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unauthorized use.

JAGS code for SSVS & abundance model for lesser prairie-chickens #####
model{

Priors

for(k in 1:nyear){ ##k = number of years
beta.p[k] ~ dnorm(0,0.1)
}

for(i in 1:R){ ## R = number of sites
eps[i] ~ dnorm(0,tau.lam) #abundance random effect
eps.p[i] ~ dnorm(0,tau.site.p) #detection random effect
}

alpha.lam ~ dnorm(0,0.1)
tau.lam <- 1/(sd.lam*sd.lam)
sd.lam ~ dunif(0,15)
tau.site.p <- pow(sd.site.p,-2)
sd.site.p ~ dunif(0,15)
tau.p <- 1/(sd.p*sd.p)
sd.p ~ dunif(0,15)

for(s in 1:ncov){

gam is the inclusion indicator for SSVS ###
beta[s] ~ dnorm(0, prec[s])
gam[s] ~ dbern(0.5)
prec[s] <- 1/variable[s]
variable[s] <- (1-gam[s])*0.01 + gam[s]*10
}

Likelihood for true abundance

for(i in 1:R){ #sites
for(k in 1:nyear){ #years
N[i,k] ~ dpois(lambda[i,k]) #latent abundance state
log(lambda[i,k]) <- alpha.lam + X[i,k,] %*% beta[] + eps[i]

#observation model for replicated counts

mu.lp[i,k] <- beta.p[k] + eps.p[i]
for(j in 1:T){ #loop over temporal reps (2)
y[i,j,k] ~ dbin(p[i,j,k],N[i,k]) #detection
p[i,j,k] <- 1/(1+exp(-lp[i,j,k]))
lp[i,j,k] ~ dnorm(mu.lp[i,k],tau.p)

```
}  
ik.p[i,k] <- mean(p[i,k])  
}}  
  
#derived quantitates  
for(k in 1:nyear){  
totalN[k] <- sum(N[,k])  
mean.detection[k] <- mean(ik.p[,k])  
}  
}
```