Updated analysis of results from data arising from the Island Closure Experiment[1]

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Summary

The results of analyses of data from the Island Closure Experiment reported in Ross-Gillespie and Butterworth (2021) are extended in three ways. First, a more consistent approach is taken for the conversions of the estimates of the effects of fishing parameters to estimates of the corresponding change in penguin population growth rate, though in implementation this leads to minimal modifications. Next the basis for contrasting the results from the aggregated and disaggregated analyses is changed from MLE to REML (or REML-equivalent) for unbiased and therefore more comparable estimates of CIs. Throughout, estimates and CIs from the two approaches remain similar, though overall a majority of aggregated approach CI's now become slightly smaller rather than slightly larger than their disaggregated counterparts than was the case previously. Finally, the aggregated approach is applied to the chick survival response variable for Dassen and Robben islands, with the results compared to those from a disaggregated approach developed by OLSPS Marine (2021). As with the other response variables, estimates and CI's from the two approaches to analyse the chick survival data are similar.

Key words: penguin, island closure, fishing impact, month, GLMM standardisation

Introduction

This paper provides a summary of the key results from Ross-Gillespie and Butterworth (2021) (referred to as FISHERIES/2021/JUN/SWG-PEL/35 or PEL/35 hereafter) (now with some adjustments) that compare the aggregated and disaggregated analysis approaches, and further includes a similar comparison for the chick survival data for Dassen and Robben islands. It also presents a concise summary of the steps followed to calculate the factors (now also somewhat adjusted in the interests of overall consistency) for converting estimates of the fishing effect δ from the island closure GLMM to estimates of change in the penguin annual population growth rate (Appendix A). Results for the various options that were considered for the aggregated analysis of the chick survival data are also included (Appendix B), with the key results from corresponding disaggregated analysis in reported in OLSPS Marine (2021) being reproduced here. Lastly, in the interest of completeness, previous results for the aggregated analysis of fledging success data (for which no disaggregated data are available) which were reported in Butterworth and Ross-Gillespie (2021) are modified slightly to correspond to the aggregated approach method used for the chick survival data (Appendix C).

Methods

Figure 2 of PEL/35 compares the estimated change in annual population growth rate for what is considered to be the "best" implementations of the aggregated and disaggregated approaches. There, the "best" aggregated approach (labelled approach A3) applies the island-closure GLMM with sample-size-weighted and island-dependent variance, while the "best" disaggregated approach (labelled approach D3) is an hierarchical island-

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closure model with island-dependent variance. The aggregated approach had to be run in ADMB to allow for the inclusion of the sample-size weighting, which has the disadvantage that ADMB does not allow for the use of the restricted maximum likelihood (REML) approach to provide unbiased estimates of standard errors (se's). As REML is the preferred approach (to adjust for bias), a REML-conversion factor was calculated for each response variable to scale the CI's to approximate the REML modification. This was achieved by running a related model (approach A2, which is approach A3 without the sample-size-weighting) in R with and without REML, and then calculating the ratio of the se's with and without REML (see Table 7b of PEL/35). This ratio was then used to scale the CI's estimated for approach A3 in ADMB. These scaled results are presented in this document for all variables other than chick survival, which are newly added here and treated slightly differently as described in the following paragraph. As the disaggregated approach can be run directly with REML in R, this was implemented for the disaggregated results presented in this paper.

In addition to the response variables reported on in PEL/35, results for chick survival have been included in this document. For this variable, an island-dependent variance could not be calculated as was the case for the A3 models for the other response variables, as disaggregated chick survival estimates are not available as such – the disaggregated data are dealt with in an entirely different manner (see Appendix D). As difficulty was experienced in estimating an island-dependent variance in ADMB, the results shown here for the aggregated approach do not take sample size into account explicitly (as the sample sizes each year are large – nearly all well over 100[3] – this choice should not have a major impact). Furthermore, they assume island-independent variance as it was found that including island-dependent variances did not make a substantial impact on the results (see Appendix B). As this model could be coded in R with REML implemented directly, the chick survival aggregated results reported here are direct REML estimates. The disaggregated chick survival results are the Laplace estimates from Table 1 of OLSPS Marine (2021), but with a modified confidence interval to attempt to take REML into account to adjust the ML-based variance estimates for bias. Similarly to the approach used above. this modification was affected by calculating the ratio of the standard errors for the GLMM with and without REML applied to the aggregated chick survival data. It was found that the REML se's were 1.12 times larger than the ML se's for the aggregated survival data, so that the CI's from OLSPS Marine (2021) were thus scaled by a factor of 1.12. It should be noted that the "REML factors" (i.e. the scale by which REML estimates of se's are bigger than the corresponding ML estimates) tend to be bigger for models applied to disaggregated data than the aggregated counterparts, as can be seen in Table 7b of Ross-Gillespie and Butterworth (2021). Thus the factor of 1.12 used here is likely to be an underestimate for the actual adjustment to take REML into account, but as there is no straightforward way to calculate this effect (note from that Table 7b that the extent to which the disaggregated REML factors are bigger varies for the different response variables), no further adjustments have been made here.

Results

Table 1 and Figure 1 compare the estimated change in annual population growth rate (expressed as an annual proportion) for what are now considered the "best" (now REML or REML-equivalent) implementations of the aggregated and disaggregated approaches, for all response variables for which disaggregated data are available (i.e. for all response variables except fledging success – excluded here because there are only aggregated, not disaggregated, results available for the variable; results for analysing these annual fledging success values have nonetheless been reported in Appendix C in the interest of completeness). The estimates for change in population growth rate are determined from the values of the fishing effect estimated by the island-closure GLMMs by use of the conversion factors developed in Appendix A.

Discussion

What follows in black are pertinent extracts from PEL/35. The material in *red italics* reflects the modifications and additions of this paper and their implications.

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[3] Table B1 of Appendix B includes the annual number of chicks sampled. For all years there are well over 100 samples at each island, except for Dassen in 2018 where there were 54 samples only.

Note that conversions from the estimates of the GLMM-based fishing effect parameter δ to changes in penguin population annual growth rate are now carried out in a more consistent manner across the response variables considered, and are reported in terms of percentages rather than proportions. The differences resulting from the changes (where applied) to conversion factors are minimal.

Key aspects of the results are as follows. Note that the authors have attempted to keep the points made below "opinion-free". Further views with arguably some subjective element are provided in Butterworth and Ross-Gillespie (2021).

- Use of aggregated vs disaggregated data:
    - The A3 and D3 approaches are put forward as representing the best implementations of the suggestions of the December 2020 International Panel.

      These chosen approaches have been replaced by REML-like and REML versions respectively of what were previously MLE estimates to obtain more comparable (and unbiased) estimates of precision for both approaches.

    - The point estimates for change in population growth rates are very similar for the aggregated (A3) and disaggregated (D3) approaches. The estimates for either approach are well within the CI for the other. This broad result is in line with the expectation expressed by the December 2020 International Panel.

      These summary comments continue to apply (see Table 1 and Figure 1), including with results for the chick survival response variable now added.

    - For chick condition and chick growth, the CIs are also similar, though the CIs estimated for the foraging data tend to be 20-40% smaller for the foraging data when the disaggregated data are used. This similarity is also generally in line with Panel expectations. In principle the same results are to be expected from both approaches (Butterworth 2020); the differences seem associated especially with instances of small sample sizes in some years for the foraging data. Note that the differences are much less than appeared to be the case in December 2020 (here the D0 approach is considered to be representative of the disaggregated approach for which results were presented in December).

      The inclusion of the REML adjustment increases the disaggregated data CI's by a greater proportion than for the aggregated data, leading to a switch in the majority of instances with a greater CI coming from aggregated data analyses compared to previously with the majority coming from disaggregated data analyses. In PEL/35, the CI's from the aggregated approach were (on average across all the response variables and islands) 6% (se 19%) larger than from the disaggregated approach selected; for the REML-adjusted refinement reported here, CI's from the aggregated approach are now 6% (se 13%)[4] smaller on average. For chick survival, the disaggregated CI range is some 15% smaller than that for the aggregated approach, but this does not allow fully for REML-associated adjustment (as explained earlier in the text). See Table 1 and Figure 1 for these results.

    - Some negative aspects of both (aggregated and disaggregated) approaches are:
        Aggregated – The sample size adjustment is approximate, and likely does not work as well at very low sample sizes.
        Disaggregated – This approach may not allow fully for pseudo-replication, which would result in smaller CIs than are appropriate. Estimates of precision can be sensitive to inappropriate selections for hierarchical structure (nesting).

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[4] Note that that these values include the chick survival estimates which were not available for PEL/35.

Both – The use of random effects (also included for year in aggregated approaches to robustify estimation given limited number of degrees of freedom) can be problematic because there are indications of estimation instability as the data are not well able to partition the contributions to the variance of different effects.

- Month standardisation
  - The month standardisation makes very little difference for chick condition and growth.
  - There is some impact for foraging data – CIs can decrease up to 60% for WC islands (e.g. Path length for Dassen).
  - The largest decreases in CI's are, however, a consequence of removing outliers.

  Month standardisation could not be applied for the fledging success and chick survival data because month information is not currently available for those datasets.

- Sensitivities
  - Incorporation of pre-2008 data
    - This does not make a substantial impact, with the notable exception that the estimates of the island closure effect switch signs for both Dassen and Robben island fledging success when the pre-2008 data are included).

      This continues to be the case for these estimates after including the refinements of this paper (see Figure C1 of Appendix C for the fledging success results). As previously, the CIs are notably larger when the pre-2008 data are included.

    - In principle, one would expect that a longer series gives more degrees if freedom and hence that better precision could be expected, but this not reflected in the results. There may be some confounding arising with all pre-2008 situations regarded as the neighbourhood of the island being open to fishing, but some catches during this period being rather small. The results in this document are all based on a "closure" estimator rather than a "catch" estimator (which would have taken that catch size into account); the reason for the former to be preferred is that the latter did not perform as well in simulation tests because of the possible positive correlation between the size of the catch and the biomass of forage fish from year to year (Ross-Gillespie and Butterworth 2016).

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Table 1: Estimates of change in population growth rate (expressed as an annual **percentage**[5]) for what is being proposed as the "best" implementations of the aggregated and disaggregated approaches. For all response variables other than chick survival, the "best" aggregated approach applies the island-closure GLMM with sample-size-weighted and island-dependent variance, while the "best" disaggregated approach is an hierarchical island-closure model with island-dependent variance. For chick survival, the aggregated approach does not take sample size into account and the variance is island-independent, and the disaggregated results are from OLSPS Marine (2021). All results have either REML adjustments or actual REML implementation (see main text for more details).

		Aggregated (A)				Disaggregated (D)				A-D				Average no. data points per year
		Est.	L95	U95	Range (A) Upper-Lower	Est.	L95	U95	Range (D) Upper-Lower	Mean(A)-Mean(D)	Range(A)-Range(D)	(Mean(A)-Mean(D)) /Range(D)	(Range(A)-Range(D)) /Range(D)	
Dassen	Condition	0.06	-0.77	0.90	1.66	-0.20	-1.05	0.64	1.69	0.27	-0.03	0.16	-0.02	474
Dassen	Growth	1.74	-0.99	4.48	5.47	1.96	-1.14	5.06	6.20	-0.22	-0.73	-0.04	-0.12	47
Dassen	MaxDist	-0.73	-2.92	1.46	4.38	-0.12	-2.55	2.30	4.85	-0.61	-0.47	-0.13	-0.10	21
Dassen	PathLength	1.26	-0.79	3.31	4.10	1.52	-0.77	3.82	4.59	-0.26	-0.49	-0.06	-0.11	21
Dassen	TripDuration	2.86	0.09	5.64	5.55	3.57	1.03	6.10	5.07	-0.71	0.48	-0.14	0.09	21
Dassen	Survival	-1.20	-2.29	-0.10	2.19	-0.84	-1.78	0.10	1.87	-0.36	0.32	-0.19	0.17	149
Robben	Condition	-0.92	-1.75	-0.09	1.67	-0.92	-1.76	-0.07	1.69	0.00	-0.02	0.00	-0.01	527
Robben	Growth	0.25	-2.67	3.16	5.83	0.08	-3.13	3.30	6.44	0.16	-0.60	0.03	-0.09	56
Robben	MaxDist	-0.16	-2.24	1.92	4.16	0.27	-2.06	2.59	4.65	-0.43	-0.49	-0.09	-0.11	27
Robben	PathLength	-0.77	-2.65	1.11	3.76	-0.17	-2.39	2.05	4.44	-0.60	-0.68	-0.14	-0.15	25
Robben	TripDuration	0.37	-2.34	3.07	5.40	0.31	-2.14	2.77	4.92	0.05	0.49	0.01	0.10	26
Robben	Survival	-0.10	-1.20	0.99	2.19	-0.51	-1.45	0.42	1.86	0.41	0.33	0.22	0.18	260
Bird	Condition	-0.26	-1.85	1.33	3.18	-0.35	-1.90	1.20	3.10	0.09	0.07	0.03	0.02	207
Bird	MaxDist	0.21	-1.03	1.46	2.49	0.78	-0.47	2.03	2.50	-0.57	-0.02	-0.23	-0.01	57
Bird	PathLength	0.87	-0.77	2.52	3.29	0.50	-1.39	2.38	3.77	0.38	-0.48	0.10	-0.13	45
Bird	TripDuration	-1.35	-2.84	0.13	2.97	-0.67	-2.69	1.35	4.04	-0.69	-1.07	-0.17	-0.27	53
StCroix	Condition	0.65	-0.83	2.14	2.97	0.26	-1.26	1.78	3.04	0.39	-0.07	0.13	-0.02	135
StCroix	MaxDist	-3.18	-4.52	-1.83	2.69	-3.92	-5.36	-2.47	2.89	0.74	-0.19	0.26	-0.07	22
StCroix	PathLength	-1.92	-3.64	-0.20	3.43	-2.64	-4.71	-0.57	4.14	0.72	-0.71	0.17	-0.17	17
StCroix	TripDuration	0.03	-1.43	1.49	2.92	-0.30	-2.46	1.85	4.31	0.33	-1.39	0.08	-0.32	19

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[5] Note that previously these results have been reported as proportions, but as the numbers are quite small, the use of percentages as here allows for clearer contrast.
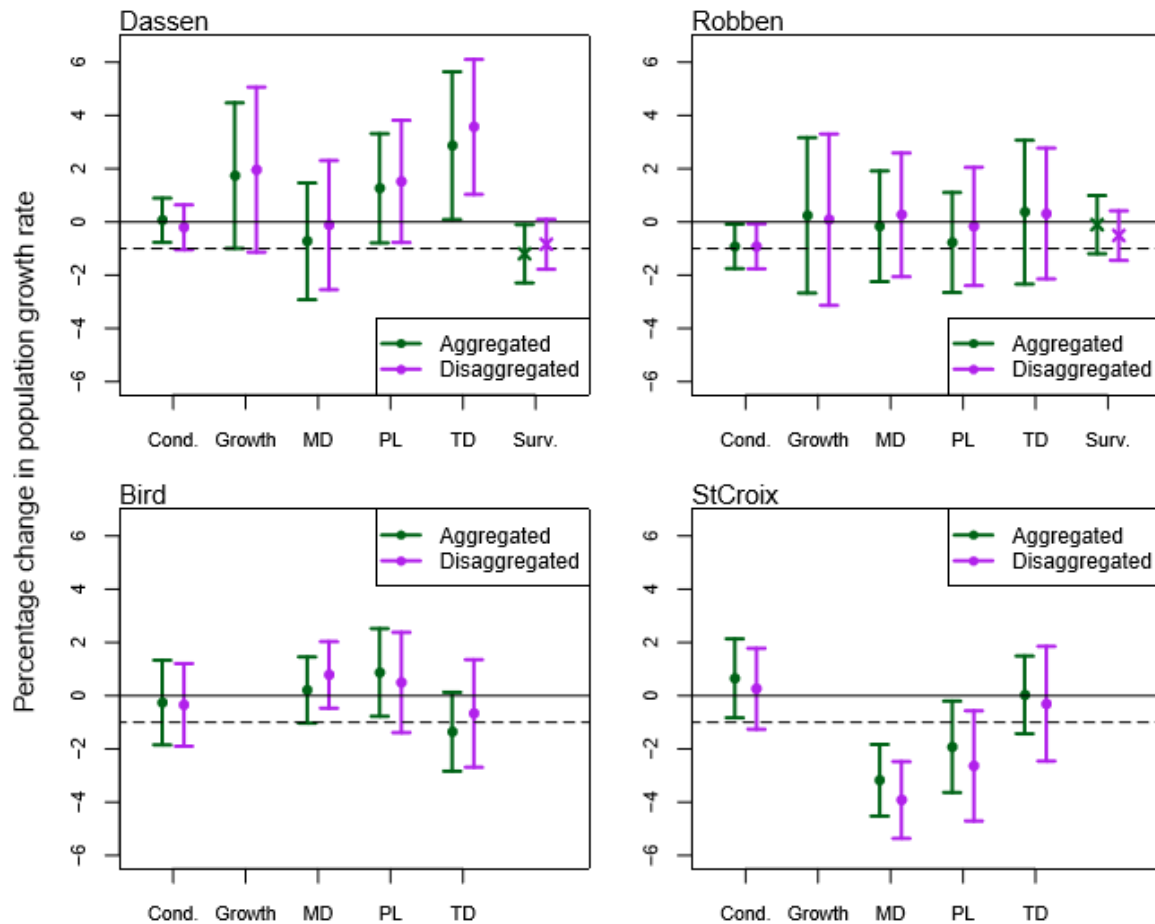
Figure 1: Comparison of the estimated change in annual population growth rate (expressed as an annual percentage[6]) for what are being put forward as the "best" implementations of the aggregated and disaggregated approaches. Point estimates and 95% CIs (given by $\pm 2se$) are shown for the various response variables for which month information is available. In the axis labels, "MD" is maximum foraging distance, "PL" is path length and "TD" is trip duration. This Figure is an update of Figure 2 of PEL/35, here taking REML adjustments for both aggregated and disaggregated approaches into account, and including chick survival results (the disaggregated survival results are the Laplace estimates from OLSPS Marine (2021), with an additional REML adjustment as described in the text).

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[6] Previously the vertical axes on these plots were shown as proportions, but these have been changed here to percentages for consistency with Table 2 and as the numbers then becomes more readily assimilated.

Appendix A: Converting the fishing effect δ estimated by the island-closure GLMM into estimates of the change in annual population growth rate (expressed as an annual proportion)

Appendix B of PEL/35 provide more details of the logic followed to derive the conversion factor for the chick condition data analysed in normal space. Table A1 below summarises this approach, but also adds the steps for the chick survival data which was also analysed in normal space, as well as the steps for obtaining a conversion factor for data analysed in log-space (the foraging data, fledging success and chick growth data were all analysed in log-space). Note that the conversion factors here differ slightly from those reported in PEL/35, where a survival rate $S = 0.867$ was assumed, which was related to the chick condition to survival rate relationship for the Macaroni penguin population. Here, $S = 0.88$ has been used instead for all except chick condition[7] as this value is arguably more appropriate here as it was estimated directly from data for the South African penguin population (at Robben Island) for the period before penguin numbers there started to decline rapidly in the early 2000's by Robinson *et al.* (2015).

In Table A1, $f(F_{i,y}) = k + \alpha_y + \beta_i + \tilde{\delta}_i X_{y,i}$ is the equation for the island-closure GLMM, with

$f(F_{i,y})$ the value of the response variable in year *y* and island *i*, with F modelled in either normal (i.e. $f(F) = F$) or log-space (i,e, $f(F) = \ln(F)$)

k is the intercept,

α_y is the random year effect reflecting prevailing environmental (e.g. related to forage fish abundance) conditions,

β_i is an island effect,

$X_{y,i}$ is a vector indicating where the island is open ($X_{y,i} = 1$) or closed ($X_{y,i} = 0$) to the fishery

δ is the general fishing effect estimated by applying the island-closure GLMM to the data,

$\tilde{\delta}$ is the specific fishing effect estimated when the GLMM is applied to data in normal space,

δ^* is the specific fishing effect estimated when the GLMM is applied to data in log-normal space,

Additionally, η is the annual relative increase in the mature female population (i.e. $\eta = N_{y+1}/N_y$), S is the mature female annual survival proportion, and H is a measure of survival rate related to the product of egg production and fledging success to the end of the first year of life.

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[7] For chick condition a value of $S = 0.867$ was assumed to be consistent with the calculations of Appendix B of PEL/35 which are based on information for the Macaroni penguin population),

Table A1: Description of the steps taken to derive the conversion factors for converting the fishing effect estimated by the island closure GLMM to an estimate of the change in annual population growth rate. These steps are shown for two possible transformations of the data: (A) normal space and (B) log space.

(A) Normal space		(B) Log space	
$$F_{i,y} = k + \alpha_y + \beta_i + \tilde{\delta}_i X_{y,i}$$	(A1)	$$\ln(F_{i,y}) = k + \alpha_y + \beta_i + \delta_i^* X_{y,i}$$	(B1)
$$\Delta F = \tilde{\delta}\Delta X = \ \tilde{\delta}$$	(A2)	$$\frac{\Delta F}{F} = \delta^*\Delta X = \delta^*$$	(B2)
$$\Delta\eta = \frac{S^3}{4\eta^3 - 3\eta^2 S}\Delta H = 0.501\Delta H$$ for $S = 0.88$ and $\eta = 1$	(A3)	$$\Delta\eta = \frac{S^3}{4\eta^3 - 3\eta^2 S}\Delta H$$ $$= \frac{S^3}{4\eta^3 - 3\eta^2 S}\Delta H * \frac{H}{H}$$ $$= \frac{S^3}{4\eta^3 - 3\eta^2 S}\frac{\Delta H}{H} * \frac{\eta^4 - \eta^3 S}{S^3}$$ $$= \frac{\eta^4 - \eta^3 S}{4\eta^3 - 3\eta^2 S}\frac{\Delta H}{H} = 0.088\frac{\Delta H}{H}$$ $$= 0.088\frac{\Delta F}{F}$$	(B3)
Conversion factor: **Chick condition:** From Appendix B of PEL/35, we have the relationship $\Delta H = 0.2321\Delta F$. The overall survival rate assumed for those calculations (based on Macaroni penguins) was $S = 0.867$, so in the interest of consistency that value is used here also. Therefore $\Delta\eta = 0.466\Delta H = 0.108\Delta F$. Hence the conversion factor for chick condition in normal space is: $$\Delta\eta = 0.108\tilde{\delta}$$	(A4a)	Conversion factor: $$\Delta\eta = 0.088\delta^*$$	(B4)
Chick survival: Assume $H = Z * S74$, where $S74$ is the proportion of chicks surviving 74 days and Z accounts for the balance of factors relating the ratio of penguins reaching 1 year of age to the parents that produced them. Using an average $S74$ value of 0.713 from the data and assuming $H = 0.176$[8], this gives $Z = 0.247$. Equation (A3) becomes: $\Delta\eta = 0.501 * (Z * \Delta S74) = 0.124\Delta S74$. So the conversion factor for chick condition in normal space is: $$\Delta\eta = 0.124\tilde{\delta}$$	(A4b)		

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[8] With $S = 0.88$ and $\eta = 1$, then $H = \frac{\eta^4 - \eta^3 S}{S^3} = 0.1761$.

Appendix B: Chick survival rate data

Table B1 lists the estimates of chick survival that were used as input to the aggregated model results presented in Figure 1 of the main text. These estimates are from OLSPS Marine (2021) using the methods described in Appendix D. Table B2 lists the results of various analyses of these data that were considered and explains the basis used to choose the final results presented in Figure 1 of the main text. Figure C1 of Appendix C plots the estimated percentage change in population growth rates along with those estimated for the fledging success response variable. Given difficulties experienced when trying to estimate island-dependent variances, and also given that the results for the various models in Table B2 are very similar, it seems reasonable to use the sample-size-invariant approach with the island-independent variance as the "best" approach for Figure 1 of the main text, i.e. to use the third row of Table B2 there.

Table B1: Estimates of chick survival from OLSPS Marine (2021). S74 is the proportion of chicks surviving 74 days, and was calculated as described in Appendix D. N indicates the sample size.

Year	Island	Closure	S (74)	N	Island	Closure	S (74)	N
2008	Dassen	Closed	0.7718	246	Robben	Open	0.6395	417
2009	Dassen	Closed	0.6062	229	Robben	Open	0.5479	252
2010	Dassen	Open	0.5314	121	Robben	Open	0.6119	227
2011	Dassen	Open	0.5394	193	Robben	Closed	0.6376	289
2012	Dassen	Open	0.7481	124	Robben	Closed	0.7092	237
2013	Dassen	Open	0.7609	160	Robben	Closed	0.7977	234
2014	Dassen	Closed	0.7677	133	Robben	Open	0.7628	188
2015	Dassen	Closed	0.7864	107	Robben	Open	0.7595	298
2016	Dassen	Closed	0.8361	119	Robben	Open	0.7200	246
2017	Dassen	Open	0.7888	156	Robben	Closed	0.8322	212
2018	Dassen	Open	0.7539	54	Robben	Closed	0.7811	262

Table B2: Estimates of the fishing effect $\tilde{\delta}$, as well as the percentage change in population growth rate estimated from the $\tilde{\delta}$ parameter, are provided for a selection of approaches in analysing the **Chick survival** response variable **in normal space**. In the Table, σ_ϵ is the component of the residual variance allowing for sample size to be taken into account, τ is the remaining component of the residual variance, and σ_α is the estimated standard deviation of the random year effect. Some points to note are listed below.

- **ADMB runs:** Where sample size has been taken into account in the variance, the formula used is $\sigma^2 = \frac{\sigma_\epsilon^2}{N} + \tau^2$. These approaches had to be coded in ADMB, and could be conducted using the MLE approach only, as REML is not available for ADMB. As convergence difficulties were experienced trying to estimate island-specific σ_ϵ's, the same σ_ϵ was assumed for each island. Furthermore, when estimated freely a $\sigma_\epsilon = 0$ was preferred, with $\tau = 0.033$. In light of this, σ_ϵ was fixed at a range of values and τ estimated, to investigate the impact on the negative log-likelihood and the estimated $\tilde{\delta}$ parameter. In this Table, ADMB results are reported for two effectively extreme cases: σ_ϵ fixed at 0, and σ_ϵ fixed at 0.49, the value for which the estimated τ parameter first becomes zero.
- **Converting δ to change in (annual) population growth rate ($\Delta\eta$):** A conversion factor of $\Delta\eta = 0.124\tilde{\delta}$ is applied, in terms of the computations shown in Appendix A.
- **Transformation sensitivity:** Repetition of these computations transforming the input estimates to log- or logit-space makes minimal difference to estimates of the change in population growth rate.

| Approach description				σ_ϵ	τ		-lnL	Fishing effect $\tilde{\delta}$				Percentage change in population growth rate ($\Delta\eta$)				σ_α	
								Dassen		Robben		Dassen		Robben			
					Estimate	se		Estimate	se	Estimate	se	Estimate	se	Estimate	se	Estimate	se
Island independent variance	No sample size adjustment	R1	MLE ADMB	0.000	0.033	0.008	-59.587	-0.100	0.043	-0.004	0.044	-1.242	0.537	-0.050	0.549	0.084	0.021
		R2	MLE R	0.000	0.033			-0.100	0.040	-0.004	0.040	-1.242	0.490	-0.050	0.490	0.084	
		R3	REML R	0.000	0.038			-0.096	0.044	-0.008	0.044	-1.194	0.546	-0.104	0.546	0.089	
	Sample size adjusted variance	R4	MLE ADMB	0.490	0.000	0.068	-59.340	-0.096	0.044	-0.026	0.043	-1.193	0.549	-0.319	0.537	0.080	0.020
Island dependent variance	No sample size adjustment	R5	MLE R	0.000	0.048*			-0.092	0.046	-0.020	0.040	-1.139	0.572	-0.250	0.491	0.081	
		R6	REML R	0.000	0.055*			-0.089	0.047	-0.024	0.040	-1.097	0.581	-0.300	0.489	0.086	

*When estimating island-dependent variance, R allocates all the variance to Dassen (i.e. $\tau_{Robben} = 0$).

Appendix C: Fledging success results

Fledging success has been analysed in an analogous manner to chick survival and the results are shown in the Table below. As for chick survival, an initial attempt was made to estimate the observation error σ_ϵ and the process error τ for the variance equation $\sigma^2 = \frac{\sigma_\epsilon^2}{N} + \tau^2$ (as there are no disaggregated data available for fledging success, an island-dependent variance could not be calculated as for the standard A3 models for the other response variables). The maximum likelihood estimate (MLE) corresponded to a $\sigma_\epsilon = 0.86$, with $\tau = 0$. In light of this, σ_ϵ was fixed at a range of values and τ estimated, to investigate the impact on the negative log-likelihood and the estimated δ^* parameter. As the difference in negative log-likelihood between the MLE of $\sigma_\epsilon = 0.86$ and fixing σ_ϵ at 0 was only 0.26 points, and further because including island-dependent variance also made little difference to the overall results, it seems defensible to choose an approach with no sample size adjustment and island-independent variance as the default approach, i.e. the third row in the Table below. Figure C1 plots the percentage change in population growth rates along with those for chick survival from Table B1 in Appendix B.

Table C1: Estimates of the fishing effect δ^*, as well as the percentage change in population growth rate estimated from the δ^* parameter, are provided for a selection of approaches in analysing the **fledging success** response variable **in log-normal space**. In the Table, σ_ϵ is the component of the residual variance allowing for sample size to be taken into account, τ is the remaining component of the residual variance, and σ_α is the estimated standard deviation of the random year effect. A conversion factor of $\Delta\eta = 0.088\delta^*$ is applied, in terms of the computations shown in Appendix A.

Approach description				σ_ϵ	τ Estimate	τ se	-lnL	Fishing effect $\tilde{\delta}$ Dassen Estimate	Dassen se	Robben Estimate	Robben se	$\Delta\eta$ Dassen Estimate	Dassen se	Robben Estimate	Robben se	σ_α Estimate	σ_α se
Island independent variance	No sample size adjustment	R1	MLE ADMB	0.000	0.085	0.024	-34.46	-0.086	0.085	0.043	0.102	-0.760	0.750	0.380	0.896	0.084	0.040
		R2	MLE R	0.000	0.085			-0.086	0.08	0.043	0.082	-0.760	0.700	0.380	0.723	0.084	
		R3a	REML R	0.000	0.101			-0.083	0.092	0.036	0.095	-0.730	0.808	0.317	0.834	0.092	
	All data (1989-2015)	R3b	REML R	0.000	0.169			0.104	0.158	-0.199	0.171	0.918	1.395	-1.747	1.500	0.296	
	Sample size adjusted variance	R4	MLE ADMB	0.860	0.000	0.114	-34.72	-0.095	0.080	0.043	0.088	-0.836	0.701	0.378	0.774	0.082	0.034
Island dependent variance	No sample size adjustment	R5	MLE R	0.000	0.084			-0.087	0.091	0.045	0.096	-0.765	0.802	0.396	0.841	0.084	
		R6	REML R	0.000	0.100			-0.083	0.092	0.037	0.095	-0.731	0.806	0.322	0.837	0.092	
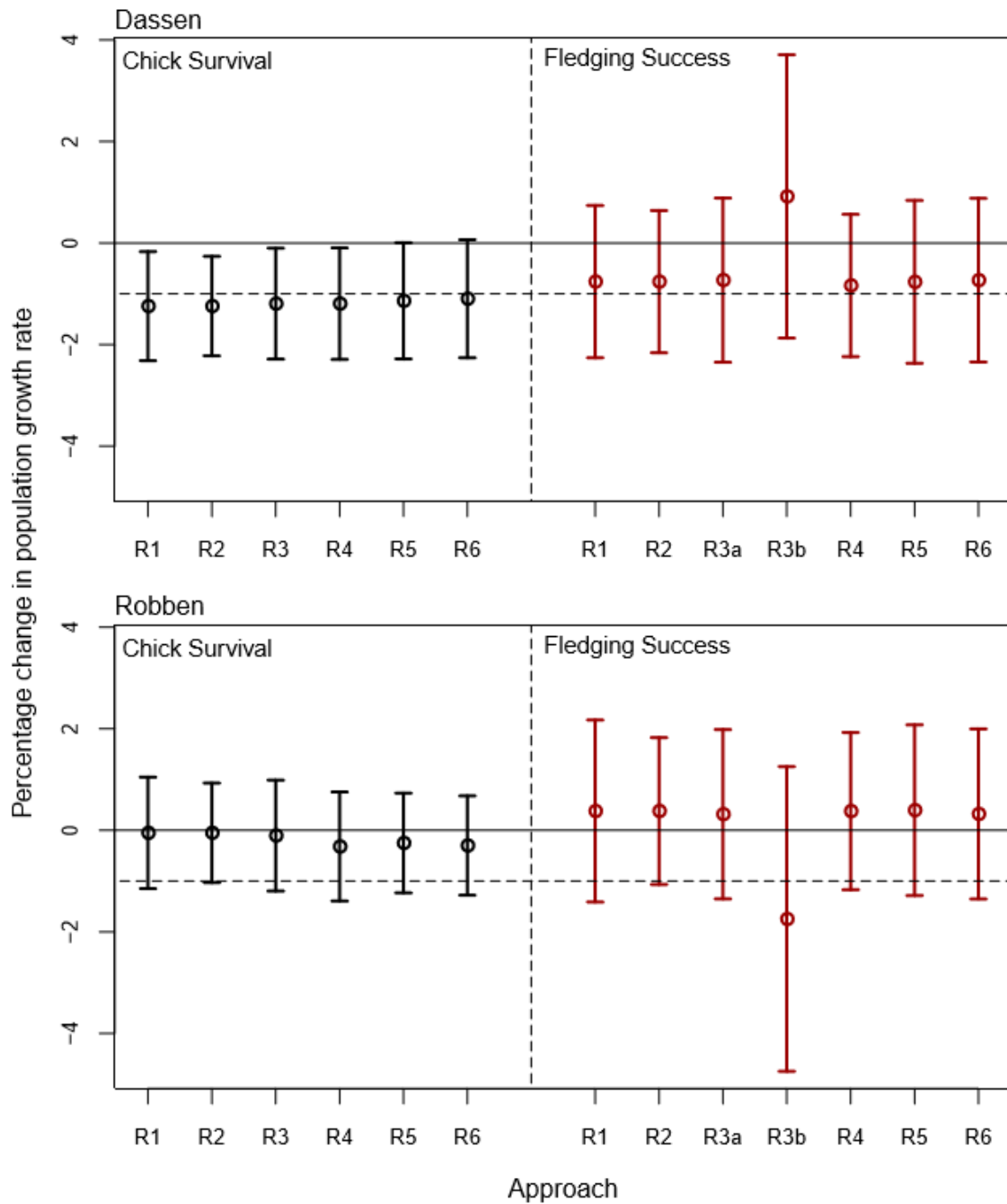
Figure C1: Zeh plots of the percentage change in population growth rate for chick survival (Table B1 of Appendix B) and fledging success (Table C1 of Appendix C) for the various approaches. R1-R4 use island-independent variance, while R5-R6 use island-dependent variance. R1-R3 do not incorporate sample size adjustment, while R4 does. R1, R2, R4 and R5 use MLE, while R3 and R6 use REML. For fledging success, there is an additional R3b, which is the same as R3a, but using all the available data.

Appendix D: Methods used to estimate chick survival proportion S(74)

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The lognormal survival function

Survival models can be characterised by 5 quantities, $S(t)$, $f(t)$, $h(t)$, $H(t)$, and $F(t)$, respectively (i) the survival function, (ii) the probability density function, (iii) the hazard function, (iv) the cumulative hazard function and (v) the cumulative density function. The quantities defined by these characteristic equations are all interrelated and can be derived if any one of the quantities (i) – (v) are given. The interrelationships for a generalised survival model are:

  i.   Survival function: $S(t) = 1 - F(t) = e^{-H(t)}$.

  ii. Pdf: $f(t) = -\frac{d}{dt}S(t) = \frac{d}{dt}F(t)$.

  iii. Hazard function: $h(t) = \frac{f(t)}{S(t)}$.

  iv. Cumulative hazard function: $H(t) = \int_0^t h(r)dr$.

  v.   Cdf: $F(t) = \int_0^t f(r)dr = 1 - e^{-H(t)}$

The characteristic equations for (i) – (v) for the lognormal survival function are as follows:

  i.   Survival function: $S(t) = 1 - \varphi\left[\frac{lnt-\mu}{\sigma}\right]$.

  ii. pdf: $f(t) = \frac{1}{\sigma t\sqrt{2\pi}}e^{-\frac{1}{2}\left(\frac{lnt-\mu}{\sigma}\right)^2}$.

  iii. Hazard function: $h(t) = \frac{\frac{1}{\sigma t\sqrt{2\pi}}e^{-\frac{1}{2}\left(\frac{lnt-\mu}{\sigma}\right)^2}}{1-\varphi\left[\frac{lnt-\mu}{\sigma}\right]}$.

  iv. Cumulative hazard function: $H(t) = -ln(1 - F(t)) = -ln(1 - \varphi\left[\frac{lnt-\mu}{\sigma}\right])$

  v.   Cdf: $F(t) = \varphi\left[\frac{lnt-\mu}{\sigma}\right]$.

where φ is the cumulative distribution function for a normal distribution with mean of zero and variance of 1. The distributional form given as characteristic for a survival function refers to the distribution of the probability density function *f(t)*, and therefore in the above *f(t)* has a lognormal form.

The aggregated approach to estimation of the survival proportion to time 74 (74 days after hatching) refers to estimating $S(74)$ for each island_year combination in such a way that there is no modelled connection between different year_island combinations. For the lognormal case, there are two parameters, μ and σ, that are estimated for each year_island combination, and the best estimate of $S(74)$ is $S(74) = 1 - \varphi\left[\frac{ln74-\hat{\mu}}{\hat{\sigma}}\right]$, where φ is the cumulative distribution function for the standard normal distribution function. The methods used to estimate μ and σ (and hence $S(74)$) are described below.

Estimation methodology

OLSPS (2020) presents a simplified approach to estimating the parameter of the survival model when the model is an exponential model. This involves a restructuring of the original dataset into an expanded format, as is described in that document. The advantage of the data restructuring approach described in FISHERIES/2020/JAN/SWG-PEL/06 is that it creates the potential for the application of GLMM techniques to incorporate the effects of other variables, including time dependent variables such as month. These

simplifications cannot be used in conjunction with GLMM techniques when the survival model is a lognormal survival model. An explicit statement of the likelihood function was therefore developed to obtain aggregated estimates of $S(74)$ using the data in its original form in which there is only one record per chick. The following is a description of that approach.

Let P_t be the probability of survival during time interval (t,t+Δt), given that survival has occurred to time t, where by the definition of $H(t)$,

$P_t = e^{-(H(t+\Delta t)-H(t))}$,

and where for the lognormal survival model *H(t)* is the cumulative hazard function for the log-normal survival function, viz. $H(t) = -\ln(1 - \varphi\left[\frac{lnt-\mu}{\sigma}\right])$, and where φ is the cumulative distribution function from a standard normal distribution.

The outcome by time $t+\Delta t$ is either 'survival' or 'death'. Consider now multiple penguin chicks observed over time. For all these data let N_t be the number of chicks that survive to the end of time interval ($t,t+\Delta t$) and let D_t be the number of chicks that die during time interval ($t,t+\Delta t$). The likelihood function for the data at time t, LF_t is:

$LF_t \propto e^{-H(t)(N_t+D_t)} P_t^{N_t}(1 - P_t)^{D_t} \propto e^{-H(t)(N_t+D_t)}\left[e^{-(H(t+\Delta t)-H(t))}\right]^{N_t}(1 - e^{-(H(t+\Delta t)-H(t))})^{D_t}$.

Considering all time periods together, an overall likelihood function is

$LF = \prod_{\forall t} LF_t \propto \prod_{\forall t} e^{-H(t)(N_t+D_t)}\left[e^{-(H(t+\Delta t)-H(t))}\right]^{N_t}\left(1 - e^{-(H(t+\Delta t)-H(t))}\right)^{D_t}$

The negative log-likelihood, $nLLF$, is:

$nLLF = \sum_{\forall t}\left\{H(t)(N_t + D_t) + N_t(H(t + \Delta t) - H(t)) - D_t \ln(1 - e^{-(H(t+\Delta t)-H(t))})\right\}$

Since there is apparently no analytical solution to the roots of the derivatives of *nLLF*, the minimisation was carried out using a derivative-free approach. This was implemented in Excel by setting up, for each {year, island} combination, the calculation of nLLF for candidate values of μ and σ, and then using the Excel solver function to minimise the value of *nLLF* with respect to μ and σ[9].

It should be noted that ultimately $S(74)$ is of interest, where

$S(74) = e^{-H(74)} = 1 - \varphi\left[\frac{ln74-\mu}{\sigma}\right]$.

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[9] The reliability of this process was verified using a simulation approach in which data was generated with given values of μ and σ and the numerical process obtained estimates of $\hat{\mu}$ and $\hat{\sigma}$ close to the original values used for data generation.