2001) relative abundance series supports lower *K* and higher *r* values than the Hedley *et al.* (2011) data. This fact is further emphasised when the model is fit to the Bannister and Hedley (2001) data only (Figure 1c), where the resulting posterior median *K* value is substantially lower and conversely the corresponding *r* value is substantially higher than when the model is fit to the Hedley *et al.* (2011) data. It is interesting to note that the results using the Bannister and Hedley (2001) data seem more consistent with the Chittleborough (1965) data, as can be seen by the fits in Figure 1c.

These observations suggest that there are either inconsistencies amongst the data sets, or that the population dynamics are not adequately captured by the model. As can be seen in Figure 1c, the estimated median population

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[6] Note that strictly speaking this is not a trajectory, but the combination of posterior median values for each year.

trajectory is substantially lower than the Hedley *et al.* (2011) absolute abundance estimate, and the rate of increase suggested by the Hedley *et al.* (2011) relative abundance series is not well matched by the slope of the median population trajectory. One possible explanation is that there has been a migration of animals in more recent years from a neighbouring breeding stock (presumably the East Australian (E1) stock). While this could account for the discrepancies between the earlier and later data sets, the model would need to be extended to explore this possibility. Details of such a modification would need to be discussed at the upcoming IWC SC meeting.

Breeding Stock E1

There was some difficulty experienced in the Sampling Importance Resampling (SIR) process because certain parameter combinations (predominantly combinations with a high r and low K) provided an exceptionally good fit to the Noad *et al.* (2011) relative abundance series. This resulted in a fairly high number of duplicates in the resampling process (between 30% and 40%), which may mean that the probability envelopes displayed in Figure 3a are too narrow. The total sample size was increased substantially to try and improve results, but there remains room for improvement. However, since the Noad *et al.* (2011) absolute and relative abundance estimates are currently the only data input to the model, and since these data seem to support a high r and a low K so strongly, it is questionable whether increasing the original sample size further will completely resolve this issue.

Figure 3b shows that the posterior median population trajectory fits the Noad *et al.* (2011) relative and absolute abundance data well. The Paton *et al.* (2011) absolute abundance estimate is also shown. Here the fit is worse, with the model-predicted population values higher than those observed (although the Paton *et al.* (2011) 95% CI includes the model-predicted population estimate). The fit to the Matsuoka *et al.* (2011) relative abundance values on the other hand seems to be reasonable.

Oceania breeding stock

Figure 4b plots the observed cumulative resightings against the median model-predicted values. The fit is reasonably good except for the last year, where the observed number of resightings lies above even the 90% probability envelope for the number predicted by the model. This suggests that the model-predicted population size in that year is larger than the true value.

Figure 4a shows the posterior median population trajectory with its 90% probability envelope. The Constantine *et al.* (2011) absolute abundance estimate has been plotted and it is noteworthy that the estimate and its 95% CI lie outside the 90% probability envelope for the model predicted value. Before making further comment on this observation, one would need to check the underlying assumptions made in obtaining the absolute abundance estimate to see how compatible these are with the assumptions of the model used in this assessment.

It should also be noted that unlike for BSD and BSE1, the N_{min} penalty comes into play for the Oceania model. This is evident in the lower bound of the N_{min} value given in Table 4, which is close to the absolute lower bound of 345 (=3*115). In order to assess what impact this has on the assessment results, the model was run without the N_{min} penalty. As can be seen in row c of Table 4, the resulting median r value is higher and median K value is lower than when the penalty is included. It should be noted that exclusion of the N_{min} penalty widens the 90% probability envelope r, suggesting that the posterior r distribution is less updated than before.

ACKNOWLEDGEMENTS

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Table 2: Assessment results for BSD for fits to four different sets of input data: (a) Model is fit to the Hedley *et al.* (2011) absolute abundance estimate as well as the Hedley *et al.* (2011) relative abundance series (Rel I); (b) Model is fit to the absolute abundance estimate and the Bannister and Hedley (2001) relative abundance series (Rel II); (c) Model is fit only to Rel II; (d) Model is fit to the absolute abundance estimate, Rel I and Rel II. The posterior median values are given with their 90% probability envelope given in square brackets.

	r		K		N_{2010}/K		N_{2040}/K		N_{min}		*Year of N_{min}*
a	0.046	[0.005,0.098]	33860	[25365, 65693]	0.896	[0.438,1.000]	0.996	[0.492,1.000]	11951	[4368,24827]	1963
b	0.054	[0.011,0.093]	30587	[23043, 56470]	0.928	[0.504,1.000]	0.999	[0.651,1.000]	8012	[2090,20597]	1964
c	0.083	[0.029,0.104]	22048	[19506, 42179]	0.893	[0.614,0.996]	1.000	[0.919,1.000]	1285	[514,15420]	1967
d	0.053	[0.015,0.092]	30178	[22559, 51453]	0.906	[0.557,1.000]	0.998	[0.740,1.000]	6501	[1776,19275]	1964

Table 3: Assessment results for BSE1 for two catches scenarios: (a) allocates 100% of the Cook Strait catches to East Australia and 0% to Oceania, while (b) allocates 100% of the Cook Strait catches to Oceania and 0% to East Australia. The posterior median values are given with their 90% probability envelope given in square brackets.

	r		K		N_{2010}/K		N_{2040}/K		N_{min}		*Year of N_{min}*
a	0.105	[0.103,0.106]	26285	[26245, 26399]	0.534	[0.484,0.589]	1.000	[0.999,1.000]	231	[204, 261]	1968
b	0.105	[0.103,0.106]	25057	[25021, 25162]	0.554	[0.503,0.608]	1.000	[1.000,1.000]	231	[203, 263]	1968

Table 4: Assessment results for the Oceania breeding stock for two catches scenarios: (a) allocates 100% of the Cook Strait catches to East Australia and 0% to Oceania, while (b) allocates 100% of the Cook Strait catches to Oceania and 0% to East Australia. (c) uses the same catch allocation as (a), but excludes the N_{min} penalty from the likelihood. The posterior median values are given with their 90% probability envelope given in square brackets.

	r		K		N_{2010}/K		N_{2040}/K		N_{min}		*Year of N_{min}*
a	0.035	[0.005,0.058]	17136	[15782, 21488]	0.195	[0.132,0.249]	0.513	[0.154,0.858]	808	[376, 2393]	1968
b	0.035	[0.005,0.059]	19178	[17285, 25292]	0.176	[0.113,0.227]	0.469	[0.129,0.832]	816	[371, 2398]	1968
c	0.060	[0.010,0.101]	15690	[14411, 20420]	0.241	[0.144,0.322]	0.866	[0.193,0.997]	347	[100, 1995]	1968
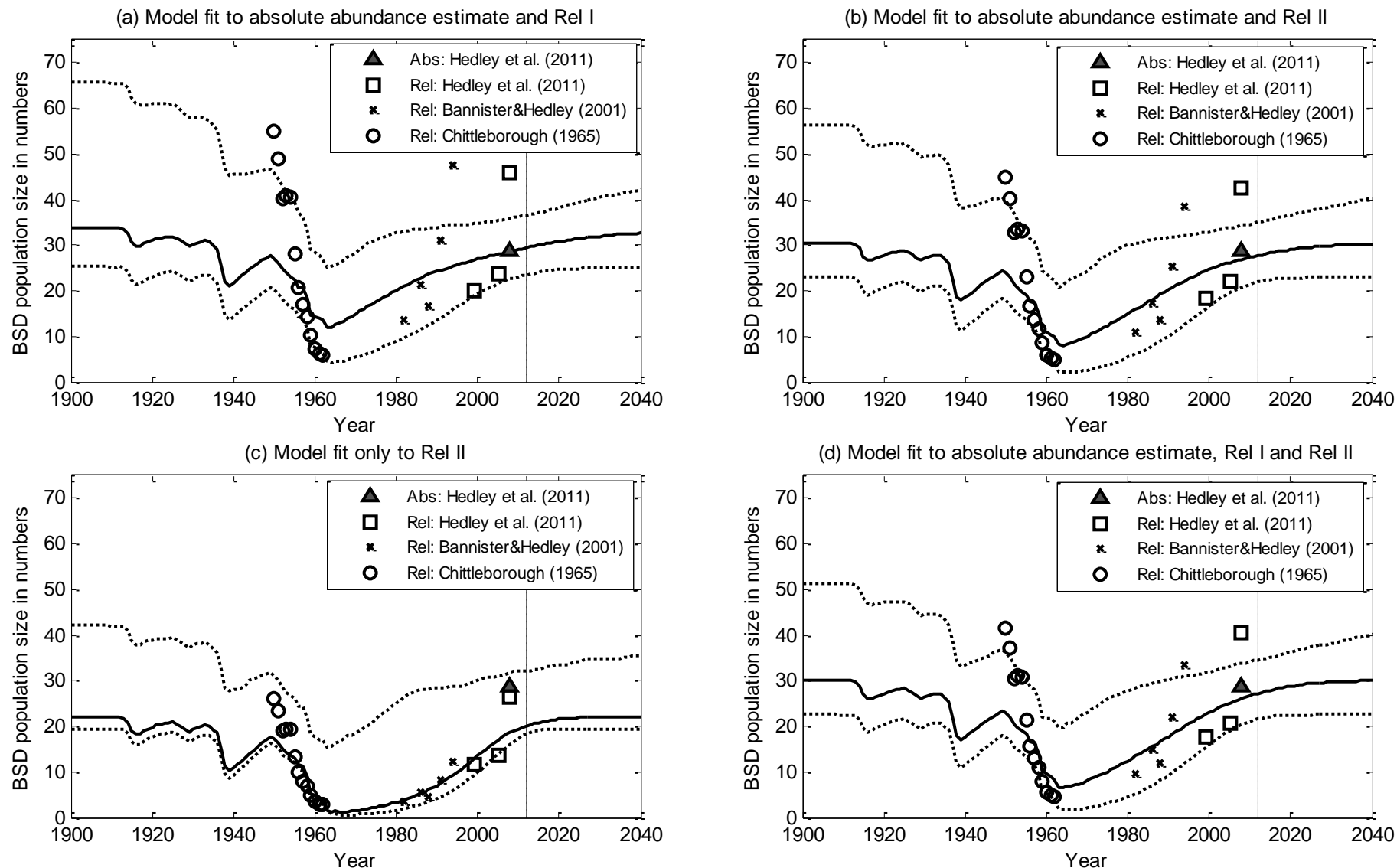
Figure 1: Posterior median population trajectories for Breeding Stock D for fits to different input data, showing the trajectories and 90% probability envelopes. Values to the right of the vertical dashed line are projections into the future under zero catch. In the figures, "Absolute abundance estimate" refers to the Hedley *et al.* (2011) absolute abundance estimate, Rel I is the Hedley *et al.* (2011) relative abundance series, Rel II is the Bannister and Hedley (2001) relative abundance series and Rel III is the Chittleborough (1965) relative abundance series.
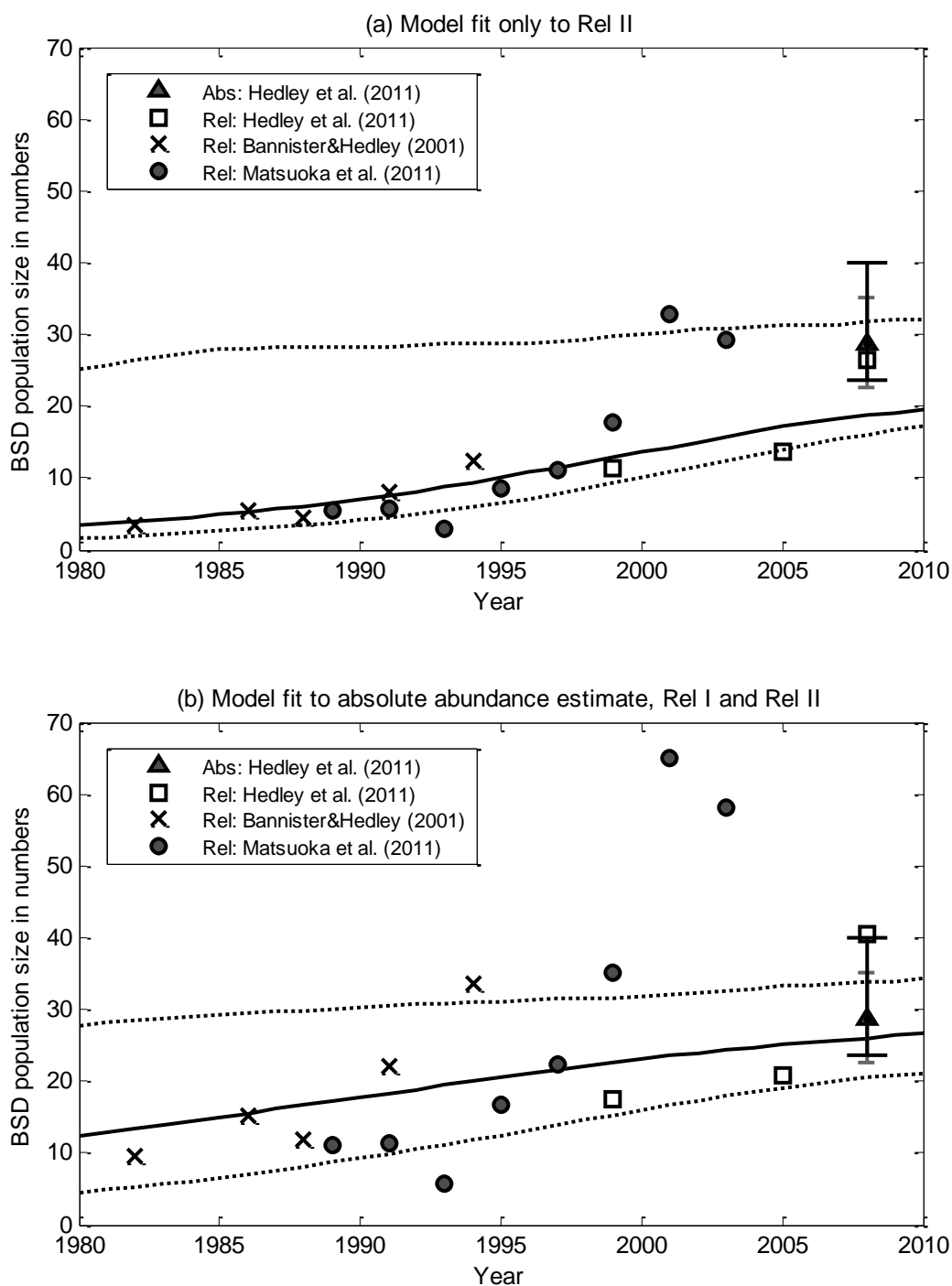
Figure 2: Repeat of Figure 1c and d, concentrating on the years 1980-2010. The 95% CI for the 2008 absolute abundance estimate as provided by Hedley *et al.* (2011) is shown by the black line with wider error bars. The 90% CI computed using the CV from footnote 7 is shown by the grey line with narrower error bars. The Matsuoka *et al.* (2011) relative abundance series (Rel IV) has been shown by the dark dots for comparison purposes.
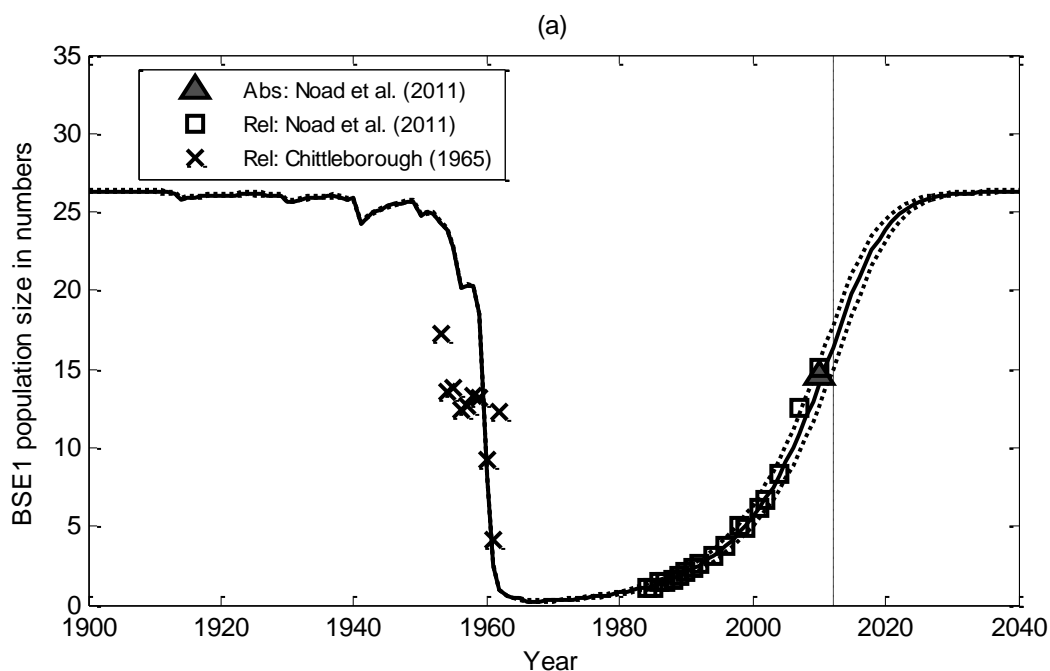
Figure 3a: Posterior median population trajectory for BSE1. The results shown are for the case where the Cook Strait catches are split 100:0 between East Australia and Oceania. Since there is very little difference between the two cases shown in Table 3, the results have not been replicated for the 0:100 split. Figure 3a shows the entire population trajectory, as well as the fits to the Noad *et al.* (2011) absolute abundance estimate and the Noad *et al.* (2011) relative abundance series (Rel I). The model was fit to both of these data sets. The Chittleborough (1965) relative abundance series (Rel II) is shown as a consistency check.
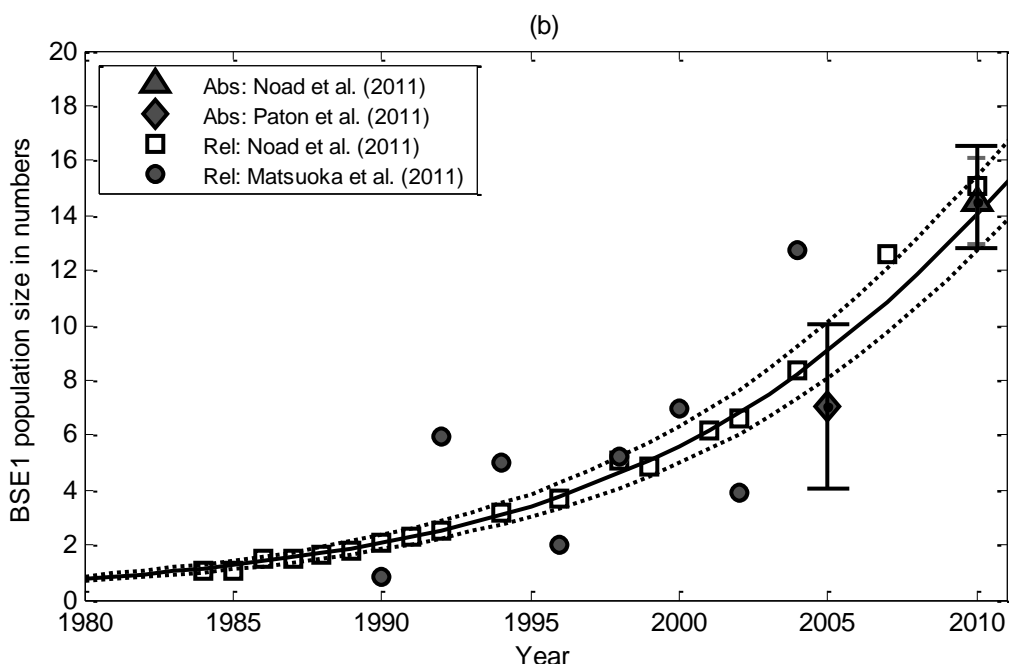
Figure 3b: Replicate of Figure 3a, except that only the years 1980-2011 are shown. The 95% CI for the 2010 absolute abundance estimate (as provided by Noad *et al.,* 2011) is shown by the black line with wider error bars. The 90% CI based on the CV calculated for this assessment is shown by the grey line with narrower error bars. The Paton *et al.* (2011) absolute abundance estimate (Abs2) is indicated by the diamond, and its 95% CI (as given in Paton *et al.,* 2011) is shown. The Matsuoka *et al.* (2011) relative abundance series for Area V is shown as a consistency check by the filled circles. Note that the Paton *et al.* (2011) and Matsuoka *et al.* (2011) estimates are not used in the model fit shown above.

(a) Posterior median popualtion trajectory for Oceania breeding stock
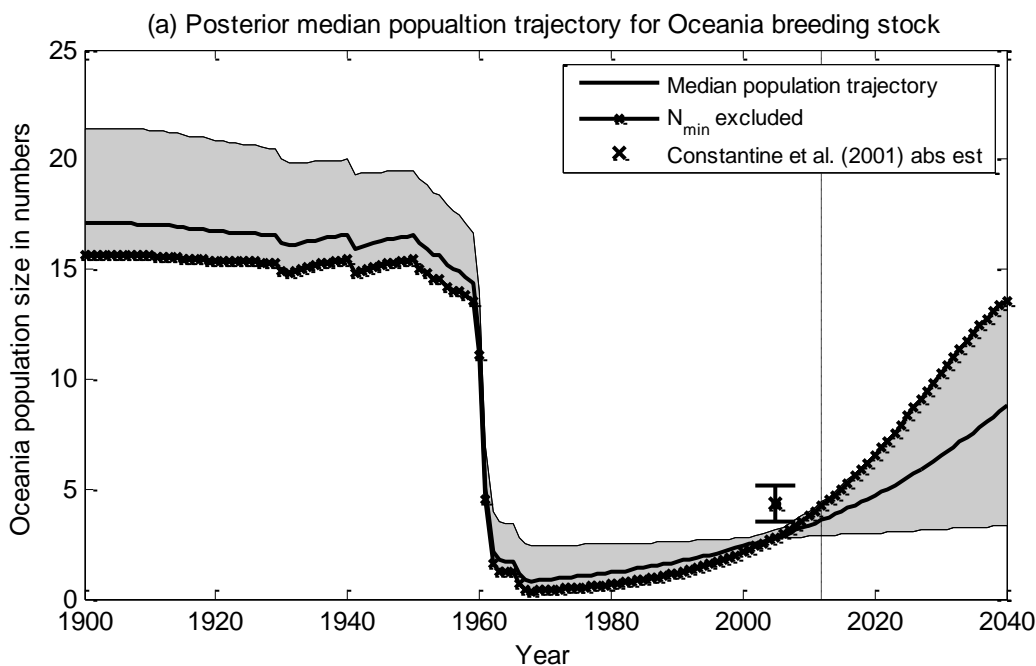
Figure 4a: Posterior median population trajectory for the Oceania breeding stock. Similarly to Figure 3a and b, the results shown in Figure 4a and b are for the case where the Cook Strait catches are split 100:0 between East Australia and Oceania, since there is very little difference between the two catch allocation cases (as can be seen in Table 4). Figure 3a shows the median population trajectory with its 90% probability envelope indicated by the shaded region. The median population trajectory has also been shown for the case where the model is run with the N_{min} penalty excluded from the likelihood. Note that the Constantine *et al.* (in press) absolute abundance estimate shown here with its 90% CI was not used in the model fitting process and is just shown as a consistency check. The model was fit instead to the underlying mark recapture data directly.

(b) Oceania model fit to mark recapture data
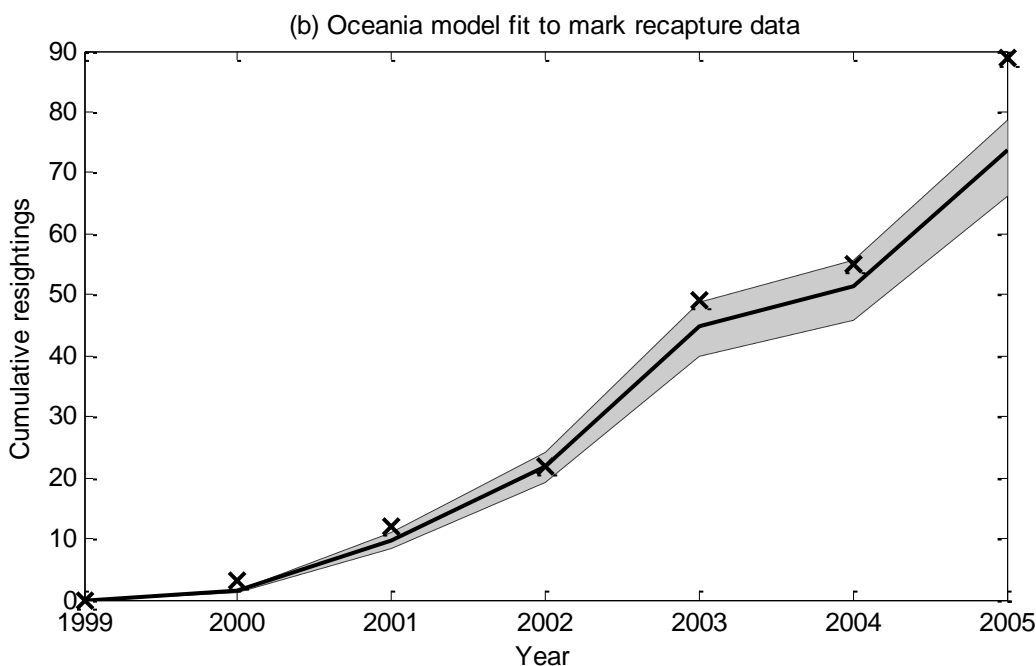
Figure 4b: Fit of the Oceania model to the Constantine *et al.* (in press) mark recapture data. The observed cumulative resightings are marked by X's. The median estimates are shown by the thick line and their 90% probability envelope is indicated by the shaded region. Note that it has been assumed that the mark recapture data apply to males only, and consequently $N_y/2$ has been used in the likelihood calculations (see Equations (7) and (8)).

APPENDIX

Table A. 1: Historic catches taken north of 40°S from Allison's database (C.Allison, *pers. comm.*).

Year	BSD	BSE1	Oceania	Cook Strait	Year	BSD	BSE1	Oceania	Cook Strait
1890	0	0	8	0	1935	0	0	0	57
1891	0	0	8	0	1936	3076	0	0	69
1892	0	0	8	0	1937	3250	0	0	55
1893	0	0	8	0	1938	917	0	0	75
1894	0	0	8	0	1939	0	0	0	80
1895	0	0	8	0	1940	0	0	0	107
1896	0	0	8	0	1941	0	0	0	86
1897	0	0	8	0	1942	0	0	0	71
1898	0	0	8	0	1943	0	0	0	90
1899	0	0	8	0	1944	0	0	0	88
1900	0	0	8	0	1945	0	0	0	107
1901	0	0	8	0	1946	0	0	0	110
1902	0	0	8	0	1947	2	0	0	101
1903	0	0	8	0	1948	4	0	0	92
1904	0	0	8	0	1949	190	0	3	141
1905	0	0	8	0	1950	388	0	0	79
1906	0	0	8	0	1951	1224	0	0	111
1907	0	0	8	0	1952	1187	600	0	121
1908	0	0	8	0	1953	1300	700	0	109
1909	0	0	16	0	1954	1320	718	0	180
1910	0	0	41	36	1955	1126	720	0	112
1911	0	0	41	36	1956	1119	720	166	127
1912	234	30	27	36	1957	1120	721	165	155
1913	993	348	56	36	1958	967	720	136	183
1914	1968	0	57	36	1959	700	810	270	214
1915	1297	0	70	36	1960	545	810	321	226
1916	388	0	25	57	1961	580	731	211	55
1917	0	0	58	36	1962	548.2	173	12	24
1918	0	0	50	40	1963	87	0	0	9
1919	0	0	72	47	1964	2	0	0	0
1920	0	0	64	43	1965	75.8	0	0	0
1921	0	0	55	34	1966	30	0	0	0
1922	155	0	40	17	1967	12	0	0	0
1923	166	0	62	17	1968	0	0	0	0
1924	0	0	55	52	1969	0	0	0	0
1925	669	0	48	48	1970	0	0	0	0
1926	735	0	35	43	1971	0	0	0	0
1927	996	0	74	53	1972	0	0	0	0
1928	1035	0	50	55	1973	0	0	3	0
1929	0	0	53	49	1974	0	0	4	0
1930	0	0	31	47	1975	0	0	8	0
1931	0	0	48	61	1976	0	0	4	0
1932	0	0	0	18	1977	0	0	4	0
1933	0	0	3	41	1978	0	0	11	0
1934	0	0	0	52	1979	0	0	0	0

Table A. 2: Historic catches taken south of 40°S from Allison's database (C.Allison, *pers. comm.*).

Year	BSD	BSE1	Oceania	Year	BSD	BSE1	Oceania
1890	0	0	0	1935	940.5	4.0	0
1891	0	0	0	1936	1427.5	0.0	0
1892	0	0	0	1937	759.0	80.5	0
1893	0	0	0	1938	757.0	126.0	0
1894	0	0	0	1939	0.0	0.0	0
1895	0	0	0	1940	171.0	1539.0	684.0
1896	0	0	0	1941	0	0	0
1897	0	0	0	1942	0	0	0
1898	0	0	0	1943	0	0	0
1899	0	0	0	1944	0	0	0
1900	0	0	0	1945	0	0	0
1901	0	0	0	1946	0	0	0
1902	0	0	0	1947	0.5	0	0
1903	0	0	0	1948	0.0	0	0
1904	0	0	0	1949	724.5	967.5	0
1905	0	0	0	1950	1112.5	42.5	445.5
1906	0	0	0	1951	879.0	286.5	311.5
1907	0	0	0	1952	191.5	191.0	339.0
1908	108.5	0	0	1953	259.0	0.0	150.0
1909	59.0	0	0	1954	26.0	762.0	518.0
1910	41.5	0	0	1955	1061.0	2421.5	334.0
1911	0	0	0	1956	0.0	0.0	43.0
1912	0	0	0	1957	1868.7	159.5	249.0
1913	0	0	0	1958	3333.7	1894.1	367.6
1914	0	0	0	1959	254.4	10430.1	2411.2
1915	0	0	0	1960	574.3	5378.5	6664.5
1916	0	0	0	1961	309.0	1039.5	2911.5
1917	0	0	0	1962	1622.2	337.2	471.9
1918	0	0	0	1963	307.7	176.6	119.0
1919	0	0	0	1964	72.8	71.8	22.5
1920	0	0	0	1965	88.5	180.2	650.8
1921	0	0	0	1966	109.5	37.0	265.5
1922	0	0	0	1967	77.5	25.0	118.0
1923	0	0	0	1968	0	0	0
1924	0	0	0	1969	0	0	0
1925	0	0	0	1970	0	0	0
1926	0	41.0	41.0	1971	0	0	1.5
1927	0	8.0	8.0	1972	0	1.0	1.0
1928	5.5	8.5	8.5	1973	0	0	0
1929	5.5	387.5	387.5	1974	0	0	0
1930	25.5	110.5	125.0	1975	0	0	0
1931	106.5	0	0	1976	0	0	0
1932	80.5	0	0	1977	0	0	0
1933	550.5	0	0	1978	0	0	0
1934	1298.0	0	0	1979	0	0	0

Breeding Stock D

Absolute abundance estimate

An estimate of absolute abundance of 28,830 individuals (95% CI[7] = 23,710-40,100) was computed from line transect aerial surveys conducted off Western Australia in 2008 and corrected for animals missed on the trackline (g(0) =0.41) (Hedley *et al.*, 2011).

Relative abundance estimates

Table A. 3: BSD Relative Abundance Index I (Hedley *et al.*, 2011). These are derived from three sets of aerial line transect surveys conducted in 1999, 2005 and 2008 (augmented with two shorter land-based surveys in 2005 and 2008) to estimate the population size of northward migrating whales.

Year	Estimate	95% CI
1999	5,130	3,380-8,750
2005	6,070	4,420-11,020
2008	11,820	9,720-16,400

Table A. 4: BSD Relative Abundance Index II (Bannister and Hedley, 2001). These are breeding ground relative abundance estimates from Bannister and Hedley (2001) for the period 1982 to 1994. No CV is available.

Year	Estimate	Year	Estimate
1982	10.2	1991	23.6
1986	16.2	1994	36.0
1988	12.7		

Table A. 5: BSD Relative Abundance Index III (Chittleborough, 1965). Catch per unit effort data are available from four catchers operating on the west coast of Australia from June 25 to August 26 each year (Chittleborough, 1965) (Area IV: 70˚E-130˚E). No CV is available.

Year	CPUE	Year	CPUE	Year	CPUE
1950	0.475	1955	0.244	1960	0.062
1951	0.424	1956	0.178	1961	0.055
1952	0.347	1957	0.146	1962	0.051
1953	0.353	1958	0.123		
1954	0.351	1959	0.090		

Table A. 6: BSD Relative Abundance Index IV (Branch, 2011). Feeding ground estimates of abundance from IDCR-SOWER CPI-CPIII surveys (south of 60˚S) associated with breeding stock D correspond to sector 60˚E-120˚E of the Southern Oceans (Branch, 2011). Current nuclear area for feeding ground catch allocation for BSD corresponds to longitudinal sector 80^oE-110^oE and margin area corresponds to 60^oE-130^oE (IWC, 2010).

Year	Estimate	CV	Estimates for comparable areas	CV
1978	1,033	0.44	1,219	0.46
1988	3,869	0.52	4,202	0.52
1997	17,959	0.17	17,959	0.17

Table A. 7: BSD Relative Abundance Index V (Matsuoka *et al.*, 2011): 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 nm from ice-edge) and southern (from ice-edge to 45 nm away). Breeding Stock D corresponds to Area IV (Matsuoka *et al.,* in press).

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

Minimum number of haplotypes

Minimum number of haplotypes for BSD from Olavarría *et al*. (2007) is 53.

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[7] This 95% CI was converted into a rough CV by assuming that the estimate was log-normally distributed. An approximation of the standard error of the log of the estimate was obtained by computing 0.5*(ln(40100)-ln(23710))/1.96. The resulting value of 0.13 was then taken to be the CV of the estimate (see footnote 3).

Breeding Stock E1

Absolute abundance estimate

   i.   BSE1 absolute abundance estimate I - Noad *et al.* (2011)
A land-based survey was conducted at Point Lookout on the east coast of Australia over 8 weeks in June and July 2010. The average number of whales passing per 10h over the peak four weeks of the northward migration was 84.7 ± 3.2 whales. A correction for whales available but missed was applied using double blind counts, as well as other corrections for sighting heterogeneity (1.212 +/- 0.049, Dunlop *et al.*, 2010). Using this correction the abundance estimate for 2010 was 14,522 whales (95% CI 12,777 – 16,504) (Noad *et al.*, 2011).

   ii.   BSE1 absolute abundance estimate I I - Paton *et al.* (2011)
From a multi-point mark-recapture estimate of absolute abundance in 2005 for the east coast of Australia. Estimate is 7,041 (95% CI = 4,075-10,008) (Paton *et al.*, 2011).

Relative abundance estimates

Table A. 8: BSE1 Relative Abundance Index I (Noad *et al.*, 2011): A count of northward migrating whales from land-based surveys conducted at Point Lookout and two other locations. The values give the number of whales passing per 10h during four weeks of the peak migration. (M. Noad, pers. comm.) and are as used for estimates of abundance provided by Noad *et al.*, (2008), Noad *et al.*, (2011). These data was used to in estimated annual rate of increase of 10.9%/year (95% CI = 10.5-11.3%/year) for a 24 year period (1984 to 2010) (Noad *et al.*, 2011).

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

Table A. 9: BSE1 Relative Abundance Index II (Chittleborough, 1965): Catch per unit effort data from two catcher boats operating on the east coast of Australia from June 10 to August 5 each year (Chittleborough, 1965) (Area V: 130˚E-170˚W). No CV available.

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

Table A. 10: BSE1 Relative Abundance Index III (Branch, 2011). Feeding ground estimates of abundance from IDCR-SOWER CPI-CPIII surveys (south of 60°S) associated with Area V (130°E-170°W).

Year	Estimate	CV	Estimates for comparable areas	CV
1980	995	0.58	1,913	0.60
1985	622	050	622	0.50
1992	2,012	0.43	3,484	0.33
2001	13,300	0.22	13,300	0.20

Table A. 11: BSE1 Relative Abundance Index IV (Matsuoka *et al.*, 2011): 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 nm from ice-edge) and southern (from ice-edge to 45 nm away). Breeding Stock E1 corresponds to Area V (Matsuoka *et al.*, 2011).

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

Minimum number of haplotypes

The minimum number of haplotypes for BSE1 is 42, with 5 of them being private to the South Pacific (Olavarría *et al.*, 2006).

Oceania breeding stock

Absolute abundance estimate

The estimate in 2005 of 4,329 individuals (CV=0.12) arises from a sighting-resighting analysis of microsatellite genotypes collected from 1999 to 2005 across four survey areas in Oceania: New Caledonia (E2), Tonga (E3), the Cook Islands and French Polynesia (F2) (Constantine *et al.*, in press). It is a doubled male-specific estimate assuming equal numbers of females in the region.

Mark recapture data

Table A. 12: Synoptic genotypic mark recapture data underlying male specific Oceania-wide abundance estimate (Constantine *et al.*, in press).

Year initial capture (males)	1999	2000	2001	2002	2003	2004	2005
Total individuals captured	25	70	112	78	114	24	82
1999	-	3	4	0	3	0	1
2000		-	5	3	8	2	6
2001			-	7	12	3	7
2002				-	4	0	6
2003					-	1	11
2004						-	3
2005							-

Relative abundance data

Table A. 13: Feeding ground estimates of abundance from IDCR-SOWER for breeding stock F correspond to sector 170°W-110°W (Branch 2011). Current nuclear area associated with Breeding Stocks E2, E3 and F is 180˚-120˚W and margin is 160˚E-100˚W (IWC, 2010).

Year	Estimate	CV	Estimates for comparable areas	CV
1980	995	0.58	1,913	0.60
1985	622	050	622	0.50
1992	2,012	0.43	3,484	0.33
2001	13,300	0.22	13,300	0.20

Minimum number of haplotypes

The minimum number of haplotypes for Oceania is 115 (Olavarría *et al.*, 2007).