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#~~~~~ 8.5.2 Static binomial N-mixture model with two species and directional interactions
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```
# Select BKTR and BLTR data
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```
str(CK <- counts.all[, , 'bktr'])
```

```
str(CL <- counts.all[, , 'bltr'])
```

```
# Bundle and summarize data set
```

```
str(abun.bltr.bktr <- list(CK = CK,
                             CL = CL,
                             nsites = nsites,
                             nreps = nreps,
                             nstream = 11,
                             dist_ms = site.covs$dist_ms,
                             water_temp = site.covs$water_temp,
                             elev = site.covs$elev,
                             pool = site.covs$pool,
                             riffle = site.covs$riffle,
                             depth_avg = site.covs$depth_avg,
                             lwd = site.covs$lwd,
                             timber_area = site.covs$timber_area,
                             rip_area = site.covs$rip_area,
                             SECONDS = seconds,
                             WET_WIDTH = wet_width))
```

```
# Specify model in BUGS language
```

```
cat(file = "Nmix4.txt", "
```

```

model {

# Model for Brook Trout (BKTR): the 'dominant' species

# Priors for intercepts and coefficients

mean.lambdaK ~ dunif(0, 35)

beta0K <- log(mean.lambdaK)

alpha0K <- logit(mean.pK)

mean.pK ~ dunif(0,1)

beta1K ~ dnorm(0, 0.1)

beta6K ~ dnorm(0, 0.1)

beta8K ~ dnorm(0, 0.1)

alpha1K ~ dnorm(0, 0.1)

tauK ~ dgamma(0.1, 0.1) # Excess-Poisson variation (precision)

sigmaK <- sqrt(1 / tauK)

# Likelihood for BKTR ('dominant')

# Ecological model

for(i in 1:nsites){

  for(s in 1:nstream){

    NK[i,s] ~ dpois(lambdaK[i,s])

    etaK[i,s] ~ dnorm(0, tauK)

    log(lambdaK[i,s]) <- beta0K + beta1K * dist_ms[i] + beta6K * depth_avg[i] + beta8K * timber_area[i] +
      etaK[i,s]

  }

}

}

```

```

# Observation model

for (j in 1:nreps){

  CK[i,j] ~ dbin(pK[i,j], NK[i,1])

  logit(pK[i,j]) <- alpha0K + alpha1K * SECONDS[i,j]

}

}

# Model for Bull Trout (BLTR): the 'subordinate' sp.

# Priors for intercepts and coefficients

mean.lambdaL ~ dunif(0, 55)

beta0L <- log(mean.lambdaL)

beta2L ~ dnorm(0, 0.1)

beta7L ~ dnorm(0, 0.1)

alpha0L <- logit(mean.pL)

mean.pL ~ dunif(0,1)

alpha1L ~ dnorm(0, 0.1)

# These are the 'interaction coefficients' !

gamma0 ~ dnorm(0, 0.1)

gamma2 ~ dnorm(0, 0.1)

gamma9 ~ dnorm(0, 0.1)

tauL ~ dgamma(0.1,0.1) # Excess-Poisson variation (precision)

sigmaL <- sqrt(1 / tauL)

```

```

# Likelihood for BLTR ('subordinate')

# Ecological model

for(i in 1:nsites){

  for(s in 1:nstream){

    NL[i,s] ~ dpois(lambdaL[i,s])

    etaL[i,s] ~ dnorm(0, tauL)

    log(lambdaL[i,s]) <- beta0L + beta2L * water_temp[i] + beta7L * lwd[i] +
      gamma0 * NK[i,s] + gamma2 * water_temp[i] * NK[i,s] + gamma9 * rip_area[i] * NK[i,s] +
      etaL[i,s]

  }

}

# Observation model

for (j in 1:nreps){

  CL[i,j] ~ dbin(pL[i,j], NL[i,1])

  logit(pL[i,j]) <- alpha0L + alpha1L * SECONDS[i,j]

}

} #j

} #i

}

")

# Initial values

Nst <- rep(20, nsites)

```

```

inits <- function() list(NK = Nst, NL = Nst)

# Parameters monitored

params <- c('mean.lambdaK', 'beta1K', 'beta6K', 'beta8K', 'mean.pK', 'alpha1K',
          'mean.lambdaL', 'beta2L', 'beta7L', 'mean.pL', 'alpha1L',
          'gamma0', 'gamma2', 'gamma9',
          'sigmaK', 'sigmaL')

# MCMC settings - actual

na <- 5000 ; nc <- 3 ; ni <- 300000 ; nb <- 110000 ; nt <- 200

#MCMC settings for testing - 3 mins

#na <- 500 ; nc <- 3 ; ni <- 3000 ; nb <- 1000 ; nt <- 2

# Call JAGS

out4 <- jags(abun.bltr.bktr, inits=NULL, params, "Nmix4.txt", n.adapt = na,
              n.chains = nc, n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)

# ~~~~~ Assess convergence ~~~~~ #

### visually from traceplots

traceplot(out4)

###Quantitatively using the R-hat statistic

out4 #All r-hat <1.1

#Convergence is good

```

