Penguin power analyses using the approach recommended by the international panel: methods and the complete set of results

A. Ross-Gillespie and D. S. Butterworth[1]

Contact email: *mlland028@myuct.ac.za*

1 Introduction

The panel report for the 2015 International Stock Assessment Workshop (IWS) provided a detailed outline of the penguin power analysis procedure which it recommended. Over the course of the last year, this procedure has nevertheless needed to be refined in consultation at times with two of the panel members, and with reference to the Penguin Task Team (PTT). This document provides the details of the refined methods and the data used, and also the results for the set of runs prioritised by the PTT in implementing the panel's recommendation.

2 Data

The data utilised in these analyses are those from Coetzee (2015). The panel for IWS 2015 recommended that a standardisation exercise be undertaken to evaluate whether there is a month-effect evident in the data. The details and the results of this standardisation exercise are provided in Appendix A. It was found that the standardised results did not differ substantially from the original data, and therefore the non-standardised data were used for these analyses as per recommendation A.2.15 of the panel report (Dunn *et al.* 2015). Panel recommendation A.2.7 (Dunn *et al.* 2015) states that instances of only three samples in a year could arguably be excluded from the analysis. This is relevant for only the foraging trip length data for Dassen Island in the years 2003 and 2009. The power analysis was conducted for both the case where the N=3 points were included and where they were excluded. In this document, however, results are only reported for the case where the N=3 points were included, for reasons explained in Appendix B.

Of the six response variables for which data were available, for only one — fledging success — could a Threshold be determined in terms of the panel's criterion set out in recommendation A.2.4. However the PTT decided to conduct analyses for three of the other variables as well: chick growth, chick condition and foraging trip length, under the assumption of a response that was linear through the origin. The variables for foraging trip duration (because of high correlation with foraging trip length) and the active nest proportions were dropped. Table 1 summarises the number of data points for each of the four data sets.

Given the large volume of analyses that were required, the PTT decided that only anchovy catches would be considered, following recommendation A.2.8 and Table 1 of the panel report (Dunn *et al.* 2015). In addition, only the 18km closure catches have been considered in the analyses presented here, which conveniently

[1]Marine Resource Assessment and Management Group, University of Cape Town, Rondebosch, 7701

removes the need for simulating increased catches in areas outside the closed regions in the years in which the island is closed to fishing. Alternative catch assumptions may need to be investigated once the methods and results presented here have been reviewed.

3 Methods

A detailed outline of the proposed power analysis approach was provided by the panel in their report for IWS 2015 (Dunn *et al.* 2015). During the course of the implementation of the recommendations, several clarifications and refinements were necessary and were undertaken in consultation with A. Punt and A. Parma, and later confirmed with the PTT. Table 2 provides a summary of the final procedure that has been followed for the analyses presented here.

The aim of the power analysis is as follows. If the true effect of fishing on the penguin population is less[2] than some negative threshold, after how many years of further data collection would the island closure experiment be able to detect with 80% probability that the effect is indeed less than this threshold?

In order to address this question, a linear model is fit to the different data sets in the same manner as has been done in the past. As per recommendation A.2.6 of the panel report (Dunn *et al.* 2015), the sub-regional biomass approach was evaluated:

$$ln(F_{y,i,s}) = K + \alpha_y + \gamma_s + \lambda \frac{C_{y,i}}{\bar{C}_i} + \delta_i X_{y,i} + \epsilon_{y,i,s} \tag{1}$$

where

- $F_{y,i,s}$ is the penguin response variable for series s for island i in year y,
- α_y is a year effect reflecting prevailing environmental conditions (assumed to be the same each year, random variation excepted, for both islands in a pair),
- γ_s is an island series effect (simply equal to island in most cases, but for fledging success there are two series for Robben Island),
- λ_i is a fishing effect,
- $C_{y,i}$ is the anchovy catch taken in year y in the neighbourhood of island i,
- $\bar{C}_{y,i}$ is the average anchovy catch taken over the years for which data are available, excluding years in which island i is closed,
- δ_i is a closure effect,
- $X_{y,i}$ is closure variable that is set to 1 in the years when the island is open to fishing and 0 when it is closed, and
- $\epsilon_{y,i,s}$ is an error term.

A value for a Threshold T in the penguin response data needs to be assumed (below this Threshold the penguin population is assumed to have been meaningfully impacted, see Section 3.1 for more details) and

[2] In these analyses, "less" equates to a more negative (i.e. more adverse) impact on the penguin population.

the probability that λ (or δ depending on the form of the model) is less than this Threshold is evaluated[3]. This is done by generating 1000 simulated data sets, and for each simulation i fixing λ at incremented values on a defined range and evaluating

$$P_i(\lambda_i < \mathrm{T}) = \int_{-\infty}^{T} \frac{1}{\sqrt{2\pi\sigma_{\hat{\lambda}_i}}} e^{-(x-\hat{\lambda}_i)^2/(2\sigma_{\hat{\lambda}_i})^2} dx \tag{2}$$

where $\hat{\lambda}_i$ is the model estimate from Equation 1 when the model is fit to data that are generated under the assumption that λ is fixed at λ_i.

The detection probability is defined as the number of times when analysing those 1000 simulations that $P_i(\lambda_i < \mathrm{T})$ is larger than P_{min}, where P_{min} is determined as described in Step 2 of Table 2. The detection probability is then integrated over a prior distribution for λ/δ to obtain a single integrated detection probability for each dataset and model combination, as described in Step 6 of Table 2.

This process is repeated simulating 1, 5, 10, 15 and 20 years into the future to ascertain the length of time the closure experiment needs to continue in order to be able to detect a meaningful fishing/closure effect if such an effect indeed applies.

More in-depth details of the process and the intermediate steps are given in Table 2, and Figure 1 provides an example illustration of the integration process. Details of the data generation process can be found in MARAM/IWS/DEC15/PengD/P1.

Computations were performed in R version 3.2.3 (R Core Team 2014).

3.1 The Threshold

The value of the threshold (referred to from now on as the Threshold, or T for short) is a biological value determined externally to the power analysis approach. It provides a decision on what proportional change in an observable penguin population variable (i.e. a change in one of the different response variables such as fledging success, chick growth etc.) would be considered to correspond to a meaningful change in the rate of penguin population growth. Since the equations for the power analysis have been set up in manner that a decrease in the observed response variable equates to a negative impact on the penguin population, the Threshold also has a negative value. A change of 1% in the penguin data, corresponding closely to a Threshold of -0.1 in the λ/δ space, was used for the base assumption for these analyses. This was based on recommendation A.2.1 of the panel report, which states that the Threshold "should be computed using a population dynamics model such as the simple model in MARAM/IWS/DEC15/PengD/BG4 or the penguin population dynamics developed by Robinson et al. (2015) given a management objective of a pre-specified change in population growth rate following elimination of fishing near islands (and assuming that fishing impacts only one population dynamics parameter)" (Dunn *et al.* 2015). See Appendix C for more details.

[3]Equation 1 is set up so that a negative value estimated for λ or δ equates to a roughly similar negative change in the penguin response variable.

3.2 Biases

There are two forms of bias that have been taken into account in these power analyses.

3.2.1 The P_{min} bias analysis in the power analysis approach

This bias is defined as the extent to which the detection probability with P_{min}=0.5 differs from 0.5 when λ (or δ for the closure model) is equal to the Threshold. To avoid confusion with other sources of bias, this bias is denoted hereafter as the "P_{min} bias". This bias is evaluated by generating data under the assumption that λ (or δ) is equal to the Threshold, and then calculating the detection probability in the same way as was done for the original analyses, except that the actual historical data are replaced by data generated with λ (or δ) equal to the Threshold (see Step 2 of Table 2).

3.2.2 Adjusting for bias in the GLM estimate — "GLM bias"

In the analyses undertaken for IWS 2015, it was established that when data are generated using the GLM point estimates corresponding to the real data, and when the same GLM was re-applied to those generated data, the estimated λ (or δ) values differed from the true underlying λ (or δ) used to generate the data. We term this bias the "GLM bias". The GLM bias is evaluated by simulating the historical data (i.e. data for those years for which actual data are available only) and re-fitting the GLM to the generated data (see Step 4 of Table 2 for technical details).

4 Weighting process

The panel for IWS 2015 recommended that for each data set and each EM, the results be weighted across the OMs with respect to two aspects.

1. The P_{min} bias values should be weighted across OMs to obtain a single bias adjustment value for each data set and each EM.
2. The integrated detection probability curves should be weighted across the OMs to obtain a single detection probability curve for each data set and EM.

When weighting the results, consideration should be given to the fact that the catch only and catch+closure OMs are effectively "double-counted" as these are evaluated for two different catch-biomass correlation values. In light of this, these two OMs should receive half the weight of the closure only OMs. The weighted averages reported have been calculated on this basis.

5 Model variants evaluated

In order to reduce the substantial number of analyses (and the associated amount of output to process and interpret) that were initially proposed by the panel for IWS 2015, the PTT agreed on a reduced set of runs (as per a meeting held in 9 August 2016, summarised in an email communication from D.S. Butterworth to

the PTT on 13 August 2016). Table 3 lists the total number runs prioritised by PTT, and for which results are reported in this document.

6 Results

Table 4 reports the adjusted P_{min} values, i.e. the values of P_{min} for which the probability $P_i(\lambda_i < \mathrm{T})$ is 0.5 when λ/δ is equal to the Threshold, and which are used to evaluate the detection probabilities (note that these depend, though to a limited extent only, on the length of the data series available).

Figures 2a and 2b are a graphical illustration of the original and GLM-adjusted estimates of λ/δ for Dassen and Robben Island, and Table 5 summarises the number of times the estimates based on the existing data fall above zero, between 0 and the Threshold and below the Threshold.

Table 6 shows the integrated detection probabilities for (i) the case where the individual P_{min} values have been used (i.e. the results that the PTT has seen previously) and (ii) the case where the OM-weighted detection probabilities are used, i.e. a single P_min adjustment value obtained by weighting across OMs is used

Table 7 repeats the probabilities from Table 6 that use the OM-weighted P_{min}, and also includes the probabilities that arise when the individual probabilities from all OM for a given EM and data set combination are weighted according to (2) above. Table 8 extracts just these OM-weighted probabilities. Figure 3 provides a graphical illustration of the integrated detection probabilities from Table 8.

Table 9 reports the integrated detection probabilities for two cases (chick growth and fledging success), when a Threshold of -0.2 is assumed. Note that owing to time constraints, these runs were conducted for the cases where the OM matches the EM only, and as such the weighting across the 10 OMs as described in Section 4 was not implemented here.

Plots of the integration process (i.e. plots of the detection probability curves superimposed onto the assumed prior distributions similar to Figure 1) for all the runs in Table 7 are available in an addendum, MARAM/IWS/DEC16/Peng/P1b . These plots also illustrate the impact of the P_{min} bias adjustments from Table 4.

7 Discussion

The results provided need to be accorded more weight for the fledging success response variable, given that only in this instance has the panel's criterion for acceptability (their recommendation A.2.4) been met.

Two sets of the results provided are of particular importance. The first is the set of (GLM-bias-corrected) current fishing/closure effect estimates which are shown graphically in Figures 2a and 2b, and summarised in Table 5. Broadly speaking, any case for fishing having a negative impact on penguin overall reproductive success is stronger for Robben than for Dassen Island.

The second is the estimates of future detection probability reported in Figure 3 and Table 8. In most cases these have already or will within 5 years reach 80%, with results for fledging success at Dassen Island being a notable exception. This may seem surprising in some cases, given that the corresponding point estimates of λ/δ are positive at this time. To understand why, it is important to be clear what this probability represents: it is the chance, IF the true value of λ/δ is less than the Threshold (here -0.1), that the estimator concerned will output such a result (note that this is a CONDITIONAL result; it does NOT indicate the probability of this event irrespective of the possible actual value of λ/δ). The surprising cases are instances where the data series are short and consequently the standard errors for the current point estimates are large; that means that even if the current point estimate for λ/δ is above zero, there remains a substantial probability that the actual value is (perhaps well) below the Threshold, and consequently the (conditional) detection probability is estimated to be high.

Table 9 shows the sensitivity in some cases to the choice of a Threshold value of -0.2 rather than -0.1. Unsurprisingly the detection probabilities become considerably lower.

Appendix B includes an examination of the sensitivity of detection probability results to the values of σ_α, given that those are not that well determined, particularly in instances where a fix is needed when the estimate from the random effects model implemented in R is zero. These results show that fortunately this sensitivity is slight only, indicating that results for the probability of detection for such cases remain reliable.

Acknowledgements

Computations were performed using facilities provided by the University of Cape Town's ICTS High Performance Computing team: http://hpc.uct.ac.za.

References

Butterworth, D. S. 2015. Suggestions re further penguin power analysis and estimator simulation test in response to panel recommendations. Document Document MARAM/IWS/DEC15/PengD/BG4.

Coetzee, J. 2015. The current set of available data for evaluation of the Island Closure Feasibility Study. Document MARAM/IWS/DEC15/PengD/BG1.

Dunn, A., Haddon, M., Parma, A. M. and Punt, A. E. 2015. International Review Panel Report for the 2015 International Fisheries Stock Assessment Workshop, 30 Nov - 4 December 2015, University of Cape Town.

Penguin Island Closure Task Team. 2015. Specifications for the operating models to evaluate bias in estimation methods in accordance with recommendation A.1 of the 2014 International Review Panel. Document MARAM/IWS/DEC15/PengD/P1.

R Core Team. 2014. R: A Language and Environment for Statistical Computing.

Robinson, W., Butterworth, D.S. and É.E Plagányi. 2015. Quantifying the projected impact of the South African sardine fishery on the Robben Island penguin colony. *ICES Journal of Marine Science* 72: 1822-1833.

Table 1: Summary of the data sets. The first column lists the total number of years which the data span, while the remaining three columns provide a break-down of the number of individual data points for each island and in total. One "individual data point" corresponds to the (unstandardised) average for the data collected in a given year. The foraging trip length values correspond to the revised data set with the years 2003 and 2004 included, and also with the data points corresponding to a sample size of three included — this is the data set that was used as input for the results presented in this document.

			Number of data points		
	Data type	No. years	Dassen	Robben	Total
(I)	Chick growth	13	12	7	19
(II)	Chick Condition	7	6	7	13
(III)	Foraging trip length	8	8	6	14
(IV)	Fledging success	23	9	23	32

Table 2: Summary of the power analysis procedure.

Step	Description
1	**Generating data**
(a)	Apply the OM to the actual data to get the estimates for V_{OM} (where V_{OM} is λ for a catch OM and δ for a closure OM) in terms of point estimate and standard error.The OM is used to condition other parameters.
(b)	Apply the EM to the actual data to get the estimate for V_{EM} (where V_{EM} is λ for a catch EM and δ for a closure EM) in terms of point estimate and standard error.
(c)	Fixing V_{OM} at a range of values on the interval $[\mu^{EM}_{data} - 3(\sigma^{EM}_{data})$; Threshold$]$[a], condition the remaining parameters of the OM for each value of V_{OM}. and use these estimates to generate future simulated data using the OM. These simulated data are appended to actual historical data.
2	**P_{min} bias**[b]
(a)	Use the OM model to generate past and future data for V_{OM}=Threshold.
(b)	Apply EM to data set from 2(a) and calculate detection probability at V_{EM}=Threshold to evaluate the value of P_{min} for which this detection probability at V_{EM}=Threshold is 0.5.
3	**Detection probability**
(a)	Apply EM to the data set generated in 1(c) to calculate detection probability with the bias-adjusted P_{min} value from 2(b), i.e. calculate the number of times in the 1000 simulations that $P_i(\lambda_i <$ T) is greater than the adjusted P_{min}. The detection probability is plotted against the V_{EM} variable (λ if the EM is a catch model or δ if the EM is a closure model).
4	**GLM bias**
(a)	Evaluate the GLM bias as follows. (i) Generate the historical data with the EM-like-OM[c] and apply the EM model to these data to obtain the mean from $\bar{V}_{EM}$ from the V_{EM}'s estimated for each of the 1000 generated data sets. (ii) Apply the EM to the actual historical data to obtain μ^{EM}_{data} as for 1(b). (iii) The bias is defined as $B = \bar{V}_{EM} - \mu^{EM}_{data}$. (iv) The adjusted value used for the mean of the starting distribution in Step 5 is $\mu^{EM*}_{data} = \mu^{EM}_{data} - B$. (v) There will thus be one GLM bias for each EM, irrespective of the OM. This (and this approach) follows conceptually from the fact that in reality one knows only the EM, whereas there are innumerable OMs which could reflect the underlying reality.
5	**Starting distribution**
(a)	The prior distribution is taken to be a normal distribution with mean from 4(a) and standard deviation from 1(b).
6	**Integrated detection probability** The detection probability is taken from 3(a) for the variable V_{EM}. The integration calculation is performed over the interval $[\mu^{EM}_{data} - 3(\sigma^{EM}_{data})$; Threshold$]$, where μ^{EM}_{data} and σ^{EM}_{data} are the EM estiamtes from the data as described in 1(b). Figure 1 provides an illustrative example of the integration process.
7	**Catch + closure OMs** In a case where the OM is a catch + closure model, the requirement is to effectively have a combined $\lambda + \delta <$ Threshold. Since there are an infinite number of combinations of λ and δ with which this can be achieved, combinations along the diagonal (i.e. λ=δ) were used, with λ (and thus δ) taking on values less than the negative Threshold value divided by two to reduce the computational burden.

[a] The interval over which V_{OM} is calculated is derived by applying the EM to the actual historical data, since the integration in Step 6 needs to be performed over the starting distribution for V_{EM}. Note that μ^{EM*}_{data} is the value of the GLM estimate μ^{EM}_{data} from 1(b) adjusted for the GLM bias as described in Step 4.

[b] The final P_{min} bias is a weighted average over the different OMs to produce a single P_{min} bias for the EM concerned.

[c] The EM-like OM is an OM that is has the same structure as the EM. Note that catch-biomass correlation is ignored in the EM for the catch model, so that a catch-biomass correlation of 0.2 will be assumed to generate the data with this "EM-like OM as the underlying OM value would not be known. Note that this means that bias adjusted estimate μ^{EM*}_{data} in Table 7 is independent of whether the OM correlation is 0.2 or 0.4 for the catch model.

Table 3: A list of the reduced set of runs to be run as a first priority, as agreed on by the PTT. Cells highlighted in blue indicate runs where the OM matches the EM, for which the results have been included in this document. Runs highlighted in purple are ones where the OM and the EM do not match. Cells highlighted in green correspond to the catch plus closure OMs, for which both a λ and a δ need to be estimated.

Run #	Data set	OM	EM	Correlation
1	Chick growth	Catch only	Catch only	0.2
2			Catch only	0.4
4			Closure only	0.2
5			Closure only	0.4
3		Closure only	Closure only	NA
6			Catch only	NA
7		Catch+closure	Catch only	0.2
8			Catch only	0.4
9			Closure only	0.2
10			Closure only	0.4
11	Chick condition	Catch only	Catch only	0.2
12			Catch only	0.4
14			Closure only	0.2
15			Closure only	0.4
13		Closure only	Closure only	NA
16			Catch only	NA
17		Catch+closure	Catch only	0.2
18			Catch only	0.4
19			Closure only	0.2
20			Closure only	0.4
21	Foraging length	Catch only	Catch only	0.2
22			Catch only	0.4
24			Closure only	0.2
25			Closure only	0.4
23		Closure only	Closure only	NA
26			Catch only	NA
27		Catch+closure	Catch only	0.2
28			Catch only	0.4
29			Closure only	0.2
30			Closure only	0.4
31	Fledging successs	Catch only	Catch only	0.2
32			Catch only	0.4
34			Closure only	0.2
35			Closure only	0.4
33		Closure only	Closure only	NA
36			Catch only	NA
37		Catch+closure	Catch only	0.2
38			Catch only	0.4
39			Closure only	0.2
40			Closure only	0.4

Table 4: The values of P_{min} at which $P_i(\lambda_i < \mathrm{T})$ from Equation 2 is 0.5 when λ/δ is equal to the Threshold (here -0.1). The runs have been sorted so that for any given data set, the runs with a common EM are grouped together. After each such grouping, the weighted P_{min} bias is listed for each year. P_{min} values for catch only and catch+closure OMs have received half the weight of those for closure only OMs, since the former are "double-counted" owing to the two correlation values.

Data set	OM	EM	Cor	(a) Dassen Island 1	5	10	15	20	(b) Robben Island 1	5	10	15	20
(I) Chick growth	1. Catch	Catch	0.2	0.46	0.44	0.42	0.41	0.42	0.49	0.48	0.49	0.49	0.47
	2. Catch	Catch	0.4	0.42	0.40	0.37	0.37	0.36	0.45	0.43	0.43	0.43	0.40
	6. Closure	Catch	-	0.11	0.08	0.06	0.05	0.04	0.13	0.11	0.07	0.05	0.03
	7. Ca+Cl	Catch	0.2	0.20	0.18	0.15	0.13	0.15	0.24	0.22	0.18	0.15	0.12
	8. Ca+Cl	Catch	0.4	0.14	0.11	0.09	0.08	0.08	0.21	0.18	0.14	0.11	0.09
	Catch EM P_{min} bias correction			0.24	0.21	0.19	0.18	0.18	0.28	0.26	0.23	0.21	0.19
	3. Closure	Closure	-	0.51	0.48	0.47	0.48	0.50	0.50	0.50	0.51	0.51	0.49
	4. Catch	Closure	0.2	0.61	0.63	0.65	0.67	0.69	0.60	0.59	0.63	0.66	0.66
	5. Catch	Closure	0.4	0.62	0.64	0.67	0.68	0.69	0.58	0.61	0.61	0.63	0.63
	9. Ca+Cl	Closure	0.2	0.57	0.58	0.60	0.61	0.63	0.54	0.56	0.57	0.57	0.58
	10. Ca+Cl	Closure	0.4	0.56	0.55	0.56	0.55	0.57	0.55	0.55	0.57	0.57	0.58
	Closure EM P_{min} bias correction			0.58	0.58	0.59	0.60	0.62	0.56	0.57	0.58	0.59	0.59
(II) Chick condition	11. Catch	Catch	0.2	0.48	0.49	0.48	0.47	0.45	0.46	0.46	0.46	0.46	0.44
	12. Catch	Catch	0.4	0.47	0.47	0.44	0.44	0.40	0.45	0.44	0.44	0.41	0.41
	16. Closure	Catch	-	0.15	0.10	0.06	0.04	0.02	0.16	0.11	0.07	0.04	0.03
	17. Ca+Cl	Catch	0.2	0.27	0.22	0.18	0.16	0.13	0.31	0.27	0.23	0.19	0.17
	18. Ca+Cl	Catch	0.4	0.24	0.20	0.17	0.14	0.11	0.29	0.25	0.19	0.16	0.15
	Catch EM P_{min} bias correction			0.29	0.26	0.23	0.21	0.19	0.30	0.27	0.24	0.22	0.20
	13. Closure	Closure	-	0.51	0.53	0.52	0.51	0.51	0.50	0.52	0.51	0.48	0.49
	14. Catch	Closure	0.2	0.67	0.70	0.72	0.75	0.76	0.65	0.66	0.70	0.73	0.75
	15. Catch	Closure	0.4	0.65	0.70	0.73	0.77	0.79	0.63	0.67	0.72	0.73	0.75
	19. Ca+Cl	Closure	0.2	0.55	0.58	0.57	0.58	0.62	0.59	0.60	0.60	0.63	0.62
	20. Ca+Cl	Closure	0.4	0.56	0.59	0.58	0.59	0.62	0.59	0.60	0.60	0.63	0.62
	Closure EM P_{min} bias correction			0.60	0.63	0.64	0.65	0.67	0.59	0.61	0.63	0.64	0.65
(III) Forage trip length	21. Catch	Catch	0.2	0.47	0.46	0.44	0.45	0.45	0.51	0.49	0.47	0.48	0.47
	22. Catch	Catch	0.4	0.44	0.43	0.40	0.42	0.41	0.49	0.46	0.44	0.44	0.44
	26. Closure	Catch	-	0.19	0.15	0.12	0.10	0.08	0.21	0.15	0.10	0.07	0.05
	27. Ca+Cl	Catch	0.2	0.33	0.28	0.27	0.24	0.22	0.40	0.35	0.31	0.27	0.25
	28. Ca+Cl	Catch	0.4	0.30	0.26	0.24	0.20	0.18	0.37	0.31	0.27	0.23	0.20
	Catch EM P_{min} bias correction			0.32	0.29	0.27	0.25	0.23	0.37	0.32	0.28	0.26	0.24
	23. Closure	Closure	-	0.49	0.50	0.50	0.50	0.50	0.47	0.48	0.47	0.47	0.47
	24. Catch	Closure	0.2	0.65	0.67	0.71	0.72	0.75	0.58	0.63	0.64	0.66	0.68
	25. Catch	Closure	0.4	0.65	0.67	0.71	0.72	0.75	0.59	0.63	0.63	0.66	0.69
	29. Ca+Cl	Closure	0.2	0.58	0.58	0.60	0.60	0.63	0.54	0.57	0.56	0.58	0.58
	30. Ca+Cl	Closure	0.4	0.55	0.54	0.60	0.60	0.60	0.54	0.57	0.56	0.58	0.59
	Closure EM P_{min} bias correction			0.59	0.60	0.63	0.63	0.66	0.54	0.57	0.58	0.59	0.61
(IV) Fledging success	31. Catch	Catch	0.2	0.36	0.38	0.38	0.36	0.33	0.23	0.22	0.23	0.23	0.23
	32. Catch	Catch	0.4	0.24	0.26	0.24	0.22	0.19	0.08	0.06	0.07	0.07	0.07
	36. Closure	Catch	-	0.13	0.13	0.10	0.07	0.05	0.04	0.03	0.02	0.02	0.02
	37. Ca+Cl	Catch	0.2	0.26	0.27	0.24	0.22	0.20	0.11	0.10	0.09	0.09	0.08
	38. Ca+Cl	Catch	0.4	0.18	0.19	0.16	0.14	0.11	0.03	0.02	0.02	0.02	0.02
	Catch EM P_{min} bias correction			0.21	0.22	0.20	0.18	0.16	0.09	0.08	0.08	0.08	0.07
	33. Closure	Closure	-	0.49	0.48	0.50	0.49	0.50	0.46	0.47	0.48	0.48	0.50
	34. Catch	Closure	0.2	0.56	0.59	0.60	0.62	0.63	0.53	0.55	0.58	0.61	0.60
	35. Catch	Closure	0.4	0.60	0.60	0.63	0.62	0.65	0.59	0.58	0.59	0.59	0.60
	39. Ca+Cl	Closure	0.2	0.54	0.54	0.56	0.56	0.57	0.54	0.55	0.54	0.55	0.56
	40. Ca+Cl	Closure	0.4	0.54	0.55	0.56	0.57	0.57	0.54	0.55	0.54	0.55	0.56
	Closure EM P_{min} bias correction			0.55	0.55	0.57	0.57	0.59	0.53	0.54	0.55	0.56	0.56

Table 5: Summary of the number of λ/δ values for which the GLM-bias-adjusted EM estimates fall above zero, between 0 and the Threshold and below the Threshold. These results are shown graphically in Figures 2a and 2b. The three columns at the end downweight the counts corresponding to catch only and catch+closure OMs by a factor of 50%. This is in line with the panel recommendation (see Appendix A of Dunn *et al.* (2015) that when combining results the catch and closure approaches be given equal weighting. Since the catch only and the catch+closure OMs are run for two different correlation values, they are effectively "double-counted" and therefore need to be downweighted.

	λ		δ		Total	Weighted		
	Dassen	Robben	Dassen	Robben		Dassen	Robben	Total
> 0	20	5	15	10	50	21	9	30
$-0.1 < \lambda/\delta < 0$	0	10	5	0	15	3	6	9
< -0.1	0	5	0	10	15	0	9	9

Table 6: Integrated detection probabilities for both islands and for two cases: (i) the case where a separate P_{min} bias adjustment value (coloured rows from Table 4) is used for each OM (i.e. the results as seen previously, with the catch+closure runs now included) and (ii) the case where the same OM-weighted P_{min} bias adjustment value (white rows in Table 4) is used for all OMs for a given EM. Grey cells indicate that the detection probability exceeds 0.80. Orange indicate cases where the present bias-adjusted λ/δ estimate is less than the Threshold.

				(a) Dassen Island												(b) Robben Island										
						(i) Individual P_{min} bias					(ii) OM-weighted P_{min} bias							(i) Individual P_{min} bias					(ii) OM-weighted P_{min} bias				
Data set	**OM**	**EM**	**Cor**	μ_{data}^{EM*}	**se**	**1**	**5**	**10**	**15**	**20**	**1**	**5**	**10**	**15**	**20**	μ_{data}^{EM*}	**se**	**1**	**5**	**10**	**15**	**20**	**1**	**5**	**10**	**15**	**20**
(I) Chick growth	1. Catch	Catch	0.2	0.05	0.10	0.11	0.41	0.60	0.70	0.75	0.34	0.69	0.81	0.87	0.90	-0.01	0.15	0.64	0.81	0.90	0.93	0.94	0.86	0.93	0.96	0.97	0.98
	2. Catch	Catch	0.4	0.05	0.10	0.13	0.43	0.62	0.71	0.76	0.33	0.66	0.80	0.86	0.88	-0.01	0.15	0.66	0.84	0.91	0.93	0.95	0.86	0.93	0.96	0.97	0.97
	3. Closure	Closure	-	0.38	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.33	0.66	0.79	0.85	0.88	0.25	0.59	0.74	0.80	0.84
	4. Catch	Closure	0.2	0.38	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.33	0.64	0.75	0.82	0.86	0.39	0.66	0.79	0.85	0.89
	5. Catch	Closure	0.4	0.38	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.36	0.62	0.78	0.84	0.88	0.39	0.67	0.80	0.86	0.89
	6. Closure	Catch	-	0.04	0.10	0.48	0.57	0.66	0.70	0.73	0.17	0.28	0.38	0.42	0.42	-0.01	0.15	0.83	0.84	0.86	0.87	0.89	0.57	0.65	0.64	0.64	0.64
	7. Ca+Cl	Catch	0.2	0.05	0.10	0.33	0.53	0.66	0.73	0.73	0.25	0.46	0.59	0.66	0.69	-0.01	0.15	0.82	0.88	0.92	0.94	0.95	0.78	0.85	0.90	0.92	0.93
	8. Ca+Cl	Catch	0.4	0.05	0.10	0.46	0.62	0.71	0.76	0.77	0.23	0.40	0.53	0.58	0.61	-0.01	0.15	0.86	0.90	0.93	0.94	0.95	0.76	0.84	0.88	0.90	0.91
	9. Ca+Cl	Closure	0.2	0.39	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.36	0.66	0.79	0.86	0.89	0.34	0.65	0.79	0.85	0.88
	10. Ca+Cl	Closure	0.4	0.39	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.35	0.67	0.80	0.86	0.89	0.34	0.66	0.80	0.85	0.89
(II) Chick condition	11. Catch	Catch	0.2	0.01	0.18	0.79	0.93	0.96	0.97	0.98	0.92	0.97	0.98	0.99	0.99	-0.21	0.15	0.99	0.98	0.98	0.99	0.99	1.00	0.99	0.99	1.00	1.00
	12. Catch	Catch	0.4	0.01	0.18	0.80	0.94	0.97	0.97	0.98	0.92	0.98	0.98	0.99	0.99	-0.21	0.15	0.99	0.98	0.99	0.99	0.99	1.00	0.99	0.99	0.99	0.99
	13. Closure	Closure	-	-0.08	0.22	0.85	0.92	0.95	0.96	0.97	0.75	0.89	0.93	0.94	0.95	-0.13	0.20	0.88	0.92	0.95	0.96	0.96	0.77	0.88	0.92	0.93	0.94
	14. Catch	Closure	0.2	-0.07	0.22	0.71	0.91	0.96	0.97	0.98	0.79	0.94	0.97	0.98	0.99	-0.14	0.20	0.71	0.91	0.95	0.97	0.97	0.78	0.92	0.96	0.98	0.98
	15. Catch	Closure	0.4	-0.07	0.22	0.73	0.91	0.96	0.97	0.98	0.80	0.94	0.97	0.98	0.99	-0.14	0.20	0.74	0.90	0.95	0.97	0.97	0.78	0.93	0.96	0.98	0.98
	16. Closure	Catch	-	0.01	0.18	0.84	0.85	0.88	0.91	0.92	0.64	0.68	0.71	0.72	0.71	-0.20	0.15	0.97	0.95	0.95	0.95	0.95	0.93	0.87	0.84	0.82	0.83
	17. Ca+Cl	Catch	0.2	0.01	0.18	0.85	0.92	0.94	0.95	0.96	0.82	0.91	0.93	0.94	0.94	-0.20	0.15	0.99	0.98	0.98	0.98	0.98	0.99	0.98	0.98	0.98	0.98
	18. Ca+Cl	Catch	0.4	0.01	0.18	0.87	0.93	0.94	0.95	0.96	0.82	0.90	0.93	0.93	0.94	-0.20	0.15	0.99	0.98	0.98	0.98	0.98	0.99	0.98	0.98	0.98	0.98
	19. Ca+Cl	Closure	0.2	-0.09	0.22	0.85	0.94	0.97	0.98	0.98	0.80	0.93	0.96	0.97	0.97	-0.12	0.20	0.79	0.91	0.95	0.96	0.97	0.78	0.91	0.94	0.96	0.97
	20. Ca+Cl	Closure	0.4	-0.09	0.22	0.85	0.94	0.97	0.98	0.98	0.81	0.93	0.96	0.97	0.97	-0.12	0.20	0.80	0.91	0.95	0.96	0.97	0.79	0.91	0.94	0.96	0.97
(III) Forage trip length	21. Catch	Catch	0.2	0.29	0.25	0.36	0.74	0.86	0.90	0.92	0.52	0.84	0.92	0.95	0.96	0.20	0.24	0.33	0.75	0.91	0.94	0.95	0.42	0.84	0.95	0.97	0.98
	22. Catch	Catch	0.4	0.29	0.25	0.38	0.75	0.87	0.90	0.93	0.52	0.84	0.92	0.94	0.96	0.20	0.24	0.33	0.76	0.91	0.94	0.95	0.42	0.83	0.95	0.97	0.97
	23. Closure	Closure	-	0.19	0.29	0.23	0.59	0.78	0.85	0.88	0.12	0.48	0.67	0.77	0.81	0.18	0.28	0.21	0.57	0.74	0.82	0.87	0.12	0.45	0.65	0.74	0.80
	24. Catch	Closure	0.2	0.19	0.29	0.08	0.58	0.82	0.90	0.92	0.14	0.67	0.86	0.92	0.94	0.16	0.28	0.24	0.59	0.80	0.88	0.91	0.28	0.64	0.84	0.91	0.93
	25. Catch	Closure	0.4	0.19	0.29	0.08	0.59	0.82	0.90	0.92	0.14	0.67	0.86	0.92	0.94	0.16	0.28	0.23	0.59	0.80	0.88	0.91	0.28	0.64	0.84	0.91	0.93
	26. Closure	Catch	-	0.30	0.25	0.41	0.58	0.68	0.73	0.75	0.25	0.41	0.49	0.53	0.54	0.19	0.24	0.40	0.63	0.70	0.74	0.79	0.18	0.41	0.46	0.47	0.51
	27. Ca+Cl	Catch	0.2	0.30	0.25	0.37	0.70	0.81	0.86	0.89	0.38	0.69	0.81	0.86	0.88	0.19	0.24	0.30	0.71	0.85	0.90	0.92	0.33	0.73	0.87	0.91	0.92
	28. Ca+Cl	Catch	0.4	0.30	0.25	0.40	0.71	0.82	0.87	0.89	0.37	0.68	0.80	0.85	0.87	0.19	0.24	0.32	0.72	0.86	0.91	0.93	0.32	0.72	0.86	0.90	0.91
	29. Ca+Cl	Closure	0.2	0.19	0.29	0.09	0.58	0.82	0.89	0.91	0.09	0.55	0.80	0.88	0.91	0.16	0.28	0.19	0.61	0.82	0.88	0.92	0.18	0.60	0.81	0.88	0.91
	30. Ca+Cl	Closure	0.4	0.20	0.29	0.11	0.62	0.81	0.88	0.91	0.08	0.54	0.79	0.87	0.90	0.16	0.28	0.18	0.61	0.82	0.88	0.91	0.17	0.60	0.81	0.88	0.91
(IV) Fledging success	31. Catch	Catch	0.2	0.08	0.09	0.04	0.20	0.35	0.48	0.57	0.09	0.39	0.60	0.70	0.77	-0.09	0.08	0.52	0.82	0.88	0.92	0.93	0.97	0.95	0.97	0.98	0.98
	32. Catch	Catch	0.4	0.08	0.09	0.07	0.31	0.49	0.58	0.65	0.08	0.36	0.55	0.63	0.69	-0.09	0.08	0.99	0.95	0.96	0.97	0.98	0.97	0.94	0.96	0.97	0.97
	33. Closure	Closure	-	0.11	0.21	0.00	0.63	0.76	0.82	0.86	0.00	0.55	0.70	0.78	0.81	-0.27	0.23	0.99	0.99	0.99	0.99	0.99	0.98	0.98	0.99	0.99	0.99
	34. Catch	Closure	0.2	0.11	0.21	0.00	0.58	0.75	0.82	0.86	0.00	0.62	0.77	0.84	0.88	-0.27	0.23	0.97	0.98	0.99	0.99	0.99	0.97	0.98	0.99	0.99	0.99
	35. Catch	Closure	0.4	0.11	0.21	0.00	0.58	0.74	0.82	0.85	0.00	0.62	0.78	0.84	0.88	-0.27	0.23	0.96	0.97	0.99	0.99	0.99	0.97	0.98	0.99	0.99	0.99
	36. Closure	Catch	-	0.09	0.09	0.11	0.43	0.54	0.58	0.60	0.06	0.24	0.32	0.34	0.33	-0.09	0.08	1.00	0.94	0.95	0.95	0.95	0.97	0.86	0.84	0.85	0.85
	37. Ca+Cl	Catch	0.2	0.08	0.09	0.06	0.30	0.46	0.52	0.56	0.08	0.37	0.52	0.59	0.63	-0.08	0.08	0.88	0.87	0.90	0.93	0.94	0.97	0.90	0.92	0.94	0.94
	38. Ca+Cl	Catch	0.4	0.08	0.09	0.09	0.40	0.56	0.60	0.62	0.07	0.34	0.47	0.51	0.54	-0.08	0.08	1.00	0.97	0.97	0.98	0.98	0.97	0.88	0.89	0.91	0.91
	39. Ca+Cl	Closure	0.2	0.11	0.21	0.00	0.63	0.77	0.84	0.87	0.00	0.62	0.76	0.83	0.86	-0.26	0.23	0.98	0.98	0.99	0.99	0.99	0.98	0.98	0.99	0.99	0.99
	40. Ca+Cl	Closure	0.4	0.11	0.21	0.00	0.63	0.77	0.84	0.87	0.00	0.62	0.77	0.83	0.86	-0.26	0.23	0.98	0.98	0.99	0.99	0.99	0.98	0.98	0.99	0.99	0.99

Table 7: Integrated detection probabilities for the case when a single OM-weighted P_{min} bias adjustment value is used for each EM (i.e. method (ii) from Table 6 and the approach recommended by the panel). The runs have been sorted so that for any given data set, the runs with a common EM are grouped together. After each such grouping, the weighted detection probability is listed for each year. The probabilities for catch only and catch+closure OMs have received half the weight of those for closure only OMs, since the former are "double-counted" owing to the two correlation values. Grey cells indicate that the detection probability exceeds 0.80. Orange indicate cases where the present bias-adjusted λ/δ estimate is less than the Threshold.

				(a) Dassen Island							(b) Robben Island						
Data set	**OM**	**EM**	**Cor**	μ_{data}^{EM*}	**se**	**1**	**5**	**10**	**15**	**20**	μ_{data}^{EM*}	**se**	**1**	**5**	**10**	**15**	**20**
(I) Chick growth	1. Catch	Catch	0.2	0.05	0.10	0.34	0.69	0.81	0.87	0.90	-0.01	0.15	0.86	0.93	0.96	0.97	0.98
	2. Catch	Catch	0.4	0.05	0.10	0.33	0.66	0.80	0.86	0.88	-0.01	0.15	0.86	0.93	0.96	0.97	0.97
	6. Closure	Catch	-	0.04	0.10	0.17	0.28	0.38	0.42	0.42	-0.01	0.15	0.57	0.65	0.64	0.64	0.64
	7. Ca+Cl	Catch	0.2	0.05	0.10	0.25	0.46	0.59	0.66	0.69	-0.01	0.15	0.78	0.85	0.90	0.92	0.93
	8. Ca+Cl	Catch	0.4	0.05	0.10	0.23	0.40	0.53	0.58	0.61	-0.01	0.15	0.76	0.84	0.88	0.90	0.91
	Catch EM, aggregated over OMs					0.25	0.46	0.58	0.63	0.65			0.73	0.81	0.83	0.84	0.84
	3. Closure	Closure	-	0.38	0.14	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.25	0.59	0.74	0.80	0.84
	4. Catch	Closure	0.2	0.38	0.14	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.39	0.66	0.79	0.85	0.89
	5. Catch	Closure	0.4	0.38	0.14	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.39	0.67	0.80	0.86	0.89
	9. Ca+Cl	Closure	0.2	0.39	0.14	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.34	0.65	0.79	0.85	0.88
	10. Ca+Cl	Closure	0.4	0.39	0.14	0.00	0.00	0.00	0.00	0.00	0.04	0.16	0.34	0.66	0.80	0.85	0.89
	Closure EM, aggregated over OMs					0.00	0.00	0.00	0.00	0.00			0.34	0.64	0.78	0.84	0.88
(II) Chick condition	11. Catch	Catch	0.2	0.01	0.18	0.92	0.97	0.98	0.99	0.99	-0.21	0.15	1.00	0.99	0.99	1.00	1.00
	12. Catch	Catch	0.4	0.01	0.18	0.92	0.98	0.98	0.99	0.99	-0.21	0.15	1.00	0.99	0.99	0.99	0.99
	16. Closure	Catch	-	0.01	0.18	0.64	0.68	0.71	0.72	0.71	-0.20	0.15	0.93	0.87	0.84	0.82	0.83
	17. Ca+Cl	Catch	0.2	0.01	0.18	0.82	0.91	0.93	0.94	0.94	-0.20	0.15	0.99	0.98	0.98	0.98	0.98
	18. Ca+Cl	Catch	0.4	0.01	0.18	0.82	0.90	0.93	0.93	0.94	-0.20	0.15	0.99	0.98	0.98	0.98	0.98
	Catch EM, aggregated over OMs					0.79	0.85	0.87	0.88	0.88			0.97	0.95	0.94	0.93	0.94
	13. Closure	Closure	-	-0.08	0.22	0.75	0.89	0.93	0.94	0.95	-0.13	0.20	0.77	0.88	0.92	0.93	0.94
	14. Catch	Closure	0.2	-0.07	0.22	0.79	0.94	0.97	0.98	0.99	-0.14	0.20	0.78	0.92	0.96	0.98	0.98
	15. Catch	Closure	0.4	-0.07	0.22	0.80	0.94	0.97	0.98	0.99	-0.14	0.20	0.78	0.93	0.96	0.98	0.98
	19. Ca+Cl	Closure	0.2	-0.09	0.22	0.80	0.93	0.96	0.97	0.97	-0.12	0.20	0.78	0.91	0.94	0.96	0.97
	20. Ca+Cl	Closure	0.4	-0.09	0.22	0.81	0.93	0.96	0.97	0.97	-0.12	0.20	0.79	0.91	0.94	0.96	0.97
	Closure EM, aggregated over OMs					0.79	0.92	0.96	0.97	0.97			0.78	0.91	0.95	0.96	0.97
(III) Forage trip length	21. Catch	Catch	0.2	0.29	0.25	0.52	0.84	0.92	0.95	0.96	0.20	0.24	0.42	0.84	0.95	0.97	0.98
	22. Catch	Catch	0.4	0.29	0.25	0.52	0.84	0.92	0.94	0.96	0.20	0.24	0.42	0.83	0.95	0.97	0.97
	26. Closure	Catch	-	0.30	0.25	0.25	0.41	0.49	0.53	0.54	0.19	0.24	0.18	0.41	0.46	0.47	0.51
	27. Ca+Cl	Catch	0.2	0.30	0.25	0.38	0.69	0.81	0.86	0.88	0.19	0.24	0.33	0.73	0.87	0.91	0.92
	28. Ca+Cl	Catch	0.4	0.30	0.25	0.37	0.68	0.80	0.85	0.87	0.19	0.24	0.32	0.72	0.86	0.90	0.91
	Catch EM, aggregated over OMs					0.38	0.65	0.74	0.77	0.79			0.31	0.66	0.76	0.78	0.80
	23. Closure	Closure	-	0.19	0.29	0.12	0.48	0.67	0.77	0.81	0.18	0.28	0.12	0.45	0.65	0.74	0.80
	24. Catch	Closure	0.2	0.19	0.29	0.14	0.67	0.86	0.92	0.94	0.16	0.28	0.28	0.64	0.84	0.91	0.93
	25. Catch	Closure	0.4	0.19	0.29	0.14	0.67	0.86	0.92	0.94	0.16	0.28	0.28	0.64	0.84	0.91	0.93
	29. Ca+Cl	Closure	0.2	0.19	0.29	0.09	0.55	0.80	0.88	0.91	0.16	0.28	0.18	0.60	0.81	0.88	0.91
	30. Ca+Cl	Closure	0.4	0.20	0.29	0.08	0.54	0.79	0.87	0.90	0.16	0.28	0.17	0.60	0.81	0.88	0.91
	Closure EM, aggregated over OMs					0.12	0.59	0.80	0.87	0.90			0.21	0.58	0.79	0.86	0.89
(IV) Fledging success	31. Catch	Catch	0.2	0.08	0.09	0.09	0.39	0.60	0.70	0.77	-0.09	0.08	0.97	0.95	0.97	0.98	0.98
	32. Catch	Catch	0.4	0.08	0.09	0.08	0.36	0.55	0.63	0.69	-0.09	0.08	0.97	0.94	0.96	0.97	0.97
	36. Closure	Catch	-	0.09	0.09	0.06	0.24	0.32	0.34	0.33	-0.09	0.08	0.97	0.86	0.84	0.85	0.85
	37. Ca+Cl	Catch	0.2	0.08	0.09	0.08	0.37	0.52	0.59	0.63	-0.08	0.08	0.97	0.90	0.92	0.94	0.94
	38. Ca+Cl	Catch	0.4	0.08	0.09	0.07	0.34	0.47	0.51	0.54	-0.08	0.08	0.97	0.88	0.89	0.91	0.91
	Catch EM, aggregated over OMs					0.07	0.32	0.46	0.52	0.55			0.97	0.90	0.90	0.92	0.92
	33. Closure	Closure	-	0.11	0.21	0.00	0.55	0.70	0.78	0.81	-0.27	0.23	0.98	0.98	0.99	0.99	0.99
	34. Catch	Closure	0.2	0.11	0.21	0.00	0.62	0.77	0.84	0.88	-0.27	0.23	0.97	0.98	0.99	0.99	0.99
	35. Catch	Closure	0.4	0.11	0.21	0.00	0.62	0.78	0.84	0.88	-0.27	0.23	0.97	0.98	0.99	0.99	0.99
	39. Ca+Cl	Closure	0.2	0.11	0.21	0.00	0.62	0.76	0.83	0.86	-0.26	0.23	0.98	0.98	0.99	0.99	0.99
	40. Ca+Cl	Closure	0.4	0.11	0.21	0.00	0.62	0.77	0.83	0.86	-0.26	0.23	0.98	0.98	0.99	0.99	0.99
	Closure EM, aggregated over OMs					0.00	0.60	0.75	0.82	0.86			0.98	0.98	0.99	0.99	0.99

Table 8: Repeat of the integrated detection probabilities from Table 7, listing only the probabilities that have been weighted across the OMs (i.e. the white rows of Table 7). Grey cells indicate that the detection probability exceeds 0.80.

		(a) Dassen Island					(b) Robben Island				
Data type	EM	**1**	**5**	**10**	**15**	**20**	**1**	**5**	**10**	**15**	**20**
Growth	Catch	0.25	0.46	0.58	0.63	0.65	0.73	0.81	0.83	0.84	0.84
	Closure	0.00	0.00	0.00	0.00	0.00	0.34	0.64	0.78	0.84	0.88
Condition	Catch	0.79	0.85	0.87	0.88	0.88	0.97	0.95	0.94	0.93	0.94
	Closure	0.79	0.92	0.96	0.97	0.97	0.78	0.91	0.95	0.96	0.97
Length	Catch	0.38	0.65	0.74	0.77	0.79	0.31	0.66	0.76	0.78	0.80
	Closure	0.12	0.59	0.80	0.87	0.90	0.21	0.58	0.79	0.86	0.89
Fledge	Catch	0.07	0.32	0.46	0.52	0.55	0.97	0.90	0.90	0.92	0.92
	Closure	0.00	0.60	0.75	0.82	0.86	0.98	0.98	0.99	0.99	0.99

Table 9: Integrated detection probabilities for two of the data sets calculated assuming a Threshold of -0.20. The corresponding results for a Threshold of -0.1 from Tables **??** and **??** have been repeated for ease of comparison. Note that the slight differences in the μ_{data}^{EM*} estimates is as a result of variation in the simulations used to evaluate the GLM-bias.

Threshold	**Island**	**Data set**	**OM**	**EM**	**Cor**	μ_{data}^{EM*}	**se**	**1**	**5**	**10**	**15**	**20**
T=-0.1	(a) Dassen	(I) Chick growth	Catch	Catch	0.2	0.05	0.10	0.11	0.41	0.60	0.70	0.75
			Catch	Catch	0.4	0.05	0.10	0.13	0.43	0.62	0.71	0.76
			*Closure	Closure	-	0.38	0.14	0.00	0.00	0.00	0.00	0.00
		(IV) Fledging success	Catch	Catch	0.2	0.08	0.09	0.04	0.20	0.35	0.48	0.57
			Catch	Catch	0.4	0.08	0.09	0.07	0.31	0.49	0.58	0.65
			Closure	Closure	-	0.11	0.21	0.00	0.63	0.76	0.82	0.86
	(b) Robben	(I) Chick growth	Catch	Catch	0.2	-0.01	0.15	0.64	0.81	0.90	0.93	0.94
			Catch	Catch	0.4	-0.01	0.15	0.66	0.84	0.91	0.93	0.95
			*Closure	Closure	-	0.04	0.16	0.33	0.66	0.79	0.85	0.88
		(IV) Fledging success	Catch	Catch	0.2	-0.09	0.08	0.52	0.82	0.88	0.92	0.93
			Catch	Catch	0.4	-0.09	0.08	0.99	0.95	0.96	0.97	0.98
			Closure	Closure	-	-0.27	0.23	0.99	0.99	0.99	0.99	0.99
Threshold	**Island**	**Data set**	**OM**	**EM**	**Cor**	μ_{data}^{EM*}	**se**	**1**	**5**	**10**	**15**	**20**
T=-0.2	(a) Dassen	(I) Chick growth	Catch	Catch	0.2	0.04	0.10	0.01	0.08	0.18	0.25	0.31
			Catch	Catch	0.4	0.04	0.10	0.02	0.09	0.20	0.26	0.34
			Closure	Closure	-	0.38	0.14	0.00	0.00	0.00	0.00	0.00
		(IV) Fledging success	Catch	Catch	0.2	0.08	0.09	0.00	0.00	0.00	0.00	0.00
			Catch	Catch	0.4	0.08	0.09	0.00	0.00	0.00	0.00	0.00
			Closure	Closure	-	0.11	0.21	0.00	0.34	0.54	0.64	0.70
	(b) Robben	(I) Chick growth	Catch	Catch	0.2	-0.02	0.15	0.37	0.58	0.78	0.86	0.88
			Catch	Catch	0.4	-0.02	0.15	0.38	0.62	0.79	0.86	0.89
			Closure	Closure	-	0.03	0.16	0.07	0.32	0.50	0.60	0.67
		(IV) Fledging success	Catch	Catch	0.2	-0.08	0.08	0.02	0.26	0.45	0.57	0.65
			Catch	Catch	0.4	-0.08	0.08	0.24	0.54	0.68	0.76	0.80
			Closure	Closure	-	-0.26	0.23	0.91	0.95	0.97	0.97	0.97

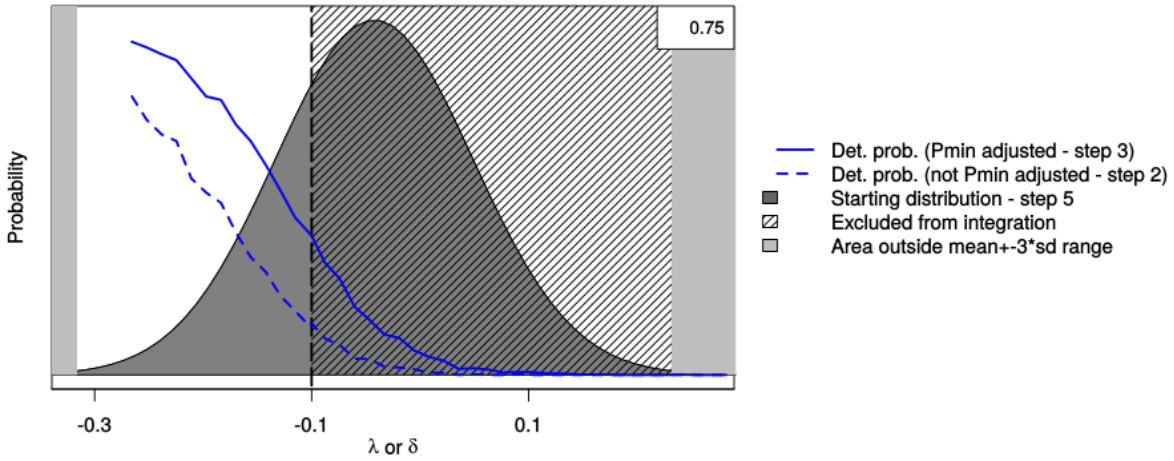

Figure 1: An example of the integration process described in Table 2 of the bias-adjusted detection probability (solid blue curve) with the prior distribution (dark grey shaded area). The horizontal axis variable corresponds to the EM variable V_{EM} (λ if the EM is catch only and δ if the EM is closure only). Only areas with a white background are included in the integration calculation, which covers the range $[\mu_{data}^{EM*} - 3(\sigma_{data}^{EM})$; Threshold] where μ_{data}^{EM*} is the GLM-bias-adjusted estimate when the EM is applied to the data (Step 4 of Table 2) and σ_{data}^{EM} the standard error from Step 1(b). The integrated detection probability is shown in the legend in the top right corner. The dashed blue line shows the detection probability prior to the P_{min} adjustment, and illustrates the effect that the P_{min} bias adjustment has on the detection probability curve.

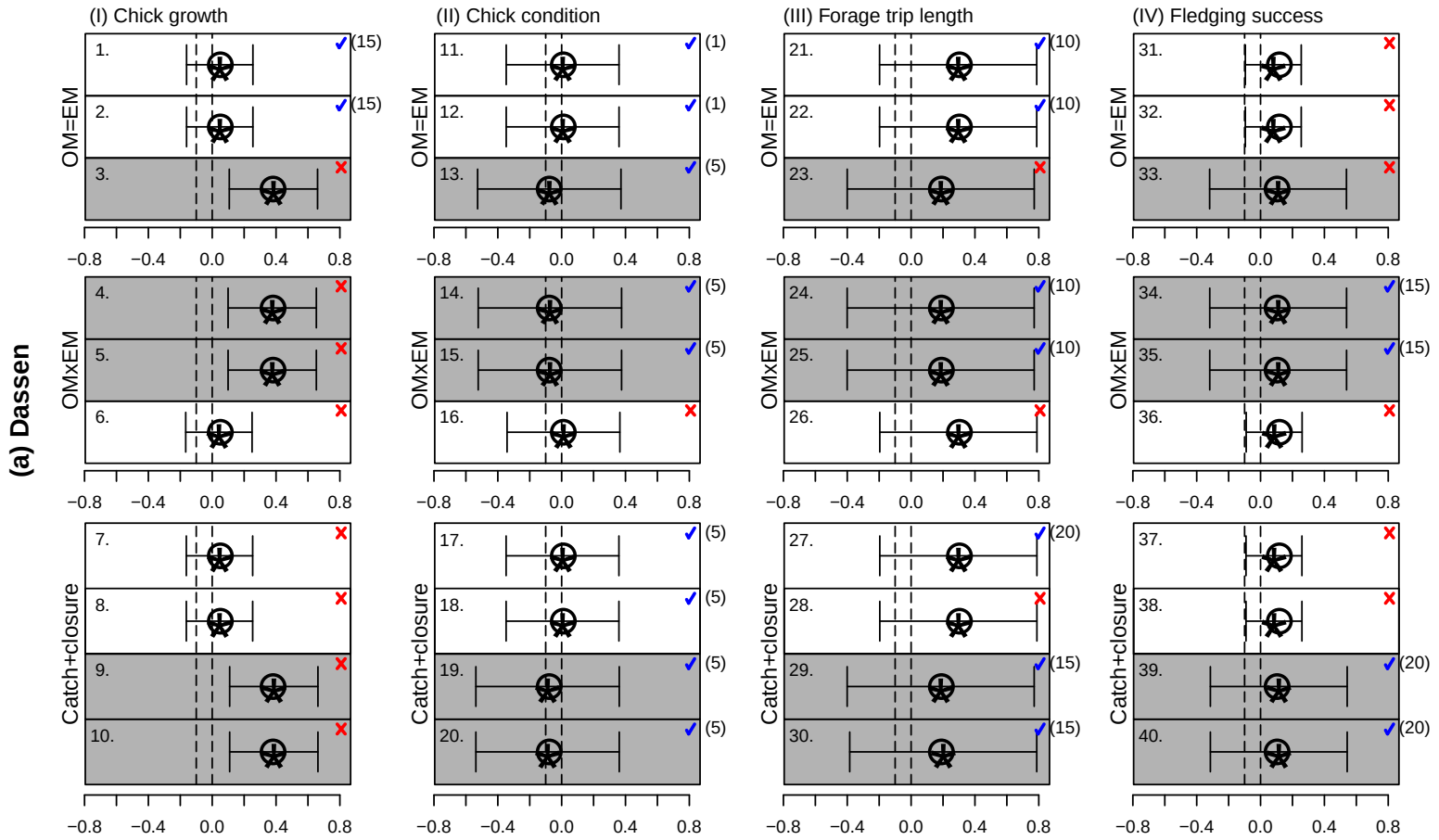

Figure 2a: Illustration of the OM estimates and GLM-bias-adjusted estimates of λ (or δ). For each of the four data sets, the estimates are shown for (i) catch only OM with catch-biomass correlation 0.2, (ii) catch only OM with catch-biomass correlation 0.4 and (iii) closure only OM. Thus the panels with a white background correspond to λ estimates and panels with a grey background correspond to δ estimates. In each panel, the star shows the GLM-bias-adjusted estimate for λ/δ and the open circle shows the original EM estimate for λ/δ. The 95% confidence interval estimated by the EM is indicated in each case. Vertical dashed lines indicate the zero mark, and the Threshold at -0.1. The top right corner of each panel shows either a red cross if the integrated detection probability fails to reach 0.8 after 20 years, or a blue tick if it has reached the 0.8 level by that time. In the latter case, the number of years taken (to the nearest 5 years) to reach 0.8 is indicated in brackets after the tick.

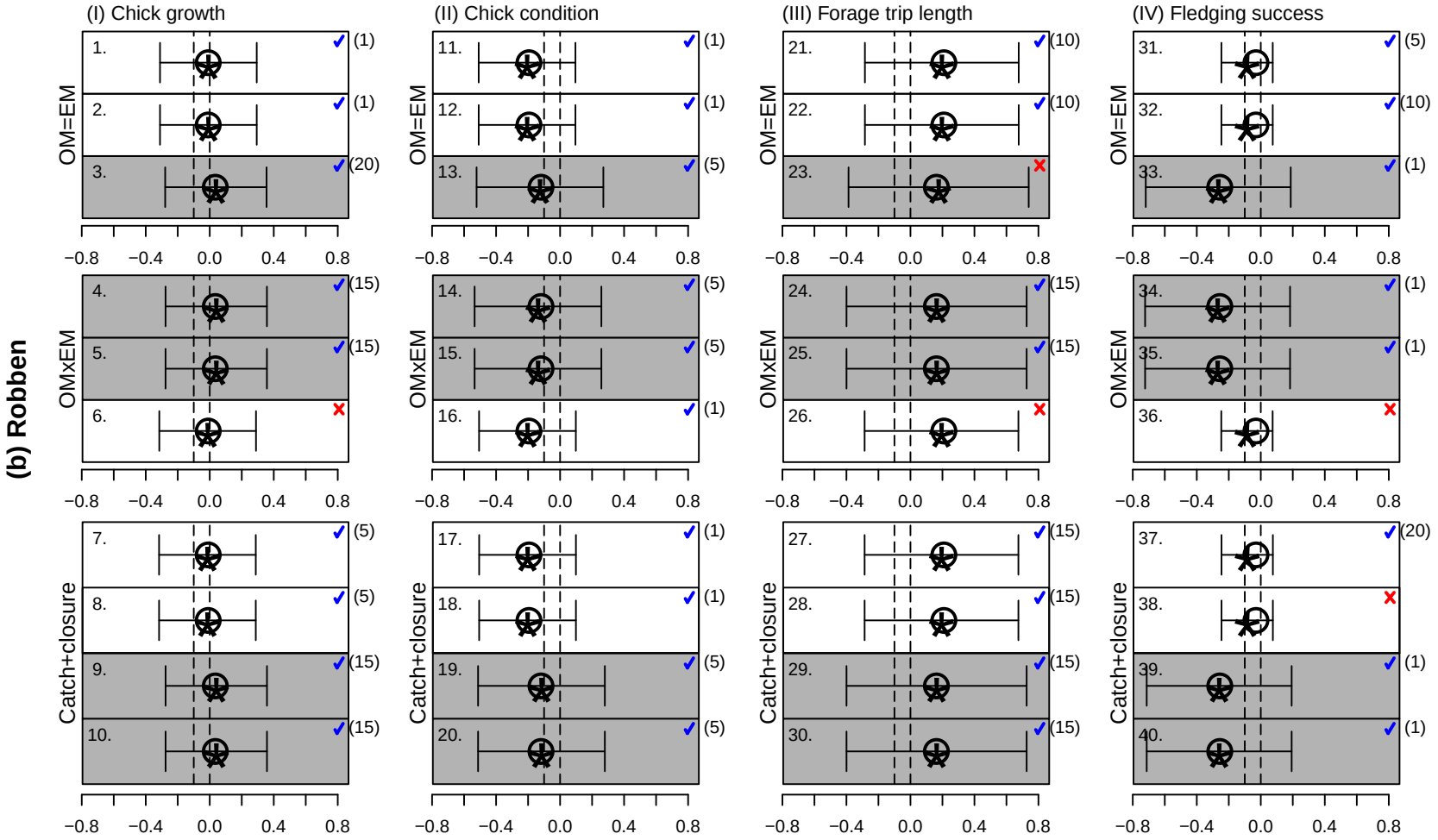

Figure 2b: Illustration of the OM estimates and GLM-bias-adjusted estimates of λ (or δ) for **Robben Island**.

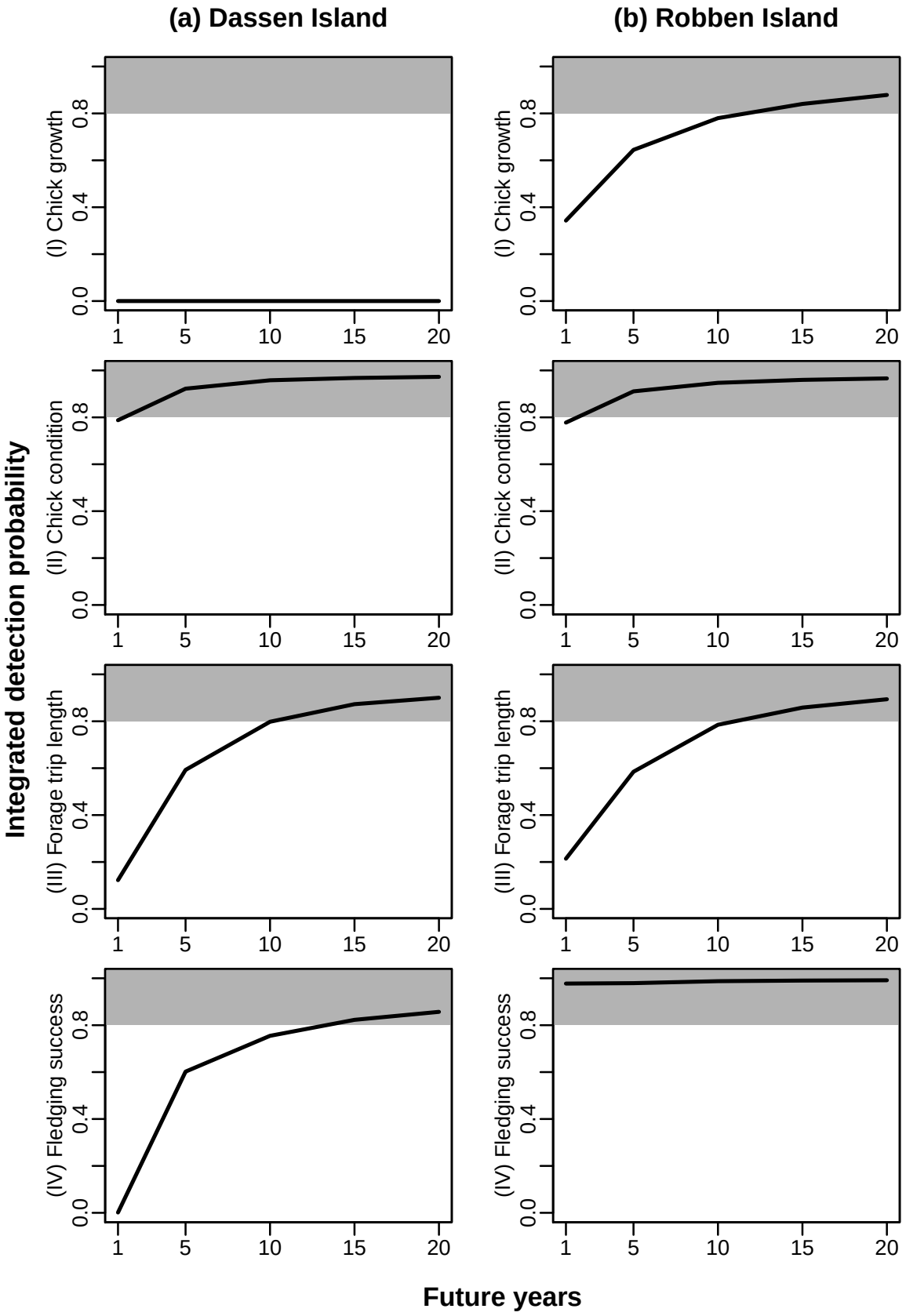

Figure 3: Plot of the integrated detection probabilities from Table 8, which have been weighted across OMs to produce a single detection probability curve for each EM.

Appendix A Data standardisation

A.1 Introduction

The panel for IWS 2015 recommended that GLM-standardised data be used only if these are statistically different to the unstandardised data. This appendix reports on the results of the standardisation process. The disaggregated data were provided by Richard Sherley (chick growth), Antje Steinfurth and Kate Robinson (foraging trip length) and Lauren Waller (chick condition), as forwarded by Janet Coetzee on 19/10/2015. Disaggregated fledging success data are not available. It is noted here for reference purposes that the disaggregated data that were provided for foraging trip length exclude the years 2003 and 2004, which have however been included in the aggregated data sets listed in Coetzee *et al.* (2015).

A.2 Method

For each data set, a separate GLM analysis was conducted for each island, since there is no reason to suppose that the year effects for the response variables for the two islands would be the same. A linear model was used for each island i and for each data type (chick growth, chick condition and foraging trip length):

$$F_{i,y,m,r} = \mu_i + \alpha_{i,y} + \beta_{i,m} \tag{A.1}$$

as well as a log-linear model:

$$lnF_{i,y,m,r} = \mu_i + \alpha_{i,y} + \beta_{i,m} \tag{A.2}$$

where

$F_{i,y,m,r}$	is the measurement for for individual penguin r on island i in month m of year y,
μ_i	is the intercept for island i,
$\alpha_{i,y}$	is the year effect for year y and island i, and
$\beta_{i,m}$	is the month effect for month m and island i.

The reference levels were set as the month and year with the most measurements (data points) for each island and data type. In these analyses, the month allocated to each sample is taken to be the month recorded in the disaggregated data set.

A.3 Results and discussion

Figures A.1 to A.3 show a selection of outputs pertinent to the standardisations, as detailed in the captions of those Figures. Results are shown for both the case where the data are log-transformed prior to standardisation (in which case negative data points in the chick growth and chick condition disaggregated data sets had to be removed) and where the data are not log-transformed.

Although for chick growth and foraging trip length the residual distributions show deviations from normality, overall the standardisations suggest little change from the means for the raw data. Consistent with the panel's recommendation A.2.15 that standardisation be effected only if it indicated marked changes (formally if

(many) instances of falling outside 95% CIs occurred), the power analyses have been conducted in all three cases with the original (unstandardised) means.

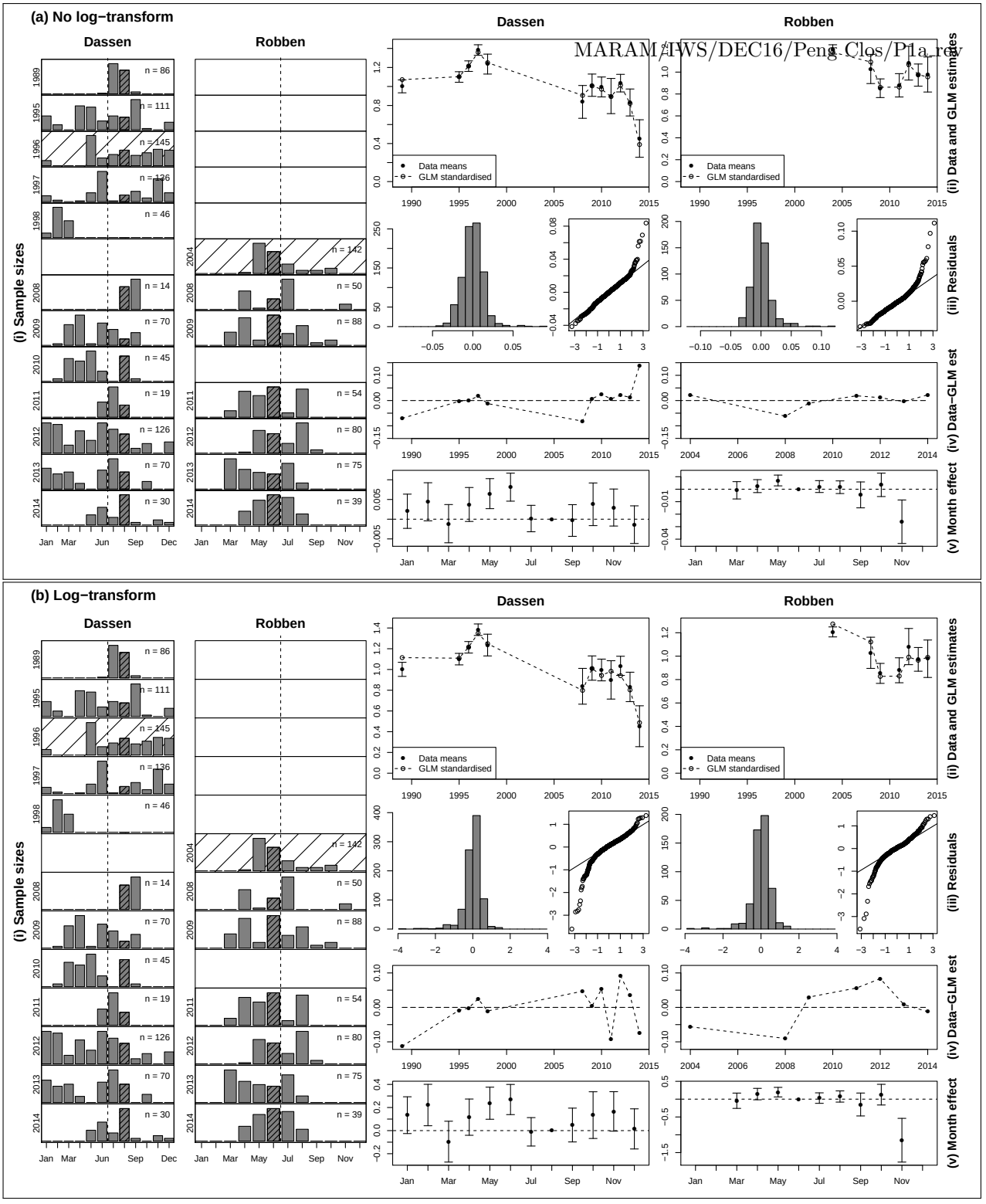

Figure A.1: Penguin data standardisation for the **chick growth** data for the case where the data (a) were not log-transformed (top set of plots) and (b) were log-transformed and negative values were excluded (bottom set of plots) prior to input into the GLM. The two panels on the left (i) show the monthly sample sizes each year. The GLM reference level year and month are marked by angled lines and correspond to the year and month with the most data points on average. The two plots in the top panel on the right (ii) show the annual (averaged) data points along with their 95% probability intervals, along with the GLM standardised estimates. The two plots in the second panel on the right show the GLM working residuals (i.e. the residuals from the last iteration of the minimisation process). The two plots in the third panel on the right (iv) show the residuals given by difference between the data means and the GLM standardised values from (ii). The two plots in the bottom panel on the right (iv) show the month effects estimated by the GLM.

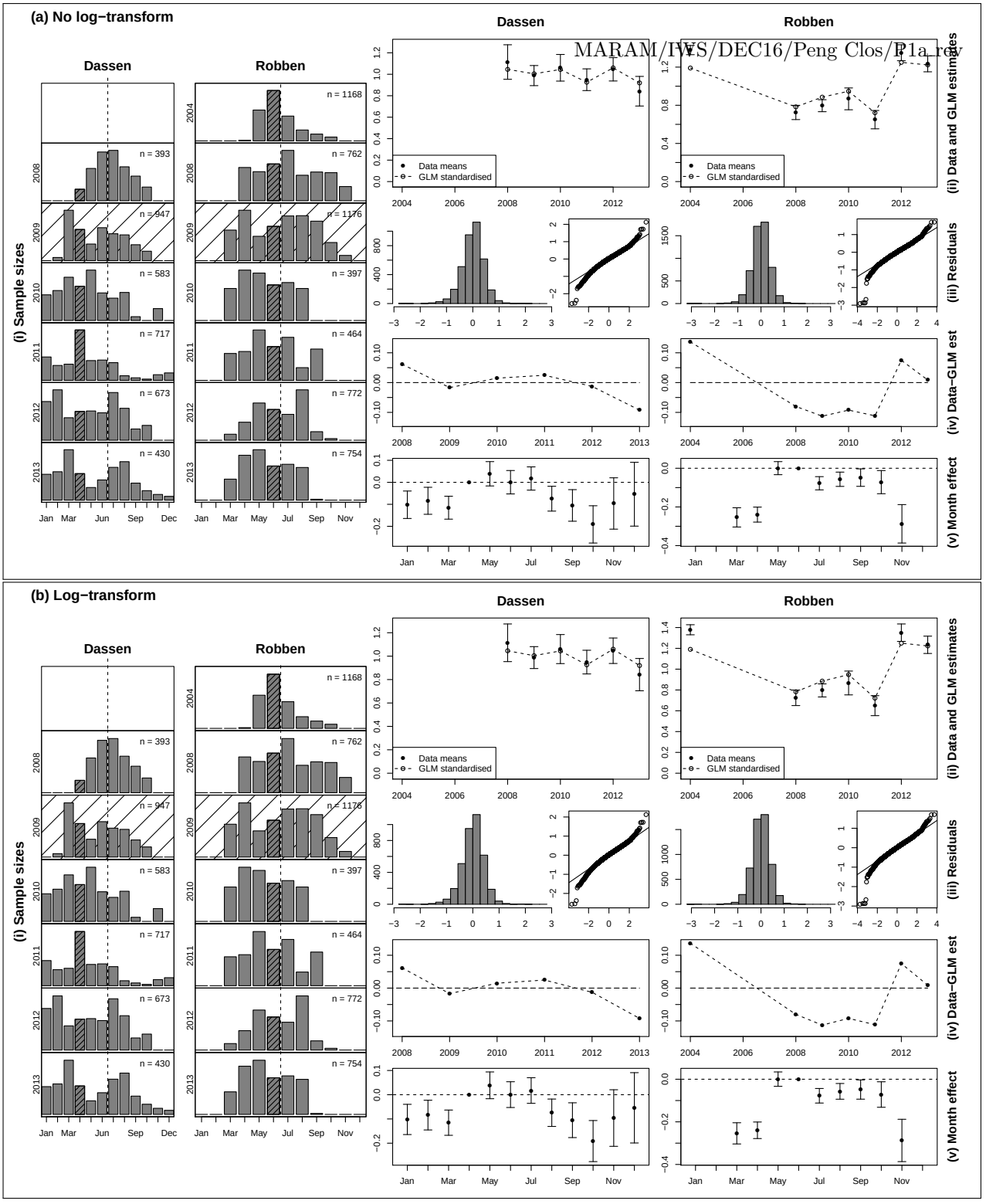

Figure A.2: Penguin data standardisation for the **chick condition** data for the case where the data (a) were not log-transformed (top set of plots) and (b) were log-transformed and negative values were excluded (bottom set of plots) prior to input into the GLM. The two panels on the left (i) show the monthly sample sizes each year. The GLM reference level year and month are marked by angled lines and correspond to the year and month with the most data points on average. The two plots in the top panel on the right (ii) show the annual (averaged) data points along with their 95% probability intervals, along with the GLM standardised estimates. The two plots in the second panel on the right show the GLM working residuals (i.e. the residuals from the last iteration of the minimisation process). The two plots in the third panel on the right (iv) show the residuals given by difference between the data means and the GLM standardised values from (ii). The two plots in the bottom panel on the right (iv) show the month effects estimated by the GLM.

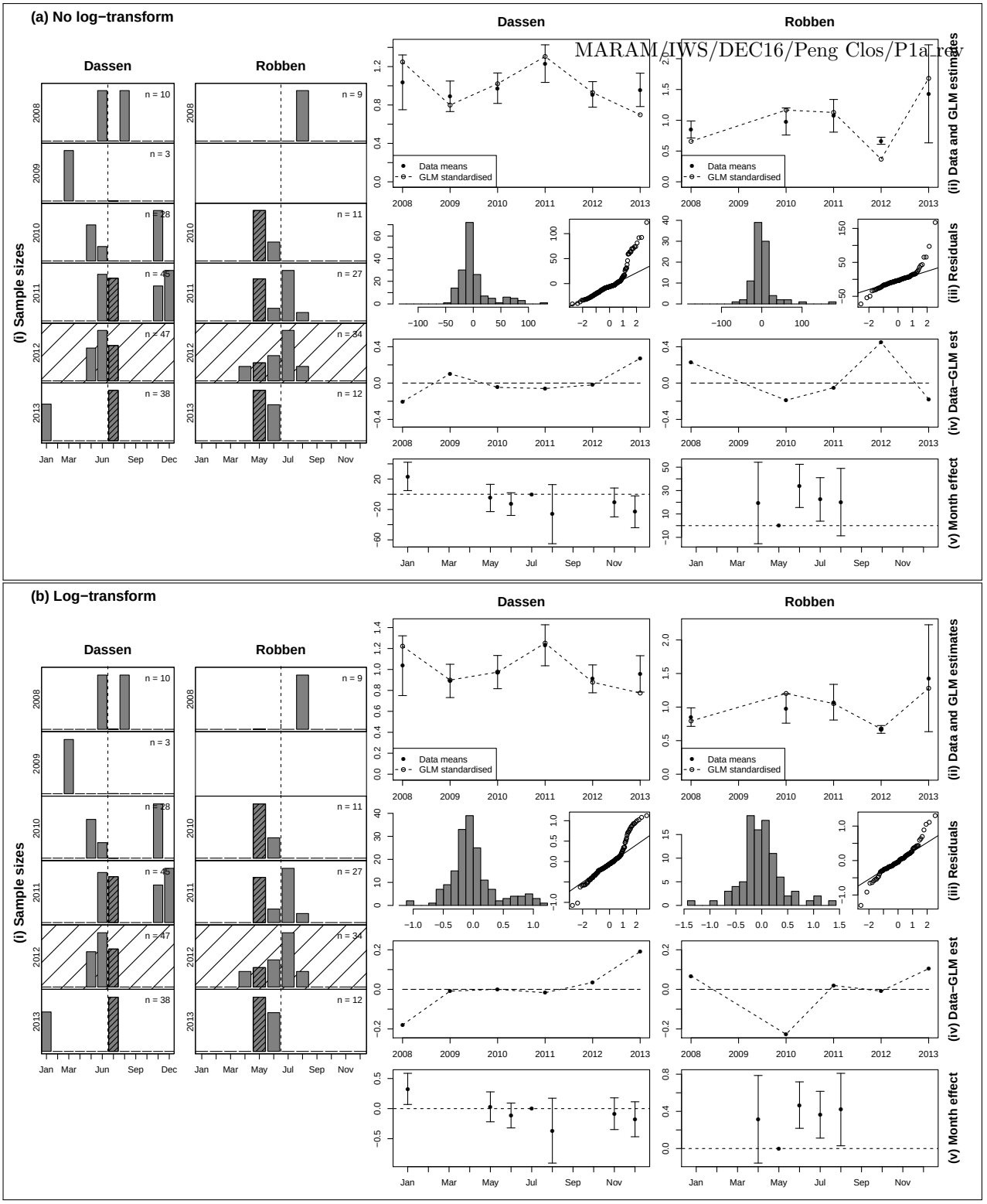

Figure A.3: Penguin data standardisation for the **foraging trip length** data for the case where the data (a) were not log-transformed (top set of plots) and (b) were log-transformed (bottom set of plots) prior to input into the GLM. The two panels on the left (i) show the monthly sample sizes each year. The GLM reference level year and month are marked by angled lines and correspond to the year and month with the most data points on average. The two plots in the top panel on the right (ii) show the annual (averaged) data points along with their 95% probability intervals, along with the GLM standardised estimates. The two plots in the second panel on the right show the GLM working residuals (i.e. the residuals from the last iteration of the minimisation process). The two plots in the third panel on the right (iv) show the residuals given by difference between the data means and the GLM standardised values from (ii). The two plots in the bottom panel on the right (iv) show the month effects estimated by the GLM.

Appendix B Dealing with σ_α=0

B.1 Introduction

A random-effects model is used to estimate the parameters of Equation 1 (page 2). One of the outputs of this model is an estimate of the standard deviation of the random year effect, σ_α. Table B.1 provides the estimates of σ_α for each of the data sets, model types, and different catch assumptions. As can be seen from the Table, in some cases the estimate of σ_α is zero, presumably as information content is limited in a situation of few degrees of freedom. This is problematic because in order to generate pseudo data for the power analysis procedure, a non-zero value of σ_α is required. The IWS 2015 panel report recommended that for such cases the mean of the sampling (or posterior) distribution be used instead (see recommendation A.2.17 of Dunn *et al.* 2015). A Bayesian approach therefore had to be developed in order to obtain an estimate of the posterior distribution of σ_α.

B.2 Methods

Although there are several packages available in R that should in theory be able to produce the posterior distribution for σ_α, some difficulty was experienced in establishing that the packages were in fact producing the desired output. It was decided to instead develop the model in AD Model Builder (ADMB) and use its MCMC option to obtain the posterior distribution. In order to accomplish this, the random year effects were treated as fixed effects, and σ_α one of the estimable parameters. A penalty was imposed to ensure that the year effect variables were normally distributed about their mean value with a variance of σ_α^2.

This penalty, however, resulted in a σ_α estimate of zero and consequently a non-positive definite Hessian matrix. Since a positive definite Hessian is required to initiate the MCMC process, a second penalty was introduced that was designed to operate when the estimate of σ_α fell below 0.01 — the value of 0.01 and the magnitude of the penalty were chosen so that this new penalty would counteract the penalty for the normal prior assumed for the year effect when σ_α was below 0.01. Effectively this amounted to placing a lower bound on the σ_α prior of about 0.07, a value lower than would be plausible anyway. The resultant MCMC chains were checked for adequate convergence.

This process was conducted not only for data set and model variant combinations for which the R estimate for σ_α was zero, but also for those for which the R estimate was not zero. The latter exercise allowed for a comparison between the posterior median σ_α estimated by the MCMC process and the estimate provided by the random-effects model implemented in R. With the aid of these comparisons, it was found that using the median of the σ_α posterior distribution (multiplied by the bias correction factor $\sqrt{n/(n-p)}$, where n is the number of data points and p the number of parameters estimated, counting 1 only for the variance parameter for those covariates treated as random effects when the model is implemented in R) gave reasonable compatibility with what was produced by the random effects model. (Note that the application of this frequentist bias correction factor to a Bayesian posterior estimate in somewhat *ad hoc*, but was considered reasonable in circumstances of relatively few degrees of freedom in the estimation process.)

Table B.2 lists the parameter estimates obtained from the random-effects model implemented in R, as well as those obtained in ADMB when σ_α is fixed at the bias-corrected MCMC median value. This Table shows that apart from a few slightly larger differences for fledging success, the parameter estimates are in general very similar, suggesting that the approach is broadly defensible.

B.3 Implementation in the power analysis process

The following procedure was then pursued for the power analysis approach. If a non-zero estimate of σ_α was available from the implementation in R, then that estimate was used for the data simulation. If the estimate of σ_α was zero, then it was replaced with the MCMC estimate from Table B.2 in order to generate data, but for the remainder of the parameters of Equation 1 the estimates from the random-effects model implemented in R were used. It could be argued that the ADMB estimates for the other parameters in Table B.2 corresponding to the σ_α that was implemented should be used instead of the R estimates, but since the power analysis requires the λ (or δ) parameter to be fixed at a range of values on an interval, this would require re-estimating these parameters externally for every λ (or δ) value on the interval evaluated. This is not computationally feasible given that an MCMC run would be required in each case. Another alternative would be to fix the remaining parameters at the same ADMB estimates for all the λ (or δ) values on the interval, but it was found that this approach did not perform well in terms of the test described below.

In order to check whether this approach worked reasonably well, a selection of data and model combinations was chosen for which the R estimate for σ_α was not zero, and the power analysis was conducted as per the approach outlined above, with the bias-corrected MCMC median estimate for σ_α replacing the non-zero R estimate. Table B.3 reports the integrated detection probabilities calculated in this way, and those calculated in the standard way using the non-zero σ_α estimate from R. As can be seen in this Table, the differences between the detection probabilities is minimal, and more importantly the broad conclusions that would have been drawn do not change. This adds weight to the earlier conclusion above of the defensibility of the approach.

B.4 Foraging trip length data

Panel recommendation A.2.7 (Dunn *et al.* 2015) states that instances of only three samples in a year could arguably be excluded from the analysis. This is relevant for only the foraging trip length data for Dassen Island in the years 2003 and 2009. The approach described in this appendix was applied to both the data set where the N=3 points were included and excluded. The case where the points where excluded, however, exhibited some numerical instabilities in the σ_α estimation for the ADMB method in that a positive definite Hessian could not be achieved for the catch+closure model. In light of this, and since the power analysis results (which were run for both data sets for the catch only and closure only models) did not result in different overall conclusions for these two models, the results in this Appendix are shown for the data set with the N=3 points included only.

Table B.1: The R estimates for σ_α for the four different data sets and four different catch radius assumptions. The 18km closure catches were used in the analyses presented in this document.

Data	Model	18km closure	10nmi	20nmi	30nmi
Chick growth	Catch only	0.04	0.07	0.02	0
	Closure only	0	0	0	0
	Catch+Closure	0.11	0.16	0.00	0
Chick condition	Catch only	0	0.00	0	0
	Closure only	0	0	0	0
	Catch+Closure	0	0	0	0
Foraging path length	Catch only	0	0.24	0	0.27
	Closure only	0.24	0.24	0.24	0.24
	Catch+Closure	0	0.25	0	0.12
Fledging success	Catch only	0.31	0.30	0.31	0.30
	Closure only	0.27	0.27	0.27	0.27
	Catch+Closure	0.27	0.28	0.27	0.28

Table B.2: Estimates for the parameters in Equation 1 are provided for two cases: rows labelled "R" list the estimates from R, for which some of the σ_α estimates are zero (in such cases the rows have been highlighted in grey), and rows labelled "MCMC" list the estimates produced by ADMB when σ_α is fixed at the MCMC posterior median value.

(I) Chick growth		K		$\gamma 1$		$\gamma 2$		λ Dassen		λ Robben		δ Dassen		δ Robben		
		Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	σ_α
(i) Catch only	R	-3.500	0.110	0.222	0.170			0.051	0.104	-0.010	0.151					0.044
	MCMC	-3.499	0.107	0.225	0.147			0.050	0.090	-0.011	0.131					0.050
(ii) Closure only	R	-3.746	0.120	0.438	0.169							0.381	0.138	0.035	0.158	0.000
	MCMC	-3.746	0.111	0.442	0.148							0.378	0.121	0.027	0.138	0.040
(iii) Catch+closure	R	-3.719	0.125	0.437	0.177			-0.096	0.101	-0.188	0.199	0.450	0.165	0.195	0.256	0.108
	MCMC	-3.728	0.109	0.424	0.142			-0.090	0.082	-0.124	0.164	0.451	0.133	0.124	0.210	0.071
(II) Chick condition		K		$\gamma 1$		$\gamma 2$		λ Dassen		λ Robben		δ Dassen		δ Robben		
		Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	σ_α
(i) Catch only	R	-1.255	0.163	0.337	0.206			0.010	0.177	-0.195	0.151					0.000
	MCMC	-1.210	0.142	0.322	0.165			-0.0069	0.142	-0.201	0.121					0.057
(ii) Closure only	R	-1.195	0.183	0.234	0.237							-0.078	0.225	-0.119	0.198	0.000
	MCMC	-1.154	0.158	0.223	0.191							-0.089	0.181	-0.123	0.160	0.055
(iii) Catch+closure	R	-1.214	0.194	0.255	0.247			0.103	0.263	-0.329	0.275	-0.162	0.315	0.207	0.340	0.000
	MCMC	-1.161	0.154	0.246	0.176			0.045	0.187	-0.323	0.196	-0.130	0.224	0.192	0.241	0.068
(III) Foraging trip length		K		$\gamma 1$		$\gamma 2$		λ Dassen		λ Robben		δ Dassen		δ Robben		
		Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	σ_α
(i) Catch only	R	-4.058	0.231	0.134	0.297			0.303	0.246	0.209	0.240					0.000
	MCMC	-4.027	0.203	0.132	0.246			0.288	0.204	0.201	0.199					0.064
(ii) Closure only	R	-3.960	0.257	0.115	0.328							0.190	0.293	0.162	0.282	0.242
	MCMC	-3.939	0.224	0.042	0.274							0.200	0.245	0.231	0.245	0.074
(iii) Catch+closure	R	-4.029	0.283	0.088	0.362			0.369	0.394	0.128	0.481	-0.108	0.458	0.116	0.574	0.000
	MCMC	-3.976	0.226	0.095	0.264			0.315	0.287	0.122	0.351	-0.070	0.335	0.105	0.418	0.092
(IV) Fledging success		K		$\gamma 1$		$\gamma 2$		λ Dassen		λ Robben		δ Dassen		δ Robben		
		Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	Est.	se	σ_α
(i) Catch only	R	-0.187	0.115	-0.439	0.127	0.037	0.147	0.118	0.088	-0.030	0.080					0.315
	MCMC	-0.401	0.094	-0.431	0.059	0.054	0.075	0.126	0.040	-0.016	0.041					0.205
(ii) Closure only	R	-0.128	0.189	-0.241	0.334	0.138	0.278					0.104	0.214	-0.256	0.227	0.267
	MCMC	-0.154	0.207	-0.284	0.307	0.066	0.281					0.091	0.185	-0.272	0.242	0.144
(iii) Catch+closure	R	-0.149	0.206	-0.261	0.337	0.125	0.292	0.114	0.114	0.025	0.128	-0.012	0.263	-0.241	0.267	0.293
	MCMC	-0.337	0.156	-0.333	0.231	0.049	0.194	0.114	0.071	0.029	0.072	-0.021	0.157	-0.178	0.200	0.162

Table B.3: Detection probabilities calculated for a selection of cases where the σ_α estimate is not zero in R, in order to compare the probabilities calculated using the standard procedure in R (labelled as "R" in the table), and those calculated by replacing the R estimate by the MCMC median when generating data, but using the R estimates for the remaining parameters (labelled as "MCMC" in the table). Note that the forage trip length results reported in this Table are for an earlier incorrect data set for which the years 2003 and 2004 are missing. Since the results for the "R" and "MCMC" methods were both based on the same uncorrected data set, the comparison remains valid. We do not plan on re-computing these runs at this stage.

Data type	Island	Method	μ*	μ se	1	5	10	15	20
Forage length, catch only	Dassen	R	0.0043	0.1630	0.72	0.92	0.95	0.97	0.97
		MCMC	0.0001	0.1630	0.78	0.94	0.97	0.97	0.98
	Robben	R	0.1098	0.1665	0.40	0.79	0.90	0.95	0.95
		MCMC	0.0524	0.1665	0.45	0.84	0.95	0.97	0.97
Data type	Island	Method	μ*	μ se	y1	y5	y10	y15	y20
Chick growth, catch only	Dassen	R	0.0495	0.1039	0.11	0.41	0.60	0.70	0.75
		MCMC	0.0458	0.1039	0.11	0.42	0.59	0.69	0.75
	Robben	R	-0.0150	0.1511	0.64	0.81	0.90	0.93	0.94
		MCMC	-0.0119	0.1511	0.68	0.84	0.92	0.94	0.95
Data type	Island	Method	μ*	μ se	y1	y5	y10	y15	y20
Fledging success, catch only	Dassen	R	0.0839	0.0876	0.04	0.20	0.35	0.48	0.57
		MCMC	0.0960	0.0876	0.03	0.17	0.31	0.40	0.46
	Robben	R	-0.0829	0.0802	0.52	0.82	0.88	0.92	0.93
		MCMC	-0.065	0.080	0.48	0.78	0.87	0.92	0.93

Appendix C

Relationship between Changes in Penguin Population Growth Rate and Changes in the Fledging Success Response Variable leading to a value for the corresponding Threshold

If penguin reproductive maturity is assumed to occur at age 4, the equation for the mature female component of the population (numbering N in year y) may be written:

$$N_{y+1} = N_y S + H_{y-3} S^3 N_{y-3} \tag{C.1}$$

where S is the mature female annual survival proportion and H is a measure related to the product of egg production and chick survival to the end of the first year (which incorporates fledging success). In a situation where the population is changing at a steady rate:

$$\eta = N_{y+1}/N_y \tag{C.2}$$

then

$$\eta^4 = \eta^3 S + HS \tag{C.3}$$

which if H changes by ΔH leads to a corresponding change in penguin growth rate $\Delta\eta$ given by:

$$\Delta\eta = \frac{S^3}{4\eta^3 - 3\eta^2 S}\Delta H \tag{C.4}$$

The Task Team decided on 1% as the pre-specified change in population growth rate (management objective), effectively then setting $\Delta\eta = 0.01$. Table C.1 below gives values of $\Delta H/H$ for ranges of plausible values for S and η which yield feasible solutions — note then that if changes in fledging success dominate any changes in η, then $\Delta H/H$ becomes equivalent to a change in the value of ln(fledging success). For much of the Table, the value 0.1 provides a good approximation to $\Delta H/H$. Accordingly power computations were performed for a Threshold value of -0.1 in λ/δ (the effect of fishing parameters) space.

Table C.1: $\Delta H/H$ values when $\Delta\eta = 0.01$.

	S	0.6	0.65	0.7	0.75	0.8	0.85	0.9	0.95
η	0.7	0.143	0.244	N/A	-	-	-	-	-
	0.75	0.107	0.14	0.241	N/A	-	-	-	-
	0.8	0.088	0.104	0.137	0.237	N/A	-	-	-
	0.85	-	0.085	0.102	0.135	0.235	N/A	-	-
	0.9	-	-	0.083	0.1	0.133	0.232	N/A	-
	0.95	-	-	0.072	0.082	0.098	0.132	0.231	N/A
	1	-	-	-	0.07	0.08	0.097	0.13	0.23
	1.05	-	-	-	-	0.069	0.079	0.095	0.129
	1.1	-	-	-	-	0.061	0.067	0.077	0.094
	1.15	-	-	-	-	-	0.059	0.066	0.076
	1.2	-	-	-	-	-	-	0.058	0.065