Supporting Information Appendix S1

A.T. Tredennick, M.B. Hooten, & P.B. Adler, "Do we need demographic data..."

Methods in Ecology and Evolution

Contents

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Hierarchical Bayesian models for vital rates

Here we describe the statistical models in complete detail, including full description of the Bayesian models and Stan code for each model. We write each model as three parts: (1) a data model (likelihood), (2) a process model, and (3) a parameter model. We then combine these three models to write the posterior and joint distributions as a single model statement. Following the full model expression we provide the Stan code that directly corresponds the statement of posterior and joint distributions. Note that Stan uses standard deviations (σ) to specify distributions rather than variances (σ^2). In our expressions of the posterior and joint distributions we use general probability notation where [.] represents some unspecified distribution. We do this for clarity of model presentation. All prior distributions are defined in the parameter model sections. For clarity, we avoid subscripting species.

Parameter to model notation keys

Table S1: Definition of parameters and model notation for IPM survival and growth models.

Parameter	Definition	Notation in statistical results tables
$\beta_{0,t}$	intercept for year t	`a[t]` where `t` is the numeric year
$\tilde{\beta}_0$	global intercept	`a_mu`
$\beta_{Q,q}$	random effect of quadrat group q	`gint[q]` where `q` is the quadrat group
$\beta_{s,t}$	size effect for year t	`b1[t]` where `t` is the numeric year
$\tilde{\beta}_s$	global size effect	`b1_mu`
$\beta_{d,1}$	effect of crowding	`w[1]`
$\beta_{d,2}$	crowding $\times$ size effect	`w[2]`
$\beta_{c,k}$	effect of climate covariate k	`b2[k]` where `k` is the climate effect
a	first parameter for growth variance	`tau`
b	second parameter for growth variance	`tauSize`

Table S2: Definition of parameters and model notation for IPM recruitment model.

Parameter	Definition	Notation in statistical results tables
$\beta_{0,t}$	intercept for year t	`a[t]` where `t` is the numeric year
$\tilde{\beta}_0$	global intercept	`a_mu`
$\beta_{Q,q}$	random effect of quadrat group q	`gint[q]` where `q` is the quadrat group
$\beta_{d,1}$	effect of plot cover	`dd`
$\beta_{c,k}$	effect of climate covariate k	`b2[k]` where `k` is the climate effect
p	mixing fraction for effective plot cover	`u`
ζ	size parameter for negative binimial likelihood	`theta`

Table S3: Definition of parameters and model notation for quadrat based model.

Parameter	Definition	Notation in statistical results tables
$\beta_{0,t}$	intercept for year t	`a[t]` where `t` is the numeric year
$\tilde{\beta}_0$	global intercept	`a_mu`
$\beta_{Q,q}$	random effect of quadrat group q	`gint[q]` where `q` is the quadrat group
$\beta_{s,t}$	cover effect for year t	`b1[t]` where `t` is the numeric year
$\tilde{\beta}_s$	global cover effect	`b1_mu`
$\beta_{c,k}$	effect of climate covariate k	`b2[k]` where `k` is the climate effect
τ	model variance in log normal likelihood	`tau`

Table S4: Climate effect key.

Integer ID (k)	Climate covariate
1	pptLag
2	ppt1
3	ppt2
4	TmeanSpr1
5	TmeanSpr2
6	ppt1 × TmeanSpr1
7	ppt2 × TmeanSpr2

Survival (IPM)

We used logistic regression to model the probability that genet i in quadrat q survives from time t to t+1 ($s_{i,q,t}$):

$$y^S_{i,q,t} \sim \text{Bernoulli}(s_{i,q,t}) \tag{1}$$

$$\text{logit}(s_{i,q,t}) = \beta_{0,t} + \beta_{s,t}x_{i,q,t} + \beta_{Q,q} + \mathbf{z}'_t\boldsymbol{\beta}_c + \beta_{d,1}w_{i,t} + \beta_{d,2}(x_{i,q,t}w_{i,q,t}) \tag{2}$$

where $x_{i,q,t}$ is the log of genet i basal area at time t, $\beta_{0,t}$ is a year specific intercept, $\beta_{Q,q}$ is the random effect for the qth quadrat to account for spatial variation, $\beta_{s,t}$ is the year-specific slope parameter for size, $\mathbf{z}$ is a vector of p climate covariates specific to year t, $\boldsymbol{\beta}_c$ is a vector of fixed climate effects of length p, $\beta_{d,1}$ is the effect of intraspecific crowding experienced by the focal genet at time t ($w_{i,q,t}$), and $\beta_{d,2}$ is a size by crowding ($x_{i,q,t}w_{i,q,t}$) interaction effect.

Data, process, and parameter models

$$
\begin{aligned}
&\texttt{data} & y^S_{i,q,t} &\sim \text{Bernoulli}(s_{i,q,t}) \quad (3)\\
&\texttt{process} & \text{logit}(s_{i,q,t}) &= \beta_{0,t} + \beta_{s,t}x_{i,q,t} + \beta_{Q,q} + \mathbf{z}_t'\boldsymbol{\beta}_c + \beta_{d,1}w_{i,t} + \beta_{d,2}(x_{i,q,t}w_{i,q,t}) \quad (4)\\
&\texttt{parameters} & \beta_{0,t} &\sim \text{Normal}(\tilde{\beta}_0, \sigma^2_{\beta_0}) \quad (5)\\
&& \beta_{s,t} &\sim \text{Normal}(\tilde{\beta}_s, \sigma^2_{\beta_s}) \quad (6)\\
&& \beta_{Q,q} &\sim \text{Normal}(0, \sigma^2_Q) \quad (7)\\
&& \boldsymbol{\beta}_c &\sim \text{Normal}(\mathbf{0}, \sigma^2_c\mathbf{I}) \quad (8)\\
&& \beta_{d,1} &\sim \text{Normal}(0, 100) \quad (9)\\
&& \beta_{d,2} &\sim \text{Normal}(0, 100) \quad (10)\\
&& \tilde{\beta}_0 &\sim \text{Normal}(0, 100) \quad (11)\\
&& \tilde{\beta}_s &\sim \text{Normal}(0, 100) \quad (12)\\
&& \sigma_Q &\sim \text{Cauchy}(0, 5) \quad (13)\\
&& \sigma_{\beta_0} &\sim \text{Cauchy}(0, 5) \quad (14)\\
&& \sigma_{\beta_s} &\sim \text{Cauchy}(0, 5) \quad (15)
\end{aligned}
$$

Full expression of posterior and joint distributions

$$
\begin{aligned}
[\boldsymbol{\beta_0}, \tilde{\beta}_0, \boldsymbol{\beta_s}, \tilde{\beta}_s, \boldsymbol{\beta_Q}, \boldsymbol{q}, \boldsymbol{\beta_c}, \beta_{d,1}, \beta_{d,2}, \sigma^2_Q, \sigma^2_{\beta_0}, \sigma^2_{\beta_s} | y^S_{i,q,t}] \propto & \quad (16)\\
\prod_{t=1}^{T}\prod_{i=1}^{n}[y^S_{i,q,t}|\beta_{0,t}, \beta_{s,t}, \beta_Q, \boldsymbol{\beta_c}, \beta_{d,1}, \beta_{d,2}]\times & \quad (17)\\
[\beta_{0,t}|\tilde{\beta}_0, \sigma^2_{\beta_0}]\times & \quad (18)\\
[\beta_{s,t}|\tilde{\beta}_s, \sigma^2_{\beta_s}][\boldsymbol{\beta_c}|\sigma^2_{\beta_c}]\times & \quad (19)\\
\prod_{q=1}^{Q_{tot}}[\beta_{Q,q}|\sigma^2_Q]\times & \quad (20)\\
[\beta_{d,1}][\beta_{d,1}][\tilde{\beta}_0][\tilde{\beta}_s][\sigma_Q][\sigma_{\beta_0}][\sigma_{\beta_s}] & \quad (21)
\end{aligned}
$$

Stan code for model

```
data{
  // All Data
  int<lower=0> N; // observations
  int<lower=0> Yrs; // years
  int<lower=0> yid[N]; // year id
  int<lower=0> Covs; // climate covariates
  int<lower=0> G; // groups
  int<lower=0> gid[N]; // group id
  int<lower=0,upper=1> Y[N]; // observation vector
  matrix[N,Covs] C; // climate matrix
  vector[N] X; // size vector
  matrix[N,2] W; // crowding matrix
  real beta_tau; // prior sdev for climate effects
}
parameters{
  real a_mu;
  vector[Yrs] a;
  real b1_mu;
  vector[Yrs] b1;
  vector[Covs] b2;
  vector[2] w;
  vector[G] gint;
  real<lower=0> sig_a;
  real<lower=0> sig_b1;
  real<lower=0> sig_G;
}
transformed parameters{
  real mu[N];
  vector[N] climEff;
  vector[N] crowdEff;
  climEff <- C*b2;
  crowdEff <- W*w;
  for(n in 1:N){
    mu[n] <- inv_logit(a[yid[n]] + gint[gid[n]] +
                        b1[yid[n]]*X[n] + crowdEff[n] + climEff[n]);
  }
}
model{
  // Priors
  a_mu ~ normal(0,10);
  w ~ normal(0,10);
  b1_mu ~ normal(0,10);
  sig_a ~ cauchy(0,5);
  sig_b1 ~ cauchy(0,5);
```

```
  sig_G ~ cauchy(0,5);
  gint ~ normal(0, sig_G);
  b2 ~ normal(0, beta_tau);
  a ~ normal(a_mu, sig_a);
  b1 ~ normal(b1_mu, sig_b1);

  // Likelihood
  Y ~ binomial(1,mu);
}
}
```

Growth (IPM)

We modeled growth as a Gaussian process describing log genet size ($y^G_{i,q,t+1}$) at time $t+1$ in quadrat q as a function of log size at time t and climate covariates:

$$y^G_{i,q,t+1} \sim \text{Normal}(\mu_{i,q,t+1}, \sigma^2_{x_{i,q,t+1}}) \tag{22}$$
$$\mu_{i,q,t+1} = \beta_{0,t} + \beta_{s,t}x_{i,q,t} + \beta_{Q,q} + \mathbf{z}'_t\boldsymbol{\beta}_c + \beta_{d,1}w_{i,q,t} + \beta_{d,2}(x_{i,q,t}w_{i,q,t}) \tag{23}$$

where $\mu_{i,q,t+1}$ is log of genet is predicted size at time $t+1$, and all other parameters are as described for the survival regression. We capture non-constant error variance in growth by modeling the variance in the growth regression ($\sigma^2_{xi,q,t+1}$) as a nonlinear function of predicted genet size:

$$\sigma^2_{x_{i,q,t+1}} = a\exp[b \times \mu_{i,q,t+1}] \tag{24}$$

where $\mu_{i,q,t+1}$ is log of predicted genet size predicted from the growth regression (Eq. 4), and a and b are constants.

Data, process, and parameter models.

$$
\begin{aligned}
&\texttt{data} & y^G_{i,q,t+1} &\sim \text{Normal}(\mu_{i,q,t+1}, \sigma^2_{x_{i,q,t+1}}) && (25)\\
&\texttt{process} & \mu_{i,q,t+1} &= \beta_{0,t} + \beta_{s,t}x_{i,q,t} + \beta_{Q,q} + \mathbf{z}_t'\boldsymbol{\beta}_c + \beta_{d,1}w_{i,q,t} + \beta_{d,2}(x_{i,q,t}w_{i,q,t}) && (26)\\
& & \sigma^2_{iQ,t} &= ae^{b\mu_{iQ,t+1}} && (27)\\
&\texttt{parameters} & \beta_{0,t} &\sim \text{Normal}(\tilde{\beta}_0, \sigma^2_{\beta_0}) && (28)\\
& & \beta_{s,t} &\sim \text{Normal}(\tilde{\beta}_s, \sigma^2_{\beta_s}) && (29)\\
& & \beta_{Q,q} &\sim \text{Normal}(0, \sigma^2_Q) && (30)\\
& & \boldsymbol{\beta}_c &\sim \text{Normal}(\mathbf{0}, \sigma^2_c\mathbf{I}) && (31)\\
& & \beta_{d,1} &\sim \text{Normal}(0, 100) && (32)\\
& & \beta_{d,2} &\sim \text{Normal}(0, 100) && (33)\\
& & \tilde{\beta}_0 &\sim \text{Normal}(0, 100) && (34)\\
& & \tilde{\beta}_s &\sim \text{Normal}(0, 100) && (35)\\
& & \sigma_Q &\sim \text{Cauchy}(0, 5) && (36)\\
& & \sigma_{\beta_0} &\sim \text{Cauchy}(0, 5) && (37)\\
& & \sigma_{\beta_s} &\sim \text{Cauchy}(0, 5) && (38)\\
& & a &\sim \text{Normal}(0, 100) && (39)\\
& & b &\sim \text{Normal}(0, 100) && (40)
\end{aligned}
$$

Full expression of posterior and joint distributions

$$
\begin{aligned}
&[\boldsymbol{\beta_0}, \tilde{\beta}_0, \boldsymbol{\beta_s}, \tilde{\beta}_s, \beta_{Q,q}, \boldsymbol{\beta_c}, \beta_{d,1}, \beta_{d,2}, \sigma^2_Q, \sigma^2_{\beta_0}, \sigma^2_{\beta_s}, a, b | y^G_{i,q,t+1}] \propto && (41)\\
&\prod_{t=1}^{T}\prod_{i=1}^{n}[y^G_{i,q,t+1}|\beta_{0,t}, \beta_{s,t}, \beta_Q, \boldsymbol{\beta_c}, \beta_{d,1}, \beta_{d,2}, a, b]\times && (42)\\
&[\beta_{0,t}|\tilde{\beta}_0, \sigma^2_{\beta_0}]\times && (43)\\
&[\beta_{s,t}|\tilde{\beta}_s, \sigma^2_{\beta_s}][\boldsymbol{\beta_c}|\sigma^2_{\beta_c}]\times && (44)\\
&\prod_{q=1}^{Q_{tot}}[\beta_{Q,q}|\sigma^2_Q]\times && (45)\\
&[\beta_{d,1}][\beta_{d,1}][\tilde{\beta}_0][\tilde{\beta}_s][\sigma_Q][\sigma_{\beta_0}][\sigma_{\beta_s}][a][b] && (46)
\end{aligned}
$$

Stan code for model

Recruitment (IPM)

Our data allows us to track new recruits, but we cannot assign a specific parent to new genets. Therefore, we model recruitment at the quadrat level. We assume the number of individuals, $y^R_{q,t+1}$, recruiting at time $t+1$ in quadrat q follows a negative binomial distribution:

$$y^R_{q,t+1} \sim \text{NegBin}(\lambda_{q,t+1}, \phi) \tag{47}$$

where λ is the mean intensity and ϕ is the size parameter. We define λ as a function of quadrat composition and climate in the previous year:

$$\lambda_{q,t+1} = \tilde{c}_{q,t} \exp\left(\beta_{0,t} + \beta_{Q,q} + \mathbf{z}'_t \boldsymbol{\beta}_c + \beta_d \sqrt{\tilde{c}_{q,t}}\right) \tag{48}$$

where $\tilde{c}_{q,t}$ is effective cover (cm^2) of the focal species in quadrat q at time t, and all other terms are as in the survival and growth regressions. Effective cover is a mixture of observed cover (c) in the focal quadrat (q) and the mean cover across the entire group ($\bar{c}$) of Q quadrats in which q is located:

$$\tilde{c}_{q,t} = pc_{q,t} + (1-p)\bar{c}_{Q,t} \tag{49}$$

where p is a mixing fraction between 0 and 1 that is estimated when fitting model.

Data, process, and parameter models

$$
\begin{aligned}
&\texttt{data} & y^R_{q,t+1} &\sim \text{NegBin}(\lambda_{q,t+1}, \phi) & (50)\\
&\texttt{process} & \lambda_{q,t+1} &= \tilde{c}_{q,t} \exp\left(\beta_{0,t} + \beta_{Q,q} + \mathbf{z}'_t \boldsymbol{\beta}_c + \beta_d \sqrt{\tilde{c}_{q,t}}\right) & (51)\\
&\texttt{parameters} & \beta_{0,t} &\sim \text{Normal}(\tilde{\beta}_0, \sigma^2_{\beta_0}) & (52)\\
& & \beta_{Q,q} &\sim \text{Normal}(0, \sigma^2_Q) & (53)\\
& & \boldsymbol{\beta}_c &\sim \text{Normal}(\mathbf{0}, \sigma^2_c \mathbf{I}) & (54)\\
& & \beta_d &\sim \text{Uniform}(-10, 10) & (55)\\
& & \tilde{\beta}_0 &\sim \text{Normal}(0, 100) & (56)\\
& & \sigma_Q &\sim \text{Cauchy}(0, 5) & (57)\\
& & \sigma_{\beta_0} &\sim \text{Cauchy}(0, 5) & (58)\\
& & \phi &\sim \text{Uniform}(0, 10) & (59)\\
& & u &\sim \text{Uniform}(0, 1) & (60)
\end{aligned}
$$

Full expression of posterior and joint distributions

$$
\begin{aligned}
&[\boldsymbol{\beta_0}, \tilde{\beta}, \boldsymbol{\beta_Q}, \boldsymbol{\beta_c}, \beta_d, \sigma^2_Q, \sigma^2_{\beta_0}, \phi, u | y^R_{q,t+1}] \propto & (61)\\
&\qquad \prod_{t=1}^{T} \prod_{i=1}^{n} [y^R_{q,t+1} | \beta_{0,t}, \beta_{Q,q}, \beta_d, \boldsymbol{\beta_c}, \phi, u] \times & (62)\\
&\qquad [\beta_{0,t} | \tilde{\beta}, \sigma^2_{\beta_0}][\boldsymbol{\beta_c} | \sigma^2_{\beta_c}] \times & (63)\\
&\qquad \prod_{q=1}^{Q_{tot}} [\beta_{Q,q} | \sigma^2_Q][\boldsymbol{\beta_c}][\beta_d][\tilde{\beta}_0][\sigma_Q][\sigma_{\beta_0}][\phi][u] & (64)
\end{aligned}
$$

Stan code for model

```
data{
  int<lower=0> N; // observations
  int<lower=0> Yrs; // years
  int<lower=0> yid[N]; // year id
  int<lower=0> Covs; // climate covariates
  int<lower=0> G; // groups
  int<lower=0> gid[N]; // group id
  int<lower=0> Y[N]; // observation vector
  matrix[N,Covs] C; // climate matrix
  vector[N] parents1; // crowding vector
  vector[N] parents2; // crowding vector
  real<lower=0> tau; // prior variance
}
parameters{
  real a_mu;
  vector[Yrs] a;
  vector[Covs] b2;
  real dd;
  real gint[G];
  real<lower=0> sig_a;
  real<lower=0> theta;
  real<lower=0> sig_G;
  real<lower=0, upper=1> u;
}
transformed parameters{
real mu[N];
vector[N] climEff;
vector[N] trueP1;
vector[N] trueP2;
vector[N] lambda;
climEff <- C*b2;
  for(n in 1:N){
    trueP1[n] <- parents1[n]*u + parents2[n]*(1-u);
    trueP2[n] <- sqrt(trueP1[n]);
    mu[n] <- exp(a[yid[n]] + gint[gid[n]] + dd*trueP2[n] + climEff[n]);
    lambda[n] <- trueP1[n]*mu[n];
  }
}
model{
// Priors
  u ~ uniform(0,1);
  theta ~ uniform(0,10);
  a_mu ~ normal(0,10);
```

```
  dd ~ uniform(-10,10);
  sig_a ~ cauchy(0,5);
  sig_G ~ cauchy(0,5);
  for(g in 1:G)
   gint[g] ~ normal(0, sig_G);
  for(y in 1:Yrs){
    a[y] ~ normal(a_mu, sig_a);
  }
  for(j in 1:Covs)
    b2[j] ~ normal(0, tau);

// Likelihood
  Y ~ neg_binomial_2(lambda, theta);
}
```

Quadrat based model (QBM)

The model for quadrat cover change from time t to $t+1$ is

$$y^P_{q,t+1} \sim \text{LogNormal}(\mu_{q,t+1}, \sigma^2)^1_0 \tag{65}$$

$$\mu_{q,t+1} = \beta_{0,t} + \beta_{s,t} x_{q,t} + \beta_{Q,q} + \mathbf{z}'_t \boldsymbol{\beta}_c \tag{66}$$

where $\mu_{q,t+1}$ is the log of proportional cover in quadrat q at time $t+1$, and all other parameters are as in the individual-level growth model (Eq. 4) except that x now represents log of proportional cover. The log normal likelihood includes a truncation (subscript 0, superscript 1) to ensure that predicted values do not exceed 100% cover.

Data, process, and parameter models.

$$
\begin{aligned}
&\texttt{data} && y^P_{q,t+1} \sim \text{LogNormal}(\mu_{q,t+1}, \sigma^2)^1_0 && (67)\\
&\texttt{process} && \mu_{q,t+1} = \beta_{0,t} + \beta_{s,t} x_{q,t} + \beta_{Q,q} + \mathbf{z}'_t \boldsymbol{\beta}_c && (68)\\
&\texttt{parameters} && \beta_{0,t} \sim \text{Normal}(\tilde{\beta}_0, \sigma^2_{\beta_0}) && (69)\\
& && \beta_{s,t} \sim \text{Normal}(\tilde{\beta}_s, \sigma^2_{\beta_s}) && (70)\\
& && \beta_{Q,q} \sim \text{Normal}(0, \sigma^2_Q) && (71)\\
& && \boldsymbol{\beta}_c \sim \text{Normal}(\mathbf{0}, \sigma^2_c \mathbf{I}) && (72)\\
& && \tilde{\beta}_0 \sim \text{Normal}(0, 100) && (73)\\
& && \tilde{\beta}_s \sim \text{Normal}(0, 100) && (74)\\
& && \sigma_Q \sim \text{Cauchy}(0, 5) && (75)\\
& && \sigma_{\beta_0} \sim \text{Cauchy}(0, 5) && (76)\\
& && \sigma_{\beta_s} \sim \text{Cauchy}(0, 5) && (77)\\
& && \sigma^2 \sim \text{Inverse Gamma}(0.001, 0.001) && (78)
\end{aligned}
$$

Full expression of posterior and joint distributions

$$
\begin{aligned}
&[\boldsymbol{\beta_0}, \tilde{\beta}_0, \boldsymbol{\beta_s}, \tilde{\beta}_s, \boldsymbol{\beta_Q}, \boldsymbol{\beta_c}, \sigma^2_Q, \sigma^2_{\beta_0}, \sigma^2_{\beta_s}, \sigma^2 | y^P_{q,t+1}] \propto && (79)\\
&\qquad \prod_{t=1}^{T} \prod_{i=1}^{n} [y_{q,t+1} | \beta_{0,t}, \beta_{s,t}, \beta_{Q,q}, \boldsymbol{\beta_c}] \times && (80)\\
&\qquad [\beta_{0,t} | \tilde{\beta}_0, \sigma^2_{\beta_0}] \times && (81)\\
&\qquad [\beta_{s,t} | \tilde{\beta}_s, \sigma^2_{\beta_s}][\boldsymbol{\beta_c} | \sigma^2_{\beta_c}] \times && (82)\\
&\qquad \prod_{q=1}^{Q_{tot}} [\beta_{Q,q} | \sigma^2_Q] \times && (83)\\
&\qquad [\tilde{\beta}_0][\tilde{\beta}_s][\sigma_Q][\sigma_{\beta_0}][\sigma_{\beta_s}][\sigma] && (84)
\end{aligned}
$$

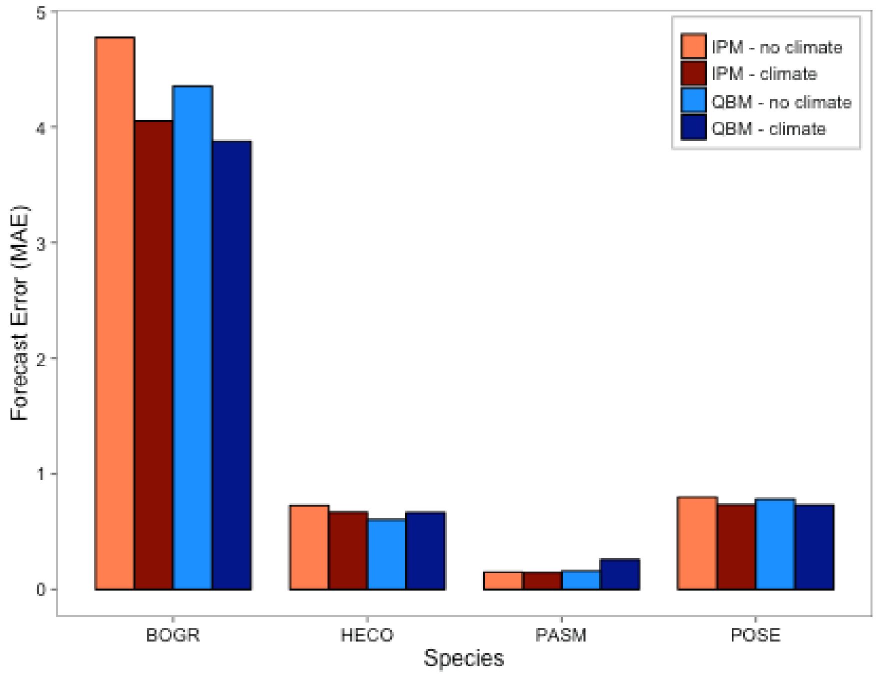
Stan code for model

```
data{
  int<lower=0> N; // observations
  int<lower=0> Yrs; // years
  int<lower=0> yid[N]; // year id
  int<lower=0> Covs; // climate covariates
  int<lower=0> G; // groups
  int<lower=0> gid[N]; // group id
  real<lower=0,upper=1> Y[N]; // observation vector
  real<lower=0> sd_clim; // prior sd on climate effects
  matrix[N,Covs] C; // climate matrix
```

```
  vector[N] X; // size vector
}
parameters{
  real a_mu;
  vector[Yrs] a;
  real b1_mu;
  vector[Yrs] b1;
  vector[Covs] b2;
  vector[G] gint;
  real<lower=0> sig_a;
  real<lower=0> sig_b1;
  real<lower=0> sig_G;
  real<lower=0> sigmaSq;
}
transformed parameters{
  real mu[N];
  vector[N] climEff;
  real<lower=0> tau;
  tau <- sqrt(sigmaSq);
  climEff <- C*b2;
  for(n in 1:N)
    mu[n] <- a[yid[n]] + gint[gid[n]] + b1[yid[n]]*X[n] + climEff[n];
}
model{
  // Priors
  a_mu ~ normal(0,10);
  b1_mu ~ normal(0,10);
  sig_a ~ cauchy(0,5);
  sig_b1 ~ cauchy(0,5);
  sig_G ~ cauchy(0,5);
  gint ~ normal(0, sig_G);
  b2 ~ normal(0,sd_clim);
  a ~ normal(a_mu, sig_a);
  b1 ~ normal(b1_mu, sig_b1);
  sigmaSq ~ inv_gamma(1, 1);

  //Likelihood
  Y ~ lognormal(mu, tau);
}
}
```

Supporting Figures



Significance Tests

	BOGR	HECO	PASM	POSE
IPM - no climate vs. QBM - no climate	$P = 1$	$P = 1$	$P = 0.15$	$P = 0.84$
IPM - climate vs. QBM - climate	$P = 0.88$	$P = 0.63$	$\mathbf{P < 0.001}$	$P = 0.68$
IPM - climate vs. IPM - no climate	$\mathbf{P = 0.01}$	$\mathbf{P = 0.017}$	$P = 0.29$	$\mathbf{P = 0.015}$
QBM - climate vs. QBM - no climate	$\mathbf{P < 0.001}$	$P = 0.87$	$P = 1$	$\mathbf{P = 0.007}$

Figure S1: Comparison of one-step-ahead, out-of-sample forecast error (mean absolute error) between the IPM and QBM models with and without the inclusion of climate covariates.

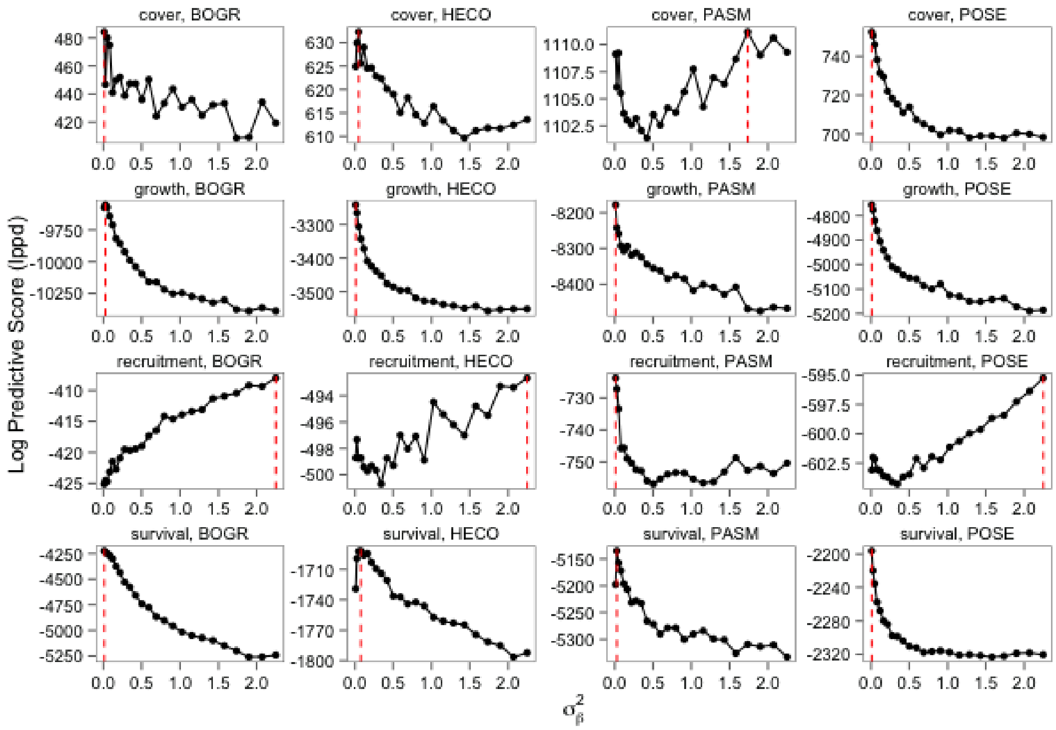


Figure S2: Results from ridge regression: summed log pointwise predictive densities (*lppd*) as a function of the prior variance of climate covariates. Dashed, red vertical lines show the highest prior variance with the highest *lppd* indicating the value of prior variance for optimal prediction.

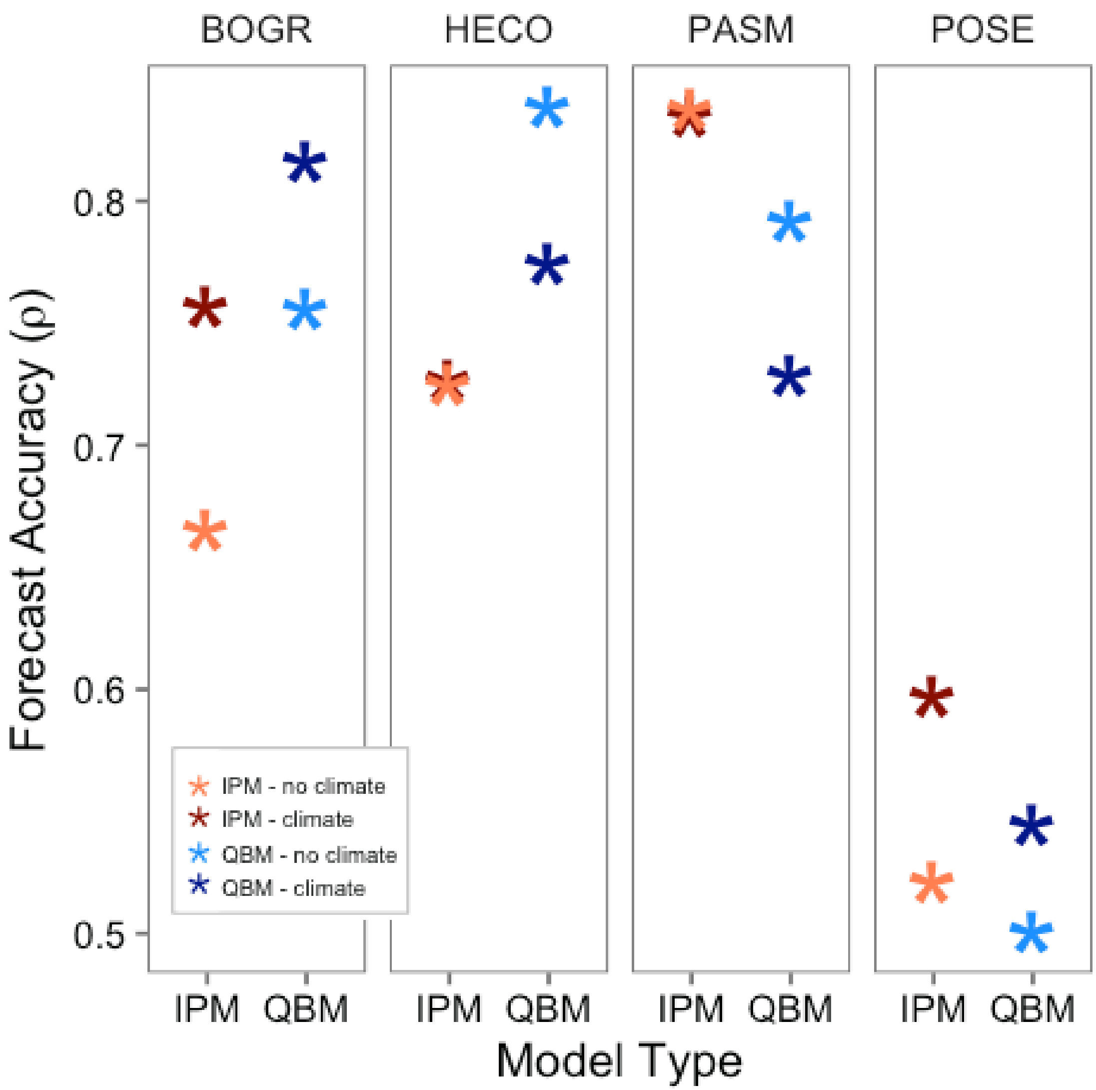


Figure S3: Comparison of one-step-ahead, out-of-sample forecast accuracy (mean correlation between observations and predictions) between the IPM and QBM models with and without the inclusion of climate covariates.

Supporting Tables

In all tables, “mean_value” is the mean parameter estimate, “sd_value” is the standard deviation of the estimate from the MCMC, “lo_BCI” is the lower limit of the 95% Bayesian Credible Interval, and “up_BCI” is the upper limit of the 95% Bayesian Credible Interval. See Tables S1-S4 for definitions and notations for model parameters.

Table S5: Statistical results from IPM survival model for *B. gracilis.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	0.64	0.29	0.06	1.21
a.1.	0.46	0.35	-0.24	1.20
a.10.	0.55	0.36	-0.15	1.25
a.11.	0.23	0.40	-0.54	1.04
a.12.	0.40	0.47	-0.53	1.35
a.13.	0.99	0.53	-0.03	2.06
a.2.	0.29	0.38	-0.46	1.02
a.3.	0.34	0.40	-0.47	1.11
a.4.	0.48	0.27	-0.05	1.00
a.5.	-0.40	0.28	-0.96	0.13
a.6.	1.62	0.25	1.16	2.14
a.7.	1.41	0.25	0.92	1.94
a.8.	1.32	0.27	0.80	1.84
a.9.	0.60	0.29	0.05	1.17
b1_mu	0.73	0.17	0.39	1.07
b1.1.	0.86	0.13	0.62	1.11
b1.10.	0.52	0.09	0.35	0.70
b1.11.	0.30	0.08	0.15	0.46
b1.12.	0.08	0.08	-0.07	0.23
b1.13.	0.11	0.10	-0.08	0.30
b1.2.	0.90	0.12	0.67	1.14
b1.3.	0.96	0.12	0.74	1.20
b1.4.	1.41	0.07	1.27	1.55
b1.5.	0.70	0.07	0.57	0.83
b1.6.	1.51	0.15	1.23	1.80
b1.7.	1.04	0.11	0.83	1.27
b1.8.	0.12	0.07	-0.03	0.26
b1.9.	0.95	0.10	0.75	1.16
b2.1.	-0.04	0.10	-0.22	0.15
b2.2.	0.05	0.09	-0.12	0.22
b2.3.	0.03	0.09	-0.16	0.21
b2.4.	-0.02	0.10	-0.21	0.16
b2.5.	-0.03	0.09	-0.19	0.15
b2.6.	0.06	0.09	-0.13	0.24
b2.7.	0.03	0.09	-0.15	0.21
gint.1.	0.08	0.17	-0.28	0.43
gint.2.	0.07	0.17	-0.28	0.41
gint.3.	-0.33	0.17	-0.68	-0.01
gint.4.	0.40	0.18	0.05	0.76
gint.5.	-0.19	0.17	-0.54	0.14
gint.6.	-0.08	0.17	-0.44	0.26
sig_a	0.70	0.19	0.43	1.16
sig_b1	0.55	0.14	0.35	0.87
sig_G	0.36	0.18	0.16	0.77
w.1.	-0.09	0.00	-0.10	-0.08
w.2.	0.02	0.00	0.02	0.03

Table S6: Statistical results from IPM survival model for *H. comata.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	1.28	0.32	0.63	1.95
a.1.	0.41	0.50	-0.58	1.36
a.10.	2.01	0.39	1.27	2.81
a.11.	0.92	0.43	0.10	1.78
a.12.	0.87	0.60	-0.29	2.09
a.13.	1.25	0.69	-0.06	2.61
a.2.	1.42	0.57	0.28	2.50
a.3.	1.03	0.64	-0.27	2.26
a.4.	1.11	0.52	0.09	2.16
a.5.	-0.34	0.45	-1.30	0.51
a.6.	2.18	0.50	1.25	3.19
a.7.	2.32	0.41	1.59	3.16
a.8.	1.70	0.35	1.07	2.47
a.9.	1.70	0.32	1.08	2.34
b1_mu	0.79	0.12	0.58	1.04
b1.1.	0.89	0.16	0.59	1.23
b1.10.	0.86	0.17	0.55	1.22
b1.11.	0.79	0.13	0.56	1.06
b1.12.	1.05	0.16	0.77	1.38
b1.13.	0.65	0.13	0.41	0.91
b1.2.	0.64	0.15	0.35	0.95
b1.3.	0.58	0.15	0.30	0.89
b1.4.	0.51	0.09	0.33	0.70
b1.5.	0.24	0.10	0.05	0.43
b1.6.	0.86	0.29	0.34	1.50
b1.7.	0.93	0.26	0.47	1.49
b1.8.	1.31	0.23	0.93	1.82
b1.9.	0.87	0.16	0.57	1.21
b2.1.	0.01	0.21	-0.41	0.43
b2.2.	0.13	0.23	-0.34	0.59
b2.3.	0.13	0.24	-0.33	0.60
b2.4.	-0.15	0.21	-0.57	0.27
b2.5.	-0.02	0.22	-0.46	0.40
b2.6.	0.13	0.24	-0.35	0.61
b2.7.	0.15	0.24	-0.32	0.61
gint.1.	0.02	0.15	-0.28	0.33
gint.2.	0.03	0.15	-0.26	0.34
gint.3.	0.22	0.16	-0.04	0.55
gint.4.	-0.16	0.16	-0.51	0.12
gint.5.	0.01	0.14	-0.28	0.30
gint.6.	-0.13	0.16	-0.47	0.15
sig_a	0.98	0.27	0.57	1.67
sig_b1	0.35	0.11	0.19	0.64
sig_G	0.23	0.15	0.03	0.59
w.1.	-0.36	0.04	-0.44	-0.28
w.2.	0.14	0.03	0.09	0.19

Table S7: Statistical results from IPM survival model for *P. smithii*.

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	2.95	0.26	2.44	3.46
a.1.	2.40	0.38	1.64	3.13
a.10.	3.13	0.25	2.66	3.62
a.11.	3.01	0.34	2.37	3.71
a.12.	3.05	0.46	2.22	4.01
a.13.	2.86	0.44	2.01	3.78
a.2.	2.26	0.39	1.44	2.97
a.3.	2.10	0.49	1.10	2.96
a.4.	3.30	0.49	2.40	4.32
a.5.	2.00	0.36	1.25	2.65
a.6.	3.66	0.44	2.86	4.59
a.7.	3.53	0.35	2.90	4.24
a.8.	3.64	0.33	3.03	4.33
a.9.	3.38	0.28	2.85	3.95
b1_mu	1.35	0.15	1.06	1.66
b1.1.	0.80	0.18	0.45	1.16
b1.10.	1.35	0.16	1.05	1.68
b1.11.	1.68	0.17	1.37	2.03
b1.12.	1.97	0.20	1.59	2.37
b1.13.	1.70	0.15	1.41	2.00
b1.2.	0.74	0.10	0.54	0.95
b1.3.	0.82	0.10	0.63	1.02
b1.4.	1.74	0.21	1.34	2.16
b1.5.	0.83	0.12	0.61	1.07
b1.6.	1.34	0.29	0.79	1.92
b1.7.	1.43	0.24	1.00	1.90
b1.8.	1.55	0.23	1.10	2.02
b1.9.	1.66	0.17	1.34	2.02
b2.1.	-0.07	0.14	-0.32	0.21
b2.2.	0.10	0.14	-0.20	0.38
b2.3.	0.13	0.15	-0.16	0.42
b2.4.	-0.22	0.15	-0.49	0.09
b2.5.	0.01	0.14	-0.27	0.28
b2.6.	0.10	0.15	-0.19	0.38
b2.7.	0.14	0.15	-0.16	0.43
gint.1.	0.13	0.10	-0.05	0.36
gint.2.	-0.18	0.11	-0.40	0.02
gint.3.	-0.03	0.10	-0.22	0.18
gint.4.	-0.01	0.12	-0.24	0.23
gint.5.	-0.06	0.11	-0.27	0.17
gint.6.	0.16	0.11	-0.03	0.39
sig_a	0.76	0.27	0.36	1.43
sig_b1	0.51	0.14	0.31	0.85
sig_G	0.20	0.12	0.08	0.46
w.1.	-0.45	0.03	-0.52	-0.39
w.2.	0.14	0.03	0.09	0.19

Table S8: Statistical results from IPM survival model for *P. secunda*.

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	1.31	0.37	0.65	2.15
a.1.	1.14	0.48	0.23	2.17
a.10.	0.53	0.37	-0.12	1.35
a.11.	0.96	0.40	0.25	1.79
a.12.	1.56	0.42	0.83	2.47
a.13.	1.45	0.45	0.62	2.42
a.2.	1.48	0.48	0.66	2.50
a.3.	1.42	0.46	0.62	2.38
a.4.	1.16	0.45	0.34	2.13
a.5.	1.35	0.41	0.62	2.16
a.6.	1.70	0.40	1.02	2.53
a.7.	1.41	0.38	0.77	2.17
a.8.	1.63	0.38	0.97	2.46
a.9.	1.29	0.37	0.65	2.05
b1_mu	0.71	0.08	0.56	0.87
b1.1.	0.75	0.19	0.38	1.13
b1.10.	0.47	0.07	0.33	0.61
b1.11.	0.52	0.09	0.34	0.70
b1.12.	0.73	0.13	0.49	0.98
b1.13.	0.85	0.12	0.62	1.09
b1.2.	0.70	0.16	0.39	1.03
b1.3.	0.60	0.16	0.28	0.90
b1.4.	1.00	0.12	0.78	1.24
b1.5.	0.74	0.11	0.53	0.97
b1.6.	0.90	0.12	0.68	1.13
b1.7.	0.63	0.09	0.46	0.81
b1.8.	0.56	0.10	0.36	0.75
b1.9.	0.86	0.09	0.70	1.03
b2.1.	-0.05	0.09	-0.21	0.12
b2.2.	-0.02	0.09	-0.19	0.15
b2.3.	-0.01	0.09	-0.19	0.16
b2.4.	0.03	0.08	-0.12	0.19
b2.5.	0.02	0.08	-0.14	0.18
b2.6.	-0.02	0.08	-0.18	0.15
b2.7.	-0.00	0.09	-0.17	0.16
gint.1.	-0.14	0.35	-0.92	0.48
gint.2.	-0.61	0.37	-1.46	0.01
gint.3.	0.16	0.35	-0.60	0.79
gint.4.	-0.15	0.37	-1.02	0.48
gint.5.	0.55	0.36	-0.21	1.22
gint.6.	0.01	0.35	-0.74	0.65
sig_a	0.44	0.13	0.25	0.76
sig_b1	0.22	0.07	0.12	0.38
sig_G	0.58	0.39	0.24	1.58
w.1.	-0.98	0.07	-1.13	-0.84
w.2.	0.21	0.05	0.11	0.31

Table S9: Statistical results from IPM growth model for *B. gracilis.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	0.74	0.22	0.33	1.20
a.1.	0.94	0.30	0.37	1.54
a.10.	1.24	0.26	0.72	1.74
a.11.	0.31	0.34	-0.34	1.01
a.12.	0.76	0.45	-0.11	1.67
a.13.	0.50	0.49	-0.43	1.48
a.2.	1.08	0.33	0.42	1.73
a.3.	0.55	0.38	-0.21	1.26
a.4.	0.68	0.30	0.11	1.28
a.5.	-0.56	0.26	-1.10	-0.07
a.6.	0.64	0.20	0.24	1.04
a.7.	1.26	0.16	0.96	1.57
a.8.	1.44	0.17	1.13	1.78
a.9.	0.78	0.20	0.41	1.18
b1_mu	0.77	0.03	0.70	0.84
b1.1.	0.88	0.05	0.79	0.98
b1.10.	0.76	0.03	0.70	0.83
b1.11.	0.88	0.04	0.80	0.95
b1.12.	0.70	0.04	0.61	0.79
b1.13.	0.78	0.04	0.70	0.86
b1.2.	0.78	0.04	0.71	0.85
b1.3.	0.74	0.04	0.67	0.81
b1.4.	0.88	0.03	0.83	0.93
b1.5.	0.57	0.05	0.47	0.66
b1.6.	0.87	0.04	0.79	0.95
b1.7.	0.67	0.03	0.61	0.73
b1.8.	0.71	0.03	0.65	0.77
b1.9.	0.79	0.03	0.73	0.86
b2.1.	-0.02	0.13	-0.27	0.23
b2.2.	0.09	0.14	-0.18	0.36
b2.3.	0.05	0.14	-0.22	0.31
b2.4.	-0.05	0.14	-0.33	0.22
b2.5.	0.06	0.13	-0.19	0.31
b2.6.	0.11	0.14	-0.16	0.38
b2.7.	0.06	0.13	-0.21	0.32
gint.1.	-0.07	0.07	-0.22	0.07
gint.2.	0.04	0.07	-0.11	0.18
gint.3.	0.09	0.07	-0.06	0.23
gint.4.	0.02	0.07	-0.12	0.17
gint.5.	0.07	0.07	-0.07	0.21
gint.6.	-0.17	0.07	-0.32	-0.04
sig_a	0.66	0.18	0.40	1.09
sig_b1	0.11	0.03	0.07	0.19
sig_G	0.14	0.08	0.06	0.35
tau	1.50	0.06	1.39	1.61
tauSize	-0.22	0.01	-0.24	-0.19
w.1.	-0.03	0.00	-0.04	-0.03
w.2.	0.01	0.00	0.00	0.01

Table S10: Statistical results from IPM growth model for *H. comata.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	0.65	0.22	0.23	1.08
a.1.	0.98	0.28	0.43	1.52
a.10.	1.08	0.15	0.79	1.39
a.11.	0.22	0.19	-0.16	0.59
a.12.	0.48	0.27	-0.03	1.01
a.13.	0.68	0.30	0.06	1.27
a.2.	0.58	0.33	-0.07	1.20
a.3.	0.01	0.37	-0.72	0.73
a.4.	0.43	0.30	-0.17	1.01
a.5.	-0.54	0.29	-1.10	0.03
a.6.	1.18	0.24	0.70	1.65
a.7.	1.88	0.12	1.65	2.11
a.8.	0.63	0.12	0.38	0.87
a.9.	0.79	0.14	0.52	1.05
b1_mu	0.62	0.06	0.49	0.74
b1.1.	0.57	0.09	0.38	0.76
b1.10.	0.72	0.03	0.66	0.79
b1.11.	0.71	0.04	0.63	0.78
b1.12.	0.77	0.04	0.70	0.84
b1.13.	0.63	0.03	0.56	0.69
b1.2.	0.73	0.09	0.55	0.92
b1.3.	0.37	0.10	0.17	0.56
b1.4.	0.60	0.05	0.50	0.70
b1.5.	0.31	0.10	0.12	0.50
b1.6.	0.65	0.12	0.41	0.89
b1.7.	0.41	0.05	0.31	0.52
b1.8.	0.87	0.04	0.79	0.96
b1.9.	0.74	0.04	0.66	0.82
b2.1.	-0.03	0.09	-0.21	0.15
b2.2.	0.04	0.09	-0.12	0.22
b2.3.	0.03	0.09	-0.16	0.21
b2.4.	-0.03	0.09	-0.21	0.15
b2.5.	0.01	0.09	-0.17	0.19
b2.6.	0.05	0.10	-0.13	0.24
b2.7.	0.03	0.10	-0.16	0.22
gint.1.	0.01	0.06	-0.10	0.12
gint.2.	0.03	0.06	-0.07	0.15
gint.3.	-0.08	0.06	-0.21	0.01
gint.4.	-0.02	0.06	-0.14	0.09
gint.5.	0.05	0.06	-0.05	0.17
gint.6.	0.02	0.06	-0.09	0.14
sig_a	0.72	0.19	0.45	1.18
sig_b1	0.20	0.06	0.12	0.34
sig_G	0.08	0.05	0.01	0.21
tau	1.31	0.06	1.19	1.43
tauSize	-0.26	0.03	-0.31	-0.21
w.1.	-0.14	0.04	-0.21	-0.07
w.2.	0.03	0.01	-0.00	0.05

Table S11: Statistical results from IPM growth model for *P. smithii.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	-0.06	0.07	-0.18	0.07
a.1.	0.01	0.12	-0.22	0.26
a.10.	0.03	0.06	-0.10	0.16
a.11.	-0.05	0.09	-0.23	0.12
a.12.	-0.14	0.11	-0.37	0.08
a.13.	-0.10	0.14	-0.38	0.17
a.2.	0.01	0.14	-0.28	0.28
a.3.	-0.09	0.14	-0.38	0.17
a.4.	-0.15	0.15	-0.45	0.14
a.5.	-0.30	0.10	-0.51	-0.10
a.6.	0.15	0.10	-0.03	0.36
a.7.	-0.12	0.06	-0.23	-0.00
a.8.	0.02	0.06	-0.08	0.13
a.9.	-0.04	0.06	-0.16	0.09
b1_mu	0.59	0.04	0.52	0.66
b1.1.	0.59	0.04	0.52	0.67
b1.10.	0.66	0.03	0.60	0.71
b1.11.	0.62	0.03	0.57	0.67
b1.12.	0.65	0.02	0.60	0.69
b1.13.	0.68	0.02	0.63	0.73
b1.2.	0.49	0.03	0.43	0.54
b1.3.	0.35	0.03	0.30	0.41
b1.4.	0.52	0.03	0.46	0.58
b1.5.	0.46	0.04	0.39	0.53
b1.6.	0.66	0.05	0.57	0.75
b1.7.	0.65	0.03	0.58	0.72
b1.8.	0.64	0.03	0.58	0.70
b1.9.	0.69	0.03	0.64	0.74
b2.1.	-0.07	0.05	-0.16	0.03
b2.2.	0.05	0.08	-0.11	0.21
b2.3.	0.02	0.08	-0.13	0.18
b2.4.	0.02	0.05	-0.08	0.11
b2.5.	0.04	0.06	-0.07	0.14
b2.6.	0.07	0.08	-0.07	0.22
b2.7.	0.03	0.07	-0.11	0.17
gint.1.	0.03	0.04	-0.05	0.11
gint.2.	-0.06	0.04	-0.15	0.02
gint.3.	-0.09	0.04	-0.18	-0.01
gint.4.	-0.00	0.05	-0.10	0.09
gint.5.	0.07	0.04	-0.02	0.15
gint.6.	0.06	0.04	-0.03	0.14
sig_a	0.17	0.05	0.09	0.29
sig_b1	0.12	0.03	0.08	0.19
sig_G	0.09	0.04	0.04	0.21
tau	0.44	0.01	0.43	0.46
tauSize	0.28	0.03	0.21	0.34
w.1.	-0.06	0.01	-0.08	-0.04
w.2.	-0.01	0.01	-0.03	0.01

Table S12: Statistical results from IPM growth model for *P. secunda*.

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	0.51	0.19	0.15	0.89
a.1.	0.77	0.30	0.22	1.36
a.10.	-0.01	0.15	-0.30	0.30
a.11.	0.06	0.23	-0.42	0.49
a.12.	0.32	0.29	-0.29	0.88
a.13.	0.65	0.34	-0.05	1.31
a.2.	0.76	0.31	0.15	1.36
a.3.	1.08	0.35	0.45	1.79
a.4.	0.03	0.30	-0.56	0.64
a.5.	0.48	0.24	0.04	0.99
a.6.	1.53	0.19	1.18	1.92
a.7.	0.22	0.15	-0.06	0.53
a.8.	0.27	0.12	0.05	0.50
a.9.	0.50	0.11	0.28	0.73
b1_mu	0.54	0.05	0.44	0.63
b1.1.	0.45	0.12	0.21	0.68
b1.10.	0.32	0.04	0.24	0.40
b1.11.	0.50	0.05	0.40	0.59
b1.12.	0.44	0.06	0.33	0.55
b1.13.	0.57	0.05	0.46	0.67
b1.2.	0.43	0.09	0.25	0.61
b1.3.	0.51	0.08	0.35	0.66
b1.4.	0.82	0.06	0.71	0.93
b1.5.	0.55	0.05	0.47	0.64
b1.6.	0.64	0.04	0.57	0.72
b1.7.	0.56	0.04	0.48	0.64
b1.8.	0.60	0.04	0.53	0.67
b1.9.	0.60	0.03	0.54	0.66
b2.1.	-0.07	0.09	-0.23	0.10
b2.2.	-0.05	0.09	-0.23	0.13
b2.3.	-0.05	0.09	-0.21	0.13
b2.4.	0.11	0.09	-0.08	0.28
b2.5.	-0.03	0.09	-0.20	0.16
b2.6.	-0.04	0.09	-0.22	0.14
b2.7.	-0.05	0.09	-0.22	0.12
gint.1.	-0.03	0.09	-0.21	0.15
gint.2.	-0.13	0.11	-0.35	0.06
gint.3.	-0.01	0.08	-0.19	0.16
gint.4.	-0.01	0.10	-0.22	0.19
gint.5.	0.23	0.09	0.05	0.42
gint.6.	-0.05	0.09	-0.23	0.12
sig_a	0.56	0.17	0.32	0.98
sig_b1	0.15	0.04	0.09	0.26
sig_G	0.18	0.09	0.07	0.41
tau	1.05	0.04	0.98	1.13
tauSize	-0.08	0.03	-0.13	-0.03
w.1.	-0.25	0.06	-0.37	-0.14
w.2.	0.07	0.03	0.01	0.12

Table S13: Statistical results from IPM recruitment model for *B. gracilis.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	1.67	0.57	0.50	2.74
a.1.	1.54	0.81	-0.28	2.92
a.10.	1.61	0.61	0.35	2.75
a.11.	1.53	0.72	0.01	2.78
a.12.	1.69	0.74	0.10	3.02
a.13.	1.78	0.69	0.33	3.06
a.2.	1.87	0.68	0.46	3.21
a.3.	1.62	0.76	-0.16	2.91
a.4.	1.57	0.78	-0.18	2.94
a.5.	1.56	0.63	0.23	2.67
a.6.	2.05	0.57	0.92	3.19
a.7.	1.71	0.55	0.59	2.76
a.8.	1.74	0.55	0.60	2.75
a.9.	1.49	0.68	0.05	2.68
b2.1.	-0.12	0.27	-0.69	0.38
b2.2.	0.20	1.12	-2.07	2.32
b2.3.	0.15	1.11	-2.14	2.25
b2.4.	0.50	0.32	-0.13	1.11
b2.5.	0.12	0.33	-0.49	0.75
b2.6.	0.43	1.03	-1.60	2.44
b2.7.	-0.51	1.03	-2.47	1.62
dd	-1.30	0.20	-1.68	-0.89
gint.1.	-0.39	0.34	-1.12	0.19
gint.2.	0.01	0.30	-0.60	0.62
gint.3.	-0.02	0.27	-0.58	0.55
gint.4.	0.02	0.32	-0.59	0.70
gint.5.	-0.05	0.31	-0.82	0.57
gint.6.	0.44	0.32	-0.07	1.13
sig_a	0.42	0.30	0.06	1.19
sig_G	0.47	0.32	0.06	1.22
theta	0.35	0.06	0.25	0.47
u	0.21	0.25	0.01	0.99

Table S14: Statistical results from IPM recruitment model for *H. comata.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	3.31	0.30	2.73	3.89
a.1.	3.07	0.72	1.52	4.44
a.10.	3.23	0.42	2.40	4.04
a.11.	3.50	0.57	2.40	4.62
a.12.	2.80	0.65	1.35	3.99
a.13.	3.23	0.76	1.78	4.82
a.2.	3.07	0.76	1.55	4.64
a.3.	3.38	0.71	1.94	4.81
a.4.	3.21	0.79	1.62	4.80
a.5.	3.20	0.48	2.26	4.14
a.6.	3.22	0.53	2.12	4.27
a.7.	4.67	0.34	4.03	5.35
a.8.	3.22	0.36	2.53	3.90
a.9.	3.33	0.42	2.47	4.14
b2.1.	-0.24	0.30	-0.82	0.33
b2.2.	-0.38	1.13	-2.68	1.85
b2.3.	-0.28	1.08	-2.43	1.84
b2.4.	-0.23	0.36	-0.94	0.51
b2.5.	-0.86	0.37	-1.55	-0.10
b2.6.	-0.40	1.03	-2.36	1.65
b2.7.	0.32	1.00	-1.63	2.33
dd	-1.32	0.16	-1.63	-0.99
gint.1.	-0.07	0.14	-0.42	0.16
gint.2.	-0.04	0.15	-0.40	0.23
gint.3.	0.08	0.14	-0.15	0.42
gint.4.	0.01	0.14	-0.29	0.31
gint.5.	0.03	0.14	-0.24	0.34
gint.6.	-0.02	0.14	-0.33	0.25
sig_a	0.78	0.31	0.38	1.55
sig_G	0.16	0.14	0.01	0.53
theta	1.31	0.20	0.97	1.75
u	1.00	0.00	1.00	1.00

Table S15: Statistical results from IPM recruitment model for *P. smithii*.

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	6.08	0.31	5.47	6.72
a.1.	7.37	0.51	6.42	8.41
a.10.	6.29	0.28	5.75	6.86
a.11.	6.64	0.33	5.99	7.27
a.12.	5.83	0.40	5.06	6.61
a.13.	5.80	0.43	5.00	6.73
a.2.	6.19	0.42	5.40	7.05
a.3.	5.06	0.45	4.14	5.91
a.4.	5.96	0.40	5.18	6.71
a.5.	4.75	0.39	3.99	5.48
a.6.	6.49	0.30	5.89	7.07
a.7.	6.25	0.28	5.72	6.82
a.8.	6.76	0.26	6.25	7.26
a.9.	5.89	0.31	5.28	6.51
b2.1.	-0.02	0.09	-0.20	0.16
b2.2.	0.05	0.10	-0.14	0.26
b2.3.	0.02	0.10	-0.16	0.20
b2.4.	-0.04	0.09	-0.21	0.15
b2.5.	0.03	0.09	-0.16	0.21
b2.6.	0.06	0.09	-0.13	0.23
b2.7.	0.03	0.09	-0.16	0.20
dd	-4.26	0.27	-4.84	-3.77
gint.1.	0.06	0.18	-0.23	0.50
gint.2.	0.01	0.18	-0.33	0.43
gint.3.	0.06	0.17	-0.23	0.48
gint.4.	-0.24	0.22	-0.73	0.06
gint.5.	0.06	0.18	-0.23	0.51
gint.6.	0.16	0.20	-0.12	0.64
sig_a	0.82	0.23	0.47	1.35
sig_G	0.25	0.22	0.02	0.73
theta	1.56	0.21	1.21	1.98
u	1.00	0.00	1.00	1.00

Table S16: Statistical results from IPM recruitment model for *P. secunda.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	3.84	0.28	3.24	4.39
a.1.	3.51	0.61	2.24	4.71
a.10.	3.59	0.39	2.82	4.33
a.11.	3.54	0.50	2.52	4.50
a.12.	3.91	0.52	2.85	4.92
a.13.	3.85	0.64	2.61	5.20
a.2.	4.03	0.62	2.81	5.31
a.3.	4.15	0.58	3.02	5.35
a.4.	3.81	0.67	2.47	5.15
a.5.	3.35	0.45	2.44	4.18
a.6.	3.91	0.43	3.04	4.75
a.7.	3.40	0.42	2.56	4.21
a.8.	4.59	0.35	3.94	5.30
a.9.	4.22	0.37	3.51	4.98
b2.1.	0.02	0.25	-0.47	0.55
b2.2.	0.09	1.10	-2.13	2.24
b2.3.	0.01	1.02	-1.98	1.91
b2.4.	0.34	0.33	-0.33	0.96
b2.5.	-0.15	0.32	-0.81	0.48
b2.6.	0.14	0.98	-1.74	2.10
b2.7.	0.17	0.96	-1.63	2.09
dd	-1.68	0.16	-1.98	-1.37
gint.1.	-0.05	0.19	-0.44	0.34
gint.2.	-0.04	0.22	-0.50	0.41
gint.3.	0.35	0.22	-0.02	0.83
gint.4.	-0.25	0.24	-0.83	0.14
gint.5.	0.01	0.21	-0.41	0.45
gint.6.	0.04	0.20	-0.35	0.46
sig_a	0.65	0.26	0.29	1.28
sig_G	0.34	0.20	0.07	0.91
theta	1.16	0.16	0.89	1.51
u	1.00	0.00	1.00	1.00

Table S17: Statistical results from QBM population model for *B. gracilis.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	-0.38	0.36	-1.07	0.29
a.1.	-0.10	0.40	-0.85	0.69
a.10.	-0.09	0.31	-0.70	0.52
a.11.	-0.20	0.33	-0.83	0.46
a.12.	-0.32	0.42	-1.15	0.54
a.13.	-0.46	0.46	-1.37	0.48
a.2.	-0.22	0.37	-0.94	0.51
a.3.	-0.94	0.38	-1.71	-0.23
a.4.	-0.18	0.41	-1.01	0.61
a.5.	-3.02	0.39	-3.82	-2.27
a.6.	0.70	0.52	-0.25	1.76
a.7.	-0.25	0.37	-0.97	0.48
a.8.	0.27	0.33	-0.38	0.91
a.9.	-0.04	0.30	-0.58	0.57
b1_mu	0.89	0.04	0.81	0.99
b1.1.	0.99	0.10	0.82	1.20
b1.10.	0.76	0.07	0.62	0.90
b1.11.	0.98	0.07	0.84	1.13
b1.12.	0.88	0.08	0.71	1.03
b1.13.	0.90	0.09	0.73	1.07
b1.2.	0.90	0.07	0.76	1.04
b1.3.	0.91	0.07	0.78	1.05
b1.4.	0.87	0.07	0.74	1.01
b1.5.	0.81	0.09	0.62	0.97
b1.6.	1.02	0.09	0.86	1.20
b1.7.	0.78	0.07	0.64	0.91
b1.8.	0.87	0.07	0.73	1.01
b1.9.	0.94	0.08	0.80	1.10
b2.1.	-0.01	0.09	-0.18	0.17
b2.2.	0.04	0.09	-0.14	0.22
b2.3.	0.03	0.10	-0.16	0.22
b2.4.	-0.04	0.10	-0.23	0.15
b2.5.	0.01	0.09	-0.18	0.19
b2.6.	0.04	0.10	-0.14	0.23
b2.7.	0.02	0.10	-0.17	0.21
gint.1.	-0.04	0.07	-0.21	0.07
gint.2.	0.02	0.07	-0.11	0.18
gint.3.	0.02	0.07	-0.11	0.17
gint.4.	0.02	0.07	-0.11	0.18
gint.5.	-0.01	0.07	-0.16	0.12
gint.6.	-0.02	0.07	-0.18	0.09
sig_a	1.07	0.32	0.62	1.81
sig_b1	0.12	0.05	0.03	0.22
sig_G	0.07	0.07	0.01	0.26
tau	0.69	0.03	0.63	0.76

Table S18: Statistical results from QBM population model for *H. comata.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	-0.68	0.37	-1.43	0.06
a.1.	-0.80	0.56	-1.86	0.32
a.10.	-0.20	0.41	-1.00	0.60
a.11.	-1.00	0.47	-1.91	-0.08
a.12.	-0.91	0.60	-2.06	0.30
a.13.	-0.82	0.67	-2.11	0.47
a.2.	-0.71	0.56	-1.81	0.36
a.3.	-0.87	0.59	-2.03	0.23
a.4.	-0.60	0.64	-1.77	0.68
a.5.	-2.55	0.55	-3.70	-1.46
a.6.	0.60	0.61	-0.61	1.79
a.7.	-0.14	0.48	-1.14	0.73
a.8.	-0.35	0.38	-1.08	0.40
a.9.	-0.52	0.39	-1.28	0.25
b1_mu	0.88	0.05	0.78	0.97
b1.1.	0.88	0.07	0.75	1.04
b1.10.	0.87	0.07	0.74	1.01
b1.11.	0.88	0.06	0.76	1.01
b1.12.	0.88	0.07	0.75	1.03
b1.13.	0.90	0.07	0.77	1.05
b1.2.	0.87	0.07	0.73	1.00
b1.3.	0.88	0.07	0.75	1.03
b1.4.	0.87	0.07	0.74	1.00
b1.5.	0.88	0.07	0.75	1.03
b1.6.	0.87	0.06	0.74	0.99
b1.7.	0.83	0.07	0.69	0.95
b1.8.	0.87	0.06	0.75	0.99
b1.9.	0.88	0.06	0.75	1.00
b2.1.	-0.12	0.18	-0.48	0.25
b2.2.	0.08	0.20	-0.28	0.46
b2.3.	0.08	0.19	-0.29	0.45
b2.4.	-0.13	0.18	-0.48	0.23
b2.5.	0.01	0.18	-0.34	0.37
b2.6.	0.09	0.19	-0.29	0.48
b2.7.	0.09	0.19	-0.29	0.48
gint.1.	0.01	0.07	-0.11	0.16
gint.2.	0.01	0.08	-0.13	0.18
gint.3.	0.00	0.07	-0.13	0.15
gint.4.	0.00	0.07	-0.13	0.16
gint.5.	-0.00	0.07	-0.14	0.15
gint.6.	-0.00	0.07	-0.16	0.14
sig_a	0.95	0.29	0.52	1.67
sig_b1	0.05	0.04	0.01	0.14
sig_G	0.06	0.07	0.00	0.25
tau	0.74	0.04	0.66	0.83

Table S19: Statistical results from QBM population model for *P. smithii*.

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	-0.83	0.23	-1.32	-0.39
a.1.	-0.87	0.33	-1.54	-0.23
a.10.	-0.70	0.30	-1.29	-0.09
a.11.	-0.78	0.30	-1.37	-0.18
a.12.	-0.97	0.31	-1.64	-0.41
a.13.	-0.87	0.36	-1.58	-0.13
a.2.	-0.79	0.36	-1.46	-0.06
a.3.	-0.86	0.33	-1.52	-0.22
a.4.	-0.89	0.34	-1.57	-0.24
a.5.	-0.99	0.31	-1.62	-0.42
a.6.	-0.64	0.33	-1.29	0.04
a.7.	-0.83	0.28	-1.39	-0.29
a.8.	-0.75	0.29	-1.31	-0.19
a.9.	-0.87	0.28	-1.43	-0.32
b1_mu	0.87	0.03	0.80	0.94
b1.1.	0.88	0.05	0.78	0.98
b1.10.	0.86	0.04	0.78	0.93
b1.11.	0.86	0.04	0.77	0.94
b1.12.	0.88	0.05	0.79	0.98
b1.13.	0.89	0.05	0.80	1.00
b1.2.	0.86	0.05	0.76	0.95
b1.3.	0.88	0.05	0.79	0.98
b1.4.	0.86	0.05	0.77	0.95
b1.5.	0.88	0.04	0.80	0.97
b1.6.	0.86	0.04	0.77	0.93
b1.7.	0.87	0.04	0.79	0.94
b1.8.	0.87	0.04	0.79	0.95
b1.9.	0.89	0.04	0.81	0.97
b2.1.	-0.16	0.13	-0.43	0.09
b2.2.	-0.38	0.97	-2.22	1.53
b2.3.	-0.04	0.85	-1.71	1.67
b2.4.	-0.15	0.20	-0.54	0.27
b2.5.	0.10	0.21	-0.31	0.51
b2.6.	0.68	0.87	-1.09	2.28
b2.7.	0.19	0.80	-1.41	1.74
gint.1.	0.06	0.09	-0.09	0.29
gint.2.	-0.05	0.10	-0.28	0.12
gint.3.	0.01	0.09	-0.15	0.20
gint.4.	-0.10	0.11	-0.37	0.06
gint.5.	0.03	0.10	-0.14	0.25
gint.6.	0.04	0.10	-0.13	0.27
sig_a	0.25	0.16	0.02	0.63
sig_b1	0.03	0.02	0.00	0.08
sig_G	0.12	0.11	0.01	0.40
tau	0.65	0.03	0.59	0.72

Table S20: Statistical results from QBM population model for *P. secunda.*

Parameter	mean_value	sd_value	lo_BCI	up_BCI
a_mu	-1.25	0.35	-1.96	-0.54
a.1.	-1.27	0.56	-2.43	-0.19
a.10.	-1.95	0.56	-3.27	-1.00
a.11.	-1.61	0.51	-2.68	-0.61
a.12.	-1.33	0.51	-2.32	-0.34
a.13.	-1.07	0.51	-2.01	0.02
a.2.	-1.24	0.53	-2.28	-0.24
a.3.	-0.70	0.55	-1.76	0.42
a.4.	-1.25	0.48	-2.10	-0.25
a.5.	-1.26	0.50	-2.15	-0.18
a.6.	-0.43	0.51	-1.50	0.54
a.7.	-1.63	0.36	-2.35	-0.94
a.8.	-1.36	0.39	-2.17	-0.57
a.9.	-1.13	0.41	-1.91	-0.32
b1_mu	0.77	0.06	0.64	0.89
b1.1.	0.77	0.08	0.60	0.93
b1.10.	0.69	0.11	0.45	0.87
b1.11.	0.79	0.09	0.63	0.98
b1.12.	0.77	0.08	0.62	0.93
b1.13.	0.76	0.08	0.61	0.91
b1.2.	0.76	0.08	0.61	0.92
b1.3.	0.74	0.08	0.57	0.90
b1.4.	0.83	0.09	0.68	1.04
b1.5.	0.83	0.09	0.67	1.03
b1.6.	0.68	0.10	0.47	0.86
b1.7.	0.78	0.09	0.60	0.98
b1.8.	0.78	0.08	0.62	0.94
b1.9.	0.77	0.08	0.63	0.93
b2.1.	-0.07	0.09	-0.27	0.11
b2.2.	-0.04	0.09	-0.22	0.13
b2.3.	-0.04	0.09	-0.22	0.14
b2.4.	0.04	0.09	-0.13	0.22
b2.5.	-0.02	0.09	-0.19	0.16
b2.6.	-0.05	0.09	-0.23	0.14
b2.7.	-0.04	0.09	-0.22	0.14
gint.1.	0.02	0.10	-0.17	0.25
gint.2.	-0.08	0.12	-0.39	0.10
gint.3.	0.04	0.10	-0.15	0.27
gint.4.	-0.08	0.12	-0.38	0.10
gint.5.	0.07	0.12	-0.12	0.37
gint.6.	0.03	0.10	-0.17	0.25
sig_a	0.59	0.26	0.14	1.18
sig_b1	0.08	0.05	0.01	0.19
sig_G	0.14	0.12	0.01	0.44
tau	0.70	0.04	0.63	0.77

Table S21: Statistical tests to assess whether models without climate covariates have higher accuracy and lower error than models with climate covariates. t-tests are one-sided.

comparison	performance_measure	test_type	test_statistic	df	p_value	species
simple IPM vs. climate IPM	rho	t	-1.196	279.000	0.884	BOGR
simple IPM vs. climate IPM	MAE	t	-2.333	280.000	0.990	BOGR
simple QBM vs. climate QBM	rho	t	-1.798	279.000	0.963	BOGR
simple QBM vs. climate QBM	MAE	t	-3.340	280.000	1.000	BOGR
simple IPM vs. climate IPM	rho	t	-0.037	169.000	0.515	HECO
simple IPM vs. climate IPM	MAE	t	-2.130	170.000	0.983	HECO
simple QBM vs. climate QBM	rho	t	0.747	169.000	0.228	HECO
simple QBM vs. climate QBM	MAE	t	1.145	170.000	0.127	HECO
simple IPM vs. climate IPM	rho	t	0.097	215.000	0.462	PASM
simple IPM vs. climate IPM	MAE	t	-0.556	216.000	0.711	PASM
simple QBM vs. climate QBM	rho	t	0.631	215.000	0.264	PASM
simple QBM vs. climate QBM	MAE	t	4.276	216.000	0.000	PASM
simple IPM vs. climate IPM	rho	t	-1.479	195.000	0.930	POSE
simple IPM vs. climate IPM	MAE	t	-2.185	196.000	0.985	POSE
simple QBM vs. climate QBM	rho	t	-1.564	195.000	0.940	POSE
simple QBM vs. climate QBM	MAE	t	-2.468	196.000	0.993	POSE

Table S22: Statistical tests of model comparisons. Table shows results from one-sided t-tests for the particular comparison.

comparison	performance_measure	test_type	test_statistic	df	p_value	species
limate IPM vs. simple IPM	rho	t	1.196	279.000	0.116	BOGR
climate IPM vs. simple IPM	MAE	t	-2.333	280.000	0.010	BOGR
climate QBM vs. simple QBM	rho	t	1.798	279.000	0.037	BOGR
climate QBM vs. simple QBM	MAE	t	-3.340	280.000	0.000	BOGR
simple IPM vs. simple QBM	rho	t	-1.757	279.000	0.960	BOGR
simple IPM vs. simple QBM	MAE	t	2.338	280.000	0.990	BOGR
climate IPM vs. climate QBM	rho	t	-1.083	279.000	0.860	BOGR
climate IPM vs. climate QBM	MAE	t	1.151	280.000	0.875	BOGR
climate IPM vs. simple IPM	rho	t	0.037	169.000	0.485	HECO
climate IPM vs. simple IPM	MAE	t	-2.130	170.000	0.017	HECO
climate QBM vs. simple QBM	rho	t	-0.747	169.000	0.772	HECO
climate QBM vs. simple QBM	MAE	t	1.145	170.000	0.873	HECO
simple IPM vs. simple QBM	rho	t	-1.638	169.000	0.948	HECO
simple IPM vs. simple QBM	MAE	t	4.011	170.000	1.000	HECO
climate IPM vs. climate QBM	rho	t	-0.704	169.000	0.759	HECO
climate IPM vs. climate QBM	MAE	t	0.329	170.000	0.629	HECO
climate IPM vs. simple IPM	rho	t	-0.097	215.000	0.538	PASM
climate IPM vs. simple IPM	MAE	t	-0.556	216.000	0.289	PASM
climate QBM vs. simple QBM	rho	t	-0.631	215.000	0.736	PASM
climate QBM vs. simple QBM	MAE	t	4.276	216.000	1.000	PASM
simple IPM vs. simple QBM	rho	t	0.552	215.000	0.291	PASM
simple IPM vs. simple QBM	MAE	t	-1.033	216.000	0.151	PASM
climate IPM vs. climate QBM	rho	t	2.022	215.000	0.022	PASM
climate IPM vs. climate QBM	MAE	t	-5.309	216.000	0.000	PASM
climate IPM vs. simple IPM	rho	t	1.479	195.000	0.070	POSE
climate IPM vs. simple IPM	MAE	t	-2.185	196.000	0.015	POSE
climate QBM vs. simple QBM	rho	t	1.564	195.000	0.060	POSE
climate QBM vs. simple QBM	MAE	t	-2.468	196.000	0.007	POSE
simple IPM vs. simple QBM	rho	t	0.297	195.000	0.383	POSE
simple IPM vs. simple QBM	MAE	t	1.027	196.000	0.847	POSE
climate IPM vs. climate QBM	rho	t	1.137	195.000	0.128	POSE
climate IPM vs. climate QBM	MAE	t	0.455	196.000	0.675	POSE

Table S23: Statistical tests of model comparisons at different forecast horizons. Table shows results from one-sided t-tests for the particular comparison.

comparison	performance_measure	test_type	test_statistic	df	p_value	species	horizon
climate IPM vs. climate QBM	rho	t	-0.122	167.000	0.549	PASM	1.000
climate IPM vs. climate QBM	rho	t	0.394	149.000	0.347	POSE	1.000
climate IPM vs. climate QBM	rho	t	-0.436	129.000	0.668	HECO	1.000
climate IPM vs. climate QBM	rho	t	-0.318	129.000	0.625	BOGR	1.000
climate IPM vs. climate QBM	rho	t	-1.015	150.000	0.844	PASM	2.000
climate IPM vs. climate QBM	rho	t	-0.876	132.000	0.809	POSE	2.000
climate IPM vs. climate QBM	rho	t	-0.790	115.000	0.784	HECO	2.000
climate IPM vs. climate QBM	rho	t	-0.049	114.000	0.519	BOGR	2.000
climate IPM vs. climate QBM	rho	t	0.610	129.000	0.272	PASM	3.000
climate IPM vs. climate QBM	rho	t	-0.719	112.000	0.763	POSE	3.000
climate IPM vs. climate QBM	rho	t	-1.871	98.000	0.968	HECO	3.000
climate IPM vs. climate QBM	rho	t	-0.006	96.000	0.503	BOGR	3.000
climate IPM vs. climate QBM	rho	t	0.761	108.000	0.224	PASM	4.000
climate IPM vs. climate QBM	rho	t	-0.168	94.000	0.566	POSE	4.000
climate IPM vs. climate QBM	rho	t	-0.600	82.000	0.725	HECO	4.000
climate IPM vs. climate QBM	rho	t	0.196	78.000	0.423	BOGR	4.000
climate IPM vs. climate QBM	rho	t	0.226	91.000	0.411	PASM	5.000
climate IPM vs. climate QBM	rho	t	-0.043	79.000	0.517	POSE	5.000
climate IPM vs. climate QBM	rho	t	-0.794	70.000	0.785	HECO	5.000
climate IPM vs. climate QBM	rho	t	0.180	65.000	0.429	BOGR	5.000
climate IPM vs. climate QBM	rho	t	-0.331	75.000	0.629	PASM	6.000
climate IPM vs. climate QBM	rho	t	0.743	66.000	0.230	POSE	6.000
climate IPM vs. climate QBM	rho	t	-0.658	59.000	0.743	HECO	6.000
climate IPM vs. climate QBM	rho	t	-0.015	54.000	0.506	BOGR	6.000
climate IPM vs. climate QBM	rho	t	0.805	62.000	0.212	PASM	7.000
climate IPM vs. climate QBM	rho	t	-0.222	53.000	0.587	POSE	7.000
climate IPM vs. climate QBM	rho	t	-1.009	50.000	0.841	HECO	7.000
climate IPM vs. climate QBM	rho	t	-0.095	44.000	0.537	BOGR	7.000
climate IPM vs. climate QBM	rho	t	-0.001	54.000	0.500	PASM	8.000
climate IPM vs. climate QBM	rho	t	-0.155	47.000	0.561	POSE	8.000
climate IPM vs. climate QBM	rho	t	-0.460	43.000	0.676	HECO	8.000
climate IPM vs. climate QBM	rho	t	-1.671	37.000	0.948	BOGR	8.000

Table S24: Statistical tests of model comparisons at different forecast horizons. Table shows results from one-sided t-tests for the particular comparison. Note the reverse order of comparisons relative to Table S23.

comparison	performance_measure	test_type	test_statistic	df	p_value	species	horizon
climate QBM vs. climate IPM	rho	t	0.122	167.000	0.451	PASM	1.000
climate QBM vs. climate IPM	rho	t	-0.394	149.000	0.653	POSE	1.000
climate QBM vs. climate IPM	rho	t	0.436	129.000	0.332	HECO	1.000
climate QBM vs. climate IPM	rho	t	0.318	129.000	0.375	BOGR	1.000
climate QBM vs. climate IPM	rho	t	1.015	150.000	0.156	PASM	2.000
climate QBM vs. climate IPM	rho	t	0.876	132.000	0.191	POSE	2.000
climate QBM vs. climate IPM	rho	t	0.790	115.000	0.216	HECO	2.000
climate QBM vs. climate IPM	rho	t	0.049	114.000	0.481	BOGR	2.000
climate QBM vs. climate IPM	rho	t	-0.610	129.000	0.728	PASM	3.000
climate QBM vs. climate IPM	rho	t	0.719	112.000	0.237	POSE	3.000
climate QBM vs. climate IPM	rho	t	1.871	98.000	0.032	HECO	3.000
climate QBM vs. climate IPM	rho	t	0.006	96.000	0.497	BOGR	3.000
climate QBM vs. climate IPM	rho	t	-0.761	108.000	0.776	PASM	4.000
climate QBM vs. climate IPM	rho	t	0.168	94.000	0.434	POSE	4.000
climate QBM vs. climate IPM	rho	t	0.600	82.000	0.275	HECO	4.000
climate QBM vs. climate IPM	rho	t	-0.196	78.000	0.577	BOGR	4.000
climate QBM vs. climate IPM	rho	t	-0.226	91.000	0.589	PASM	5.000
climate QBM vs. climate IPM	rho	t	0.043	79.000	0.483	POSE	5.000
climate QBM vs. climate IPM	rho	t	0.794	70.000	0.215	HECO	5.000
climate QBM vs. climate IPM	rho	t	-0.180	65.000	0.571	BOGR	5.000
climate QBM vs. climate IPM	rho	t	0.331	75.000	0.371	PASM	6.000
climate QBM vs. climate IPM	rho	t	-0.743	66.000	0.770	POSE	6.000
climate QBM vs. climate IPM	rho	t	0.658	59.000	0.257	HECO	6.000
climate QBM vs. climate IPM	rho	t	0.015	54.000	0.494	BOGR	6.000
climate QBM vs. climate IPM	rho	t	-0.805	62.000	0.788	PASM	7.000
climate QBM vs. climate IPM	rho	t	0.222	53.000	0.413	POSE	7.000
climate QBM vs. climate IPM	rho	t	1.009	50.000	0.159	HECO	7.000
climate QBM vs. climate IPM	rho	t	0.095	44.000	0.463	BOGR	7.000
climate QBM vs. climate IPM	rho	t	0.001	54.000	0.500	PASM	8.000
climate QBM vs. climate IPM	rho	t	0.155	47.000	0.439	POSE	8.000
climate QBM vs. climate IPM	rho	t	0.460	43.000	0.324	HECO	8.000
climate QBM vs. climate IPM	rho	t	1.671	37.000	0.052	BOGR	8.000