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Year. An open population hierarchical distance sampling model. *Ecology* XXX.

APPENDIX A. Simulation results: log-linear trend data and log-linear trend model.

Methods

We simulated island scrub-jay abundance at J sites across T primary occasions with a log-linear trend model where

$$N_{jt} \sim \text{Negative Binomial}(\lambda_{jt}, r)$$

$$\log(\lambda_{jt}) = \alpha + \beta_1 * Chap + \beta_2 * Elevation + \beta_3 * Chap^2 + \beta_4 * (t - 1).$$

Values for all parameters were taken from Sillett et al. (2012), except for the log-linear time effect, β_4 , which we set at -0.05 and -0.11, corresponding to population rates of change of 0.95 and 0.9, respectively. Conditional on these N_{jt} we generated distance sampling data, using the observation model from Sillett et al. (2012), by placing individuals i at random distances, d_i , between 0 and 300m from the survey point. To do so, we calculated the areas $A(D)$ of rings around the survey point at distances $D=1,2,\dots,300$ m. Then \mathbf{d} has a multinomial distribution:

$$\mathbf{d} \sim \text{Multinomial}(N_j, \boldsymbol{\pi})$$

where $\boldsymbol{\pi} = A(D) / \sum A(D)$.

We performed these simulations using all 307 sampling points, as well as random subsets of 200 and 100 points. We generated 100 data sets for each scenario and analyzed them with the data generating model. We report the average parameter estimates with root mean square error (rmse), average relative bias, 95% Bayesian confidence interval coverage and, for the linear time effect of the independent model, β_4 , the number of times the downward population trend was

deemed significant, defined as the 95% BCI not overlapping 0. We further report the number of local extinction and recolonization events, and the size of the latter, for the data generated under the log-linear trend model.

Results

Data generated under the log-linear trend model using all 307 sampling points and with $\beta_4 = -0.05$ showed, on average 332.13 (SD 12.15) local extinctions (sites going from >0 to 0 individuals between t and $t+1$) and 310.43 (SD 11.32) local recolonizations (sites going from 0 to >0 individuals between t and $t+1$). During recolonization events, numbers of individuals jumped from 0 to, on average, 61.35 individuals (SD 20.23), with a maximum of 140 individuals.

With $\beta_4 = -0.11$, there were, on average 333.72 (SD 12.38) local extinctions and 321.04 (SD 12.87) local recolonizations. During recolonization events, numbers of individuals jumped from 0 to, on average, 68.19 individuals (SD 25.26), with a maximum of 144 individuals.

Results from the simulations described above are summarized in the following tables.

TABLE A1. Simulation results for estimating annual population decline using log-linear trend data and model, considering different numbers of survey points; 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.

Model	True value	Mean	RMSE	Bias	CI coverage	Sign.
307 points	-0.11	-0.103	0.036	-0.019	93	86
	-0.05	-0.053	0.034	0.039	94	36
200 points*	-0.11	-0.102	0.038	-0.036	99	65
	-0.05	-0.046	0.039	-0.098	97	22
100 points*	-0.11	-0.112	0.062	0.067	94	50
	-0.05	-0.049	0.057	-0.043	97	15

* Randomly chosen subset of the full set of 307 points

TABLE A2. Simulation results for estimating open population distance sampling parameters related to abundance (λ) and detection (σ) under two log-linear population declines (β_d), using a log-linear trend model on abundance; mean parameter estimate (Mean), root mean square error (RMSE), relative bias (Bias), and 95% confidence interval coverage (CI coverage) across 100 simulations; all 307 sampling points considered.

Parameter	β_d	True value ^c	Mean	RMSE	Bias	CI coverage
λ (Intercept)	-0.11	0.83	0.822	0.115	-0.005	97
	-0.05		0.841	0.122	0.018	92
λ (chap) ^a	-0.11	1.43	1.433	0.088	0.001	98

	-0.05		1.430	0.080	-0.001	97
λ (chap ²) ^a	-0.11	-0.38	-0.379	0.051	0.009	97
	-0.05		-0.382	0.050	0.016	97
λ (elev) ^b	-0.11	-0.23	-0.228	0.061	0.005	96
	-0.05		-0.232	0.059	0.024	95
r	-0.11	-1.03	-1.008	0.105	-0.011	95
	-0.05		-1.011	0.084	-0.007	98
σ (Intercept)	-0.11	4.68	4.681	0.034	0.000	94
	-0.05		4.674	0.028	-0.001	95
σ (chap) ^a	-0.11	-0.20	-0.200	0.028	0.006	96
	-0.05		-0.197	0.026	-0.008	93

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.