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*Wildlife Research*

### Supplementary Material

#### Improved house mouse control in the field with a higher dose zinc phosphide bait

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## Supplementary Materials: Data Analysis

We used the mark-recapture data to estimate the number of mice at each site during each survey (pre- and post-treatment). The approach, described in (Royle, 2009), allowed us to model heterogeneity in detection probabilities arising from individual differences among mice, and differences between nights in capture probability, by implementing the model in a Bayesian framework via data augmentation. We allowed the probability of capture to differ between nights because we observed that the number of mice captured at each site tended to increase over successive nights during each survey (Figure S1).

For the  $i$ th individual mouse ( $i = 1$  to  $n_{jk}$ ) captured on the  $j$ th site during the  $k$ th survey (pre- or post-treatment), we had data on whether that individual was captured on the  $m$ th night ( $y_{ijkm}=1$ ) or not ( $y_{ijkm}=0$ ), with four nights trapping pre-treatment and five nights trapping post-treatment.

To allow for individuals that were present at a site but not detected, we augmented the  $n_{jk}$  individuals with  $s_{jk}$  pseudo-individuals that were captured zero times. We specified the total number of captured plus pseudo-individuals at each site to be 400, which was a sufficiently large number to ensure that we were specifying a non-informative prior for the total number of individuals present at a site during a survey. We then defined an indicator variable,  $z_{ijk}$ , which took the value one for each of the  $n_{jk}$  individuals captured on a site during a survey and was missing for each of the  $s_{jk}$  pseudo-individuals, and specified that  $z_{ijk} \sim \text{Bernoulli}(\psi_{jk})$ , where  $\psi_{jk}$  can be interpreted as the probability that a pseudo-individual was actually present on the  $j$ th site at the  $k$ th survey. The total number of individuals,  $N_{jk}$ , on each site at each survey is then given by: 
$$N_{jk} = \sum_{i=1}^{n_{jk}+s_{jk}} z_{ijk}$$

Our model comprised the following:

$$\begin{aligned} z_{ijk} &\sim \text{Bernoulli}(\psi_{jk}) \\ y_{ijkm} &\sim \text{Bernoulli}(z_{ijk} * p_{ijkm}) \\ \text{logit}(p_{ijkm}) &\sim \text{Normal}(d_m, \sigma) \end{aligned} \tag{1}$$

Where  $p_{ijkm}$  is the probability of capture for the  $i$ th individual on the  $j$ th site during the  $k$ th survey on the  $m$ th night,  $d_m$  is the mean capture probability for the  $m$ th night, and  $\sigma^2$  is additional variation in capture probability attributable to individual heterogeneity.

Being a Bayesian model, we had to specify prior distributions for the unknown parameters. We followed (Link, 2013) in specifying a scale prior for the prior distribution of  $\psi_{jk}$ :

$$\psi_{jk} \sim \text{Beta}(0.001, 1)$$

We specified a hierarchical prior for each night's capture probability:

$$\begin{aligned} d_m &\sim \text{Normal}(\mu, \sigma_m) \\ \mu &\sim \text{Normal}(0, 100) \end{aligned}$$

And uniform priors for the standard deviation parameters:

$$\begin{aligned} \sigma &\sim \text{Uniform}(0, 10) \\ \sigma_m &\sim \text{Normal}(0, 10) \end{aligned}$$

The model was fitted in a Bayesian framework using Markov Chain Monte Carlo (MCMC) methods as implemented in the JAGS software (Plummer, 2003) using the package jagsUI (Kellner, 2015) called from R v. 4.0.1 (R Core Team (2020)). The model was run with 3 chains for 10,000 iterations following a burn-in of 5,000 iterations, which was sufficient to achieve convergence as judged by the Gelman-Rubin statistic (Gelman & Rubin, 1992).

The outcome of model fitting was an estimate of the number of mice at each site during each survey, expressed as a posterior distribution specifying the probability that the number of individuals took a particular value, having accounted for variation in capture probability among sites, nights, and individuals. There was clear increase in the probability of capture with each successive trapping night (Figure S2), which justified modelling the between-night heterogeneity.

## References

- Gelman, A., & Rubin, D. B. (1992). Inference from iterative simulation using multiple sequences. *Statistical Science*, 7(4), 457–472.
- Kellner, K. (2015). *jagsUI: A wrapper around rjags to streamline JAGS analyses*. <https://cran.r-project.org/web/packages/jagsUI/index.html>
- Link, W. A. (2013). A cautionary note on the discrete uniform prior for the binomial N. *Ecology*, 94(10), 2173–2179. <https://doi.org/10.1890/13-0176.1>
- Plummer, M. (2003). JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. In K. Hornik, F. Leisch, & A. Zeileis (Eds.), *Proceedings of the 3rd international workshop on distributed statistical computing* (Vol. 124, p. 10). Vienna, Austria.
- R Core Team. (2020). *R: A language and environment for statistical computing*. <https://www.R-project.org/>. <https://www.R-project.org/>
- Royle, J. A. (2009). Analysis of capture–recapture models with individual covariates using data augmentation. *Biometrics*, 65(1), 267–274. <https://doi.org/10.1111/j.1541-0420.2008.01038.x>

## Supplementary Figures

Figure S1: The number of mice captured at each of nine sites by night of capture showing a general increase in the number of mice caught per night over time both pre- and post-treatment.

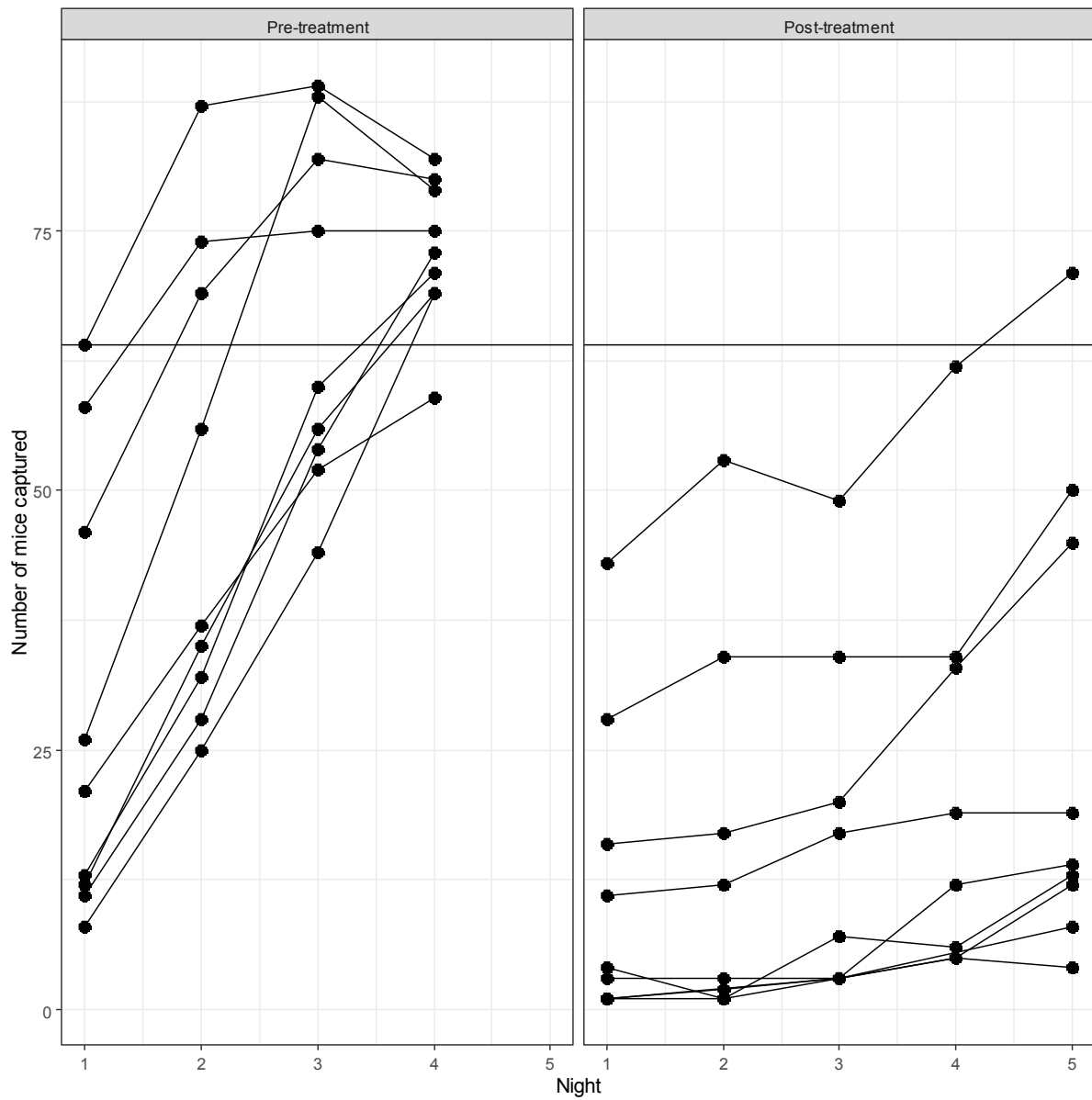


Figure S2: Estimated probability of capture as a function of trapping night. Points are the mean and bars the 95% credible intervals of the posterior distributions of capture probabilities.

