

Appendix 3. Description of model structure.

Our models closely followed the model developed by Sollmann et al. (Sollmann et al. 2016). Bird abundance was modeled with a negative binomial distribution with a mean of $\lambda_{j,t,s}$ for point j , year t , and species s and a dispersion parameter r . Bird abundances were modeled in separate models for spring and winter. There were also two separate models within each season, one which included a categorical OHV use effect, and one with a continuous covariate of trail area in OHV use areas. We modeled mean abundance $\lambda_{j,t,s}$ as a function of covariates such that:

$$N_{j,t,s} \sim \text{Negative Binomial}(\lambda_{j,t,s}, r)$$

For the categorical OHV use model:

$$\log(\lambda_{j,t,s}) = \alpha_{0,s} + OHVuse_s + Year_{t,s} + HABeff_{k,s}$$

For the trail area model:

$$\log(\lambda_{j,t,s}) = \alpha_{0,s} + \alpha_{1,s} * TrailArea_j + Year_{t,s} + HABeff_{k,s}$$

The $OHVuse_s$ term represents the categorical effect of OHV use on each species s included in the model. $Year_{t,s}$ represents the categorical effect of year t of survey on species s , with the effect of $Year_{1,s}$ set to zero for identifiability and corresponding to the first year surveyed. $HABeff_{k,s}$ represents the categorical effect of habitat class k on species s , with $HABeff_{1,s}$ set to zero for identifiability and corresponding to chaparral habitat. $TrailArea_j$ represents the area covered by trails within a 100 m radius of a bird survey point j at points open to OHV users. The $\alpha_{0,s}$ term is the species specific intercept and $\alpha_{1,s}$ is the coefficient representing the effect of OHV trail area on species s .

Detection probability $g(x)$ for each species was modeled as a function of distance x to each bird observed, by either a negative-exponential function;

$$g(x) = \exp\left(\frac{-x}{\sigma}\right)$$

or half-normal function;

$$g(x) = \exp\left(\frac{-x^2}{2\sigma^2}\right)$$

and covariates on detection were linked to the detection function such that:

$$\log(\sigma_{j,t,s}) = \beta_{0,s} + \beta'_s Y_{j,t}$$

Where $\sigma_{j,t,s}$ is the scale parameter which describes how detection probability varies for species s which was detected at point j during year t . The parameter $\beta_{0,s}$ is a species specific intercept for σ , and β'_s represents all coefficients for each detection covariate Y included in the model. The inclusion of either the negative-exponential or half-normal detection in the final model, and the determination of which detection covariates to include was based on the Bayesian P -value of the detection models. Detection probability was linked to abundance such that:

$$n_{jts} \sim \text{Binomial}(N_{jts}, p_{jts})$$

where detection probability, p_{jts} , is the output of the detection function $g(x)$ defined above and n_{jts} is the observed count of bird clusters (see Methods for definition) for for species s which was detected at point j during year t .

Parameters for each species, with the exception of the zero inflation parameter r , and their mean and standard deviation are drawn from a common distribution informed by all species in each model. This means we assumed that the estimate of a parameter came from an overall community distribution, which we call the hyperdistribution. For instance, the intercept for abundance $\alpha_{0,s}$ is drawn such that:

$$\alpha_{0,s} \sim \text{Normal}(\mu\alpha_0, \sigma\alpha_0)$$

Hyperparameters for $\alpha_{0,s}$, mean $\mu\alpha_0$ and standard deviation $\sigma\alpha_0$ given precision $\tau\alpha_0$, are drawn such that:

$$\mu\alpha_0 \sim \text{Normal}(0, 10)$$

$$\sigma\alpha_0 = \frac{1}{\sqrt{\tau\alpha_0}}$$

$$\tau\alpha_0 \sim \text{gamma}(0.1, 0.1)$$

References:

Sollmann, R., B. Gardner, K. A. Williams, A. T. Gilbert, and R. R. Veit. 2016. A hierarchical distance sampling model to estimate abundance and covariate associations of species and communities. *Methods in Ecology and Evolution* 7:529–537. doi: 10.1111/2041-210X.12518