**S1 APPENDIX.** R/JAGS code for generation and analysis of simulated data

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#### function for generating data in R ####

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data.fn <- function(R=40, T=5, K=6, #sites, surveys, seasons

 x1mean=2, #covariate of detection

 x2min=-1.5, x2max=1.5, #abundance covariate

 x3n=T\*K, x3mean=2, #covariate of availability

 Talpha.om=2.2, #true values of parameters

Talpha.nu=-1.39, #alpha.om and alpha.nu vary by scenario

Talpha.lam=1.5,

 Tbeta.om=1,

 Tbeta.lam=0.8,

 Tbeta.nu=-0.5){

 y <- array(dim=c(R,T,K)) #array for counts

 N.tr <- array(dim=c(R,K)) #array for true abundance per site per season

 #### ecological process ####

 X2 <- (runif(n=R, min=x2min, max=x2max)) #create site-level covariate

 lam.tr <- exp(Talpha.lam + Tbeta.lam\*X2) #abundance-covariate relationship

 for (k in 1:K){

 N.tr[,k] <- rpois(n=R, lambda=lam.tr) #add Poisson variation

 }

 #### observation process ####

X3 <- array((rep((rpois(x3n,x3mean)),each=R)), dim=c(R,T,K)) #survey covariate

nu.tr <- plogis(Talpha.nu + Tbeta.nu\*X3) #availability-covariate relationship

 X1 <- array((rpois(n=R\*T\*K, x1mean)), dim=c(R,T,K)) #site\*survey covariate om.tr <- plogis(Talpha.om + Tbeta.om\*X1) #conditional p-covariate relationship

 p.tr <- nu.tr\*om.tr #overall detection probability

 #### count process ####

 for (i in 1:R){

 for (k in 1:K){

 for (j in 1:T){

 y[i,j,k] <- rbinom(1, size=N.tr[i,k], prob=p.tr[i,j,k])

 }}}

 #### return data ####

 return(list(R=R, T=T, X1=X1, X2=X2, X3=X3, y=y, N.tr=N.tr))

} #end data function

####################################################################

#### TE binomial mixture model #### run in R, requires “R2jags” ####

####################################################################

sink("TEsim.txt")

cat("

 model {

 ## priors

 alpha.om ~ dunif(-4.6,4.6) #equates to (.01, .99) on probability scale

 alpha.nu ~ dunif(-4.6,4.6) #to prevent numerical overflow/underflow

 alpha.lam ~ dunif(-5,5)

 beta.om ~ dunif(-5,5)

 beta.lam ~ dunif(-5,5)

 beta.nu ~ dunif(-5,5)

 ## ecological model

 for (k in 1:6){

 for (i in 1:R){

 N[i,k] ~ dpois(lambda[i,k])

 log(lambda[i,k]) <- alpha.lam + beta.lam\*X2[i]

 ## observation model

 for (j in 1:T){

 y[i,j,k] ~ dbin(p[i,j,k],N[i,k])

 p[i,j,k] <- (om[i,j,k])\*(nu[i,j,k])

 om[i,j,k] <- exp(logit.om[i,j,k])/(1+exp(logit.om[i,j,k]))

 logit.om[i,j,k] <- alpha.om + beta.om\*X1[i,j,k]

 nu[i,j,k] <- exp(logit.nu[i,j,k])/(1+exp(logit.nu[i,j,k]))

 logit.nu[i,j,k] <- alpha.nu + beta.nu\*X3[i,j,k]

 } #close j loop

 } #close i loop

 } #close k loop

 # Derived quantities

 for (k in 1:6){

 totalN[k] <- sum(N[,k]) #total population for each season (across all sites)

 }

 } #close model loop

 ",fill=TRUE)

sink()

##initial values

Ninit <- apply(y, c(1,3), max) + 1 #max for each site and season +1 (so no 0’s)

inits <- function() list(N=Ninit, alpha.lam=runif(1,-1, 1), alpha.om=runif(1,-1, 1), alpha.nu=runif(1,-1, 1), beta.lam=runif(1,-1,1), beta.om=runif(1,-1, 1), beta.nu = runif(1,-1, 1))

##parameters monitored

params <- c("alpha.lam", "alpha.om", "alpha.nu", "beta.nu", "beta.om", "beta.lam", "N", "totalN")

#MCMC settings

ni <- 10000

nt <- 2

nb <- 5000

nc <- 3

#call JAGS for each simulation

 data <- data.fn()

 out <- jags(data, inits, params, "TEsim.txt", n.chains = nc, n.thin = nt,

 n.iter = ni, n.burnin = nb, working.directory = getwd())