

**Rahel Sollmann, Beth Gardner, Richard B. Chandler, J. Andrew Royle, T. Scott Sillett. An open population hierarchical distance sampling model. *Ecology* XXX.**

Appendix B: Simulation results: log-linear trend data analyzed with Markov and generalized Markov model.

## Methods

We simulated island scrub-jay abundance at  $J$  sites across  $T$  primary occasions with the log-linear trend model (Eq. 2) and generated distance sampling data conditional on these abundances, as described in Appendix A. We simulated data for 307 sampling points and with log-linear time effects,  $\beta_t$ , of -0.05 and -0.11, corresponding to population rates of change of 0.95 and 0.9, respectively. We generated 100 data sets for each scenario and analyzed them with the Markovian model described in Eq. 1.

Under the negative binomial distribution, data generated from the log-linear trend model exhibit population dynamics that are highly unrealistic for a long lived species like the island scrub-jay. Local extinctions and recolonizations were frequent, and recolonizations occurred in jumps of 60 individuals (Appendix A). Because of the complete dependence of  $N$  at  $t$  on  $N$  at  $t-1$ , the Markov model does not allow recolonization, and we expected it to perform poorly on the data from the model without temporal correlation. We therefore also specified a generalized version of the Markov model (henceforth generalized Markov model), where, for  $t > 1$ ,

$$N_{j,t} \sim \text{Poisson}(N_{j,t-1}\gamma + \varepsilon_t),$$

$$\log(\varepsilon_t) \sim \text{Normal}(0, \tau).$$

Here, even when  $N_{j,t-1} = 0$ ,  $\varepsilon_t$  allows for a non-zero population size at  $t$  and  $\varepsilon$  represents immigration from other sites. By setting  $\varepsilon = 0$ , the generalized Markov model becomes the Markov model (Eq. 2). We expect  $\gamma$  and  $\varepsilon$  to be confounded, because there is no information in the data as to the origin of recruits. We therefore estimated a derived population rate of change,  $\gamma^*$ , as the average over all  $\Sigma_j N_{j,t} / \Sigma_j N_{j,t-1}$  for the generalized Markov model.

We report average parameter estimates with root mean square error (rmse), average relative bias, 95% Bayesian confidence interval coverage and, for the population rates of change  $\gamma$  and  $\gamma^*$ , the number of times the downward population trend was deemed significant, defined as the 95% BCI not overlapping 1.

## Results

TABLE B1. Simulation results for estimating annual population rate of change using the Markovian model with abundance data generated under a log-linear trend model; mean parameter estimate (Mean), root mean square error (RMSE), relative bias (Bias), 95% confidence interval coverage (CI coverage) and percentage of simulations where population decline came out as significant (Sign.), across 100 simulations.

Parameter	$\gamma$	True value <sup>c</sup>	Mean	RMSE	Bias	CI coverage	Sign.
$\lambda$ (Intercept)	0.90	0.83	1.206	0.390	0.460	0	
	0.95		1.215	0.398	0.470	2	
$\lambda$ (chap) <sup>a</sup>	0.90	1.43	1.040	0.404	-0.274	2	
	0.95		1.016	0.425	-0.290	1	

$\lambda$ (chap <sup>2</sup> ) <sup>a</sup>	0.90	-0.38	-0.325	0.076	-0.134	87	
	0.95		-0.313	0.079	-0.168	84	
$\lambda$ (elev) <sup>b</sup>	0.90	-0.23	-0.202	0.073	-0.109	92	
	0.95		-0.211	0.067	-0.072	96	
$\gamma$	0.90	0.9	0.870	0.037	-0.033	76	100
	0.95	0.95	0.914	0.045	-0.038	55	98
$r$	0.90	-1.03	1.37	2.392	-2.345	0	
	0.95		1.417	2.437	-2.391	0	
$\sigma$ (Intercept)	0.90	4.68	4.573	0.107	-0.023	0	
	0.95		4.569	0.111	-0.023	0	
$\sigma$ (chap) <sup>a</sup>	0.90	-0.20	-0.091	0.11	-0.544	0	
	0.95		-0.091	0.11	-0.543	0	

a. Percent chaparral in survey plot with 300-m radius

b. Elevation of survey plot

c. Values taken from Sillett et al. (2012)

TABLE B2. Simulation results for estimating annual population decline using the generalized Markovian model allowing for recolonization, with abundance data generated under a log-linear trend model; mean parameter estimate (Mean), root mean square error (RMSE), relative bias (Bias), 95% confidence interval coverage (CI coverage) and percentage of simulations where population decline came out as significant (Sign.), across 100 simulations.

Parameter	$\gamma$	True value <sup>c</sup>	Mean	RMSE	Bias	CI coverage	Sign.
$\lambda$ (Intercept)	0.90	0.83	0.871	0.128	0.055	93	
	0.95		0.853	0.125	0.032	90	
$\lambda$ (chap) <sup>a</sup>	0.90	1.43	1.503	0.160	0.049	93	
	0.95		1.516	0.168	0.059	92	
$\lambda$ (chap <sup>2</sup> ) <sup>a</sup>	0.90	-0.38	-0.461	0.118	0.228	84	
	0.95		-0.458	0.112	0.218	83	
$\lambda$ (elev) <sup>b</sup>	0.90	-0.23	-0.254	0.099	0.119	96	
	0.95		-0.272	0.108	0.199	92	
$\gamma$	0.90	0.9	0.879	0.034	-0.024	75	100
	0.95	0.95	0.924	0.040	-0.027	57	92
$r$	0.90	-1.03	0.532	1.586	-1.523	0	
	0.95		0.64	1.687	-1.628	0	
$\sigma$ (Intercept)	0.90	4.68	4.68	4.652	0.035	-0.006	
	0.95		4.648	0.037	-0.007	73	
$\sigma$ (chap) <sup>a</sup>	0.90	-0.20	-0.13	0.072	-0.348	10	
	0.95		-0.132	0.071	-0.336	12	

a. Percent chaparral in survey plot with 300-m radius

b. Elevation of survey plot

c. Values taken from Sillett et al. (2012)

## LITERATURE CITED

Sillett, S., R. B. Chandler, J. A. Royle, M. Kéry, and S. A. Morrison. 2012. Hierarchical distance sampling models to estimate population size and habitat-specific abundance of an island endemic. *Ecological Applications* 22:1997–2006.