Appendix B: Detailed description of model selection, parameterization, and posterior parameter estimates.

Model Selection and Parameterization

Hierarchical Bayesian disease and survival models were fit independently in JAGS (Plummer 2003) in the R statistical programming environment (R Development Core Team 2010) using the `rjags` and `coda` packages. For both disease and survival models, model selection using indicator variables (Kuo and Mallick 1998), but no plot-level random effects, was carried out using 300000 iterations, discarding the initial 100000 iterations as burnin. Gibbs samplers used the `glm` module of the `rjags` package to improve fitting. As an example, consider the model for disease incidence with no random effects. The effect of covariate m on disease incidence depends on both the regression parameters β_m and indicator variables I_m, where $I_m = 1$ indicates inclusion of covariate m and $I_m = 0$ indicates otherwise. Therefore, $\beta = [\beta_0 I_0, \ldots, \beta_m I_m, \ldots, \beta_{M-1} I_{M-1}]$ so that element m of β equals 0 when $I_m = 0$ and β_m when $I_m = 1$. The indicator variable was modeled as a Bernoulli process $I_m \sim Bernoulli(\pi)$, where π is the probability of including any given parameter m in the model.

Bayesian model selection often relies on the posterior probability of models (Hoeting et al. 1999) or the marginal probabilities of individual parameter inclusion (O'Hara and Sillanpää 2009), each of which have advantages and disadvantages. For example, median probability models (i.e., the model including all parameters with marginal probability of inclusion $\pi_k > 0.5$) perform better in terms of prediction than the individual model with the highest posterior predictive probability (Barbieri and Berger 2004). Given that the large number of models being considered in this analysis (i.e., $2^{[\text{number of main, quadratic, and interaction} = 34]} = 2.25 \times 10^{15}$) would require

impractically large MCMC simulations to fully explore posterior model probabilities, we report the median probability model for predicting disease incidence responses to covariates.

The marginal probability of inclusion for each parameter was then calculated by taking the mean of each indicator variable for thinned series of predictions (every 40th iteration out of 200000 Gibbs steps). Next, model fitting was carried out using the median probability model and plot-level random effects. In both cases, priors for regression parameters were taken to be weak, such as $\beta \sim N(0,1000)$. For model selection, the prior for the probability of parameter inclusion π was *Beta*(2, 8). For the model fitting, the prior probability for the variance (τ^2 and ω^2) in the plot-level random effects was $Gamma^{-1}(0.1, 0.1)$.

Posterior Parameter Estimates

Parameter estimates, model predictions, and all other inference outside of model selection were based on the fitting of the median probability model. Following model selection and the fitting of the median probability model, the first 40000 iterations of the Gibbs sampler were discarded and 2000 iterations of the remaining 40000 steps were randomly selected for disease and mortality models. Mean posterior parameter estimates along with 68% and 95% credible intervals were calculated for the effects of covariates on the probability of observing disease in aspen trees (Table B1), the probability of aspen mortality for undiseased, or healthy, trees (Table B2), and the probability of aspen mortality for diseased trees (Table B3). 68% and 95% credible intervals for the random effects for each plot were calculated similarly to provide evidence concerning which plots exhibited higher or lower disease or mortality rates than would otherwise be expected (Fig. B2). The fact that many plots exhibited non-zero random effects for the disease (43%) and the mortality (35%) models supported the incorporation of random effects to account for variation not otherwise explained by the covariates.

TABLE B1. Mean parameter estimates for the disease incidence model with 68% and 95% credible intervals are provided for effects most often incorporated in the model ($\pi_k > 0.5$; Table 2).

	Covariate	Parameter Estimate ($\beta_k \mid I_k = 1$)		
		mean	68% interval	95% interval
Main Effects	intercept	-0.59	(-1.35, 0.17)	(-2.07, 0.91)
	d_{ijk}	1.62	(1.08, 2.15)	(0.57, 2.67)
	s_{ijk}	-2.12	(-2.61, -1.64)	(-3.04, -1.19)
	c_{ijk}	0.18	(-0.15, 0.52)	(-0.46, 0.79)
	b_{jk}	-0.25	(-0.46, -0.04)	(-0.67, 0.18)
	r_{jk}	-0.01	(-0.68, 0.65)	(-1.30, 1.29)
	T_k	0.67	(0.00, 1.32)	(-0.60, 1.92)
	P_k	-2.10	(-2.84, -1.37)	(-3.60, -0.65)
	t_k	0.02	(-0.58, 0.61)	(-1.19, 1.16)
	p_k	-0.16	(-0.90, 0.57)	(-1.63, 1.34)
Quadratic Effects	$d_{ijk}\ d_{ijk}$	0.91	(-0.87, 2.66)	(-2.55, 4.58)
	$s_{ijk} \times s_{ijk}$	2.17	(-0.05, 4.34)	(-2.10, 6.53)
	$r_{jk} \times r_{jk}$	-1.09	(-3.18, 0.97)	(-5.05, 3.09)
	$T_k \times T_k$	-5.40	(-8.16, -2.54)	(-11.19, -0.18)
	$P_k \times P_k$	6.15	(3.74, 8.55)	(1.59, 10.83)
	$t_k \times t_k$	3.63	(1.38, 5.77)	(-0.86, 8.10)
	$p_k \times p_k$	0.92	(-2.01, 3.89)	(-5.40, 6.89)
Interaction Effects	$s_{ijk} \times r_{jk}$	-4.23	(-6.91, -1.61)	(-9.64, 1.13)
	$s_{ijk} \times T_k$	5.30	(2.37, 8.23)	(-0.33, 10.87)
	$s_{ijk} \times P_k$	6.34	(3.74, 8.89)	(1.32, 11.33)
	$s_{ijk} \times t_k$	0.52	(-2.03, 3.02)	(-4.42, 5.42)
	$s_{ijk} \times p_k$	1.26	(-1.81, 4.11)	(-4.26, 7.17)
	$d_{ijk} \times s_{ijk}$	0.56	(-3.17, 4.28)	(-6.68, 8.08)
	$d_{ijk} \times r_{jk}$	1.64	(-1.09, 4.37)	(-3.94, 7.00)
	$d_{ijk} \times T_k$	2.95	(0.26, 5.66)	(-2.39, 8.30)
	$d_{ijk} \times P_k$	4.48	(2.19, 6.81)	(0.03, 9.13)
	$d_{ijk} \times t_k$	-1.64	(-3.91, 0.67)	(-5.91, 2.77)
	$d_{ijk} \times p_k$	-0.45	(-3.03, 2.17)	(-5.39, 4.72)
	$c_{ijk} \times r_{jk}$	2.10	(0.04, 4.17)	(-1.90, 6.31)
	$c_{ijk} \times T_k$	6.27	(4.06, 8.59)	(1.56, 10.80)
	$r_{jk} \times T_k$	-7.83	(-11.14, -4.39)	(-14.79, -1.09)
	$r_{jk} \times P_k$	5.14	(1.93, 8.33)	(-1.45, 11.37)
	$r_{jk} \times t_k$	-3.46	(-6.31, -0.65)	(-9.42, 2.03)
	$r_{jk} \times p_k$	-0.81	(-4.28, 2.58)	(-7.67, 6.14)
	$T_k \times P_k$	3.48	(0.85, 5.99)	(-1.60, 8.31)
	$T_k \times t_k$	-3.56	(-6.87, -0.30)	(-10.28, 2.99)
	$P_k \times p_k$	2.69	(-1.32, 6.69)	(-5.62, 10.65)
	$t_k \times p_k$	-2.33	(-6.40, 1.61)	(-9.68, 5.71)

TABLE B2. Mean parameter estimates for the diseased tree survival model with 68% and 95% credible intervals are provided for effects most often incorporated in the model ($\pi_k > 0.5$; Table 2).

	Covariate	Parameter Estimate ($\beta_k \mid I_k = 1$)		
		mean	68% interval	95% interval
Main Effects	Intercept	-4.20	(-4.94, -3.45)	(-5.64, -2.79)
	d_{ijk}	-4.89	(-5.43, -4.34)	(-5.98, -3.81)
	s_{ijk}	-1.93	(-2.37, -1.48)	(-2.86, -1.04)
	c_{ijk}	2.32	(1.90, 2.74)	(1.50, 3.16)
	b_{jk}	-0.11	(-0.38, 0.16)	(-0.61, 0.41)
	r_{jk}	0.09	(-0.35, 0.56)	(-0.78, 0.95)
	T_k	2.60	(2.15, 3.08)	(1.63, 3.51)
	P_k	1.21	(0.64, 1.76)	(0.08, 2.30)
	t_k	0.13	(-0.31, 0.58)	(-0.82, 0.99)
	p_k	-0.85	(-1.34, -0.36)	(-1.81, 0.11)
Quadratic Effects	$d_{ijk}\, d_{ijk}$	0.68	(-1.53, 2.86)	(-3.81, 5.17)
	$s_{ijk} \times s_{ijk}$	5.36	(3.76, 6.92)	(2.34, 8.39)
	$c_{ijk} \times c_{ijk}$	-2.65	(-4.12, -1.22)	(-5.46, 0.16)
	$b_{jk} \times b_{jk}$	-0.21	(-0.87, 0.47)	(-1.50, 1.08)
	$r_{jk} \times r_{jk}$	1.93	(0.66, 3.18)	(-0.59, 4.46)
	$P_k \times P_k$	-5.19	(-7.02, -3.33)	(-8.92, -1.52)
	$t_k \times t_k$	1.08	(-0.53, 2.70)	(-2.32, 4.28)
Interaction Effects	$s_{ijk} \times r_{jk}$	0.06	(-1.89, 2.02)	(-3.76, 3.74)
	$s_{ijk} \times T_k$	0.10	(-1.92, 2.13)	(-3.85, 3.86)
	$s_{ijk} \times P_k$	2.16	(0.13, 4.25)	(-2.15, 6.45)
	$s_{ijk} \times t_k$	4.40	(2.15, 6.68)	(-0.05, 8.87)
	$s_{ijk} \times p_k$	-1.13	(-3.89, 1.75)	(-6.52, 4.44)
	$d_{ijk} \times s_{ijk}$	-5.40	(-9.17, -1.68)	(-13.02, 1.76)
	$d_{ijk} \times c_{ijk}$	-12.10	(-14.97, -9.17)	(-17.55, -6.26)
	$d_{ijk} \times r_{jk}$	5.47	(2.73, 8.04)	(0.32, 10.70)
	$d_{ijk} \times P_k$	0.09	(-2.24, 2.49)	(-4.59, 4.75)
	$d_{ijk} \times t_k$	-3.19	(-5.78, -0.52)	(-8.31, 1.91)
	$d_{ijk} \times p_k$	-11.90	(-15.20, -8.58)	(-18.13, -5.60)
	$c_{ijk} \times b_{jk}$	2.52	(1.57, 3.53)	(0.68, 4.40)
	$c_{ijk} \times t_k$	-5.07	(-6.84, -3.25)	(-8.52, -1.43)
	$c_{ijk} \times p_k$	-5.65	(-8.28, -3.11)	(-10.66, -0.67)
	$r_{jk} \times T_k$	-4.27	(-6.65, -1.97)	(-9.12, -0.01)
	$r_{jk} \times p_k$	-1.05	(-4.18, 2.02)	(-7.13, 5.18)
	$T_k \times P_k$	-5.61	(-7.71, -3.44)	(-9.72, -1.41)

TABLE B3. Mean parameter estimates for the healthy tree survival model with 68% and 95% credible intervals are provided for effects most often incorporated in the model ($\pi_k > 0.5$; Table 2).

	Covariate	Parameter Estimate ($\beta_k \mid I_k = 1$)		
		mean	**68% interval**	**95% interval**
Main Effects	Intercept	-3.43	(-3.80, -3.05)	(-4.24, -2.66)
	d_{ijk}	-2.91	(-3.34, -2.48)	(-3.75, -1.99)
	b_{jk}	-0.40	(-0.63, -0.17)	(-0.83, 0.04)
	T_k	1.48	(0.94, 2.01)	(0.43, 2.54)
	P_k	0.31	(-0.10, 0.72)	(-0.51, 1.14)
Interaction Effects	$T_k \times P_k$	-4.05	(-5.83, -2.24)	(-7.72, -0.44)

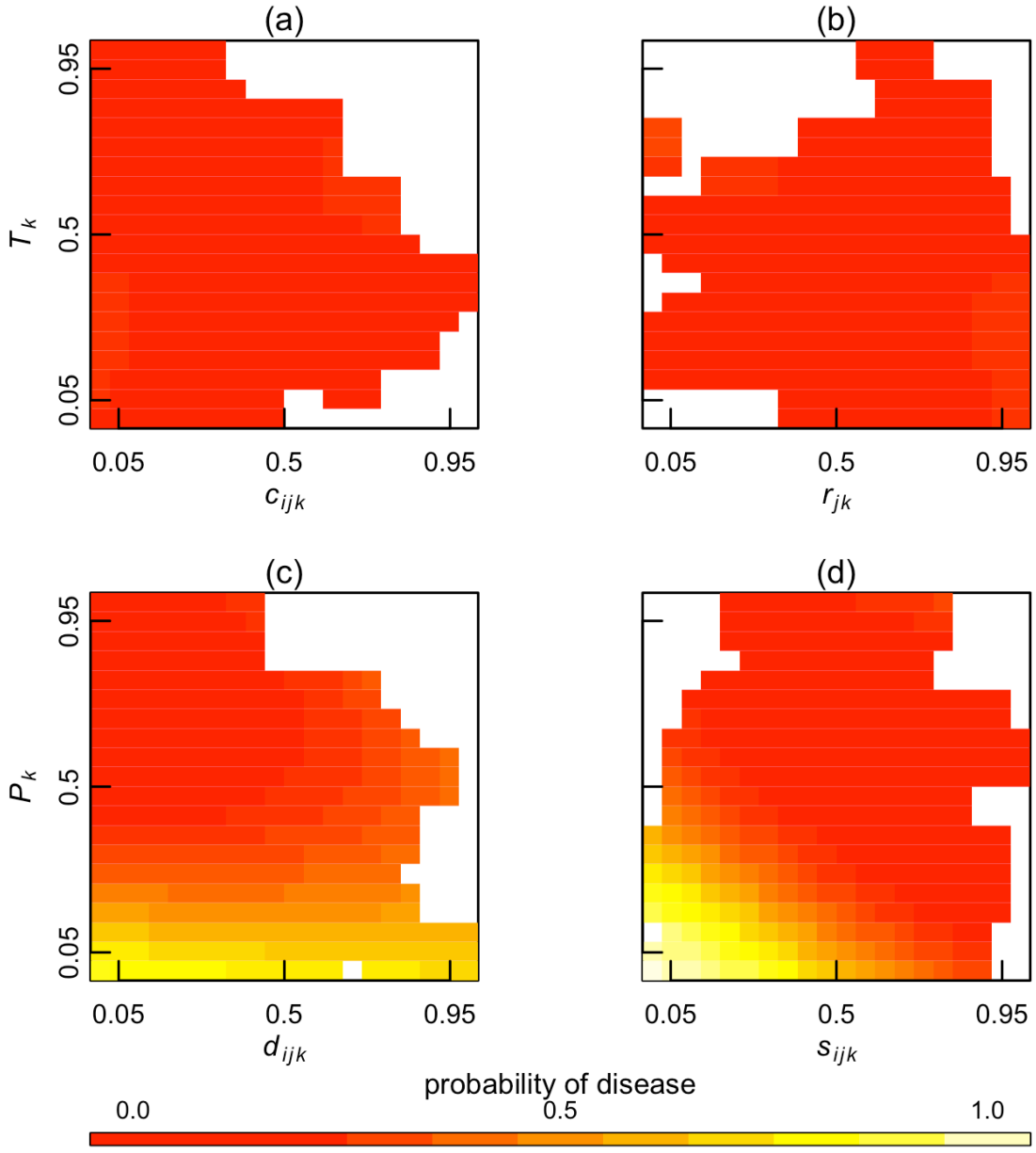

FIG. B1. Disease prevalence as a function of interacting covariates where yellow indicates high and red indicates low predicted probabilities of disease. White regions represent covariate space for which there were no plots. For each panel, all variables except for the two variables of interest were held constant at the mean observed values. See table 1 for definitions of variables.

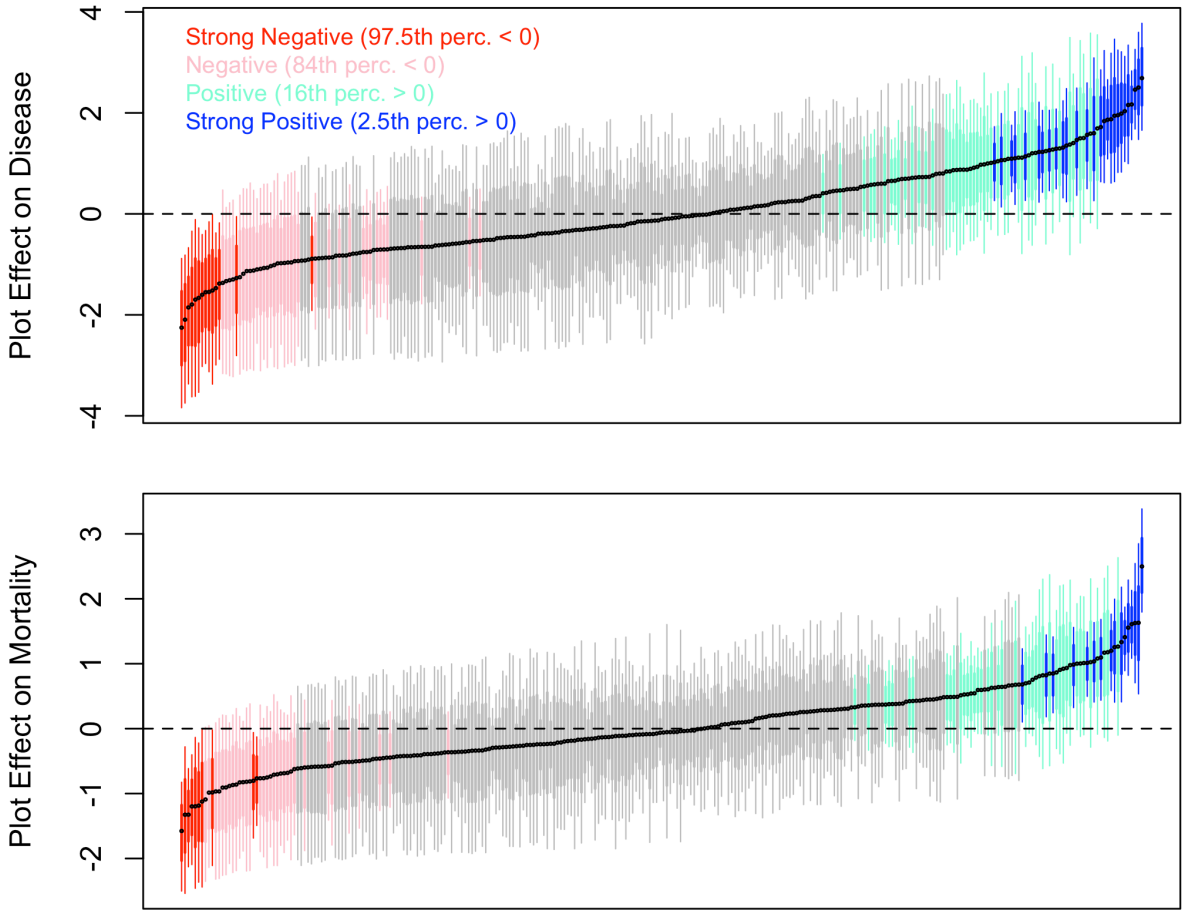

FIG. B2. Plot-level random effects on disease (upper; α_k) and mortality (lower; $-\gamma_k$) showing that plots exhibit strong negative (4.9% and 3.5%, respectively), moderate negative (12.8% and 11.3%, respectively), moderate positive (16.0% and 14.9%, respectively), and strong positive (9.6% and 5.7%, respectively) plot-level random effects for disease and mortality, respectively. Strong effects were classified as those where the 95% credible interval for the plot effect did not include zero and moderate effects were classified as those where the 95% credible interval included zero, but the 68% credible interval did not. Within each panel, plots are sorted in ascending mean plot random effect order.

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