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).

```r
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
```