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# Manuscript: Spatiotemporal patterns of urban mosquitoes are modulated by
socioeconomic status and environmental traits in the United States
# Date: 08-08-2022
# Script: Bayesian spatial regression model to reproduce table 2 results for
larvae and pupae


#=====load libraries==================
library(spBayes)
library(knitr)
library(dplyr)
library(kableExtra)

#=====import data=====================
# Example import larvae dataset in csv format
baltimore = read.csv("tlarvae.csv", stringsAsFactors = FALSE, na.strings =
"NA")


#=====Longitude and Latitude============
baltimore$long=jitter(baltimore$long)
baltimore$lat=jitter(baltimore$lat)
coords = cbind(baltimore$long,baltimore$lat)


#=====Gaussian process gradient model====
form = as.formula(cii~ndvi*mhi*ab)
gaussNS <- glm(form, data = baltimore, family="gaussian")
beta.starting <- coefficients( gaussNS )    # to initialize spBayes
beta.tuning   <- t(chol(vcov( gaussNS )))   # to start proposals
betaNS        <- matrix(beta.starting)     # non-spatial estimates
AICNS         <- summary(gaussNS)$aic       # non-spatial AIC

# arguments for spatial generalized linear model
n.batch      <- 10
batch.length <- 1500
n.samples <- n.batch*batch.length

# model parameters
library(truncnorm)
priors <-  list("beta.Flat", "phi.Unif" = c(.05, 4), "sigma.sq.IG" = c(50,
20))
betaS  <- rnorm(length(betaNS),betaNS,abs(betaNS)*.1)
phiS   <- dtruncnorm(1,0.1,2,0.05,1)
sigS   <- dtruncnorm(1,0,3,3,1)

# fit spatial model
out <- spGLM(form, data = baltimore, family="poisson", coords=coords,
             starting=list("beta"=betaS, "phi"= phiS,"sigma.sq"= sigS,
"w"=0),
             tuning=list("beta"=beta.tuning, "phi"=0.4,"sigma.sq"=1,
"w"=0.1),
             priors=priors,
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              amcmc=list("n.batch"=n.batch,"batch.length"=batch.length,
                         "accept.rate"=0.43),
              cov.model="exponential", verbose=T, n.report=500)

out$DIC <- unlist( spDiag(out, verbose=F) )['DIC4']

# plotting variable and parameters
burn.in   <- 0.8*n.samples
sub.samps <- burn.in:n.samples
out$p.samples[,"phi"] <- 3/out$p.samples[,"phi"]
par(mar=c(1,1,1,1))
plot(out$p.beta.theta.samples)

coeff <- t(apply( out$p.beta.theta.samples, 2, quantile, c(.5, .025, .975) ))
se    <- apply( out$p.beta.theta.samples, 2, sd )
coeff <- cbind( coeff[,1], se, coeff[,2:3])


# Table of estimates
coeff %>%
  kbl() %>%
  kable_styling(bootstrap_options = c("striped", "hover", "condensed",
"responsive"))
```