

Appendix C: Description of the bobcat data and integrated analysis

1. Bobcat data

The bobcat data consist of recorded histories of the LR data type for non-collared individuals and complete encounter histories for collared individuals. We applied our bilateral model for the LR data type to estimate N using the recorded histories from the $N - m$ non-collared individuals and the complete encounter histories from the m collared individuals. These data are summarized in Table C1.

Table C1: Detection history data used in an integrated photo-ID analyses from $T = 8$ camera trap surveys of a southern California bobcat population. The data consist of complete encounter histories for 27 collared individuals and recorded histories of the LR data type for the non-collared individuals.

Collared individuals		Non-collared individuals	
ID	Complete history	ID	Recorded history
1	RR000000		
2	00000LL0		
3	00LRLRR0		
4	0000L000		
5	0000R000		
6	L0000000		
7	00L0000L		
8	0L000000		
9	000000R0		
<i>continued on next page</i>			

Collared individuals		Non-collared individuals	
ID	Complete history	ID	Recorded history
10	00000R00		
11	0000R000		
12	RRRLBR0R		
13	00000R0L		
14	0000000B		
15	000000R0		
16	00000000		
17	00000000		
18	00000000		
19	00000000		
20	00000000		
21	00000000		
22	00000000		
23	00000000		
24	00000000		
25	00000000		
26	00000000		
27	00000000		
		28	0LLLL000
		29	L00000L0
		30	0000L00L
		31	000L0LL0
		32	000L0000
		33	L0000000

continued on next page

Collared individuals		Non-collared individuals	
ID	Complete history	ID	Recorded history
		34	L0000000
		35	000L0000
		36	0000L000
		37	00000L00
		38	000000L0
		39	0000000L
		40	0000000L
		41	0000000L
		42	00R000R0
		43	000000RR
		44	R00000RR
		45	0000R000
		46	000000R0
		47	R0000000
		48	0R000000
		49	00R00000
		50	00R00000
		51	000R0000
		52	0000R000
		53	00000R00
		54	000000R0

2. Bobcat analysis

We used our integrated model for the LR data type and the Bayesian analysis methods described in Appendix A. To incorporate the complete encounter histories for the $m = 27$ collared individuals, we simply constrained the latent history frequencies \mathbf{x} to be greater

than or equal to the known frequencies for the collared individuals. For example, because 12 collared individuals had encounter history $\omega_1 = 00000000$, we constrained $x_1 \geq 12$ within our MCMC algorithm.

To evaluate models with (model M_t) and without (model M_0) temporal variation in detection probability, as well as models assuming $\delta^L = \delta^R$ and $\delta^L \neq \delta^R$, we used reversible jump steps (e.g., Green 1995) within the algorithm described in Appendix A. Switching from one model to another involves adding or removing parameters within each iteration of the Markov chain. For model M_0 (i.e., $p_t = p$ for $t = 1, \dots, T$), we assign the prior

$$[p] \sim \text{Beta}(a_0, b_0),$$

and set $a_0 = b_0 = 1$. For models assuming $\delta^L = \delta^R$, we assign the prior

$$[\tau] \sim \text{Beta}(c_0^{LR}, c_0^B),$$

where $\boldsymbol{\delta} = (\delta^L, \delta^R, \delta^B) = (\tau/2, \tau/2, 1 - \tau)$, and set $c_0^{LR} = c_0^B = 1$.

Assuming equal prior model probabilities, two different model updates were proposed during each iteration:

1. If currently in model M_0 , propose a jump to model M_t by proposing

$\mathbf{p}^* = (p_1^*, p_2^*, \dots, p_T^*)$ from the full conditional distribution:

$$[p_t^* \mid \cdot] \sim \text{Beta}(a^t, b^t),$$

where

$$a^t = a_0^t + \sum_i x_i \mathbf{I}(\omega_{it} \neq 0),$$

and

$$b^t = b_0^t + \sum_i x_i \mathbf{I}(\omega_{it} = 0)$$

for $t = 1, \dots, T$. Accept this proposed model move with probability

$$R = \min \left(\frac{[\mathbf{x} \mid \mathbf{p}^*, \cdot][\mathbf{p}^*][p \mid \cdot]}{[\mathbf{x} \mid p, \cdot][p][\mathbf{p}^* \mid \cdot]}, 1 \right).$$

Alternatively, propose a jump from model M_t to model M_0 by proposing p^* from the full conditional distribution:

$$[p^* \mid \cdot] \sim \text{Beta}(a, b),$$

where

$$a = a_0 + \sum_i \sum_t x_i \mathbf{I}(\omega_{it} \neq 0),$$

and

$$b = b_0 + \sum_i \sum_t x_i \mathbf{I}(\omega_{it} = 0).$$

Accept this proposed model move with probability

$$R = \min \left(\frac{[\mathbf{x} \mid p^*, \cdot][p^*][\mathbf{p} \mid \cdot]}{[\mathbf{x} \mid \mathbf{p}, \cdot][\mathbf{p}][p^* \mid \cdot]}, 1 \right).$$

2. If $\delta^L \neq \delta^R$ in the current model, propose a jump to $\delta^L = \delta^R$ by proposing τ^* from the full conditional distribution:

$$[\tau^* \mid \cdot] \sim \text{Beta}(c^{LR}, c^B),$$

where

$$c^{LR} = c_0^{LR} + \sum_i x_i \sum_t \mathbf{I}(\omega_{it} = L) + \sum_i x_i \sum_t \mathbf{I}(\omega_{it} = R),$$

and

$$c^B = c_0^B + \sum_i x_i \sum_t \mathbf{I}(\omega_{it} = B).$$

Accept this proposed model move with probability

$$R = \min \left(\frac{[\mathbf{x} \mid \boldsymbol{\delta}^*, \cdot][\tau^*][\boldsymbol{\delta} \mid \cdot]}{[\mathbf{x} \mid \boldsymbol{\delta}, \cdot][\boldsymbol{\delta}][\tau^* \mid \cdot]}, 1 \right).$$

Alternatively, propose a jump from $\delta^L = \delta^R$ to $\delta^L \neq \delta^R$ by proposing $\boldsymbol{\delta}^*$ from the full conditional distribution:

$$[\boldsymbol{\delta}^* \mid \cdot] \sim \text{Dirichlet}(c^L, c^R, c^B),$$

where

$$c^L = c_0^L + \sum_i x_i \sum_t \mathbf{I}(\omega_{it} = L),$$

$$c^R = c_0^R + \sum_i x_i \sum_t \mathbf{I}(\omega_{it} = R),$$

and

$$c^B = c_0^B + \sum_i x_i \sum_t \mathbf{I}(\omega_{it} = B).$$

Accept this proposed model move with probability

$$R = \min \left(\frac{[\mathbf{x} \mid \boldsymbol{\delta}^*, \cdot][\boldsymbol{\delta}^*][\tau \mid \cdot]}{[\mathbf{x} \mid \boldsymbol{\delta}, \cdot][\tau][\boldsymbol{\delta}^* \mid \cdot]}, 1 \right).$$

By performing these model updates at each iteration, posterior model probabilities can be estimated as the proportion of iterations the Markov chain spends in each of the four possible models. Monte Carlo estimates (including model-averaged estimates) may also be obtained for each of the parameters from this single Markov chain.

To investigate potential sensitivity to our prior specification for N , we conducted additional analyses assuming a scale prior:

$$N \propto \frac{1}{N}.$$

For all analyses, we found the scale prior on N had virtually no effect on posterior model probabilities. However, model-averaged N estimates were slightly lower when using the scale prior. We believe this is due to the scale prior favoring smaller values relative to the uniform prior, particularly when N is small as for this population. Having no a priori justification for favoring smaller values of N , we prefer use of the uniform prior on N .

LITERATURE CITED

Green, P. J. 1995. Reversible jump Markov chain Monte Carlo computation and Bayesian model determination. *Biometrika* **82**:711–732.