Homework 2

Stat 597a: Spatial Models

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Due September 28, 2017

Problem 1:

First, read over this section. There is one key change we will make compared to Wikle's analysis, which is that I have first transformed the coordinates from longitude and latitude to UTM coordinates. This is because the geoRglm package only uses Euclidean distances. Using it with longitude and latitude will not give accurate distances between the points. Another way we could do it, if we were coding this from scratch, would be to keep longitude and latitude, but work with great circle distances when calculating the distance matrix.

Given this new coordinate system, the prior for the range parameter ϕ that we'll use is a discrete uniform distribution from 500 to 300,000, in increments of 500. The reasons for the discrete prior are again due to the constraints of the geoRglm package.

With this change, write down the three layers of the hierarchical model as defined on slide 8 of Lecture 8. That is, what distributions make up the data model, process model, and prior model?

From the lecture, we know there are going to be 3 components to our model: the data model, the process model, and the parameter model. That is, $f(\eta, \theta|\mathbf{Y}) \propto f(\mathbf{Y}, \eta, \theta) \times f(\eta|\theta) \times \pi(\theta)$.

According to the textbook, Hierarchical Model with Spatial Data, we will model this data according to the genearlized linear spatial modeling framework.

So, the data model is as follows:

$$f(Y(s_i)|\lambda(s_i), \phi) \sim \text{ independent } Poisson(\lambda(s_i)), i = 1, ..., m$$

where we employ a Gaussian spatial process model to describe the spatial variation in $\lambda(s_i)$ and use the canonical log-link function. So, $log(\lambda(s_i)) = \beta + \eta(s_i)$ where $\eta(s_i)$ is a Guassian process with mean 0, variance σ_n^2 and correlation function $r(s_i, s_j; \phi)$. Specifically, $r_\eta(s_i, s_j; \phi) = exp(-||s_i - s_j||/\phi)$. We were told in the problem statement that ϕ followes a discrete uniform distribution from 500 to 300,000, in increments of 500. Therefore, the process model is as follows:

$$log(\lambda(s_i)) = \beta + \eta(s_i) \text{ where}$$

$$f(\eta(s_i)|\phi) \sim \text{GP}(mean = 0, \text{variance} = \sigma_n^2, \text{correlation function} = r_\eta(s_i, s_j; \phi) = exp(-||s_i - s_j||/\phi)$$

and the parameter model is as follows:

$$\pi(\phi) \sim Uniform(500, 300{,}000) \text{ with breaks as described above.}$$

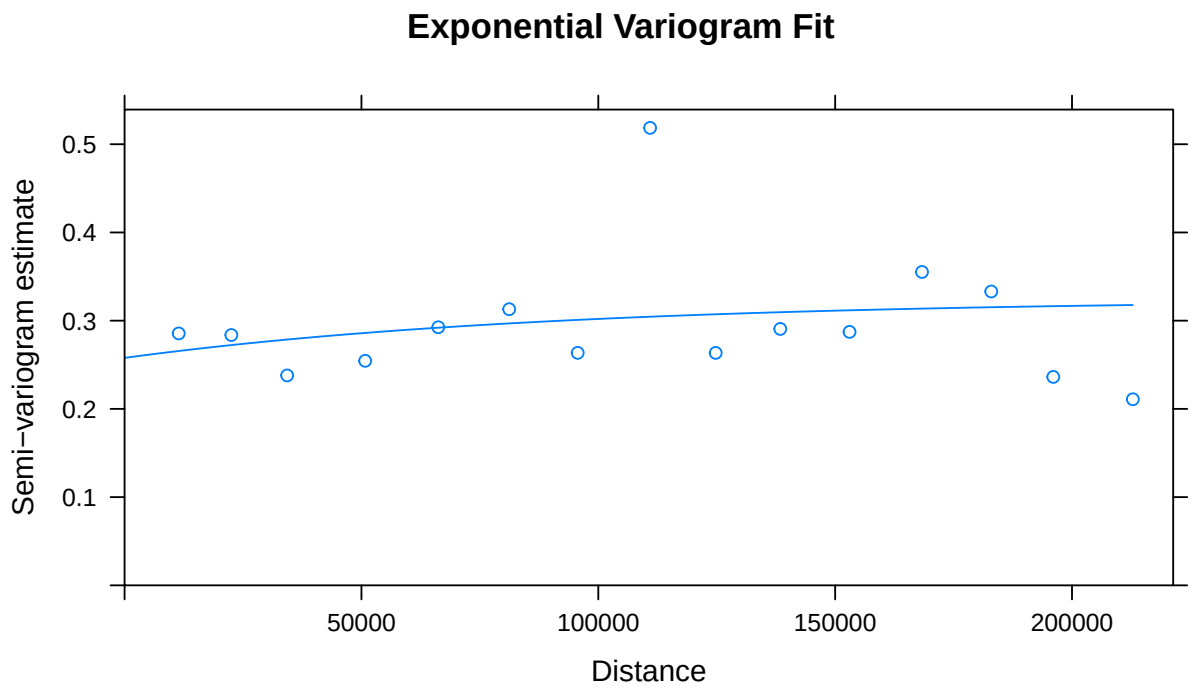
Also, the parameter model for β is flat, so $\pi(\beta) \propto 1$ and σ^2 has a uniform prior, according to the book.

Problem 2

Transform the original observations using $Z_i = log(Y_i)$ and use classical geostatistical techniques to get preliminary estimates of σ^2 and ϕ by treating the Z_i as normally distributed given η (i.e. fit a model with a nugget, and extract just the estimates for σ^2 and ϕ).

We have our estimates of σ^2 as 0.06637062 and our estimate of ϕ to be 91436.2.

```
plot(vg, fitvg.3, xlab = "Distance", ylab = "Semi-variogram estimate", layout=c(2,1), main = "Exponenti
```



Above, we have also included the fitted exponential variogram, which seems like a pretty good fit of our data. Therefore, we will proceed into the MCMC.

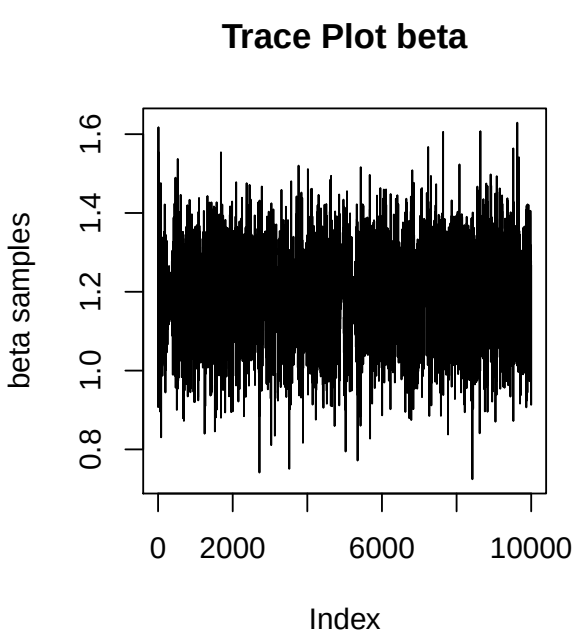
Problem 3

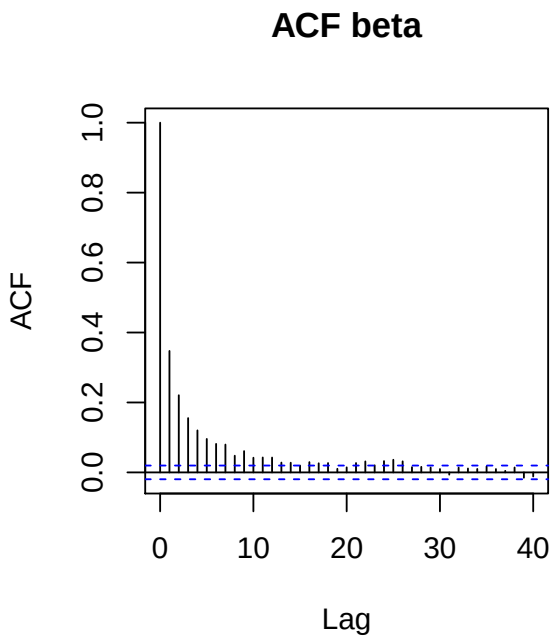
Use model.glm.control, prior.glm.control, mcmc.control, and pois.krige.bayes to run an initial MCMC chain, fixing ϕ at your estimate from (1). The goal here is to experiment with changing S.scale to achieve an acceptance rate of about 60% for the process samples, which is optimal for the algorithm pois.krige.bayes is using to sample the vector of process values.

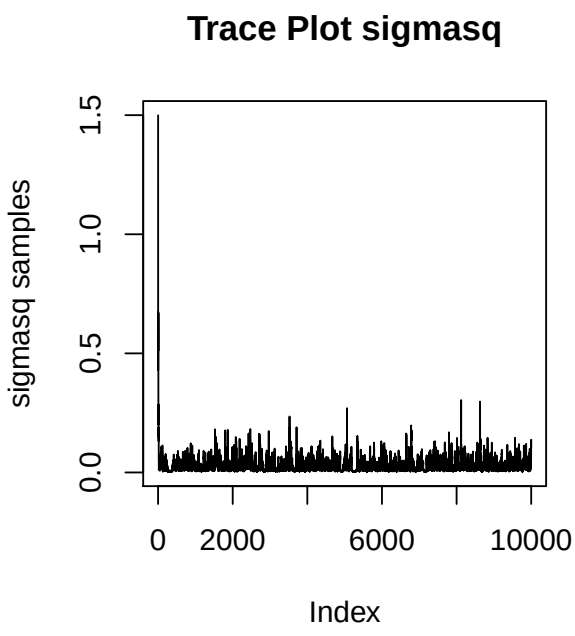
The choice of niter = 100000 and thin = 10 is just to keep things manageable at this stage. We will eventually run a much longer chain. I suggest you always keep burn.in = 0 and then discard the initial samples yourself after seeing the results.

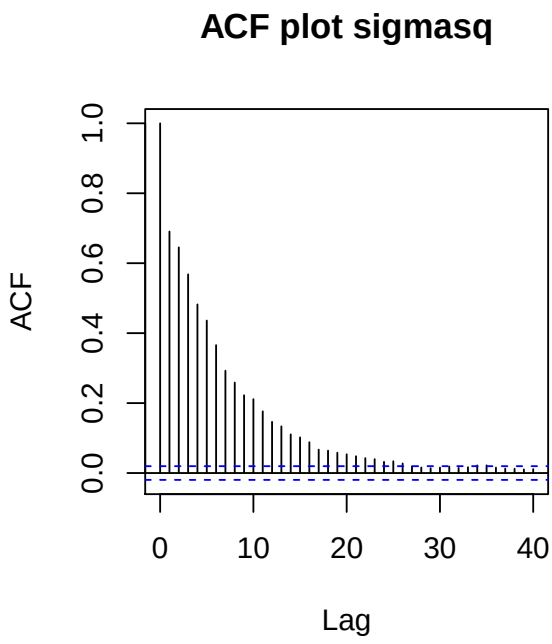
After I ran the MCMC, I include ACF and trace plots below. It was not too difficult to achieve an acceptance rate of 60% in this case, although this was exceedingly difficult to do later on. I also note that in the ACF and trace plots below, there is not too much autocorrelation. There is a bit more autocorrelation in the trace and ACF plots for σ^2. For this example, I achieved an acceptance rate that is also included below.

```
## iter.numb  Acc.rate
##  1.00e+05  5.75e-01
```









Problem 4

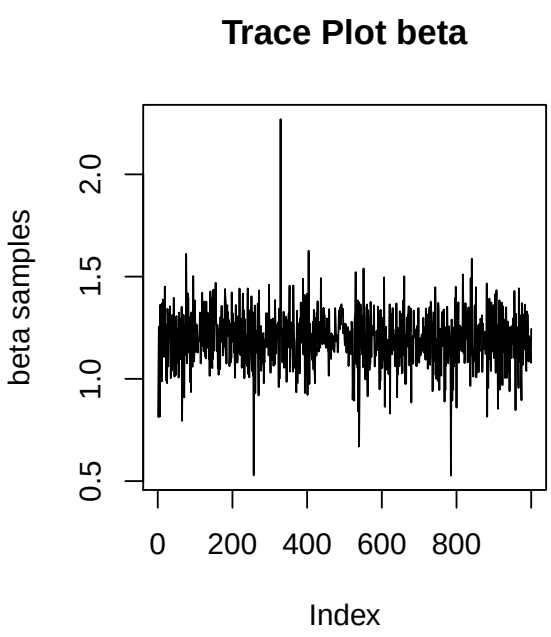
Now duplicate and modify the code from (3) to include sampling phi. Experiment with changing S.scale and phi.scale to get acceptance rates of about 60% and 25%, respectively. (Note:

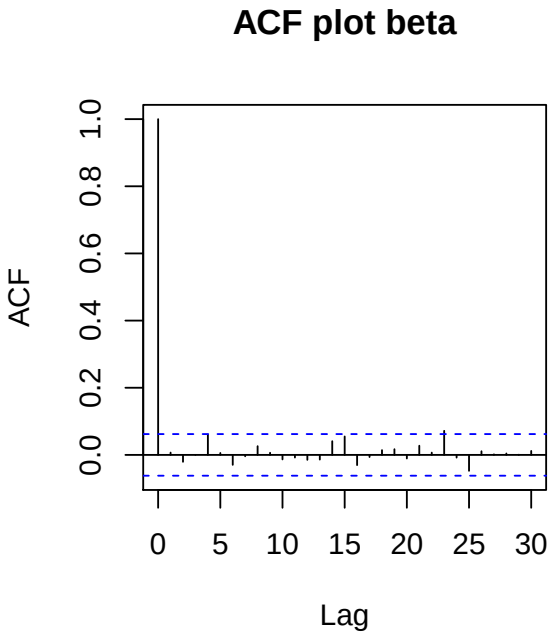
I found the acceptance rates fluctuated over the course of my chain. Just aim to get in the right ballpark.) I suggest you also take thin = 100 and n.iter = 100000 here. Make trace plots and ACF plots of the parameters $\sigma^2, \phi,$ and β. You will likely see a LOT of autocorrelation.

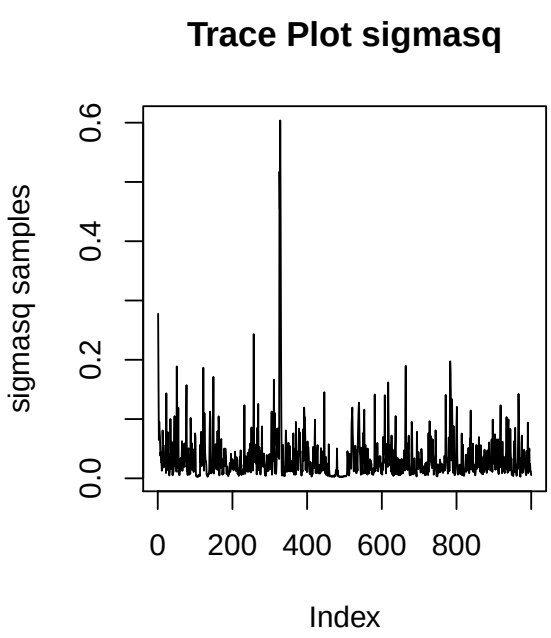
As in Problem 3, I have run the MCMC code and I include the ACF and trace plots below. I also include the acceptance rates below. For this iteration, I had a very difficult time trying to find the values of S.scale and phi.scale that would lead anywhere close to the "acceptable" acceptance rates.

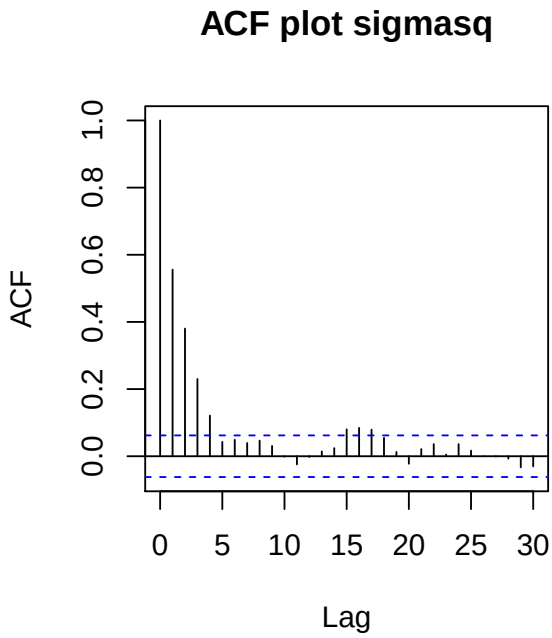
When I look at the acf and trace plots again for this example, I notice that there is quite a bit of autocorrelation, as we expected to see. This is especially relevant for the plots of $sigma^2$ and phi, with ϕ having the most autocorrelation.

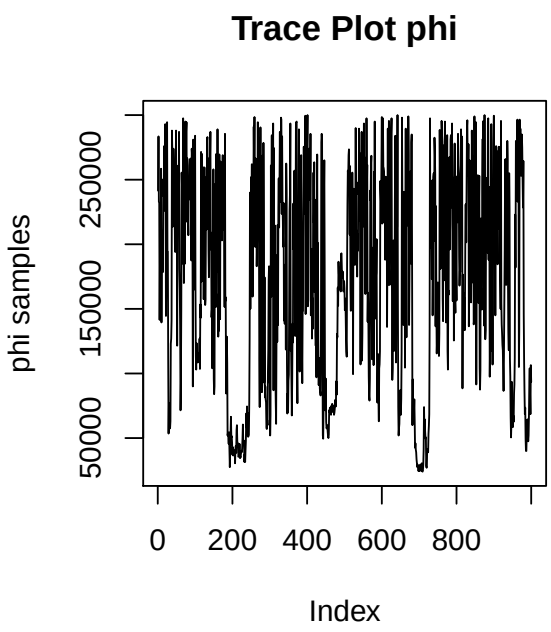
```
##     iter.numb     Acc.rate Acc.rate.phi
##      1.00e+05     6.74e-01     1.91e-01
```

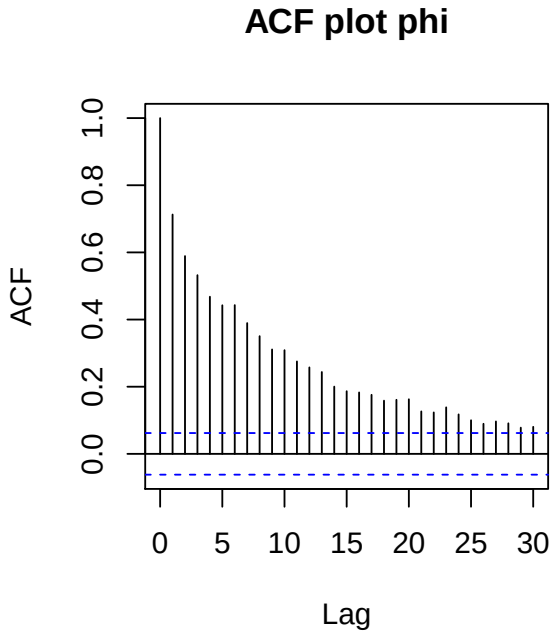












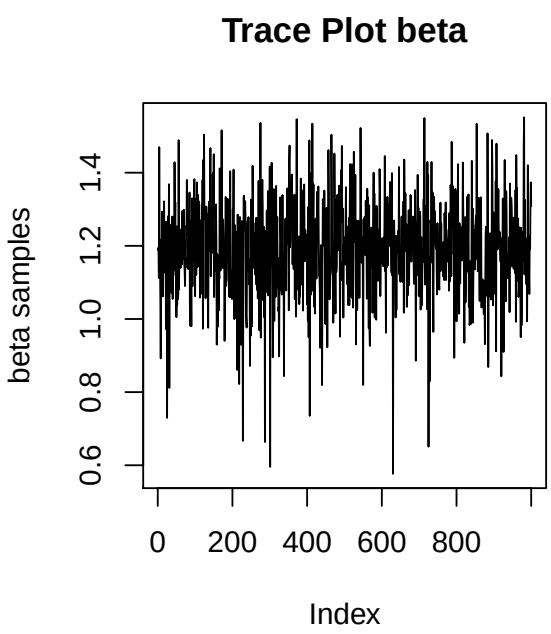
Problem 5

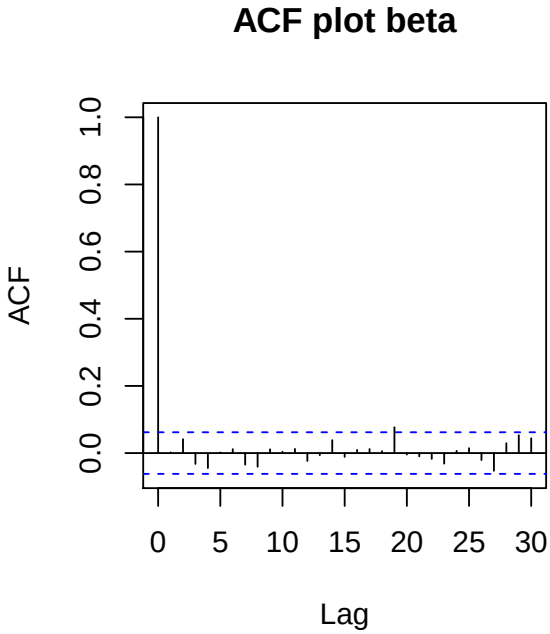
There is not much beyond changing S.scale and phi.scale that we can do to reduce the autocorrelation. So we will run a long chain and subsample it. Run the same code as in part (4), increasing to thin = 1e4 and n.iter = 1e7. Now do the following with your sampled parameters.

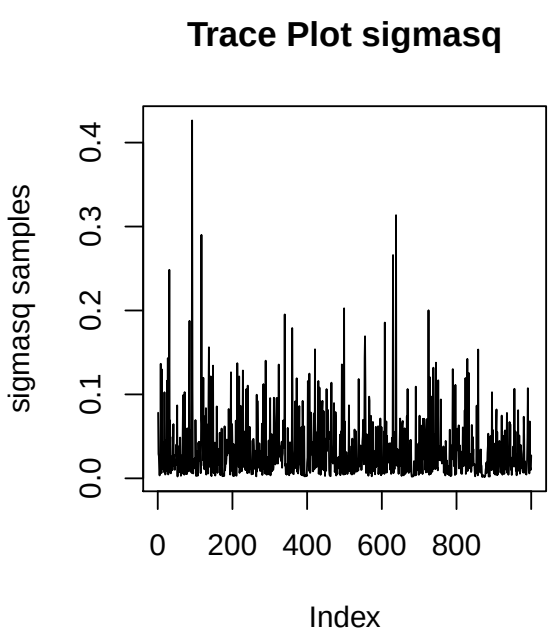
- **Make trace plots and ACF plots. Choose a burn-in to discard and make them again.**
- **Calculate the effective sample size you have for each parameter. If they are not at least 100 for each parameter, go back and run a longer chain.**
- **Plot the marginal posterior distributions for each parameter using histograms and/or kernel density estimators.**

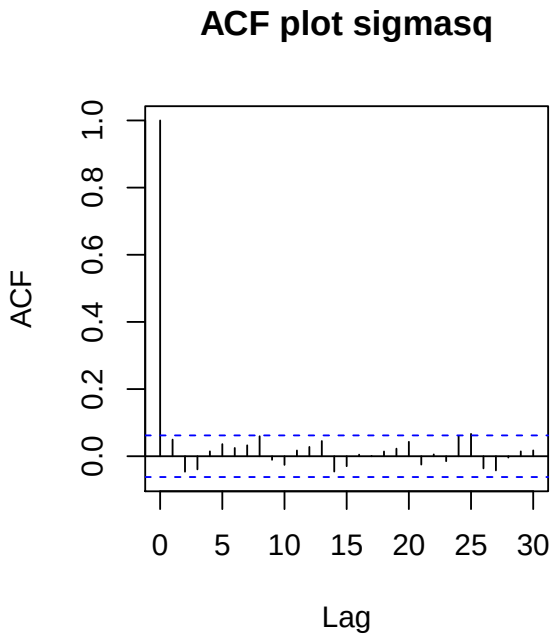
Once again, I include my acceptance rate below as well as my trace and ACF plots. For this example, I chose my burnin value to be 50,000 I notice that the plots vary quite a bit less after I get rid of the burnin.

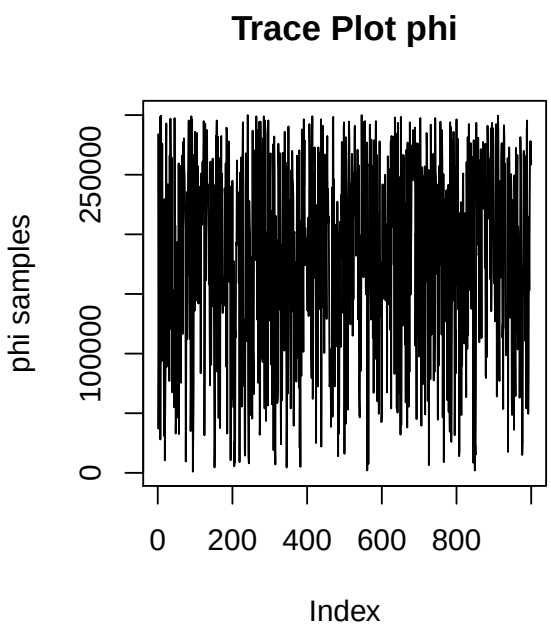
```
##    iter.numb     Acc.rate Acc.rate.phi
##     1.00e+07     7.37e-01     3.71e-01
```

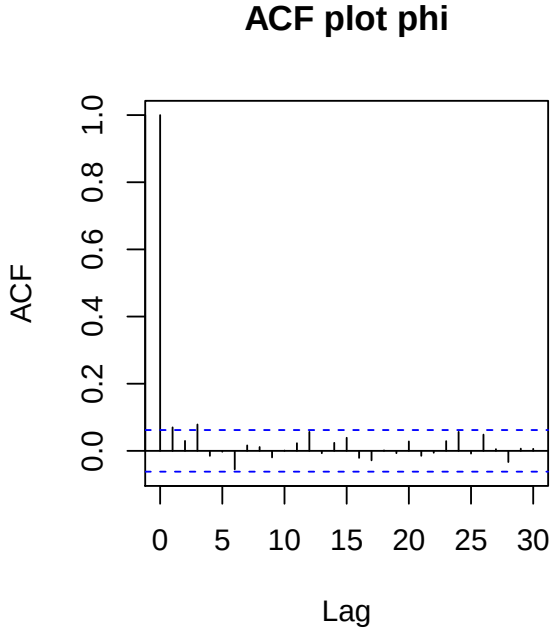




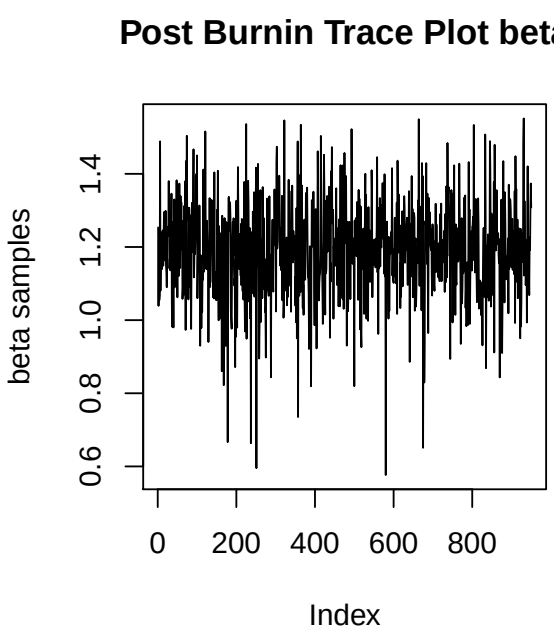


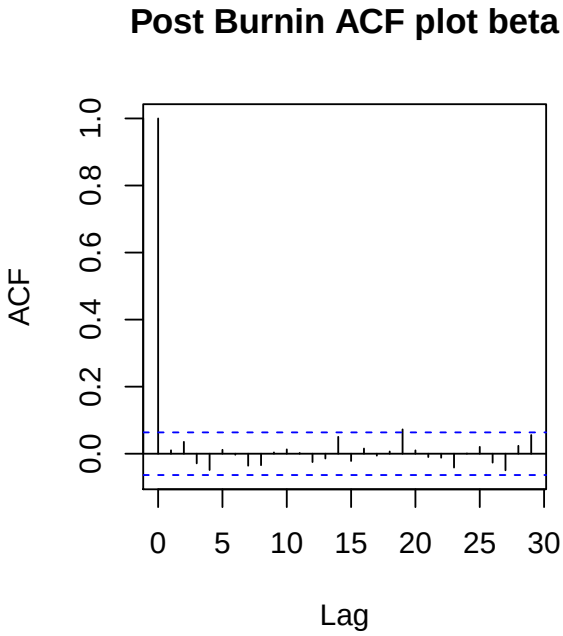


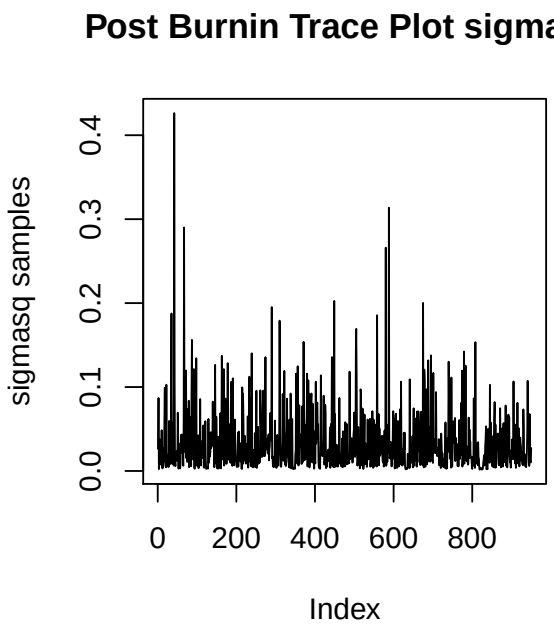


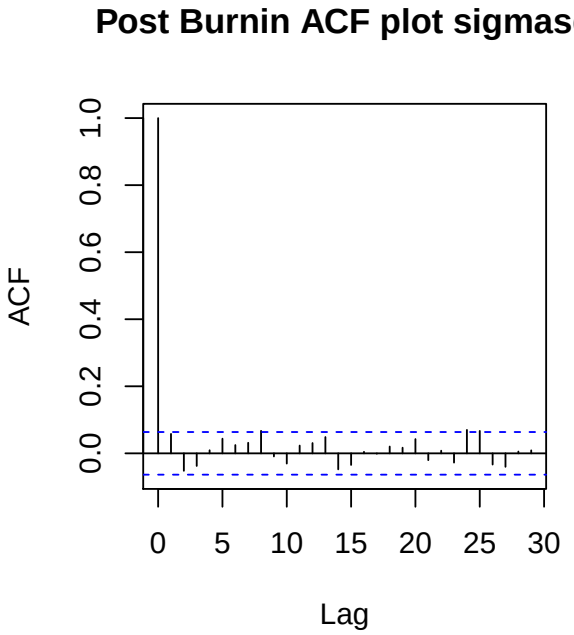


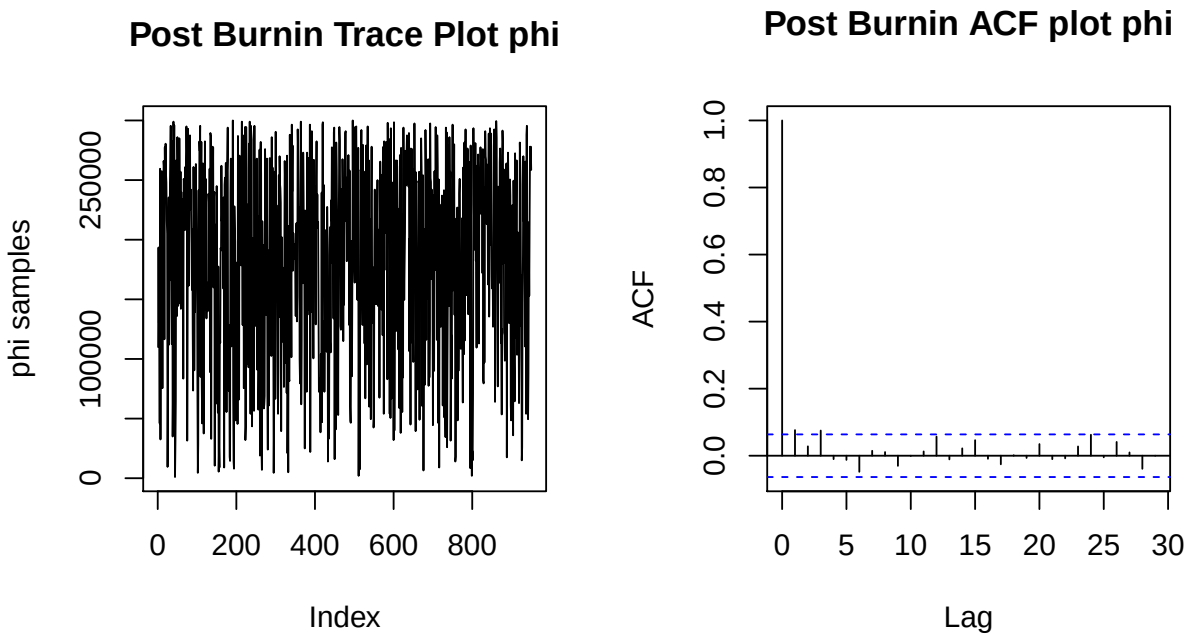
I remove the burnin and re-create the plots.


Post Burnin Trace Plot beta
beta samples
0.6
0.8
1.0
1.2
1.4
0
200
400
600
800
Index


Post Burnin ACF plot beta
ACF
0.0
0.2
0.4
0.6
0.8
1.0
0
5
10
15
20
25
30
Lag


Post Burnin Trace Plot sigmasq
sigmasq samples
0.0
0.1
0.2
0.3
0.4
0
200
400
600
800
Index

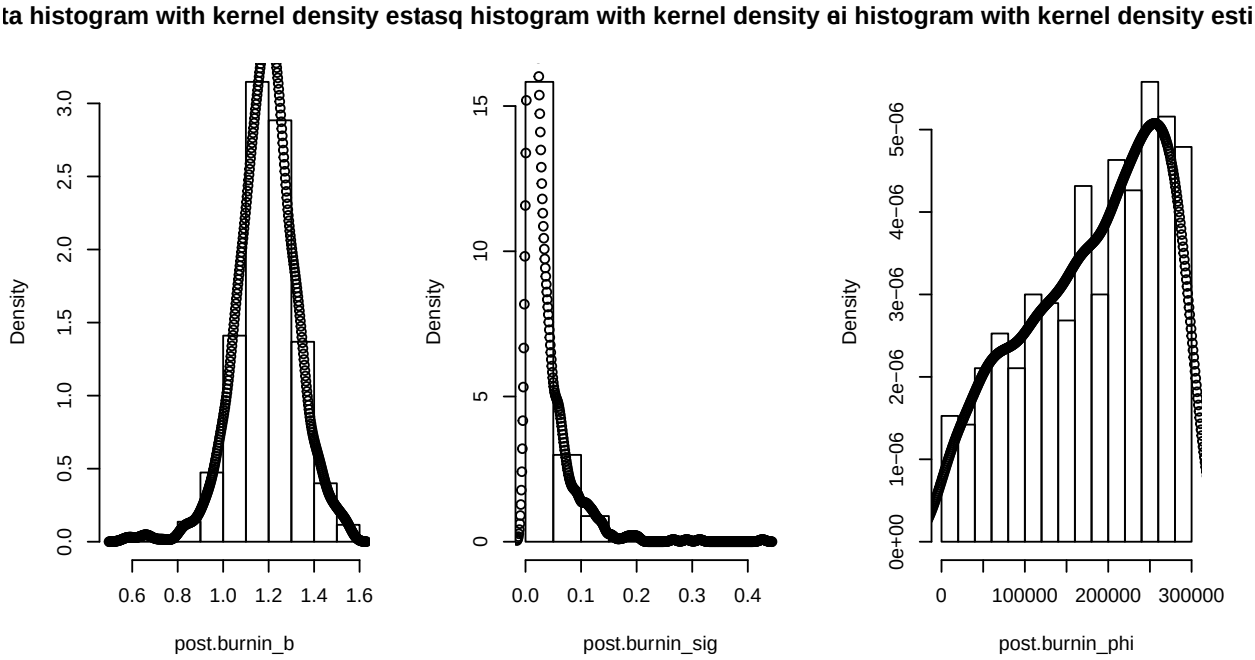

Post Burnin ACF plot sigmasq
ACF
0.0
0.2
0.4
0.6
0.8
1.0
0
5
10
15
20
25
30
Lag



My effective sample sizes for each parameter are included below, and are all above 100.

I have also included plots for the marginal posterior distributions for each parameter, which includes a histogram and the kernel density esimtators.

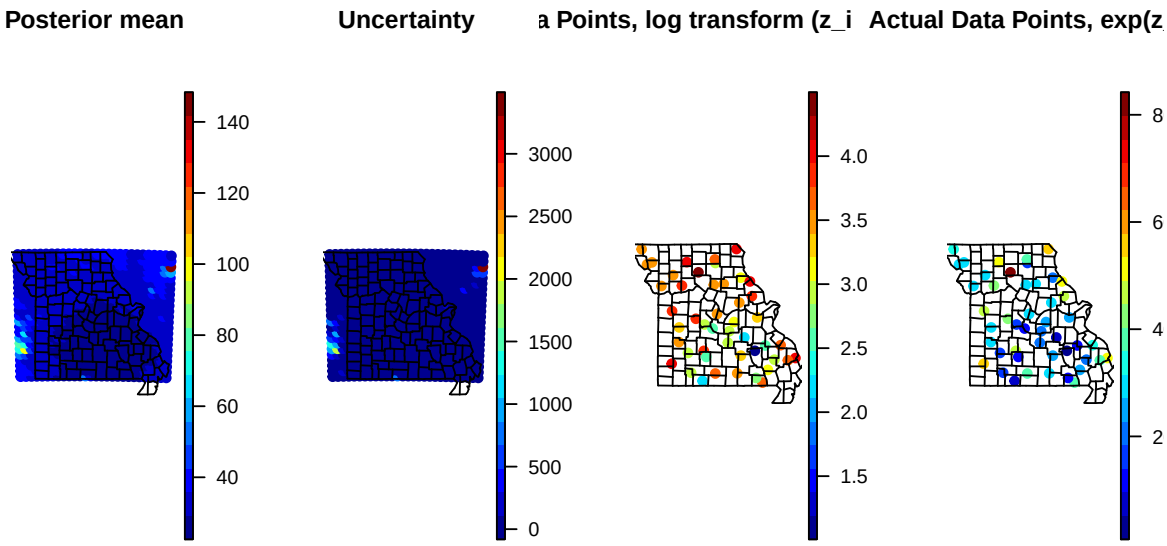
```
## [1] "Sigmasq effective sample size is  725.140499701841"
## [1] "Phi effective sample size is  661.791408132617"
## [1] "Beta effective sample size is  1221.49959530374"
```



Problem 6

Do one final run of the chain, the same as in (5), but this time specifying the burn-in value you chose in (5) and also modifying the code to include prediction at the locations in dove.grid. Create two color or grayscale plots, showing the posterior mean and standard deviation for the underlying mean surface (exp η) at each location in dove.grid.

Once again, I have made a final run of the chain, as in (5), but I specified the burnin value that I chose in (5) in the function. I also included my two plots with the posterior mean and standard deviation of the underlying mean surface below. I also included a plot of the original observations. I see that the mean surface corresponds pretty well with this graph and that the standard deviation is highest where there aren't many observations. It just so happens that the lowest standard deviations (where there are more observations) occur where there are also low dove counts, in the middle of the state.




```
##
#Problem 2
##

#load the data
load("C:/Users/ckell/OneDrive/Penn State/2017-2018/597/spatial_statistics_597/Homework 2/data/dove.RData

#transform the original observations
dove$counts <- log(dove$counts)

#use classical geostatistical techniques to get preliminary estimates of $\sigma^2$ and $\phi$

#Fitting the preliminary linear model
linmod <- lm(counts~coords.x1+coords.x2, data=dove)
#linmod <- lm(z~1, data=dove)
summary(linmod)
#storing the residuals so I can plot them
dove$resid <- linmod$resid

##  Nonparametric estimation of the variogram
vg <- variogram(resid ~ 1, data = dove)#, width=75)
#print(vg)
plot(vg, xlab = "Distance", ylab = "Nonparametric Semi-variogram estimate", width=5, main = "Exponentia

##  Fitting the variogram parametrically
# fitvg <- fit.variogram(vg, vgm(1, "Exp", range=47, nugget=1), fit.method = 2)
# print(fitvg)
# fitvg.2 <- fit.variogram(vg, vgm(1, "Exp", 47, 0.05))
# print(fitvg.2)
fitvg.3 <- fit.variogram(vg, vgm("Exp"))
print(fitvg.3)
```

```r
s2.hat <- fitvg.3$psill[2]
phi.hat <- fitvg.3$range[2]
tau2.hat <- fitvg.3$psill[1]
```

```r
##
#Problem 3
##

dove_mcmc <- as.geodata(dove)

#run an initial MCMC chain, fixing phi at your estimate from
#achieve an acceptance rate of about 60% for the process samples
sim.model <- model.glm.control(cov.model= "exponential")#, kappa = NA, not required for exponential
#0.017
set.seed(132)
sim.prior <- prior.glm.control(phi.prior = "fixed", phi = phi.hat)
sim.mcmc <- mcmc.control(S.scale = 0.0098, Htrunc = "default", S.start = "random",
                         burn.in = 0, thin = 10, n.iter = 100000)
sim.posterior <- pois.krige.bayes(dove_mcmc, model=sim.model, prior=sim.prior,
                                  mcmc.input=sim.mcmc)#, keep.mcmc.sim=TRUE)

nrow(sim.posterior$posterior$acc.rate)
sim.posterior$posterior$acc.rate[100,]
```

```r
##
#Problem 3 images
##
sim.posterior$posterior$acc.rate[100,]
par(mfrow=c(1,2))

#ACF and trace plots
plot(sim.posterior$posterior$beta$sample, type = "l", ylab = "beta samples", main = "Trace Plot beta")
acf(sim.posterior$posterior$beta$sample, main = "ACF beta")

plot(sim.posterior$posterior$sigmasq$sample, type = "l", ylab = "sigmasq samples", main = "Trace Plot si
acf(sim.posterior$posterior$sigmasq$sample, main = "ACF plot sigmasq")
```

```r
##
#Problem 4
##

#run an initial MCMC chain, fixing phi at your estimate from
sim.model <- model.glm.control(cov.model= "exponential")#, kappa = NA, not required for exponetnial
sim.prior <- prior.glm.control(phi.prior = "uniform", phi.discrete = seq(500,300000,500))
# Experiment with changing S.scale and phi.scale to get acceptance rates of about 60%
# and 25%, respectively.
set.seed(134)
sim.mcmc <- mcmc.control(S.scale = 0.008, phi.scale=1000e6, Htrunc = "default",
                         S.start = "random",
                         burn.in = 0, thin = 100, n.iter = 100000)
sim.posterior <- pois.krige.bayes(dove_mcmc, model=sim.model, prior=sim.prior,
                                  mcmc.input=sim.mcmc)

mean(sim.posterior$posterior$acc.rate[,2])
```

```r
mean(sim.posterior$posterior$acc.rate[,3])

nrow(sim.posterior$posterior$acc.rate)
sim.posterior$posterior$acc.rate[100,]
```

```r
##
#Problem 4 images
##

sim.posterior$posterior$acc.rate[100,]

par(mfrow=c(1,2))
#acf and trace plots for beta
plot(sim.posterior$posterior$beta$sample, ylab = "beta samples", type = "l", main = "Trace Plot beta")
acf(sim.posterior$posterior$beta$sample, main = "ACF plot beta")

#acf and trace plots for sigmasq
plot(sim.posterior$posterior$sigmasq$sample, ylab = "sigmasq samples", type = "l", main = "Trace Plot si
acf(sim.posterior$posterior$sigmasq$sample, main = "ACF plot sigmasq")

#acf and trace plots for phi
plot(sim.posterior$posterior$phi$sample, ylab = "phi samples", type = "l", main = "Trace Plot phi")
acf(sim.posterior$posterior$phi$sample, main = "ACF plot phi")
```

```r
##
#Problem 5
##

#Run the same code as in part (4), increasing to thin = 1e4 and n.iter = 1e7.
#run an initial MCMC chain, fixing phi at your estimate from
sim.model <- model.glm.control(cov.model= "exponential")#, kappa = NA, not required for exponetnial
sim.prior <- prior.glm.control(phi.prior = "uniform", phi.discrete = seq(500,300000,500))
# Experiment with changing S.scale and phi.scale to get acceptance rates of about 60%
# and 25%, respectively.
# S.scale 0.007
set.seed(134) #80%, 26
sim.mcmc <- mcmc.control(S.scale = 0.008, phi.scale=1000e6, Htrunc = "default",
                         S.start = "random",
                         burn.in = 0, thin = 1e4, n.iter = 1e7)
sim.posterior <- pois.krige.bayes(dove_mcmc, model=sim.model, prior=sim.prior,
                                  mcmc.input=sim.mcmc)

n <- nrow(sim.posterior$posterior$acc.rate)
sim.posterior$posterior$acc.rate[n,]
```

```r
##
#Problem 5 images
##

sim.posterior$posterior$acc.rate[n,]

par(mfrow=c(1,2))
#acf and trace plots for beta
plot(sim.posterior$posterior$beta$sample, ylab = "beta samples", type = "l", main = "Trace Plot beta")
```

```r
acf(sim.posterior$posterior$beta$sample, main = "ACF plot beta")

#acf and trace plots for sigmasq
plot(sim.posterior$posterior$sigmasq$sample, ylab = "sigmasq samples", type = "l", main = "Trace Plot si
acf(sim.posterior$posterior$sigmasq$sample, main = "ACF plot sigmasq")

#acf and trace plots for phi
plot(sim.posterior$posterior$phi$sample, ylab = "phi samples", type = "l", main = "Trace Plot phi")
acf(sim.posterior$posterior$phi$sample, main = "ACF plot phi")

#choose a burnin to discard and make them again
burnin <- 1:50
#length(sim.posterior$posterior$sigmasq$sample)
post.burnin_sig <- sim.posterior$posterior$sigmasq$sample[-c(burnin)]
post.burnin_b <- sim.posterior$posterior$beta$sample[-c(burnin)]
post.burnin_phi <- sim.posterior$posterior$phi$sample[-c(burnin)]
```

```r
par(mfrow=c(1,2))
#acf and trace plots for beta
plot(post.burnin_b, ylab = "beta samples", type = "l", main = "Post Burnin Trace Plot beta")
acf(post.burnin_b, main = "Post Burnin ACF plot beta")

#acf and trace plots for sigmasq
plot(post.burnin_sig, ylab = "sigmasq samples", type = "l", main = "Post Burnin Trace Plot sigmasq")
acf(post.burnin_sig, main = "Post Burnin ACF plot sigmasq")

#acf and trace plots for phi
plot(post.burnin_phi, ylab = "phi samples", type = "l", main = "Post Burnin Trace Plot phi")
acf(post.burnin_phi, main = "Post Burnin ACF plot phi")
```

```r
#calculate the effective sample size for each parameter
##if they are not all at least 100 for each parameter, go back and run a longer chain
print(paste("Sigmasq effective sample size is " ,ess(post.burnin_sig)))
print(paste("Phi effective sample size is " , ess(post.burnin_phi)))
print(paste("Beta effective sample size is ", ess(post.burnin_b)))

#plot the marginal and posterior distributions for each parameter using histograms and/or kernel densit
#par(mfrow = c(1,3))
#
par(mfrow=c(1,3))
hist(post.burnin_b,freq=F, main ="beta histogram with kernel density estimator")
points(density(post.burnin_b))
hist(post.burnin_sig, freq=F, main = "sigmasq histogram with kernel density estimator")
points(density(post.burnin_sig))
hist(post.burnin_phi,freq=F, main = "phi histogram with kernel density estimator")
points(density(post.burnin_phi))
```

```r
##
#Problem 6
##

#Do one final run of the chain, the same as in (5), but this time specifying the burn-in value you chos
sim.model <- model.glm.control(cov.model= "exponential")#, kappa = NA, not required for exponetnial
sim.prior <- prior.glm.control(phi.prior = "uniform", phi.discrete = seq(500,300000,500))
```

```
#S.scale = 0.5, 0.2, 0.7
# Experiment with changing S.scale and phi.scale to get acceptance rates of about 60%
# and 25%, respectively.
set.seed(130) #80%, 26
sim.mcmc <- mcmc.control(S.scale = 0.008, phi.scale=1000e6, Htrunc = "default",
                         S.start = "random",
                         burn.in = 50e3, thin = 1e4, n.iter =  1e7)
#keep MCMC sample
sim.posterior <- pois.krige.bayes(dove_mcmc, model=sim.model, prior=sim.prior,
                                  mcmc.input=sim.mcmc, locations=dove.grid, output =
                                  output.glm.control(keep.mcmc.sim=TRUE, sim.predict = TRUE))


pred_sim <- sim.posterior$predictive$simulations
#test2 <- sim.posterior$posterior$simulations

post_med <- sim.posterior$predictive$median
uncertainty <- sim.posterior$predictive$uncertainty

pred_sim <- exp(pred_sim)

post_mean <- apply(pred_sim, 1, mean)
post_sd <- apply(pred_sim, 1, sd)
```

```
##
#Problem 6 images
##
ploteqc <- function(spobj, z, breaks, ...){
  pal <- tim.colors(length(breaks)-1)
  fb <- classIntervals(z, n = length(pal),
                       style = "fixed", fixedBreaks = breaks)
  col <- findColours(fb, pal)
  plot(spobj, col = col, ...)
  image.plot(legend.only = TRUE, zlim = range(breaks), col = pal)
}


library(rgdal)
utms <- SpatialPoints(cbind(dove.grid$x, dove.grid$y),
                      proj4string=CRS("+proj=utm +zone=15"))
dove.longlat <- spTransform(utms, CRS("+proj=longlat"))
utms2 <- SpatialPoints(dove, proj4string=CRS("+proj=utm +zone=15"))
dove.longlat2 <- spTransform(utms2, CRS("+proj=longlat"))



par(mfrow=c(1,4))

ploteqc(dove.longlat, post_mean, seq(min(post_mean),max(post_mean),length=20), pch=19)
map("county", region = "missouri", add = TRUE)
title("Posterior mean")

ploteqc(dove.longlat, post_sd, seq(min(post_sd),max(post_sd),length=20), pch=19)
map("county", region = "missouri", add = TRUE)
```

```r
title("Uncertainty")
points(dove)

ploteqc(dove.longlat2, dove$counts, seq(min(dove$counts),max(dove$counts),length=20), pch=19)
map("county", region = "missouri", add = TRUE)
title("Actual Data Points, log transform (z_i= log(count_i))")

dove$counts <- exp(dove$counts)
ploteqc(dove.longlat2, dove$counts, seq(min(dove$counts),max(dove$counts),length=20), pch=19)
map("county", region = "missouri", add = TRUE)
title("Actual Data Points, exp(z_i)")




# plot(dove)
#
# range(post_med)
# breaks <- seq(8, 70, by = 0.01)
#
#
# ploteqc(dove.grid, post_med, breaks, pch = 19)
# map("county", region = "missouri", add = TRUE)
# title(main = "Posterior Median")
#
#
# range(uncertainty)
# breaks <- seq(2, 35, by = 0.01)
# ploteqc(dove.grid, uncertainty, breaks, pch = 19)
# #map("county", region = "missouri", add = TRUE)
# title(main = "Posterior Mean")
# points(dove)
```