Ecography

Supplementary material

Appendix 1

The goodness-of-fit test of the general Cormark-Jolly-Seber capture-recapture model

Under the assumption that individuals share the same parameters, i.e. the homogeneity assumption, the distribution of individual encounter histories can be written as a combination of two probabilities: the probability that an individual survives the interval i to i+1 (i.e. the survival probability at i, generally noted Φ_i) and the probability that an individual known to be alive, is caught, or seen, at i+1 (i.e. the recapture probability at i+1, denoted p_{i+1}). The goodness-of-fit test of homogeneity deployed here is divided into four different sets of contingency tables, that help to identify whether the survival (mainly tests 3.SR and 3.SM,) or recapture processes (mainly test 2.CT and 2.CL) depend on an individual encounter history (see also Tavecchia et al. 2008). The component 3SR assesses, in particular, if the survival probability after marking is different from subsequent survival probabilities. In birds marked as fledglings, this is equivalent to a test of age-dependence in local survival while in adult birds this is a test for the presence of

transient animals, i.e. birds seen only at marking and never seen after (Pradel et al. 1997). The results of the homogeneity goodness-of-fit tests based on a model in which all parameters are time dependent, i.e. the Cormark-Jolly Seber model (CJS), are shown for birds marked as adults and as fledglings in Table S1. A variance inflation factor, ĉ, for the general Cormark-Jolly-Seber model can be calculated as follows:

$$\widehat{c} = \frac{\sum_{groups} \chi^2(3.SR + 3.SM + 2.CT + 2.CL)}{\sum_{groups} df(3.SR + 3.SM + 2.CT + 2.CL)}$$

If test 3.SR is significant, model selection should begin from a model including specific parameters for the survival of newly marked animals (Pradel et al. 1997); and c-hat should be calculated for this new model as follows:

$$\widehat{c} = \frac{\sum_{groups} \chi^2(3.SM + 2.CT + 2.CL)}{\sum_{groups} df(3.SM + 2.CT + 2.CL)}$$

This is the starting model that we developed in our capture-mark-recapture analysis of birds marked as adults; and this model without time for birds marked as fledglings.

Table S1. Testing assumptions of the Cormark-Jolly Seber model, including time- and group-dependent parameters for birds at Marettimo "M" and at Benidorm ("B1" and "B2" for birds marked at Cave 1 and 2, respectively). Significant chi-square statistics (p<0.05) are in bold.

Goodness-of-fit components	M		B1		B2	
	χ^2	np	χ^2	np	χ^2	np
Birds marked as fledglings						
3.SR transient effect	**70.25**	**11**	**96.35**	**9**	**81.29**	**6**
3.SM	11.20	8	13.38	7	6.61	4
2.CT trap-dependence effect	17.27	10	12.87	7	4.47	6
2.CL	**30.02**	**16**	3.24	8	9.79	9
Total	**128.73**	**45**	**125.84**	**31**	**102.12**	**25**
Birds marked as adults						
3.SR transient effect	**37.26**	**11**	**42.35**	**12**	19.03	11
3.SM	16.57	17	8.34	11	15.44	10
2.CT trap-dependence effect	**16.79**	**8**	**27.01**	**11**	8.92	10
2.CL	19.78	24	8.54	8	6.98	7
Total	**90.41**	**60**	**86.24**	**42**	50.35	38

Appendix 2

Population matrix modelling

If N_i is a vector containing the number of birds in the n age classes at occasion i, the population at i+1 is $N_{i+1} = A\ N_i$ (Caswell 2001), the matrix A is denoted as the transition matrix and contains the n-age-dependent parameters where n is the number of age classes necessary to describe the focal species life-cycle (in our case n=6; Table S2). The matrix A takes the form:

$$A = \begin{pmatrix} \phi_1\pi_1 F_1 & \phi_2\pi_2 F_2 & .... & \phi_n\pi_n F_n \\ \phi_1 & 0 & ... & 0 \\ 0 & \phi_2 & ... & 0 \\ 0 & 0 & ... & 0 \\ 0 & 0 & ... & \phi_n \end{pmatrix}$$

Where:
Φ_j = the average survival of birds from age j-1 to age j
π_j = proportion of birds breeding at age j
F_j = the average number of female fledglings per breeding female
$B_j = (\Phi_j\ \pi_j\ F_j)$ the number of females born per breeding female of age j
Here, the vector N_i is unknown but the matrix formulation permits to estimate the asymptotic population growth, λ, as the dominant eigenvalue of A. In a stable population the population growth rate is equal to 1. Lower values indicate a decreasing trend. The 95% confidence interval of λ can be estimated by combining parameter variance and sensitivity (Lande 1988). Perturbation analyses permit the investigation of the sensitivity of the population growth rate to each entry in the matrix A (Caswell 2000). The sensitivity analysis gives an indication of how a change of a specific parameter affects the population growth rate. Note that in our case not all parameters were available for each colony. The breeding success in Marettimo, for example, was not available and was assumed to be similar to Cave 2 from Benidorm which experienced the lower predation pressure relative to Cave 1 over the study period (Table S2).

Table S2. Age- and colony-dependent estimates (se) of demographic parameters and sensitivity of matrix model entries. Fertility is the number of females born per breeding female of age j (see matrix A).

Colony	Age	Survival	Sensitivity survival	Breeding proportion	Breeding success	Fertility	Sensitivity fertility
Marettimo	1	0.57 (0.05)	0.110	0.07 (0.02)	0.30 (0.11)	0.005 (0.003)	0.065
	2	0.57 (0.05)	0.109	0.15 (0.03)	0.30 (0.11)	0.012 (0.005)	0.038
	3	0.89 (0.03)	0.068	0.65 (0.07)	0.30 (0.11)	0.076 (0.031)	0.023
	4	0.89 (0.03)	0.064	0.64 (0.08)	0.62 (0.08)	0.155 (0.034)	0.021
	5	0.89 (0.03)	0.059	1	0.62 (0.08)	0.243 (0.047)	0.019
	6	0.89 (0.03)	**0.685**	1	0.60 (0.07)	0.235 (0.044)	0.223
Benidorm (Cave 1)	1	0.47 (0.04)	0.057	0	0	0	0
	2	0.47 (0.04)	0.057	0	0	0	0
	3	0.47 (0.04)	0.057	0.11 (0.06)	0.21 (0.09)	0.005 (0.003)	0.008
	4	0.86 (0.04)	0.030	0.92 (0.16)	0.54 (0.08)	0.188 (0.098)	0.049
	5	0.86 (0.04)	0.029	1	0.55 (0.07)	0.208 (0.050)	0.004
	6	0.86 (0.04)	**0.850**	1	0.53 (0.06)	0.201 (0.047)	0.125
Benidorm (Cave 2)	1	0.55 (0.03)	0.073	0	0	0	0
	2	0.55 (0.03)	0.073	0	0	0	0
	3	0.55 (0.03)	0.071	0.97 (0.14)	0.30 (0.11)	0.070 (0.029)	0.013
	4	0.94 (0.02)	0.040	1	0.62 (0.08)	0.256 (0.057)	0.007
	5	0.94 (0.02)	0.038	1	0.62 (0.08)	0.256 (0.057)	0.007
	6	0.94 (0.02)	**0.801**	1	0.60 (0.07)	0.248 (0.054)	0.143