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Appendix S1. Detailed methods for the deer mouse mark-recapture analysis on Santa Barbara Island

We calculated deer mouse densities based on mark-recapture data collected annually by the National Park Service on two plots during the spring season (March) as well as once during the fall/winter season (September-December) from 2007-2012 [1]. Mouse captures in 2013 were far too low to reliably estimate abundance and density, so instead we calculated the minimum number known alive (MNKA). The mouse monitoring protocol is described in detail in Fellers et al. [2]. Briefly, each plot has 100 permanent trap stations that are arranged in a 10 X 10 pattern spaced 7 m apart, at which one small Sherman live-trap is placed during trapping sessions that are conducted typically over three consecutive nights. Mice were weighed, sexed, and given a uniquely numbered ear tag before release.

We used Program MARK [3] to construct models and estimate detection probabilities and abundance for each of the capture history matrices in the mouse monitoring data set. We analyzed the capture-recapture data for each site $\times$ season $\times$ year combination using Huggins (1991) [4] closed-population capture-recapture models to estimate detection probabilities. Detection probabilities were explicitly modeled as a function of covariates such as sex and weight. Models were fit with maximum likelihood functions that condition on captures so abundance ( N ) was not explicitly part of the likelihood function and was therefore estimated as a derived parameter (see [4] for details). For capture history matrices where fewer than $20 \%$ of the values for sex were missing, the proportion (p) of males in the capture history matrix was computed and the missing values were randomly assigned a value of 1 (male) with probability $p$, and 0 (female) with probability 1-p. For capture history matrices where less than $20 \%$ of the values for weight were missing, the average of the non-missing weight values was computed and the missing values were assigned that average weight. In cases where $\geq 20 \%$ of the values for sex (weight) were missing, we omitted covariate data for sex (weight) from the analysis.

The most general model we analyzed was additive and allowed for capture probabilities (p) and recapture probabilities (c) to vary across capture occasions (time) and among individuals as a function of sex and weight. We also analyzed all possible subsets of this model where p and c were not constrained to be equal, which for 3 capture occasions (the most common number of days a grid was run) yielded a total of 32 models. We then constrained $\mathrm{p}=\mathrm{c}$ and constructed all possible subsets of an additive time, sex, and weight model, which for 3 capture occasions yielded a total of 16 models. Thus, in the typical case where there were 3 capture occasions, a total of 48 models were constructed and their parameters estimated. Once all models had been run they were ranked by their AICc values, and the weights for the $i$ th model $\left(\mathrm{w}_{\mathrm{i}}\right)$ were computed [5]. We deleted models with $\mathrm{w}_{\mathrm{i}}<0.01$ because the weights were so small they indicated there was little support for such models. In addition, when data were sparse and the results for many of
the models indicated the numerical optimization routine failed to converge on reasonable values, the model was deleted from consideration. Generally, this included models meeting one or more of the following criteria: (1) One or more of the parameters were singular; (2) the lower and upper bounds on the confidence interval for $p$ (or c) were near 0 and 1, respectively; (3) the estimated abundance or standard error were unrealistically large, or the standard error equaled 0 ; or (4) the coefficient of variation on a parameter was unrealistically large. Once inappropriate models were deleted, we model-averaged the remaining models to obtain a model-averaged estimate of abundance and its unconditional standard error [5]. Program MARK does this computation automatically.

Density $(D)$ was estimated as $N / A(W)$, where $N$ is estimated abundance and $A(W)$ is the estimated area sampled by the trapping grid, which depends on an estimated buffer strip around the grid of width $W$. Following Parmenter et al. (2003) [6], we let $A(W)=L^{2}+4 L W+\pi W^{2}$, where $L$ is the length of the side of the square formed by the trapping grid (i.e., 63 m ), and the buffer strip $W$ was estimated using the mean maximum distance moved (MMDM) by mice trapped at least twice on the grid. In previous studies MMDM was found to perform well for estimating $W$ [6]. In cases where fewer than two mice were captured twice, we set $W=0$ and therefore $A(W)=L^{2}$ (following [6] $\left.\operatorname{Var}(A(W))=(4 L+2 \pi W)^{2} \operatorname{Var}(W)\right)$.

## References:

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