

Initial exploration of single-stock, two-stock and three-stock population models for humpback breeding stocks D, E1 and Oceania under different Antarctic stock boundaries assumptions

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ABSTRACT

A three-stock model with feeding and breeding ground interchange was proposed at IWC 64 for the assessment of Southern Hemisphere humpback whale breeding stocks D (West Australia), E1 (East Australia) and Oceania, with the aim of addressing some inconsistencies that arose in the single-stock assessments. First a two-stock (D+E1) and then a three-stock model with only mixing of stocks on the feeding grounds were developed, but it was found that neither removed these inconsistencies. It was found, however, that substantial improvements could be obtained by shifting the customary Antarctic stock boundaries to allow for more of the Antarctic catches to be allocated to breeding stock D. This paper presents the results of the single-stock, two-stock and three-stock models for both the original Antarctic boundaries, as well as the proposed new boundaries. The aim of the paper is to illustrate the effect of moving the boundaries and to provide a platform for further discussion and development at IWC 65.

INTRODUCTION

Paper SC/64/SH29 presented preliminary results for three single stock models for the respective West Australian (D), East Australian (E1) and Oceania (O) breeding stocks. Two inconsistencies of concern were evident:

1. The reference case trend and abundance data used for the West Australian breeding Stock (Breeding Stock D, or BSD) comprised an absolute abundance estimate (Hedley *et al.* 2011) and a relative abundance series (Hedley *et al.* 2011). The model-predicted population trajectory was unable to simultaneously fit this absolute abundance estimate as well as reflect the high growth rate suggested by the relative abundance series.
2. Haplotype data give an indication of the minimum size a population under study could have realistically been in the past. Constraints in the model do not allow the model estimated population trajectory to go below this N_{min} value. It was found that the minimum population size the model predicted for the Oceania breeding stock (BSO) violated the N_{min} constraint, i.e. if the constraint was removed from the model, the other data led to a posterior median population trajectory went below this N_{min} constraint.

It was suggested at IWC 64 that feeding and breeding ground interchange between the breeding stocks might help resolve these inconsistencies. A model was proposed that allowed for (a) migration of whales from one breeding stock to another on the breeding grounds, and (b) movement of the whales on the feeding grounds so that catches traditionally associated with one stock might in part be allocated to another stock as well.

The authors proposed to undertake the development of this model in three steps: (1) a two-stock model between D and E1, (2) a three-stock model for D, E1 and Oceania, with only the feeding ground interchange, since it was assumed that the feeding ground interchange would have a more substantial effect on the model results than the relatively small breeding ground interchange indicated by tag-recapture data, so that this would therefore be a simpler but nevertheless good starting place, and (3) update the three-stock model from (2) to include breeding ground interchange.

It was found, however, that neither the two-stock model for D and E1, nor the three-stock model with feeding ground interchange provided any substantial resolution of the inconsistencies mentioned above. It was considered

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unlikely that including breeding-ground interchange would improve the situation, since such interchange rates seemed likely to be low.

Given the nature of the inconsistencies, the hypothesis that the somewhat arbitrary boundaries used for allocating the Antarctic catches to the different breeding stocks might be the root of the problem came under consideration. Both the West and East Australia populations must have been depleted to fairly low numbers historically in order to experience the high growth rate indicated by the trend data. If not enough catches are allocated to BSD with the current Antarctic boundaries, this will lead to less extreme depletion levels in the model, and might explain why the model-predicted population trajectory cannot reflect the high increase rate suggested by the data. Similarly, too many catches allocated to the Oceania stock could explain why the model-predicted population went below the biologically realistic minimum population size indicated by genetic data. Therefore it seemed reasonable to investigate whether moving the Antarctic boundaries might be a better way to resolve the inconsistencies.

A total of 16 different Antarctic catch boundaries were explored, and it was found that it was possible to obtain a much better fit to the BSD data without a substantial loss of fit to the BSE1 data by moving the boundaries. The results of these 16 models are not presented here, but they indicated that moving the D-E1 boundary from 120E to 150E, and moving the E1-O boundary from 170E to 150W yielded the best results. The single-stock models, the two-stock (D and E1) model and three-stock model (D, E1 and O) were run for the new boundaries. Diagrammatic representations of the two-stock and three-stock models are given in Figure B. 2 of Appendix B. Results are presented in this paper for the new boundaries, as well as for the old boundaries for comparison purposes.

The purpose of this paper is to illustrate the improvement of the model fits (in particular for BSD) obtained by shifting the boundaries, and hence to create a platform for further discussion at IWC 65 regarding the boundaries for and development of the models. Mixing proportions for the Antarctic feeding grounds are available (Pastene *et al.*, 2012) and give the proportion of animals from the different stocks occurring in each feeding area. These proportions will have to be revised given these suggested new Antarctic boundaries. It is suggested that the revision occurs once the sub-committee has had a chance to review the findings presented in this paper and has come to an agreement regarding the most appropriate placement of the Antarctic boundaries.

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 E1 and 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 have been split equally between BSE1 and Oceania.

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.

Abundance and trend data

The data used in this assessment are listed in the Appendix. A summary is given below of which data were used for the base case and which were used for independent consistency checks, as recommended at IWC 64. 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

Breeding ground data		Reference Case	Sensitivity	Consistency Check
<i>Breeding Stock D</i>				
Absolute abundance	Hedley <i>et al.</i> (2011)	X		
Relative abundance	Hedley <i>et al.</i> (2011)	X		
Relative abundance	Bannister and Hedley (2001)		X	
Relative abundance	Chittleborough (1965)			X
Min number of haplotypes	Olavarria <i>et al.</i> (2007)	X		
<i>Breeding Stock E1</i>				
Absolute abundance	Noad <i>et al.</i> (2011)	X		
Absolute abundance	Paton <i>et al.</i> (2011)			X
Relative abundance	Noad <i>et al.</i> (2011)	X		
Relative abundance	Chittleborough (1965)			X
Relative abundance	Forestell <i>et al.</i> (2011)			
Mark-recapture (photo-ID)	Forestell <i>et al.</i> (2011)			X
Mark-recapture (genetic)	Jackson <i>et al.</i> (2012)			X
Mark-recapture (photo-ID)	Paton <i>et al.</i> (2011)			X
Min number of haplotypes	Olavarria <i>et al.</i> (2007); Valsecchi <i>et al.</i> (2010)	X		
<i>Oceania breeding stock</i>				
Mark-recapture (photo-ID)	Constantine <i>et al.</i> (2011)	X		
Absolute abundance	Constantine <i>et al.</i> (2011) ²			X
Mark-recapture (genetic)	Jackson <i>et al.</i> (2012)			X
Min number of haplotypes	Olavarria <i>et al.</i> (2007)	X		
<i>Data informing interchange</i>				
Mark-recapture (photo-ID)	Pacific Whale Organisation – D and E1			
Mark-recapture (genetic)	Anderson <i>et al.</i> (2007) – D and E1			
Mark-recapture (genetic)	Jackson <i>et al.</i> (2012) – E1 and Oceania			
Feeding ground data		Reference Case	Sensitivity	Consistency Check
Relative abundance	Matsuoka <i>et al.</i> (2011)		X	X
Relative abundance	Branch (2011)		X	X
Mixing proportions	Pastene <i>et al.</i> (2013)			

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.

METHODS

Population dynamics

The population dynamics are given by the following equation:

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

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) $r^i \sim U[0, 0.106]$ ³
- 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) 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 $\tilde{N}_{target}^{i,obs}$ 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.

Priors for the mixing proportion parameters which come into play in the two- and three-stock models, and described in Appendix B.

³ Note that an importance function was used for r^{E1} to improve sampling efficiency. Details are given later.

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 deviation⁴. Thus the negative log likelihood contribution is:

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

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

- I_y is the relative abundance estimate for year y ,
- q is a constant of proportionality⁵,
- 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:

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

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:

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

⁴ 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 .

⁵ 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 $[r, \ln N_{target}]$. 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.

In the Bayesian context, \boldsymbol{q} and $\boldsymbol{\sigma}$ 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 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 distribution⁶, with the associated likelihood contribution given by:

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

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:

⁶ 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.

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

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

Importance function for BSE1

The trend data for BSE1 (Noad *et al.*, 2011) are highly informative, and as such high r^{EI} values have a much higher likelihood associated with them and have a much better chance of being resampled. Since r^{EI} is sampled from a uniform prior on the interval $[0,0.106]$, small values of r^{EI} 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 values are sampled repeatedly). A very large initial sample has to then be drawn in order to generate enough samples with high r 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^{EI} values and reduces the number of essentially wasted low r values in the sample. To counter the fact that the resulting distribution of the n_1 values of r^{EI} sampled is no longer uniform as required by the uniform prior distribution, the final likelihood values are weighted up in the same proportion as the probability of picking a particular r^{EI} in the initial sample was weighted down.

The importance function used is shown in Figure 1 below. Given this function, the likelihood associated with any sample containing an r^{EI} valued between 0 and 0.05 is up-weighted by a factor of 20, the likelihood associated with any sample containing an r^{EI} valued between 0.05 and 0.07 is up-weighted by a factor of 5, etc.

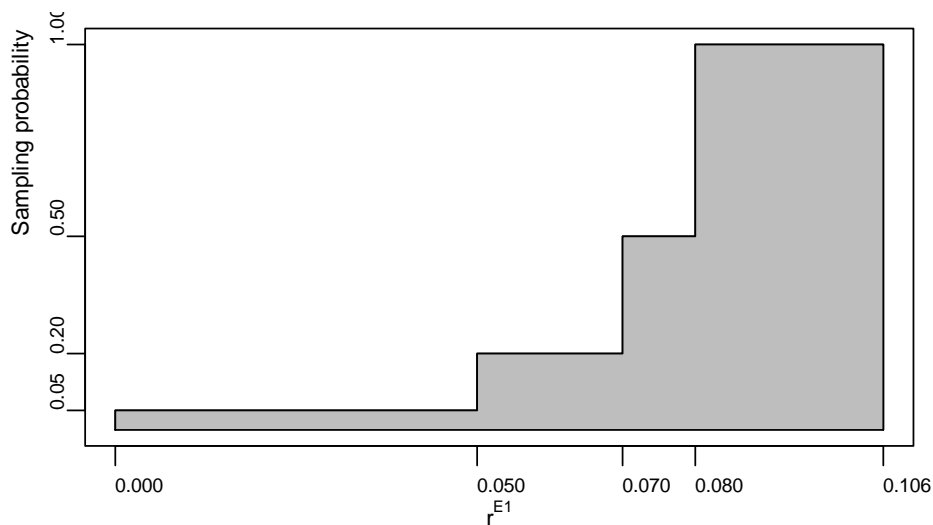


Figure 1: Importance function used when sampling for r^{EI} . The horizontal axis shows the step values of r^{EI} at which the importance function increases, and the vertical axis shows the probability of accepting an r^{EI} sample from a particular range. In other words, if a value between 0 and 0.05 is drawn 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

The posterior median values and their 90% probability intervals for r , K , N_{min} , N_{2012}/K and N_{2040}/K are given in Table 2. Results are given for the single-stock, two-stock and three-stock models for BSD and BSDE1 (Table 2(a) and (b)), and for the single-stock and three-stock model for BSO (Table 2(c)). Results are presented for both the old and the new Antarctic catch boundaries. Posterior median values and their 90% probability intervals for the interchange parameters in the two-stock and three-stock models are given in Table 2(d).

Plots of the median trajectories with the 90% probability envelopes are given in Figure 2 (BSD), Figure 3 (BSE1) and Figure 4 (BSO). Fits to abundance and trend data are shown where such data are available for the stock in question. Fits to mark-recapture data in the form of cumulative resightings are shown in Figure 4 (BSE1 fits to the Forestell *et al.* (2011) data and the Jackson *et al.* (2012) (sexes combined) data) and Figure 6 (BSO fits to the Constantine *et al.* (2011) and the Jackson *et al.* (2012) (sexes combined) data).

DISCUSSION

The primary purpose of this document is to report on results of the model put forward at IWC 64⁷ and to illustrate the effects of moving the Antarctic catch boundaries, in order to facilitate further discussion at IWC 65. In light of this, discussion will aim to highlight points that should be noted and discussed further by the sub-committee.

Breeding Stock D

Figure 2: Moving the Antarctic boundaries results in a substantial improvement for the BSD fit to trend data, in particular to the Bannister and Hedley (2001) relative abundance series (although the model is not (here) fit to this series directly). This boundary shift is supported by the analyses of the genetic data from the JARPA and JARPA II programmes, which indicate a large proportion (24%) of BSD whales in the region from 120E to 170E (T. Kitakado, *pers. comm.*). The fit to the Hedley *et al.* (2011) relative abundance series is still fairly poor. Moving from the single-stock to the two-stock and three-stock models does not seem to make a substantial difference to the model results. The estimated intrinsic growth rate parameter does change (Table 2(a)), but the wide probability envelope about the estimate is a reflection of the fact that the data have not updated the prior for this parameter very much (see Figures B3 and B4). This will change if it is decided to also include the earlier time series of relative abundance estimates for BSD (Bannister and Hedley, 2001) in the likelihood.

Breeding Stock E1

Figure 3: Fits to the Noad *et al.* (2011) relative abundance are exceptionally good in all cases. This abundance series is highly informative, resulting in a consistently high estimate of the growth rate with a very narrow probability envelope. A point worth consideration is to what extent the Noad *et al.* (2011) data will dominate the other likelihood components in the two-stock and three-stock models. It is interesting to note that, although no mark-recapture data have been incorporated into the likelihood, the Forestell *et al.* (2011) mark-recapture data appears to be consistent with the model results, but the Jackson *et al.* (2012) fits are poor (Figure 4). For these cumulative resightings plots the points to consider are most likely the last in the series. The resightings are accumulated over the years and as such the last points should ideally lie within the probability envelope for the model estimate. For the Jackson *et al.* (2012) data, the observed cumulative resightings are substantially higher than the model estimate, suggesting that the model-estimated population is too large.

Breeding Stock O

Figure 4: The problem with the N_{min} constraint seems to have remained, as the median population trajectory goes below the N_{min} value if the penalty is removed from the likelihood. Another way of looking at the effect of this constraint is to consider what fraction of the initial sample of n_i violate the N_{min} constraint (and therefore are unlikely to be resampled given the N_{min} penalty). For the single-stock BSO model with the old boundaries, 31% of the samples violated the N_{min} constraint. With the new boundaries, this decreases to 18%. Therefore while the N_{min} constraint is clearly still raises a problem, the new boundaries have ameliorated it somewhat. Fits to the Constantine *et al.* (2011) data are shown in Figure 6. The observed cumulative resightings are consistently higher

⁷ It is noted again that the three-stock model presented here is an adapted version of the model proposed at IWC64, since breeding ground interchange has not been included at this stage yet.

than the model estimate, suggesting that the model-estimated population is too large. Fits to the Jackson *et al.*, (2012) data are good, so although these data have not been included in the likelihood, they appear to be consistent with the model.

General points for discussion and further model development

The plausibility of the existing and proposed new Antarctic boundaries should be discussed in light of the improved fit to the BSD data obtained by shifting the boundaries. Once a reference set has been decided on, reanalyses of the Pastene *et al.* (2011) mixing proportions in the Antarctic feeding grounds should be undertaken to obtain estimates of the proportions of the three stocks in the new feeding areas. These estimates can be included in the likelihood when fitting the two-stock and three-stock models.

Much of the information on the stocks has yet to be included in the likelihood when fitting the model. This needs to be discussed at IWC 65 to specify updated reference cases. These in turn should result in more updating of the priors for intrinsic growth rate and stock mixing parameters than is broadly evident (aside from r for BS E1) from the plots in Figures B3 and B4.

Consideration should be given to potential errors in the genetic mark recapture data which could result in false negatives and so bias results.

Breeding ground interchange has not yet been implemented at this stage. Once a reference case feeding ground catch allocation has been decided on, the breeding ground interchange will be explored.

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Table 2(a)-(d): Posterior median values of key model parameters are given, with their 90% probability intervals, for the various models run. Table 2(a) gives the results for BSD, Table 2(b) those for BSE1 and Table 2(c) those for BSO. Table 2(d) gives the same posterior statistics for the mixing proportion parameters the two-stock and three-stock models.

(a) BSD		r	K	N_{\min}	N_{2012}/K	N_{2040}/K
Old boundaries	Single-stock	0.047 [0.005,0.100]	33421 [24420,66218]	11712 [3166,25475]	0.908 [0.442,1.000]	0.996 [0.496,1.000]
	Two-stock	0.056 [0.012,0.098]	30341 [22384,55051]	8847 [2061,20880]	0.944 [0.539,1.000]	0.999 [0.682,1.000]
	Three-Stock	0.054 [0.010,0.093]	32936 [23447,56833]	11438 [5102,21333]	0.968 [0.476,1.000]	0.999 [0.590,1.000]
New boundaries	Single-stock	0.056 [0.008,0.099]	36486 [28347,72227]	4759 [1065,21091]	0.831 [0.415,1.000]	0.996 [0.516,1.000]
	Two-stock	0.068 [0.023,0.102]	31706 [24165,52949]	4400 [930,14997]	0.926 [0.549,1.000]	1 [0.816,1.000]
	Three-Stock	0.060 [0.006,0.099]	33060 [25634,74051]	5269 [1431,23786]	0.91 [0.403,1.000]	0.999 [0.485,1.000]

(b) BSE1		r	K	N_{\min}	N_{2012}/K	N_{2040}/K
Old boundaries	Single-stock	0.105 [0.103,0.106]	25666 [25631,25775]	230 [203,260]	0.632 [0.578,0.685]	1 [1.000,1.000]
	Two-stock	0.105 [0.103,0.106]	26504 [21792,29691]	204 [171,242]	0.624 [0.543,0.730]	1 [0.999,1.000]
	Three-Stock	0.105 [0.103,0.106]	28121 [22948,32299]	222 [193,262]	0.594 [0.506,0.690]	1 [0.999,1.000]
New boundaries	Single-stock	0.105 [0.103,0.106]	27477 [27442,27598]	230 [204,264]	0.597 [0.548,0.654]	1 [0.999,1.000]
	Two-stock	0.105 [0.104,0.106]	29015 [23320,34271]	224 [199,260]	0.572 [0.485,0.696]	1 [0.999,1.000]
	Three-Stock	0.105 [0.103,0.106]	28890 [23601,33797]	226 [198,261]	0.574 [0.495,0.690]	1 [0.999,1.000]

(c) BSO		r	K	N_{\min}	N_{2012}/K	N_{2040}/K
Old boundaries	Single-stock	0.035 [0.005,0.058]	18169 [16545,23338]	827 [375,2393]	0.196 [0.124,0.257]	0.483 [0.144,0.832]
	Two-stock	-	-	-	-	-
	Three-Stock	-	-	-	-	-
New boundaries	Single-stock	0.038 [0.005,0.059]	5803 [5038,9372]	750 [367,2379]	0.592 [0.312,0.742]	0.929 [0.359,0.993]
	Two-stock	0.040 [0.010,0.057]	16995 [11434,25497]	675 [388,2112]	0.231 [0.128,0.336]	0.647 [0.174,0.886]
	Three-Stock	0.044 [0.007,0.067]	6495 [3306,12686]	669 [355,2230]	0.533 [0.254,0.955]	0.926 [0.314,1.000]

(d) Interchange		β_{DE}	β_{ED}	γ	γ^*	β_{EO}	β_{OE}
Old boundaries	Two-stock	0.044 [0.003,0.234]	0.368 [0.030,0.840]	-	-	-	-
	Three-Stock	0.418 [0.007,0.832]	0.169 [0.012,0.410]	0.108 [0.005,0.448]	0.387 [0.100,0.773]	0.238 [0.045,0.637]	0.036 [0.002,0.125]
New boundaries	Two-stock	0.071 [0.006,0.305]	0.393 [0.048,0.832]	-	-	-	-
	Three-Stock	0.271 [0.011,0.818]	0.161 [0.029,0.456]	0.184 [0.024,0.536]	0.323 [0.088,0.642]	0.24 [0.015,0.460]	0.065 [0.005,0.300]

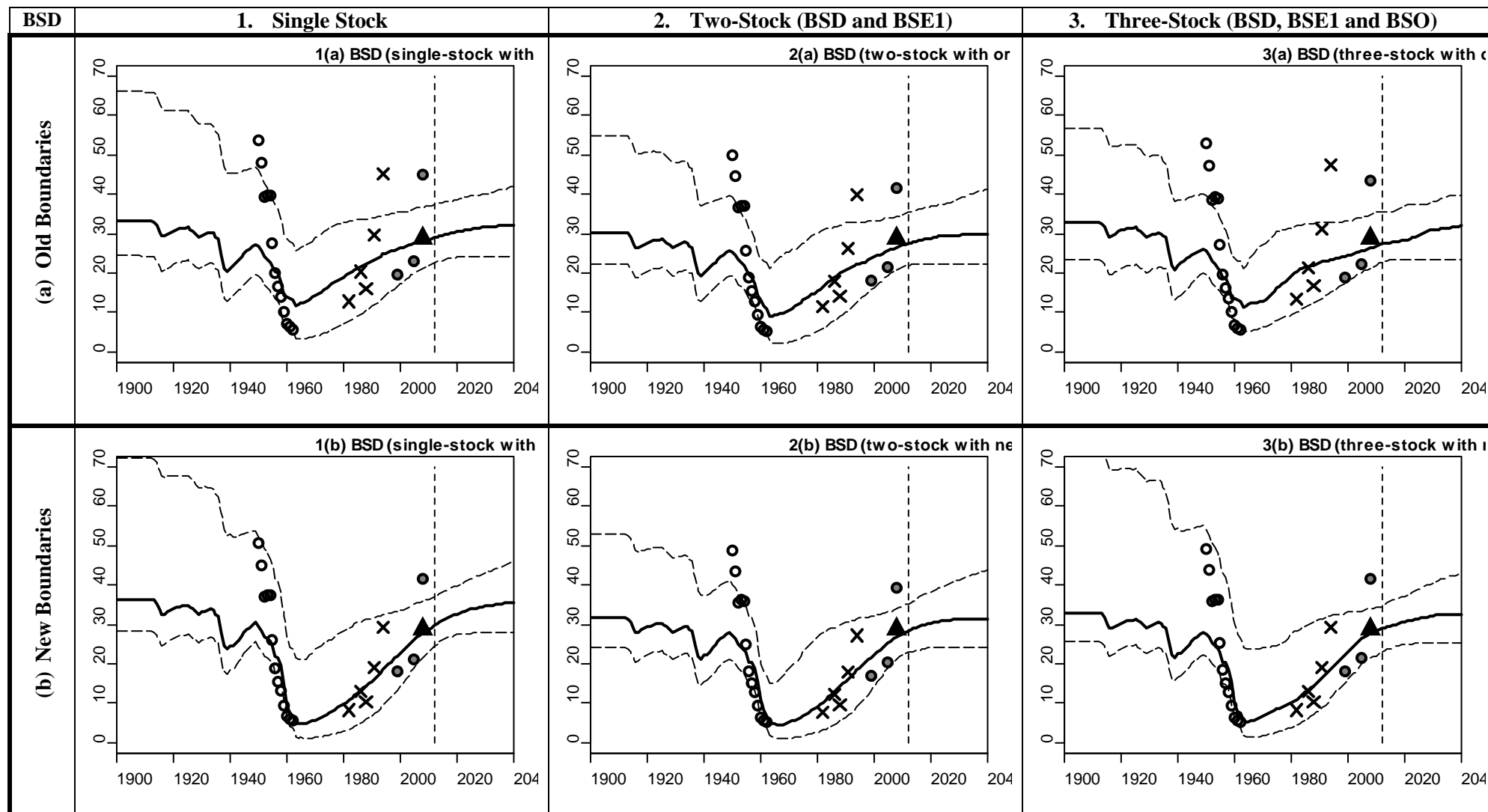


Figure 2: Posterior median population trajectories for BSD, showing the trajectories and the 90% probability envelopes. Results are shown for single-stock, two-stock and three-stock models using the old boundaries, and are repeated for the new boundaries. Plots show fits to the Chittleborough (1965) relative abundance series (open circles), the Bannister and Hedley (2001) relative abundance series (crosses), the Hedley *et al.* (2011) relative abundance series (grey circles) as well as the Hedley *et al.* (2011) absolute abundance estimate (black triangle). In all cases the model was fit to the Hedley *et al.* (2011) relative and absolute abundance estimates. The Chittleborough (1965) and Bannister and Hedley (2001) relative abundance series are shown as consistency checks. The trajectory to the right of the vertical dashed 2012 line shows projection into the future under the assumption of zero catch.

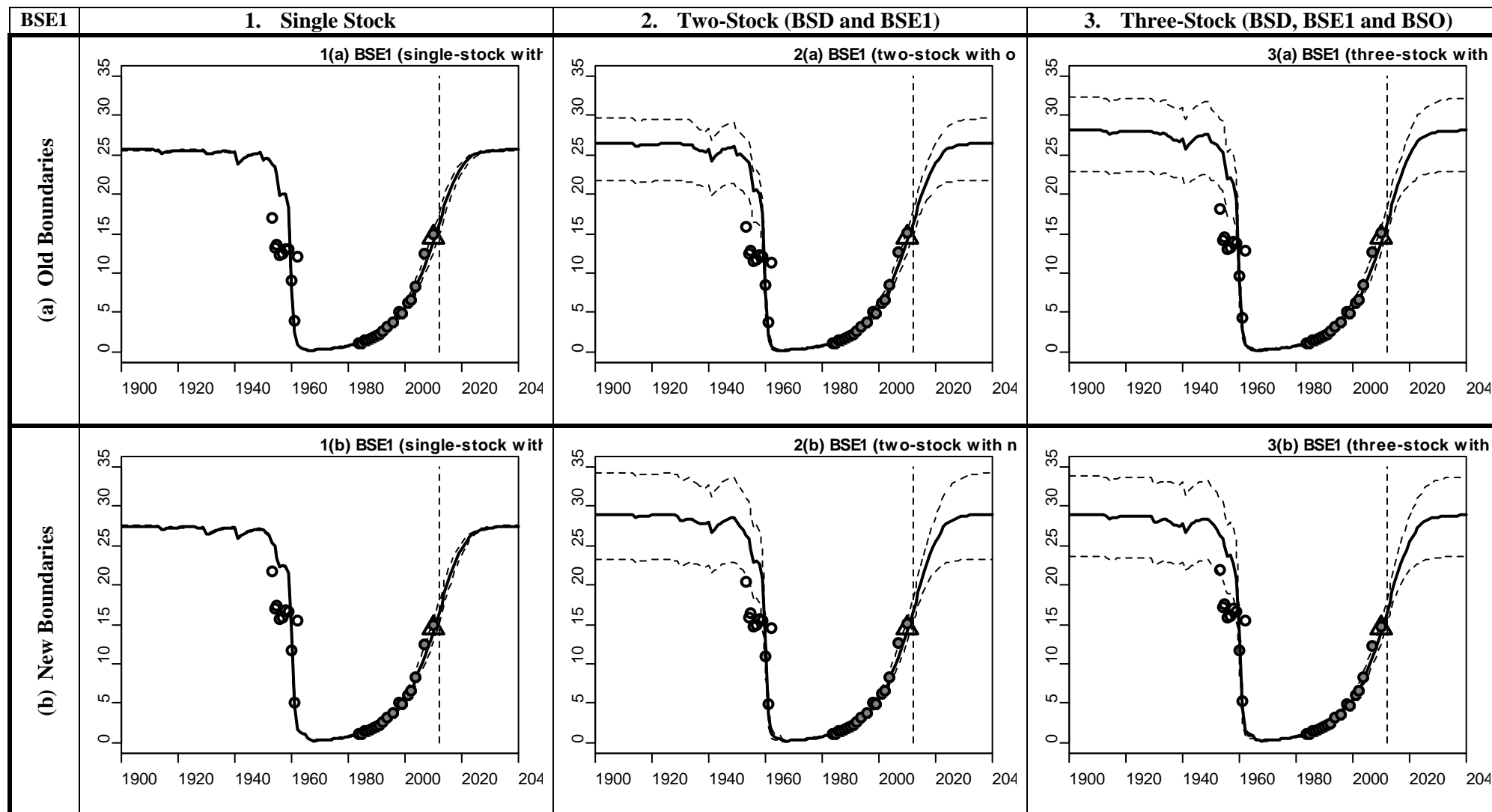


Figure 3: Posterior median population trajectories for BSE1, showing the trajectories and the 90% probability envelopes. Results are shown for single-stock, two-stock and three-stock models using the old boundaries, and are repeated for the new boundaries. Plots show fits to the Chittleborough (1965) relative abundance series (open circles), the Noad *et al.* (2011) relative abundance series (grey circles) as well as the Noad *et al.* (2011) absolute abundance estimate (black triangle). In all cases the model was fit to the Noad *et al.* (2011) relative and absolute abundance estimates. The Chittleborough (1965) relative abundance series is shown as a consistency check. The trajectory to the right of the vertical dashed 2012 line shows projection into the future under the assumption of zero catch.

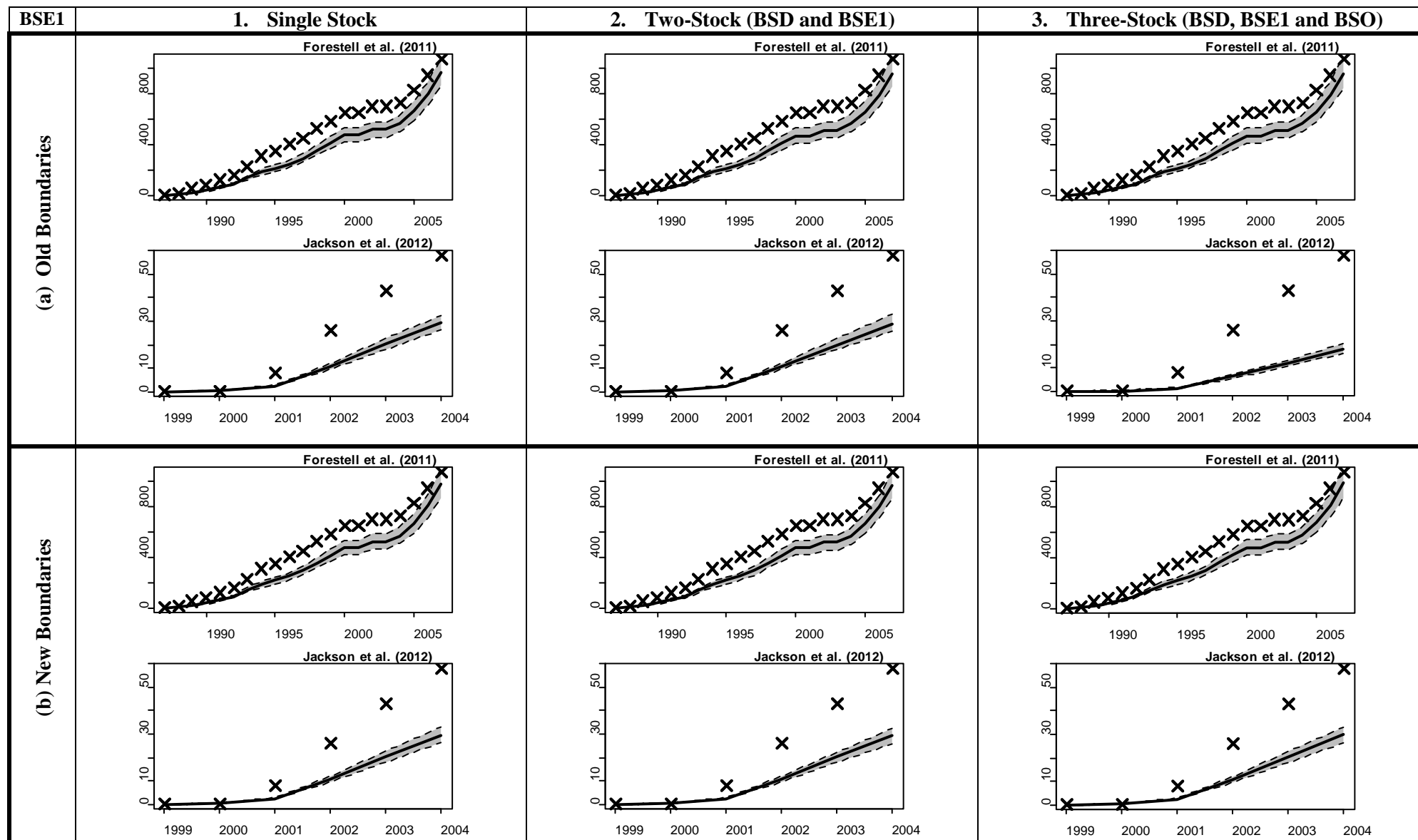


Figure 4: Plots showing model fit to mark-recapture data. Note that these mark-recapture data have not been included in the likelihood, and the fits are shown as a consistency check. The cumulative observed re-sightings are marked by X's. The median estimates are shown by the thick line and their 90% probability envelope is indicated by the shaded region.

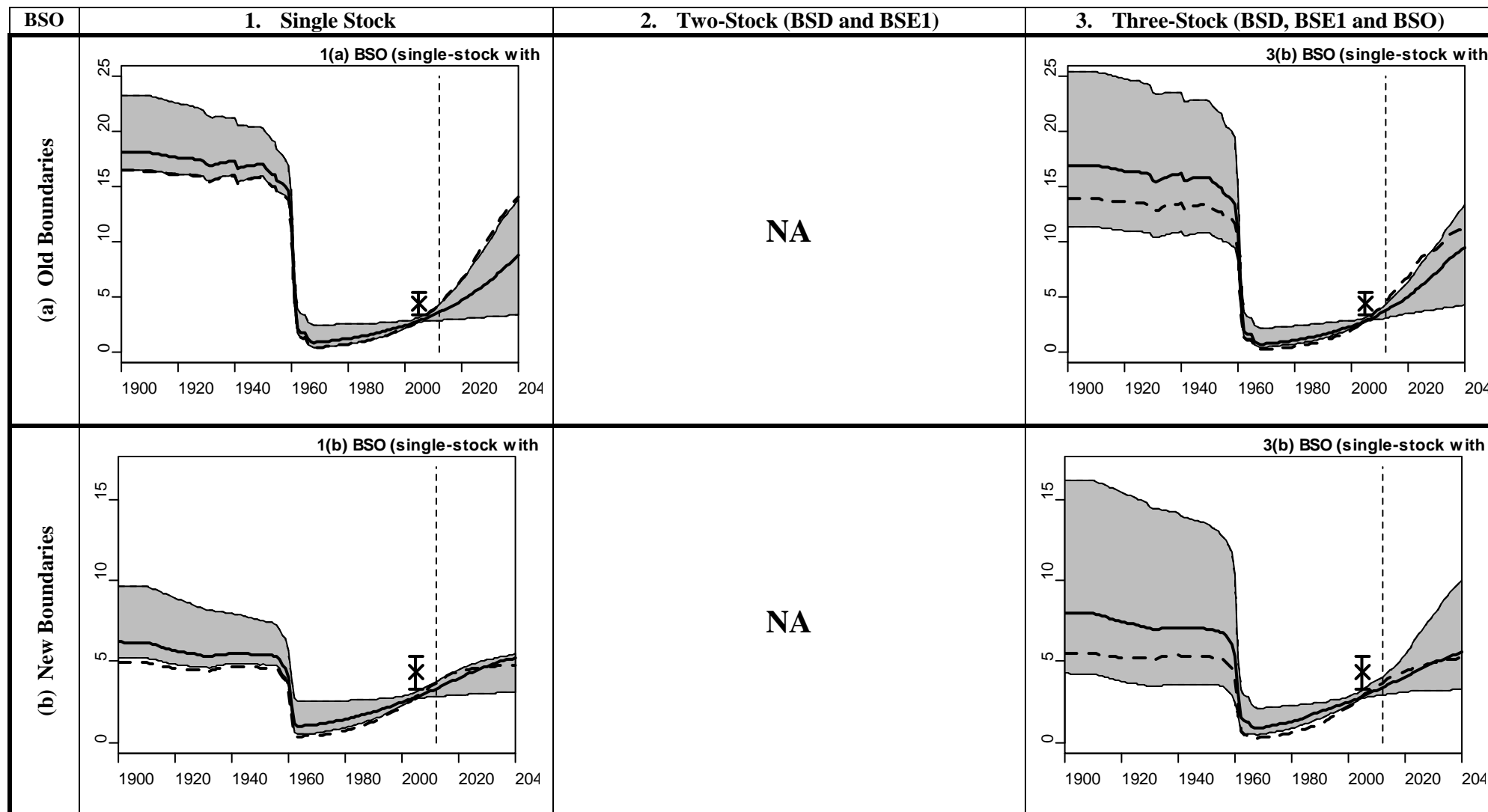


Figure 5: Posterior median population trajectories for BSO. The 90% probability envelopes are indicated by the grey areas. Results are shown for single-stock and three-stock models using the old boundaries, and are repeated for the new boundaries. A two-stock model for BSE1 and BSO was not undertaken for this analysis. In all cases the model was fit to the Constantine *et al.* (2011) mark-recapture data. The dashed curves show the posterior median population trajectory for the case when the model was run without the N_{min} constraint to illustrate the impact which this constraint has. The Constantine *et al.* (2011) absolute abundance estimate is shown as a consistency check. The trajectory to the right of the vertical dashed 2012 line shows projection into the future under the assumption of zero catch.

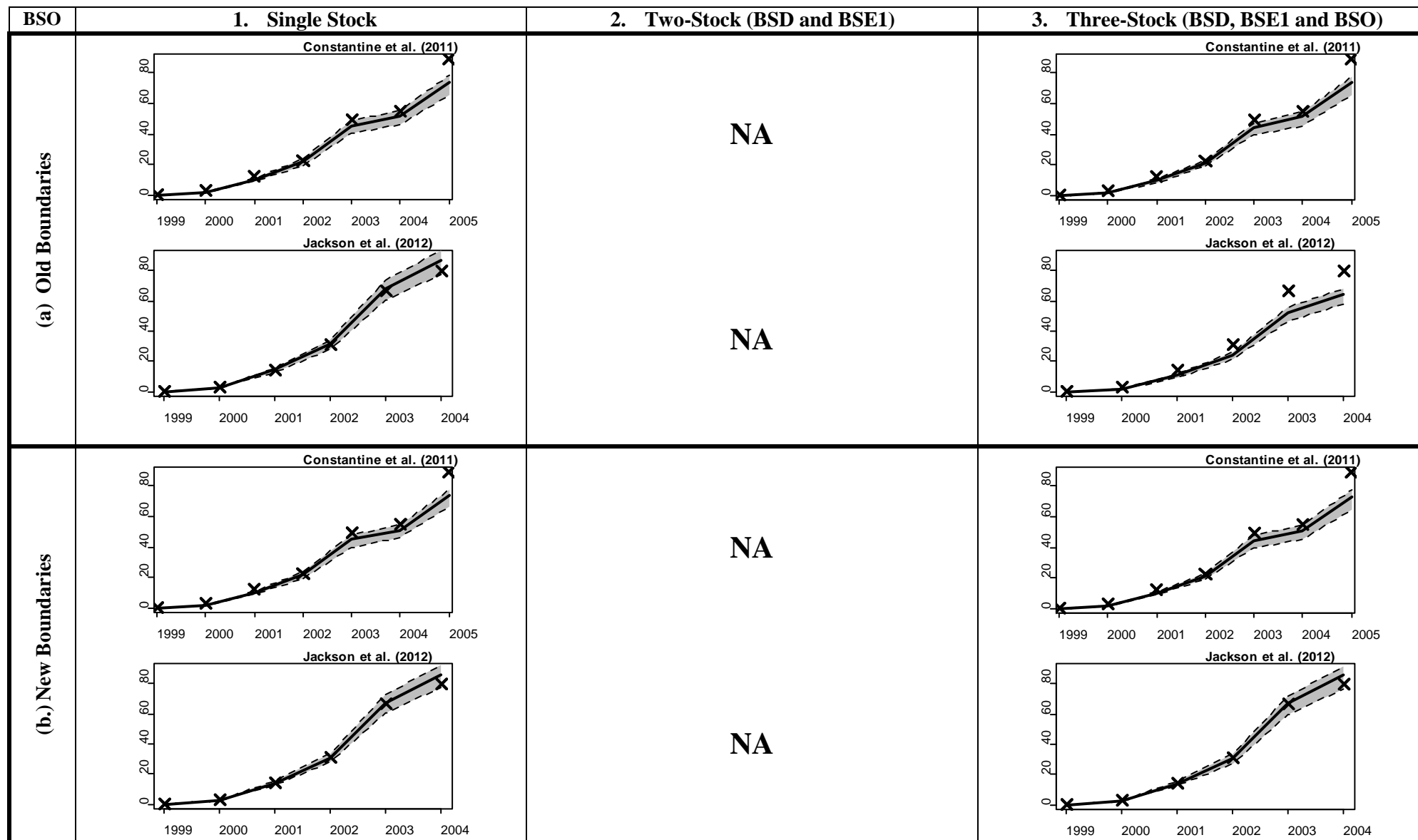


Figure 6: Plots showing model fit to mark-recapture data. Note that only the Constantine *et al.* (2011) data has been included in the likelihood. The fit to the Jackson *et al.* (2012) data (sexes combined) has been shown as a consistency check. The observed cumulative re-sightings are marked by X's. The median estimates are shown by the thick line and their 90% probability envelope is indicated by the shaded region.

APPENDIX A: CATCH, ABDUNANCE AND TREND DATA

Table A. 1: Historic catches taken north of 40°S from Allison's database (C.Allison, *pers. comm*). Note that for the assessments in this paper, the Cook Strait catches have been split equally between the East Australia and Oceania stocks.

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	Total	28406	7801	2601	4060

Table A. 2: Historic catches taken south of 40°S from Allison's database (C.Allison, *pers. comm*), given in 10 degree longitude bands.

Year	60-69E	70-79E	80-89E	90-99E	100-109E	110-119E	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
1908	217	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1909	118	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1910	83	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1911	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1912	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1913	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1914	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1915	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1916	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1917	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1918	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1919	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1920	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1921	0	0	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	0	0	0
1923	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1924	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1926	0	0	0	0	0	0	0	0	0	0	0	82	0	0	0	0	0	0	0	0
1927	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0	0
1928	11	0	0	0	0	0	0	0	0	0	0	17	0	0	0	0	0	0	0	0
1929	11	0	0	0	0	0	0	0	0	0	0	775	0	0	0	0	0	0	0	0
1930	3	1	16	4	3	0	1	0	32	49	3	55	96	0	0	0	0	0	0	0
1931	0	109	51	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1932	2	1	38	41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1933	20	81	457	43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1934	9	83	964	266	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1935	0	1	744	196	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0
1936	0	15	597	755	68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1937	1	56	337	125	188	129	32	0	0	0	0	0	0	0	0	0	0	0	0	0
1938	0	0	0	173	482	180	24	24	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	0	0
1940	0	0	0	0	0	0	342	342	342	342	342	342	342	0	0	0	0	0	0	0

Year	60-69E	70-79E	80-89E	90-99E	100-109E	110-119E	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
1941	0	0	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	0	0
1943	0	0	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	0	0
1945	0	0	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	0	0
1947	0	1	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	0	0
1949	0	0	516	48	101	10	109	30	760	118	0	0	0	0	0	0	0	0	0	0
1950	0	5	351	599	160	0	0	0	0	0	85	86	316	0	0	1	0	0	0	0
1951	0	104	268	0	358	170	232	0	1	0	66	103	189	37	0	0	1	0	0	0
1952	1	2	0	190	0	0	0	0	0	0	166	216	135	13	0	0	0	0	0	0
1953	0	0	0	259	0	0	0	0	0	0	0	14	136	0	0	0	0	0	0	0
1954	0	0	0	20	6	0	0	2	0	749	5	17	167	269	69	2	0	0	0	0
1955	0	111	274	162	110	508	411	769	416	777	0	0	0	278	56	0	0	0	0	0
1956	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	3	27	39	
1957	3	67.3	510.2	977.8	339.5	12	0	30	19	38	133	0	0	0	35	27	29	76	31	0
1958	9.8	287.5	1214	652	240	1275.9	882.1	104.7	157.1	185.7	525.8	209.4	0	0	0	0	0	0	0	0
1959	5.2	6.4	16.9	91.1	97.7	41	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
1960	2	49.6	54.2	77.6	295.5	171.3	71	163.7	742.3	1184.3	3703.8	2630.2	740	962.5	565.3	508.3	428.6	292.9	0	0
1961	0	2	33	145	63	120	14	14	61	436	581	342	123	226	1010	401	452	189	54	44
1962	21	99	151	906	417	118.2	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
1963	46	33.2	105.4	116	34.8	23.5	0.2	1.2	23.6	20.9	225	13	0	0	0	0	0	0	0	0
1964	5	11	5.6	31.2	19	17	0.9	2.8	11.3	26.2	45	0	0	0	0	0	0	0	0	0
1965	0	6.5	10.6	51.5	14.3	8.8	8.8	12.6	43.6	26.6	80	97.1	85.3	474.6	1.3	1	0	0	0	0
1966	2	4	24	41	25	26	7	4	3	1	11	14	16	93	118	26	0	0	0	0
1967	5	6	19	26	21	5	7	0	1	11	12	2	1	6	47	57	0	0	0	0
1968	0	0	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	0	0
1970	0	0	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	0	0	0	0	0	0	3	0
1972	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Total	575	1143	6757	5997	3064.8	2815.7	2245	2561.7	6709.4	7677.4	8431.3	6023.6	2322.1	2973.4	2062.47	1195.2	1055.27	652.167	207.2	114.4

Breeding Ground Data

Breeding Stock D

Absolute abundance estimate

An estimate of absolute abundance of 28,830 individuals (95% CI⁸ = 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
1982	10.2
1986	16.2
1988	12.7
1991	23.6
1994	36.0

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 CVs are available.

Year	CPUE
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

Minimum number of haplotypes

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

⁸ 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 4).

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% CI⁹ 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. 6: 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
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

⁹ Similar to BSD, 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 (see footnote 4).

Table A. 7: 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 CVs are available.

Year	Estimate
1953	0.97
1954	0.76
1955	0.78
1956	0.7
1957	0.71
1958	0.75
1959	0.74
1960	0.52
1961	0.23
1962	0.69

Mark-recapture data

Table A. 8: BSE1 microsatellite genotypic mark-recapture data for males and females combined (Jackson *et al.*, 2012).

Sexes combined	1999	2000	2001	2002	2003	2004
Total individual captures	4	72	187	222	154	126
1999	X	0	0	0	0	0
2000		X	8	6	1	0
2001			X	12	8	5
2002				X	8	5
2003					X	5
2004						X

Table A. 9: BSE1 microsatellite genotypic mark-recapture data for males only (Jackson *et al.*, 2012).

Males	1999	2000	2001	2002	2003	2004
Total individual captures	2	38	96	128	84	80
1999	X	0	0	0	0	0
2000		X	3	3	1	0
2001			X	6	4	3
2002				X	3	4
2003					X	4
2004						X

Table A. 10: BSE1 microsatellite genotypic mark-recapture data for females only (Jackson *et al.*, 2012).

Females	1999	2000	2001	2002	2003	2004
Total individual captures	2	34	91	94	70	46
1999	X	0	0	0	0	0
2000		X	5	3	0	0
2001			X	6	4	2
2002				X	5	1
2003					X	1
2004						X

Table A. 11: BSE1 photo-ID mark-recapture data from Forestell *et al.* (2011), provided by E. Martinez (*pers. comm*)

	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07
n	30	179	156	105	129	120	212	173	89	126	160	236	189	219	0	173	0	232	451	587	649
87	X	9	2	3	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1
88		X	40	10	9	8	8	6	3	2	3	4	1	4	0	1	0	1	1	3	2
89			X	18	16	9	11	8	6	1	2	4	4	1	0	4	0	0	1	0	1
90				X	10	10	10	4	2	0	1	2	3	2	0	0	0	0	1	1	2
91					X	11	18	11	2	7	2	5	2	1	0	0	0	1	2	1	1
92						X	20	15	1	4	2	7	1	4	0	2	0	0	1	2	0
93							X	38	13	9	6	6	8	1	0	4	0	1	7	4	2
94								X	16	20	8	9	8	3	0	4	0	1	6	3	0
95									X	7	2	6	1	4	0	1	0	3	6	1	1
96										X	17	11	5	6	0	2	0	1	5	4	0
97											X	25	5	7	0	8	0	1	2	5	0
98												X	21	13	0	10	0	2	8	7	5
99													X	18	0	4	0	2	8	5	9
00														X	0	11	0	5	15	11	3
01															X	0	0	0	0	0	0
02																X	0	9	17	12	9
03																	X	0	0	0	0
04																		X	17	16	11
05																			X	45	22
06																				X	57
07																					X

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							-

Table A. 13: Oceania microsatellite genotypic mark-recapture data for males and females combined (Jackson *et al.*, 2012).

Sexes combined	1999	2000	2001	2002	2003	2004
Total individual captures	52	114	183	130	216	79
1999	X	3	5	3	2	1
2000		X	6	5	9	2
2001			X	9	18	6
2002				X	7	2
2003					X	2
2004						X

Table A. 14: Oceania microsatellite genotypic mark-recapture data for males only (Jackson *et al.*, 2012).

Males	1999	2000	2001	2002	2003	2004
Total individual captures	27	72	120	84	131	41
1999	X	3	2	0	1	0
2000		X	5	3	6	1
2001			X	7	10	3
2002				X	4	0
2003					X	1
2004						X

Table A. 15: Oceania microsatellite genotypic mark-recapture data for females only (Jackson *et al.*, 2012).

Females	1999	2000	2001	2002	2003	2004
Total individual captures	25	42	63	46	85	38
1999	X	0	3	3	1	1
2000		X	1	2	3	1
2001			X	2	8	3
2002				X	3	2
2003					X	1
2004						X

Minimum number of haplotypes

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

Feeding Ground Data

Breeding Stock D

Table A. 16: 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°E-110°E and margin area corresponds to 60°E-130°E (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. 17: 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
1989	5325	0.302
1991	5408	0.188
1993	2747	0.153
1995	8066	0.142
1997	10657	0.166
1999	16751	0.143
2001	31134	0.123
2003	27783	0.115

Breeding Stock E1

Table A. 18: 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	0.50	622	0.50
1992	2,012	0.43	3,484	0.33
2001	13,300	0.22	13,300	0.20

Table A. 19: 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
1989	5325	0.302
1991	5408	0.188
1993	2747	0.153
1995	8066	0.142
1997	10657	0.166
1999	16751	0.143
2001	31134	0.123
2003	27783	0.115

Oceania breeding stock**Table A. 20:** 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	0.50	622	0.50
1992	2,012	0.43	3,484	0.33
2001	13,300	0.22	13,300	0.20

Data informing interchange**D and EI****Table A. 21:** Inter-regional recaptures between West and East Australia (Anderson and Brasseur, 2007). The first row gives the total number of East Australia animals that were sighted in 2002 and 2003, while the second row gives the total number of West Australia animals that were sighted in 2002 and 2003. Entries above the diagonal of X's would reflect animals that were first seen in West Australia and then later re-seen in East Australia. Entries below the diagonal would reflect animals first seen in East Australia and later resighted in West Australia

	EA 2002	EA 2003
Total East Australia	216	131
Total West Australia	89	144
WA 2002	X	0
WA 2003	0	X

EI and Oceania**Table A. 22:** Inter-regional recaptures between East Australia and Oceania, from microsatellite genotypic mark-recapture data for males and females combined (Jackson *et al.*, 2012). Note that entries above the diagonal of the matrix reflect animals that were first seen in Oceania, and later re-sighted in EA, while entries below the diagonal reflect animals that were first seen in EA and later re-sighted in Oceania.

Sexes combined	1999	2000	2001	2002	2003	2004
Total East Australia	4	72	187	222	154	126
Total Oceania	52	114	183	130	216	79
1999	X	1	0	1	0	0
2000	0	X	0	0	0	0
2001	0	0	X	2	0	2
2002	0	0	0	X	0	0
2003	0	1	0	1	X	0
2004	0	0	0	0	0	X

Table A. 23: Inter-regional recaptures between East Australia and Oceania, from microsatellite genotypic mark-recapture data for males and females combined (Jackson *et al.*, 2012).

Males	1999	2000	2001	2002	2003	2004
Total East Australia	2	38	96	128	84	80
Total Oceania	27	72	120	84	131	41
1999	X	1	0	1	0	0
2000	0	X	0	0	0	0
2001	0	0	X	1	0	2
2002	0	0	0	X	0	0
2003	0	1	0	1	X	0
2004	0	0	0	0	0	X

Table A. 24: Inter-regional recaptures between East Australia and Oceania, from microsatellite genotypic mark-recapture data for males and females combined (Jackson *et al.*, 2012).

Females	1999	2000	2001	2002	2003	2004
Total East Australia	4	72	187	222	154	126
Total Oceania	52	114	183	130	216	79
1999	X	1	0	1	0	0
2000	0	X	0	0	0	0
2001	0	0	X	2	0	2
2002	0	0	0	X	0	0
2003	0	1	0	1	X	0
2004	0	0	0	0	0	X

APPENDIX B – MODEL DIAGRAMS AND CATCH ALLOCATIONS

This Appendix contains the model diagrams for the single-stock, two-stock and three-stock models for both the old and the new boundaries.

Single-stock models

Catches are allocated according to the boundaries given in Figure B. 1. Note that the traditional approach using core and marginal regions (where 100% of the core catches are allocated to the respective stocks, and catches from the marginal regions are shared equally between neighbouring stocks) has not been used here.

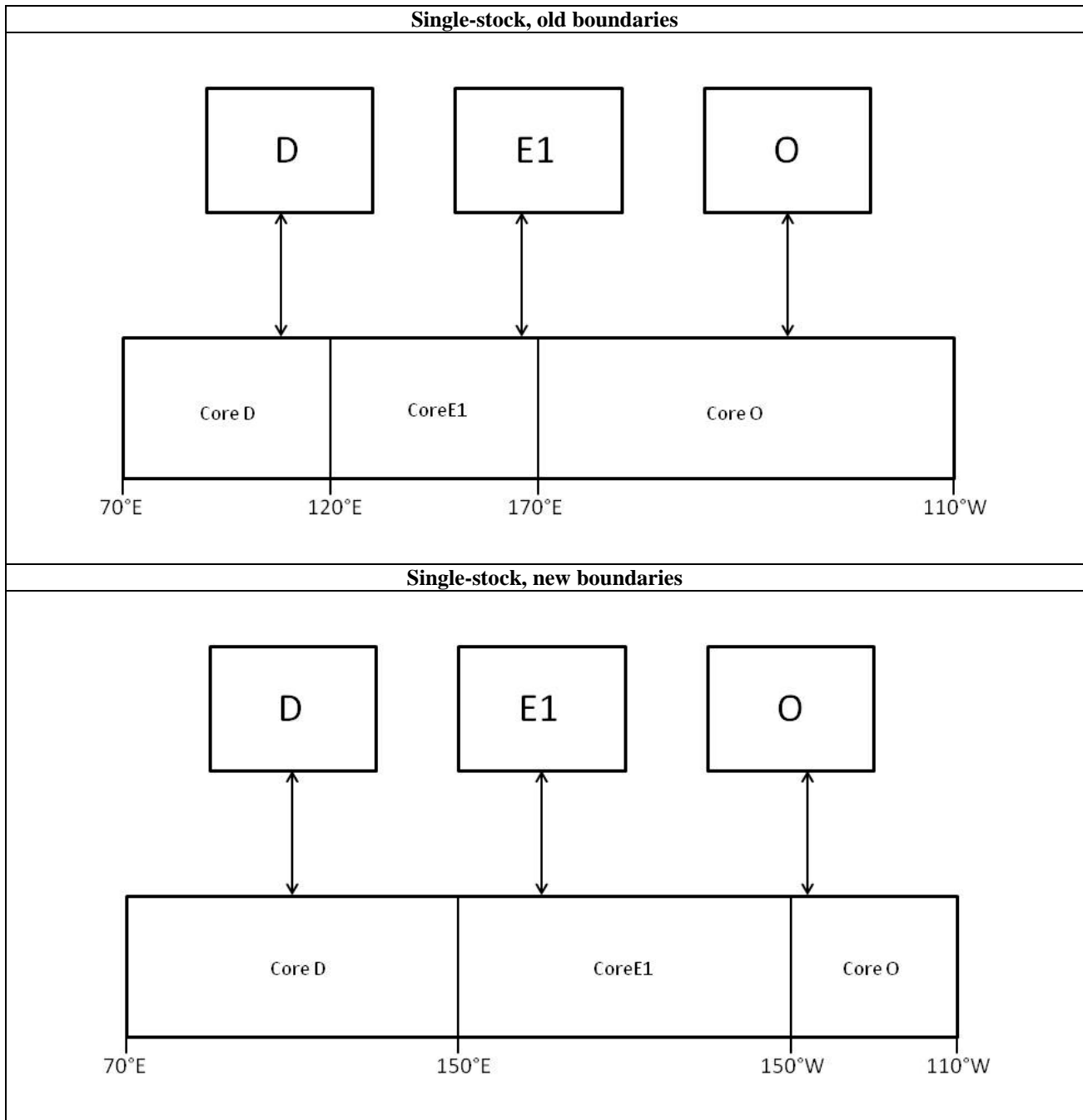


Figure B. 1: Diagrammatic representations of the single-stock boundaries used for allocating the Antarctic catches, both for the original boundaries, and the new boundaries.

Two-stock model (D and E1)

The two-stock model assumes that each year a proportion of D animals feed in the core E1 feeding area and conversely a proportion of E1 animals feed in the core D feeding area. Diagrammatic representations of the two-stock models for the old and new Antarctic boundaries are given in Figure B. 2.

Since a mixture of D and E1 animals are assumed to occur on the Antarctic feeding grounds, the catches taken there need to be allocated in proportion to number of each stock present. In order to do this, the total numbers of animals found on each of the two feeding grounds need to be calculated:

$$N_y^{Core D} = (1 - \beta_{DE})N_y^D + \beta_{ED}N_y^{E1} \quad (B.1)$$

$$N_y^{Core E1} = \beta_{DE}N_y^D + (1 - \beta_{ED})N_y^{E1} \quad (B.2)$$

where

$N_y^{Core D}$ is the total number of whales in the core D Antarctic feeding area in year y (see Figure B. 2),

$N_y^{Core E1}$ is the total number of whales in the core E1 Antarctic feeding area in year y (see Figure B. 2),

β_{DE} is the proportion of BSD whales that feed in the core E1 Antarctic feeding area each year, and

β_{ED} is the proportion of BSE1 whales that feed in the core D Antarctic feeding area each year.

The total feeding ground catches allocated to the two stocks are then given by:

$$C_y^{F,D} = \frac{(1 - \beta_{DE})N_y^D}{N_y^{Core D}} C_y^{Core D} + \frac{\beta_{DE}N_y^D}{N_y^{Core E1}} C_y^{Core E1} \quad (B.3)$$

$$C_y^{F,E1} = \frac{\beta_{ED}N_y^{E1}}{N_y^{Core D}} C_y^{Core D} + \frac{(1 - \beta_{ED})N_y^{E1}}{N_y^{Core E1}} C_y^{Core E1} \quad (B.4)$$

where

$C_y^{F,D}$ is the total Antarctic catch allocated to BSD,

$C_y^{F,E1}$ is the total Antarctic catch allocated to BSE1,

$C_y^{Core D}$ is the total Antarctic catch taken in the core D feeding region, and

$C_y^{Core E1}$ is the total Antarctic catch taken in the core E1 feeding region.

$C_y^{Core D}$, $C_y^{E1,W}$, $C_y^{E1,E}$, $C_y^{Core O}$ are calculated according to the boundaries given in see Figure B. 2.

Priors for the mixing proportion parameters

β_{DE} and β_{ED} are drawn from uniform priors on the interval [0,1]. A constraint needs to be placed on the values of β_{DE} and β_{ED} , as the uniform priors do not prevent a situation where nearly all of the BSD stock feeds in the E1 feeding area, and nearly all of the BSE1 stock feeds in the D feeding area, which is biologically implausible. The approach of Johnston and Butterworth (2005) was taken whereby the constraint is added that the proportion of BSE1 whales going to the E1 feeding area must be greater than the proportion of BSD whales, and *vice versa*. Mathematically this amounts to the constraint that $\beta_{DE} + \beta_{ED} < 1$. The resulting prior distributions are shown in Figure B. 4.

Three-stock model

Similar to the two-stock model, the three-stock model allows for a proportion of animals from one stock to feed in a neighbouring feeding ground. In order to prevent a situation where all three stocks mix on a single feeding ground, four feeding areas are used in the model: a core D feeding area, an E1 west (E1,W) feeding area, an E1 east (E1,E) feeding area, and a core O feeding area. BSD and BSE1 mix on the core D and E1,W feeding areas, while BSE1 and

BSO mix on the E1,E and core O feeding areas. It is assumed that no D animals go further east than the E1,W feeding ground, and similarly no BSO animals go further west than the E1,E feeding ground. The diagrammatic representations of the three-stock model for the new and the old boundaries are given in Figure B. 2. The total numbers of whales in each of the four feeding areas are given by:

$$N_y^{CoreD} = (1 - \beta_{DE})N_y^D + \beta_{ED}N_y^{E1} \quad (B.5)$$

$$N_y^{E1,W} = \beta_{DE}N_y^D + \gamma N_y^{E1} \quad (B.6)$$

$$N_y^{E1,E} = \gamma^* N_y^{E1} + \beta_{OE}N_y^O \quad (B.7)$$

$$N_y^{CoreO} = (1 - \beta_{OE})N_y^O + \beta_{EO}N_y^{E1} \quad (B.8)$$

where

N_y^{CoreD} is the total number of whales in the core D Antarctic feeding area in year y (see Figure B. 2),

$N_y^{E1,W}$ is the total number of whales in the E1 western Antarctic feeding area in year y (see Figure B. 2),

$N_y^{E1,E}$ is the total number of whales in the E1 eastern Antarctic feeding area in year y (see Figure B. 2),

N_y^{CoreO} is the total number of whales in the core Oceania Antarctic feeding area in year y (Figure B. 2),

β_{DE} is the proportion of BSD whales that feed in the E1,W feeding area each year,

β_{ED} is the proportion of BSE1 whales that feed in the core D feeding area each year,

β_{EO} is the proportion of BSE1 whales that feed in the core O feeding area each year,

β_{OE} is the proportion of BSO whales that feed in the E1,E feeding area each year,

γ is the proportion of BSE1 whales that feed in the E1,W feeding area each year, and

γ^* is the proportion of BSE1 whales that feed in the E1,E feeding area each year

(note that $\beta_{ED} + \beta_{EO} + \gamma + \gamma^* = 1$).

The feeding-ground catch allocations to the three stocks are given as follows:

$$C_y^{F,D} = \frac{(1 - \beta_{DE})N_y^D}{N_y^{CoreD}} C_y^{CoreD} + \frac{\beta_{DE}N_y^D}{N_y^{E1,W}} C_y^{E1,W} \quad (B.9)$$

$$C_y^{F,E1} = \frac{\beta_{ED}N_y^{E1}}{N_y^{CoreD}} C_y^{CoreD} + \frac{\gamma N_y^{E1}}{N_y^{E1,W}} C_y^{E1,W} + \frac{\gamma^* N_y^{E1}}{N_y^{E1,E}} C_y^{E1,E} + \frac{\beta_{EO}N_y^{E1}}{N_y^{CoreO}} C_y^{CoreO} \quad (B.10)$$

$$C_y^{F,O} = \frac{\beta_{OE}N_y^O}{N_y^{E1,E}} C_y^{E1,E} + \frac{(1 - \beta_{OE})N_y^O}{N_y^{CoreO}} C_y^{CoreO} \quad (B.11)$$

where

$C_y^{F,D}$ is the total Antarctic catch allocated to BSD,

$C_y^{F,E1}$ is the total Antarctic catch allocated to BSE1,

$C_y^{F,O}$ is the total Antarctic catch allocated to BSO,

C_y^{CoreD} is the total Antarctic catch taken in the core D feeding region,

$C_y^{E1,W}$ is the total Antarctic catch taken in the E1,W feeding region,

$C_y^{E1,E}$ is the total Antarctic catch taken in the E1,E feeding region, and

C_y^{CoreO} is the total Antarctic catch taken in the core O feeding region.

C_y^{CoreD} , $C_y^{E1,W}$, $C_y^{E1,E}$, C_y^{CoreO} are calculated according to the boundaries given in Figure B. 2.

Priors for the interchange parameters

As for the two-stock model, β_{DE} and β_{DE} are drawn from uniform priors on the interval [0,1] with the added constraint that $\beta_{DE} + \beta_{DE} < 1$. Following similar logic, β_{EO} and β_{OE} are drawn from uniform priors on the interval [0,1] with the added constraint that $\beta_{EO} + \beta_{OE} < 1$. In order to ensure that the BSE1 proportions sum to 1, (i.e. $\beta_{DE} + \beta_{EO} + \gamma + \gamma^* = 1$), an approach was taken whereby β_{DE} , β_{DE} , β_{EO} and β_{OE} were drawn according to the above-mentioned constraints, and γ and γ^* were drawn from a uniform prior on the interval [0,1]. Any samples where $|1 - \beta_{DE} + \beta_{EO} + \gamma + \gamma^*| > 0.01$ were discarded. The remaining samples were rescaled so that $\beta_{DE} + \beta_{EO} + \gamma + \gamma^* = 1$. The resulting prior distributions are shown in Figure B. 5.

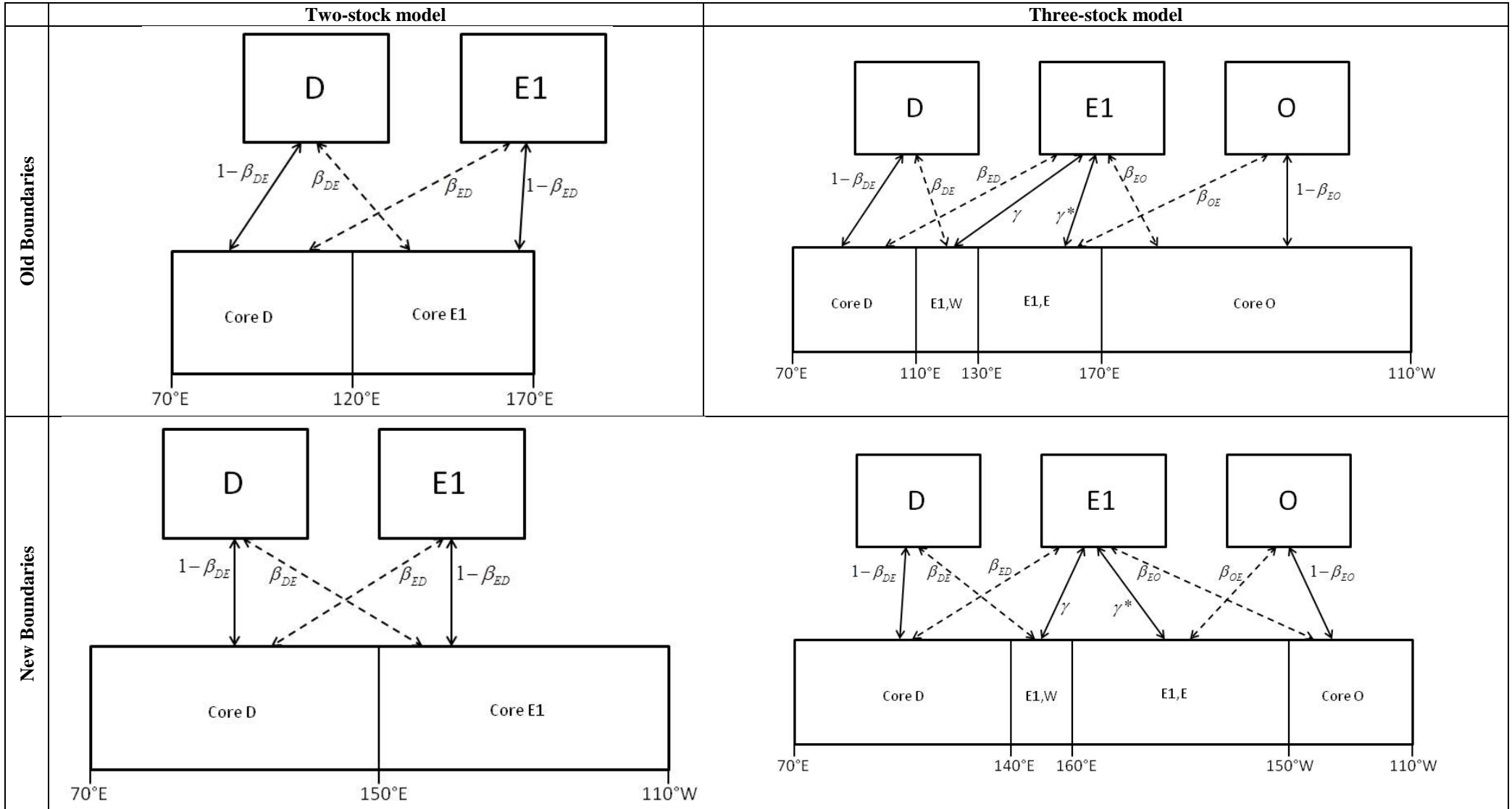


Figure B. 2: Diagrammatic representation of the two-stock and three-stock models, for both the old Antarctic boundaries and the new Antarctic boundaries.

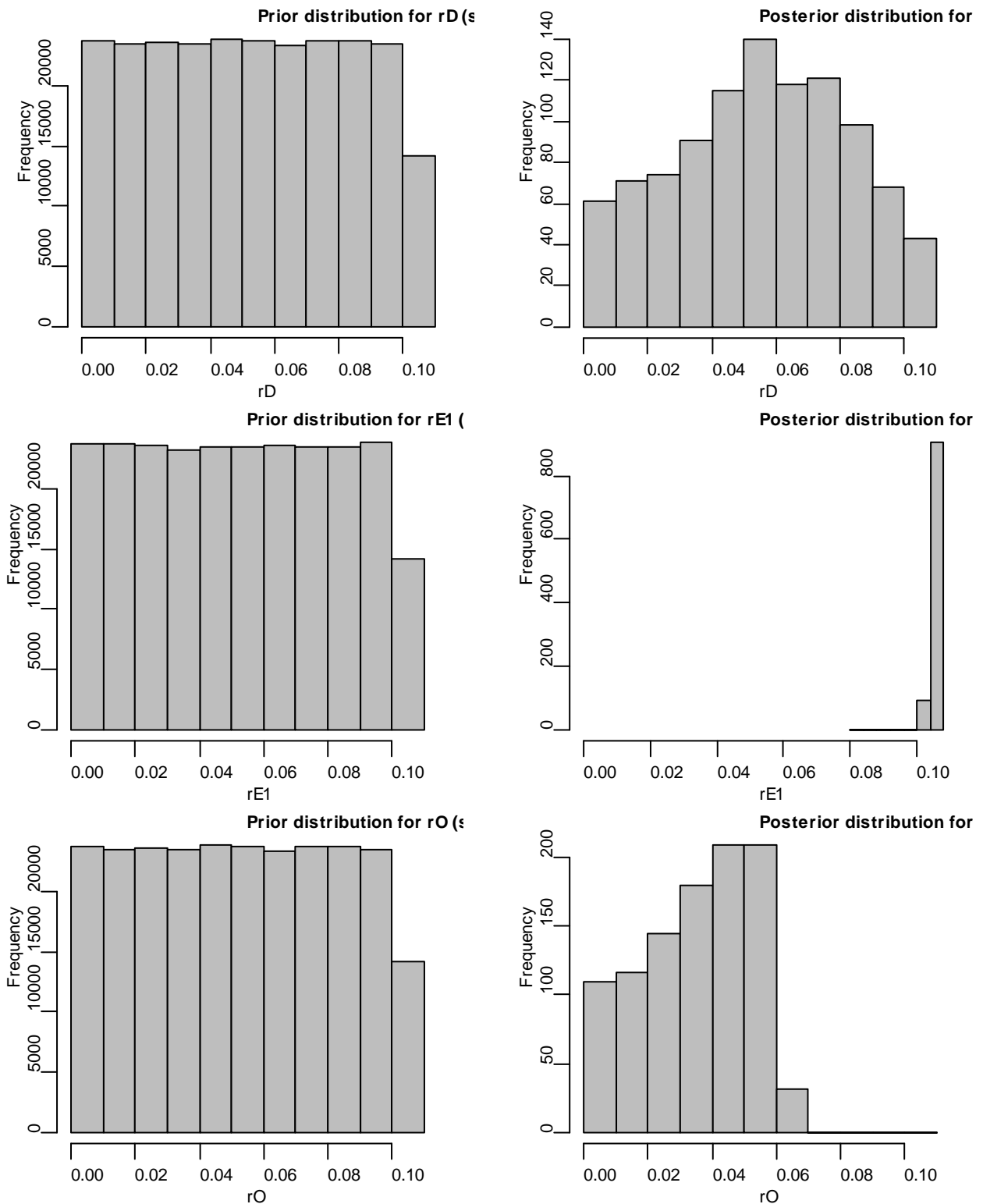


Figure B. 3: Plots of the prior and posterior distributions for the growth rates estimated in the BSD, BSE1 and BSO single stock models. Posterior distributions have been shown here only for the analyses using the new boundaries.

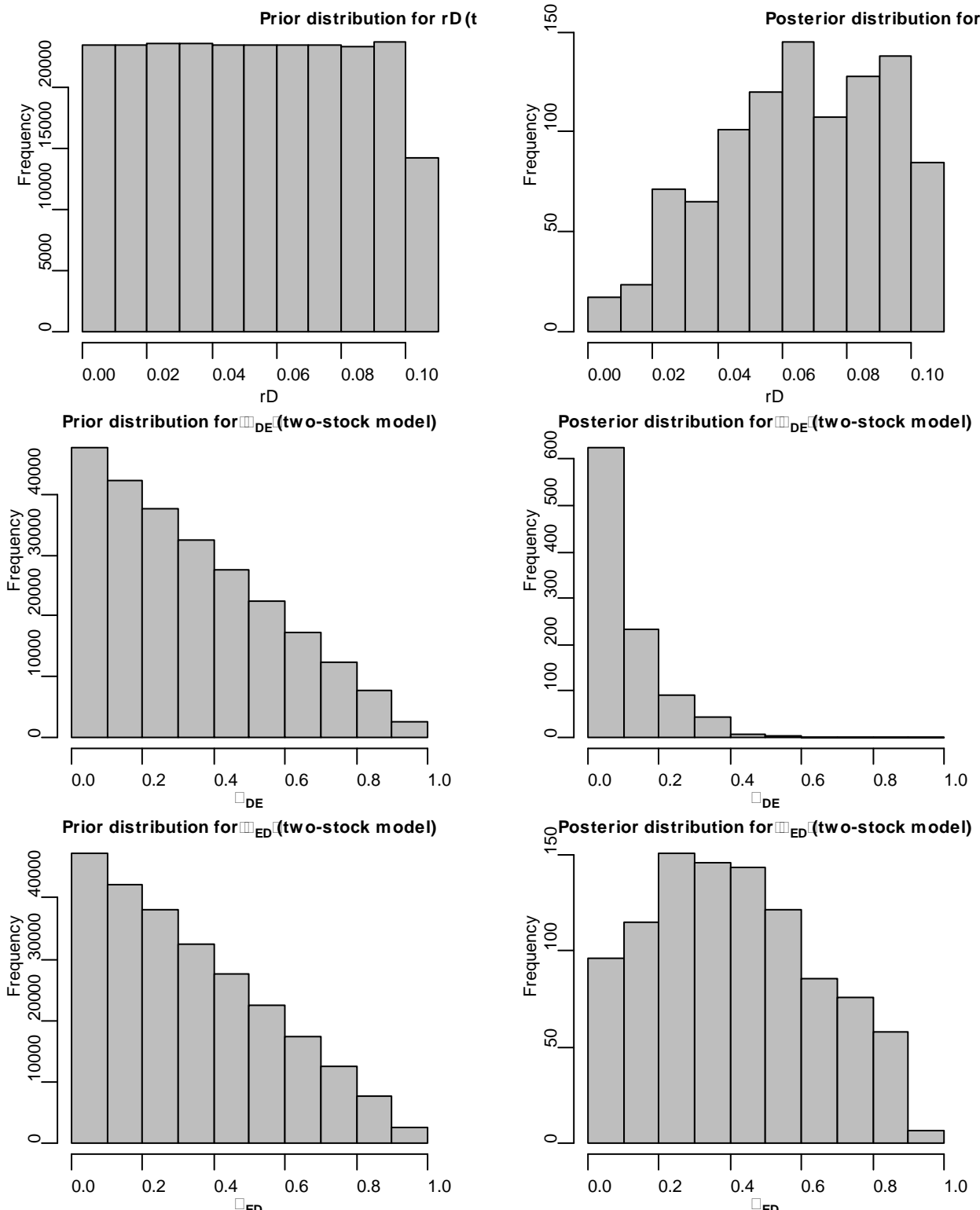


Figure B. 4: Plots of the prior and posterior distributions for the BSD growth rate estimated in the BSD+BSE1 two-stock model, as well as the mixing proportion parameters. Results are shown here only for analyses using the new boundaries. The prior and posterior distributions for r^{E1} have not been included here, as they are virtually identical to those shown in Figure B. 3.

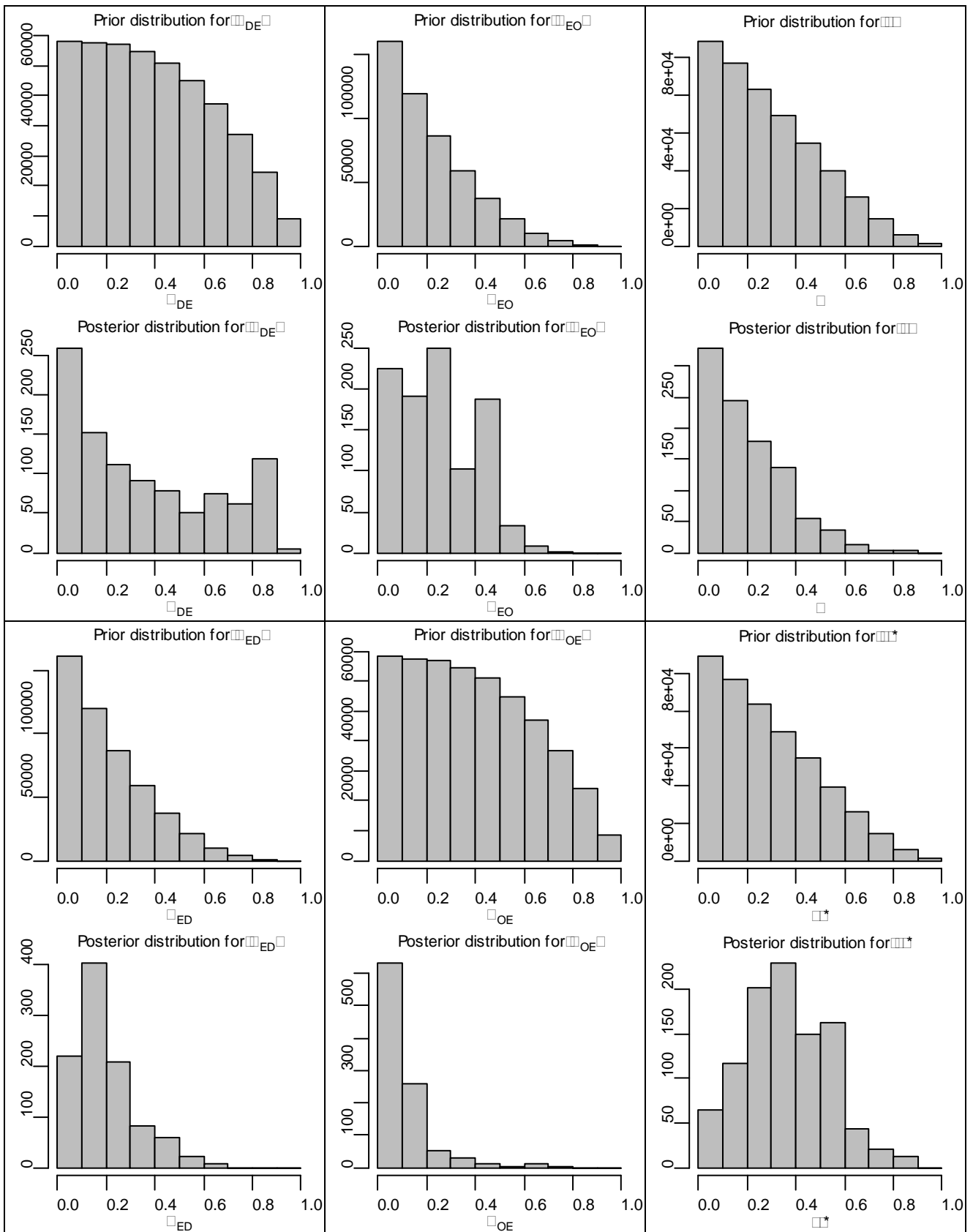


Figure B. 5: Plots of the prior and posterior distributions for the mixing proportion parameters of the three-stock model. Results are shown here only for analyses using the new boundaries.