Supporting Methods

Bayesian hierarchical model of community dynamics

This model uses observed year-to-year transitions in 2-cm^2 cells to fit survival and colonization regressions in which the independent variables are the relative abundances of the three grass species (*Bouteloua hirsuta*, *Bouteloua curtipendula*, and *Schizachyrium scoparium*) in each cell's local neighborhood.

The Data Model. Each 2-cm cell can only be occupied by one of four available states (the three species and bare ground) at any one time. Because the data take a multinomial distribution, we write the state of cell j at time t as a vector of three 0s and a 1. For example, cell 23 in year 1968 occupied by bare ground would be written:

$$\mathbf{k}_{23,1968} = [0,0,0,1]$$.

We link the observed data (the $\mathbf{k}_{j,t}$s) to a multinomial distribution with unknown probabilities for each state ($\hat{\mathbf{k}}_{j,t}$) and a sample size of 1:

$$\mathbf{k}_{j,t} \sim \text{multinom}(\hat{\mathbf{k}}_{j,t},1)$$.   [3]

Taking the product over all js and ts gives the likelihood of our data given the model predictions.

The Process Model. The unknown probabilities that determine the state of each cell at year j and time t ($\hat{\mathbf{k}}_{j,t}$) depend on the state of the cell in the previous time step, $\mathbf{k}_{j,t-1}$, and on species-specific survival and colonization functions. For example, the probability that a cell occupied by *S. scoparium* will remain occupied in the next time step is the probability that *S. scoparium* survives plus the probability that *S. scoparium* dies but then

colonizes the cell, given that neither *B. hirsuta* nor *B. curtipendula* colonizes that cell (Table 2).

The logistic regressions used to estimate the probabilities of cell survival and colonization, as a function of the cell's identity and the composition of its local neighborhood, are described in *Materials and Methods* (Eqs. **1** and **2**).

Parameter Models and Parameter Estimation. We fit the year- and species-specific survival and colonization functions by using a hierarchical Bayesian model (1). This approach accommodated both the nonlinear model structure and our desire to estimate both year-specific and average values of the parameters by setting year as a random effect. Thus, our statistical model quantifies survival and colonization regression parameters for each year of the time series; these values, in turn, are random draws from underlying normal distributions that represent the average across-year values of these parameters.

Put more formally, we can write the year-specific survival intercepts of species *i* as a vector, $\boldsymbol{\alpha}_i$, of dimension T (total number of years). This vector is a multivariate normal draw from a normal distribution with a mean, $\overline{\alpha}_i$, and variance $\sigma^2_{\alpha_i}$:

$$N_T(\boldsymbol{\alpha}_i \mid \overline{\alpha}_i, \sigma_{\alpha_i}{}^2)$$. **[4]**

The mean intercept is itself a univariate normal distribution with a mean of 0 and large (vague) variance (i.e., a diffuse prior):

$$N(\overline{\alpha}_i \mid 0, 1000)$$. **[5]**

The likelihood of the variance is an inverse gamma distribution (IG) with prior parameters 1 and 100, also diffuse:

$$IG(\sigma^2_{\alpha_i} \mid 1,100) \, .$$ **[6]**

The colonization intercepts are handled in a directly analogous way:

$$N_T(\boldsymbol{\delta}_i \mid \overline{\delta}_i, \sigma_{\delta_i}^{2})$$ **[7]**

$$N(\overline{\delta}_i \mid 0,1000)$$ **[8]**

$$IG(\sigma^2_{\delta_i} \mid 1,100) \, .$$ **[9]**

The coefficients for the survival neighborhood effects also take multivariate normal distributions. For example, parameters for the effect of within-plant conspecifics cells (*self*) on survival of species *i* is:

$$N_T(\boldsymbol{\beta}_i^{self} \mid \overline{\beta}_i^{self}, \sigma_{\beta_i^{self}}^{2}) \, .$$ **[10]**

The effects of *B. curtipendula* (*bc*), *B. hirsuta* (*bh*), or *S. scoparium* (*ss*) are handled in the same way. We used a prior variance of 5,000 for these coefficients because neighborhood abundance values (by which these coefficients are multiplied) often have very small values, leading to large values for the coefficients:

$$N(\overline{\beta}_i^{self} \mid 0,5000) \, .$$ **[11]**

We gave the variance parameter ($\sigma^2_{\beta_i^{self}}$) an IG prior:

$$IG(\sigma^2_{\beta_i^{self}} \mid 1,100) \, .$$ **[12]**

Parameters for colonization neighborhood effects take the same form. Here we show the parameter for the effect of *B. curtipendula* on colonization of species *i* as an example (*bh* and *ss* are equivalent):

$$N_T(\lambda_i^{bc} \mid \overline{\lambda}_i^{bc}, \sigma_{\lambda_i^{bc}}^2) \tag{13}$$

$$N(\overline{\lambda}_i^{bc} \mid 0,5000) \tag{14}$$

$$IG(\sigma_{\lambda_i^{bc}}^2 \mid 1,100). \tag{15}$$

We modeled quadrat intercepts for survival and colonization as fixed effects because introducing them as random effects dramatically slowed convergence of the fitting algorithm. Thus, the likelihood of the quadrat effects for survival of species *i* is a multivariate normal distribution of dimension $Q - 1$ (the value for the last quadrat is fixed at 0) with a mean of 0 and variance of 1,000:

$$N_{Q-1}(\varphi_i \mid 0,1000) \tag{16}$$

and for the colonization case

$$N_{Q-1}(\theta_i \mid 0,1000) \tag{17}$$
.

After accounting for missing censuses in 1964 and 1969 and for some inconsistencies in the 1971 data, the dataset included 29 year-to-year transitions. We removed any cells located within 10 cm of the edge of the quadrats, although these cells were used to calculate the neighborhoods of interior cells. In addition, we removed records involving transitions to or from species not included in the model and also removed records whose neighborhoods included these other species in neighborhood abundances >0.05%, thus

reducing the dataset from 198,400 to 126,019 records. Contact P.B.A. to obtain these data, formatted for WinBUGS.

Because the high-dimensional posterior of this model is intractable, we simulated it by using Markov Chain Monte Carlo (MCMC), implemented with WinBUGS 1.4 (script provided in *Supporting Code*) and R 2.1 (2). Initial runs showed that deviance was lowest for data generated using a neighborhood distance-weighting exponent of –2 (Fig. 4). Using these data, we then ran two MCMC chains for 10,000 iterations, discarding the first 3,000 iterations. For all parameters, the scale reduction factor, $\hat{r}$, was <1.2, indicating convergence (1). Deviance averaged 118,997. The model closely reproduces observed changes in abundance from one year to another (Fig. 5).

1. Gelman, A., Carlin, J. B., Stern, H. S. & Rubin, D. B. (2004) *Bayesian Data Analysis* (Chapman & Hall/CRC, Boca Raton, FL).

2. R Development Core Team (2005) *R: A Language and Environment for Statistical Computing* (R Foundation for Statistical Computing, Vienna).