Appendix A – Site-structured demographic model.

We developed a site-structured demographic model to synthesize categorical count data while estimating habitat effects and population dynamics. Following De Valpine (2003), we use a demographic model both to ensure that estimates are plausible given species life history, and to account for the implied repeated-measures design, wherein the same location is surveyed multiple times within and among years. Specifically, we specified the number of individuals $N_{s,t}$ at site s and in the first year of available data (i.e., $t=1$) as a Poisson-distributed random variable:

$$N_{s,t=1} \sim Poisson(\lambda)$$

where λ is a parameter representing the expected value of initial abundance, where the expected value λ is constant among sites while the realized initial abundance $N_{s,t=1}$ varies among sites. Survival was specified as binomially distributed:

$$S_{s,t+1} \sim Binomial(N_{s,t,}\psi)$$

where ψ is the annual survival rate (which in our analyses is fixed *a priori* at a biologically plausible value) and $S_{s,t+1}$ is the number of individual surviving to year $t+1$, and recruitment $R_{s,t}$ was distributed according to a Poisson distribution:

$$R_{s,t} \sim Poisson(r_{s,t})$$

where $r_{s,t}$ is the expected recruitment for that site and year. Expected recruitment was affected by year-specific environmental factors and habitat-specific environmental factors:

$$\ln(r_{s,t}) = \rho_t + \sum_{h=1}^{n_h} \eta_h I(h = H_s)$$

where ρ_t is the median recruitment rate (in log-space) across all habitats in a given year t, η_h is the effect of habitat h on expected recruitment rates, H_s is the habitat-type for site s, and $I(x=X)$ is an indicator function that equals *1* when $x=X$ and *0* otherwise (and hence $I(h=H_s)$ is used to

associate each site with its appropriate habitat-specific effect). Both habitat and temporal effects on recruitment were specified hierarchically as random effects to facilitate comparison of the relative magnitude of variation in recruitment caused by both effects:

$$\rho_t \sim Normal(\mu_\rho, \sigma^2_\rho)$$

and

$$\eta_h \sim Normal(0, \sigma^2_\eta)$$

where μ_ρ is the median recruitment rate across all habitats and years, and σ^2_ρ and σ^2_η are the variance of year and habitat-specific effects on recruitment. Abundance at a given site and year was then the sum of survival and recruitment:

$$N_{s,t} = S_{s,t} + R_{s,t}$$

for all years $t>1$.

Finally, the observation process was approximated using a binned-Poisson distribution:

$$\Pr(c_{s,t,r} = 0) = \varphi + (1-\varphi)\frac{\left(pN_{s,t}\right)^0}{0!}e^{-pN_{s,t}}$$

$$\Pr(c_{s,t,r} = 1) = (1-\varphi)\frac{\left(pN_{s,t}\right)^1}{1!}e^{-pN_{s,t}}$$

$$\Pr(10 \geq c_{s,t,r} \geq 2) = (1-\varphi)\sum_{C=2}^{10}\frac{\left(pN_{s,t}\right)^C}{C!}e^{-pN_{s,t}}$$

$$\Pr(c_{s,t,r} \geq 11) = (1-\varphi)\left(1 - \sum_{C=0}^{10}\frac{\left(pN_{s,t}\right)^C}{C!}e^{-pN_{s,t}}\right)$$

where $c_{s,t,r}$ is the r-th survey at site s in year t, p is a parameter representing the expected number of times that each individual is detected in each sampling occasion (which we call "detectability"), and φ is the probability that a given sampling occasion will have a zero count (beyond that expected from the Poisson sampling distribution, called the "zero-inflation"

parameter). Given that we are using a zero-inflated binned-Poisson distribution for expected counts, we do not have a nonlinear relationship between the mean and variance of expected counts. This nonlinear relationship is generally used to estimate detectability in occupancy models (Royle 2004). However, detectability is still estimable in our demographic model because we have a time series of observations with which to discriminate between process and measurement variance (analogous to conventional state-space population models, e.g., de Valpine and Hastings 2002, and as noted by Dail and Madsen (2011) for their model). Model misspecification may in some cases result in miscalibrated estimates of detectability (Martin et al. 2011). However, the ratio of estimated parameters (e.g., abundance in years t_1 and t_2) may still be unbiased in some cases when detection probability is estimated with bias (Thorson et al. 2013).

To provide for exact inference regarding credible intervals, we use a Bayesian statistical paradigm and Markov chain Monte Carlo. We therefore must specify priors for all parameters, i.e., $ln(\lambda) \sim Uniform(-5,5)$, $p \sim Uniform(0.0001,10)$, $\sigma_\rho \sim Uniform(0,10)$, $\sigma_\eta \sim Uniform(0,10)$, $\varphi \sim Uniform(0,1)$, and $ln(\mu_\rho) \sim Uniform(-5,5)$, where we confirm for each parameter that these arbitrary upper bounds are not approached during sampling. The model was implemented in JAGS (Plummer 2003) called from *R* (R Core Development Team 2012) using the *R2jags* package (Su and Yajima 2012). We ran three sampling chains, each with 100,000 discarded samples followed by 100,000 monitored samples and a thinning rate of 100, resulting in 3,000 retained samples from the posterior distribution. We checked for evidence of non-convergence using trace plots, the Gelman-Rubin *R*-statistic, and estimated effective sample sizes, and confirmed that the effective samples size was >100 for all parameters (corresponding to a Gelman-Rubin generally <1.02).

LITERATURE CITED

Dail, D., and L. Madsen. 2011. Models for estimating abundance from repeated counts of an open metapopulation. Biometrics 67:577–587.

Martin, J., J. A. Royle, D. I. Mackenzie, H. H. Edwards, M. Kéry, and B. Gardner. 2011. Accounting for non-independent detection when estimating abundance of organisms with a Bayesian approach. Methods in Ecology and Evolution 2:595–601.

Plummer, M. 2003. JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003). Vienna, Austria.

R Core Development Team. 2012. R: A Language and Environment for Statistical Computing. Vienna, Austria.

Royle, J. A. 2004. N-Mixture Models for Estimating Population Size from Spatially Replicated Counts. Biometrics 60:108–115.

Su, Y.-S., and M. Yajima. 2012. R2jags: A Package for Running jags from R.

Thorson, J. T., S. Zhou, A. E. Punt, and T. D. M. Smith. 2013. A stepwise-selected spline approximation to time-varying parameters, with application to occupancy modelling. Methods in Ecology and Evolution 4:123–132.

De Valpine, P. 2003. Better inferences from population-dynamics experiments using Monte Carlo state-space likelihood methods. Ecology 84:3064–3077.

De Valpine, P., and A. Hastings. 2002. Fitting population models incorporating process noise and observation error. Ecological Monographs 72:57–76.