



Quantitative modelling of Antipodean wandering albatross

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C.T.T. Edwards,
J.O. Roberts,
K. Walker
G. Elliott

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EXECUTIVE SUMMARY

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Management of New Zealand's marine bird species is guided by a risk assessment framework that can prioritise research on those species considered to be most at risk. This framework has identified the Antipodean wandering albatross (*D. antipodensis antipodensis*) as High Risk, motivating further work to understand the drivers behind its population dynamics. The current project is aimed at fulfilling this requirement, detailing the development of a quantitative demographic model with which to estimate vital rates and predict population changes into the future. The model is parameterised using extensive mark-recapture and census data, which allowed the estimation of time-variant survivorship and breeding parameters.

Although the survivorship has changed over time, it is apparent from both the modelling and an empirical review of the data that changes in the breeding rate, success and age of first breeding are primarily responsible for temporal changes in the population abundance. The model predicts that the population has declined in numbers since 2007 and will continue to do so unless these demographic vital rates recover. Furthermore it predicts that reduced adult survivorship as a result of fishing induced mortalities within New Zealand waters is likely to be having a negligible impact, although the impact of unquantified mortalities arising from potential species misidentification or captures outside of New Zealand waters could not be evaluated due to a lack of data.

Project code: PRO2012-10

1. Introduction

Two wandering albatross taxa are endemic to the New Zealand region and were originally regarded as populations of a single circum-polar wandering albatross species *Diomedea exulans*. In 2004, however, these two populations were classified as subspecies of a new species *Diomedea antipodensis*. The birds nesting on Antipodes Island (with smaller numbers - two to five pairs - on the Campbell and Chatham Islands) are now classified as *D. antipodensis antipodensis* (Antipodean wandering albatross) and those nesting on the Auckland Islands as *D. antipodensis gibsoni* (Gibson's wandering albatross).

Antipodean wandering albatross forage largely in the Pacific Ocean east of New Zealand, and to a lesser extent in the Tasman Sea (Walker & Elliott, 2006). They are a rare, but regular bycatch in a wide variety of New Zealand surface longline, trawl, and bottom longline fisheries. Numbers actually caught are likely to be considerably higher than those reported, as many long-line hooks set in New Zealand waters are from small unobserved domestic vessels, and there are substantial unobserved long-line fleets in international waters in the south Pacific Ocean where the birds forage (Walker & Elliott, 2006).

Due to the vulnerability of this long-lived and slow breeding species to fisheries bycatch, their survival, productivity, recruitment and population trends have been monitored during almost annual visits to the Antipodes Island since 1994. No monitoring occurred during the 2006 season, and the scale of the monitoring was reduced from 2007 to 2011, but restored in 2012. In the 1990s the population increased following a major decline during the 1980s, most likely due to fishing induced mortality (Elliott & Walker, 2005, Walker & Elliott, 2005). However, around 2006 there was a drop in the size of the breeding population, and it has continued to decline since then (Elliott & Walker, 2014).

1.1. Previous work

Both of the New Zealand species of wandering albatross have been subjected to a risk assessment based on a comparison of estimated annual potential fatalities with an analogue of the Potential Biological Removal (PBR), which is an estimate of the number of individuals that can be caught as bycatch without jeopardizing maintenance of the population above 50% of carrying capacity with high certainty (Richard & Abraham, 2013a,b, Richard et al., 2011). Both were ranked as being at High Risk, although it was found to be unlikely that commercial fishing-induced mortality within New Zealand's EEZ exceeded the analogue of PBR (used as a limit reference point) for either species (table 9 in Richard & Abraham, 2013b). Gibson's albatross was identified as the more at risk (i.e., subject to the higher rate of fishing related mortality) of the two and has been subjected to an independent analysis (Francis et al., 2015).

The seabird risk assessment approach adopted for New Zealand's 2013 NPOA Seabirds (Richard & Abraham, 2013a,b, see also www.mpi.govt.nz/document-vault/3962) represents a Level 2, semi-quantitative risk assessment (*sensu* Hobday et al., 2011). It is dependent on three main sources of information, namely an estimate of the total fatalities across all fishing fleets operating within New Zealand waters, productivity of the population and the current population size. Productivity is itself primarily dependent on the adult survival, age at first reproduction and the proportion of adults that breed. The greatest uncertainty in the initial risk assessment for these populations came from information on average adult survival, with the most recent estimates at the time being from Walker

& Elliott (1999), and from unknown levels of bycatch in global fisheries. As well as providing the demographic parameters required for prediction of population dynamics, this current work aims to provide a more robust estimate of adult survival for the risk assessment.

1.2. Report outline and objectives

Given that extensive mark-recapture information from a long time period is now available for Antipodean wandering albatross (Elliott & Walker, 2014), comprehensive modelling of the population is used in this study as a first step towards a fully quantitative Level 3 risk assessment. Most importantly the modelling yields updated estimates of adult survival and predicts the immediate population trajectory. The modelling further provides a platform with which to evaluate the efficacy of management strategies designed to mitigate fisheries bycatch (or other stressors) and allow the population to recover.

A Level 3 risk assessment has been conducted for Gibson's wandering albatross (Francis et al., 2015) and concluded with high certainty that the population has been declining, due to a combination of low adult survival and low breeding success. Similar, high quality data are available for Antipodean wandering albatross. A model is developed to estimate important demographic parameters, partition mortality into fishing-related and non-fishing-related components, and provide for the testing of different approaches to managing bycatch (management strategies). This specifically requires estimates of fisheries bycatch (including cryptic and out-of-zone mortality) to assess the extent to which fishery-related mortality has contributed to historic trends of the population, and the influence of current levels on its future viability.

Specific objectives for the study are as follows:

- (a) To develop a fully quantitative population model of Antipodean albatross to assess population trend and key demographic rates for this population;
- (b) To use the model to assess the effect of fisheries mortality on population viability; and,
- (c) To use the model, as information permits, to assess the effect of alternative management strategies.

2. Data and Methods

2.1. Raw empirical data

Data have been collected from Antipodes Island during annual summer visits for almost every year since 1994 (the one exception being 2006). Three types of data have been collected, namely census counts of breeding pairs, whether or not these pairs successfully fledge a chick, and mark-recapture data.

Census data consists of counts of breeding pairs in three demarcated blocks as described by Walker & Elliott (2005): block 1 (referred to hereafter as the “study area” or SA); block 5 (which encloses the more intensively studied MCBA); and block 32. In addition to these, a whole island census was conducted in 1994, 1995 and 1996. These three years of data provided an average ratio of abundance between the whole island and the smaller study blocks, which was used to rescale census data from the study blocks and reconstruct an abundance index for the whole island (Elliott & Walker, 2014). For all modelling work shown here, we used this reconstructed whole island census time series, since

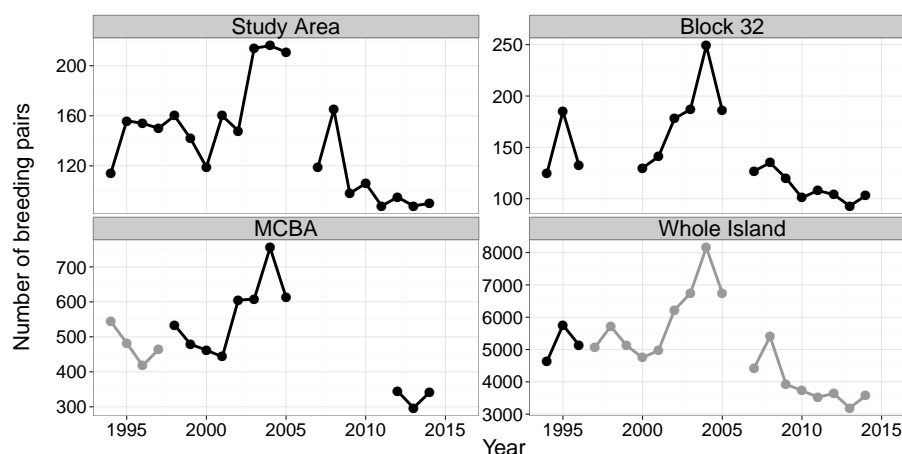


Figure 1: Census data (number of breeding pairs) from Antipodes Island. Observations are in black; reconstructed estimates are in grey. No data were collected during 2006 from any of the census blocks. Reconstructed estimates for MCBA were based on counts from the larger enclosing block 5 (Walker & Elliott, 2005). Reconstructed estimates for the whole island were based on the average ratio of counts for the study area, block 32 and MCBA to the whole island in years 1994 to 1996, which was used to scale up the population counts from these areas to the whole island in subsequent years (Elliott & Walker, 2014).

the absolute population size is important for the assessment of fishing induced mortalities. These data are shown in Figure 1.

The mark-recapture data can be split into two categories: those marked as chicks (“known age”) and those marked as breeders (“unknown age”). Most marks are made when the birds are nesting within the SA, however some breeders and their chicks are marked opportunistically when nesting nearby. Recapture data are recorded from within the SA, and again occasionally from nearby. However only if the birds are breeding is the location (SA or non-SA) relevant as birds only show strong site fidelity when nesting. Non-breeding birds are therefore not distinguished as either SA or non-SA. Birds that habitually nest in the SA are often seen outside it when not breeding. A list of the recorded categories is given in Table 1. The raw data are illustrated in Figures 2 and 3.

Chicks have been tagged fairly consistently since 1995, but only started to appear as mature individuals around 2003, since when the majority have been recorded as non-breeders. For the unknown ages, only very few were marked or resighted between 1994 and 1997, but in 1998 this number increased markedly and has remained high. A feature of both of these data sets is the absence of any data from 2006, as there was no survey conducted that year. This has the additional effect of meaning that breeders in 2005 could not be easily categorised as having failed or succeeded, since this is usually determined from examining the nest the following year and banding any chicks produced. This shortcoming is most noticeable in the unknown age data. For the known age data, there were only a few breeders in 2005 anyway. Unfortunately, no chicks were marked in 2007 as their nest from the previous year had not been mapped.

General data considerations With reference to Table 1, the category of resting birds is redundant. Resting birds may have a lower resight probability than other non-breeders that have not bred in the year before, but they can nevertheless be accounted for by the non-breeding category. The distinction between birds marked and resighted within or outside of the study area was also ignored. For non-breeders, this distinction is irrelevant anyway. For breeders, the numbers recorded outside of

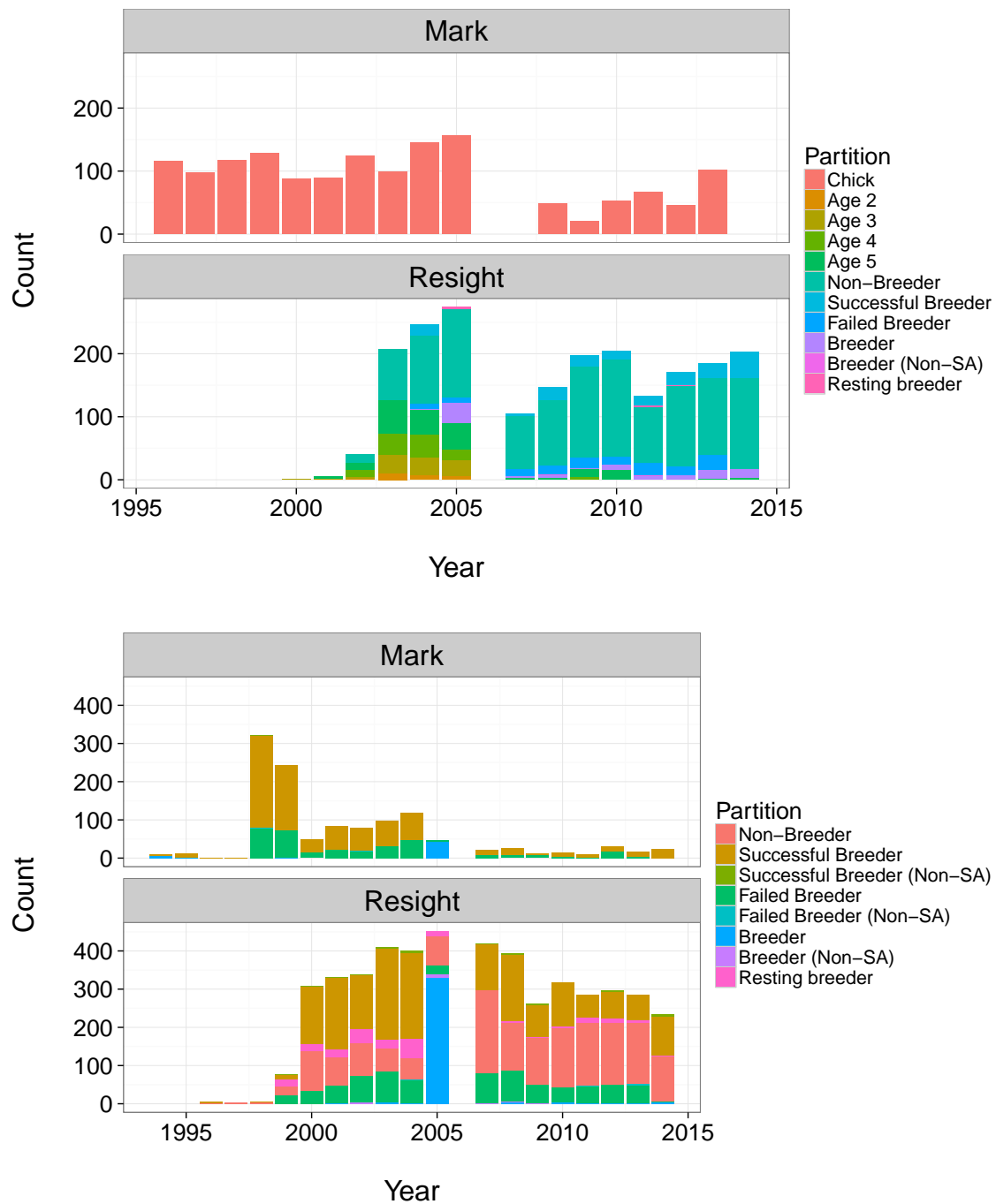


Figure 2: Raw mark-recapture observational data for known and unknown age individuals, with the known age individuals all marked as chicks (top panel). The bar graph shows the number of observations of marked and resighted individuals by year and data category. Note that the number of resights for the unknown age data are approximately double the number of resights for the mark-recapture data of known age.

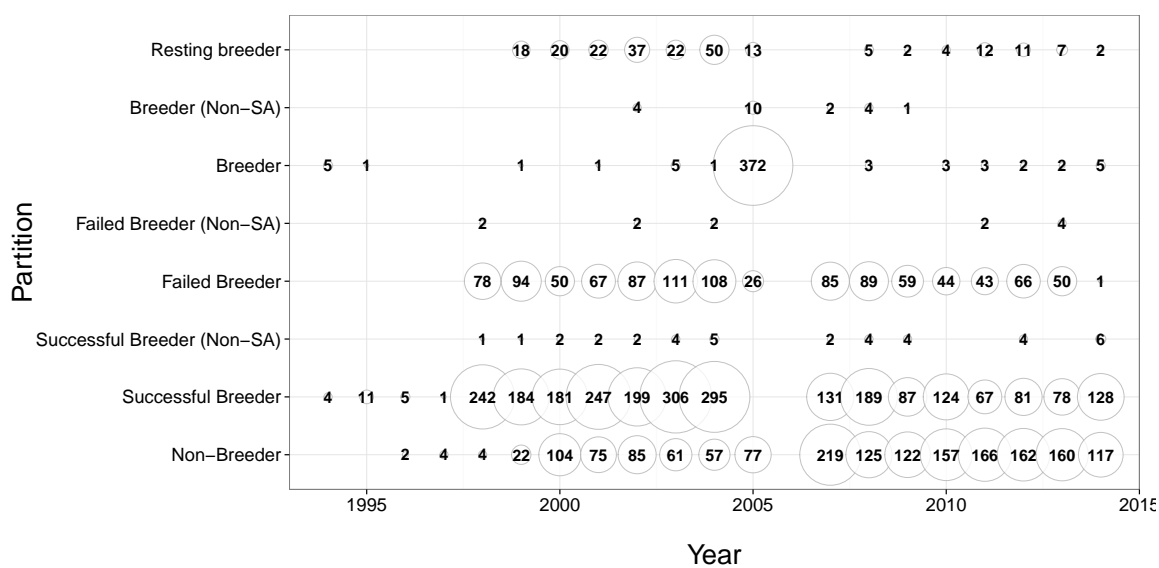
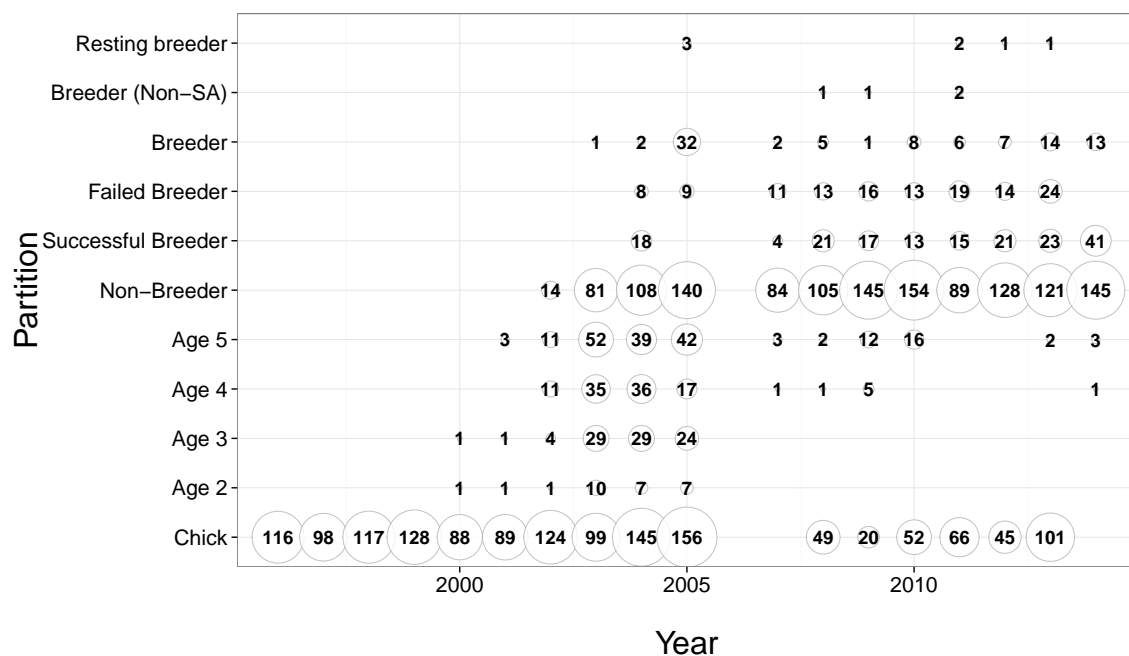


Figure 3: Alternative representation of the raw mark-recapture observational data for known and unknown age individuals, with the known age individuals all marked as chicks (top panel). The bubble plots illustrate the combined number of observations of marked and resighted individuals by year and data category.

Table 1: List of mark-recapture data categories. Breeders are distinguished according to whether or not they are nesting within the study area; this distinction is not made for ages 1 – 6, resting birds or non-breeders. Only individuals banded as chicks are of known age, and therefore the mature breeding categories contain individuals of known and unknown ages.

Category	Description
Chick (age 0)	Newly hatched chicks
Ages 1 – 5	Fledged chicks that are assumed to be immature (i.e. have not attempted breeding before)
Resting	Mature individuals that are not nesting, but were successful breeders in the previous year
Non-breeders	Mature individuals that are not nesting, and were either failed breeders in the previous year, or have not attempted to breed before
Successful breeders	Nesting individuals that successfully fledge a chick
Failed breeders	Nesting individuals that do not fledge a chick
Breeders	Nesting individuals with unknown outcome

the study area was very small (Figure 3). Making use of the non-SA to SA distinction for inferential purposes is therefore impossible. However discarding the non-SA data could bias estimation of survival, and instead the data were collated. Finally, it is possible to age the birds tagged as chicks, even though the ages were not recorded when older than five years.

2.2. Empirical data analysis

Given that these data will be used to parameterise a population dynamics model, it is useful to first analyse the empirical mark-recapture data directly so as to inform construction of the model itself. Field observations suggested that, post-2005 fewer adult pairs attempted to breed, and there were fewer young new breeders; established pairs briefly attended the breeding grounds to contact their mates but then left without laying. Through an examination of the data collected, we were able to yield quantifiable insights into these processes of maturation and breeding. Since breeding is related to whether or not birds return to the island, we also examine changes in the resight probability with age and time.

Maturation and breeding Maturation is an age dependent process characterised in this case not by physical maturity – birds reach sexual maturity when they achieve a threshold weight (Weimerskirch, 1992) – but by the age at which individuals first attempt to breed, which we assume occurs at the same time. Maturation can be identified in the known age mark-recapture data as the first age that individuals are recorded as breeders (successful or failed breeders, or part of the combined composite group; Table 1). The ages at first breeding, by year marked, are shown as frequency histograms in Figure 4a. In the histograms for 1996 – 1999 there is a gap corresponding to 2006 (when no survey was undertaken), but there nevertheless appears to be a bimodal distribution of ages with peaks around ages 8 and 12. Of the individuals tagged as chicks post-1999, there are clearly far fewer recorded as first breeding at around age 8. For chicks marked in years 2000 – 2002 (so that enough time has elapsed subsequently), there instead appears to be a higher relative frequency of individuals first breeding around age 12. This indicates that reaching a threshold weight and breeding might have been delayed in more recent cohorts. Unfortunately cohorts cannot be tracked by the SeaBird model (Francis & Sagar, 2012) used here, which instead interprets the data on an annual basis with

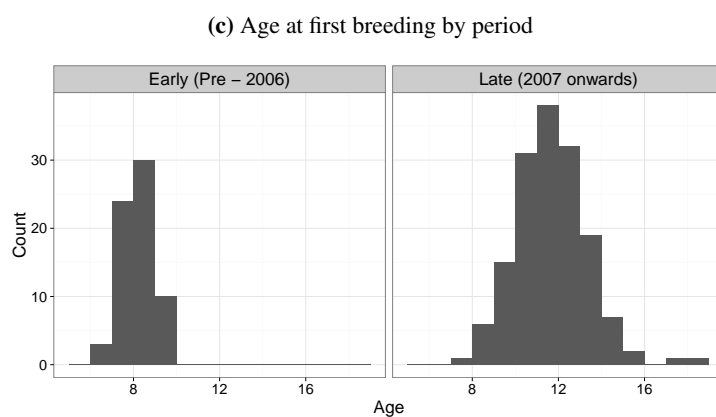
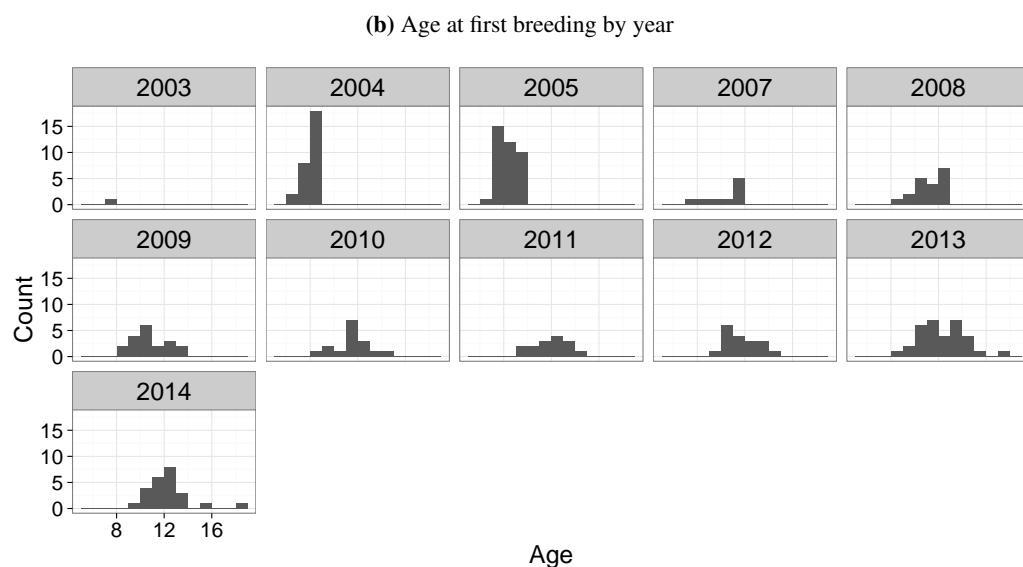
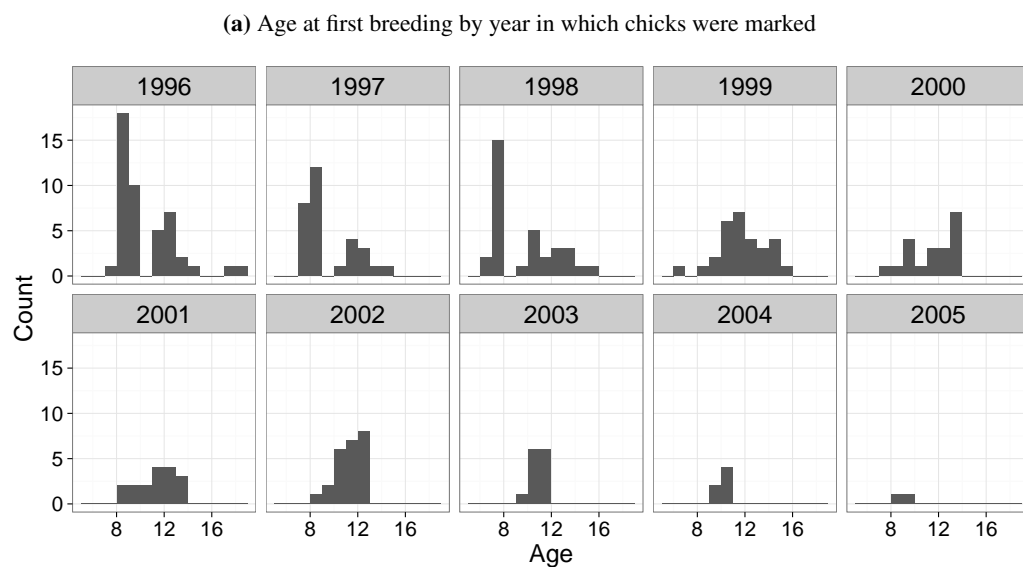


Figure 4: Frequency histograms showing the age at first breeding from known-age mark-recapture data.

individuals marked at different times treated equally. The ages at first breeding by year are shown in Figure 4b. Aggregating the data into early and late periods (pre- and post-2006) clearly yields distinct pictures of the maturation process (Figure 4c).

A suitable functional form to describe the maturation process is the bi-logistic curve $g(x)$, which effectively combines two logistic curves, each of which can be taken to represent an alternative breeding strategy (i.e. individuals that breed early compared to those that delay the age at first breeding):

$$g(x) = \frac{P[\text{early}]}{1 + \exp(-(x - a_{50}^{\text{early}}))} + \frac{1 - P[\text{early}]}{1 + \exp(-(x - a_{50}^{\text{late}}))} \quad (1)$$

where $P[\text{early}]$ is the probability of breeding early, and a_{50}^{early} and a_{50}^{late} are the mean ages of maturation for the early and late breeders respectively.

Of those individuals that have already started to breed, we can next examine temporal trends in the overall probability of breeding, which is the probability of breeding for an individual that has bred at least once already and that is known to be alive (because it is resighted at a later date). For this, both the known- and unknown-age data were combined, for the former discarding all records prior to the age at first breeding (so as to make the data sets equivalent). The resultant probability over time is shown in Figure 5a, as well as the probability of being a successful breeder. The breeding success rate is shown directly in 5b. There has clearly been a decline in both the probability of breeding, and the probability of breeding successfully, with these probabilities post-2010 being markedly different from pre-2005. This trend is also apparent in Figure 2, which for the unknown age data in particular shows an apparent increase in the observation of non-breeders and a decline in the record of successful breeders. Based on these observations it is reasonable to infer that the success, age and frequency of breeding may be having an influence on the population dynamics, and need to be incorporated into the population dynamics model.

Resight probability It is also possible to use the raw data to investigate the resight probability. This is important for the estimation of survival from mark-recapture data because it indicates whether individuals not seen are likely to have died. However there are some confounding factors that can impair inference: individuals may emigrate; and, for species that do not return to breed every year, resight probability is confounded with the probability of return to the island when not breeding. Emigration is impossible to estimate without further data from other study sites, but for other wandering albatross species is known to be extremely rare in adults (e.g. Gauthier et al., 2010). In the current model emigration is considered as an additional mortality. To account for birds not returning to the island when not breeding, the resight probability for breeders and non-breeders can be segregated in the model so as to facilitate better estimation of survival.

From the known-age mark-recapture data we can plot the resight probability at age, based on the numbers seen and the numbers known to be alive (because they are seen later). Figure 6 shows this probability for individuals that have not bred yet (immature), individuals that have bred (or attempted to breed) at least once (mature), and members of the mature category that are not breeding (non-breeders). The resight probability for the immature individuals increases with age and appears to plateau at around the same probability as that for the mature individuals. This is interesting. First, because the asymptote suggests that at least 20% of resident individuals still alive are not seen in any one year, even after they have started breeding – consistent with the fact that a proportion of the non-breeders do not return to the island. And second, that there is a continuity (with age) in the resight probability between immature and mature individuals.

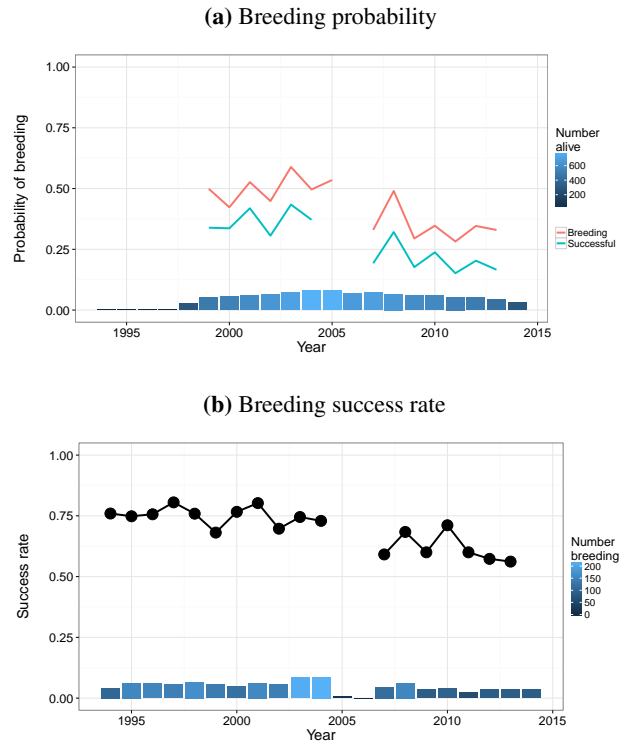


Figure 5: Breeding probability and success rate calculated from the combined mark-recapture data sets (known- and unknown-age). Note that for 2005, even though over 200 hundred nests were recorded that year, only very few could be categorised as either successful or not, because there was no survey in 2006.

From inspection of the empirical data plots, a suitable asymptotic function describing resight probability for non breeding individuals (both mature and immature) at age x would be:

$$h(x) = \begin{cases} 0 & \text{if } x \leq b \\ a \cdot (1 - \exp(-(x - b)/\delta)) & \text{if } x > b \end{cases} \quad (2)$$

where a is the asymptotic resight value, denoted as either $R_{\infty}^{[IMM]}$ for immature individuals or $R_{\infty}^{[MNB]}$ for mature non-breeders. The parameter b is an intercept term, and δ determines the rate at which the asymptote is reached. The resight probability for mature breeders was assumed to be one: $R^{[SBR]} = R^{[FBR]} = 1$ (i.e. if an individual breeds or attempts to breed then it is certain to be seen).

The resight probability has also changed over time (Figure 7), particularly for mature non-breeders. However there are a range of causal possibilities. The first is that resight effort has changed. This is in fact true: from 2006 to 2011 the study area was checked only 3 – 4 times, whereas before and after that period it has been checked around 20 times per season. Since the effort has dropped, one might expect the resight probability to also drop. However this does not appear to have happened. Instead, the resight probability has increased. An alternative explanation, and one that accords with field observations, is that birds are returning with a consistent frequency but are less likely to breed, meaning that the number of non-breeders observed increases. Out of the total number known to be alive, this would yield the apparent increase in resight probability shown in Figure 7. As such this increase may be indicative of a decline in the breeding probability, rather than a change in the probability of non-breeders returning to the island to be sighted.

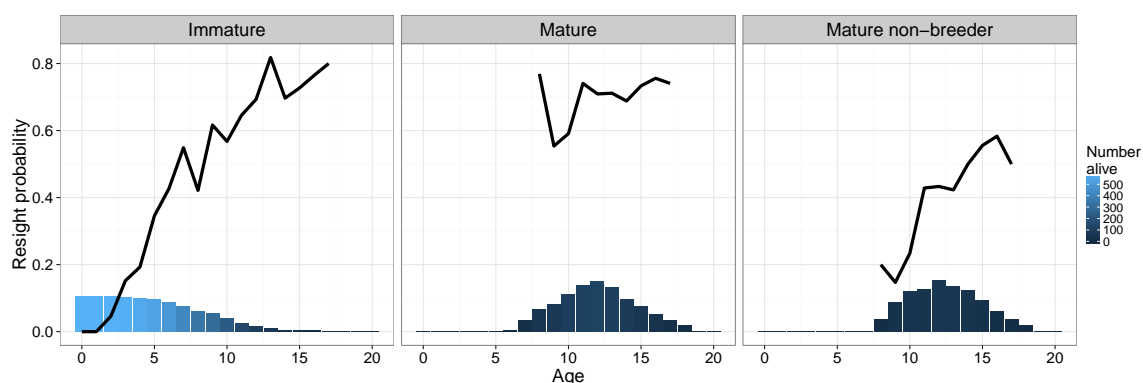


Figure 6: Resight probability at age from known-age resight data. Immature individuals are those that have never bred. Mature individuals are those that have bred at least once, and includes both breeders and non-breeders. Non-breeders are individuals that have started breeding (i.e. part of the mature class) but are not breeding at that age. The resight probability is the number seen at age divided by the number alive. The number alive represents those marked individuals known to be alive because they are resighted at an older age. For non-breeders, the number alive is the number of marked individuals that have bred at least once and are resighted at an older age, minus the number resighted as breeders for that age category. Ages for which the number alive was less than 10 are not shown.

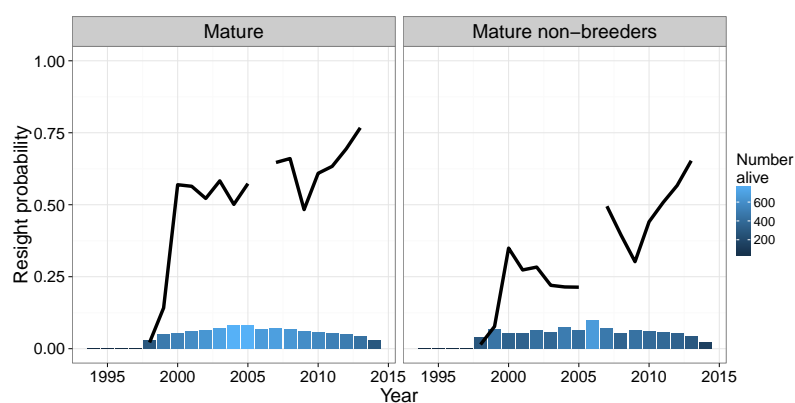


Figure 7: Empirical resight probability by year from mark-recapture data, using unknown-age data combined with known-age data. All resight data from known ages prior to first breeding were discarded. See Figure 6 for a full description of how resight probabilities were calculated.

2.3. Population dynamics model

The dynamics are described by a transition matrix model implemented in the programme SeaBird (Francis & Sagar, 2012), which is able to combine a variety of data sources, including census observations and mark-recapture data, to produce estimates of dynamic rate parameters and population size. As is typical for matrix models the population is partitioned into discrete and non-overlapping classes that include all individuals being modelled in only one class. We can therefore describe the modelled population using a vector \mathbf{N} which may contain individuals classified according to, for example, age, sex or breeding status. The inter-annual dynamics are specified in chronological order by the matrices \mathbf{R} , \mathbf{S} and \mathbf{T} . Respectively, these represent the number of new birds added to the youngest partition (recruitment), the survivorship in each class, and the transition probabilities between classes. The dynamics from years t to $t + 1$ can therefore be written as:

$$\mathbf{N}_{t+1} = \mathbf{T}_t \mathbf{S}_t \mathbf{R}_t \mathbf{N}_t$$

The numbers vector contains age classes from chicks (age 0) to age 15, with age 15 being a plus group. All birds of age 15 and over therefore have the same survivorship (i.e. there is no senescence). For ages 6 and upwards, birds are represented in the model as non-breeders, successful breeders or failed breeders (Table 2). The non-breeding category includes those that have never bred (immature) plus those that are mature but not currently breeding. Following the notation in Table 2, and with ages given as subscripts, the numbers vector can therefore be written as:

$$\mathbf{N} = \left[N_0^{[IMM]}, N_1^{[IMM]}, \dots, N_5^{[IMM]}, N_6^{[NBR]}, N_6^{[SBR]}, N_6^{[FBR]}, \dots, N_{15}^{[NBR]}, N_{15}^{[SBR]}, N_{15}^{[FBR]} \right]^T$$

Since the non-breeding age classes can be considered as being made up of physically mature birds that have bred and have never bred, they are in effect a combination of two latent (unobserved) classes:

$$\mathbf{N}^{[NBR]} = \mathbf{L}^{[IMM]} + \mathbf{L}^{[MNB]}$$

with the proportions in each latent category determined by the maturation ogive $m_x = g(x)$ (equation 1):

$$\begin{aligned} \mathbf{L}^{[MNB]} &= m_x \cdot \mathbf{N}^{[NBR]} \\ \mathbf{L}^{[IMM]} &= (1 - m_x) \cdot \mathbf{N}^{[NBR]} \end{aligned}$$

When calculating the probability of breeding, we are specifically concerned about the probability of transition from $\mathbf{L}^{[MNB]}$ to either $\mathbf{N}^{[SBR]}$ or $\mathbf{N}^{[FBR]}$.

Resight probabilities Because the mature and immature components of the non-breeding categories follow different resight probabilities at age (Figure 6), two resight ogives were estimated, with the functional forms following that given in equation 2. The asymptote parameters $R_\infty^{[IMM]}$ and $R_\infty^{[MNB]}$ (parameter a in equation 2) were estimated, whilst the intercept parameter b was fixed. Because immature individuals banded as chicks are first resighted at age 2, we fixed $b = 1.5$ for the immature category. For mature individuals, we fixed $b = 5.5$, since birds reach physical maturity at age 6. The rate parameter δ (which determines the speed at which the asymptote is reached) was estimated. During preliminary model explorations it was found to be equivalent for both resight ogives and was therefore shared in all model fits presented here. In summary, the resight probabilities can be written as:

$$R_x^{[IMM]} = \begin{cases} 0 & \text{if } x \leq 1.5 \\ R_\infty^{[IMM]} \cdot (1 - \exp(-(x - 1.5)/\delta)) & \text{if } x > 1.5 \end{cases} \quad (3a)$$

$$R_x^{[MNB]} = \begin{cases} 0 & \text{if } x \leq 5.5 \\ R_\infty^{[MNB]} \cdot (1 - \exp(-(x - 5.5)/\delta)) & \text{if } x > 5.5 \end{cases} \quad (3b)$$

These are combined to give the resight probability for all immature and mature non-breeding individuals. Using the maturation ogive: $m_x = g(x)$ (equation 1); the resight probabilities are:

$$R_x^{[IMM \cup NBR]} = \begin{cases} 0 & \text{if } x \leq 1.5 \\ R_x^{[IMM]} & \text{if } 1.5 < x \leq 5.5 \\ (1 - m_x) \cdot R_x^{[IMM]} + m_x \cdot R_x^{[MNB]} & \text{if } x > 5.5 \end{cases} \quad (4)$$

We used $R_x^{[IMM \cup NBR]}$ as the resight probability at age for all non-breeders in the known-age mark-recapture data. From Figure 6 it can be seen that $R_\infty^{[IMM]}$ approximates the overall resight probability for all mature birds (i.e. breeding and non-breeding birds that have bred at least once before), meaning that:

$$R_\infty^{[IMM]} \approx P[BR] + R_\infty^{[MNB]}(1 - P[BR])$$

remembering that the resight probability for breeders is one, and where $P[BR]$ is the probability of a mature individual breeding. According to this simplification, if $P[BR]$ and $R_\infty^{[IMM]}$ are estimated, then $R_\infty^{[MNB]}$ is redundant. Unfortunately we were not able to explore this alternative parameterisation further and instead estimated all three as independent parameters.

Finally, this leaves the non-breeder resight probability for mark-recapture data of unknown age. We might expect this to be a numbers weighted average of $R_x^{[MNB]}$:

$$\tilde{R}_x^{[MNB]} = \frac{m_x \cdot N_x^{[NBR]}}{\sum m_x \cdot N_x^{[NBR]}} \cdot R_x^{[MNB]} \quad \text{for } x \geq 5.5$$

however, again, this parameterisation was not explored further. Instead, $\tilde{R}_x^{[MNB]}$ was estimated directly as a constant for all ages of 10 years and older, this being an arbitrary age above which we might expect the resight probability to be approximately the same (Figure 6).

Survivorship Survivorship was estimated separately for adults (model classes $N^{[NBR]}$, $N^{[SBR]}$ and $N^{[FBR]}$) and juveniles (model class $N^{[IMM]}$). Juvenile survivorship was kept constant over time, whereas adult survivorship was constant for 1990 – 1999 and then allowed to be time variant for years 2000 – 2013 inclusive. This model property was included for all model runs based on an assumption that changes in survivorship are at least partly responsible for the dynamics that have been observed, and to allow these changes to be included in the projections used to inform our understanding of future population changes.

2.4. Outline of analysis

The analysis is broken down into the following five stages:

1. Model development: Alternative models of different complexity are fitted to the data using Maximum Posterior Density (MPD) estimation and examined to determine the one most suitable for describing and understanding the population dynamics. The selected model is known as the *basecase*.

2. Model fit: The basecase model is fitted to the data using Markov chain Monte Carlo (MCMC).
3. Sensitivity tests: The basecase model is fitted to alternative data configurations, to examine which data are responsible for the model parameter estimates and whether there are conflicts between data or data types.
4. Assessment of fishing impact: The basecase model is refitted with an assumed annual mortality attributed to fishing. Projections are then performed under different assumed fishing mortality scenarios, to quantify the impact of fishing on future population dynamics. Further sensitivity testing was included in this stage, utilising the results from the previous step.
5. Estimation of maximum survivorship: Part of the project aim is to provide input for the seabird risk assessment framework (see Richard & Abraham, 2013a), which requires a value for the maximum survivorship of each species. For this purpose the basecase model was restructured to estimate a constant survivorship and fitted to the data using MCMC. The results from this analysis are shown separately from the main report in Appendix III.

Table 2: Table of model classes, showing numbers N and latent categories L .

Class label	Description	Age range
$N^{[IMM]}$	Immature: chicks and individuals that have never tried to breed	0 – 5
$L^{[IMM]}$	Latent immature: individuals that have never tried to breed	6 – 15
$L^{[MNB]}$	Latent mature non-breeders: individuals that have bred at least once but are not currently breeding	6 – 15
$N^{[NBR]}$	Non-breeders: equal to $L^{[IMM]} + L^{[MNB]}$	6 – 15
$N^{[SBR]}$	Mature successful-breeders: individuals that are currently breeding and successfully fledge chicks	6 – 15
$N^{[FBR]}$	Mature failed-breeders: individuals that are currently breeding but do not successfully fledge chicks	6 – 15

Table 3: Table of model runs. Maturation was blocked into two periods: 1990 – 2005 and 2006 onwards. Breeding probability and success rate were allowed to be time variant from 2000 onwards. The resight probability was set to zero from 1990 – 1999 in all models, and when blocked was split into two periods: 2000 – 2005 and 2006 onwards. In all runs survivorship was time variant for the year 2000 onwards.

Label	Maturation	Breeding probability	Breeding success rate	Resight Probability
A01	Constant	Constant	Constant	Constant
B01	Blocked	Constant	Constant	Constant
B02	Blocked	Time variant	Constant	Constant
B03	Blocked	Constant	Time variant	Constant
C01	Blocked	Time variant	Constant	Constant
C02	Blocked	Time variant	Time variant	Constant
C03	Blocked	Time variant	Constant	Blocked
C04	Blocked	Time variant	Time variant	Blocked

3. Results

3.1. Model development

From the empirical data exploration we identified the following temporal trends for potential inclusion in the final model:

- There is a trend towards an older age at first breeding, being approximately 12 years of age in more recent years.
- Considering only those individuals that have bred at least once, the probability of subsequent breeding in any one year is about 0.5 for years up to 2005–06 (i.e. breeding once every two years) but declines thereafter to about 0.3 in 2013 (i.e. breeding once every three years).
- The breeding success rate is constant at around 0.75 until 2005–06 but then also declines to 0.55 between 2007 and 2013.
- There is a trend towards an increased resight probability at age in individuals that have not bred.
- After individuals have bred for the first time, the resight probability drops, but then increases with age thereafter.
- The resight probability for non-breeders is around 0.25 prior to 2005–06, and then increases thereafter.
- The mark-recapture data for years prior to 2000 should be ignored, since the resight probability is unusually low.

In summary, we were able to identify age dependent relationships with the maturation and resight probabilities, and noticeable temporal trends in the age at first breeding, breeding rate, breeding success and non-breeder resight probability. Initial model runs were therefore devised to examine how best to represent these temporal changes (Table 3).

The bilogistic maturation ogive was included by default based on explorations of the empirical data, with two periods for $P[early]$ (the probability of breeding at an early age as defined by a_{50}^{early}), from 1990 – 2005 and from 2006 onwards (Figure 4). We then investigated whether the data exhibited any evidence of time variant changes in breeding probability or success. Figure 8 shows the different fits to census data indicating that out of models B01 – B03, B02 (with a time variant breeding rate but constant probability of success) has a substantially improved fit to the census data. Taking this forward, we examined whether either a time variant breeding success rate or blocked resight probability further improved the model fit to the data (models C01 – C04). Figure 8 shows that fits to the census data are not much affected. However from Figures 9 and 10 it can be seen that the blocked resight probability does have a marked effect on the fits to the resight probability. More specifically, it seems to reduce the quality of the fit to the data from non-breeders of known age (Figure 9), but improves the fit to non-breeders of unknown age (Figure 10). There is therefore an apparent conflict between these mark-recapture data, with the model showing preference towards the data of unknown age. This preference is due to the data quantity, with there being more unknown age mark-recapture data (Figure 2). This preference is further illustrated by Table 4, which shows that according to the AIC, model C03 should be preferred (i.e. a blocked resight probability should be included). Despite exhibiting a trend in the empirical data, a time variant breeding success rate did not improve the model fit. This may be because the effect of a change in breeding success could be partly accommodated by time variant adult survivorship (included in the model by default), which can adjust the number of breeders entering the population each year.

Final model In the final (basecase) model: maturation was represented by equation 1, with two time periods for $P[early]$ from 1990–2005 and 2006 onwards (Figure 4c); the probability of a mature individual breeding (i.e. the probability of transition from $N^{[NBR]}$ to either $N^{[SBR]}$ or $N^{[FBR]}$) was

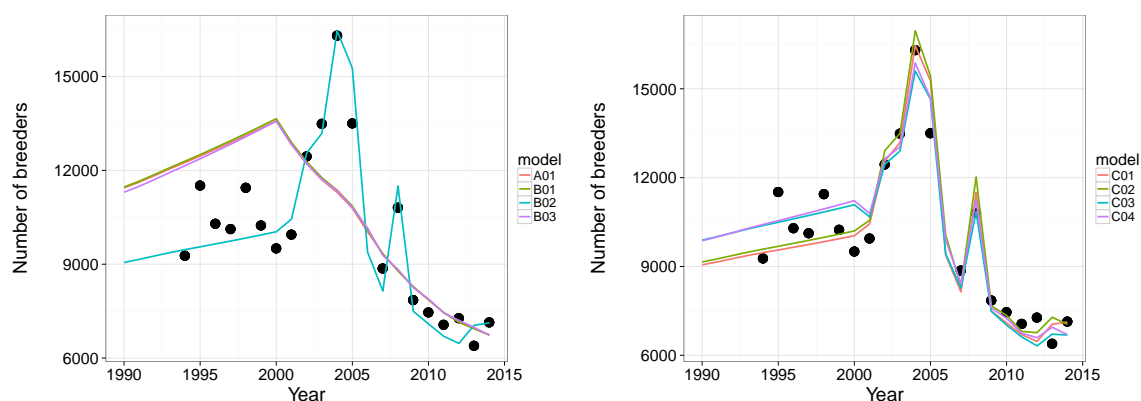


Figure 8: Model fits to empirical whole island census data. Empirical data are shown as black dots, with model estimated values as coloured lines.

allowed to be time-variant from 2000 onwards (Figure 5a); the breeding success rate was kept constant; and finally the resight probability for non-breeders was split into two time blocks (Figure 7).

Table 4: Alternative model runs with associated AIC values

Model	n	-ln(L)	AIC
A01	26	84970	169992
B01	27	84970	169994
B02	40	84770	169620
B03	40	84960	170000
C01	40	84770	169620
C02	53	84760	169626
C03	43	84650	169386
C04	56	84650	169412

3.2. Model fit

Taking model C03 forward, we then proceeded to implement a full Bayesian fit to the data using MCMC. A single chain was first initialised at the maximum posterior density values and run for 10 000 iterations, following which the covariance matrix used for parameter resamples was recalculated to improve mixing. This was repeated a second time, all iterations were discarded as burn-in, and three independent chains were then run for 100 000 iterations, keeping every 10th sample. The chains are illustrated in Figure A1, with each chain plotted over-lapping so as to allow diagnosis of convergence. The three chains were then combined to obtain the posterior density distribution for each parameter. The estimated parameter values from this posterior are listed in Table 5.

3.3. Sensitivity tests

Sensitivity runs were conducted to examine the behaviour of the model under different data configurations, so as to better understand which data components are driving the derived model estimates. Three sensitivity runs were performed, with the posterior distributions of important model parameters illustrated in Figure 11:

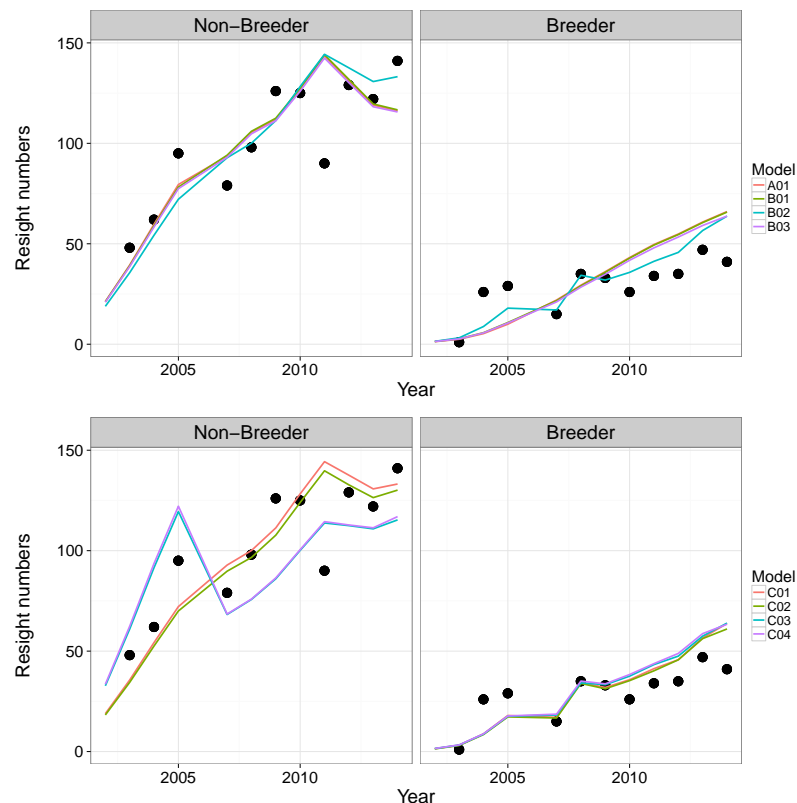


Figure 9: Model fits to empirical mark recapture data of known age. Empirical data are shown as black dots, with model estimated values as coloured lines.

1. No census data: Removing the census data has no noticeable influence on the posterior estimates of survivorship or breeding probability. However it does lead to a change in the estimates of maturation. This suggests that including the census data leads to lower values for $P[early]$ in both time periods (i.e. that the probability of breeding early is smaller). The effect of the census data on estimates of $a50[early]$ and $a50[late]$ is less marked.
2. No unknown age mark recapture data: Inclusion of unknown age mark recapture data into an age-structured model can create conflicts, due to the structural assumptions required to achieve this. In our case, we have specifically assumed that unknown age mark recapture are equally likely to be of ages 10 – 15 when marked. If this is not true, for example if unknown age bandings are usually of individuals older than 15, then this may bias our estimation of age-dependent vital rates (even if these vital rates are not represented as age dependent in the model). Fortunately, excluding the unknown age data has a negligible effect on the survivorship estimates. However it does have an effect on the breeding probability, leading to higher probabilities of breeding from 2007 onwards. This means that our inclusion of these data lowers our estimates of $P[breed]$. Inclusion also leads to lower estimates of $P[early]$, offset by younger mean ages at maturation $a50[early]$ and $a50[late]$.
3. Female only data. If males and females have different survivorship, or the same survivorship but different maturation ogives or probabilities of breeding, then estimates of model properties and the derived population dynamics might depend on how sexual differences are considered. The basecase model does not partition between the sexes. We therefore performed an additional run using female only data to examine whether this has an effect. The model structure was

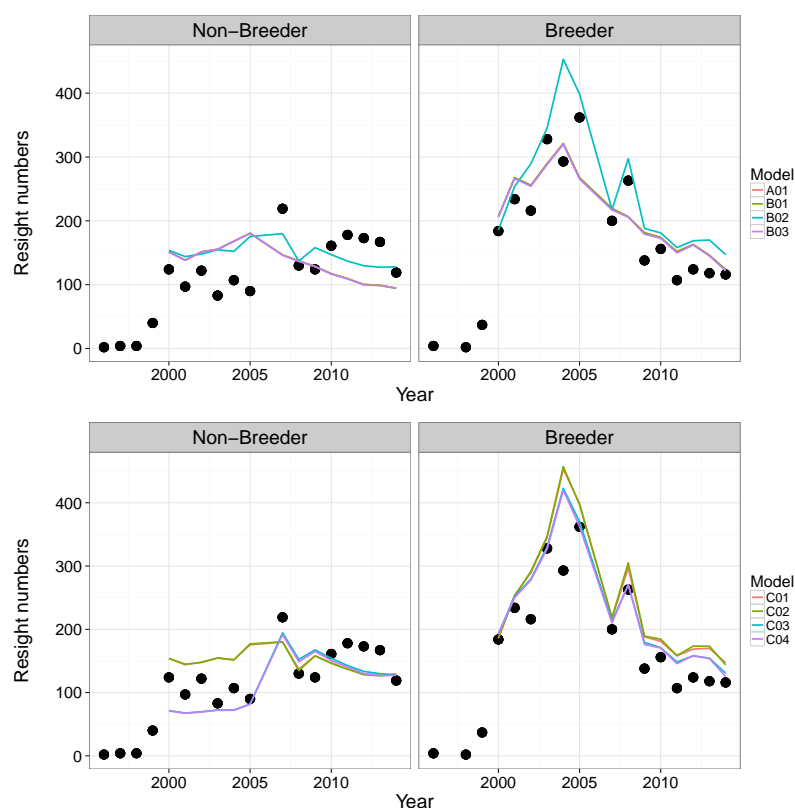


Figure 10: Model fits to empirical mark recapture data of unknown age. Empirical data are shown as black dots, with model estimated values as coloured lines.

otherwise the same as the basecase, with the exception that juvenile survivorship was not estimated but fixed at the basecase value. This is because banded birds could only be sexed after they had survived the juvenile stages, meaning that juvenile survival could not be estimated. Fitting to the female data only seemed to have only a small impact on survivorship and breeding probability. However it led to a noticeable shift in the age at first breeding towards younger ages, indicating that females breed at younger ages. There is also a loss of any noticeable distinction between $P[early]$ in the early and late periods.

3.4. Assessment of fishing impact

Projections were performed by sampling parameter values from their posterior distributions and predicting the dynamics twenty years into the future (from 2015 – 2034). The fishing impact was assessed by re-fitting the model with an assumed fishing related mortality of 89 individuals per year (from Richard & Abraham, 2015), and then projecting assuming either: a continued 89 individuals per year; or, no fishing mortality. The difference between these two scenarios represents the likely impact of fishing related mortality within the New Zealand EEZ. Three evaluations were performed, illustrated in Figure 12:

1. Basecase model with vital rates sampled from most recent ten years of estimates (2004 – 2013): This indicates that the population is most likely to continue to decline unless the underlying demographic rate parameters improve relative to the most recent decade.
2. Basecase model with vital rates sampled from an earlier period of estimates (1995 – 2004)

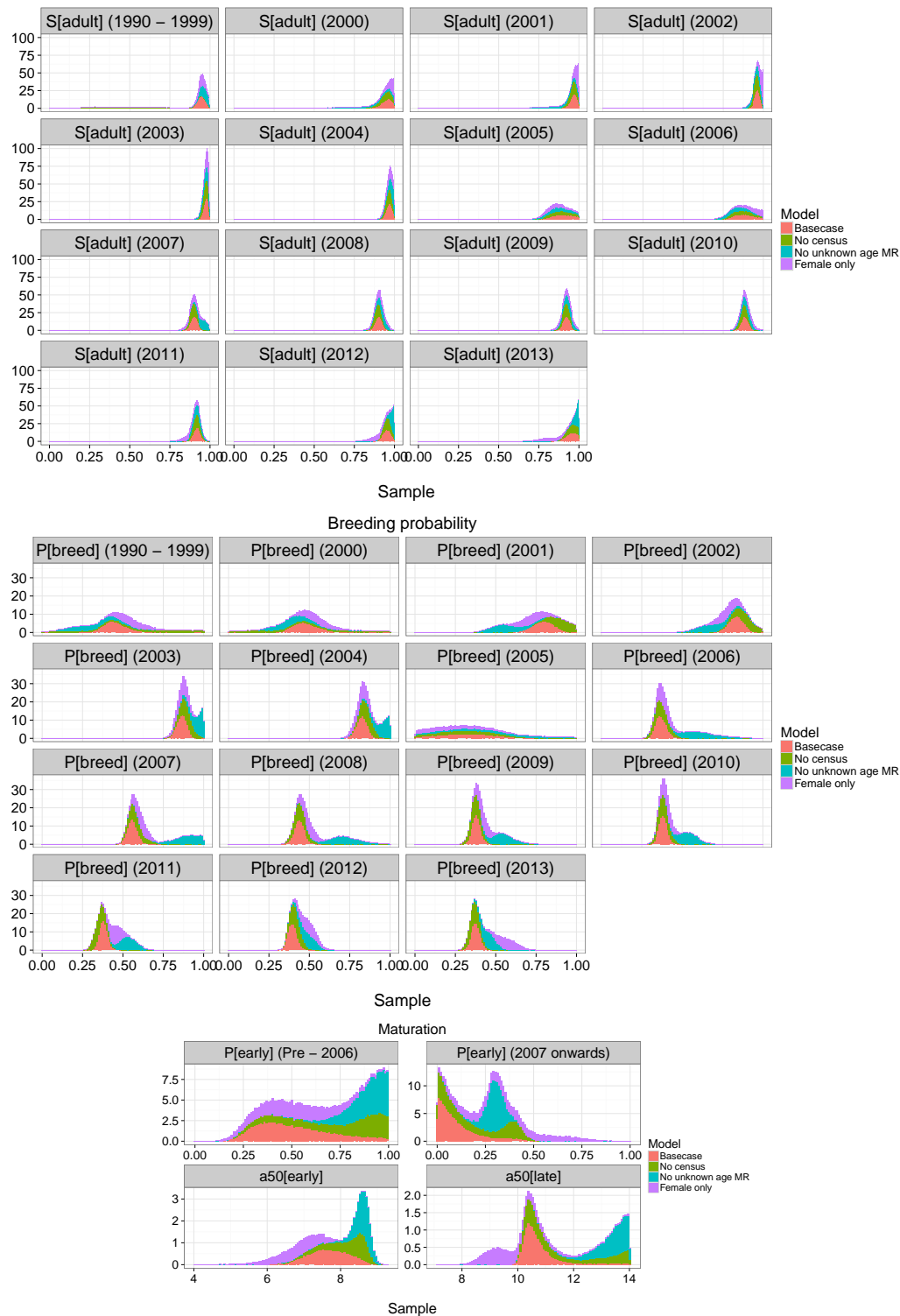


Figure 11: Selected posterior probability distributions for alternative sensitivity tests. A complete set of parameter estimates is in Appendix II.

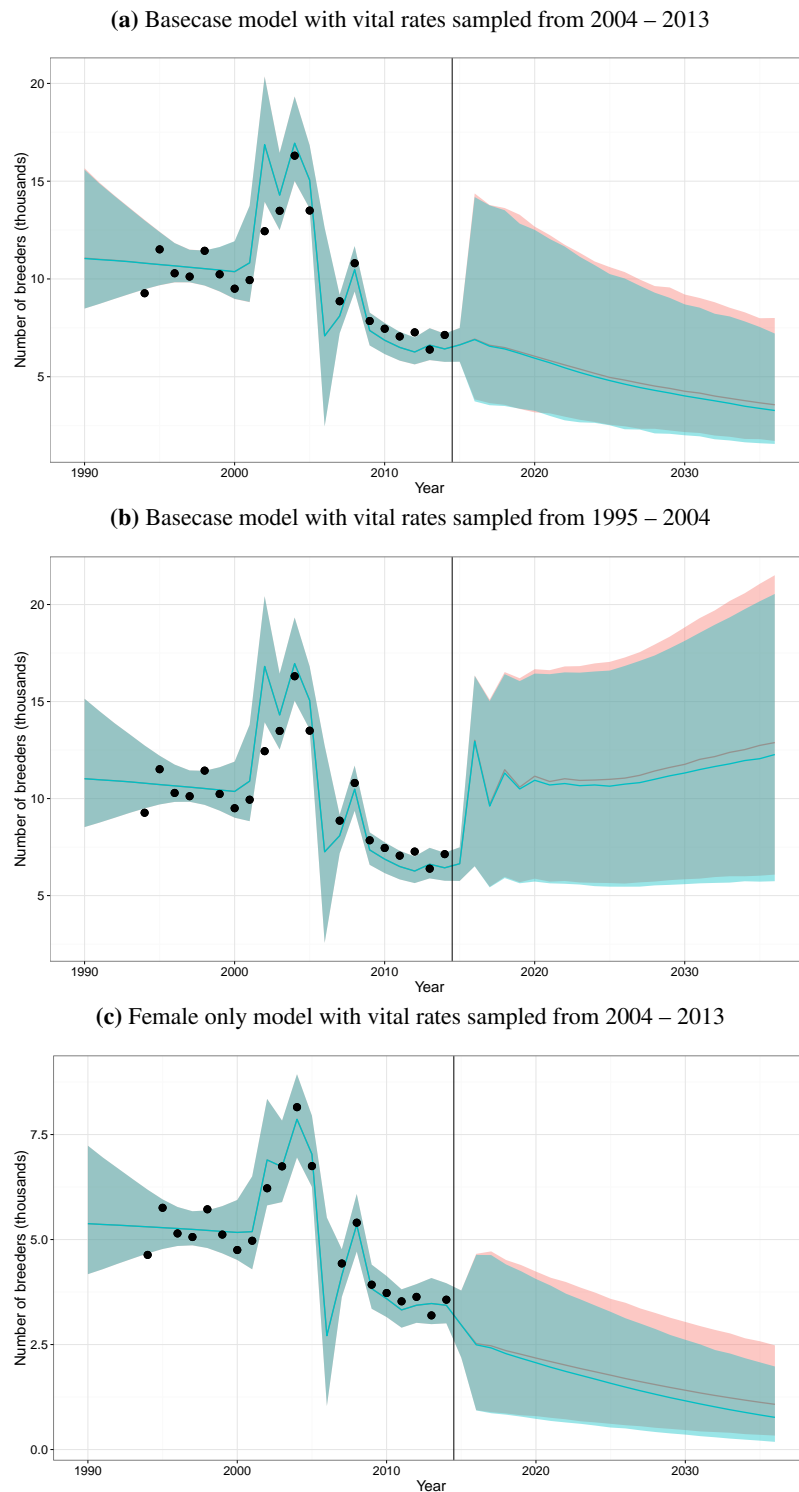


Figure 12: Predicted population dynamics for the whole island, showing the number of breeders from 2015 – 2034. Predicted dynamics with and without fishing pressure are superimposed. The median and 95% confidence intervals are shown for each scenario. The vertical line indicates the limit of the empirical data, with subsequent dynamics representing an extrapolation. Empirical census data are also shown.

during which the survivorship was higher (Table 5); noting that these were estimated in the basecase as a constant from 1990 – 1999: This scenario implies a sudden (and probably unrealistic) jump in the short term breeding probability, but nevertheless indicates in the projection results that the population could stabilise if demographic conditions improved.

3. Females only model with vital rates sampled from most recent ten years of estimates (2004 – 2013): The predicted dynamics are similar to basecase, being similarly pessimistic.

Clearly, the prospects for species recovery are dependent on whether or not the future vital rates are closer to their most recent values or to values from the previous decade, these latter rates producing much more optimistic results. Either way, the apparent impact of fishing within the New Zealand EEZ is small. The impact of fishing-related mortality outside New Zealand's EEZ is much less certain and, given the species distribution across the Pacific (Debski et al., 2016) it can be expected that the effect of such mortality will be non-trivial (Small et al., 2013).

4. Summary and Conclusions

This report has outlined the development of a quantitative model with which to represent the population dynamics of Antipodean wandering albatross. It is parameterised using extensive mark-recapture and census data, which allowed the estimation of time-variant survivorship and breeding parameters. Although the survivorship has changed over time, it is apparent from both the modelling and an empirical review of the data that changes in the breeding rate, success and age of first breeding are important determinants of temporal changes in the population abundance, all of which are consistent with a hypothesis that nutritional stress is impacting the population. The model strongly indicates that the population has declined in numbers since 2007 and will continue to do so unless demographic vital rates recover.

The model was also able to quantify the likely effect of fishing induced mortality, at least for that which occurs within the New Zealand Exclusive Economic Zone. It demonstrates that the best estimate of adult mortality attributed to these fleets is likely to have had a negligible effect on population dynamics. However we were unable to draw any conclusions regarding the impact of unknown levels of fishing related mortality outside of New Zealand waters and therefore note that this species was ranked by Small et al. (2013) as the 5th most at-risk species in the waters of the Western Central Pacific Fisheries Commission. Since there are currently no good estimates available for this additional mortality, a more sophisticated risk assessment framework would be required (e.g. Moore & Curtis, 2016), which is outside the scope of the present study.

5. Acknowledgements

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Table 5: Posterior parameter estimates for the basecase model. S[adult] is the survivorship for model classes: $N^{[NBR]}$, $N^{[SBR]}$, $N^{[FBR]}$; whilst S[juvenile] is the survivorship for classes: $N^{[IMM]}$.

Category	Parameter	Median	95% CI
N0	N0	11045.1	[8460.45, 15093.01]
Survivorship	S[adult] (1990 - 1999)	0.95	[0.9, 0.99]
	S[adult] (2000)	0.95	[0.87, 1]
	S[adult] (2001)	0.97	[0.92, 1]
	S[adult] (2002)	0.96	[0.93, 0.99]
	S[adult] (2003)	0.98	[0.95, 1]
	S[adult] (2004)	0.97	[0.93, 1]
	S[adult] (2005)	0.9	[0.79, 0.99]
	S[adult] (2006)	0.88	[0.79, 0.99]
	S[adult] (2007)	0.9	[0.86, 0.94]
	S[adult] (2008)	0.9	[0.86, 0.94]
	S[adult] (2009)	0.92	[0.88, 0.96]
	S[adult] (2010)	0.88	[0.84, 0.92]
	S[adult] (2011)	0.92	[0.88, 0.96]
	S[adult] (2012)	0.95	[0.91, 0.99]
	S[adult] (2013)	0.95	[0.88, 1]
Maturation	S[juvenile]	0.88	[0.87, 0.89]
	P[early] (1990 - 2005)	0.49	[0.23, 0.94]
	P[early] (2006 onwards)	0.08	[0, 0.41]
	a50[early]	7.68	[6.63, 8.64]
Breeding	a50[late]	10.6	[10.09, 13.34]
	P[breed FBR]	0.68	[0.65, 0.71]
	P[breed NBR] (1990 - 1999)	0.47	[0.43, 0.51]
	P[breed NBR] (2000)	0.45	[0.33, 0.61]
	P[breed NBR] (2001)	0.47	[0.35, 0.66]
	P[breed NBR] (2002)	0.8	[0.66, 0.91]
	P[breed NBR] (2003)	0.83	[0.74, 0.92]
	P[breed NBR] (2004)	0.87	[0.8, 0.92]
	P[breed NBR] (2005)	0.82	[0.76, 0.89]
	P[breed NBR] (2006)	0.31	[0.03, 0.63]
	P[breed NBR] (2007)	0.37	[0.31, 0.44]
	P[breed NBR] (2008)	0.56	[0.5, 0.62]
	P[breed NBR] (2009)	0.44	[0.38, 0.5]
	P[breed NBR] (2010)	0.38	[0.33, 0.43]
	P[breed NBR] (2011)	0.38	[0.33, 0.43]
	P[breed NBR] (2012)	0.38	[0.33, 0.43]
	P[breed NBR] (2013)	0.4	[0.35, 0.45]
Resight	P[success]	0.38	[0.33, 0.43]
	R[mature] (2000-2005)	0.22	[0.19, 0.26]
	R[mature] (2006 onwards)	0.43	[0.41, 0.46]
	R[immature] (2000-2005)	1.97	[1.63, 2.6]
	R[immature] (2006 onwards)	0.91	[0.73, 1.28]
	R[non-breeder] (2000-2005)	0.88	[0.38, 1]
	R[non-breeder] (2006 onwards)	0.98	[0.91, 1]
	δ	12.42	[10.16, 17.03]

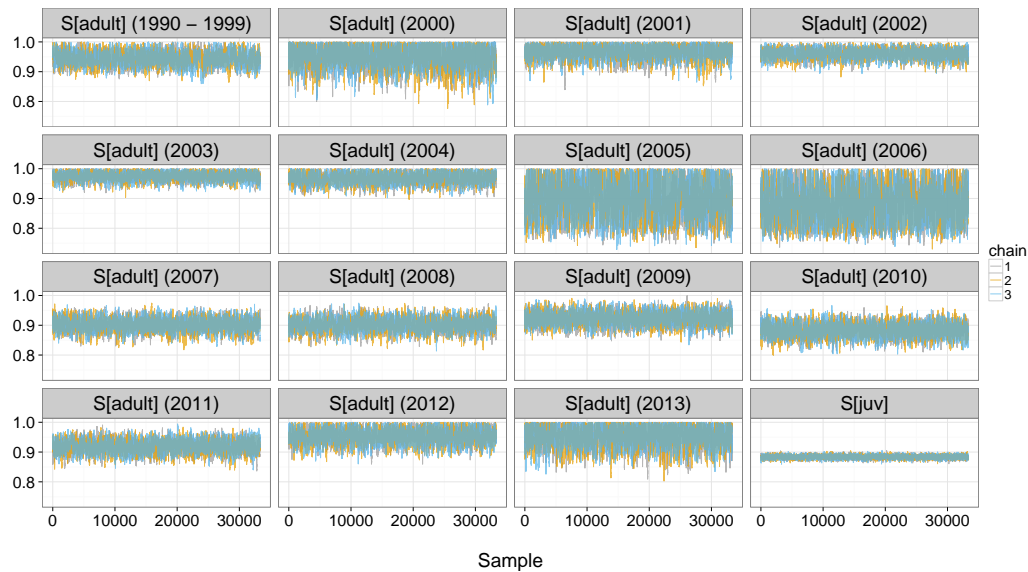
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Appendix I: MCMC trace outputs

(a) Survivorship - Trace plots



(b) Survivorship - Cumulative Plots

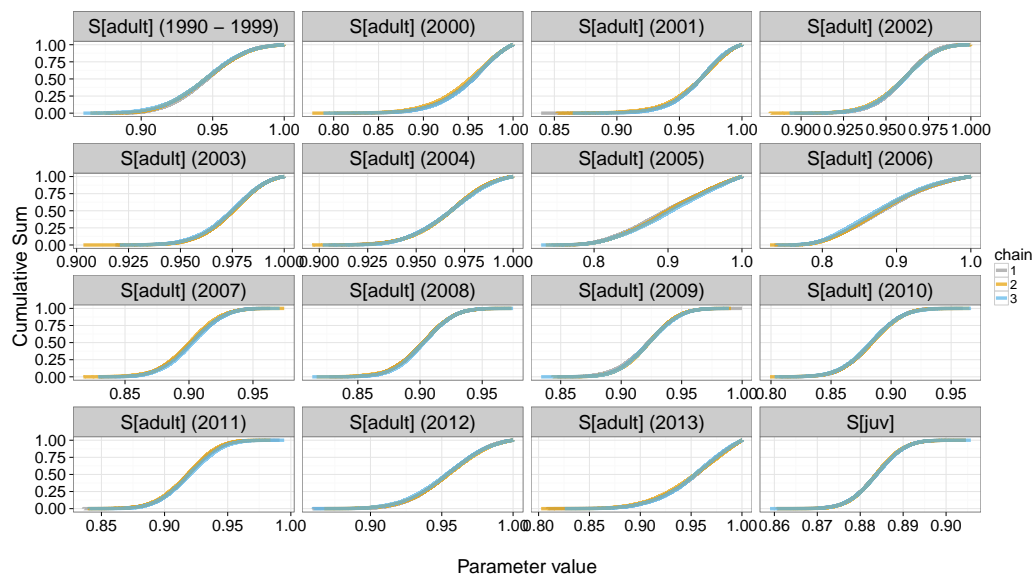
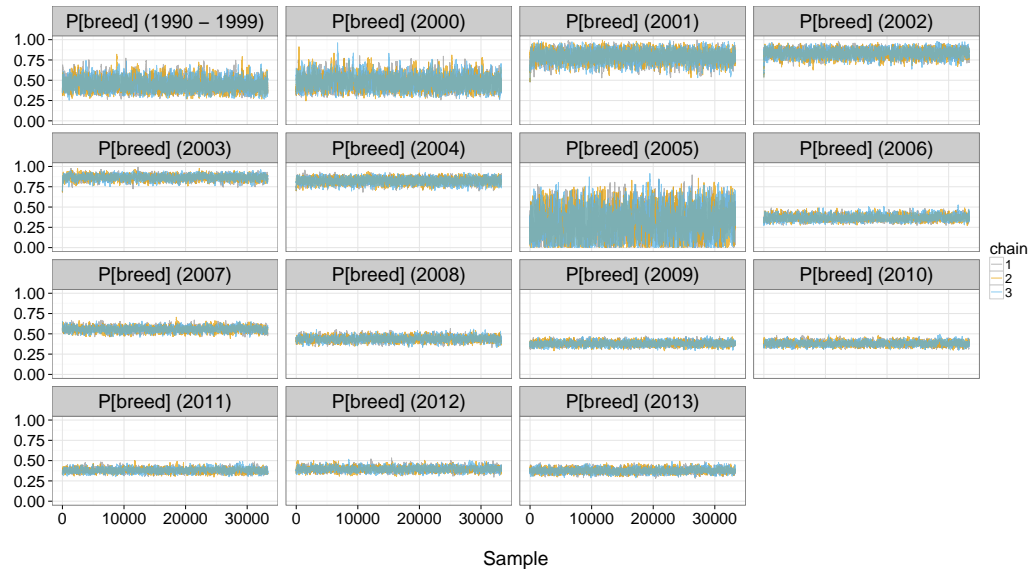


Figure A1: MCMC chains.

(c) Breeding rate - Trace plots



(d) Breeding rate - Cumulative Plots

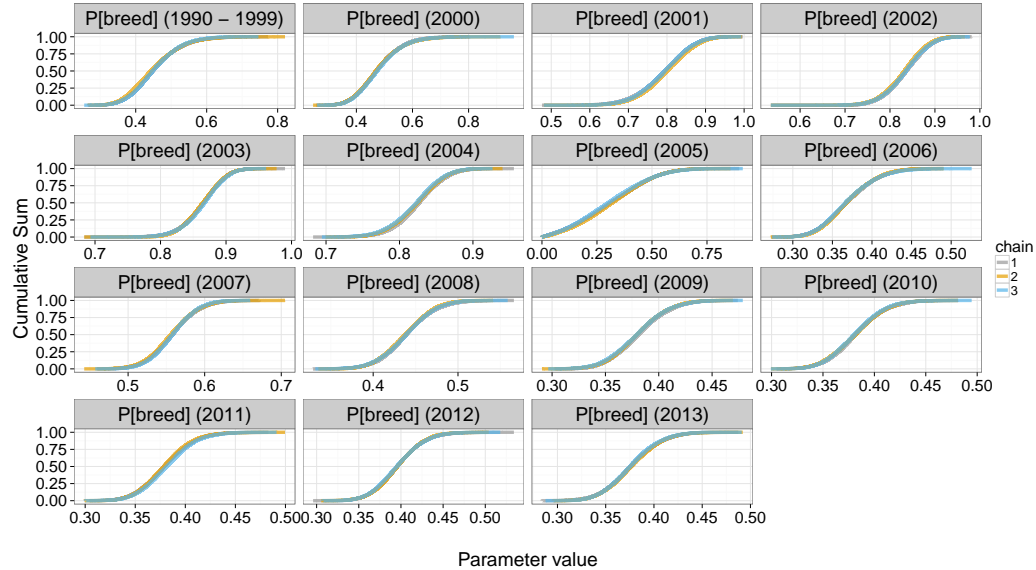
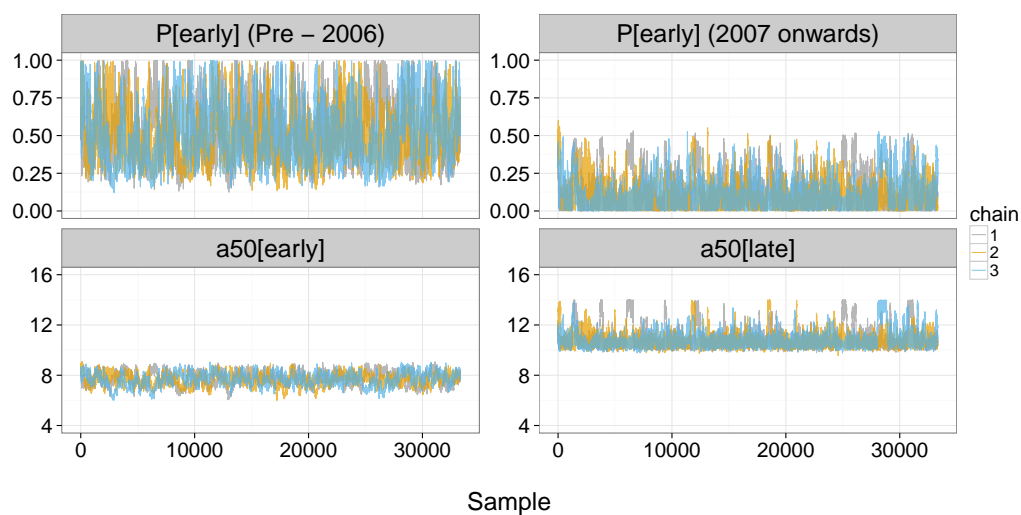


Figure A1: MCMC chains (continued).

(e) Maturation - Trace plots



(f) Maturation - Cumulative Plots

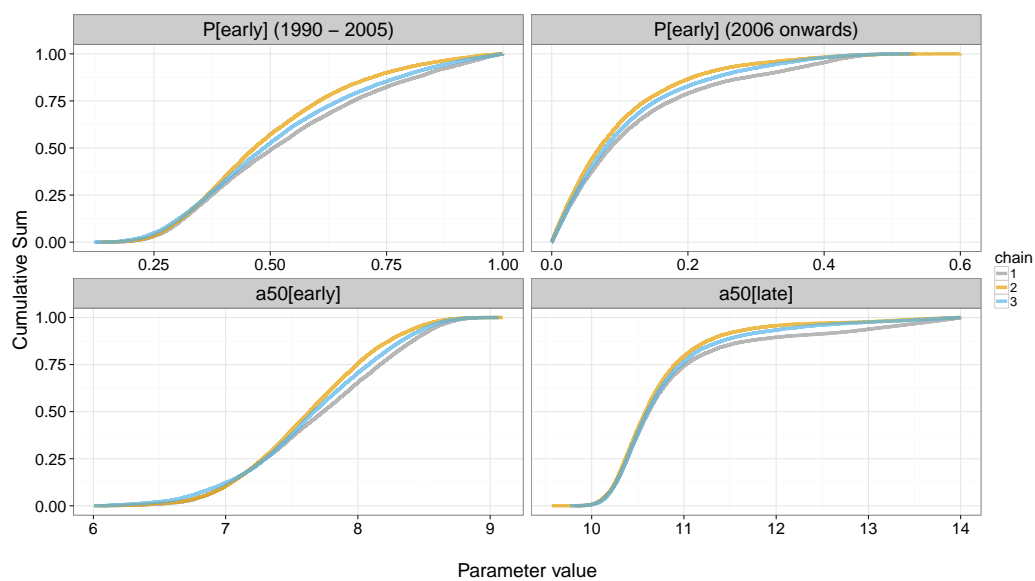
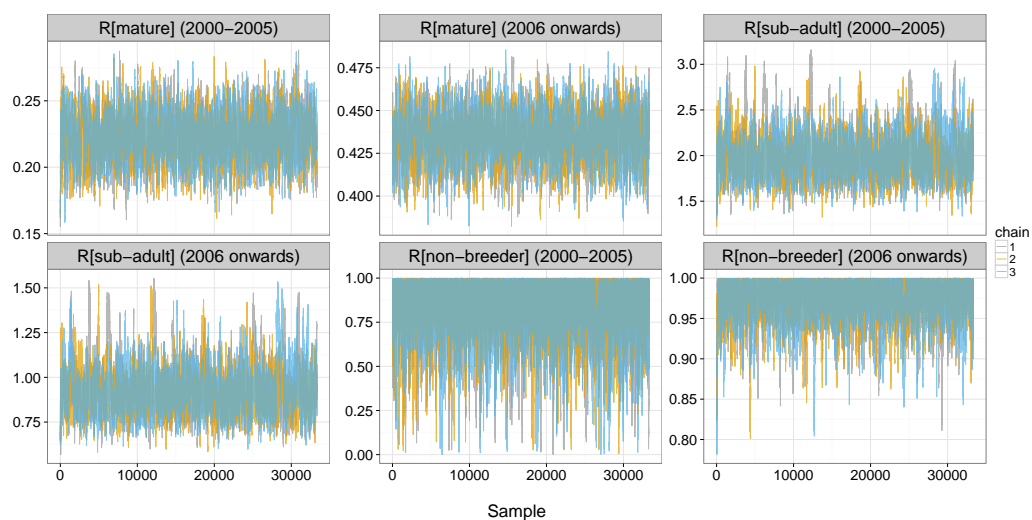


Figure A1: MCMC chains (continued).

(g) Resight probability - Trace plots



(h) Resight probability - Cumulative Plots

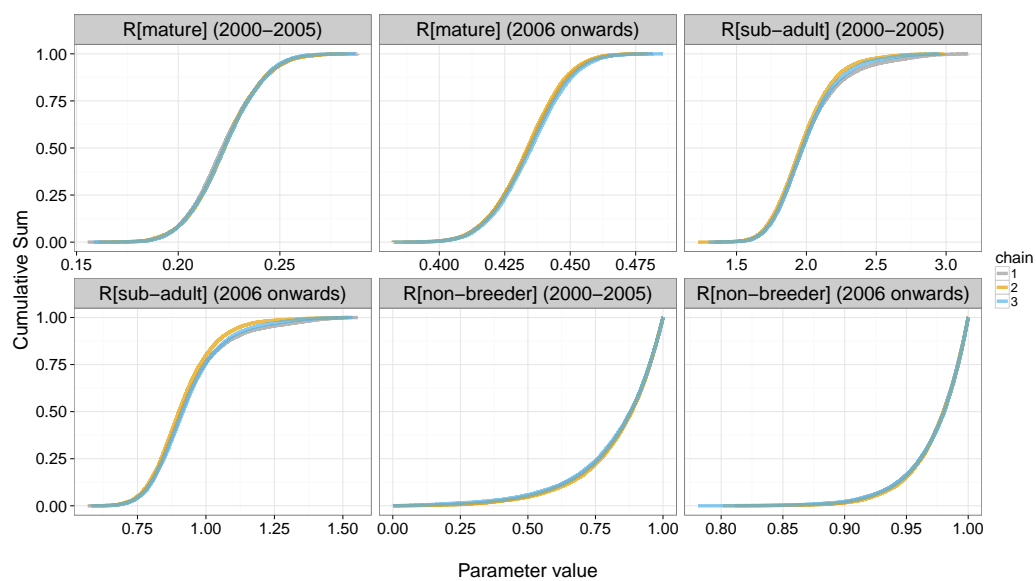


Figure A1: MCMC chains (continued).

Appendix II: Parameter estimates for sensitivity runs

Table A1: Posterior parameter estimates for the “no census data” sensitivity run.

Category	Parameter	Median	95% CI
N0	N0	26002.1	[1426.22, 48666.4]
Survivorship	S[adult] (1990 - 1999)	0.47	[0.09, 0.95]
	S[adult] (2000)	0.95	[0.85, 0.99]
	S[adult] (2001)	0.96	[0.91, 1]
	S[adult] (2002)	0.95	[0.92, 0.99]
	S[adult] (2003)	0.97	[0.94, 1]
	S[adult] (2004)	0.97	[0.93, 1]
	S[adult] (2005)	0.88	[0.77, 0.99]
	S[adult] (2006)	0.87	[0.77, 0.99]
	S[adult] (2007)	0.89	[0.85, 0.93]
	S[adult] (2008)	0.89	[0.85, 0.94]
	S[adult] (2009)	0.92	[0.87, 0.96]
	S[adult] (2010)	0.88	[0.83, 0.92]
	S[adult] (2011)	0.92	[0.87, 0.96]
	S[adult] (2012)	0.96	[0.91, 1]
	S[adult] (2013)	0.96	[0.88, 1]
Maturation	S[juvenile]	0.88	[0.87, 0.89]
	P[early] (1990 - 2005)	0.79	[0.27, 0.99]
	P[early] (2006 onwards)	0.2	[0.01, 0.46]
	a50[early]	8.31	[6.78, 8.84]
Breeding	a50[late]	11.11	[10.13, 13.94]
	P[breed FBR]	0.68	[0.65, 0.7]
	P[breed NBR] (1990 - 1999)	0.47	[0.42, 0.51]
	P[breed NBR] (2000)	0.59	[0.06, 0.98]
	P[breed NBR] (2001)	0.49	[0.02, 0.97]
	P[breed NBR] (2002)	0.91	[0.76, 0.99]
	P[breed NBR] (2003)	0.89	[0.77, 0.99]
	P[breed NBR] (2004)	0.89	[0.82, 0.97]
	P[breed NBR] (2005)	0.86	[0.78, 0.93]
	P[breed NBR] (2006)	0.33	[0.03, 0.68]
	P[breed NBR] (2007)	0.37	[0.29, 0.48]
	P[breed NBR] (2008)	0.58	[0.5, 0.7]
	P[breed NBR] (2009)	0.44	[0.36, 0.53]
	P[breed NBR] (2010)	0.37	[0.31, 0.44]
	P[breed NBR] (2011)	0.38	[0.32, 0.46]
	P[breed NBR] (2012)	0.35	[0.29, 0.42]
	P[breed NBR] (2013)	0.42	[0.35, 0.49]
	P[success]	0.36	[0.3, 0.43]
Resight	R[mature] (2000-2005)	0.22	[0.19, 0.26]
	R[mature] (2006 onwards)	0.43	[0.41, 0.46]
	R[immature] (2000-2005)	2.1	[1.64, 2.91]
	R[immature] (2006 onwards)	0.99	[0.74, 1.45]
	R[non-breeder] (2000-2005)	0.89	[0.41, 1]
	R[non-breeder] (2006 onwards)	0.98	[0.9, 1]
	δ	13.29	[10.2, 19.21]

Table A2: Posterior parameter estimates for the “no unknown-age mark recapture data” sensitivity run.

Category	Parameter	Median	95% CI
N0	N0	10752.35	[8601.42, 14424.81]
Survivorship	S[adult] (1990 - 1999)	0.96	[0.92, 1]
	S[adult] (2000)	0.85	[0.39, 0.99]
	S[adult] (2001)	0.9	[0.56, 1]
	S[adult] (2002)	0.96	[0.88, 1]
	S[adult] (2003)	0.97	[0.92, 1]
	S[adult] (2004)	0.98	[0.92, 1]
	S[adult] (2005)	0.86	[0.73, 0.99]
	S[adult] (2006)	0.82	[0.71, 0.96]
	S[adult] (2007)	0.95	[0.89, 0.99]
	S[adult] (2008)	0.92	[0.86, 0.97]
	S[adult] (2009)	0.93	[0.87, 0.98]
	S[adult] (2010)	0.89	[0.83, 0.95]
	S[adult] (2011)	0.92	[0.86, 0.97]
	S[adult] (2012)	0.99	[0.93, 1]
	S[adult] (2013)	0.99	[0.94, 1]
Maturation	S[juvenile]	0.88	[0.87, 0.89]
	P[early] (1990 - 2005)	0.9	[0.64, 1]
	P[early] (2006 onwards)	0.3	[0.18, 0.38]
	a50[early]	8.61	[8.09, 8.95]
	a50[late]	13.46	[11.86, 13.98]
Breeding	P[breed FBR]	0.59	[0.54, 0.64]
	P[breed NBR] (1990 - 1999)	0.36	[0.27, 0.45]
	P[breed NBR] (2000)	0.31	[0.1, 0.65]
	P[breed NBR] (2001)	0.38	[0.2, 0.6]
	P[breed NBR] (2002)	0.56	[0.4, 0.79]
	P[breed NBR] (2003)	0.69	[0.52, 0.91]
	P[breed NBR] (2004)	0.96	[0.85, 1]
	P[breed NBR] (2005)	0.96	[0.82, 1]
	P[breed NBR] (2006)	0.49	[0.03, 0.96]
	P[breed NBR] (2007)	0.61	[0.45, 0.88]
	P[breed NBR] (2008)	0.9	[0.71, 0.99]
	P[breed NBR] (2009)	0.71	[0.54, 0.92]
	P[breed NBR] (2010)	0.54	[0.41, 0.69]
	P[breed NBR] (2011)	0.53	[0.42, 0.66]
	P[breed NBR] (2012)	0.53	[0.43, 0.64]
	P[breed NBR] (2013)	0.49	[0.39, 0.58]
	P[success]	0.45	[0.37, 0.54]
Resight	R[mature] (2000-2005)	0.48	[0.03, 0.97]
	R[mature] (2006 onwards)	0.49	[0.03, 0.97]
	R[immature] (2000-2005)	2.74	[2.21, 3.07]
	R[immature] (2006 onwards)	1.33	[1.07, 1.5]
	R[non-breeder] (2000-2005)	0.84	[0.23, 0.99]
	R[non-breeder] (2006 onwards)	0.97	[0.89, 1]
	δ	18.18	[14.36, 19.92]

Table A3: Posterior parameter estimates for the “female only data” sensitivity run.

Category	Parameter	Median	95% CI
N0	N0	5378.95	[4176.05, 7234.46]
Survivorship	S[adult] (1990 - 1999)	0.95	[0.9, 0.99]
	S[adult] (2000)	0.98	[0.88, 1]
	S[adult] (2001)	0.99	[0.94, 1]
	S[adult] (2002)	0.99	[0.95, 1]
	S[adult] (2003)	0.98	[0.95, 1]
	S[adult] (2004)	0.97	[0.91, 1]
	S[adult] (2005)	0.85	[0.75, 0.99]
	S[adult] (2006)	0.94	[0.79, 1]
	S[adult] (2007)	0.89	[0.82, 0.96]
	S[adult] (2008)	0.91	[0.83, 0.98]
	S[adult] (2009)	0.92	[0.84, 0.99]
	S[adult] (2010)	0.89	[0.81, 0.98]
	S[adult] (2011)	0.88	[0.79, 0.97]
	S[adult] (2012)	0.9	[0.8, 0.99]
	S[adult] (2013)	0.84	[0.69, 0.98]
Maturation	P[early] (1990 - 2005)	0.52	[0.2, 0.91]
	P[early] (2006 onwards)	0.36	[0.03, 0.8]
	a50[early]	6.83	[5.15, 7.78]
	a50[late]	9.67	[8.39, 13.5]
Breeding	P[breed FBR]	0.68	[0.65, 0.72]
	P[breed NBR] (1990 - 1999)	0.48	[0.43, 0.55]
	P[breed NBR] (2000)	0.55	[0.4, 0.75]
	P[breed NBR] (2001)	0.54	[0.4, 0.74]
	P[breed NBR] (2002)	0.73	[0.59, 0.88]
	P[breed NBR] (2003)	0.78	[0.66, 0.89]
	P[breed NBR] (2004)	0.87	[0.78, 0.94]
	P[breed NBR] (2005)	0.82	[0.73, 0.9]
	P[breed NBR] (2006)	0.25	[0.01, 0.62]
	P[breed NBR] (2007)	0.38	[0.32, 0.48]
	P[breed NBR] (2008)	0.61	[0.53, 0.69]
	P[breed NBR] (2009)	0.49	[0.41, 0.58]
	P[breed NBR] (2010)	0.42	[0.35, 0.5]
	P[breed NBR] (2011)	0.4	[0.34, 0.48]
	P[breed NBR] (2012)	0.45	[0.38, 0.53]
	P[breed NBR] (2013)	0.49	[0.4, 0.6]
Resight	P[success]	0.57	[0.45, 0.7]
	R[mature] (2000-2005)	0.2	[0.16, 0.25]
	R[mature] (2006 onwards)	0.25	[0.22, 0.29]
	R[immature] (2000-2005)	2.71	[1.5, 3.62]
	R[immature] (2006 onwards)	1.31	[0.68, 2]
	R[non-breeder] (2000-2005)	0.71	[0.06, 0.99]
	R[non-breeder] (2006 onwards)	0.88	[0.59, 0.99]
	δ	14.73	[7.46, 19.58]

Appendix III: Maximum survivorship estimate

The description of work for this project states that: *Given that extensive mark-recapture information from a long time period is available for Antipodean wandering albatross, comprehensive modelling of that population should generate estimates of average survival that could be used to refine the seabird risk assessment for this population....* The survival estimates used in the risk assessment should, to the extent possible, represent survivorship under optimal conditions (Richard & Abraham, 2013a). Given the temporal changes in survival we have estimated here, we therefore performed an additional model fit with the adult survivorship estimated as a constant value from 1990 – 2004. From the basecase model fit, this time period has a high and stable survivorship estimate, with median estimates of $S \geq 0.95$ (Table 5). For 2005 and 2006 survivorship is poorly estimated (Figure A1), and thereafter it remains at $S < 0.95$ until 2012. We therefore concluded that a constant estimate of survivorship for this early blocked period would be most appropriate. Apart from this change the model was exactly the same as the basecase. The posterior distribution is shown in Figure A2. Currently a value of $\mu = 0.957; \sigma = 0.007$ is used in the most recent seabird risk assessment (Table A-1; Richard & Abraham, 2015). From the current model we can report revised mean value that is almost identical, but with a larger standard error $\mu = 0.956; \sigma = 0.024$.

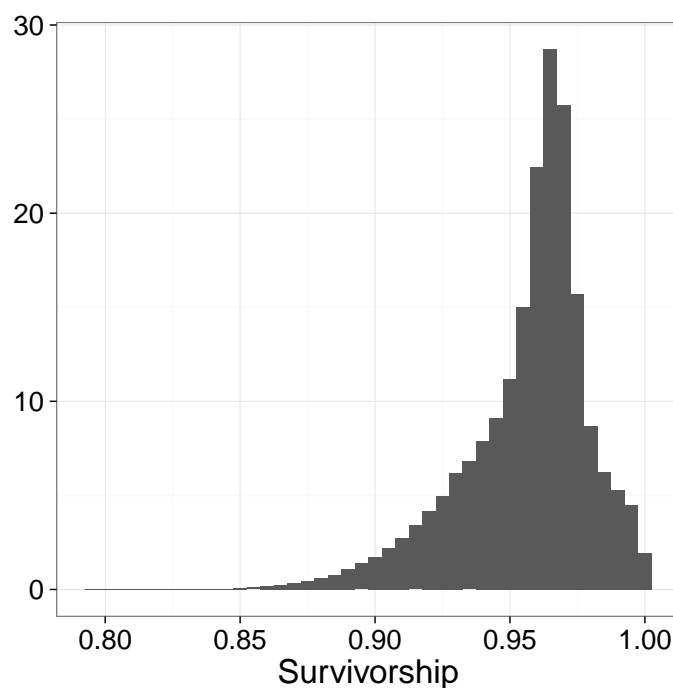


Figure A2: Posterior distribution of “maximum” survivorship, represented as a constant value for years 1990 – 2004.