Consolidated analyses produced in implementation of the approaches described in document MARAM/IWS/DEC15/PengD/P1

Penguin Island Closure Task Team [1]

This consolidated document includes a series of analyses, conducted under the auspices of the Task Team, implementing the simulation approach detailed in MARAM/IWS/DEC15/PengD/P1. The analyses are divided into the following sections, arranged in the order in which they were produced.

Note that text in blue indicates a clickable hyperlink.

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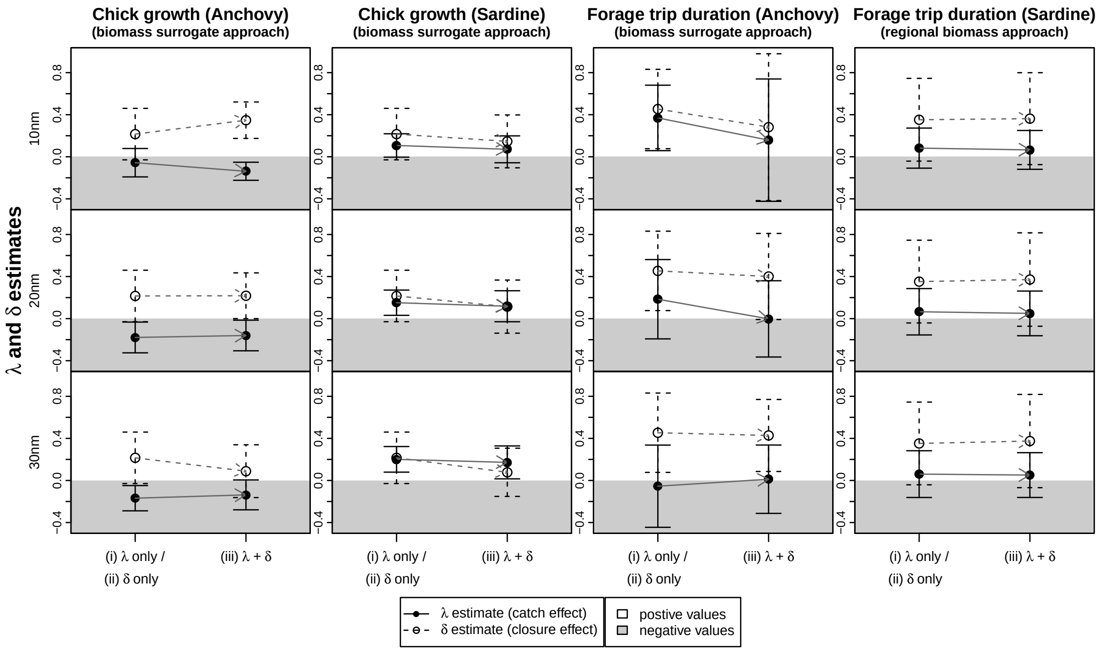
[1] The Task Team consisted of M.O. Bergh, D.S. Butterworth, K.L. Cochrane (chair), T.L. Morris, R.B. Sherley and H. Winker. A. Ross-Gillespie undertook, on behalf of the Team, all the analyses and tests described in these working papers, under the supervision of D.S. Butterworth.

1 Some initial results for the penguin simulation conditioning process

(a) Dassen Island



(b) Robben Island

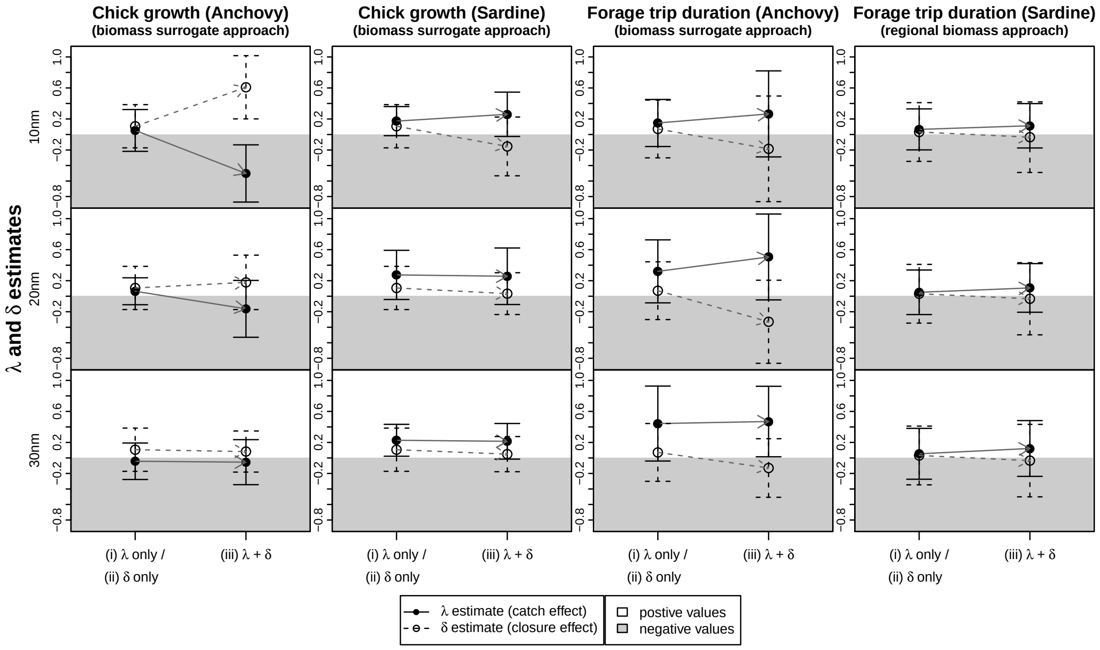
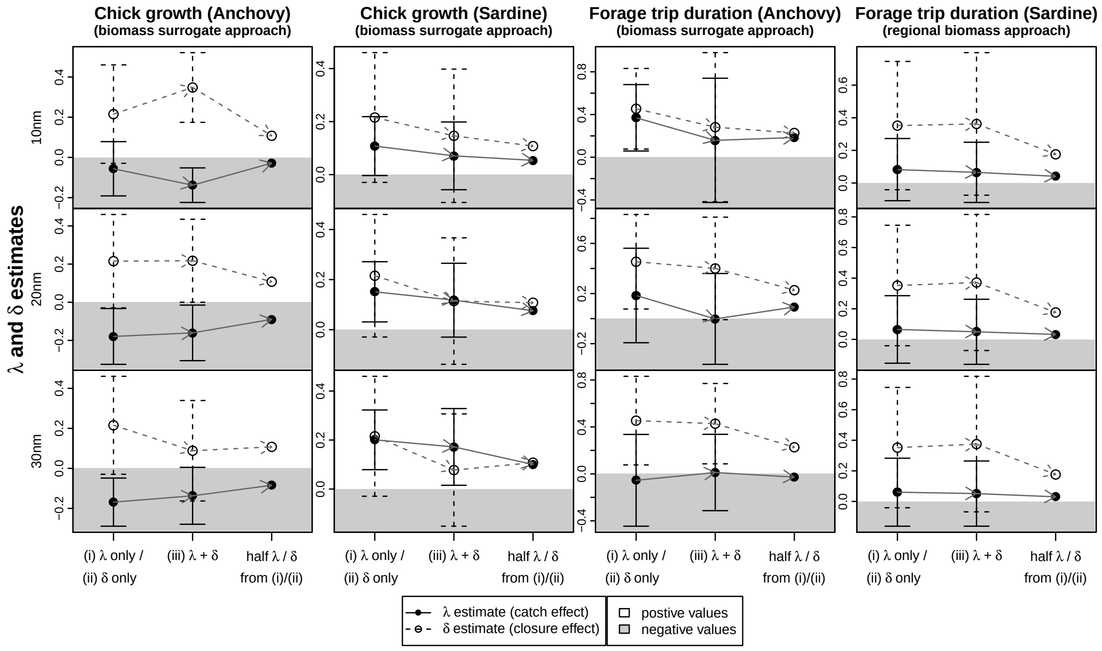


Figure 1.1: Graphical representation of the λ and δ estimates and 95% confidence intervals (twice standard error) for "(i) catch only / (ii) closure only" and "(iii) catch+closure" forms of the operating model (see MARAM/IWS/DEC15/PengD/P1). Estimates are shown for four different different scenarios and three catch zones. The grey shaded areas indicate negative values. Note that the adjusted variance of Equation (2) of MARAM/IWS/DEC15/PengD/P1 has not yet been implemented, and that data from MARAM/IWS/DEC15/PengD/BG1 were used to generate the results presented here. For the regional biomass approach, the spawner biomass surveys of the previous November have been used.

(a) Dassen Island



(b) Robben Island

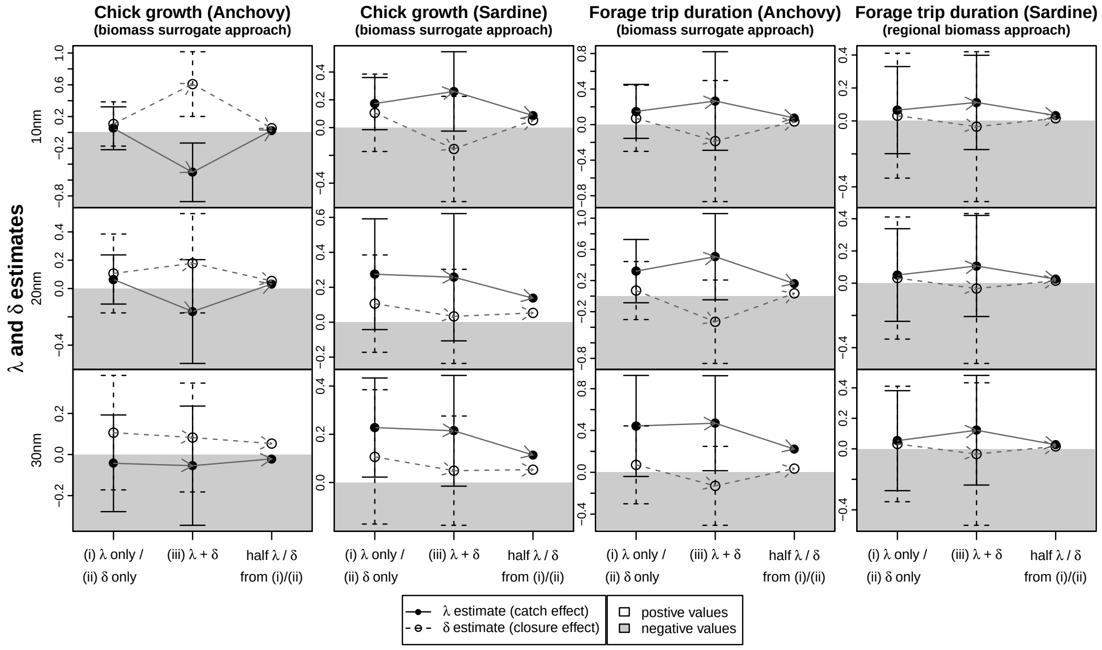


Figure 1.2: Graphical representation of the λ and δ estimates and 95% confidence intervals (twice standard error) for "(i) catch only / (ii) closure only" and "(iii) catch+closure" forms of the operating model (see MARAM/IWS/DEC15/PengD/P1), **as well as estimates given by half the value of the estimates from the individual catch/closure only operating model**. Estimates are shown for four different different scenarios and three catch zones. The grey shaded areas indicate negative values. Note that the vertical axes are not to the same scale. As for Figure 1.1, the adjusted variance of Equation (2) of MARAM/IWS/DEC15/PengD/P1 has not yet been implemented, and data from MARAM/IWS/DEC15/PengD/BG1 have been used. For the regional biomass approach, the spawner biomass surveys of the previous November have been used.

2 Penguin process vs observation error variance analysis

Note that these analyses are based on data presented in FISHERIES/2015/AUG/SWG-PEL/PENG/DATA1 (draft5).

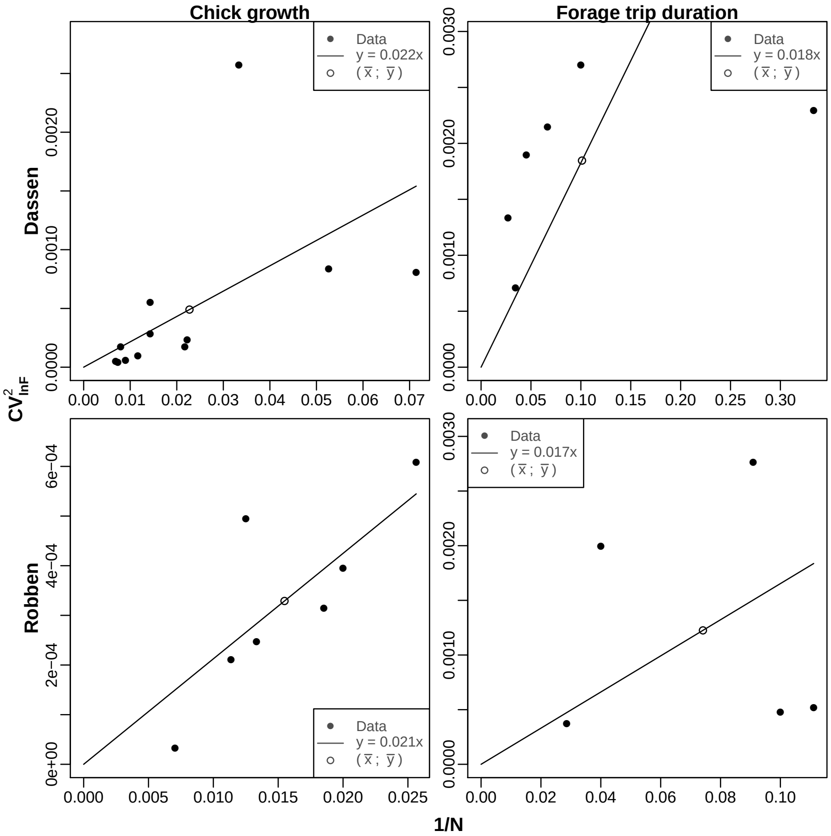


Figure 2.1: Plots of the square of the CVs of the log of the response variables chick growth and forage trip duration against the inverse of the sample size. Values are plotted for each year for which data are available. The line $y = mx$ is shown, where $m = \bar{y}/\bar{x}$, as well as the point $(\bar{x}; \bar{y})$.

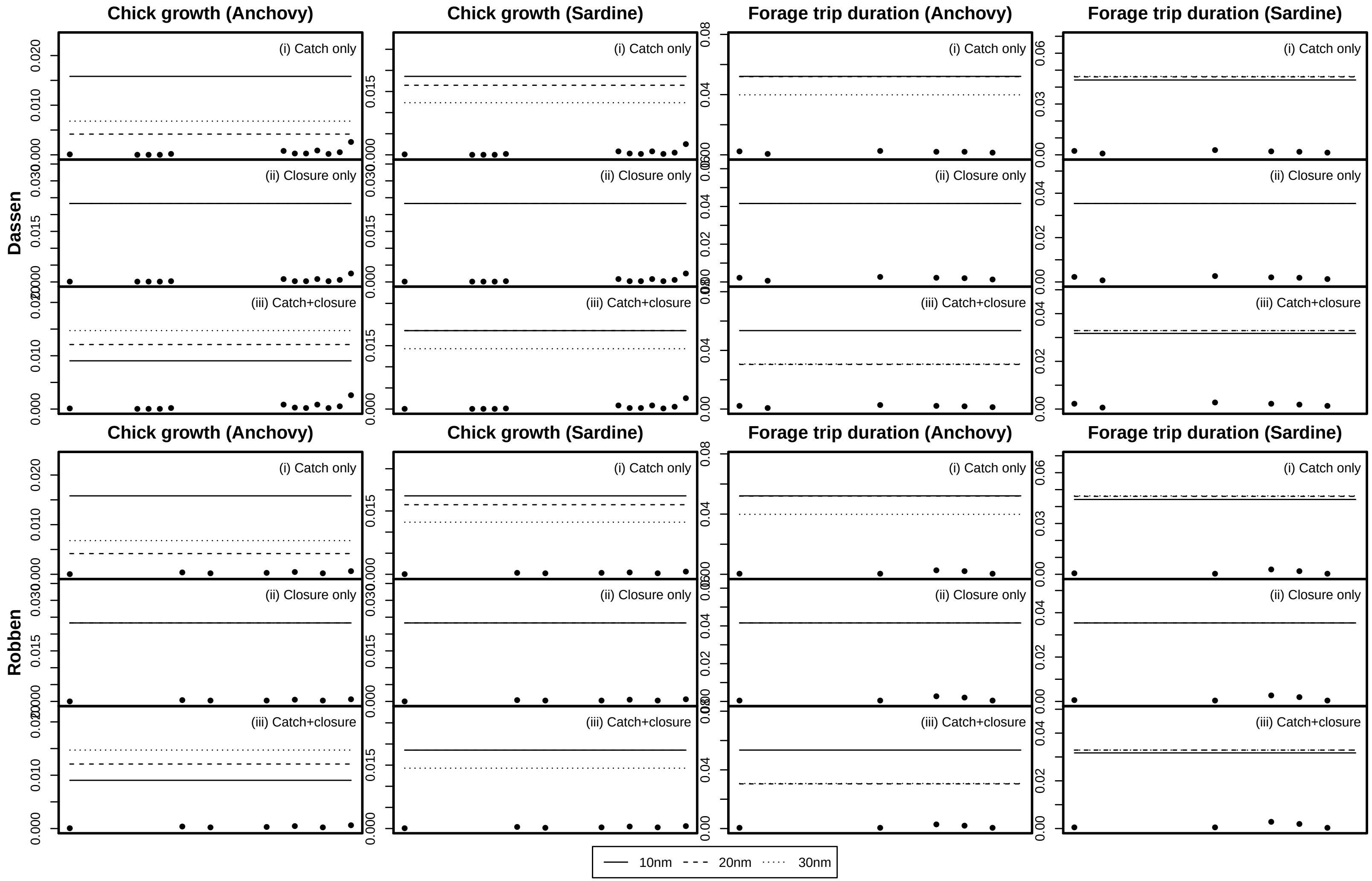


Figure 2.2: Plots comparing the GLM variance estimates σ^2 and the squared CVs from the data. The horizontal lines indicate the σ^2 values from the GLM for each of the 10nm, 20nm and 30nm catch zones. The black points show the CV^2 values from the data for the years for which these are available.

Table 2.1: Table corresponding to **Figure 2.2**. In each case, "Range" is the range of the observed CV^2s when standardised so that their mean is 1. For the 10nm, 20nm and 30nm catch zones, the GLM residual variance (σ^2) values are given as a multiples of the mean of the standardised **observed** CV^2 i.e. as multiples of one.

Dassen		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.09 5.24	0.09 5.24	0.38 1.46	0.38 1.46
(i) Catch only	10nm	32	38	28	24
	20nm	9	34	28	25
	30nm	14	25	22	25
(ii) Closure only	10nm	47	47	23	19
	20nm	47	47	23	19
	30nm	47	47	23	19
(iii) Catch+closure	10nm	18	38	29	17
	20nm	25	38	16	18
	30nm	30	29	17	18
Robben		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.10 1.85	0.10 1.85	0.31 2.26	0.31 2.26
(i) Catch only	10nm	48	56	43	36
	20nm	13	50	42	38
	30nm	21	38	33	38
(ii) Closure only	10nm	71	71	34	29
	20nm	71	71	34	29
	30nm	71	71	34	29
(iii) Catch+closure	10nm	28	56	44	26
	20nm	37	56	25	27
	30nm	45	43	25	27

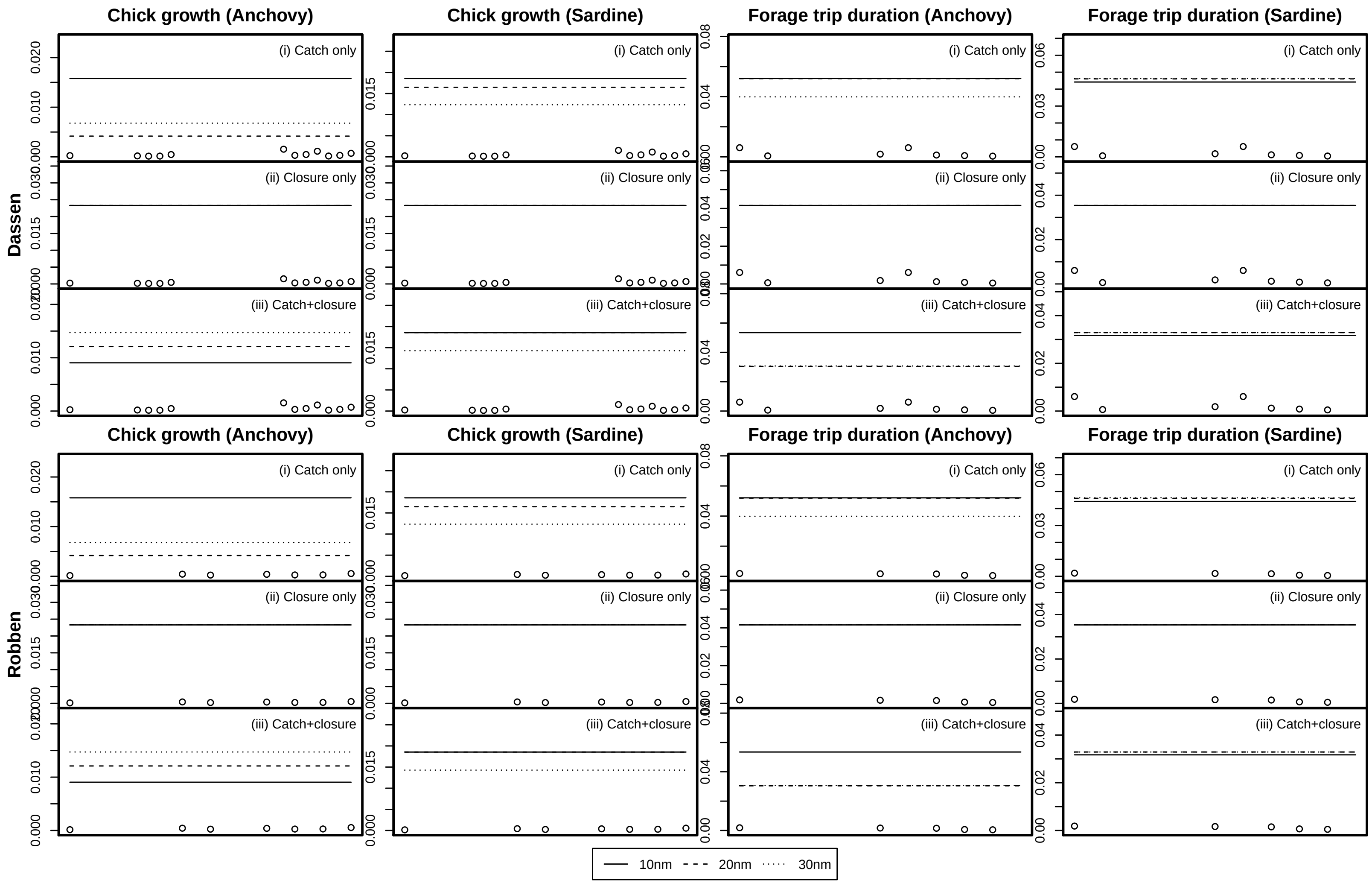


Figure 2.3: Same as Figure 2.2, except that the CV^2 values indicated by open circles are now the square of the expected CVs given by $CV^2_{exp} = m/N(y)$, where $m = \bar{y}/\bar{x}$ and $N(y)$ is the samples size for year y.

Table 2.2: Table corresponding to **Figure 2.3**. In each case, "Range" is the range of the expected CV^2s when standardised so that their mean is 1. For the 10nm, 20nm and 30nm catch zones, the GLM residual variance (σ^2) values are given as a multiples of the mean of the standardised **expected** CV^2 i.e. as multiples of one.

Dassen		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.30 3.14	0.30 3.14	0.20 2.48	0.20 2.48
(i) Catch only	10nm	32	38	21	18
	20nm	9	34	21	19
	30nm	14	25	16	19
(ii) Closure only	10nm	47	47	17	14
	20nm	47	47	17	14
	30nm	47	47	17	14
(iii) Catch+closure	10nm	18	38	22	13
	20nm	25	38	12	13
	30nm	30	29	13	13
Robben		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.45 1.66	0.45 1.66	0.39 1.50	0.39 1.50
(i) Catch only	10nm	48	56	43	36
	20nm	13	50	42	38
	30nm	21	38	33	38
(ii) Closure only	10nm	71	71	34	29
	20nm	71	71	34	29
	30nm	71	71	34	29
(iii) Catch+closure	10nm	28	56	44	26
	20nm	37	56	25	27
	30nm	45	43	25	27

2rev Penguin process vs observation error variance analysis — update with all available se values taken into account

Note that these analyses are based on data presented in an updated version of FISHERIES/2015/AUG/SWG-PEL/PENG/DATA1 from 16 October 2015.

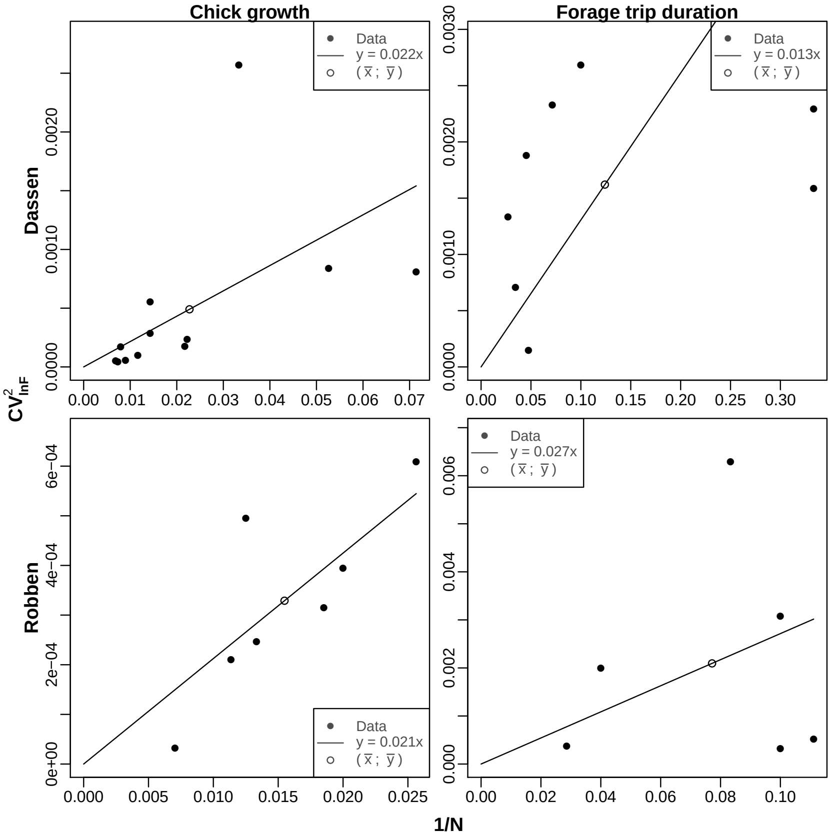


Figure 2rev.1: Plots of the square of the CVs of the log of the response variables chick growth and forage trip duration against the inverse of the sample size. Values are plotted for each year for which data are available. The line $y = mx$ is shown, where $m = \bar{y}/\bar{x}$, as well as the point $(\bar{x}; \bar{y})$.

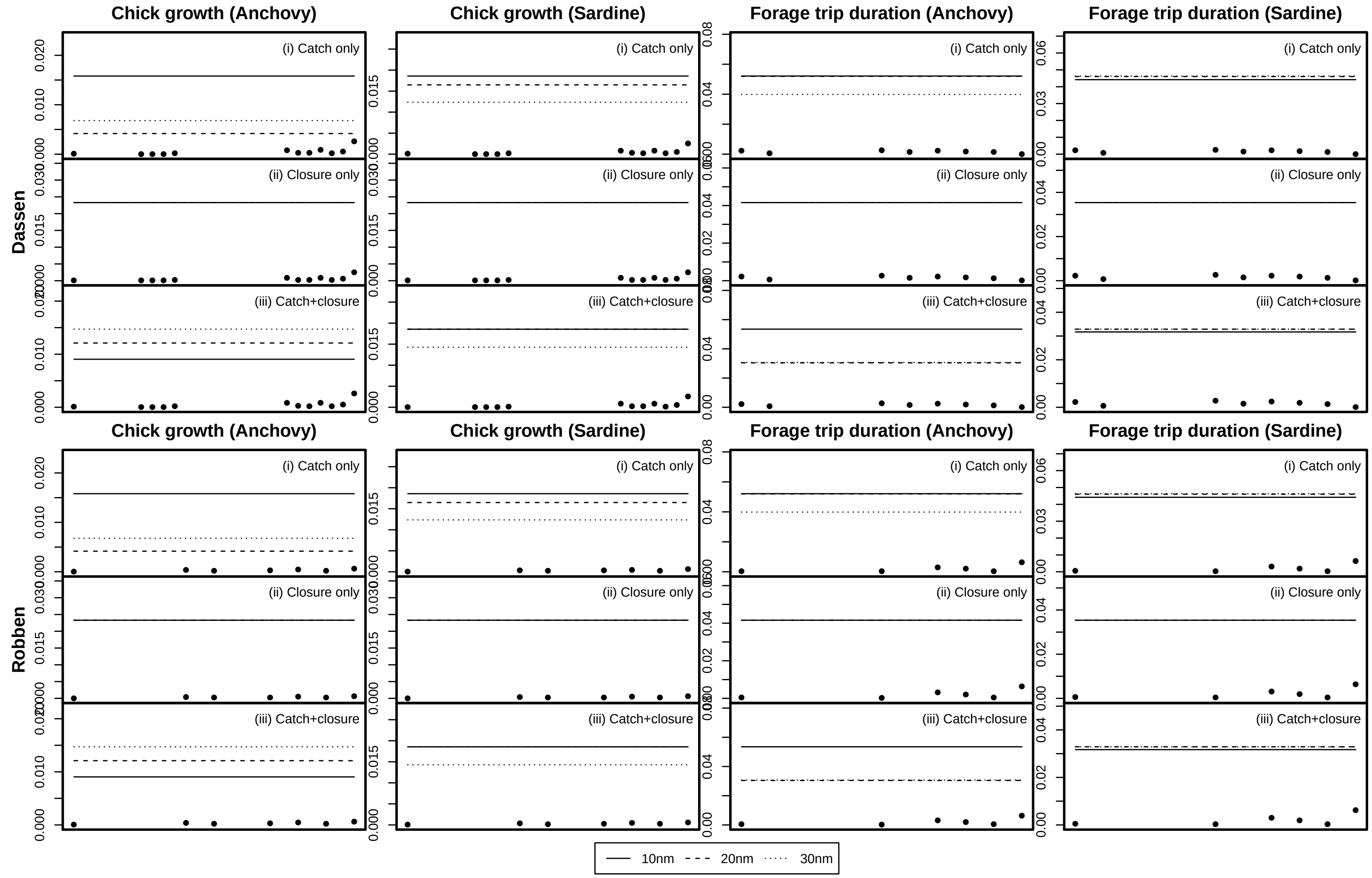


Figure 2rev.2: Plots comparing the GLM variance estimates σ^2 and the squared CVs from the data. The horizontal lines indicate the σ^2 values from the GLM for each of the 10nm, 20nm and 30nm catch zones. The black points show the CV^2 values from the data for the years for which these are available.

Table 2rev.1: Table corresponding to **Figure 2rev.2**. In each case, ”Range” is the range of the observed CV^2s when standardised so that their mean is 1. For the 10nm, 20nm and 30nm catch zones, the GLM residual variance (σ^2) values are given as a multiples of the mean of the standardised **observed** CV^2 i.e. as multiples of one.

Dassen		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.09 5.24	0.09 5.24	0.09 1.66	0.09 1.66
(i) Catch only	10nm	32	38	32	27
	20nm	9	34	32	28
	30nm	14	25	25	29
(ii) Closure only	10nm	47	47	26	22
	20nm	47	47	26	22
	30nm	47	47	26	22
(iii) Catch+closure	10nm	18	38	33	20
	20nm	25	38	19	20
	30nm	30	29	19	20
Robben		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.10 1.85	0.10 1.85	0.15 3.00	0.15 3.00
(i) Catch only	10nm	48	56	25	21
	20nm	13	50	25	22
	30nm	21	38	19	22
(ii) Closure only	10nm	71	71	20	17
	20nm	71	71	20	17
	30nm	71	71	20	17
(iii) Catch+closure	10nm	28	56	26	15
	20nm	37	56	15	16
	30nm	45	43	15	16

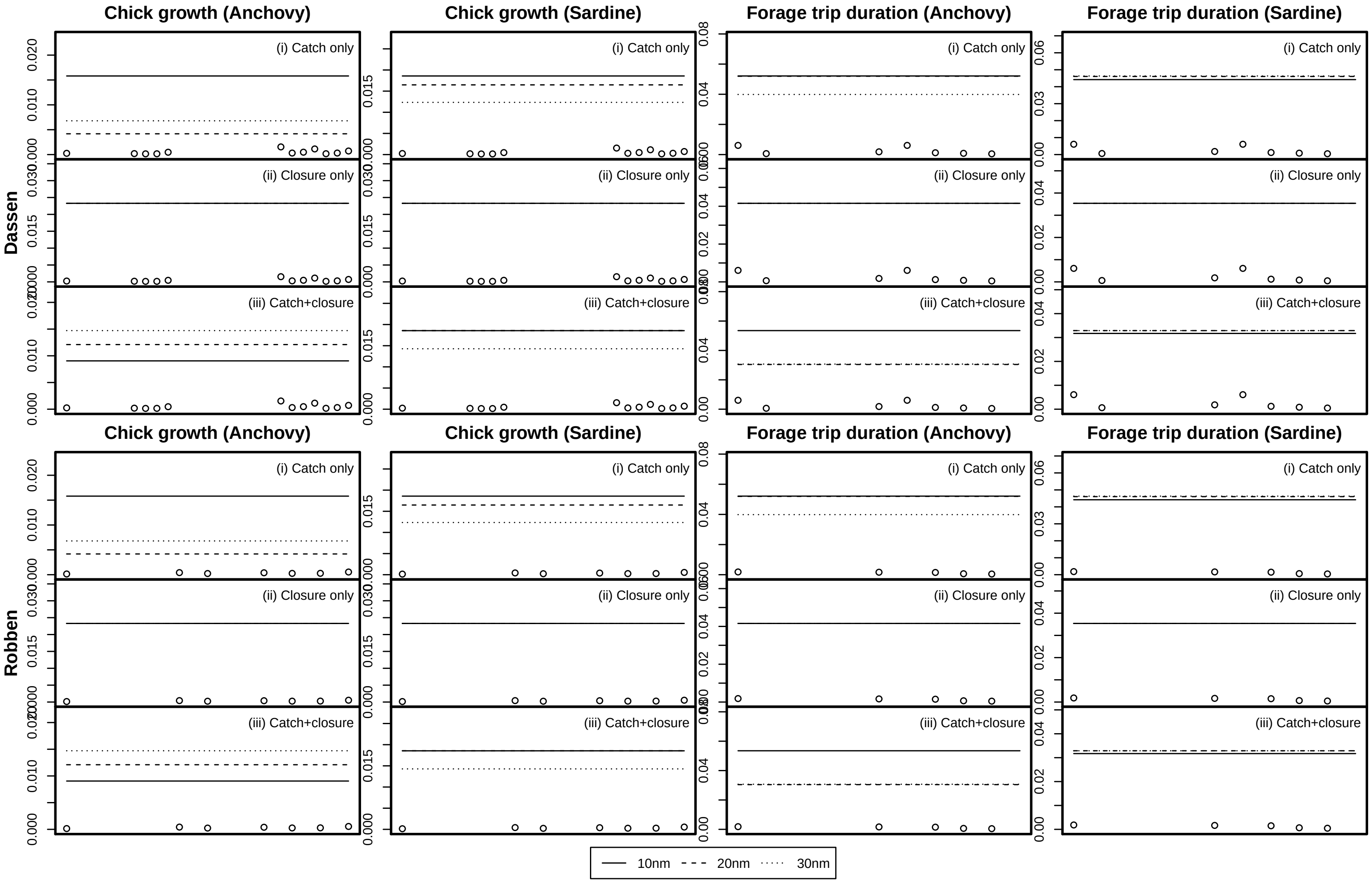


Figure 2rev.3: Same as Figure 2rev.2, except that the CV^2 values indicated by open circles are now the square of the expected CVs given by $CV^2_{exp} = m/N(y)$, where $m = \bar{y}/\bar{x}$ and $N(y)$ is the samples size for year y.

Table 2rev.2: Table corresponding to **Figure 2rev.3**. In each case, ”Range” is the range of the expected CV^2s when standardised so that their mean is 1. For the 10nm, 20nm and 30nm catch zones, the GLM residual variance (σ^2) values are given as a multiples of the mean of the standardised **expected** CV^2 i.e. as multiples of one.

Dassen		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.30 3.14	0.30 3.14	0.22 2.69	0.22 2.69
(i) Catch only	10nm	32	38	32	27
	20nm	9	34	32	28
	30nm	14	25	25	29
(ii) Closure only	10nm	47	47	26	22
	20nm	47	47	26	22
	30nm	47	47	26	22
(iii) Catch+closure	10nm	18	38	33	20
	20nm	25	38	19	20
	30nm	30	29	19	20
Robben		**Growth (Anchovy)**	**Growth (Sardine)**	**Duration (Anchovy)**	**Duration (Sardine)**
	Range	0.45 1.66	0.45 1.66	0.37 1.44	0.37 1.44
(i) Catch only	10nm	48	56	25	21
	20nm	13	50	25	22
	30nm	21	38	19	22
(ii) Closure only	10nm	71	71	20	17
	20nm	71	71	20	17
	30nm	71	71	20	17
(iii) Catch+closure	10nm	28	56	26	15
	20nm	37	56	15	16
	30nm	45	43	15	16

3 Generating pseudo data — evaluating correlation for all years in which catch and biomass are available

All years for which biomass and catch data are available (anchovy recruitment biomass from Table 12 and anchovy 10nm catches from Table 8 of MARAM/IWS/DEC15/PengD/BG1) are used in the calculations. Catches are generated from

$$C_{y,i,p} = \bar{C} + m(B_y - \bar{B}) + \eta_i$$

where

$\eta_i \sim N(0, \sigma_\eta^2)$

$B_y - \bar{B} \sim N(0, \sigma_B^2)$

$m = \phi \frac{\sigma_C}{\sigma_B}$

$\sigma_\eta = \sqrt{1-\phi^2}\sigma_c$

$\sigma_B^2 = \sigma_{Bobs}^2 - \left(\sum_y \sigma_{B_y} / \sum_y 1\right)^2$ with B_y now corresponding to the entire available biomass series, and

σ_C is the standard deviation of the entire catch series available.

Jack-knife estimates of variance of the correlation estimate from full catch-biomass series

Dassen: mean=0.408, $var_{jacknife}$=0.039, $\sqrt{var_{jacknife}}$=0.20

Robben: mean=0.195, $var_{jacknife}$=0.051, $\sqrt{var_{jacknife}}$=0.23

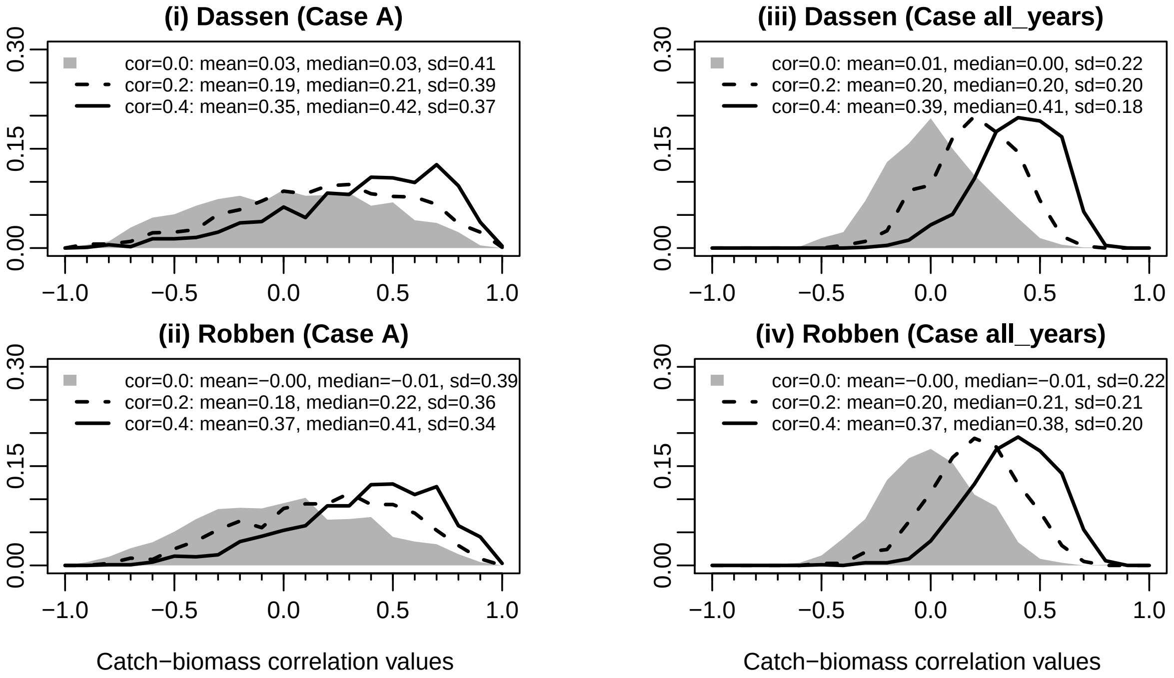


Figure 3.1: Distribution of the correlation between catch and biomass. Case (A) is as described in Section 4 and only takes years for which response data are available into account and "all_years" takes all years for which biomass and catch are available into account.

4 Generating pseudo data — some initial results

The results below are based on mixed model results for the sub-regional biomass surrogate approach (Equation 1 of MARAM/IWS/DEC15/PengD/P1), catch only ($\delta = 0$), response variable chick growth, fish species anchovy and $10nm$ catches. The variance adjustment of Equation (2) of MARAM/IWS/DEC15/PengD/P1 has not been implemented. Further, pseudo data have been generated using an autocorrelation value of $\mu = 0$ (Equation 8 of MARAM/IWS/DEC15/PengD/P1). σ_ϵ for Equation (8) does not take sample size into account, and the σ_0 value is the biomass surrogate model estimate of the residual standard deviation.

NB: The chick growth values used here are the **median** growth rates up to 2012, these being the data available at the time these simulation exercises were initiated.

Table 4.1: Mean and standard deviation of the observed and generated response variable chick growth (F_y), calculated for both islands are provided. "Observed" corresponds to the mean and standard deviation of the values in Table 2 of MARAM/IWS/DEC15/PengD/BG1. Results are further given for 1000 generated series of F_y, with N_y years in each series. The mean, standard deviation and standard error of the mean of the $1000 * N_y$ estimates of F_y are given. Note that the generated data correspond to those for Case A from Table 4.2.

	Dassen			Robben		
Observed	Mean	sd		Mean	sd	
	0.0348	0.0059		0.0364	0.0058	
1000 generated sets	Mean	sd	sem	Mean	sd	sem
$\phi = 0.0$	0.0351	0.0063	0.0001	0.0384	0.0069	0.0001
$\phi = 0.2$	0.0351	0.0061	0.0001	0.0382	0.0069	0.0001
$\phi = 0.4$	0.0349	0.0059	0.0001	0.0383	0.0070	0.0001

Table 4.2: Estimate and standard error of λ from the biomass surrogate model when applied to the actual data are reported for Dassen island. The biomass surrogate model was applied to the 1000 generated data sets and a lambda value estimated for each set. The mean, median, standard deviation and standard error of the mean of the 1000 estimated λ values are provided. The m^{calc} values calculated from Equation (6) of MARAM/IWS/DEC15/PengD/P1 for each value of ϕ are provided, as well as the regression $\hat{m}$ values from Table 1 of MARAM/IWS/DEC15/PengD/P1 alongside the correlation values calculated for each these $\hat{m}$ values from Equation (6) of MARAM/IWS/DEC15/PengD/P1. $\Delta_{\phi_0}^{mean/med}$ gives the difference between $\lambda_{\phi=0.2} - \lambda_{\phi=0}$ and $\lambda_{\phi=0.4} - \lambda_{\phi=0}$ for the mean/median estimates of λ.

Partitions of the table correspond to the following:

(A) is a repetition of the results previously circulated.

(B) is a re-run of (A) where the biomass values are constrained to be positive by putting the boundaries $\hat{\alpha} \pm \frac{\bar{B}}{\sigma_B}\sigma_\alpha$ instead of $\hat{\alpha} \pm 2\sigma_\alpha$.

(C) is a re-run of (A) where samples corresponding to the first and fourth quantiles of correlation values have been removed from the set of 1000 samples.

(D) is a re-run of (A) except that $\hat{\alpha}_y$ is sampled with replacement from the biomass surrogate model estimates for α_y (instead of sampled from a normal distribution), but $\eta_i \sim N(0, \sigma_\eta^2)$ as before (Equation 4 of MARAM/IWS/DEC15/PengD/P1).

(E) is a re-run of (D) for the case where $\phi = 0$ and η is now sampled with replacement from the $C_y - \bar{C}$, where C_y is the catch series in question (Equation 4 of MARAM/IWS/DEC15/PengD/P1).

Dassen λ estimates							
Biomass surrogate model estimate applied to actual data	-0.0564		(se = 0.0675)				
Generated data	Regression $\hat{m} = 2.26 \implies$		$\phi^{calc} = 0.37$				
(A) 1000 generated sets	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	-0.0487		-0.0480		0.0636	0.0020	0.00
$\phi = 0.2$	-0.0347	(0.0141)	-0.0315	(0.0165)	0.0634	0.0020	1.42
$\phi = 0.4$	-0.0205	(0.0282)	-0.0171	(0.0309)	0.0583	0.0018	2.85
(B) Biomass forced positive	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	-0.0518		-0.0500		0.0573	0.0018	0.00
$\phi = 0.2$	-0.0350	(0.0168)	-0.0340	(0.0160)	0.0615	0.0019	1.42
$\phi = 0.4$	-0.0224	(0.0293)	-0.0219	(0.0281)	0.0577	0.0018	2.85
(C) Exclude 1^{st} and 4^{th} quantiles	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	-0.0473		-0.0453		0.0620	0.0020	0.00
$\phi = 0.2$	-0.0333	(0.0140)	-0.0272	(0.0181)	0.0655	0.0021	1.42
$\phi = 0.4$	-0.0220	(0.0253)	-0.0170	(0.0284)	0.0590	0.0019	2.85
(D) Method 2	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	-0.0490		-0.0480		0.0536	0.0017	0.00
$\phi = 0.2$	-0.0436	(0.0054)	-0.0414	(0.0066)	0.0543	0.0017	1.42
$\phi = 0.4$	-0.0353	(0.0137)	-0.0333	(0.0147)	0.0503	0.0016	2.85
(E) Method 3	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	-0.0449		-0.0430		0.0472	0.0015	0.00

Table 4.3: Repeat of Table 4.2 for Robben island.

Robben λ estimates							
Biomass surrogate model estimate applied to actual data	0.0524		(se = 0.1349)				
Generated data	Regression $\hat{m} = 2.26 \implies$		$\phi^{calc} = 0.37$				
(A) 1000 generated sets	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	0.0345		0.0312		0.0781	0.0025	0.00
$\phi = 0.2$	0.0405	(0.0060)	0.0393	(0.0048)	0.0784	0.0025	2.68
$\phi = 0.4$	0.0458	(0.0113)	0.0422	(0.0110)	0.0755	0.0024	5.35
(B) Biomass forced positive	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	0.0328		0.0341		0.0688	0.0022	0.00
$\phi = 0.2$	0.0381	(0.0053)	0.0392	(0.0064)	0.0728	0.0023	2.68
$\phi = 0.4$	0.0426	(0.0098)	0.0417	(0.0076)	0.0734	0.0023	5.35
(C) Exclude 1^{st} and 4^{th} quantiles	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	0.0346		0.0347		0.0778	0.0025	0.00
$\phi = 0.2$	0.0394	(0.0048)	0.0438	(0.0092)	0.0794	0.0025	2.68
$\phi = 0.4$	0.0465	(0.0119)	0.0430	(0.0082)	0.0780	0.0025	5.35
(D) Method 2	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	0.0369		0.0362		0.0665	0.0021	0.00
$\phi = 0.2$	0.0383	(0.0014)	0.0353	(-0.0016)	0.0661	0.0021	2.68
$\phi = 0.4$	0.0446	(0.0077)	0.0402	(0.0041)	0.0674	0.0021	5.35
(E) Method 3	Mean	$\Delta_{\phi_0}^{mean}$	Median	$\Delta_{\phi_0}^{med}$	sd	sem	m^{calc}
$\phi = 0.0$	0.0321		0.0324		0.0612	0.0019	0.00

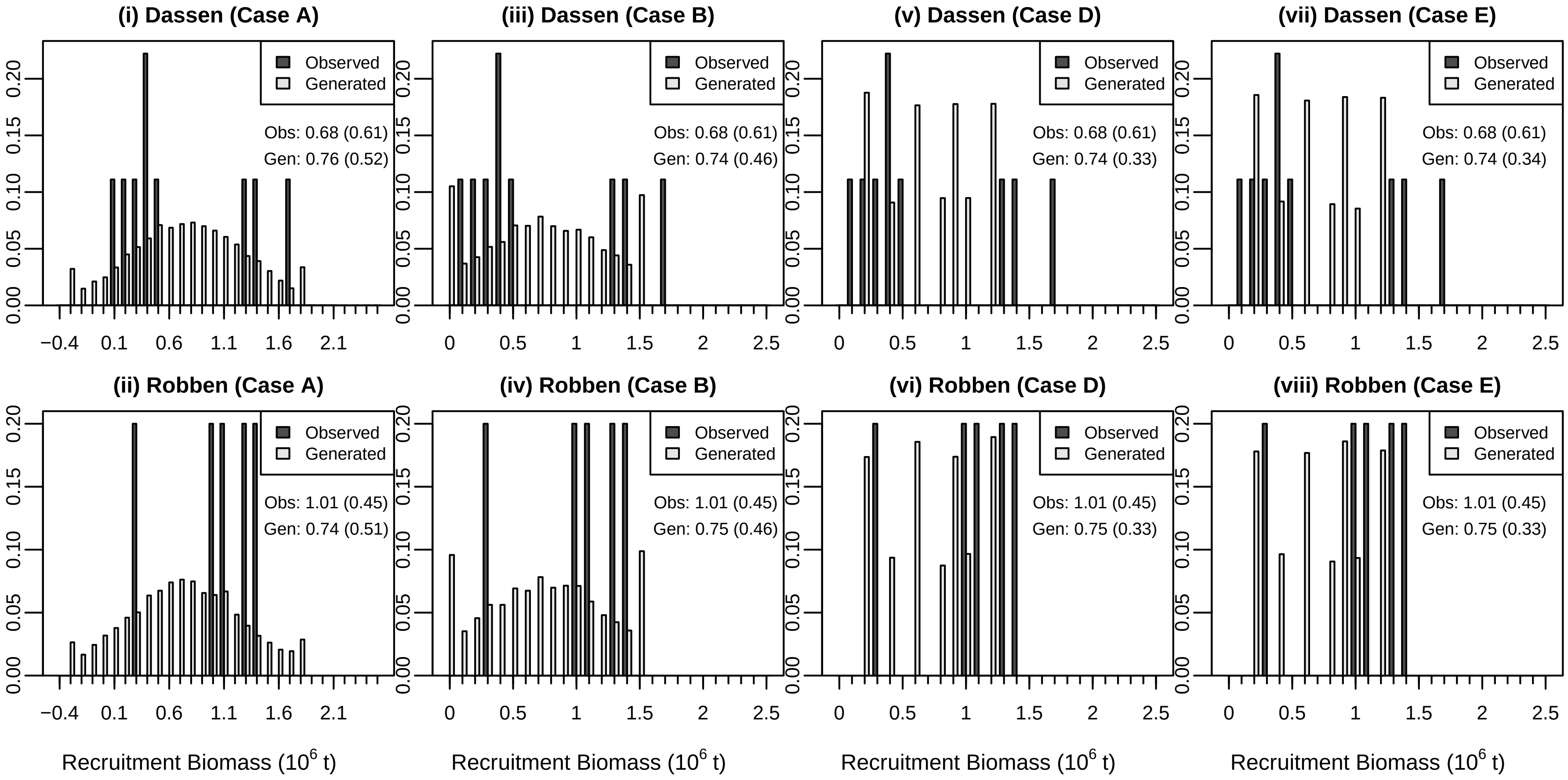
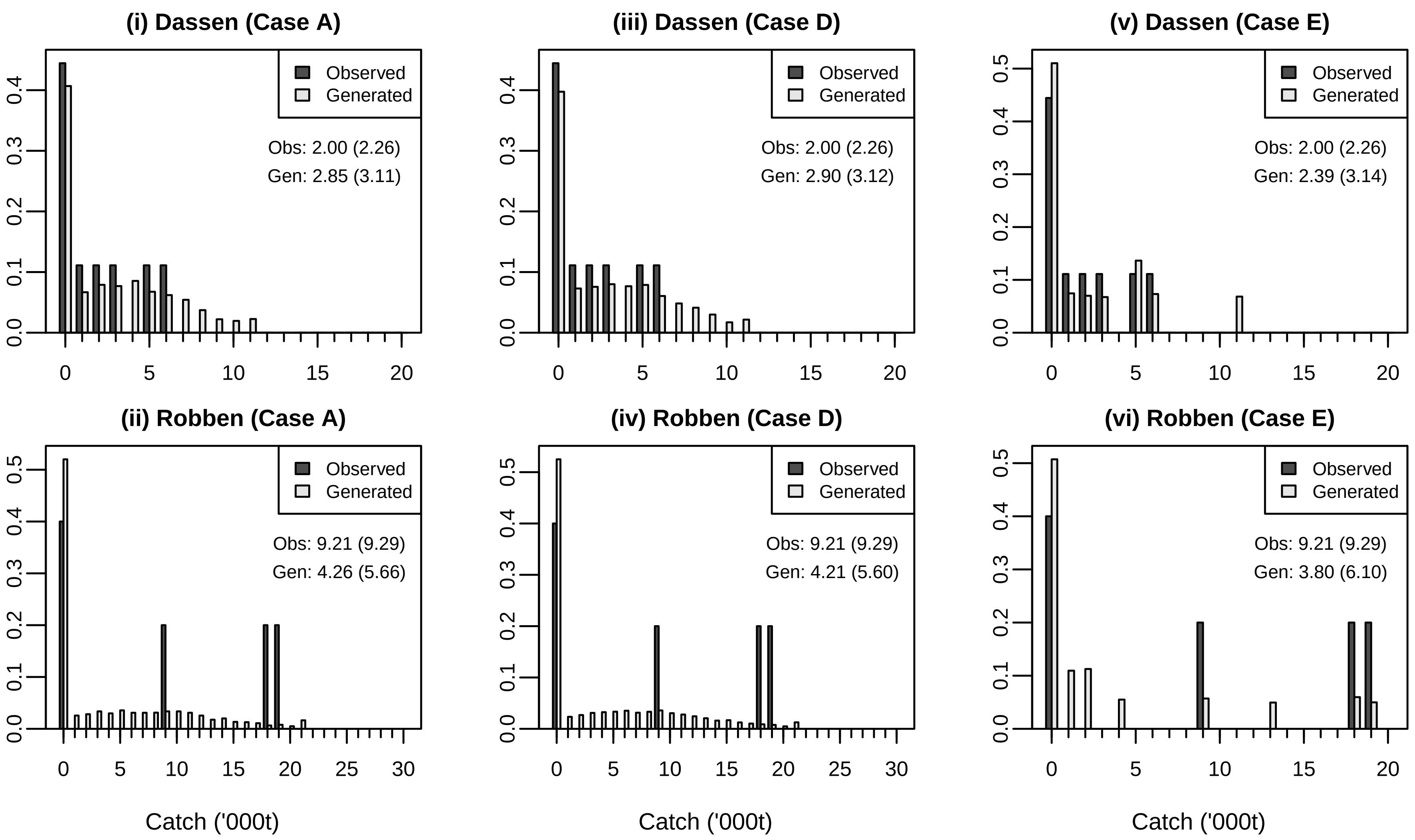


Figure 4.1: Distributions of the observed and generated recruitment biomass data are provided for four cases. (A) is a repetition of the results previously circulated, (B) is a re-run of (A) where the biomass values are constrained to be positive, (D) is a re-run of (A) except that $\hat{\alpha}_y$ is sampled with replacement from the biomass surrogate model estimates for α_y, and (E) is a re-run of (D) for the case where $\phi = 0$ and η is now sampled with replacement from the $C_y - \bar{C}$. In all cases except (E), $\phi = 0.2$. Note that for each island only years for which chick growth data are available have been used. Mean values and standard deviations are also provided.



(i) Dassen (Case A)

(iii) Dassen (Case D)

(v) Dassen (Case E)

(ii) Robben (Case A)

(iv) Robben (Case D)

(vi) Robben (Case E)

Figure 4.2: Distributions of the observed and generated catch data are provided for three cases. (A) is a repetition of the results previously circulated, (D) is a re-run of (A) except that $\hat{\alpha}_y$ is sampled with replacement from the biomass surrogate model estimates for α_y, and (E) is a re-run of (D) for the case where $\phi = 0$ and η is now sampled with replacement from the $C_y - \bar{C}$. In all cases except (E), $\phi = 0.2$. Note that for each island only years for which chick growth data are available have been used. Mean values and standard deviations are also provided.

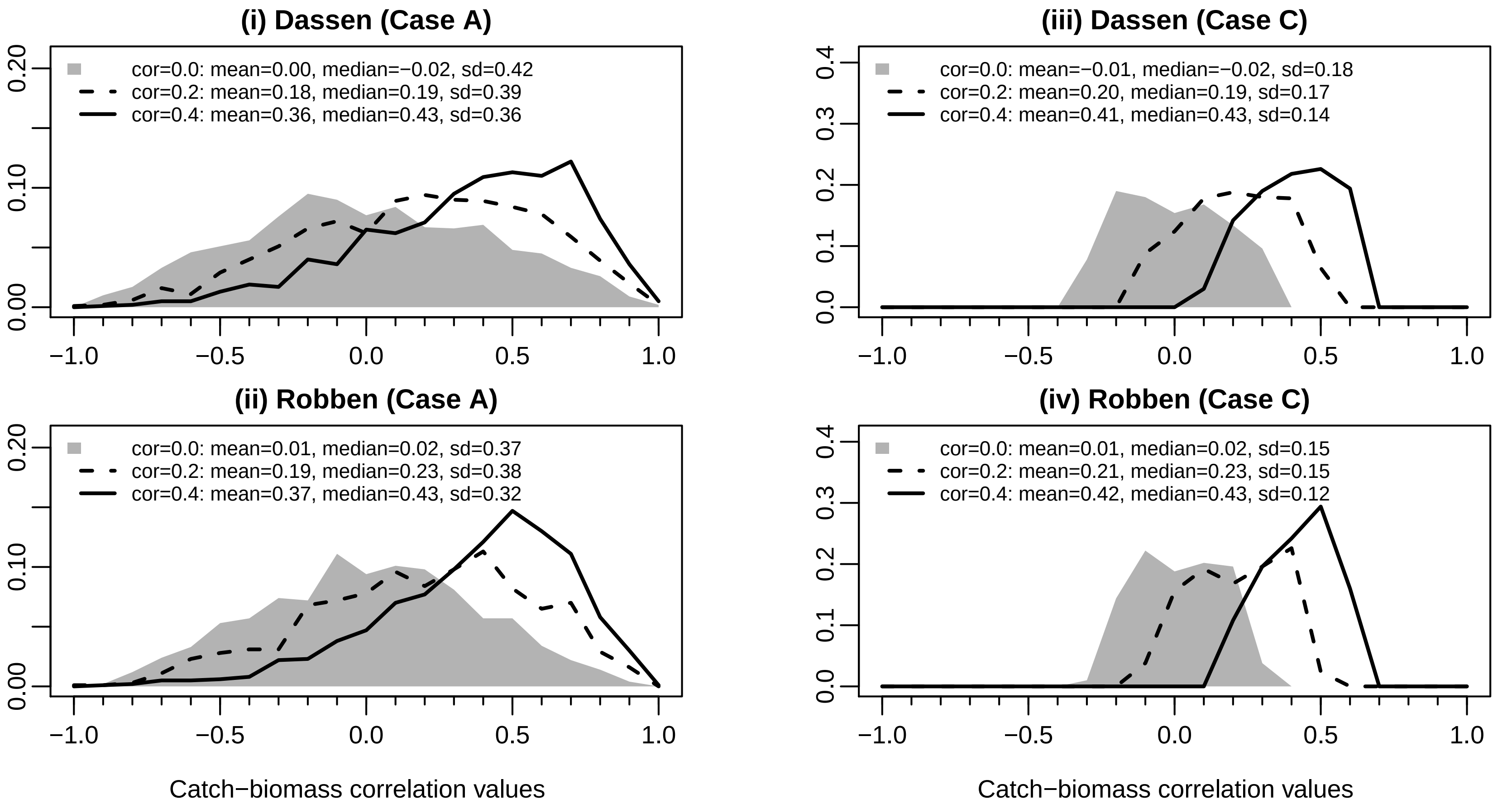


Figure 4.3: Distribution of the correlation between catch and biomass estimated for each of the 1000 simulated data sets, for two cases. (A) is a repetition of the results previously circulated, and (C) is a re-run of (A) where samples corresponding to the first and fourth quantiles of correlation values have been removed from the set of 1000 samples. The grey shaded areas, dashed lines and solid lines show the distributions for a correlation ϕ of 0, 0.2 and 0.4 respectively. The mean, median and standard deviation of each distribution are shown in the legend. Note that for each island, only years for which chick growth data are available have been used to calculate the correlation values. Also note that the edges of the distributions for Case C are not straight simply as a result of how the data have binned.

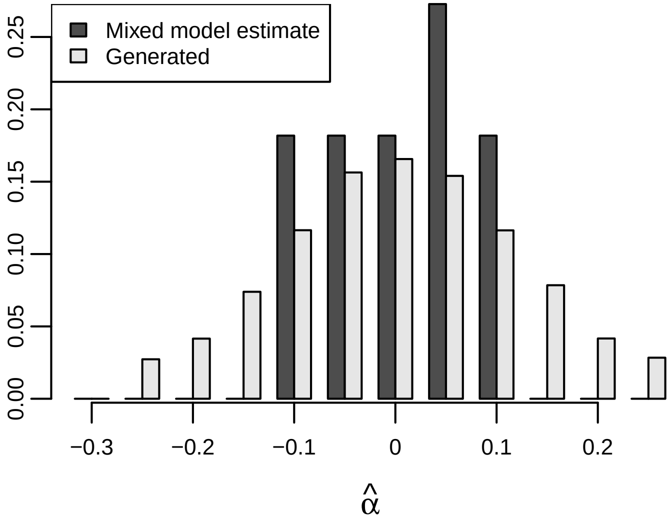


Figure 4.4: Distribution of the generated $\hat{\alpha}$ values plotted alongside the estimates from the biomass surrogate model, for **Case A** with $\boldsymbol{\phi = 0.2}$.

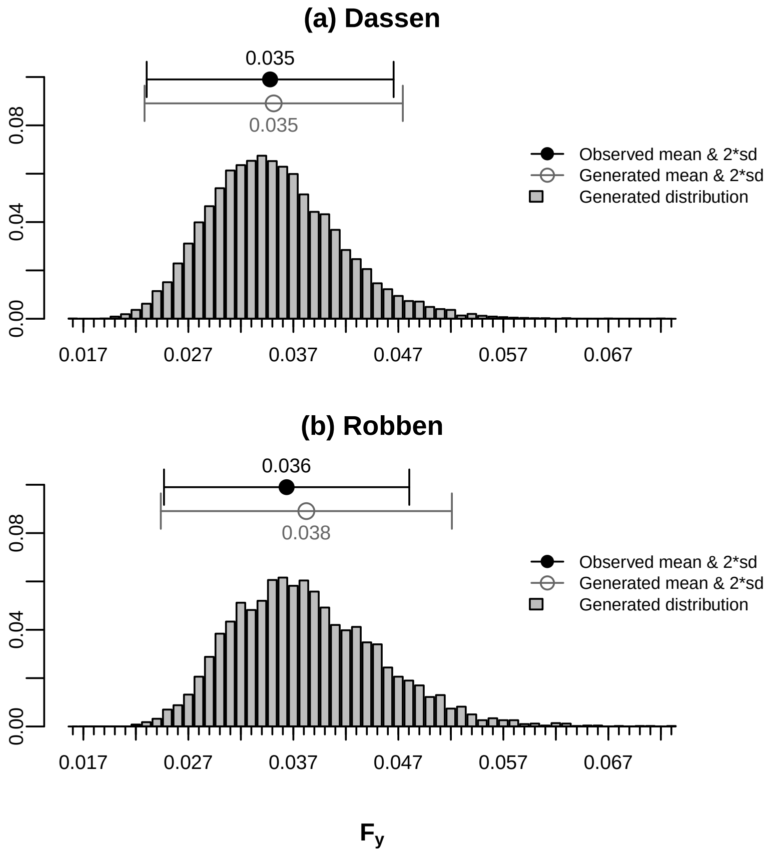


Figure 4.5: Distributions of the $N_y * 1000$ generated F_y values are shown for **Case A** and $\boldsymbol{\phi = 0.2}$ by the grey bars. The mean and 95 % confidence interval (twice standard deviation) are shown by black dots and error bars for the observed data, and by grey open circles and grey error bars for the generated data.

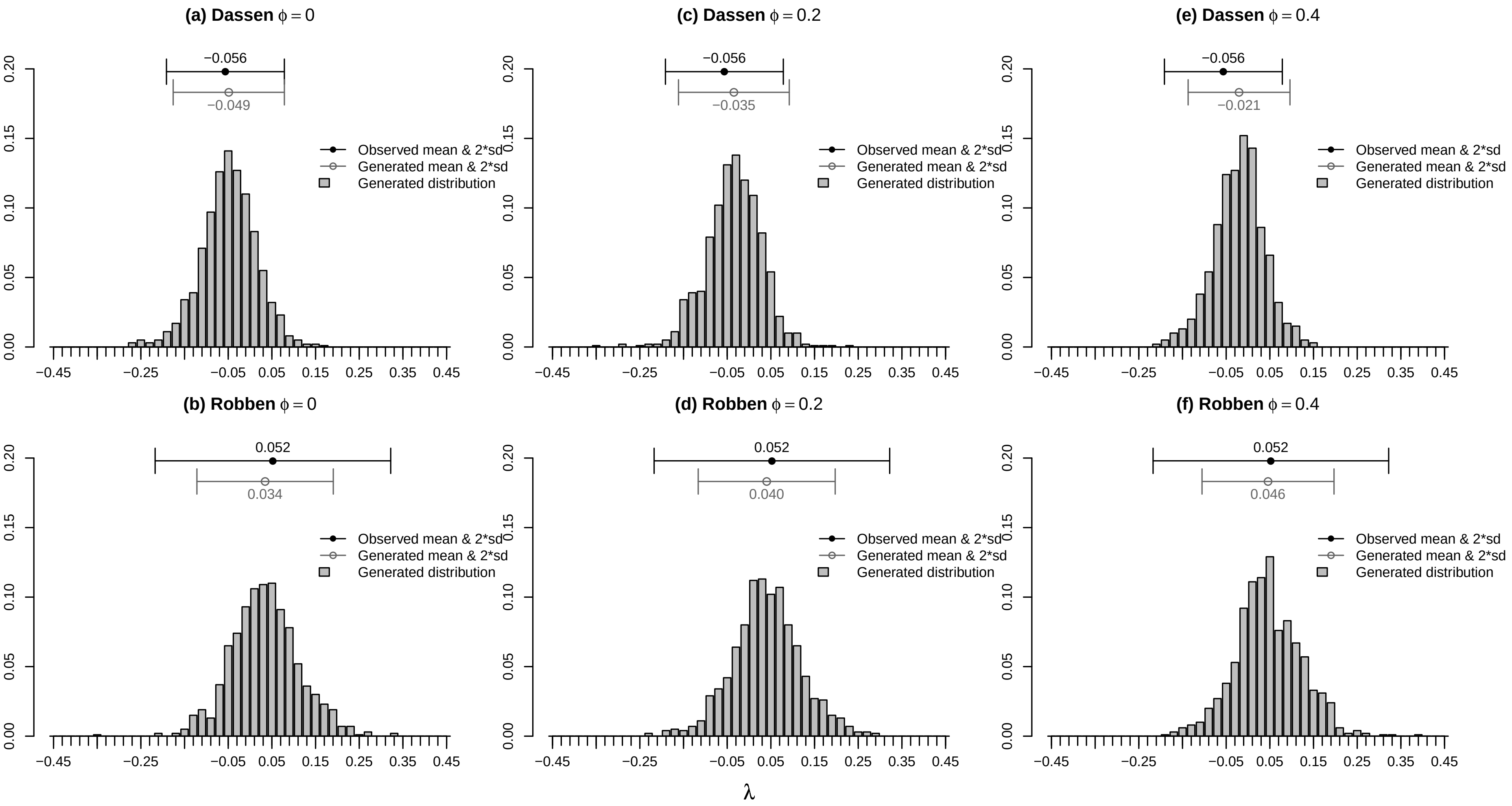


Figure 4.6: Distributions of the λ values estimated for the 1000 generated data sets are shown for **Case A** by the grey bars. The mean and 95% confidence interval (twice standard error) are shown by black dots and error bars for the λ estimate of the biomass surrogate model applied to the observed data and by grey open circles and grey error bars for the biomass surrogate model applied to the generated data.

5 A problem detected with the biomass surrogate approach

When point estimates of λ and δ were computed to construct Figures 5.1 and 5.2, which have been extended from Figures 1.1 and 1.2 to include results for $C_{closure}$ catches corresponding to a circle radius of 18km around the island), given the urgency that prevailed at the time the individual fits of the random effects models were not examined closely.

Now however, with the generation of further pseudo-data for simulation testing purposes imminent, a closer examination has revealed that in a number of cases the standard deviation of the random effects α year parameter is zero (see Table 5.1). In these cases it would seem that the REML estimator prefers treating the year effect parameter (the biomass surrogate) as constant over time — presumably a consequence of working with data sets with relative few degrees of freedom for the estimator being applied. In these circumstances it would certainly not be realistic to assume this standard deviation to be zero when generating pseudo-data. Furthermore the estimates of λ or of δ in these circumstances must themselves be open to question.

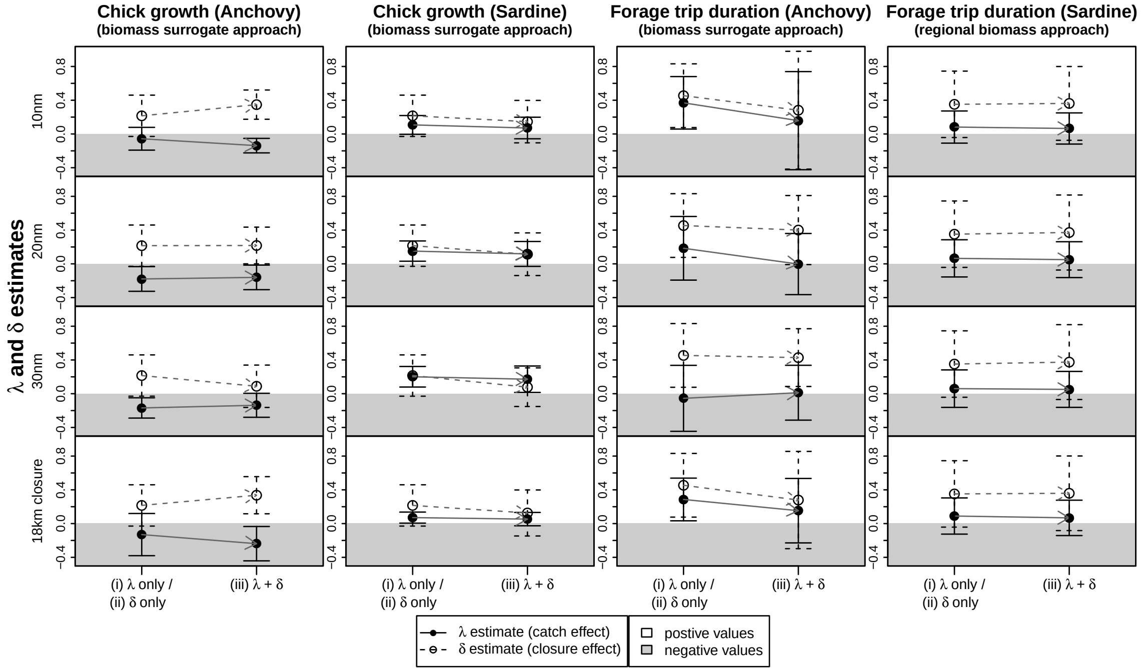
While ad hoc solutions to this problem could be suggested (e.g. fixing the standard deviation of the random effects in the estimator in such instances to the average of the values obtained when estimation is satisfactory — and appears to yield values of about 0.12 fairly consistently), this would require further checking as to the reliability of such an approach. In the shorter term then, it is proposed that such instances be omitted from further consideration at this time, with the associated estimates of λ or δ also regarded as unreliable at this stage and not taken further. Note that this includes omitting catch+closure cases where one of the two variables considered in isolation yielded a zero standard deviation for α — these cases are grey-highlighted in Table 5.1 below.

Table 5.1: Estimates of the standard deviation of the random effects variable $\hat{\alpha}$.

		Chick Growth Anchovy	Chick Growth Sardine	Forage Trip Duration Anchovy
(i) Catch only	10nm	0.12	0	0
	20nm	0.14	0	0.12
	30nm	0.11	0	0.16
	18km closure	0.14	0	0
(i) Closure only	10nm	0	0	0.12
	20nm	0	0	0.12
	30nm	0	0	0.12
	18km closure	0	0	0.12
(i) Catch+closure	10nm	0	0	0.08
	20nm	0.08	0	0.14
	30nm	0.08	0	0.12
	18km closure	0	0	0

Table 5.2: A summary of the number of years for which data are available and number of years within that period for which the islands were closed to fishing is provided.

		No. years for which data are available	No. years for which data are available and island was closed
Chick growth (median)	Dassen	9	2
	Robben	5	2
	Total	11	4
Forage trip duration	Dassen	8	2
	Robben	6	3
	Total	8	5


(a) Dassen Island

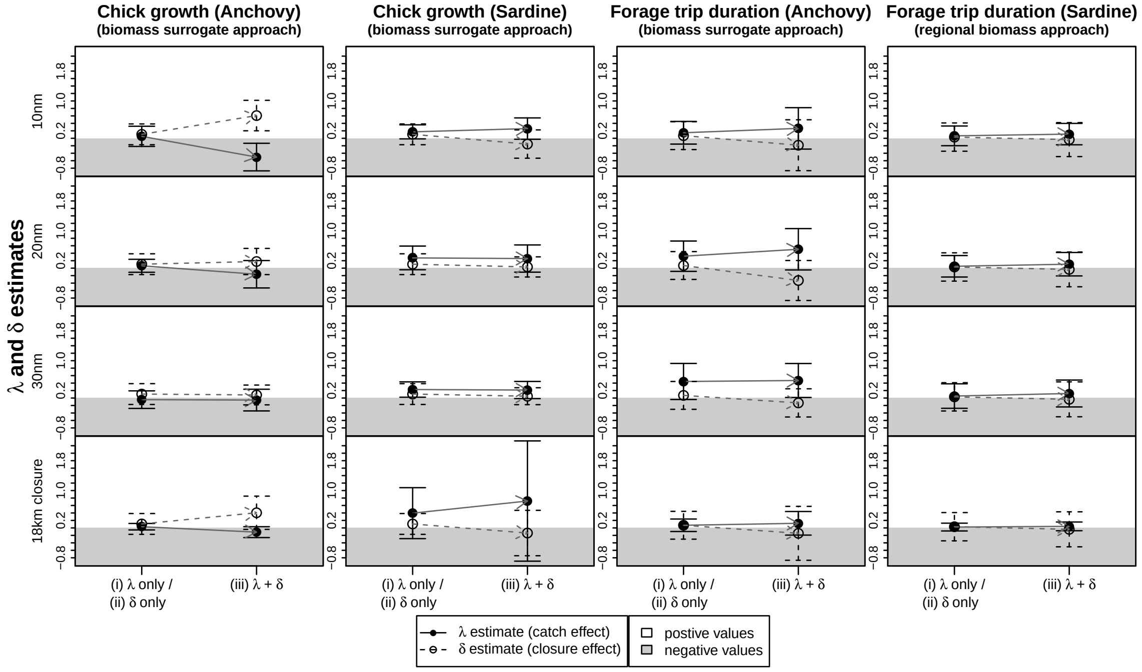
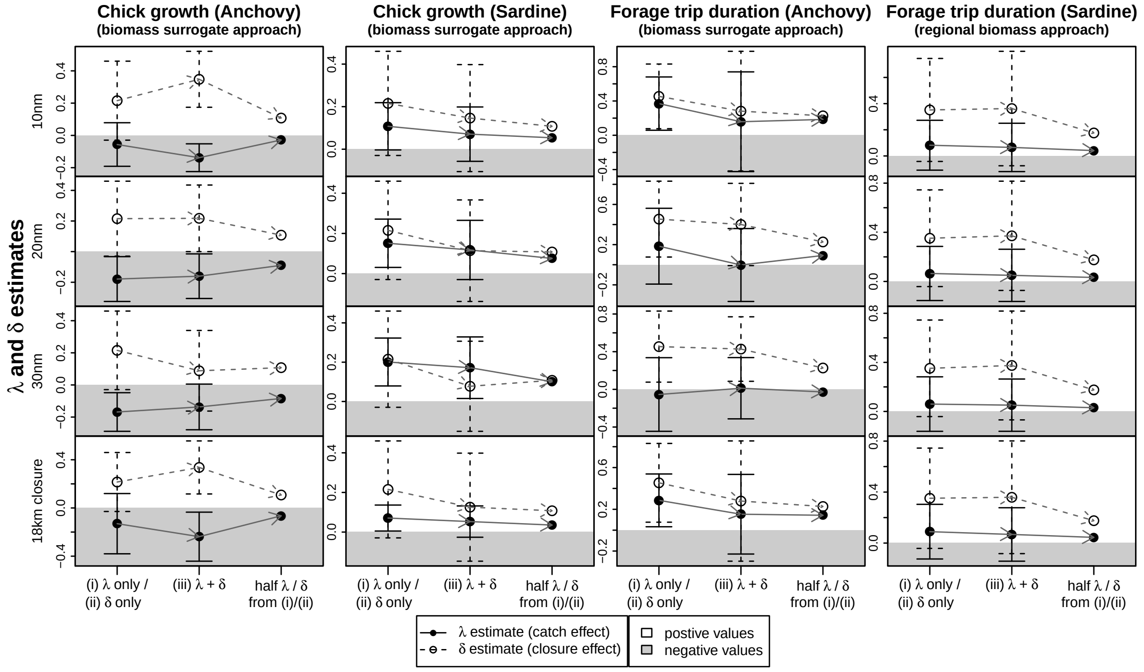

(b) Robben Island

Figure 5.1: Graphical representation of the λ and δ estimates and 95% confidence intervals (twice standard error) for "(i) catch only / (ii) closure only" and "(iii) catch+closure" forms of the operating model (see MARAM/IWS/DEC15/PengD/P1). Estimates are shown for four different different scenarios and **four** catch zones. The grey shaded areas indicate negative values. Note that the adjusted variance of Equation (2) of MARAM/IWS/DEC15/PengD/P1 has not yet been implemented, and that data from MARAM/IWS/DEC15/PengD/BG1 were used to generate the results presented here. For the regional biomass approach, the spawner biomass surveys of the previous November have been used.

(a) Dassen Island



(b) Robben Island

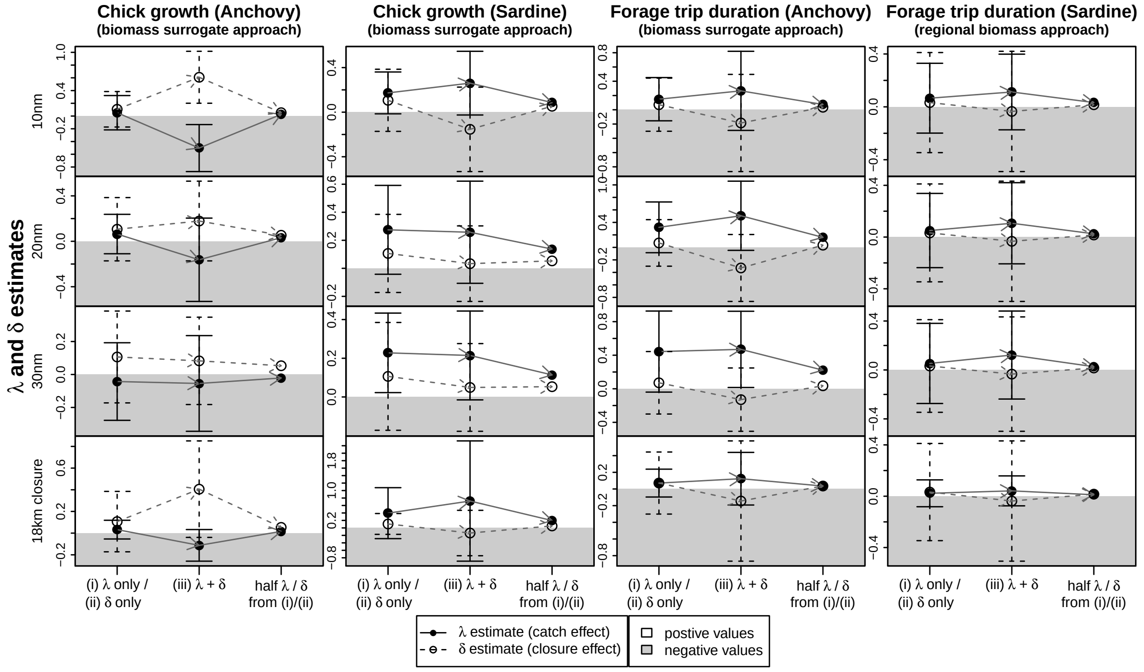


Figure 5.2: Graphical representation of the λ and δ estimates and 95% confidence intervals (twice standard error) for "(i) catch only / (ii) closure only" and "(iii) catch+closure" forms of the operating model (see MARAM/IWS/DEC15/PengD/P1), **as well as estimates given by half the value of the estimate from the individual catch/closure only operating model**. Estimates are shown for four different different scenarios and **four** catch zones. The grey shaded areas indicate negative values. Note that the vertical axes are not to the same scale. As for Figure 5.1, the adjusted variance of Equation (2) of MARAM/IWS/DEC15/PengD/P1 has not yet been implemented, and data from MARAM/IWS/DEC15/PengD/BG1 have been used. For the regional biomass approach, the spawner biomass surveys of the previous November have been used.

6 Possible further analyses (in rough priority order)

Completing ones already specified that remain viable

This involves repeat of bias analyses similar to that presented in Table 4.2 of the chick growth analysis, though only for one (or at most two) pseudo-data generation approaches (to be agreed at the meeting of the Penguin Task Team Tuesday 27 October 2015). Same specifications as for that chick growth analysis unless otherwise specified.

1. Biomass surrogate approach — forage trip duration — anchovy — 20 nm
2. Regional biomass approach forage trip duration — sardine
    (a) Without taking sample size into account
    (b) Taking sample size into account

Priorities for further biomass surrogate approach runs

1. Closure rather than catch — forage trip duration — anchovy — 20 nm
2. Effect of autocorrelation of residuals — chick growth — anchovy — 10nm+20nm
3. Effect of autocorrelation of residuals — forage trip duration — anchovy — 20nm - closure
4. Effect of different distance to define catches — chick growth — 20 nm
5. Effect of both catch and closure — forage trip duration — anchovy — 20 nm
6. Use of simpler estimator — eg Panel proposal of a unique island closure effect
7. Repeat for further response variables
8. (A few) other combinations of factors (priority to closure in place of catch)

Priorities for further regional biomass approaches

1. Repeat options of previous section to extent possible

Note: The main purpose of the above is to see the Panel in December placed in a position to advise on the appropriate approach to complete further calculations thereafter to the extent required to provide a basis for a decision regarding island closures in the future.

Use of individual sample data

Suggest a GLM analysis to standardise taken month as a factor (who will do this?). Repeat estimation with standardised to compare with nominal results for estimators performing well in simulations.

Power analyses

Approach to be used to be discussed at next meeting. This to include identification of priorities for attention, including catch vs closure comparison and implications of residual autocorrelation

7 Evaluating small-sample-size bias

Concern was expressed over the bias exhibited between the mean λ value estimated from the generated data ($\hat{\lambda}$) and the underlying biomass surrogate model estimate of λ used to generate the data (λ^{true}) when the correlation ϕ was set to zero. This document explores whether the small sample sizes of data available (in particular the five years for Robben island) are responsible for this bias. Two approaches were used to investigate this:

- Generate further data into the future and utilise these additional data to estimate $\hat{\lambda}$. Note that for this initial run, closure was not simulated for future years, i.e. islands were taken to be open for all years.
- No future data are generated, but instead "gaps" in past data are filled. Previously, if chick growth data are available in a particular year y for Dassen but not for Robben, then that year y would be included for Dassen but excluded for Robben (and *vice versa*). In this alternative approach, this year y is included for both Robben and Dassen. Thus where nine years for Dassen and five years for Robben were utilised previously to calculate λ, 11 years are now used for each island.

As before, the results here are based on biomass surrogate model results for the sub-regional biomass surrogate approach (Equation 1), catch only ($\delta = 0$), response variable chick growth, fish species anchovy and 10nm catches. The variance adjustment of Equation (2) has not been implemented. Further, pseudo data have been generated using an autocorrelation value of $\mu = 0$ (Equation 8). σ_ϵ for Equation (8) does not take sample size into account, and the σ_0 value is the biomass surrogate model estimate of the residual standard deviation.

NB: The chick growth values used here are the **median** growth rates up to 2012, these being the data available at the time these simulation exercises were initiated.

Discussion

The results shown in Tables 7.1 and 7.2 and in Figure 7.1 show that the bias under examination reduces to zero as extra years of data are added, and further that "gap filling" for the period of the existing data reduces this bias, especially for Robben.

This seems to confirm that there is a small-sample-size bias associated with the estimates from existing data, which is exacerbated by the unbalanced nature of these data.

Also evident is that as the period for which data are available is increased, the additional bias associated with the estimator ignoring catch-biomass correlation ($\Delta_{\phi 0}$) increases, more so for Robben.

Table 7.1: The estimate and standard error of λ from the biomass surrogate model when applied to the actual data are reported for Dassen island. The biomass surrogate model was applied to the 1000 generated data sets and a λ value estimated for each set. The mean, standard deviation and standard error of the mean of the 1000 estimated λ values are provided, as well as the difference between the average λ estimated from the generated data and the underlying "true" λ biomass surrogate model estimate ($\hat{\lambda} - \lambda^{true}$, i.e. the bias) and the root mean squared error (RMSE) of the estimates. The m^{calc} values calculated from Equation (6) of MARAM/IWS/DEC15/PengD/P1 for each value of ϕ are provided, as well as the regression $\hat{m}$ values from Table 1 of MARAM/IWS/DEC15/PengD/P1 alongside the correlation values calculated for each these $\hat{m}$ values from Equation (6) of MARAM/IWS/DEC15/PengD/P1. Δ_{ϕ_0} gives the difference between $\lambda_{\phi=0.2} - \lambda_{\phi=0}$ and $\lambda_{\phi=0.4} - \lambda_{\phi=0}$ for the mean estimates of λ.

Partitions of the table correspond to the following:

(A) is a repetition of the results previously circulated. Generated biomass is not constrained to be positive.

(A1) is a re-run of (A), where past years for which data are available for one island and not the other (these years would have previously been excluded for the island with the "gap" in the data) are now included for both islands. In other words, 11 years of data are used for both islands, whereas previously nine were used for Dassen and five for Robben, corresponding to the years for which chick growth data are available for each island.

(A2) is a re-run of (A), where data has been generated for 10 years into the future. λ values are calculated taking all future years into account, but past years have only been taken into account where penguin response data are available for each island in question.

(A3) is the same as (A2), except that data have been generated for 20 years into the future.

Dassen λ estimates							
Biomass surrogate model estimate applied to actual data	-0.056	(se = 0.067)					
Generated data	Regression $\hat{m} = 2.26 \implies$	$\phi^{calc} = 0.37$					
(A) 1000 generated sets	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	-0.049		0.008	0.064	0.064	0.002	0.00
$\phi = 0.2$	-0.035	(0.014)	0.022	0.063	0.067	0.002	1.42
$\phi = 0.4$	-0.021	(0.028)	0.036	0.058	0.068	0.002	2.85
(A1) Fill gaps in past years	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	-0.053		0.003	0.054	0.054	0.002	0.00
$\phi = 0.2$	-0.034	(0.019)	0.023	0.054	0.059	0.002	1.42
$\phi = 0.4$	-0.020	(0.033)	0.037	0.056	0.067	0.002	2.85
(A2) Generate 10 years into the future	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	-0.050		0.007	0.039	0.040	0.001	0.00
$\phi = 0.2$	-0.037	(0.013)	0.020	0.038	0.043	0.001	1.52
$\phi = 0.4$	-0.022	(0.027)	0.034	0.038	0.051	0.001	3.04
(A3) Generate 20 years into the future	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	-0.055		0.002	0.034	0.034	0.001	0.00
$\phi = 0.2$	-0.037	(0.018)	0.020	0.033	0.039	0.001	1.52
$\phi = 0.4$	-0.019	(0.036)	0.038	0.033	0.050	0.001	3.04

Table 7.2: Repeat of Table 7.1 for Robben island.

Robben λ estimates							
Biomass surrogate model estimate applied to actual data	0.052	(se = 0.135)					
Generated data	Regression $\hat{m} = 2.26 \implies$	$\phi^{calc} = 0.37$					
(A) 1000 generated sets	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	0.034		-0.018	0.078	0.080	0.002	0.00
$\phi = 0.2$	0.040	(0.006)	-0.012	0.078	0.079	0.002	2.68
$\phi = 0.4$	0.046	(0.011)	-0.007	0.076	0.076	0.002	5.35
(A1) Fill gaps in past years	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	0.045		-0.008	0.059	0.060	0.002	0.00
$\phi = 0.2$	0.063	(0.018)	0.010	0.058	0.059	0.002	2.68
$\phi = 0.4$	0.077	(0.032)	0.024	0.055	0.060	0.002	5.35
(A2) Generate 10 years into the future	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	0.046		-0.006	0.045	0.045	0.001	0.00
$\phi = 0.2$	0.061	(0.015)	0.009	0.047	0.048	0.001	2.71
$\phi = 0.4$	0.075	(0.029)	0.023	0.046	0.052	0.001	5.41
(A3) Generate 20 years into the future	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem	m^{calc}
$\phi = 0.0$	0.049		-0.004	0.039	0.039	0.001	0.00
$\phi = 0.2$	0.067	(0.018)	0.015	0.037	0.040	0.001	2.71
$\phi = 0.4$	0.085	(0.036)	0.033	0.039	0.051	0.001	5.41

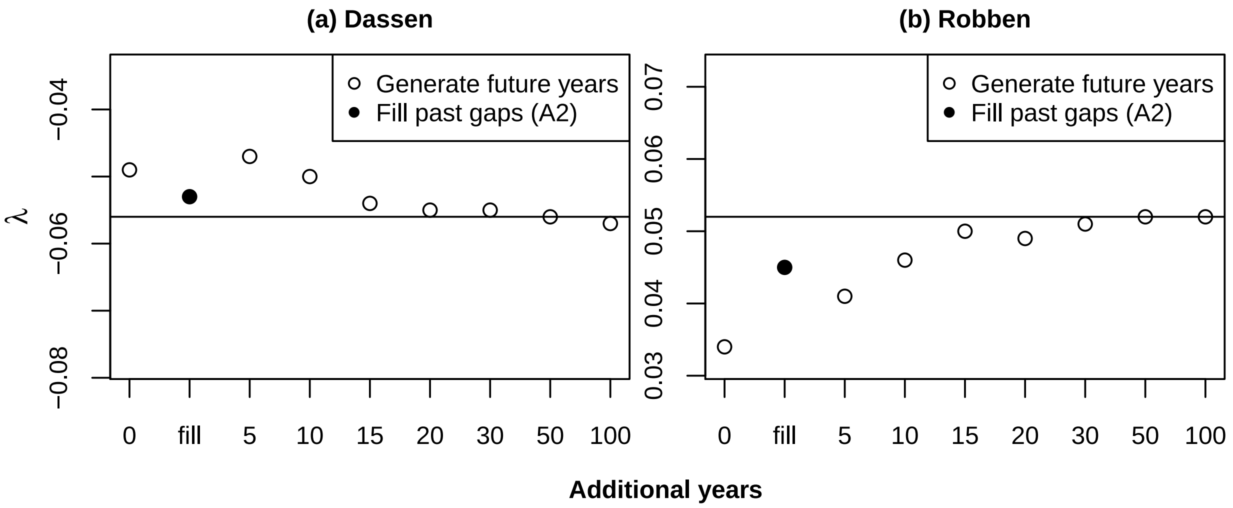


Figure 7.1: Graph showing how the bias between the mean λ estimate from the generated data in relation to the underlying "true" estimate from the biomass surrogate model used to generate the data decreases as more years are included in the generated data set. These plots are for the case $\phi = 0$. More details are given in the text.

8 Further runs for simulating pseudo data as recommended in Section 6

These further runs use the approach of Case (A) (see Section 4), i.e. biomass is not constrained to be positive, and both $\hat{\alpha}$ and η are sampled from normal distributions. All simulations presented here utilise the biomass surrogate approach.

Summaries of runs for **chick growth** are provided below. CG0 is treated as a base case and corresponds to Case (A) of WP04. Bold lettering has been used to highlight aspects of the simulation that have been changed from CG0.

(CG0) Catch only - chick growth - anchovy - 10nm
(CG1) Catch only - chick growth - anchovy - 10nm - **autocor.** $\mu = 0.2, 0.5$
(CG2) Catch only - chick growth - anchovy - **20nm**
(CG3) Catch only - chick growth - anchovy - **20nm** - **autocor.** $\mu = 0.2, 0.5$
(CG4) Catch only - chick growth - anchovy - **18km closure**

Summaries of runs undertaken for the response variable **forage trip duration** are also provided. Again, TP0 is treated as a base case and bold lettering has been used to highlight aspects of the simulation that have been changed for each run.

(TD0) Catch only - forage trip duration - anchovy - 20nm
(TD1) Catch only - forage trip duration - anchovy - 20nm - **autocor.** $\mu = 0.2, 0.5$
(TD2) **Closure only** - forage trip duration - anchovy - 20nm
(TD3) **Closure only** - forage trip duration - anchovy - 20nm - **autocor.** $\mu = 0.2, 0.5$
(TD4) **Catch+closure** - forage trip duration - anchovy - 20nm

Note that the variance adjustment of Equation (2) of MARAM/IWS/DEC15/PengD/P1 has not been implemented. Further, pseudo data have been generated using an autocorrelation value of $\mu = 0$ (Equation 8 of ALL1) unless specified otherwise. σ_ϵ for Equation (8) of ALL1 does not take sample size into account, and the σ_0 value is the biomass surrogate model estimate of the residual standard deviation.

Also note the following regarding the data utilised:

1. The chick growth values used here are the **median** growth rates up to 2012, these being the data available at the time these simulation exercises were initiated.
2. Owing to some difficulties that arose when the forage trip duration values that correspond to a sample size of three (Dassen 2003 and 2009) were removed, these two points have been included in the analyses presented here.

Initial summary impression from results

The results in Table 8.1a for chick growth show that when the distance from the island used to define nearby anchovy catches is increased from 10 nm to 20 nm, this results in both larger estimates for λ and larger changes in the bias of λ estimates as the catch-biomass correlation (ϕ) is increased. For the case of Robben and a 20 nm distance, if this correlation is 0.4, the bias becomes sufficiently large that correcting for it would change the sign of the estimate of λ from positive to negative. Adding autocorrelation (μ) to the time series of residuals has minimal impact. The small-sample-size bias (the difference between the estimate from the actual data and the mean of estimates from the pseudo-data when the catch-biomass correlation is zero) is minimal for Dassen for a 20 nm distance, and some 0.01 for Robben (i.e. somewhat less than for the 10 nm case).

More care must be taken against possibly over-interpreting the results in Table 8.2a and b for the forage trip duration response variable, as standard errors of the mean (typically about 0.007) are some three times larger than for the chick growth results. For the catch only estimator, the small-sample-size bias is again about 0.01 for both islands, and the changes in the estimates of the bias of λ are once more in the direction expected as the catch-biomass correlation is increased. Adding autocorrelation to the residuals causes the mean of the estimates of λ from the pseudo-data to increase slightly (hence making an increased contribution to bias) for Dassen, but there is no clear trend for Robben.

When instead the closure only estimator is considered for forage trip duration in Table 8.2a and b, Robben shows a small-sample-size bias of about 0.01 for the closure effect δ, but there is no such effect evident for Dassen. The impact of the catch-biomass correlation on bias in the estimates of δ is of a lesser magnitude than for the catch only estimator, but in the opposite direction. Adding autocorrelation to the residuals has minimal impact on the results for Dassen; however for Robben, there is some (though inconsistent) indication of an increased contribution to bias, with an associated clearer pattern of a slight increase in the standard deviation of the distribution of the estimates of δ from the pseudo-data as the extent of this autocorrelation is increased.

For the case when both catch and closure effects are estimated together, the small-sample-size bias effects are generally minimal. The consequences of catch-biomass correlation are in most cases similar to those when either effect is estimated in isolation.

The small impact in most cases of introducing autocorrelation into the residuals that is reported above may be surprising. The reason is that in a regression context, this introduction has more impact on estimates of intercepts (such as K) (and specifically their precision), than on estimates of "slope" parameters (such as λ or δ). This is evident from the results shown in Table 8.3, which reflect smallish but consistent increases in the standard deviation of the distributions of the estimates of the estimator constant K as the residual autocorrelation μ is increased.

Table 8.1a: The estimates and standard errors of λ from the biomass surrogate model when applied to the actual data are reported for **Dassen Island** for the **chick growth** penguin response variable for various scenarios. The biomass surrogate model was applied to the 1000 generated data sets for each scenario and a λ value estimated for each set. The mean, standard deviation and standard error of the mean of the 1000 estimated λ values are provided, as well as the difference between the average λ estimated from the generated data and the underlying "true" λ biomass surrogate model estimate ($\hat{\lambda} - \lambda^{true}$, i.e. the bias) and the root mean squared error (RMSE) of the estimates. Δ_{ϕ_0} gives the difference between $\lambda_{\phi=0.2} - \lambda_{\phi=0}$ and $\lambda_{\phi=0.4} - \lambda_{\phi=0}$ for the mean estimates of λ.

Biomass surrogate model estimate (10nm)	-0.056		(se = 0.067)			
(CG0) 10nm catches and $\mu = 0$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.049		0.008	0.064	0.064	0.002
$\phi = 0.2$	-0.035	(0.014)	0.022	0.063	0.067	0.002
$\phi = 0.4$	-0.021	(0.028)	0.036	0.058	0.068	0.002
(CG1a) 10nm catches and $\mu = 0.2$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.052		0.005	0.062	0.062	0.002
$\phi = 0.2$	-0.033	(0.018)	0.023	0.059	0.063	0.002
$\phi = 0.4$	-0.023	(0.029)	0.034	0.061	0.069	0.002
(CG1b) 10nm catches and $\mu = 0.5$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.047		0.010	0.060	0.061	0.002
$\phi = 0.2$	-0.036	(0.010)	0.020	0.061	0.064	0.002
$\phi = 0.4$	-0.022	(0.025)	0.035	0.061	0.070	0.002
Biomass surrogate model estimate (20nm)	-0.179		(se = 0.073)			
(CG2) 20nm catches and $\mu = 0$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.174		0.006	0.106	0.106	0.003
$\phi = 0.2$	-0.131	(0.043)	0.048	0.107	0.117	0.003
$\phi = 0.4$	-0.097	(0.077)	0.083	0.097	0.127	0.003
(CG3a) 20nm catches and $\mu = 0.2$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.182		-0.003	0.109	0.109	0.003
$\phi = 0.2$	-0.135	(0.046)	0.044	0.103	0.112	0.003
$\phi = 0.4$	-0.096	(0.086)	0.083	0.096	0.127	0.003
(CG3b) 20nm catches and $\mu = 0.5$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.177		0.002	0.105	0.105	0.003
$\phi = 0.2$	-0.133	(0.043)	0.046	0.103	0.113	0.003
$\phi = 0.4$	-0.092	(0.085)	0.087	0.103	0.135	0.003
Biomass surrogate model estimate (18km)	-0.130		(se = 0.125)			
(CG4) 18km closure catches	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
$\phi = 0.0$	-0.109		0.021	0.073	0.075	0.002
$\phi = 0.2$	-0.094	(0.015)	0.036	0.068	0.077	0.002
$\phi = 0.4$	-0.075	(0.034)	0.055	0.069	0.088	0.002

Table 8.1b: Repeat of Table 8.1a for **Robben Island** for the **chick growth** penguin response variable.

Biomass surrogate model estimate (10nm)		0.052		(se = 0.135)			
(CG0)	10nm catches and $\mu = 0$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.034		-0.018	0.078	0.080	0.002
	$\phi = 0.2$	0.040	(0.006)	-0.012	0.078	0.079	0.002
	$\phi = 0.4$	0.046	(0.011)	-0.007	0.076	0.076	0.002
(CG1a)	10nm catches and $\mu = 0.2$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.036		-0.016	0.077	0.079	0.002
	$\phi = 0.2$	0.043	(0.006)	-0.009	0.073	0.073	0.002
	$\phi = 0.4$	0.047	(0.011)	-0.005	0.080	0.080	0.003
(CG1b)	10nm catches and $\mu = 0.5$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.034		-0.018	0.074	0.077	0.002
	$\phi = 0.2$	0.043	(0.009)	-0.009	0.078	0.078	0.002
	$\phi = 0.4$	0.049	(0.016)	-0.003	0.077	0.077	0.002
Biomass surrogate model estimate (20nm)		0.064		(se = 0.087)			
(CG2)	20nm catches and $\mu = 0$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.054		-0.010	0.161	0.161	0.005
	$\phi = 0.2$	0.102	(0.048)	0.038	0.155	0.160	0.005
	$\phi = 0.4$	0.139	(0.086)	0.076	0.161	0.178	0.005
(CG3a)	20nm catches and $\mu = 0.2$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.069		0.005	0.150	0.150	0.005
	$\phi = 0.2$	0.099	(0.030)	0.035	0.154	0.158	0.005
	$\phi = 0.4$	0.135	(0.067)	0.071	0.139	0.156	0.004
(CG3b)	20nm catches and $\mu = 0.5$	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.060		-0.004	0.162	0.162	0.005
	$\phi = 0.2$	0.094	(0.034)	0.030	0.148	0.151	0.005
	$\phi = 0.4$	0.141	(0.081)	0.077	0.164	0.181	0.005
Biomass surrogate model estimate (18km)		0.032		(se = 0.1043)			
(CG4)	18km closure catches	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.021		-0.011	0.073	0.073	0.002
	$\phi = 0.2$	0.033	(0.011)	0.000	0.075	0.075	0.002
	$\phi = 0.4$	0.036	(0.015)	0.004	0.077	0.077	0.002

Table 8.2a: Repeat of Table 8.1a for **Dassen Island** for the **forage trip duration** penguin response variable.

Catch only biomass surrogate model estimate of λ		0.184		(se = 0.189)			
(TD0)	Catch only, $\mu = 0$ (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.172		-0.013	0.211	0.212	0.007
	$\phi = 0.2$	0.219	(0.047)	0.035	0.228	0.231	0.007
	$\phi = 0.4$	0.256	(0.084)	0.071	0.219	0.230	0.007
(TD1a)	Catch only, $\mu = 0.2$ (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.182		-0.002	0.218	0.218	0.007
	$\phi = 0.2$	0.225	(0.043)	0.040	0.203	0.207	0.006
	$\phi = 0.4$	0.278	(0.096)	0.094	0.209	0.229	0.007
(TD1b)	Catch only, $\mu = 0.5$ (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.183		-0.001	0.210	0.210	0.007
	$\phi = 0.2$	0.235	(0.052)	0.050	0.203	0.209	0.006
	$\phi = 0.4$	0.274	(0.091)	0.090	0.201	0.220	0.006
Closure only biomass surrogate model estimate of δ		0.454		(se = 0.189)			
(TD2)	Closure only, $\mu = 0$ (δ)	Mean	Δ_{ϕ_0}	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.455		0.001	0.203	0.203	0.006
	$\phi = 0.2$	0.460	(0.005)	0.006	0.202	0.202	0.006
	$\phi = 0.4$	0.453	(-0.002)	-0.001	0.205	0.205	0.006
(TD3a)	Closure only, $\mu = 0.2$ (δ)	Mean	Δ_{ϕ_0}	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.457		0.003	0.205	0.205	0.006
	$\phi = 0.2$	0.451	(-0.006)	-0.003	0.217	0.217	0.007
	$\phi = 0.4$	0.445	(-0.012)	-0.008	0.204	0.204	0.006
(TD3b)	Closure only, $\mu = 0.5$ (δ)	Mean	Δ_{ϕ_0}	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.469		0.015	0.206	0.207	0.007
	$\phi = 0.2$	0.446	(-0.023)	-0.008	0.215	0.215	0.007
	$\phi = 0.4$	0.448	(-0.021)	-0.006	0.207	0.207	0.007
Catch+closure biomass surrogate model estimate of λ		-0.002		(se = 0.181)			
Catch+closure biomass surrogate model estimate of δ		0.400		(se = 0.205)			
(TD4)	Catch+Closure (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	-0.002		0.000	0.221	0.221	0.007
	$\phi = 0.2$	0.053	(0.055)	0.056	0.219	0.225	0.007
	$\phi = 0.4$	0.089	(0.091)	0.091	0.226	0.244	0.007
	Catch+Closure (δ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.399		-0.002	0.222	0.221	0.007
	$\phi = 0.2$	0.393	(-0.005)	-0.007	0.208	0.208	0.007
	$\phi = 0.4$	0.389	(-0.010)	-0.011	0.217	0.217	0.007

Table 8.2b: Repeat of Table 8.2a for **Robben Island** for the **forage trip duration** penguin response variable.

Catch only biomass surrogate model estimate of λ		0.321		(se = 0.203)			
(TD0)	Catch only, $\mu = 0$ (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.311		-0.010	0.237	0.237	0.007
	$\phi = 0.2$	0.357	(0.046)	0.036	0.252	0.254	0.008
	$\phi = 0.4$	0.383	(0.072)	0.063	0.233	0.241	0.007
(TD1a)	Catch only, $\mu = 0.2$ (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.311		-0.010	0.243	0.243	0.008
	$\phi = 0.2$	0.363	(0.052)	0.042	0.241	0.244	0.008
	$\phi = 0.4$	0.380	(0.069)	0.059	0.240	0.247	0.008
(TD1b)	Catch only, $\mu = 0.5$ (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.323		0.002	0.234	0.234	0.007
	$\phi = 0.2$	0.347	(0.024)	0.026	0.240	0.241	0.008
	$\phi = 0.4$	0.388	(0.064)	0.067	0.214	0.225	0.007
Closure only biomass surrogate model estimate of δ		0.071		(se = 0.186)			
(TD2)	Closure only, $\mu = 0$ (δ)	Mean	Δ_{ϕ_0}	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.063		-0.008	0.198	0.199	0.006
	$\phi = 0.2$	0.081	(0.018)	0.010	0.198	0.198	0.006
	$\phi = 0.4$	0.068	(0.005)	-0.003	0.196	0.196	0.006
(TD3a)	Closure only, $\mu = 0.2$ (δ)	Mean	Δ_{ϕ_0}	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.079		0.008	0.203	0.203	0.006
	$\phi = 0.2$	0.087	(0.008)	0.016	0.204	0.204	0.006
	$\phi = 0.4$	0.073	(-0.007)	0.002	0.207	0.207	0.007
(TD3b)	Closure only, $\mu = 0.5$ (δ)	Mean	Δ_{ϕ_0}	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.072		0.000	0.217	0.217	0.007
	$\phi = 0.2$	0.074	(0.003)	0.003	0.210	0.210	0.007
	$\phi = 0.4$	0.063	(-0.008)	-0.008	0.224	0.224	0.007
Catch+closure biomass surrogate model estimate of λ		0.506		(se = 0.277)			
Catch+closure biomass surrogate model estimate of δ		-0.329		(se = 0.268)			
(TD4)	Catch+Closure (λ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	0.512		0.006	0.267	0.267	0.008
	$\phi = 0.2$	0.543	(0.031)	0.037	0.273	0.275	0.009
	$\phi = 0.4$	0.573	(0.061)	0.067	0.257	0.266	0.008
	Catch+Closure (δ)	Mean	Δ_{ϕ_0}	$\hat{\lambda} - \lambda^{true}$	sd	RMSE	sem
	$\phi = 0.0$	-0.328		0.001	0.235	0.235	0.007
	$\phi = 0.2$	-0.338	(-0.010)	-0.009	0.235	0.235	0.007
	$\phi = 0.4$	-0.321	(0.007)	0.008	0.229	0.229	0.007

Table 8.3: Mean and standard deviation of the 1000 K values estimated from the sets of simulated data, shown for different values of the autocorrelation value μ.

Chick growth K estimates				Forage trip duration K estimates			
(CG0)	10nm, $\mu = 0$	Mean	sd	(TD0)	Catch only, $\mu = 0$	Mean	sd
	$\phi = 0$	-3.315	0.084		$\phi = 0$	-2.794	0.228
	$\phi = 0.2$	-3.332	0.085		$\phi = 0.2$	-2.838	0.245
	$\phi = 0.5$	-3.348	0.085		$\phi = 0.5$	-2.876	0.230
(CG1a)	10nm, $\mu = 0.2$	Mean	sd	(TD1a)	Catch only, $\mu = 0.2$	Mean	sd
	$\phi = 0$	-3.316	0.089		$\phi = 0$	-2.800	0.242
	$\phi = 0.2$	-3.330	0.083		$\phi = 0.2$	-2.849	0.225
	$\phi = 0.5$	-3.342	0.086		$\phi = 0.5$	-2.898	0.231
(CG1b)	10nm, $\mu = 0.5$	Mean	sd	(TD1b)	Catch only $\mu = 0.5$	Mean	sd
	$\phi = 0$	-3.318	0.092		$\phi = 0$	-2.807	0.241
	$\phi = 0.2$	-3.325	0.092		$\phi = 0.2$	-2.848	0.228
	$\phi = 0.5$	-3.343	0.096		$\phi = 0.5$	-2.892	0.242
(CG2)	20nm, $\mu = 0$	Mean	sd	(TD2)	Closure only $\mu = 0$	Mean	sd
	$\phi = 0$	-3.198	0.113		$\phi = 0$	-2.985	0.172
	$\phi = 0.2$	-3.243	0.114		$\phi = 0.2$	-2.988	0.170
	$\phi = 0.5$	-3.271	0.106		$\phi = 0.5$	-2.982	0.177
(CG3a)	20nm, $\mu = 0.2$	Mean	sd	(TD3a)	Closure only $\mu = 0.2$	Mean	sd
	$\phi = 0$	-3.191	0.114		$\phi = 0$	-2.985	0.178
	$\phi = 0.2$	-3.234	0.116		$\phi = 0.2$	-2.981	0.187
	$\phi = 0.5$	-3.275	0.106		$\phi = 0.5$	-2.974	0.180
(CG3a)	20nm, $\mu = 0.5$	Mean	sd	(TD3b)	Closure only $\mu = 0.5$	Mean	sd
	$\phi = 0$	-3.192	0.118		$\phi = 0$	-2.973	0.198
	$\phi = 0.2$	-3.240	0.115		$\phi = 0.2$	-2.978	0.205
	$\phi = 0.5$	-3.278	0.116		$\phi = 0.5$	-2.996	0.193

9 Testing a simple estimator

Biomass surrogate model estimates from three scenarios ((i)-(iii) below) were utilised to generate three batches of 1000 pseudo-data sets. Throughout, the catch-biomass correlation ϕ is zero.

i. Chick growth (CG), for anchovy 10nm catches, catch only form

ii. Forage trip duration (TD), for anchovy 20nm catches, catch only form

iii. Forage trip duration (TD), for anchovy 20nm catches, closure only form

The following three models were applied to each data set in each batch:

- The simple estimator model (Equation 2 below), for which a singe island-independent δ is estimated
- The biomass surrogate model with closure only (Equation 1 below with $\lambda_i = 0$), for which two island-dependent δ_i values are estimated
- The biomass surrogate model with catch only (Equation 1 below with $\delta_i = 0$), for which two island-dependent λ_i values are estimated

Biomass surrogate model equation (cross-reference Equation 1 of MARAM/IWS/DEC15/PengD/P1):

$$lnF = K + \alpha_y + \gamma_s + \lambda_i \frac{C_{yip}}{\bar{C}_{ip}} + \delta_i X_{yi} + \epsilon_{yis} \tag{1}$$

Simple estimator model:

$$lnF = K + \delta X_{yi} + \epsilon_{yis} \tag{2}$$

Discussion

The motivation for these runs was the 2015 IWS panel suggestion to investigate the simplest estimator possible (which has advantages in terms of reduced estimation variance). Equation (2) attempts to capture that intent.

Although λ and δ are comparable in very broad terms, as both reflect the difference in the log response for closure vs (in some sense) an average catch situation, only the results under scenario (iii) in Tables 9.1a and 9.1b report strictly comparable estimation performances for two different approaches to estimate the closure effect δ. For both islands, the simple estimator is outperformed by the biomass surrogate model closure only estimator in RMSE terms — the variance advantages of the simple estimator are outweighed by the extent of its bias for the forage trip duration data.

It is notable also that the biomass surrogate model catch only estimator performs better in RMSE terms than either closure estimator when the pseudo-data are generated from a catch only model. For the reverse situation, that conclusion does not apply universally. These comparisons do however suffer from the reservation noted above.

Table 9.1a: Biomass surrogate model estimates from three scenarios ((i)-(iii) in the table below) were utilised to generate three batches of 1000 pseudo-data sets. The following three models were applied to each pseudo-data set in each batch:

- The simple estimator model (Equation 2 above), for which a singe island-independent δ is estimated
- The biomass surrogate model with closure only (Equation 1 above with $\lambda_i = 0$), for which two island-dependent δ_i values are estimated
- The biomass surrogate model with catch only (Equation 1 above with $\delta_i = 0$), for which two island-dependent λ_i values are estimated

The mean, standard deviation and standard error of the mean of the 1000 estimated λ (or δ) values are provided for each scenario, as well as the difference between the average λ (or δ) estimated from the pseudo-data and the underlying "true" λ (or δ) biomass surrogate model estimate (i.e. the bias) and the root mean squared error (RMSE) of the estimates. Note that in some cases the mean of the estimated λ values is compared to an underlying "true" δ estimate (or *vice versa*) and this should be taken into account when interpreting the difference. These cases have been emphasised by italics. Rows marked by a * indicate that the biomass surrogate model in question was the model used to generate the pseudo data.

Dassen Island

(i) CG data generated for anchovy, 10nm, catch only

Biomass surrogate model estimate λ_i^{true}: -0.056 (se = 0.067)

Model applied to pseudo-data	Mean	$\hat{\lambda} - \lambda^{true}$	$\hat{\delta} - \lambda^{true}$	sd	RMSE	sem
Simple estimator (δ)	-0.030		*0.026*	0.104	0.108	0.003
Biomass surrogate model closure only (δ_i)	-0.068		*-0.011*	0.148	0.148	0.005
Biomass surrogate model catch only (λ_i)*	-0.049	0.008		0.064	0.064	0.002

(ii) TD data generated for anchovy, 20nm, catch only

Biomass surrogate model estimate for λ_i^{true}: 0.184 (se = 0.189)

Model applied to pseudo-data	Mean	$\hat{\lambda} - \lambda^{true}$	$\hat{\delta} - \lambda^{true}$	sd	RMSE	sem
Simple estimator (δ)	-0.021		*-0.205*	0.174	0.269	0.005
Biomass surrogate model closure only (δ_i)	-0.002		*-0.187*	0.247	0.309	0.008
Biomass surrogate model catch only (λ_i)*	0.172	-0.013		0.211	0.212	0.007

(iii) TD data generated for anchovy, 20nm, closure only

Biomass surrogate model estimate for δ_i^{true}: 0.454 (se = 0.189)

Model applied to pseudo-data	Mean	$\hat{\lambda} - \delta^{true}$	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
Simple estimator (δ)	0.252		-0.202	0.126	0.238	0.004
Biomass surrogate model closure only (δ_i)*	0.455		0.001	0.203	0.203	0.006
Biomass surrogate model catch only (λ_i)	0.002	*-0.451*		0.261	0.521	0.008

Table 9.1b: Repeat of Table 9.1a for **Robben Island**.

Robben Island						
(i) CG data generated for anchovy, 10nm, catch only						
Biomass surrogate model estimate λ_i^{true}:	0.052	(se = 0.135)				
Model applied to pseudo-data	Mean	$\hat{\lambda} - \lambda^{true}$	$\hat{\delta} - \lambda^{true}$	sd	RMSE	sem
Simple estimator (δ)	-0.030		*0.026*	0.104	0.108	0.003
Biomass surrogate model closure only (δ_i)	0.061		*0.008*	0.177	0.177	0.006
Biomass surrogate model catch only (λ_i)*	0.034	-0.018		0.078	0.080	0.002
(ii) TD data generated for anchovy, 20nm, catch only						
Biomass surrogate model estimate for λ_i^{true}:	0.321	(se = 0.203)				
Model applied to pseudo-data	Mean	$\hat{\lambda} - \lambda^{true}$	$\hat{\delta} - \lambda^{true}$	sd	RMSE	sem
Simple estimator (δ)	-0.021		*-0.205*	0.174	0.269	0.005
Biomass surrogate model closure only (δ_i)	-0.004		*-0.325*	0.289	0.435	0.009
Biomass surrogate model catch only (λ_i)*	0.311	-0.010		0.237	0.237	0.007
(iii) TD data generated for anchovy, 20nm, closure only						
Biomass surrogate model estimate for δ_i^{true}:	0.071	(se = 0.186)				
Model applied to pseudo-data	Mean	$\hat{\lambda} - \delta^{true}$	$\hat{\delta} - \delta^{true}$	sd	RMSE	sem
Simple estimator (δ)	0.252		-0.202	0.126	0.238	0.004
Biomass surrogate model closure only (δ_i)*	0.063		-0.008	0.198	0.199	0.006
Biomass surrogate model catch only (λ_i)	0.002	*-0.070*		0.222	0.232	0.007