Fragmentation of habitat affects communities and movement of nekton in salt marsh tidal creeks

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Supplement. Code modified from Kéry (2010) for fitting random-intercept binomially distributed generalized linear mixed models (GLMMs) (logit links) via Bayesian inference to data on movement of adult *Fundulus heteroclitus* past road and reference crossings in North Carolina tidal creeks. GLMMs were run through *R* software by calling *JAGS* software. Similar code was used for additional models fitted to other combinations of covariates (see Table 3).

```
model {

###### Priors
for (i in 1:n.creeks) {
    alpha[i] ~ dnorm (mu.int, tau.int)   #prior for population random intercepts
    }

    mu.int ~ dnorm (0,0.000001)   #hyperprior for grand mean random intercepts
    sigma.int ~ dunif (0, 100)        #  hyperprior for standard deviation of random intercepts
    tau.int <- 1 / (sigma.int*sigma.int)   #calculated precision for random intercepts

    beta1 ~ dnorm (0,0.000001)
    beta2 ~ dnorm (0,0.000001)
    beta3 ~ dnorm (0,0.000001)
    beta4 ~ dnorm (0,0.000001)

###### likelihood
for (i in 1:n.obs) {
  C[i] ~ dbin(p[i], N[i])
    logit(p[i]) <-  alpha[CreekCode[i]] + beta1*PercentMarsh[i] + beta2*CurrentVelocity[i]
                    + beta3*CurrentVelocitySquared[i]
                    + beta4*PercentMarsh[i]*CurrentVelocitySquared[i]

###### Posterior predictive check using a chi-square discrepancy measure
ExpC[i] <- N[i] * p[i]
E[i] <- pow((C[i]-ExpC[i]),2) / (ExpC[i] + 0.5)
C.new[i]~dbin(p[i], N[i])   #Create replicate data set
E.new[i] <- pow((C.new[i]-ExpC[i]),2) / (ExpC[i] + 0.5)

}

fit <- sum(E[])   #sum of squared residuals for actual data set
fit.new <- sum(E.new[])   #sum of squared residuals for new data set
test <- step(fit.new-fit)   #Bayesian probability value

} #end model
```