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SUPPLEMENTARY MATERIAL

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8 **Capture–recapture models accounting for individual heterogeneity in capture** 9 **probabilities**

10 Two additional Pollock’s closed robust design (PCRD) models with two point finite
11 mixtures (Norris and Pollock 1996; Pledger 2000) were fitted to the data. The first model
12 allows for individual capture probabilities to be heterogeneous (M_{th}), while the second
13 model allows individual capture probabilities to be heterogeneous *and* to vary with time
14 (M_{th}). Under the two point finite mixtures approach animals may belong to one group of
15 animals with capture probability p_1 or another group of animals with capture probability p_2 .
16 The best performing model of these as well as other models fitted to the data was PCRD
17 with full heterogeneity (M_{th}) in which: apparent survival (φ) was kept constant (.);
18 temporary emigration parameters (γ'' and γ') were allowed to vary with time (t) and set
19 equal (random temporary emigration); and capture probability (p) was set equal to
20 recapture probability (c) and also allowed to vary with time.

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22 Although the above model best fitted the data, with ΔAIC_c of 243.3316 to the next model
23 (PCRD $\varphi(.)\gamma''(t)\gamma'(t)p(t)$ with $\gamma'' = \gamma'$ and $p=c$), the model consisted of 71 parameters
24 in comparison to the 38 parameters in the PCRD model that did not account for
25 heterogeneity. When comparing the parameter estimates for abundance and temporary
26 emigration between the two models, it was apparent that estimates were very similar
27 (Tables 1 and 2). The estimated apparent survival of 0.95 (SE 0.02) was also identical

28 between the two models. The estimate of abundance and temporary emigration are more
 29 precise for more estimates in the PCRDR model without accounting for heterogeneity and,
 30 in terms of number of parameters included, was also more parsimonious. For this reason
 31 we have focused on the models that did not include heterogeneity in this study.

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33 Table 1. Comparison of population abundance estimates obtained from Pollock's closed
 34 robust design (PCRDR) and PCRDR with full heterogeneity (M_{th}) to account for
 35 heterogeneous capture probabilities. For both modelling approaches, model
 36 $\varphi(.)\gamma''(t)\gamma'(t)p(t)$, with random temporary emigration pattern, best fit the data and was
 37 used for parameter estimations.

38 Notation: SE=Standard error, 95%CI= 95% confidence interval, n = number of identified
 39 individuals, \hat{N} = Estimated population size, φ = survival, γ'' = emigration, γ' = immigration
 40 and p = capture probability. Recapture probability (c) was set equal to p and, therefore, is
 41 not included in the model description.

Year	n	PCRDR			PCRDR with full heterogeneity		
		\hat{N}	SE	95% CI	\hat{N}	SE	95% CI
2007	105	112	3.5	108-123	115	5	109-130
2008	99	107	3.8	103-118	102	2.3	100-110
2009	186	193	2.9	189-201	197	4.0	192-208
2010	132	194	15.4	170-232	214	30.8	172-299
2011	96	160	20.0	131-212	147	20.9	119-206

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52 Table 2. Comparison of temporary emigration estimates obtained from Pollock’s closed
53 robust design (PCRD) and PCRD with full heterogeneity (M_{th}). Model $\varphi(\cdot)\gamma''(t)\gamma'(t)p(t)$
54 with random temporary emigration pattern was used for parameter estimation.

55 Notation: SE=Standard error, 95%CI= 95% confidence interval, \hat{N} = Estimated population
56 size, φ = survival, γ'' = emigration, γ' = immigration and p = capture probability. Recapture
57 probability (c) was set equal to p and therefore is not included in the model description.

Year	PCRD	PCRD with full heterogeneity
	$\gamma'' = \gamma'$ (SE)	$\gamma'' = \gamma'$ (SE)
2007-08	0.66 (0.05)	0.68 (0.05)
2008-09	0.33 (0.05)	0.31 (0.05)
2009-10	0.33 (0.07)	0.26 (0.12)
2010-11	0.50 (0.08)	0.54 (0.08)

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59 **References**

60 Norris, J. L., III, and Pollock, K. H. (1996). Nonparametric MLE under two closed
61 capture–recapture models with heterogeneity. *Biometrics* **52**, 639–649.

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63 Pledger, S. (2000). Unified maximum likelihood estimates for closed capture–recapture
64 models using mixtures. *Biometrics* **56**, 434–442.

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