$$y_{tj} \sim \begin{cases} 0, Z_{t} = 0 \\ 0, Z_{t} = 1, U_{tj} < 0 \\ 1, Z_{t} = 1, U_{tj} > 0 \end{cases}$$

Jandakes sombling occasion

20 N Beta (dy, Pp)

Roje and Doratio robotion

d NN(Ma, Za)

B ~ N(以B, ZB)

0 NN (ho, 28)

Posterior Distribution:

[2, 2, P, U, V, P, \alpha, \beta, \beta, \beta] \ \ \frac{1}{\tau} \left([y_{ti} | \beta_t, u_i] [u_i | \alpha]

fikelihood?

[201.] ~ [2, 12] [2, 14]

$$\propto \left[\frac{1}{2} \frac{2}{2} \frac{1}{2} \frac{1}{2$$

$$\left[(1-4) \left(1^{55-03} 1^{56-03} + 1^{55-03} 1^{56-03} \right) \right]_{x}^{50}$$

$$\left[(1-4) \left(1^{55-03} 1^{56-03} + 1^{55-03} 1^{56-03} \right) \right]_{x}^{1-50}$$

$$\left[(1-4) \left(1^{55-03} 1^{56-03} + 1^{55-03} 1^{56-03} \right) \right]_{x}^{1-50}$$

$$\left[(1-4) \left(1^{55-03} 1^{56-03} + 1^{55-03} 1^{56-03} \right) \right]_{x}^{1-50}$$

$$\propto \left[\psi \varphi^{\overline{z}_1} (1-\varphi)^{1-\overline{z}_1}\right]^{\overline{z}_0} \left[(1-\psi) \gamma^{\overline{z}_1} (1-\gamma)^{1-\overline{z}_1}\right]^{1-\overline{z}_0}$$
 $\propto \operatorname{Bern}(\overline{\psi})$

$$\gamma = \frac{A}{A+B}$$

$$\left[\int_{\mathbb{R}^{-1}}^{\mathbb{R}^{-1}} \left(1_{\{y_{k_{1}}=0\}} 1_{\{u_{k_{1}}\leq0\}} + 1_{\{y_{k_{1}}=1\}} 1_{\{u_{k_{1}}>0\}} \right) + 1_{\{z_{k_{1}}=1\}} 1_{\{q_{k_{1}}>0\}} + 1_{\{z_{k_{1}}=1\}} 1_{\{q_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=1\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=1\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=1\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} + 1_{\{z_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}} 1_{\{q_{k_{1}}=0\}}$$

((antinue d...)

$$\Psi = \frac{A}{A+B}$$

$$\begin{bmatrix} 2_{7} | \cdot \end{bmatrix} \propto \frac{1}{11} ([Y_{7i} | Z_{7}, U_{7i}]) [Z_{7} | Z_{7-1}]$$

$$\propto \frac{1}{11} (1_{\{Y_{7i} = 0\}} 1_{\{U_{7i} = 0\}} + 1_{\{Y_{7i} = 0\}} 1_{\{U_{7i} > 0\}} + 1_{\{Y_{7i} = 0\}} 1_{\{U_{7i} > 0\}} + 1_{\{Y_{7i} = 0\}} 1_{\{U_{7i} > 0\}} \times 1_{\{Y_{7i} = 0\}} 1_{\{Y_{7i} = 0\}} 1_{\{U_{7i} = 0\}} 1_{\{U_{7i}$$

(colonization)

$$[U_{ij}] \cdot J \propto [Y_{ij}] Z_{e}, U_{ij}] [U_{ij}] \propto I$$

$$U_{ij} = 0$$

$$U_{ij} \cdot J \propto \left(\frac{Z_{e}}{1} \sum_{i \neq j = 0}^{2} \frac{1}{2} \sum_{i \neq j = 0}^{2} \sum_{i \neq j = 0}^{2} \frac{1}{2} \sum_{i \neq j = 0}^{2} \frac{1}{2} \sum_{i \neq$$

[4][4]68] 6 [4][4]

$$\propto \left(\psi^{2\sigma}\left(1-\psi\right)^{1-2\sigma}\right)\left(\psi^{\alpha-1}\left(1-\psi\right)^{3-1}\right)$$

$$\alpha + \frac{20+\alpha-1}{(1-20)+(\beta-1)}$$

- Imperfect ditec Zio~ Bern(4) (- loops) 4 ~ Betal du, 54) - add falsi puiltine r detection - handle いいけんとしかがら、より NA's by 0, Vitto, 2:t-1=0 0, 4itto 2:t-1=1 トンタンパーN(Xにない、コ) olay + yen 1-4) & 91+~ N(X1/50, 1) 1] qit 70, zit-1=1 silte ON N(Ma, Ed) \$=ρ(Surval) Bo~N(Mg, 2g,)

Bo~N(Mg, 2g) 9 (p)t) = Wit & 0 = p(colonization) 更(句) = と:1月ので **ず(8) = X/gg** Full conditionals [Z, 20, 4, V, 4, U, &, Ba, Ba/y] attitude 1 Systems Systems · Isvije sus + Ingijtas Imijtas ([Uijt d]) I szitevi I sviesus + I (zit=1) · I (Vit>u) + I zit-1] (qit=u) | (qit=u) | (qit=u) | (qit=u) | [Vit| Br] [41|Br) [Zio]4] [4] [D] [Bo) [Bo) [Bo] [2,0]] x TT] [-2,0] +] [-2,0] +] [-2,0] +] [-2,0] +] [-2,0] +] [-2,0] + 1 [+17=1) Tigition) [+10] +] Z.O=1 x 4 (1-4) + Z.J = A 7 = 4/A+B

Z.0=0 d(1-4) (1-2) X = B

$$\begin{bmatrix}
2 + \frac{1}{2} + \frac{1}{2}$$

Zitle de Title I sy je d'I + IZIT-11 + SYIENS) L (Isympton I Sunteus I Tympton + The Internal Invition is $2(p_{ij}r_{ij}r_{(i-p_{ij}r_{i})}r_{ij}r$ [Zit]] = Bern(4) Q=A A=pij (1-pijt) Wil y-2it-1 p2it-1 B=(1-0) -317-1 (1-0) 0 B Zit-1=0 at I svitos + I vitter [Vit | Ba] Zit=0 2 TN(X: Rx, 1)-00 Zit=1 aTN(Xib,1)00 [B+1-] = N((X'X+2")"X'Z,(X'X+2")")

(E1 t-1=0)

```
probit_det_z0na_ms_msp_0908 <- function(Y,n.mcmc,n.burn,X,W){</pre>
  library(truncnorm)
  library(mvtnorm)
  library(Rlab)
  library(boot)
  library(abind)
  library(MASS)
  library(msm)
  library(MCMCpack)
  n \leftarrow dim(Y)[1]
  J \leftarrow dim(Y)[2]
  T \leftarrow dim(Y)[3]
  N \leftarrow dim(Y)[4]
  #####
  #####Save samples
  #####
  psi.save <- array(0,dim=c(n.mcmc,dim(X)[2],N))</pre>
  beta.psi.save <- array(0,dim=c(n.mcmc,dim(X)[2],N))
  sigma.beta.psi.save <- array(0,dim=c(dim(X)[2],dim(X)[2],n.mcmc))</pre>
  mu.beta.psi.save <- array(0,dim=c(n.mcmc,dim(X)[2]))</pre>
  phi.save <- array(0,dim=c(n.mcmc,dim(X)[2],N))</pre>
  beta.phi.save <- array(0,dim=c(n.mcmc,dim(X)[2],N))
  sigma.beta.phi.save <- array(0,dim=c(dim(X)[2],dim(X)[2],n.mcmc))</pre>
  mu.beta.phi.save <- array(0,dim=c(n.mcmc,dim(X)[2]))</pre>
  gamma.save <- array(0,dim=c(n.mcmc,dim(X)[2],N))</pre>
  beta.gamma.save <- array(0,dim=c(n.mcmc,dim(X)[2],N))
  sigma.beta.gamma.save <- array(0,dim=c(dim(X)[2],dim(X)[2],n.mcmc))</pre>
```

```
mu.beta.gamma.save <- array(0,dim=c(n.mcmc,dim(X)[2]))</pre>
  p.save <- array(0,dim=c(n.mcmc,J,N))</pre>
  alpha.save <- array(0,dim=c(n.mcmc,dim(W)[2],N))</pre>
  sigma.alpha.save <- array(0,dim=c(dim(W)[2],dim(W)[2],n.mcmc))</pre>
 mu.alpha.save <- array(0,dim=c(n.mcmc,dim(W)[2]))</pre>
  #####
 #####Set up variables for each species
  #####
  zi <- NULL:</pre>
 Y.nz.idx <- NULL:
  for(i in 1:N){
    Y.tmp <- Y[,,,i]
    Ys <- colSums(aperm(Y.tmp, c(2,1,3)),na.rm=TRUE)
    zi.tmp \leftarrow array(0,dim = c(n,T))
    zi.tmp[Ys>0] <- 1 ##zi matrix for when a species was observed at least once at a
site, per year
    Y.nz.temp <- zi.tmp==1 #index for when a species was observed at least once
    Y.nz.idx <- abind(Y.nz.idx,Y.nz.temp,along=3)</pre>
    zi <- abind(zi,zi.tmp,along=3)</pre>
 ##get priors for alpha
 mu.mu.alpha <- matrix(rep(0, dim(W)[2]), ncol=1)</pre>
  sigma.mu.alpha <- matrix(0, nrow=dim(W)[2], ncol=dim(W)[2])</pre>
 diag(sigma.mu.alpha) <- 1.5</pre>
  sigma inv.mu.alpha <- solve(sigma.mu.alpha)</pre>
 V.alpha <- diag(2)*1.5
```

```
##get priors for beta psi
mu.mu.beta.psi <- matrix(rep(0, dim(X)[2]), ncol=1)</pre>
sigma.mu.beta.psi <- matrix(0, nrow=dim(X)[2], ncol=dim(X)[2])</pre>
diag(sigma.mu.beta.psi) <- 1.5
sigma inv.mu.beta.psi <- solve(sigma.mu.beta.psi)</pre>
V.beta.psi \leftarrow diag(2)*1.5
nu.beta.psi <- 100
##get prior mean and cov for beta Phi, it does not change with every iteration
mu.mu.beta.phi <- matrix(rep(0, dim(X)[2]), ncol=1)</pre>
sigma.mu.beta.phi <- matrix(0, nrow=dim(X)[2], ncol=dim(X)[2])</pre>
diag(sigma.mu.beta.phi) <- 1.5</pre>
sigma inv.mu.beta.phi <- solve(sigma.mu.beta.phi)</pre>
V.beta.phi \leftarrow diag(2)*1.5
nu.beta.phi <- 100
##get prior mean and cov for beta Gamma, it does not change with every iteration
mu.mu.beta.gamma <- matrix(rep(0, dim(X)[2]), ncol=1)</pre>
sigma.mu.beta.gamma \leftarrow matrix(0, nrow=dim(X)[2], ncol=dim(X)[2])
diag(sigma.mu.beta.gamma) <- 1.5</pre>
sigma inv.mu.beta.gamma <- solve(sigma.mu.beta.gamma)</pre>
V.beta.gamma <- diag(2)*1.5
nu.beta.gamma <- 100
##starting values for the betas for psi
```

nu.alpha <- 100

```
x.psi \leftarrow as.matrix(cbind(c(1,1),c(1,0)))
beta.psi <- array(0,dim=c(N,dim(X)[2]))</pre>
psi \leftarrow array(0,dim=c(n,N))
##starting values for psi
for(i in 1:N){
  beta.psi[i,] <- glm(zi[,T-2,i] \sim X[,2],family=binomial)$coefficients
  psi[,i] <- inv.logit(X%*%beta.psi[i,])</pre>
##setting up the new zi matrix
zi.2 \leftarrow array(NA, dim=c(n,T+1,N))
for(i in 1:N){
  zi.2[,2:(T+1),i] \leftarrow zi[,,i] ##add the zi
  zi.2[,1,i] \leftarrow rbern(n,mean(psi[i]))
Y.nz2.idx <- zi.2==1
mu.beta.psi <- apply(beta.psi,2,mean)</pre>
sigma.beta.psi <- matrix(0, nrow=dim(X)[2], ncol=dim(X)[2])</pre>
                                                                                    2
diag(sigma.beta.psi) <- apply(beta.psi,2,var)</pre>
sigma.beta.psi inv <- solve(sigma.beta.psi)</pre>
                                                                                 2
##starting value for the alphas for detection
                                                                                 2
alphas <- array(0,dim=c(N,dim(W)[2]))</pre>
p \leftarrow array(0,dim=c(dim(W)[1],N))
p.mean \leftarrow array(0,dim=c(dim(W)[1],N))
##starting values for detection (p)
for(i in 1:N){
 Y.temp <- Y[,,,i]
```

```
alphas[i,] \leftarrow glm(c(t(Y.temp[,,T-2]))[Y.nz.idx[,T-2,i]] \sim W[Y.nz.idx[,T-2,i],2:dim(W)]
[2]], family=binomial)$coefficients#get starting values for alpha
    p[,i] <- inv.logit(W%*%alphas[i,])</pre>
    p.mean[,i] \leftarrow p[,i]
                                                                                             Persistance
  mu.alpha <- apply(alphas,2,mean)</pre>
  sigma.alpha <- matrix(0, nrow=dim(W)[2], ncol=dim(W)[2])</pre>
  diag(sigma.alpha) <- apply(alphas,2,var)</pre>
  sigma.alpha_inv <- solve(sigma.alpha)</pre>
  ##starting value for the betas for persistence
  x.phi \leftarrow as.matrix(cbind(c(1,1),c(1,0)))
  x2.phi <- do.call(rbind, replicate(T, X, simplify=FALSE))
  beta.phi <- array(0,dim=c(N,dim(X)[2]))</pre>
  phi <- array(0,dim=c(n,N))</pre>
  ##starting values for persistence (Phi)
  for(i in 1:N){
    z.pers1.indx.temp \leftarrow zi[,T-2,i]==1
    beta.phi[i,] <- glm(zi[z.pers1.indx.temp,T-1,i]~ X[z.pers1.indx.temp,
2].family=binomial)$coefficients
    phi[,i] <- inv.logit(X%*%beta.phi[i,])</pre>
  mu.beta.phi <- apply(beta.phi,2,mean)</pre>
  sigma.beta.phi <- matrix(0, nrow=dim(X)[2], ncol=dim(X)[2])</pre>
  diag(sigma.beta.phi) <- apply(beta.phi,2,var)</pre>
  sigma.beta.phi_inv <- solve(sigma.beta.phi)</pre>
```

```
#Starting value for the betas for colonization
  x2.gamma <- do.call(rbind, replicate(T, X, simplify=FALSE))</pre>
  x.gamma \leftarrow as.matrix(cbind(c(1,1),c(1,0)))
  beta.gamma <- array(0,dim=c(N,dim(X)[2]))</pre>
  gamma <- array(0,dim=c(n,N))</pre>
  ##starting values for colonization (Gamma)
  for(i in 1:N){
    z.col0.indx.temp <-zi[,2,i]==0 ##how many sites were empty
    beta.gamma[i,] <- glm(zi[z.col0.indx.temp,3,i] ~ X[z.col0.indx.temp,
2].family=binomial)$coefficients
    gamma[,i] <- inv.logit(X%*%beta.gamma[i,])</pre>
  mu.beta.gamma <- apply(beta.gamma,2,mean)</pre>
  sigma.beta.gamma \leftarrow matrix(0, nrow=dim(X)[2], ncol=dim(X)[2])
  diag(sigma.beta.gamma) <- apply(beta.gamma,2,var)</pre>
  sigma.beta.gamma inv <- solve(sigma.beta.gamma)</pre>
  for(k in 1:n.mcmc){
    if(k % 100 == 0) cat(k, " "); flush.console()
    ####
          Sample mu.alpha
    ####
    temp.alpha.var <- solve(N*sigma.alpha inv + sigma inv.mu.alpha)
    temp.alpha.mean <- temp.alpha.var%*%(sigma.alpha_inv%*%apply(alphas,2,sum))
    mu.alpha <- matrix(rmvnorm(1, temp.alpha.mean, temp.alpha.var,method="chol"), ncol=1)</pre>
```

```
####
          sigma.alpha
    ####
    ####
    mu.alphas <- matrix(mu.alpha,N,dim(W)[2],byrow = TRUE)</pre>
    alpha.mu.diff <- alphas - mu.alphas
    V.alpha.temp <- crossprod(alpha.mu.diff)</pre>
    sigma.alpha_inv <- rwish((N + nu.alpha),solve(V.alpha.temp+V.alpha*nu.alpha))</pre>
    ####
    ####
          Sample mu.beta.psi
    ####
    temp.beta.psi.var <- solve(N*sigma.beta.psi_inv + sigma_inv.mu.beta.psi)
    temp.beta.psi.mean <- temp.beta.psi.var%*%(sigma.beta.psi_inv%*%apply(beta.psi,
2, sum))
    mu.beta.psi <- matrix(rmvnorm(1, temp.beta.psi.mean,</pre>
temp.beta.psi.var.method="chol"), ncol=1)
    ####
          sigma.beta.psi
    ####
    ####
    mu.beta.psis <- matrix(mu.beta.psi,N,2,byrow = TRUE)</pre>
    beta.psi.mu.diff <- beta.psi - mu.beta.psis
    V.psi.temp <- crossprod(beta.psi - mu.beta.psis)</pre>
    sigma.beta.psi_inv <- rwish((N + nu.beta.psi),solve(V.psi.temp</pre>
+V.beta.psi*nu.beta.psi))
    ####
          Sample mu.beta.phi
    ####
    ####
```

```
temp.beta.phi.var <- solve(N*sigma.beta.phi_inv + sigma_inv.mu.beta.phi)
    temp.beta.phi.mean <- temp.beta.phi.var%*%(sigma.beta.phi_inv%*%apply(beta.phi,
2.sum))
    mu.beta.phi <- matrix(rmvnorm(1, temp.beta.phi.mean,</pre>
temp.beta.phi.var,method="chol"), ncol=1)
    ####
          sigma.beta.phi
    ####
    ####
    mu.beta.phis <- matrix(mu.beta.phi,N,2,byrow = TRUE)</pre>
    beta.phi.mu.diff <- beta.phi - mu.beta.phis</pre>
    V.phi.temp <- crossprod(beta.phi - mu.beta.phis)</pre>
    sigma.beta.phi_inv <- rwish((N + nu.beta.phi), solve(V.phi.temp</pre>
+V.beta.phi*nu.beta.phi))
    ####
          Sample mu.beta.gamma
    ####
    temp.beta.gamma.var <- solve(N*sigma.beta.gamma inv + sigma inv.mu.beta.gamma)
    temp.beta.gamma.mean <- temp.beta.gamma.var%*%(siqma.beta.gamma inv%*
%apply(beta.gamma,2,sum))
    mu.beta.gamma <- matrix(rmvnorm(1, temp.beta.gamma.mean,</pre>
temp.beta.gamma.var,method="chol"), ncol=1)
    ####
          sigma.beta.gamma
    ####
```

```
mu.beta.gammas <- matrix(mu.beta.gamma,N,2,byrow = TRUE)</pre>
    beta.gamma.mu.diff <- beta.gamma - mu.beta.gammas
    V.gamma.temp <- crossprod(beta.gamma - mu.beta.gammas)</pre>
    sigma.beta.gamma_inv <- rwish((N + nu.beta.gamma), solve(V.gamma.temp)
+V.beta.gamma*nu.beta.gamma))
    for(j in 1:N) {
        cat(j, " ")
#
      ####
      ####
            Sample Zi0
      ####
      if(sum(is.na(zi.2[,,j]))>1){
           zi.2[,2:(T+1),i] \leftarrow zi[,,j]
          zi.2[,1,i] <- rbern(n,mean(psi[i]))</pre>
      }
      z0.tmp.numer \leftarrow (phi[,j]^zi.2[,2,j])*((1-phi[,j])^(1-zi.2[,2,j]))
      z0.temp.denom \leftarrow (gamma[,j]^zi.2[,2,j])*((1-gamma[,j])^(1-zi.2[,2,j]))
      z0.psi.tmp=z0.tmp.numer/(z0.tmp.numer+z0.temp.denom)
      zi.2[,1,j] \leftarrow rbern(dim(zi.2)[1],z0.psi.tmp)
      ####
             Sample Zi2 to T-1
      ####
      ####
      ##get rid of loop if possible
         for(t in 2:T){## from 2 to five in zi.2, but from year 1 to 4 in real data
```

```
tmp.numer <- prod(dbinom(Y[,,t-1,j],1,t(matrix(p,J,n))),na.rm=TRUE)*((1-
phi[,j])^(1-zi.2[,t-1,j]))*
                                   (phi[,j]^zi.2[,t+1,j])*(gamma[,j]^(1-zi.2[,t-1,j]))*(phi[,j]^zi.2[,t-1,j])
                             temp.denom <- ((1-gamma[,j])^{(1-zi.2[,t+1,j])}*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*(gamma[,j]^zi.2[,t+1,j])*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+1,j]))*((1-zi.2[,t+
phi[,i])^{(1-zi.2[,t-1,i])}*((1-qamma[,i])^{(1-zi.2[,t-1,i])})
                             psi.tmp=tmp.numer/(tmp.numer+temp.denom)
                             zi.2[!Y.nz2.idx[,t,j],t,j]=rbern(sum(!Y.nz2.idx[,t,j]),psi.tmp[!
Y.nz2.idx[,t,j]])
                 ####
                                  Sample ZiT
                 ####
                 tmp.numer <- prod(dbinom(Y[ ,,T,j],1,t(matrix(p,J,n))),na.rm=TRUE)*(gamma[,j]^(1-</pre>
zi.2[.T.i]))*(phi[.i]^zi.2[.T.i])
                 temp.denom <- ((1-gamma[,j])^{(1-zi.2[,T,j])}*((1-phi[,j])^{(zi.2[,T,j])})
                 psi.tmp=tmp.numer/(tmp.numer+temp.denom)
                 zi.2[!Y.nz2.idx[,T+1,j],T+1,j]=rbern(sum(!Y.nz2.idx[,T+1,j]),psi.tmp[!Y.nz2.idx[,T
+1, j]])
                 ####
                                  Sample u
                 ####
                 ####
                 u.all <- NULL:
                 W.all <- NULL:
                 for(t in 1:T){
                 z.year.1.idx <- c(t(matrix(zi[,t,j],n,J)==1))##fills in occupied sites with 1 in a
vector same length as Y
                 Y.zi1 <- c(t(Y[,,t,j]))[z.year.1.idx]##creates a vector for the occupied sites only
```

```
Y.zil.idx <- Y.zil==1 & !is.na(Y.zil)##index of when yij==1 for the occupied sites
      Y.zi0.idx <- Y.zi1==0 & !is.na(Y.zi1)##index of when yij==0 for the occupied sites
      u.mean <- as.vector(W[z.year.1.idx,] %*% alphas[j,])##get mu for u to sample from
the truncated normal
      u <- rep(NA, dim(W[z.year.1.idx,])[1])</pre>
      u[Y.zi1.idx] <- rtruncnorm(sum(Y.zi1.idx), a=0,b=Inf,mean=u.mean[Y.zi1.idx],</pre>
sd=1)##sample from a left truncated normal
      u[Y.zi0.idx] <- rtruncnorm(sum(Y.zi0.idx), a=-Inf,b=0,mean=u.mean[Y.zi0.idx],</pre>
sd=1)##sample from a right truncated normal
      u.all <- c(u.all,u)
      W.all <- rbind(W.all, W[z.year.1.idx,])</pre>
      ####
            Sample alpha.p
      ####
      ####
      V.alpha <- solve(sigma.alpha_inv + t(W.all) %*% W.all)</pre>
      u.na.red <- u.all[!is.na(u.all)]</pre>
      u.na.idx <- !is.na(u.all)</pre>
      W.na.1 <- t(W.all)
      W.na.red <- W.na.1[,u.na.idx]</pre>
      sigma.alpha <- solve(sigma.alpha_inv)</pre>
      alpha.mean <- V.alpha %*% (sigma.alpha%*%mu.alpha + (W.na.red %*% u.na.red))
      alphas[j,] <- matrix(rmvnorm(1, alpha.mean, V.alpha), ncol=1)</pre>
    ####
          Sample m
    ####
    ####
```

```
m.mean.1t <- as.vector(X %*% beta.psi[j,])##get mu for m to sample from the truncated
normal
    ##indicator for all cases where zit==1
    zi.m1.idx <- zi.2[,1,j] == 1
    m = rep(NA, length(m.mean.1t))
    ##sample from a left TN, when mit > 0
    m[zi.m1.idx] <- rtruncnorm(sum(zi.m1.idx), a=0,b=Inf,mean=m.mean.1t[zi.m1.idx], sd=1)</pre>
    ##sample from a right TN, when mit =< 0
    m[!zi.m1.idx] <- rtruncnorm(sum(!zi.m1.idx), a=-Inf,b=0,mean=m.mean.1t[!zi.m1.idx],</pre>
sd=1)
    ####
          Sample Beta.psi
    ####
    m.beta <- solve(sigma.beta.psi_inv + (t(X) %*% X))</pre>
    sigma.beta.psi<- solve(sigma.beta.psi_inv)</pre>
    beta.psi.mean <- m.beta %*% (sigma.beta.psi%*%mu.beta.psi + (t(X) %*% m))
    beta.psi[j,] <- matrix(rmvnorm(1, beta.psi.mean, m.beta), ncol=1)##sample from a
multivariate normal
    ####
          Sample q
    ####
    ####
    q.mean.1t <- as.vector(X %*% beta.phi[j,])##get mu for q to sample from the truncated</pre>
```

```
normal
    q.mean.all <- rep(q.mean.1t,T) ##repeat this for all the sites and years
    ##indicator for all cases where zit-1==1, and where zit=0 or =1
    zi.q1 \leftarrow c(zi.2[,1:T,j]) ## create a vector from z0 to T-1
    zi.q2 \leftarrow c(zi.2[,2:(T+1),j])
    zi.q10.idx <- zi.q1 == 1 \& zi.q2 == 0
    zi.q11.idx <- zi.q1 == 1 & zi.q2 == 1
    zi.q1.idx \leftarrow zi.q1 == 1
    q = rep(NA, length(q.mean.all))
    ##sample from a left TN, when zit = 1, vit > 0, zit-1=1
    q[zi.q11.idx] <- rtruncnorm(sum(zi.q11.idx), a=0,b=Inf,mean=q.mean.all[zi.q11.idx],
sd=1)
    ##sample from a right TN, when zit = 0, vit =< 0, zit-1=1
    q[zi.q10.idx] <- rtruncnorm(sum(zi.q10.idx), a=-Inf,b=0,mean=q.mean.all[zi.q10.idx],
sd=1)
      ####
            Sample Beta.phi
      ####
      q.beta <- solve(sigma.beta.phi_inv + (t(x2.phi[zi.q1.idx,]) %*%</pre>
x2.phi[zi.q1.idx,]))
      x2.phi.red <- x2.phi[zi.q1.idx,] ##take the elongated X cov matrix for phi, and
index those sites where zit-1=1
      q.red <- q[zi.q1.idx] ##take only those values for when zit-1=1</pre>
      sigma.beta.phi<- solve(sigma.beta.phi_inv)</pre>
      beta.phi.mean <- q.beta %*% (sigma.beta.phi%*%mu.beta.phi + (t(x2.phi.red) %*%
q.red))
```

```
beta.phi[j,] <- matrix(rmvnorm(1, beta.phi.mean, q.beta), ncol=1)##sample from a
multivariate normal
      ####
            Sample v
      ####
      v.mean.1t <- as.vector(X %*% beta.gamma[j,])##get mu for v to sample from the
truncated normal
      v.mean.all <- rep(v.mean.1t,T)</pre>
      ##indicator for all cases where zit-1==0
      zi.v1 \leftarrow c(zi.2[,1:T,j])
      zi.v2 \leftarrow c(zi.2[,2:(T+1),j])
      zi.v00.idx <- zi.v1 == 0 & zi.v2 == 0
      zi.v01.idx <- zi.v1 == 0 & zi.v2 == 1
      zi.v0.idx \leftarrow zi.v1 == 0
      v = rep(NA, length(v.mean.all))
      ##sample from a left TN, when zit = 1, vit > 0, zit-1=0
      v[zi.v01.idx] <- rtruncnorm(sum(zi.v01.idx), a=0,b=Inf,mean=v.mean.all[zi.v01.idx],</pre>
sd=1)##sample from a left TN, when zit = 1, zit-1=0, vit-1=0
      ##sample from a right TN, when zit = 0, vit =< 0, zit-1=0
      v[zi.v00.idx] <- rtruncnorm(sum(zi.v00.idx), a=-
Inf, b=0, mean=v.mean.all[zi.v00.idx], sd=1)##sample from a right TN, when zit = 0,
zit-1=0, vit-1=0
        ####
              Sample Beta.gamma
        ####
        ####
```

```
V.beta <- solve(sigma.beta.gamma_inv + (t(x2.phi[zi.v0.idx,]) %*%</pre>
x2.phi[zi.v0.idx,]))
        x2.gamma.red <- x2.phi[zi.v0.idx,] ##take the elongated X cov matrix for gamma,
and index those sites where zit-1=0
        v.red <- v[zi.v0.idx] ##take only those values for when zit-1=0
        sigma.beta.gamma <- solve(sigma.beta.gamma_inv)</pre>
        beta.gamma.mean <- V.beta %*% (sigma.beta.gamma%*%mu.beta.gamma +
(t(x2.gamma.red) %*% v.red)) ##a n by cov X matrix * V that's n dims
        beta.gamma[j,] <- matrix(rmvnorm(1, beta.gamma.mean, V.beta), ncol=1)##sample
from a multivariate normal
      ####
            Sample psi, p, Phi and Gamma
      ####
      p[,j] <- as.vector(pnorm(W%*%alphas[j,]))</pre>
      psi[,j] <- as.vector(pnorm(X %*% beta.psi[j,]))</pre>
      phi[.j] <- as.vector(pnorm(X %*% beta.phi[j,]))</pre>
      gamma[,i] <- as.vector(pnorm(X %*% beta.gamma[j,]))</pre>
      ####
            Save samples
      ####
      ####
      psi.save[k,,j] <- unique(psi[,j])</pre>
      beta.psi.save[k,,j] <- t(beta.psi[j,])</pre>
```

```
phi.save[k,,j] <- unique(phi[,j])
  beta.phi.save[k,,j] <- t(beta.phi[j,])
  gamma.save[k,,j] <- unique(gamma[,j])
  beta.gamma.save[k,,j] <- t(beta.gamma[j,])
  p.save[k,,j] <- p[1:J,j]
  alpha.save[k,,j] <- t(alphas[j,])
}

sigma.beta.psi.save[,,k] <- sigma.beta.psi
  mu.beta.psi.save[k,] <- t(mu.beta.psi)
  sigma.beta.phi.save[,,k] <- sigma.beta.phi
  mu.beta.phi.save[k,] <- t(mu.beta.phi)
  sigma.beta.gamma.save[,,k] <- sigma.beta.gamma
  mu.beta.gamma.save[k,] <- t(mu.beta.gamma)
  sigma.alpha.save[k,] <- t(mu.beta.gamma)
}</pre>
```

list(psi.save=psi.save, beta.psi.save=beta.psi.save, phi.save=phi.save, beta.phi.save=beta.phi.save, gamma.save=gamma.save, beta.gamma.save=beta.gamma.save, p.save=p.save, alpha.save=alpha.save, sigma.beta.psi.save=sigma.beta.psi.save, mu.beta.psi.save=mu.beta.psi.save, sigma.beta.gamma.save, mu.beta.phi.save=mu.beta.phi.save, sigma.beta.gamma.save=sigma.beta.gamma.save, mu.beta.gamma.save=mu.beta.gamma.save, sigma.alpha.save=sigma.alpha.save=mu.alpha.save=mu.alpha.save, Y=Y, X=X, W=W)

}