

Implementing the 2014 three-stock model for Southern Hemisphere Breeding Stocks E1, Oceania and G

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ABSTRACT

The three stock model approach with mixing on feeding grounds, which was implemented in 2014 to assess the BSD, BSE1 and BSO breeding stocks, is applied in a similar manner to the BSE1, BSO and BSG breeding stocks. This is intended as a first step in applying this approach consecutively around the globe to check for consistency of results in circumstances of uncertainty in the allocation of feeding ground catches. Compared to earlier assessments of the BSE1, BSO and BSG breeding stocks in partly separate analyses, there is an appreciable change in that the pre-exploitation level is estimated higher for BSE1 and lower for BSO; correspondingly, BSE1 is estimated as less and BSO as more recovered towards those pre-exploitation levels. Comparable likelihoods do not differ greatly for data for these stocks used in both the 2014 BSD+BSE1+BSO and the 2015 BSE1+BSO+BSG assessments, suggesting that the data used here do not contain sufficient information to distinguish these rather different results.

INTRODUCTION

In 2014, a three-stock approach was implemented in order to jointly assess the West Australian Breeding Stock D (BSD), East Australian Breeding Stock E1 (BSE1) and the Oceania breeding stock (BSO). The rationale behind a three-stock approach was primarily to address the uncertainty about how to allocate the historical feeding ground catches between the three stocks (IWC 2014). The three-stock model defined a western and an eastern feeding ground with a boundary at 130°E. BSD and an estimable proportion of the BSE1 stock feed (and were caught) in the western feeding ground west of 130°E, while BSO and the remaining proportion of BSE1 feed in the eastern feeding ground. These assumptions were used to allocate the historical catches to breeding stocks in proportion to the abundances of the populations present in each feeding ground.

Allocation of feeding ground catches remains a challenge for the assessment of the Southern Hemisphere humpback whale populations, since assumptions have to be made about where to place the boundaries for each stock. An attempt was made to develop an all-stock assessment which combined seven breeding populations into a single assessment (Müller *et al.* 2010), where all feeding ground catches could be allocated in proportion to population abundances present on the feeding ground, rather than fixed on input. This work, however, was not completed owing to convergence issues which arose as a result of too many estimable parameters. Another possible approach would be to utilise the less ambitious three-stock model to successively assess all the stocks, i.e. to follow the D+E1+O assessment with a E1+O+G assessment and so on, in order to allow flexibility in the allocation of historical feeding ground catches for all the stocks and so to assess how key parameter estimates change for each iteration. The aim would be to assess the potential of using successive three-stock models to develop a combined assessment of all the stocks.

This paper presents the results of a three-stock E1+O+G model. Similar to the D+E1+O model, a western and eastern feeding area are defined (Figure 1). The western region runs from 120°E to 100°W and BSE1 and a proportion (γ^O) of the BSO population are assumed to feed there. The eastern region runs between 100°W and 50°W and BSG and the remaining proportion ($1 - \gamma^O$) of the BSO population are assumed to feed there. Figure 2 provides a juxtaposition of the D+E1+O and the E1+O+G models in order to provide comparison of the boundaries and total catches taken in the respective western and eastern feeding areas.

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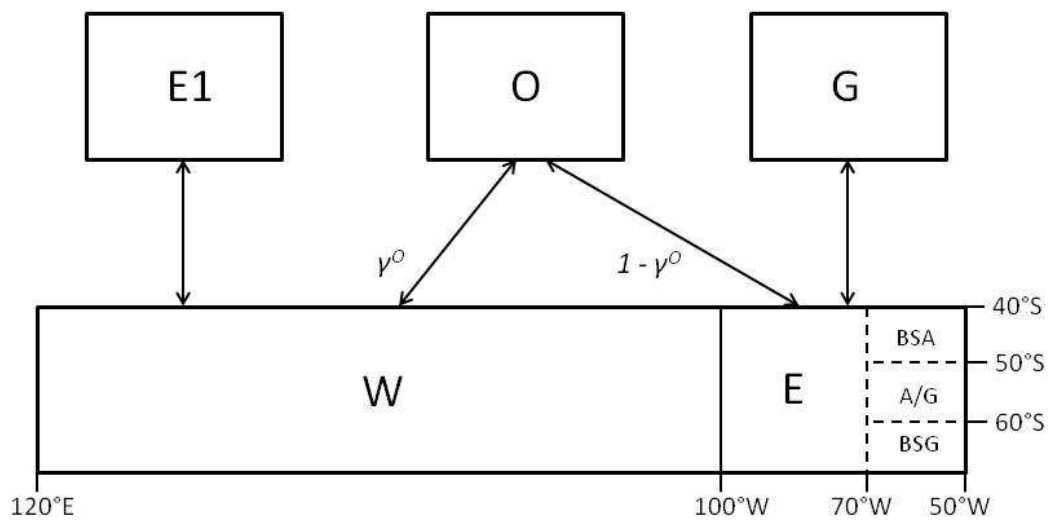


Figure 1: Diagrammatic representation of the E1+O+G three-stock model. BSE1 and a proportion (γ^O) of the BSO population feed in the western feeding area, while BSG and the remaining proportion ($1-\gamma^O$) of the BSO population feed in the eastern feeding ground. Historical feeding ground catches from each feeding ground are allocated to the different stocks in proportion to the model-predicted abundances in each area. Catches taken between 70°W and 50°W are further split between the eastern feeding ground and the Brazilian Breeding Stock A, as described later in the text.

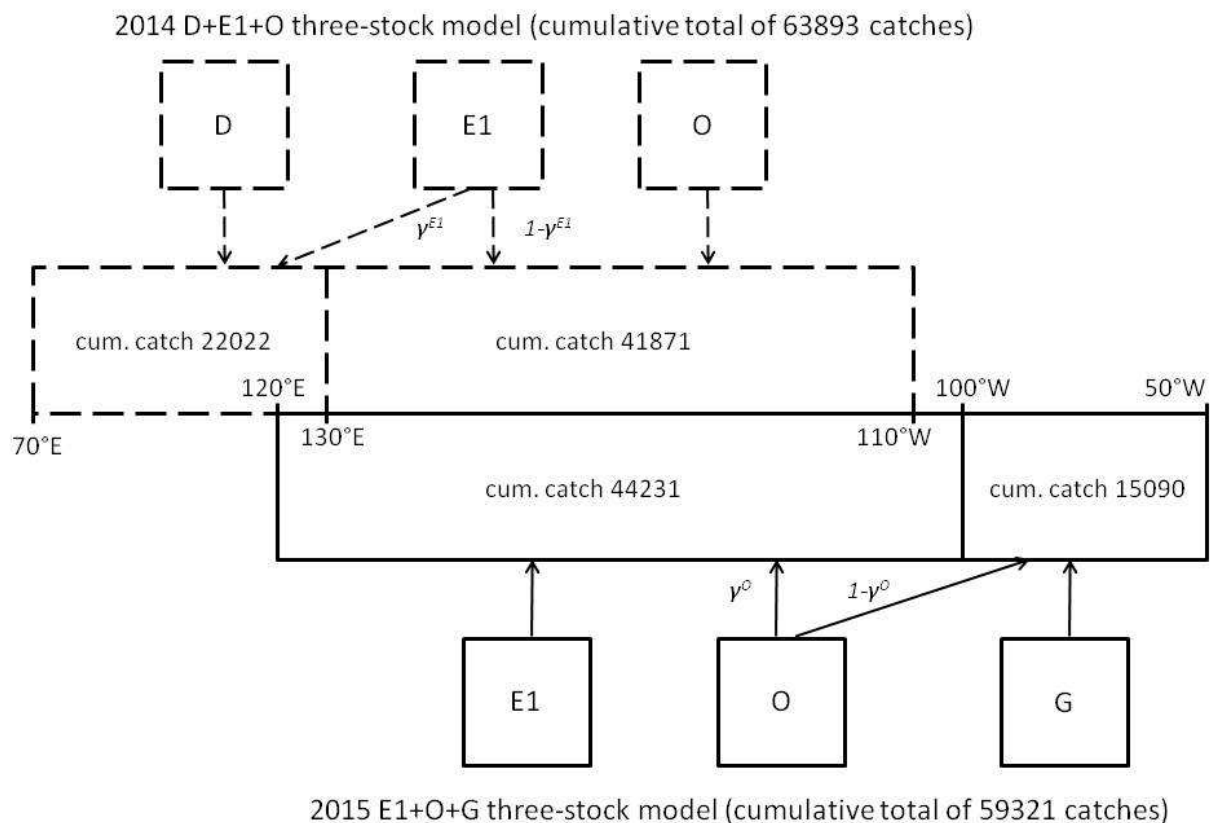


Figure 2: Juxtaposition of the 2014 D+E1+O three-stock model (dashed lines) with the 2015 E1+O+G three-stock model (solid lines), illustrating the boundaries of the respective eastern and western feeding areas, as well as the total historical catches taken in each area. In IWC (2014) γ^{E1} was estimated to be 0.068, i.e. 6.8% of BSE1 feed in western feeding area.

DATA

Historical catch data

There are two sets of historical 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 Eland Oceania

The catches for E1 and Oceania are given by landing station. Catches landed at LochTay, Tangalooma and Byron Bay have been allocated to BSE1. Catches landed at Norfolk Island, Tonga and Polynesia have been allocated to the Oceania breeding stock. Catches landed at Rakiura and Prince George, New Zealand, Kaikoura, Cook Strait and Tory Channel, Great Barrier Island, Whangamumu and Bay of Island are allocated to BSE1 and Oceania in proportion to the model-predicted population abundances.

Breeding Stock G

Catches labelled “Chile”, “Ch/Per/E” and “Peru” in the database have been allocated to BSG.

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

ii) Catches south of 40°S

These catches are given for 10 degree longitude bands, as shown in Table A. 2. Catches taken between 120°E and 100°W are allocated to the western feeding ground and catches taken between 100°W and 70°W are allocated to the eastern feeding ground. IWC (2010) splits the area between 70°W and 50°W into three blocks: one from 40°S-50°S (allocated to the Brazilian breeding stock BSA), one from 50°S-60°S (shared between BSA and BSG) and lastly one south of 60°S (see Figure 6). In light of this, all catches between 70°W and 50°W and south of 60°S were added to the eastern feeding ground catches for the three-stock model. Further, half the catches between 70-50°W and 50-60°S were added to the eastern feeding ground catches.

Abundance and trend data

Breeding Stock E1 was fit to the Noad *et al.* (2011) absolute abundance estimate, as well as the Noad *et al.* (2011) relative abundance series. Breeding Stock Oceania was fit to the Constantine *et al.* (2012) mark-recapture data. Breeding Stock G was fit to the Felix *et al.* (2011) absolute abundance estimate. The data are listed in the Appendix along with further details.

In their assessment of Breeding Stock G, Johnston *et al.* (2011) fit to the Felix *et al.* (2011) absolute abundance estimate, but also to the Branch (2011) IDCR/SOWER relative abundance series. This series was derived for the feeding ground area between 110°W and 70°W, and since these boundaries correspond closely to the eastern feeding ground (100°W-70°W, with only 114 catches taken between 110°W-100°W), the population feeding in the eastern area of E1+O+G three-stock model $((1-\gamma^O)N^{BSO} + N^{BSG})$ was fit to the IDCR/SOWER relative abundance series as a sensitivity.

N_{min} constraint

The minimum population constraint was taken to be three times the minimum number of haplotypes (IWC 2012). The minimum number of haplotypes utilised were: 5 for BSE1 (IWC 2014), 33 for BSO (IWC 2014) and 27 for BSG (Rosenbaum *et al.* 2006).

METHODS

Population dynamics

The population dynamics are given by the following equation:

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

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 (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) $r^i \sim U[0, 0.106]^2$
- ii) $\ln \tilde{N}_{target}^{i,obs} \sim U[\ln N_{target}^{i,obs} - 4CV, \ln N_{target}^{i,obs} + 4CV]$

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 – at least over lengthy periods) 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 the target abundance estimate $\tilde{N}_{target}^{i,obs}$ is drawn at random is uniform on a natural logarithmic scale. The upper and lower bounds, whose only purpose is to render the computations more efficient, are set by the CV of the abundance estimate multiplied by four.

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

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. Details for calculating the components of the negative log likelihood are given below.

Likelihood function

Absolute abundance data

Given an absolute abundance estimate, N_{target}^{obs} , this is assumed to be log-normally distributed with the log of the estimate as the mean and the CV as the standard deviation³. Thus the negative log likelihood contribution is:

$$\frac{1}{2\sigma^2} (\ln N_{target}^{obs} - \ln N_{target})^2 \quad (2)$$

where

- N_{target}^{obs} is the absolute abundance estimate obtained from observations,
- N_{target} is the model-estimated population size for the year of the abundance estimate, and
- σ^2 is the variance of $\ln N_{target}^{obs}$.

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:

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

where

² Note that an importance function was used for r^{EI} to improve sampling efficiency. Details are given later.

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 $\sqrt{e^{\sigma^2} - 1}$. Since the CV of N is relatively small, σ has been approximated here by the value of the CV of N .

- I_y is the relative abundance estimate for year y ,
 q is a constant of proportionality,
 N_y is the model estimate of observed population size at the start of year y , and
 \mathcal{E}_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:

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

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:

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

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

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

In the Bayesian context, q and σ are “nuisance parameters, i.e. parameters that need to be estimated but are not of great 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 a region in year y , then the number of animals captured in year y is given by:

$$n_y = p_y N_y \quad (7)$$

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:

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

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 distribution⁴, with the associated likelihood contribution given by:

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

⁴ 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.

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

$$\sum_{y=y_0}^{y_f-1} \sum_{y'=y+1}^{y_f} [-m_{y,y'} \ln \hat{m}_{y,y'} + \hat{m}_{y,y'}] \quad (10)$$

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 re-seen 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_i s is generated.

This sample is then resampled with replacement n_2 times with probability equal to weight w_j , where:

$$w_j = \frac{\tilde{L}(\theta_j / data)}{\sum_{j=1}^{n_1} \tilde{L}(\theta_j / data)} \quad (11)$$

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

Importance functions for BSE1

The trend data for BSE1 (Noad *et al.*, 2011) are highly informative, and as such high r^{E1} values have a much higher likelihood associated with them and have a much better chance of being resampled. Since r^{E1} is sampled from a uniform prior on the interval [0,0.106], small values of r^{E1} will form a substantial proportion of the initial sample of n_1 , even though they are not likely to be chosen in the resampling process. This leads to sampling inefficiency and a high number of duplicates (where the same high r^{E1} values are sampled repeatedly). A very large initial sample has to then be drawn in order to generate enough samples with high r^{E1} values to be able to resample without a high number of duplicates. In order to increase the sampling efficiency, an importance function was used. This function increases the likelihood of sampling high r^{E1} values and reduces the number of essentially wasted low r^{E1} values in the sample. To counter the fact that the resulting distribution of the n_1 values of r^{E1} sampled is no longer uniform as required by the uniform prior distribution, the final likelihood values are weighted upwards in the same proportion as the probability of picking a particular r^{E1} in the initial sample was weighted down. The importance function is shown in Figure 3 below.

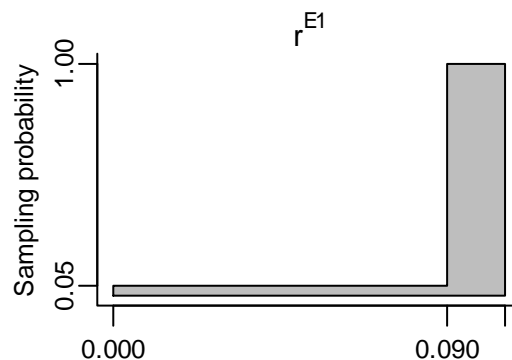


Figure 3: Importance functions used when sampling for r^{E1} . The horizontal axis shows the step values of r at which the importance function increases, and the vertical axis shows the probability of accepting an r sample from a particular range. In other words, if a value between 0 and 0.090 is drawn for r^{E1} from the uniform prior, it has a 95% chance of being discarded.

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.

RESULTS

Table 1(a) gives the posterior median values and 90% probability intervals for key parameter estimates for the E1+O+G three-stock model. Since Johnston *et al.* (2011) fit to the Branch (2011) IDCR/SOWER feeding ground relative abundance series in their assessment of BSG, Table 1(b) reports on the results of the E1+O+G three-stock model where the number of whales feeding in the eastern feeding ground is also fit to the Branch (2011) series. Table 1(c) gives the posterior median values and 90% probability intervals for the BSE1, BSO and BSG populations from previous assessments: the BSE1 and BSO results are from the 2014 D+E1+O assessment (IWC 2014) and BSG results are from the Johnston *et al.* (2011) assessment.

Figure 4 is a graphical representation of the r , K , N_{2015}/K parameter estimates for the three stocks from Table 1(a)-(c), comparing the median estimates and 90% probability intervals for the E1+G+O model, the E1+G+O model fit to the IDCR/SOWER data as well for the previous assessments. Figure 5 shows the posterior median trajectories and 90% probability envelopes for the E1+O+G model and for previous assessments.

Table 2 gives the likelihood components (in terms of median values) for the D+E1+O and the E1+O+G models. Likelihood components are reported for BSE1 and BSO, i.e. the two stocks common across the two three-stock models.

Table 3 gives the cumulative catches allocated in the models to each breeding stock.

DISCUSSION

The main point of interest is how compatible the results of the E1+O+G model are with the 2014 D+E1+O three-stock model, in order to assess whether a combined assessment of all the stocks could be undertaken by using successive three-stock models.

As can be seen from Figure 5 (a) and (b), there are substantial differences between the results of the two models. Table 3 helps elucidate the reason underlying these differences, namely that the E1+O+G model allocated substantially more catches to BSE1 and fewer catches to BSO than the D+E1+O model, thus resulting in the higher BSE1 and lower BSO carrying capacity values. This illustrates not only the impact that the catch allocations have on model outputs, but also the impact that the neighbouring populations have on any one breeding stock when catches are shared between neighbouring stocks. For example, the BSE1 population requires a fairly large number of catches to be allocated to it in order for the population to be sufficiently depleted to achieve the high growth rate observed by Noad *et al.* (2011). For the D+E1+O model, the BSE1 population shares a total of 63892 catches with a larger BSD population to the west and a smaller BSO population to the east (Figure 2), and as such there is some flexibility in the model for balancing the catch allocation between BSD+BSE1 and BSE1+BSO. For the E1+O+G model, the BSE1 population shares a total of 59321 catches with a smaller BSO population to the east (Figure 2) and all the BSE1 catches are those shared with the western BSO population. While there are many intricate interacting factors that play a role in the final model outputs, it is clear that the different set-up of the two three-stock models can easily lead to appreciably different results. Interestingly, the likelihoods in Table 2, while showing a small difference for the BSE1 fit to the Noad *et al.* (2011) relative abundance data, otherwise do not differ greatly amongst the models, suggesting that the data do not provide sufficient information to clearly prefer one model to the other.

Some thought could be given to developing a gradient-like boundary, rather than the hard boundaries from Figure 1 and Figure 2, so that the catches from outside the current boundaries can still be allocated to the western- and eastern-most stocks of the three-stock model and perhaps produce more compatible results when the three-stock model is shifted from one group of neighbouring stocks to the next.

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Table 1 (a): Posterior median values of key model parameters are given with their 90% probability intervals for the E1+O+G three-stock model. Results are from a re-sample of 1000 from an initial sample of 2 000 000. The model was fit to the Noad *et al.* (2011) absolute and relative abundance estimates for BSE1, the Constantine *et al.* (2012) mark-recapture data for BSO and the Felix *et al.* (2011) absolute abundance estimate for BSG.

	BSE1		BSO		BSG	
r	0.105	[0.103,0.106]	0.056	[0.010,0.087]	0.055	[0.006,0.103]
K	36682	[29092,38717]	5700	[2861,15644]	8629	[5620,18096]
γ	0.359 [0.043,0.798] (Proportion of BSO feeding in western feeding area)					
N_{\min}	227	[204,259]	529	[175,2033]	1470	[233,5676]
N_{2015}	21765	[19760,23727]	3579	[2818,5285]	7254	[5274,9591]
N_{\min}/K	0.006	[0.005,0.008]	0.098	[0.024,0.273]	0.163	[0.034,0.431]
N_{2015}/K	0.602	[0.544,0.709]	0.713	[0.223,0.998]	0.921	[0.375,1.000]
N_{2020}/K	0.811	[0.760,0.885]	0.818	[0.240,0.999]	0.961	[0.379,1.000]
N_{2040}/K	0.999	[0.999,1.000]	0.986	[0.304,1.000]	0.998	[0.435,1.000]

Table 1 (b): Repeat of the model run from Table 1, except that in addition to the input data described there, the eastern feeding ground population $(1-\gamma^O)*N^{BSO}+N^{BSG}$ was also fit to the Branch (2011) feeding ground relative abundance series.

	BSE1		BSO		BSG	
r	0.105	[0.103,0.106]	0.067	[0.036,0.087]	0.068	[0.030,0.105]
K	37328	[31185,38724]	4469.0	[2897,10743]	8109	[5840,10913]
γ	0.357 [0.041,0.764] (Proportion of BSO feeding in western feeding area)					
N_{\min}	226	[202,257]	335	[175,790]	520	[225,2268]
N_{2015}	21719	[19909,23796]	3726	[2844,5182]	7280	[5534,8703]
N_{\min}/K	0.006	[0.005,0.008]	0.077	[0.025,0.169]	0.066	[0.033,0.210]
N_{2015}/K	0.594	[0.532,0.674]	0.859	[0.416,0.996]	0.944	[0.644,1.000]
N_{2020}/K	0.805	[0.749,0.865]	0.931	[0.510,0.999]	0.975	[0.696,1.000]
N_{2040}/K	0.999	[0.998,0.999]	0.998	[0.840,1.000]	0.999	[0.899,1.000]

Table 1 (c): Posterior median values from previous assessments are given with their 90% probability intervals. For BSE1 and BSO these previous assessment results are from the 2014 D+E1+O three-stock model (IWC 2014), which was fit to Bannister and Hedley (2001) and Hedley *et al.* (2011) relative abundance series for BSD, the Noad *et al.* (2011) absolute and relative abundance estimates for BSE1 and the Constantine *et al.* (2012) mark-recapture data for BSO. The BSG previous assessment results are from Johnston *et al.* (2011), where the model was fit to the Felix *et al.* (2011) absolute abundance estimate and the Branch (2011) IDCR/SOWER feeding ground relative abundance series.

	BSE1		BSO		BSG	
r	0.105	[0.103,0.106]	0.091	[0.071,0.101]	0.063	[0.023, 0.093]
K	26133	[21605,29033]	14115	[10198,19651]	11584	[10590,14878]
γ	0.068 [0.007,0.190] (Proportion of BSE1 feeding in western feeding area)					
N_{\min}	237	[203,272]	132	[103,250]	731	[238,2959]
N_{2015}	19614	[17643,21454]	6404	[5491,7595]	9173	[6829,10857]
N_{\min}/K	0.009	[0.008,0.011]	0.010	[0.007,0.014]	0.063	[0.022, 0.198]
N_{2015}/K	0.762	[0.692,0.841]	0.466	[0.291,0.657]	0.792	[0.512,0.956]
N_{2020}/K	0.915	[0.872,0.950]	0.648	[0.409,0.846]	0.885	[0.575, 0.988]
N_{2040}/K	1.000	[0.999,1.000]	0.993	[0.926,0.999]	0.994	[0.818,1.00]

Table 2: Likelihood components for BSE1 and BSO (the two stocks common across the two three-stock models) are given in terms of the posterior median values. Likelihood values are given for the 2014 D+E1+O three stock model, the current E1+O+G three stock model as well as the E1+O+G three-stock model where the eastern feeding ground population is fit to the IDCR/SOWER relative abundance trend.

BSE1	D+E1+O model	E1+O+G model	E1+O+G model, fitting to IDCR
Absolute abundance estimate (Noad et al. 2011)	0.2531	0.2046	0.2445
Relative abundance series (Noad et al. 2011)	-39.61	-41.37	-41.52
BSO	D+E1+O model	E1+O+G model	E1+O+G model, fitting to IDCR
Mark-recapture (Constantine <i>et al.</i> 2012)	-58.81	-59.04	-59.17

Table 3: Posterior medians of the cumulative catches allocated in the model to the various breeding stocks for (i) the E1+O+G three stock model, (ii) the E1+O+G three stock model where the IDCR/SOWER feeding ground estimates (Branch 2011) have been included in the likelihood fit and (iii) the 2014 D+E1+O three stock model. The 5th and 95th percentiles have been given in parenthesis.

	BSD	BSE1	BSO	BSG
(i) E1+O+G	-	41284 [31271, 43875]	7702 [2542, 21791]	10392 [5729, 13340]
(ii) E1+O+G (with IDCR/SOWER)	-	42048 [31271, 43875]	7278 [2542, 21791]	9991 [5729, 13340]
(iii) D+E1+O	19967 [16821, 21782]	27657 [20473, 33809]	16439 [11707, 22771]	-

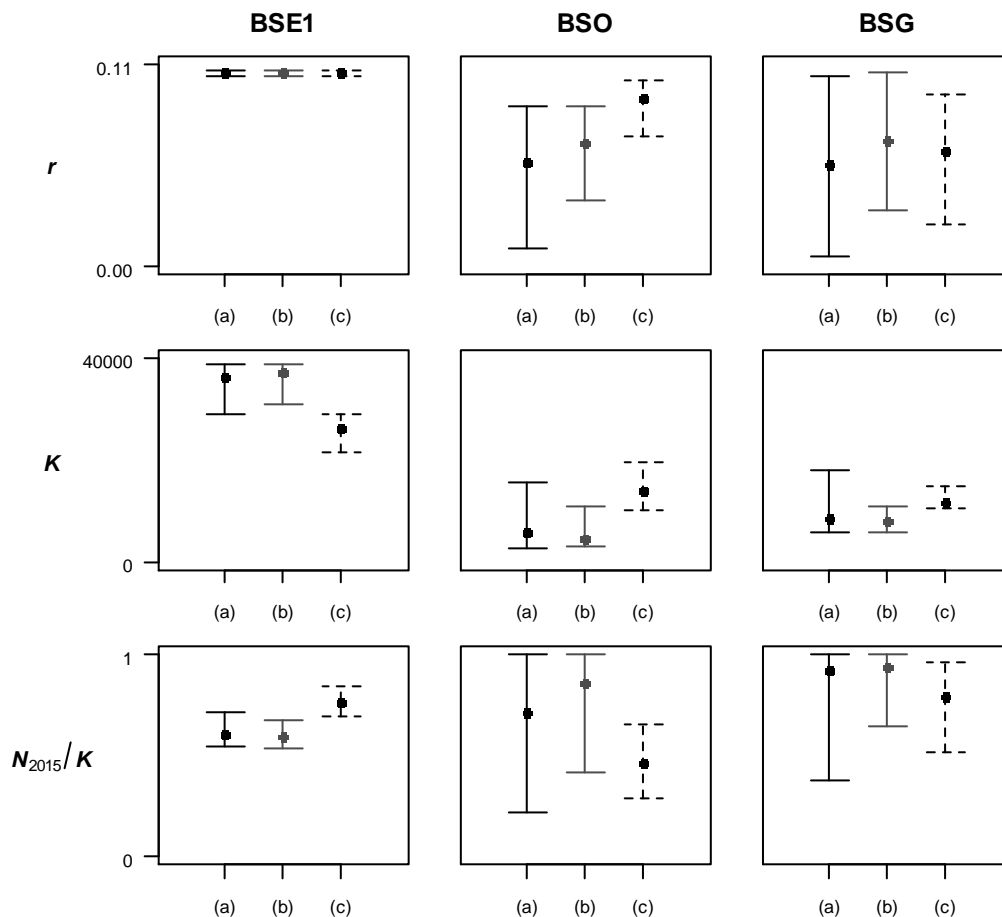


Figure 4: Graphical representation of the r , K , N_{2015}/K parameter estimates from Table 1. Median estimates are indicated by points and the 90% probability intervals by bars. Estimates are shown for all three stocks for (a) the E1+O+G three stock model, (b) the E1+O+G three stock model where the IDCR/SOWER feeding ground estimates (Branch 2011) have been included in the likelihood fit and (c) previous assessments (the 2014 D+E1+O model for BSE1 and BSO, and the Johnston *et al.* 2011 assessment for BSG).

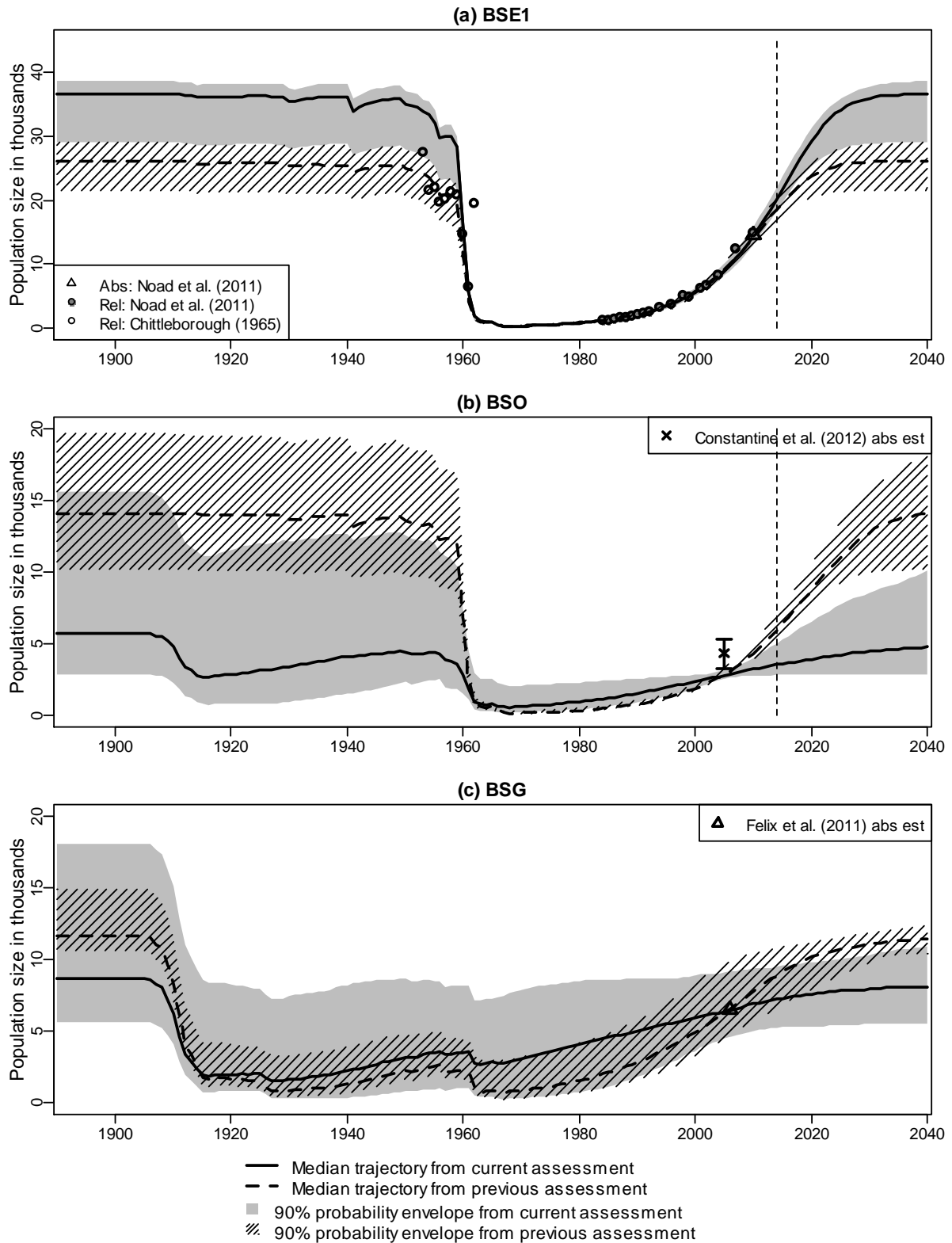


Figure 5: Posterior median population trajectories and their 90% probability envelopes (PE) for the three stocks. Trajectories for the E1+O+G three-stock model are shown by the solid lines and their 90% P.E. by the grey shaded areas. Posterior median trajectories from previous assessments are shown by dashed lines and their 90% P.E. by the areas filled with diagonals. For BSE1 and BSO these previous assessment results are from the 2014 D+E1+O three-stock model. The BSG previous assessment results are from Johnston *et al.* (2011). Fits to various input data are indicated in the legends.

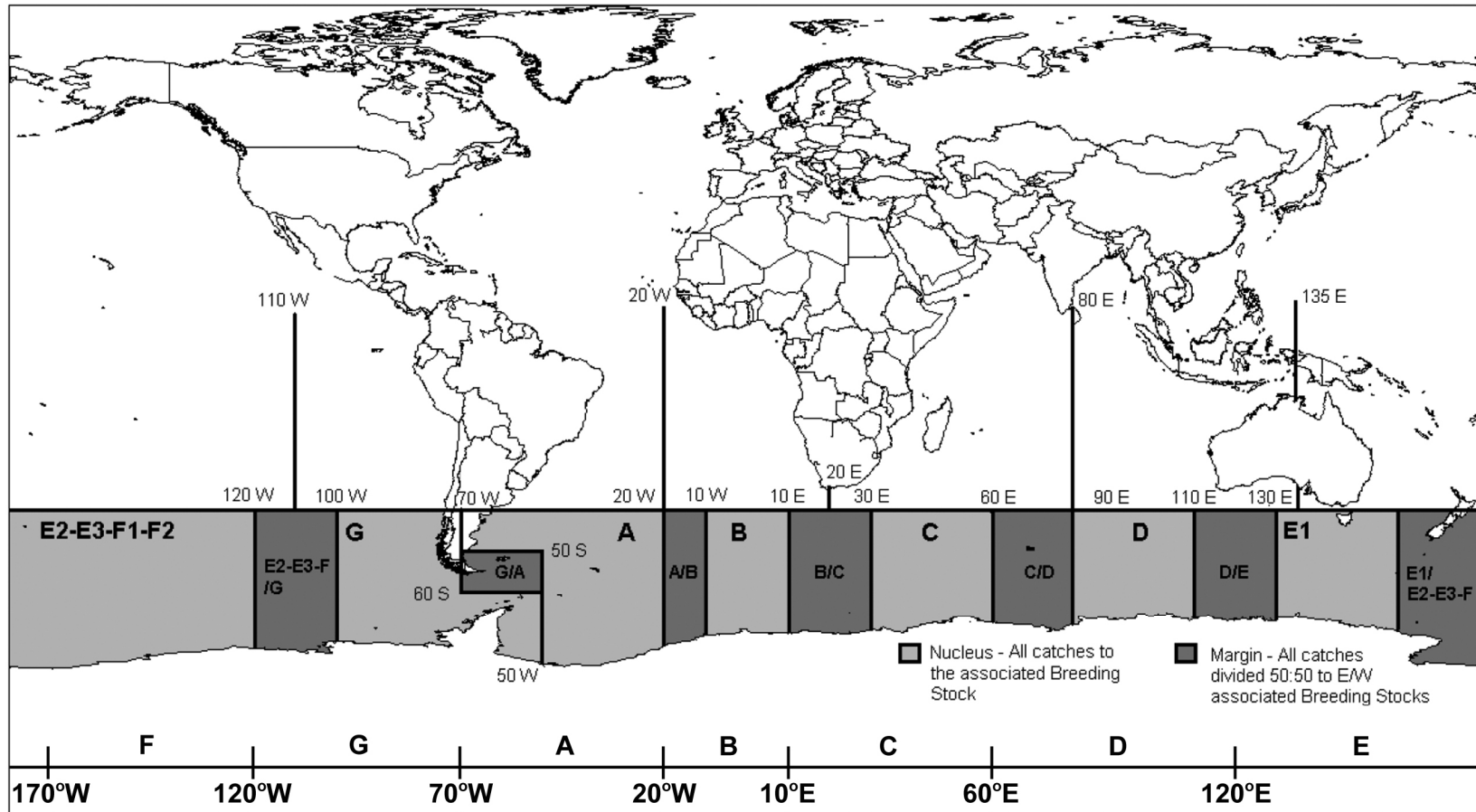


Figure 6: Nucleus and Margin regions associated with each of the seven breeding stocks according to Hypothesis 1 (map adapted from IWC, 2010).

APPENDIX A: CATCH, ABDUNANCE AND TREND DATA

Table A. 1: Historical catches taken north of 40°S from Allison’s database (C.Allison, *pers. comm*). The catches for E1 and Oceania are available by landing station. Catches landed at LochTay, Tangalooma and Byron Bay have been allocated to BSE1. Catches landed at Norfolk Island, Tonga and Polynesia have been allocated to the Oceania breeding stock. Catches landed at Rakiura and Prince George, New Zealand, Kaikoura, Cook Strait and Tory Channel, Great Barrier Island, Whangamumu and Bay of Island are allocated to BSE1 and Oceania in proportion to the model-predicted population abundances (labelled BSE1/BSO in the table). Catches labelled “Chile”, “Ch/Per/E” and “Peru” in the database have been allocated to BSG.

Year	BSE1	BSO	BSE1/ BSO	BSG	Year	BSE1	BSO	BSE1/ BSO	BSG
1890	0	0	8	0	1935	0	0	57	31
1891	0	0	8	0	1936	0	0	69	18
1892	0	0	8	0	1937	0	0	55	28
1893	0	0	8	0	1938	0	0	75	6
1894	0	0	8	0	1939	0	0	80	7
1895	0	0	8	0	1940	0	0	107	0
1896	0	0	8	0	1941	0	0	86	0
1897	0	0	8	0	1942	0	0	71	0
1898	0	0	8	0	1943	0	0	90	0
1899	0	0	8	0	1944	0	0	88	0
1900	0	0	8	0	1945	0	0	107	0
1901	0	0	8	0	1946	0	0	110	15
1902	0	0	8	0	1947	0	0	101	19
1903	0	0	8	0	1948	0	0	92	5
1904	0	0	8	0	1949	0	3	141	6
1905	0	0	8	0	1950	0	0	79	5
1906	0	0	8	0	1951	0	0	111	26
1907	0	0	8	0	1952	600	0	121	27
1908	0	0	8	16	1953	700	0	109	29
1909	0	0	16	44	1954	718	0	180	106
1910	0	0	77	62	1955	720	0	112	7
1911	0	0	77	92	1956	720	150	143	10
1912	0	0	93	86	1957	721	136	184	5
1913	348	0	92	45	1958	720	136	183	0
1914	0	0	93	195	1959	810	166	318	3
1915	0	0	106	30	1960	810	186	361	2
1916	0	0	82	15	1961	731	186	80	3
1917	0	0	94	15	1962	173	4	32	4
1918	0	0	90	23	1963	0	0	9	1
1919	0	0	119	24	1964	0	0	0	35
1920	0	0	107	21	1965	0	0	0	143
1921	0	0	89	21	1966	0	0	0	58
1922	0	0	57	19	1967	0	0	0	0
1923	0	0	79	16	1968	0	0	0	3
1924	0	0	107	34	1969	0	0	0	1
1925	0	0	96	248	1970	0	0	0	0
1926	0	0	78	277	1971	0	0	0	0
1927	0	0	127	40	1972	0	0	0	0
1928	0	0	105	36	1973	0	3	0	0
1929	0	0	102	26	1974	0	4	0	0
1930	0	0	78	33	1975	0	8	0	0
1931	0	0	109	53	1976	0	4	0	0
1932	0	0	18	21	1977	0	4	0	0
1933	0	0	44	11	1978	0	11	0	0
1934	0	0	52	13	Total	7771	1001	5690	2119

Table A. 2: Historical catches taken south of 40°S from Allison's database (C.Allison, *pers. comm*), given in 10 degree longitude bands. Catches taken between 120°E and 100°W were allocated to the western feeding ground and catches taken between 100°W and 70°W were allocated to the eastern feeding ground. Catches in the column 'S. Shet/Falk' are 100% of catches taken between 70°W and 50°W and south of 60°S as well as 50% of catches taken between 70-50°W and 50-60°S. These catches were allocated to the eastern feeding ground.

Year	120-129E	130-139E	140-149E	150-159E	160-169E	170-180E	180-170W	169-160W	159-150W	149-140W	139-130W	129-120W	119-110W	109-100W	99-90W	89-80W	79-70W	S. Shet/Falk
1903	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
1904	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1905	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23
1906	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	498
1907	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	366
1908	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1250.5
1909	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1528
1910	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2562
1911	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2047.5
1912	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	980
1913	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1041.5
1914	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	662
1915	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	219
1916	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21
1917	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69
1918	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81
1919	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	181
1920	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	149
1921	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1922	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	189
1923	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96
1924	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	102
1925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	163
1926	0	0	0	0	0	82	0	0	0	0	0	0	0	0	0	0	0	101
1927	0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	3
1928	0	0	0	0	0	17	0	0	0	0	0	0	0	0	0	0	0	16
1929	0	0	0	0	0	775	0	0	0	0	0	0	0	0	0	0	0	0
1930	1	0	32	49	3	55	96	0	0	0	0	0	0	0	0	0	0	1
1931	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1932	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1933	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1934	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1935	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1936	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Year	120-129E	130-139E	140-149E	150-159E	160-169E	170-180E	180-170W	169-160W	159-150W	149-140W	139-130W	129-120W	119-110W	109-100W	99-90W	89-80W	79-70W	S. Shet/ Falk
1937	32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1938	24	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1939	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1940	342	342	342	342	342	342	342	0	0	0	0	0	0	0	0	0	0	1
1941	0	0	0	0	0	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	0	0	0	0
1943	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1944	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1945	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1946	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1947	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1948	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1949	109	30	760	118	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1950	0	0	0	0	0	85	86	316	0	0	1	0	0	0	0	0	0	271.8
1951	232	0	1	0	66	103	189	37	0	0	1	0	0	0	0	0	0	0
1952	0	0	0	0	166	216	135	13	0	0	0	0	0	0	0	0	0	0
1953	0	0	0	0	0	0	14	136	0	0	0	0	0	0	0	0	0	0
1954	0	2	0	749	5	17	167	269	69	2	0	0	0	0	0	0	0	0
1955	411	769	416	777	0	0	0	278	56	0	0	0	0	0	0	14	0	0
1956	0	0	0	0	0	0	0	0	0	0	7	3	27	39	571	11	8	37.6
1957	0	30	19	38	133	0	0	0	35	27	29	76	31	0	37	18	4	0
1958	882.1	104.7	157.1	185.7	525.8	209.4	0	0	0	0	0	0	0	0	0	0	0	26.2
1959	44.8	1043.5	4057.1	3673	2228.5	998.7	317.8	112.8	73.2	106.8	73.2	73.2	74.1	7	14	5	0	182
1960	71	163.7	742.3	1184.3	3703.8	2630.2	740	962.5	565.27	508.3	428.57	292.87	0	0	0	0	81	10.9
1961	14	14	61	436	581	342	123	226	1010	401	452	189	54	44	806	334	24	2.5
1962	58.2	18.2	35.4	39.7	302.2	9.2	10	49.5	87.7	66.1	63.5	18.1	18.1	24.4	36.2	70	88.1	85.5
1963	0.2	1.2	23.6	20.9	225	13	0	0	0	0	0	0	0	0	0	0	0	0
1964	0.9	2.8	11.3	26.2	45	0	0	0	0	0	0	0	0	0	0	0	0	0
1965	8.8	12.6	43.6	26.6	80	97.1	85.3	474.6	1.3	1	0	0	0	0	0	0	0	0
1966	7	4	3	1	11	14	16	93	118	26	0	0	0	0	0	0	0	0
1967	7	0	1	11	12	2	1	6	47	57	0	0	0	0	0	0	0	0
1968	0	0	0	0	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	0	0	0	0
1970	0	0	0	0	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	0	3	0	0	0	0	0
1972	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Total	2245	2561.7	6709.4	7677.4	8431.3	6023.6	2322.1	2973.4	2062.47	1195.2	1055.27	652.17	207.2	114.4	1464.2	452	205.1	12969

Breeding Stock E1

Absolute abundance estimate

A land-based survey was conducted at Point Lookout on the east coast of Australia over eight weeks in June and July 2010 (Noad *et al.* 2011). 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% CI⁵ 12,777 – 16,504) (Noad *et al.*, 2011).

Relative abundance estimates

Table A. 3: 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 were 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
1984	6.12
1985	5.92
1986	8.25
1987	8.53
1988	9.15
1989	10.22
1990	11.58
1991	12.93
1992	14.36
1994	17.75
1996	20.91
1998	28.45
1999	27.45
2001	34.67
2002	37.34
2004	47.11
2007	70.73
2010	84.7

Minimum number of haplotypes

The minimum number of haplotypes for BSE1 5 (IWC 2014).

⁵ 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 $0.5 * (\ln(16504) - \ln(12777)) / 1.96$. The resulting value of 0.065 was then taken to be the CV of the estimate.

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.*, 2012). It is a doubled male-specific estimate assuming equal numbers of males and females in the region.

Mark recapture data

Table A. 4: Synoptic genotypic mark recapture data underlying male specific Oceania-wide abundance estimate. This is the males-only subset of the sexes combined dataset from Constantine *et al.* (2012), as provided by Jackson (*pers. comm.*, 2012).

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							-

Minimum number of haplotypes

The minimum number of haplotypes for Oceania is 33 (IWC 2014).

BREEDING STOCK G

Absolute abundance estimate

A breeding ground estimate of 6504 (CV=0.21) for the year 2006 is from a photographic capture-recapture study in Ecuador, and is based on Chapman modified-Peterson estimator (Felix *et al.*, 2011).

Relative abundance estimates

Table A. 5: IDCR/SOWER estimates for the feeding grounds (Branch 2011). The area for G is 110°W-50°W, south of 60°S.

Year	N	CV
1982	1452	0.65
1989	2817	0.38
1996	3310	0.21

Minimum number of haplotypes

The minimum number of haplotypes for BSG is 27 (Rosenbaum *et al.* 2006).