

Demographic characteristics of Australian humpback dolphins reveal important habitat toward the southwestern limit of their range

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SUPPLEMENT 1

Photo-identification protocol

Individual humpback dolphins were primarily identified based on the unique natural marks on their dorsal fins (Würsig and Jefferson 1990), which included nicks, notches, and scoops on the leading and trailing edges of the dorsal fin, and loss of pigmentation (LOP) in the upper region of the dorsal fin and/or saddle patch (see Brown et al. 2016 for LOP definitions). Secondary features such as scarring, small patches of LOP and peduncle nicks/notches were also used for individual identification. All photographs taken were examined and subject to a modified quality (Q) and distinctiveness (D) grading protocol (derived from Urian et al. 1999, 2015) to minimise misidentification and heterogeneity in capture probabilities. All photographs (JPEG format) were examined and classified into three grades (excellent, good, and poor) according to four image quality parameters: (1) clarity – refers to the sharpness/level of focus of an image, (2) contrast – refers to the range of tones in the image, where too much contrast causes detail of small features to wash out to white and too little contrast the dorsal fin is lost into the background and features lack definition, (3) angle – refers to the angle of the dolphin’s dorsal fin relative to the camera, and (4) partial – refers to how much of the dorsal fin is visible in the image, includes where water droplets may be present on the fin and obstructing features. Each of these image quality parameters received a score between 2 and 10 (where 10 is excellent and 2 is poor). These scores were then summed and divided by four to achieve an overall image quality (Q) score out of 10. Photographs of excellent grade were those with a Q value 8-10, those with a good grade were Q5-7, and a poor grade was Q<5.

Once a Q value had been assigned to an image, distinctiveness was assessed for each individual photo based on the relative distinctive features displayed on the dorsal fin. A distinctiveness score (D1, D2, D3 or Clean) was assigned to each individual photo, independent of image quality, where; D1 = highly distinctive features (singular or multiple), includes individuals with missing tops, extended tips, large notches or multiple notches, and/or extensive LOP; D2 = medium distinctive features – single feature (e.g. notch), or multiple smaller less distinctive nicks and notches, fins with substantial scarring, and/or some LOP evident; and D3 = not distinctive features - fins basically clean except for minor scarring or small waves, or very small nicks. Images that were considered ‘Clean’ did not display any distinctive features, except for very minor scars that were sufficient enough to delineate different individuals within a sighting and ascertain total dolphin school sizes. Only excellent and good quality ($Q \geq 5$) photographs displaying distinctive individuals (D1 and D2) were used to identify individuals and develop an identification catalogue for the analysis of abundance, site fidelity and residency patterns.

All individual images of dorsal fins were processed, matched to the catalogue and managed in the photo-identification data management software ‘Discovery’ (Gailey & Karczmarksi 2012). Before matching or adding new individuals to the identification catalogue, photographs were cross-checked by a minimum of two experienced research assistants against all images in the catalogue. After a match was confirmed (or a new individual identification number assigned), individual capture data was entered into the Discovery database before being verified by the lead author. Juveniles of

sufficient distinctiveness were included in capture histories for analysis, however, calves were excluded from all analyses because they typically do not possess sufficient markings to ensure their future recognition without error.

SUPPLEMENT 2

Proportion of marked individuals in the population

The proportion of marked (i.e. distinct) individuals in the population ($\hat{\theta}$) was estimated as the average number of marked individuals (D1 & D2) found in each sighting where photographic coverage was $\geq 50\%$ (determined by total number of animals photographically identified per sighting over the best school size estimated in the field, excluding calves) (modified from Nicholson et al. 2012).

To estimate the total population size, we adjusted the model estimates to take into account the proportion of marked individuals in the population (Wilson et al. 1999, Nicholson et al. 2012) as follows:

$$\hat{N}_{total} = \frac{\hat{N}_m}{\hat{\theta}},$$

where \hat{N}_{total} is the estimated total population size, \hat{N}_m is the estimated marked population size and $\hat{\theta}$ is the estimated proportion of marked individuals in the population. Standard errors of total population sizes were calculated as per Williams et al. (2002), where n is the total number of photographs from which $\hat{\theta}$ was derived:

$$SE(\hat{N}_{total}) = \sqrt{\hat{N}_{total}^2 \left(\frac{SE(\hat{N}_m)^2}{\hat{N}_m^2} + \frac{1 - \hat{\theta}}{n\hat{\theta}} \right)}$$

Lower and upper log-normal 95% confidence intervals were calculated as

$$\hat{N}_{total}^{Lower} = \frac{\hat{N}_{total}}{C}, \quad \hat{N}_{total}^{Upper} = \hat{N}_{total} \times C \quad (\text{Burnham et al. 1987}) \text{ where:}$$

$$C = \exp \left(1.96 \sqrt{\ln \left(1 + \left(\frac{SE(\hat{N}_{total})}{\hat{N}_{total}} \right)^2 \right)} \right).$$

SUPPLEMENT 3

Validation of model assumptions and goodness-of-fit results

PCRD models assume: (1) the population is closed within P-periods, (2) all individuals (marked and unmarked) have equal probability of being captured within a sampling period, (3) all individuals have equal probability of survival, (4) marks are unique, permanent and identified correctly, (5) each individual's probability of capture is independent of all others, (6) the study area remains constant, and (7) the sampling interval for a particular s-period is instantaneous (i.e. that is sampling periods are short and birth, death, immigration and emigration do not occur during the recapture process) (Pollock 1982, Pollock et al. 1990, Williams et al. 2002).

POPAN models assume: (1) all individuals (marked and unmarked) have equal probability of being captured within a sampling period, (2) all individuals have equal probability of survival, (3) marks are unique, permanent and identified correctly, (4) sampling is instantaneous, and (5) the study area remains constant (Pollock et al. 1990, Williams et al. 2002).

Australian humpback dolphins do not associate at random (Parra et al. 2011), thus, the assumption of independent individual capture probability may have been violated, given that close associates of an individual are more likely to be captured over other individuals. However, associations are dynamic and change often with time (Parra et al. 2011). We therefore deemed

violation of this assumption to cause minor bias in our estimates. Secondary sampling periods were kept as short as possible (3 to 31 days); and thus we considered biases due to births, deaths and migration to be negligible given these dolphins' lifespan (decades).

To test the assumption that the population is closed within each P-period, we used the Otis et al. (1978) closure test for capture-recapture data implemented in the CloseTest software (Stanley & Richards 2005, Stanley & Richards 2011). Further, we used U-CARE to carry out TEST 2.CT for heterogeneity in capture probabilities, including testing for a trap response, and used TEST 3.SR to test for a transience effect (i.e. dolphins sighted only once during the study period more often than expected). We also used TEST 3.SM to examine any difference in the expected time of first recapture between the 'new' and 'old' individuals captured at any occasion and then seen again at least once (Choquet et al. 2005).

Table S1. Results from goodness-of-fit tests run in Program RELEASE and U-CARE for the six primary sampling periods of Australian humpback dolphin surveys conducted during 2013-2015 (April to October) around the North West Cape, Western Australia. Global test results (Test 2 + Test 3) and corresponding \hat{c} values are also included. χ^2 = chi-squared statistic, df = degrees of freedom, N/A = statistic not available for this test.

Program	Parameters	TEST 3.SR	TEST 3.SM	TEST 2.CT ^a	Global test	\hat{c}
RELEASE	χ^2	2.06	6.80	0.39	9.24	0.99
	df	4	3	3	10	
	<i>p</i> -value	0.72	0.08	0.94	0.51	
U-CARE	Statistic	1.01	N/A	-0.58	N/A	1.33
	χ^2	2.57	7.78	1.11	16.00	
	df	4	3	3	12	
	<i>p</i> -value	0.31	0.05	0.57	0.19	

^a This test is referred to as TEST 2.C in RELEASE.

SUPPLEMENT 4

Table S2. Reduced set of Pollock's Closed Robust Design models fitted to the capture histories of Australian humpback dolphins to estimate population size (N), apparent survival rate (ϕ), emigration (γ'' , γ') and capture probability (p). The notation ' \bullet ' indicates that a given parameter was kept constant, ' t ' indicates that a given parameter was allowed to vary with time, and ' $season$ ' indicates that emigration parameters were allowed to vary by seasons Autumn-Winter (April to July; P1^a, P3 & P5) and Winter-Spring (August to October; P2, P4, & P6). Capture probability was allowed to vary with time among and within primary sampling periods (t, s). Recapture probability (c) was set equal to p and therefore is not included in the model description. The top three ranked models are shown in **bold**.

Model	Rank	AICc	Δ AICc	AICc weights	Cumulative AICc weight (%)	Number of parameters
$\phi(\bullet) \gamma''(season) \neq \gamma'(\bullet) p(t,s)$	1	585.3	0.0	0.331	33.12%	47
$\phi(\bullet) \gamma''(season) \neq \gamma'(season) p(t,s)$	2	585.4	0.1	0.318	64.92%	48
$\phi(\bullet) \gamma''(season) = \gamma'(season) p(t,s)$	3	586.9	1.5	0.154	80.30%	46
$\phi(t) \gamma''(season) = \gamma'(season) p(t,s)$	4	589.3	4.0	0.046	84.87%	50
$\phi(\bullet) \gamma''(t) \neq \gamma'(\bullet) p(t,s)$	5	589.9	4.6	0.033	88.19%	50
$\phi(t) \gamma''(\bullet) = \gamma'(\bullet) p(t,s)$	6	590.0	4.7	0.032	91.41%	49
$\phi(\bullet) \gamma''(\bullet) \neq \gamma'(\bullet) p(t,s)$	7	591.3	6.0	0.016	93.06%	46
$\phi(t) \gamma''(season) \neq \gamma'(\bullet) p(t,s)$	8	591.8	6.5	0.013	94.34%	51
$\phi(t) \gamma''0 = \gamma'0 p(t,s)$	9	592.0	6.6	0.012	95.54%	48
$\phi(t) \gamma''(\bullet) \neq \gamma'(\bullet) p(t,s)$	10	592.5	7.2	0.009	96.46%	50
$\phi(\bullet) \gamma''(\bullet) = \gamma'(\bullet) p(t,s)$	11	592.6	7.2	0.009	97.35%	45
$\phi(t) \gamma''(season) \neq \gamma'(season) p(t,s)$	12	593.3	8.0	0.006	97.96%	52
$\phi(\bullet) \gamma''(t) = \gamma'(t) p(t,s)$	13	593.7	8.4	0.005	98.46%	49
$\phi(t) \gamma''(\bullet) \neq \gamma'(season) p(t,s)$	14	593.8	8.5	0.005	98.93%	51
$\phi(\bullet) \gamma''(\bullet) \neq \gamma'(season) p(t,s)$	15	593.9	8.6	0.005	99.38%	47
$\phi(t) \gamma''(t) = \gamma'(t) p(t,s)$	16	594.6	9.3	0.003	99.70%	52
$\phi(t) \gamma''(\bullet) \neq \gamma'(t) p(t,s)$	17	596.1	10.8	0.002	99.86%	52
$\phi(t) \gamma''(t) \neq \gamma'(\bullet) p(t,s)$	18	597.1	11.8	0.001	99.95%	53
$\phi(\bullet) \gamma''0 = \gamma'0 p(t,s)$	19	600.4	15.1	<0.001	99.96%	44
$\phi(\bullet) \gamma''(t) \neq \gamma'(t) p(t,s)$	20	600.6	15.3	<0.001	99.98%	53
$\phi(t) \gamma''(t) \neq \gamma'(t) p(t,s)$	21	601.2	15.8	<0.001	99.99%	55
$\phi(\bullet) \gamma''(\bullet) \neq \gamma'(t) p(t,s)$	22	601.7	16.4	<0.001	100.00%	49

^a Emigration parameters for P1 cannot be obtained given it is the first sampling occasion with no previous sampling occasion to reference and derive an estimate

Table S3. Weighted-average estimates of capture probabilities (p) for all 22 Robust Design models (for model descriptions see Table S2). P-period = primary sampling period, s-period = secondary sampling period, LCI = 95% Lower Confidence Interval limit, UCI = 95% Upper Confidence Interval limit, p_P = effective detection probability per P-period: $p_P = 1 - (1-p_{s1})(1-p_{s2})\dots(1-p_{sK})$, where s_1, s_2, \dots, s_K , are the s-period capture probabilities in each P-period.

Parameter	P-period	s-period	Estimate	LCI	UCI	p_P
p	1	1	0.11	0.05	0.25	
p	1	2	0.10	0.04	0.22	0.55
p	1	3	0.32	0.17	0.53	
p	1	4	0.16	0.07	0.32	
p	2	5	0.18	0.09	0.31	
p	2	6	0.25	0.14	0.39	0.66
p	2	7	0.09	0.04	0.20	
p	2	8	0.33	0.21	0.49	
p	2	9	0.11	0.05	0.22	
p	3	10	0.08	0.04	0.18	0.71
p	3	11	0.07	0.03	0.16	
p	3	12	0.01	0.00	0.09	
p	3	13	0.18	0.11	0.29	
p	3	14	0.29	0.19	0.42	
p	3	15	0.07	0.03	0.16	
p	3	16	0.22	0.14	0.34	
p	3	17	0.18	0.11	0.29	
p	4	18	0.13	0.06	0.25	
p	4	19	0.22	0.13	0.35	
p	4	20	0.40	0.27	0.55	0.86
p	4	21	0.20	0.11	0.33	
p	4	22	0.07	0.03	0.18	
p	4	23	0.16	0.09	0.29	
p	4	24	0.31	0.20	0.45	
p	4	25	0.20	0.11	0.33	
p	5	26	0.24	0.16	0.36	0.50
p	5	27	0.21	0.13	0.32	
p	5	28	0.02	0.01	0.09	
p	5	29	0.11	0.06	0.20	
p	5	30	0.05	0.02	0.12	
p	6	31	0.11	0.05	0.22	0.71
p	6	32	0.07	0.03	0.18	
p	6	33	0.04	0.01	0.13	
p	6	34	0.39	0.25	0.55	
p	6	35	0.07	0.03	0.18	
p	6	36	0.25	0.14	0.39	
p	6	37	0.16	0.08	0.29	

Table S4. Real parameter estimates of apparent survival (ϕ), capture probability (p), temporary emigration (γ' , γ), and abundance (N) for the Robust Design model $\phi(\bullet)$ $\gamma'(season) \neq \gamma(\bullet)$ $p(t,s)$ (Rank 1). N_m = estimate of number of marked animals in the population. P-period = primary sampling period, s-period = secondary sampling period, SE = standard error, LCI = 95% Lower Confidence Interval limit, UCI = 95% Upper Confidence Interval limit.

Parameter	P-period	s-period	Estimate	SE	LCI	UCI
ϕ	ALL	-	0.99	0.07	0.00	1.00
γ'	P2, P4, & P6	-	0.31	0.07	0.20	0.45
γ'	P3 & P5	-	<0.001	<0.001	<0.001	<0.001
γ	Constant	-	0.80	0.11	0.50	0.94
p	1	1	0.11	0.05	0.05	0.25
p	1	2	0.10	0.04	0.04	0.22
p	1	3	0.32	0.10	0.17	0.53
p	1	4	0.16	0.06	0.07	0.32
p	2	5	0.17	0.05	0.09	0.30
p	2	6	0.24	0.06	0.14	0.38
p	2	7	0.09	0.04	0.04	0.20
p	2	8	0.33	0.07	0.21	0.48
p	2	9	0.10	0.04	0.05	0.22
p	3	10	0.08	0.03	0.04	0.18
p	3	11	0.07	0.03	0.03	0.16
p	3	12	0.01	0.01	0.00	0.09
p	3	13	0.18	0.05	0.11	0.29
p	3	14	0.29	0.06	0.20	0.42
p	3	15	0.07	0.03	0.03	0.16
p	3	16	0.22	0.05	0.14	0.34
p	3	17	0.18	0.05	0.11	0.29
p	4	18	0.12	0.04	0.06	0.24
p	4	19	0.21	0.06	0.12	0.34
p	4	20	0.39	0.07	0.26	0.53
p	4	21	0.20	0.05	0.11	0.32
p	4	22	0.07	0.03	0.03	0.18
p	4	23	0.16	0.05	0.08	0.28
p	4	24	0.30	0.06	0.19	0.44
p	4	25	0.20	0.05	0.11	0.32
p	5	26	0.25	0.05	0.16	0.36
p	5	27	0.21	0.05	0.13	0.32
p	5	28	0.02	0.02	0.01	0.09
p	5	29	0.11	0.04	0.06	0.21
p	5	30	0.05	0.02	0.02	0.13
p	6	31	0.10	0.04	0.04	0.21
p	6	32	0.07	0.03	0.02	0.17
p	6	33	0.03	0.02	0.01	0.13
p	6	34	0.37	0.07	0.24	0.52
p	6	35	0.07	0.03	0.02	0.17
p	6	36	0.23	0.06	0.14	0.37
p	6	37	0.15	0.05	0.08	0.27
N_m	1	-	61.63	14.61	44.44	107.12
N_m	2	-	57.46	8.26	46.76	81.20
N_m	3	-	72.39	7.26	62.36	92.12
N_m	4	-	54.66	3.91	49.98	66.68
N_m	5	-	83.29	12.97	64.77	117.55
N_m	6	-	56.14	7.44	46.59	77.69

Table S5. Real parameter estimates of apparent survival (ϕ), capture probability (p), temporary emigration (γ' , γ), and abundance (N) for the Robust Design model $\phi(\bullet)$ $\gamma'(season) \neq \gamma(season)$ $p(t,s)$ (Rank 2). N_m = estimate of number of marked animals in the population. P-period = primary sampling period, s-period = secondary sampling period, SE = standard error, LCI = 95% Lower Confidence Interval limit, UCI = 95% Upper Confidence Interval limit.

Parameter	P-period	s-period	Estimate	SE	LCI	UCI
ϕ	ALL	-	1.00	0.07	0.00	1.00
γ'	P2, P4, & P6	-	0.35	0.06	0.23	0.48
γ'	P3 & P5	-	<0.001	<0.001	<0.001	<0.001
γ	P2, P4, & P6	-	0.56	0.19	0.21	0.85
γ	P3 & P5	-	1.00	0.18	0.00	1.00
p	1	1	0.11	0.05	0.05	0.25
p	1	2	0.10	0.04	0.04	0.22
p	1	3	0.32	0.10	0.17	0.53
p	1	4	0.16	0.06	0.07	0.32
p	2	5	0.18	0.06	0.10	0.32
p	2	6	0.25	0.07	0.15	0.40
p	2	7	0.09	0.04	0.04	0.20
p	2	8	0.34	0.08	0.21	0.50
p	2	9	0.11	0.04	0.05	0.23
p	3	10	0.08	0.03	0.04	0.17
p	3	11	0.07	0.03	0.03	0.16
p	3	12	0.01	0.01	0.00	0.09
p	3	13	0.18	0.05	0.10	0.29
p	3	14	0.29	0.06	0.19	0.41
p	3	15	0.07	0.03	0.03	0.16
p	3	16	0.22	0.05	0.14	0.33
p	3	17	0.18	0.05	0.10	0.29
p	4	18	0.13	0.05	0.06	0.25
p	4	19	0.23	0.06	0.13	0.36
p	4	20	0.41	0.07	0.28	0.56
p	4	21	0.21	0.06	0.12	0.34
p	4	22	0.08	0.04	0.03	0.18
p	4	23	0.17	0.05	0.09	0.30
p	4	24	0.32	0.07	0.20	0.46
p	4	25	0.21	0.06	0.12	0.34
p	5	26	0.23	0.05	0.15	0.35
p	5	27	0.20	0.05	0.12	0.31
p	5	28	0.02	0.02	0.01	0.09
p	5	29	0.11	0.03	0.05	0.20
p	5	30	0.05	0.02	0.02	0.12
p	6	31	0.11	0.04	0.05	0.22
p	6	32	0.07	0.03	0.03	0.18
p	6	33	0.04	0.02	0.01	0.13
p	6	34	0.39	0.08	0.25	0.55
p	6	35	0.07	0.03	0.03	0.18
p	6	36	0.25	0.06	0.14	0.39
p	6	37	0.16	0.05	0.08	0.29
N_m	1	-	61.63	14.61	44.44	107.12
N_m	2	-	55.96	7.90	45.88	78.94
N_m	3	-	73.42	7.54	62.96	93.87
N_m	4	-	53.51	3.53	49.41	64.59
N_m	5	-	87.35	14.34	66.90	125.30
N_m	6	-	54.23	6.86	45.56	74.36

Table S6. Real parameter estimates of apparent survival (ϕ), capture probability (p), temporary emigration (γ'' , γ'), and abundance (N) for the Robust Design model $\phi(\bullet) \gamma''(\text{season}) = \gamma'(\text{season}) p(t,s)$ (Rank 3). N_m = estimate of number of marked animals in the population. P-period = primary sampling period, s-period = secondary sampling period, SE = standard error, LCI = 95% Lower Confidence Interval limit, UCI = 95% Upper Confidence Interval limit.

Parameter	P-period	s-period	Estimate	SE	LCI	UCI
ϕ	ALL	-	0.85	0.05	0.73	0.92
$\gamma'' = \gamma'$	P2, P4, & P6	-	0.31	0.06	0.20	0.45
$\gamma'' = \gamma'$	P3 & P5	-	<0.001	<0.001	<0.001	<0.001
p	1	1	0.11	0.05	0.05	0.25
p	1	2	0.10	0.04	0.04	0.22
p	1	3	0.32	0.10	0.17	0.53
p	1	4	0.16	0.06	0.07	0.32
p	2	5	0.18	0.06	0.09	0.31
p	2	6	0.25	0.07	0.14	0.40
p	2	7	0.09	0.04	0.04	0.20
p	2	8	0.34	0.08	0.21	0.50
p	2	9	0.11	0.04	0.05	0.23
p	3	10	0.08	0.03	0.04	0.17
p	3	11	0.07	0.03	0.03	0.16
p	3	12	0.01	0.01	0.00	0.09
p	3	13	0.18	0.05	0.10	0.29
p	3	14	0.29	0.06	0.19	0.41
p	3	15	0.07	0.03	0.03	0.16
p	3	16	0.22	0.05	0.14	0.33
p	3	17	0.18	0.05	0.10	0.29
p	4	18	0.13	0.05	0.06	0.26
p	4	19	0.23	0.06	0.13	0.36
p	4	20	0.42	0.07	0.29	0.56
p	4	21	0.21	0.06	0.12	0.34
p	4	22	0.08	0.04	0.03	0.19
p	4	23	0.17	0.05	0.09	0.30
p	4	24	0.32	0.07	0.21	0.47
p	4	25	0.21	0.06	0.12	0.34
p	5	26	0.24	0.05	0.16	0.36
p	5	27	0.21	0.05	0.13	0.31
p	5	28	0.02	0.02	0.01	0.09
p	5	29	0.11	0.04	0.06	0.20
p	5	30	0.05	0.02	0.02	0.12
p	6	31	0.11	0.04	0.05	0.22
p	6	32	0.07	0.04	0.03	0.18
p	6	33	0.04	0.03	0.01	0.13
p	6	34	0.39	0.08	0.26	0.55
p	6	35	0.07	0.04	0.03	0.18
p	6	36	0.25	0.06	0.15	0.39
p	6	37	0.16	0.05	0.08	0.29
N_m	1	-	61.63	14.61	44.44	107.12
N_m	2	-	56.31	8.11	45.99	79.96
N_m	3	-	73.29	7.36	63.02	93.13
N_m	4	-	53.30	3.44	49.31	64.15
N_m	5	-	85.18	13.52	65.85	120.87
N_m	6	-	53.89	6.74	45.38	73.71

Table S7. POPAN open models fitted to the capture histories of Australian humpback dolphins to estimate super population size, apparent survival (ϕ), capture probability (p) and probability of entry into the study area ($pent$). Each model incorporates either constant (\bullet) or time-varying (t) parameters.

Model	Rank	AICc	Δ AICc	AICc weights	Cumulative AICc weights (%)	Number of parameters
$\phi(t) p(\bullet) pent(t)$	1	485.3	0.0	0.439	43.9%	11
$\phi(t) p(t) pent(t)$	2	485.5	0.2	0.401	84.0%	14
$\phi(\bullet) p(t) pent(t)$	3	488.5	3.2	0.090	93.0%	12
$\phi(\bullet) p(\bullet) pent(t)$	4	489.0	3.7	0.070	100%	8
$\phi(t) p(t) pent(\bullet)$	5	48376.7	47891.4	0.000	100%	10
$\phi(\bullet) p(\bullet) pent(\bullet)$	6	48410.6	47925.2	0.000	100%	3

SUPPLEMENT 5

Table S8. Models fitted to observed LIR data of Australian humpback dolphins on the North West Cape, Western Australia. For description of model equations see Whitehead (2001). The models that best fitted the data according to Akaike's Information Criterion, corrected for small sample size and overdispersion (QAICc) are shown in **bold**. Δ QAIC indicates how well the data support the less favoured model (Burnham & Anderson 2002).

Model equation	Model explanation	QAIC	Δ QAIC	Model parameter explanation ^d
$a2 \cdot \exp(-a1 \cdot td)$	Emigration/mortality^a	2437.8	0.0	$a1$=emigration rate; $1/a2=N$
$(1/a1) \cdot \exp(-td/a2)$	Emigration/mortality^a	2437.8	0.0	$a1=N$; $a2$=mean residence time
$a3 \cdot \exp(-a1 \cdot td) + a4 \cdot \exp(-a2 \cdot td)$	Emigration + reimmigration + mortality	2440.0	2.2	$a1=N$; $a2$ =mean time in study area; $a3$ =mean time out of study area; $a4$ =mortality rate
$a2 + a3 \cdot \exp(-a1 \cdot td)$	Closed: emigration + reimmigration ^b	2441.0	3.2	$a1$ =emigration rate; $a2/(a2+a3)$ =proportion of population in study area at any time
$a1$	Closed (no movement) ^c	2441.4	3.6	$a1=N$
$1/a1$	Closed (no movement) ^c	2441.4	3.6	$1/a1=N$
$(\exp(-a4 \cdot td)/a1) \cdot ((1/a3) + (1/a2) \cdot \exp(-(1/a3 + 1/a2) \cdot td)) / (1/a3 + 1/a2)$	Emigration + reimmigration + mortality	2441.8	4.0	$a1=N$; $a2$ =mean time in study area; $a3$ =mean time out of study area; $a4$ =mortality rate

^{a,c} Both model equations are considered the same but are parameterized differently, and yielded identical QAIC values.

^b The corresponding emigration + reimmigration model $[(1/a1) \cdot ((1/a3) + (1/a2) \cdot \exp(-(1/a3 + 1/a2) \cdot td)) / (1/a3 + 1/a2)]$ from Whitehead (2001, 2009) is not reported. This model includes the best fitting model plus one parameter, and given $QAIC = -2 \log(\text{Likelihood}) / \hat{c} + 2K$ (where K is the number of parameters), it is therefore constrained to have $\Delta QAIC$ within 2 of the best fitting model (because Log-Likelihood cannot decrease). It is therefore not a representative model of proper fit to the data and is not reported (Hal Whitehead, pers. comm. 17 January 2016).

^d For each model with a 'td' parameter, this refers to 'time lag'. Parameters $a1$, $a2$, $a3$ and $a4$ differ slightly amongst models and are therefore explained in the table. 'N' refers to the population size (at any one time) in the study area (Whitehead 2009).

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