

¹ A height threshold for seed production by Willow (*Salix*
² *spp.*): implications for state change following wolf
³ reintroduction in Yellowstone

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Abstract

13 The removal of a top predator leading to an alternative stable state is a major area
14 of ecological research. The movement into the alternative state is often caused when
15 the ecosystem crosses a critical threshold. In many situations, it is the objective of
16 managers to revert that ecosystem back to its historical state. This is accomplished by
17 identifying a threshold for restoration. Yellowstone National Park is an iconic example
18 of a system that shifted into an alternative stable state following the removal of wolves
19 (*Canis lupus*) in the early 1900s. Wolves were then reintroduced in 1995 with the
20 goal of transitioning the ecosystem back to its original state. However, after almost 20
21 years of wolf presence in Yellowstone, the willow (*Salix*) populations in Yellowstone's
22 riparian areas have not recovered. There may be several reasons for this phenomena,
23 but one problem may be that willow are not producing enough seeds. A willow height
24 threshold for restoration has been proposed for Yellowstone National Park's willow (Kay
25 and Chadde 1991). Here, we present a Bayesian, zero-inflated Poisson regression which
26 uses height and seed rain data from 21 randomly selected observational site across
27 Yellowstone's Northern Range to estimate a willow height threshold for restoration.
28 We found that the threshold height for willow seed production is very close to 100
29 cm from stem base to tallest stem. This model gives managers a new perspective on
30 estimating ecological thresholds as well as rigorous basis for a willow height threshold
31 for restoration.

32 1 Introduction

33 A wealth of empirical data has substantiated the seminal theoretical prediction of Lewontin
34 and Cohen (1969) and Holling (1973) that populations, communities, and ecosystems can
35 undergo abrupt, qualitative changes in response to biotic and environmental drivers (Scheffer
36 et al. 2009). The point at which these changes occur is known as an ecological threshold, or
37 in somewhat more contemporary language, a tipping point (Dakos and Hastings 2013). The
38 movement of systems beyond ecological thresholds can result in alternative states, some of
39 which resist reorganization to their original configuration over broad ranges of environmental
40 conditions (Suding et al. 2004). A much-studied threshold in ecology is population growth
41 rate. When the instantaneous growth rate is less than 0, the population will decline, even-
42 tually to extinction. Qualitative shifts in population growth from increases to declines can
43 ripple throughout ecosystems, causing changes in the structure of communities that stabilize
44 alternative states (Scheffer et al. 2001).

45 Changes in landscape conditions on the northern range of Yellowstone National Park
46 after the loss of wolves from the ecosystem and the subsequent release of the park's elk
47 population from control by predators has been widely cited as a landmark example of an
48 alternative state that developed following the reorganization of a terrestrial food web (Ripple
49 and Beschta 2012; Suding et al. 2004; Terborgh et al. 2001; Wolf et al. 2007). A key feature of
50 this state was the loss willows from riparian zones. The disappearance of willows was caused,
51 at least in part, by the failure of young plants to establish, leading to an age-distribution
52 where young plants were dramatically underrepresented (Wolf et al. 2007) and providing
53 evidence for a negative population growth rate. The loss of willows from the system, in turn,
54 led to self-reinforcing feedbacks to the major source of riparian disturbance, dam building by
55 beaver (Beschta and Ripple 2006). This feedback occurred because beaver require willows for
56 food and for dam building materials and willows require beaver to create habitat suitable for
57 plant establishment. Seed production alone is not sufficient to assure willow reproduction –
58 viable seeds must disperse to suitable sites on the landscape, which in the case of willow, are

59 patches of bare, moist soil with shallow water tables, conditions that accompany disturbance
60 of streams by beaver. Thus, seed production is a necessary if not a sufficient condition for
61 willow reproduction, and hence, for restoration of riparian communities on the northern
62 range. The restoration of wolves to Yellowstone has raised the possibility that the system
63 could reorganize to a configuration resembling the state that prevailed before wolves were
64 extirpated. Demonstrating this reconfiguration depends on identifying ecological thresholds
65 that can be measured on the landscape and that can be functionally related to key processes
66 controlling state transition. Willow height has been widely used as an ecological threshold
67 for ecosystem restoration in Yellowstone. Browsing by elk can eliminate reproduction by
68 willows because browsed stems cannot produce catkins, and hence, produce no seeds (Singer
69 et al. 1994). Excessive browsing can reduce the stature of willows to the point that all stems
70 are within reach of browsers, and as a result, production of catkins is virtually eliminated,
71 a condition that was observed for decades following the loss of wolves from the system
72 (Bilyeu et al. 2007). These observations gave rise to a widely used threshold for willow
73 restoration, 200 cm, the height at which the upper canopy of willows can reliably escape
74 browsing. Although the 200 cm threshold is based on appealing, rough-hewn logic and is
75 widely cited in papers on ecosystem restoration in Yellowstone (Gage and Cooper 2005;
76 Johnston et al. 2011; Bilyeu et al. 2008; Johnston et al. 2007; Kay and Chadde 1991), no one
77 has demonstrated a quantitative, functional basis for a ecological threshold based on willow
78 height.

79 In this paper, we report investigations of the relationship between willow height and seed
80 production on Yellowstone's northern range. We use this relationship to estimate a threshold
81 at which seed production by willows increases above zero. We offer this threshold as an
82 indicator of necessary conditions for restoration of the riparian zone following reintroduction
83 of wolves.

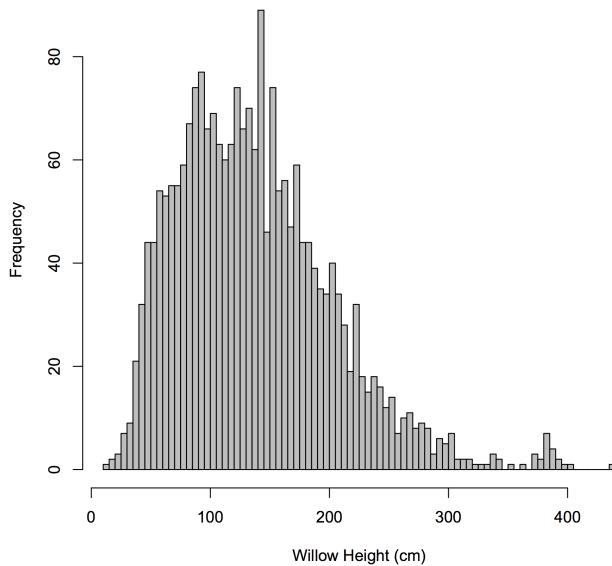


Figure 1: A histogram of the willow heights from over 2200 willows (*Salix*) randomly sampled across Yellowstone's Northern Range. Here we see that most of the willows are between 50 cm and 200 cm suggesting that very little seed is being produced (Kay and Chadde 1991).

84 2 Materials and Methods

85 2.1 Study Area

86 Observations of willow height and seed production were collected from 21 randomly selected
87 riparian sites on the northern range of Yellowstone National Park during June and July of
88 2010. These 21 observational sites were chosen from a sampling frame of stream sections
89 that were either historically known to have beaver or were hypothesized to be a potential
90 habitat for beaver based on gradient and stream order (Marshall et al. 2013). Sites were
91 selected from the frame using a spatially balanced random sampling algorithm (Theobald
92 et al. 2007). Each observational site ran parallel to a stream for 100m and extended 25m
93 away from the stream margin.

94 2.2 Observations

95 Willow seeds were collected using seed traps constructed from 30 cm² and 60 cm² plywood
96 boards covered with a layer of adhesive (Tree Tanglefoot[©] Contech Inc.). Boards were staked
97 into the ground using shelf brackets which were secured to the underside of each board. Two
98 seed traps were placed 25 m from the margin of the 100 m river length transect line within
99 5 m of the river bank. These seed traps capture the ambient seed rain for the entire site. A
100 third trap (measuring 30 cm²) was placed on an area within the transect determined optimal
101 for seedling establishment. Willow seeds at each site were counted then removed from all
102 traps each week during the willow seed production season. Every willow within each site
103 was measured from the center of the root base to the highest branch in centimeters.

104 2.3 Analysis

105 We sought to estimate a threshold height for willow seed production (\tilde{h}). The number of
106 plants exceeding this threshold should effect the number of seeds produced that exceeded
107 the threshold height required for seed production to occur, so we represent the data with
108 the following equation:

$$x_i = \sum_{j=1}^{J_i} I_{\{h_{ij} \geq \tilde{h}\}} \quad (1)$$

$$\tilde{h} \sim \text{Discrete Uniform}(0, 300) \quad (2)$$

109 where j indexes the individual plants, i indexes site, and $I_{\{h_{ij} \geq \tilde{h}\}}$ is an indicator variable =
110 1 when the condition within the {} is true and 0 otherwise. Thus, x_i is a count of plants
111 equal to or above the estimated threshold height (\tilde{h}) at each site.

112 We needed to account for two sources of zeros in counts of seeds: zeros that occurred
113 because there was no seed production at a site and zeros that occurred as a result of sampling
114 error when the true state of average seed production was > 0 . These considerations motivated
115 us to use a zero inflated Poisson distribution to represent the relationship between seed

116 production and the number of willows in a stand exceeding the threshold height:

$$y_{ik} \sim \begin{cases} 0 & , x_i = 0 \\ \text{Poisson}(\lambda_i w_{ik}) & , x_i > 0 \end{cases} \quad (3)$$

117 where y_{ik} is the number of seeds per seed trap k at a site i , and w_{ik} is an offset giving the
118 area of each seed trap in m^2 . Equation 3 simply says that when there are no plants at the
119 site are above the threshold height ($x_i = 0$), then we will observe 0 seeds with probability 1.
120 Otherwise, the number of seeds will be a Poisson distributed random variable with mean λ_i .

121 We estimated the mean seed production (i.e., λ_i , the intensity parameter of the Poisson)
122 using

$$\log(\lambda_i) = \beta_0 + \beta_1 \log(x_i) + \gamma_i \quad (4)$$

$$\boldsymbol{\beta} \sim \text{Multivariate Normal}(\mathbf{0}, \sigma^2 \mathbf{I}) \quad (5)$$

$$\gamma_i \sim \text{Normal}(0, 1) \quad (6)$$

where $\sigma^2 = 5$. An extra set of random effect parameters (γ_i) were added to account for variation in seed detection between sites. Without these parameters, the posterior predictive p-value for the mean squared error was equal to .005, and with these parameters, the dispersion is improved slightly (p-value = 0.07). The full posterior expression is given here,

$$\begin{aligned} [\boldsymbol{\gamma}, \boldsymbol{\beta}, \tilde{h} \mid \mathbf{y}, \mathbf{x}] &\propto \prod_{i=1}^{21} \prod_{k=1}^3 \left(I_{\{y_i=0\}}^{I_{\{x_i=0\}}} \text{Poisson} \left(y_{ik} \mid \lambda_i w_{ik} \right)^{I_{\{x_i>0\}}} \right) \\ &\times \text{Multivariate Normal} \left(\boldsymbol{\beta} \mid \mathbf{0}, \sigma^2 \mathbf{I} \right) \text{Discrete Uniform} \left(\tilde{h} \mid 0, 300 \right) \text{Normal}(\gamma_i \mid 0, 1) \end{aligned} \quad (7)$$

123 **2.3.1 Parameter Model**

124 There are twenty-four unobserved quantities in this model, $\tilde{h}, \beta_0, \beta_1$, and γ_i . We chose
125 priors based on simulated data that closely imitated the behavior of the observed data. The

₁₂₆ threshold height parameter has a discrete uniform prior because the willow heights were
₁₂₇ measured to the nearest centimeter resulting in a discrete height dataset.

₁₂₈ **2.3.2 Implementation**

₁₂₉ Marginal posterior distributions of states, parameters, and model predictions were estimated
₁₃₀ using Markov chain Monte Carlo (MCMC) methods in the R computing environment (Team
₁₃₁ 2013). Parameters were estimated using a random walk Metropolis-Hastings algorithm with
₁₃₂ discrete uniform and normal proposal distributions tuned to provide an acceptance rate of
₁₃₃ between 20% and 60% (See Appendix for full conditional distributions). Three chains were
₁₃₄ chosen for each estimated quantity. Convergence was assured by inspection of trace plots
₁₃₅ with varying initial conditions (Brooks and Gelman 1998). All code and trace plots for this
₁₃₆ model can be found in the appendix.

₁₃₇ **3 Results**

₁₃₈ In Figure 2, we show the marginal posterior distributions of the model parameters, and in
₁₃₉ Table 1 we report the means and 95% credible intervals of each parameter. The parameters
₁₄₀ converged after 20,000 iterations of the MCMC Sampler as indicated by visual inspection of
₁₄₁ the trace plots for all parameters with a 4,000 iteration burn-in. It is also notable that the
₁₄₂ model has estimated the lower bound of the seed producing plots as the threshold for seed
₁₄₃ production (Figure 3).

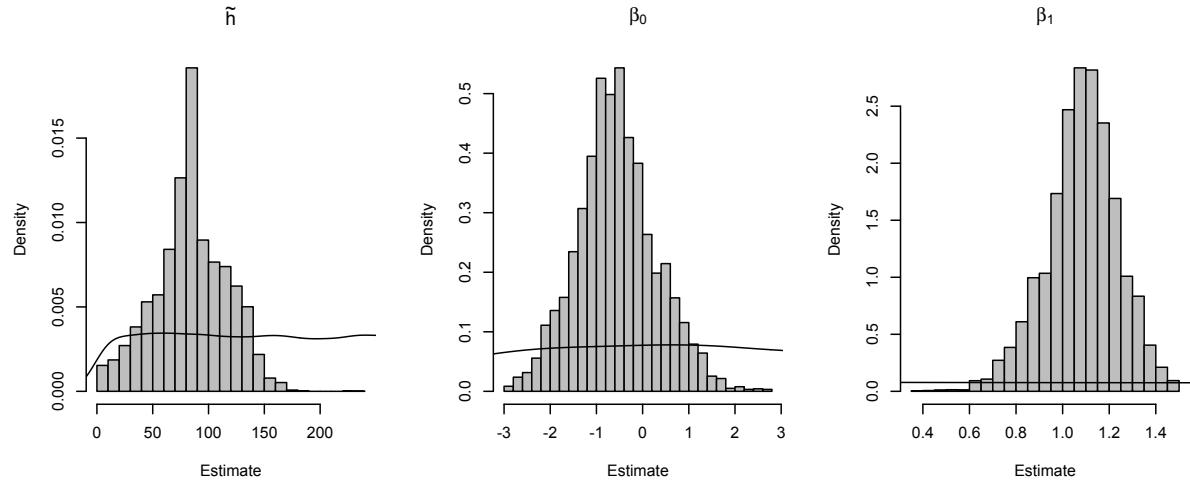


Figure 2: The marginal posterior distributions of the parameters of interest: threshold height parameter (\tilde{h}), the intercept β_0 , and the slope β_1 . The horizontal line is the prior distribution we defined for the parameter.

Parameter	Lower 95% Credible Interval	Mean	Upper 95% Credible Interval
\tilde{h}	27	85	145
β_0	-1.93	-0.60	1.22
β_1	.81	1.09	1.38

Table 1: The means and 95% credible intervals for each parameter estimated in the model.

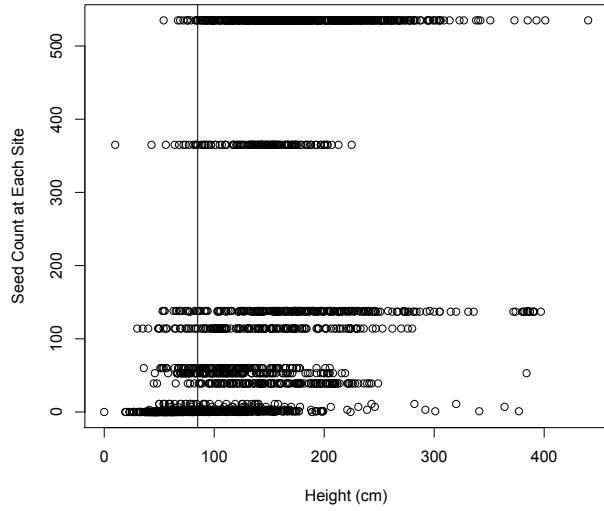


Figure 3: This plot shows the distribution of willow heights compared to the number of seeds counted at each plot. The vertical line represents the estimated mean of the threshold height for seed production parameter $(E(\tilde{h}) = 85 \text{ cm})$.

¹⁴⁴ 4 Discussion

¹⁴⁵ 4.1 The Willow Height Threshold

¹⁴⁶ Ecological thresholds have important implications for ecosystem management and ecological
¹⁴⁷ theory. Yellowstone National Park has been a premier example of a major shift over a criti-
¹⁴⁸ cal threshold from one alternative stable state to another following the extirpation of a top
¹⁴⁹ predator (Wolf et al. 2007). The reintroduction of the wolf reduced elk populations by 70%
¹⁵⁰ supposedly paving the way for riparian willow recovery (Ripple and Beschta 2012). However,
¹⁵¹ alternative evidence suggests that wolves are not the only species needed to restore the area's
¹⁵² original willow populations. Beaver depend on willow for nourishment and protection, so
¹⁵³ following the extreme decrease in the willow population beavers vacated Yellowstone. With-
¹⁵⁴ out beaver, willows have been unable to reestablish to historic levels. This self-reinforcing
¹⁵⁵ feedback has caused researchers to conclude that Yellowstone has shifted to an elk grassland
¹⁵⁶ stable stage (Wolf et al. 2007). We know that beavers are critical in the process of shifting
¹⁵⁷ Yellowstone's ecosystem back to its historical stable state, but we do not know when wil-

158 lows will be able to produce seeds in order to begin the reestablishment process. With this
159 model and randomly collected data, we estimate that the threshold height for willow seed
160 production on Yellowstone's Northern Range has an average of 85 cm. This is well below
161 the previous estimate of by Kay and Chadde (1991) who believed that the threshold height
162 for seed production was around 200cm. However, we can see in figure 4 that our model
163 has estimated the lower bound of the heights of seed producing sites and that the non seed
164 producing sites have very few willows at or above this threshold height.

165 The increase of riparian willow is the key to the restoration of Yellowstone, but it cannot
166 occur until more willows are producing seeds. In this study the heights of over 2200 willow
167 were measured and 77% of willow were above the threshold height of 85 cm (Figure 4). In
168 spite of this high percentage, only 14 of the 21 sites had more than 6 tall willows present. All
169 but one site had several up and coming willows between 25 - 50 cm. This suggests that some
170 sites are on the verge of recovery while other sites still lag behind. Willows will continue to
171 grow because herbivore populations have decreased, but that there do not yet seem to be
172 enough tall plants to allow the willow communities to expand to historic levels at all sites.
173 A tall and populated willow community that facilitates seedling recruitment will allow for
174 willow recovery, but returning to this state may be impossible without beaver to increase
175 water availability and exposed soil for seedling establishment in the riparian corridors.

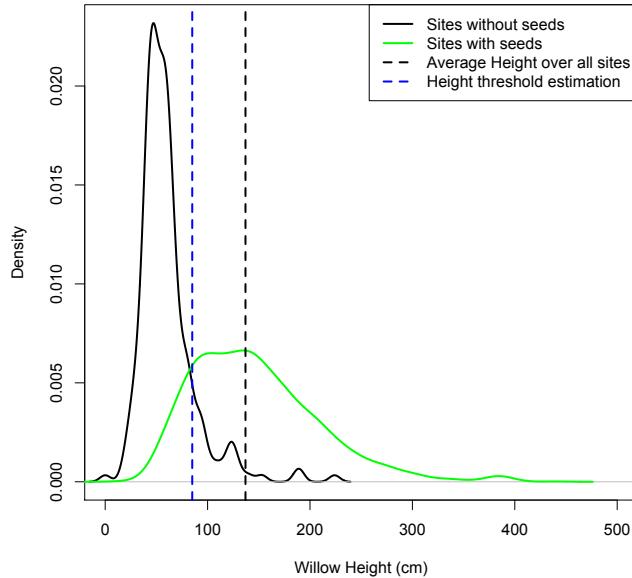


Figure 4: This is a density plot of the willow heights measured in this study. The black curve is the density of willow heights for sites that did not produce seeds. The green curve is the density of willow heights for the sites that did produce seeds. The black dotted line is the average willow height across all sites, and the blue dotted line is the mean of the estimated height threshold (\hat{h}).

¹⁷⁶ **4.2 Threshold Modeling: Generalizations for Management**

¹⁷⁷ We have provided a Bayesian structure that can allow managers to input their own knowledge
¹⁷⁸ through data, informed priors, and increased number of covariates in a intuitive and rigorous
¹⁷⁹ way to determine a threshold value in their own system and to quantify the uncertainty
¹⁸⁰ associated with those estimates. This gives the manager and the researcher a Bayesian
¹⁸¹ alternative to the piecewise regression described in Toms and Lesperance 2003. Our use of
¹⁸² an indicator variable in the process model signals to the flexibility of this methodology.

¹⁸³ Change-point models are becoming more critical as our world continues to change. Shifts
¹⁸⁴ in ecosystems are occurring rapidly. It will be important for managers to understand ecolog-
¹⁸⁵ ical thresholds and have a quantitative basis for estimating their values (Estes et al. 2011).
¹⁸⁶ Thresholds often form the basis for management action plans as well as the interpretation of
¹⁸⁷ the type of stable state an ecosystem is realizing (Groffman et al. 2006). Mistakes in these
¹⁸⁸ estimations could lead to mismanagement which could lead to further ecological harm. In

189 Yellowstone National Park, managers need to know these types of critical details for willow
190 reestablishment in order to return the ecosystem to its historical stable state. They have
191 taken courageous steps to reduce the herbivore population by reintroducing wolves, and now
192 they seek to know more about what needs to happen to reconstruct their riparian corridors.
193 Knowing an ecological threshold and the inherent uncertainty is one step in a very com-
194 plicated problem that can help managers and researchers further understand the transition
195 from one stable state to another.

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258 Appendix

259 R Code for MCMC Algorithm

```
260 change.pt.pois.regMCMC.no.inflat1 <- function(n.mcmc,X,y.seed,opt.ht.  
261     strt,hshape1,hshape2,beta,beta.mns,beta.tune,beta.var,error.var,  
262     error.tune){  
263  
264     #####  
265     ##### Subroutines and Libraries  
266     #####  
267  
268     library(mvtnorm)  
269     library(data.table)  
270     dunifdisc<-function(x, min=0, max=1) ifelse(x>=min & x<=max &  
271         round(x)==x, 1/(max-min+1), 0)  
272     runifdisc<-function(n, min=0, max=1) sample(min:max, n, replace  
273         =T)  
274  
275  
276     #####  
277     ##### Storage  
278     #####  
279  
280     opt.ht.save=rep(0,n.mcmc)  
281     beta.save=matrix(0,n.mcmc,2)  
282     error.save=matrix(0,21,n.mcmc)  
283  
284     mse.y=rep(0,n.mcmc)  
285     mse.ypred=rep(0,n.mcmc)
```

```

286     msediffsave=rep(0,n.mcmc)
287     ypred=matrix(0,length(y.seed[,1])*3,n.mcmc)
288     msesave=rep(0,n.mcmc)

289

290

291     #####
292     ##### Initial Conditions
293     #####
294
295     opt.ht = opt.ht.strt
296     error=rep(0,21)
297     error.mns=rep(0,21)
298     W = matrix(c(.5,.25,.25),1,3)
299     X1 = data.table(X)
300     x = cbind(1,log(X1[,list(A=sum(V3>opt.ht),B=V1[,A])))

301
302     beta = beta
303
304     accept.opt.ht = 0
305     accept.beta = 0
306
307     #####
308     ##### Begin MCMC
309     #####
310
311     for(k in 1:n.mcmc){
312       if(k%%1000==0) cat(k," ")
313       flush.console()
314     #####

```

```

315      ##### Sample Opt.ht
316      #####
317      if (TRUE){
318          opt.ht.star = runifdisc(1,opt.ht-100,opt.ht+100)
319
320          if (opt.ht.star>0 & opt.ht.star<=max(X[,3])){
321
322              x.star = cbind(1,log(X1[,list(A=sum(V3>opt.ht.star),B=V1)[,A
323                  ])) )
324
325              mh1.ht = sum(dpois(as.vector(y.seed[x.star[,2]>=0]),as.
326                  vector(exp(x.star[x.star[,2]>=0,]*%*%beta+error[x.star
327                  [,2]>=0])%*%W),log=TRUE) ) + dunifdisc(opt.ht.star,hshape1,
328                  hshape2) + dunifdisc(opt.ht,opt.ht.star-100,opt.ht.star
329                  +100)
330
331              mh2.ht = sum(dpois(as.vector(y.seed[x.star[,2]>=0]),as.
332                  vector(exp(x[x.star[,2]>=0,]*%*%beta+error[x.star[,2]>=0])
333                  %*%W),log=TRUE) ) + dunifdisc(opt.ht,hshape1,hshape2) +
334                  dunifdisc(opt.ht.star,opt.ht-100,opt.ht+100)
335
336              mh.ht = exp(mh1.ht - mh2.ht)
337
338              if (mh.ht > runif(1)){
339                  opt.ht=opt.ht.star
340                  accept.opt.ht=accept.opt.ht+1
341                  x=x.star
342              }
343

```

```

344
345
346 #####  

347 ##### Sample Betas  

348 #####
349
350 if (TRUE) {
351     beta.star = rnorm(2,beta,beta.tune)
352
353     mh1.beta = sum(dpois(as.vector(y.seed[x[,2]>=0,]),as.vector(
354         exp(x[x[,2]>=0,]*beta.star+error[x[,2]>=0])%*%W),log=
355         TRUE))+dmvnorm(beta.star,beta.mns,beta.var*diag(2),log=
356         TRUE)
357
358     mh2.beta = sum(dpois(as.vector(y.seed[x[,2]>=0,]),as.vector(
359         exp(x[x[,2]>=0,]*beta+error[x[,2]>=0])%*%W),log=TRUE))+
360         dmvnorm(beta,beta.mns,beta.var*diag(2),log=TRUE) #rep(beta
361         .var,2)*diag(2)#solve(t(x[x[,2]>0,])%*%x[x[,2]>0,])
362
363     mh.beta = exp(mh1.beta-mh2.beta)
364
365     if (mh.beta > runif(1)){
366         beta = beta.star
367         accept.beta = accept.beta+1
368     }
369
370 #####  

371 ##### Sample Error  

372 #####

```

```

373
374 if (TRUE) {
375   error.star = rnorm(21,error,error.tune)
376
377   if (min(exp(x[,2]>=0,)%*%beta.star+error.star[x[,2]>=0,])%*%
378     W)>=0){
379
380
381   mh1.error = dpois(y.seed[x[,2]>=0,],exp(x[,2]>=0,)%*%beta.
382     star+error.star[x[,2]>=0,])%*%W,log=TRUE)+dnorm(error.star[
383     x[,2]>=0],error.mns[x[,2]>=0],error.var,log=TRUE)
384   mh2.error = dpois(y.seed[x[,2]>=0,],exp(x[,2]>=0,)%*%beta+
385     error[x[,2]>=0,])%*%W,log=TRUE)+dnorm(error[x[,2]>=0],error
386     .mns[x[,2]>=0],error.var,log=TRUE) #rep(beta.var,2)*diag
387     (2)#solve(t(x[x[,2]>0,])%*%x[x[,2]>0,])
388   mh.error = exp(mh1.error-mh2.error)
389
390   mh.index=which(mh.error > runif(length(mh.error[,1])*length(
391     mh.error[1,]))),arr.ind=TRUE)
392   error[unique(mh.index[,1])] = error.star[unique(mh.index[,1])]
393   ]
394 }
395 }
396
397 #####
398 ##### Calculate Posterior Predictive Checks
399 #####
400
401
```

```

402 mn.nbinom=exp(x%*%beta+error)%*%W
403 ypred[,k]=rpois(length(mn.nbinom),mn.nbinom)
404
405 mse.y[k]=mean((as.vector(y.seed)-mn.nbinom)^2)
406 mse.ypred[k]=mean((ypred-as.vector(mn.nbinom))^2)
407
408
409 #####
410 ##### Save Values
411 #####
412
413 opt.ht.save[k] = opt.ht
414 beta.save[,] = beta
415 msediffsolve[k]=mse.ypred[k]-mse.y[k]
416 error.save[,k]=error
417
418 }
419
420 #####
421 ##### Create Plots
422 #####
423 n.burn=round(.2*n.mcmc)
424 p.value=sum(mse.ypred[n.burn:n.mcmc] > mse.y[n.burn:n.mcmc]) /
425 (n.mcmc - n.burn)
426
427
428 layout(matrix(1:3,3,1))
429 plot(opt.ht.save[n.burn:n.mcmc],type="l",main="Threshold Height
430 ")

```

```

431 plot(beta.save[n.burn:n.mcmc,1], type="l", main=expression(paste(
432   beta[0])))
433 plot(beta.save[n.burn:n.mcmc,2], type="l", main=expression(paste(
434   beta[1])))
435
436
437
438 list(error.save=error.save, ypred=ypred, msediffs.save=msediffs.save, p.
439   value=p.value, opt.ht.save=opt.ht.save, beta.save=beta.save, accept
440   .beta=accept.beta, accept.opt.ht=accept.opt.ht)
441 }

```

442 R Code for Script to Run MCMC Algorithm

```

443 rm(list=ls())
444 #####
445 ##### Load and Molt Data
446 #####
447
448 setwd("/Users/raiho/Documents/Willows")
449 library(reshape)
450 library(segmented)
451 raw_seeds=read.csv("raw_seeds.csv")
452 melt.raw.seeds=melt(raw_seeds)##id=c("Site","Trap.Type","X..Seeds
453 ") ,na.rm=TRUE)
454 cast.raw.seeds=cast(melt.raw.seeds, Site ~ Trap.Type , sum)
455 #cast.raw.seeds1=cast(melt.raw.seeds, Site ~ Trap.Type , sum)
456 remove=c( 11, 12, 20) #,22 to remove WBT1
457 cast.raw.seeds.remove=cast.raw.seeds[-remove,]

```

```

458
459 remove.cols=c(3,4,5,6,7,8)
460 seed.count.traps=cast.raw.seeds.remove[,-remove.cols]
461 as.numeric(seed.count.traps[,1])
462
463 y.seed=as.matrix(seed.count.traps[,2:4])
464
465 seed.count=rowSums(cast.raw.seeds.remove[,2:10])
466
467 ht.obs=(read.csv("sex_obs_sites.csv"))
468 seed1=(read.csv("seedrain1.csv"))
469 ht.obs$sex<-NULL
470 ht.obs$species<-NULL
471 head(ht.obs)
472 ht.obs=ht.obs[ht.obs[,1]!="Rose",] #Takes Rose out because it has
473 no heights
474 ht.obs[,1]=as.numeric(factor(ht.obs[,1])) #Giving index
475
476 ht.obs3=matrix(0,1,3)
477 ht.obs=matrix(rbind(as.matrix(ht.obs),ht.obs3),2229,3)
478
479 ##### Run MCMC #####
480 ##### Run MCMC #####
481 #####
482
483 n.mcmc=20000
484 setwd("~/Documents/Willows")

```

```

485 source("change.pt.pois.regMCMC.no.inflat1.R")
486 output5 = change.pt.pois.regMCMC.no.inflat1(n.mcmc=n.mcmc,X=ht.obs
487 [1:2228],y.seed=y.seed,opt.ht strt=50,hshape1=0,hshape2=300,
488 beta=c(-1,1.5),beta.mns=c(0,0),beta.var=c(1,1),beta.tune=c
489 (.5,.1),error.var=.000001,error.tune=.01)

```

490 **Trace Plots**

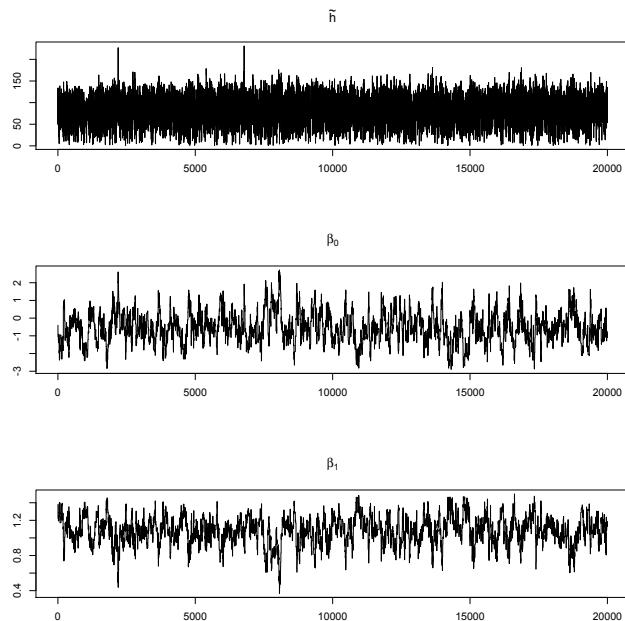


Figure 5: Trace plots for parameters for parameters of interest.

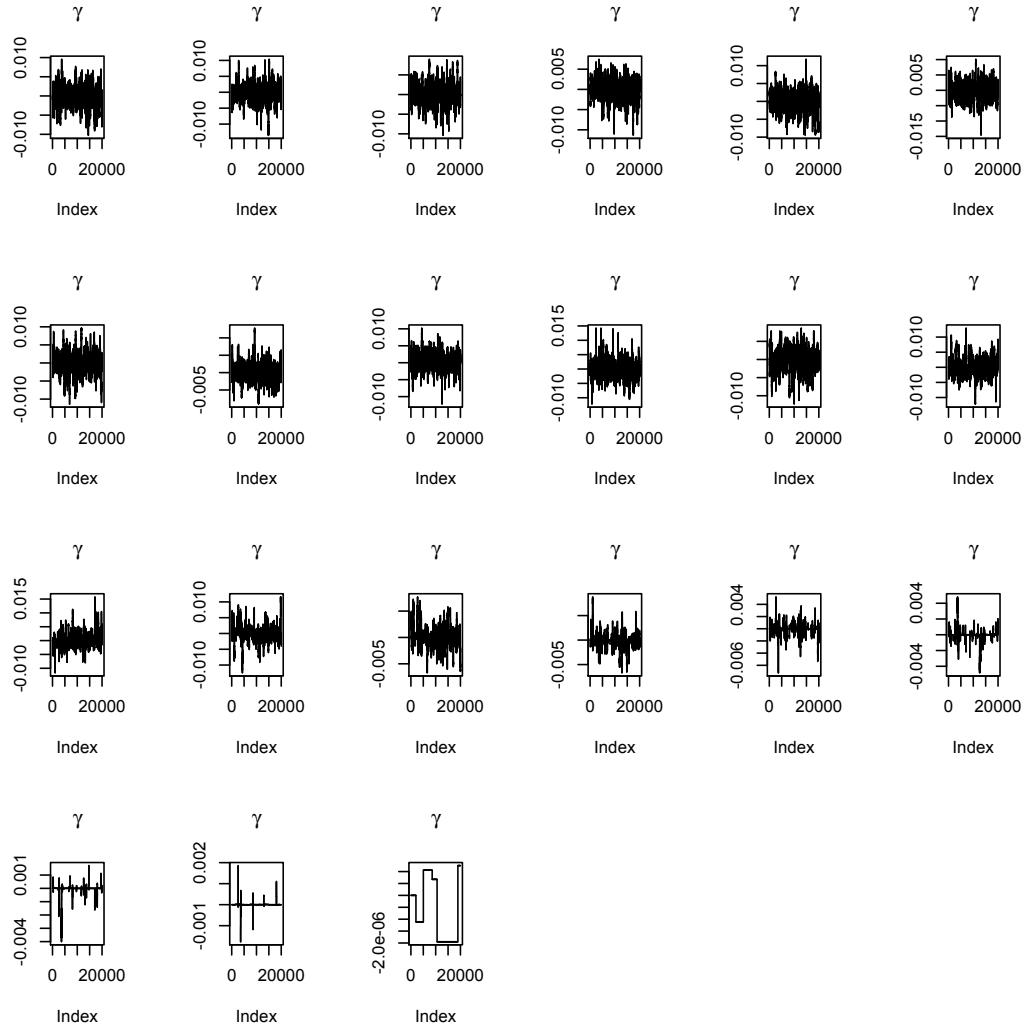


Figure 6: Trace plots of the error parameters for each site (γ_i).

491 Full Conditionals

$$\begin{aligned}
 [\tilde{h} | \cdot] &\propto \prod_{i=1}^n \prod_{k=1}^3 (1_{\{y_i=0\}} 1_{\{x_i=0\}} + 1_{\{x_i>0\}} \text{Poisson}(y_{ik} | \lambda_i w_k)) \text{Discrete Uniform}(\tilde{h} | 0, 400) \\
 [\boldsymbol{\beta} | \cdot] &\propto \prod_{x_i>0} \prod_{k=1}^3 \text{Poisson}(y_{ik} | \lambda_i w_k) N(\boldsymbol{\beta} | \mathbf{0}, \sigma_\beta^2 I) \\
 [\boldsymbol{\gamma} | \cdot] &\propto \prod_{x_i>0} \prod_{k=1}^3 \text{Poisson}(y_{ik} | \lambda_i w_k) N(\boldsymbol{\gamma} | \mathbf{0}, \sigma_\gamma^2 I)
 \end{aligned}$$