Beta regression for the microbiome data

Chapter 4.3.3: Generalized linear models

This model regresses a measure of microbiome species richness onto features of the home from which the sample was taken. Let OTU_{ij} be the abundance of Operational Taxonomic Unit (OTU) j in sample i. The response variable is the proportion of the abundance attributed to the most abundant OTU,

$$Y_i = \frac{\max\{OTU_{i1}, \ldots, OTU_{im}\}}{\sum_j OTU_{ij}} \in (0,1).$$

There are eight covariates (X_{ij}):

1. Longitude
2. Latitude
3. Annual average temperature
4. Annual average precipitation
5. Net primary production
6. Elevation
7. The binary indicator of whether it is a single-family home
8. Number of bedrooms

The regression model is

$$Y_i \sim \text{Beta}(rq_i, r(1-q_i)) \text{ where } \text{logit}(q_i) = \sum_{l=1}^{p} X_{ij}\beta_j,$$

so that the expected value of Y_i is $q_i \in [0,1]$ and the concentration around q_i is determined by $r > 0$. The regression coefficients have uninformative priors $\beta_j \sim \text{Normal}(0, 10^2)$ and the concentration parameter has prior $r \sim \text{Gamma}(0.1, 0.1)$.

Load the data

```
set.seed(0820)

load("S:\\Documents\\My Papers\\BayesBook\\Data\\Microbiome\\homes.RData")
ls()
```

```
## [1] "homes" "OTU"
```

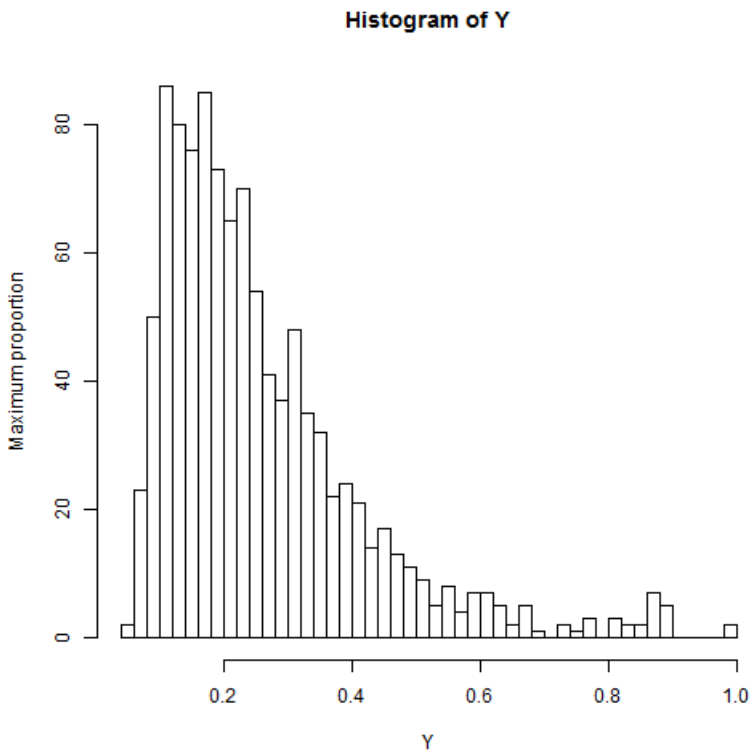
```
city     <- homes[,2]
state    <- homes[,3]
lat      <- homes[,4]
long     <- homes[,5]
temp     <- homes[,6]
precip   <- homes[,7]
NPP      <- homes[,8]
elev     <- homes[,9]
house    <- ifelse(homes[,10]=="One-family house detached from any other house",1,0)
bedrooms <- as.numeric(homes[,11])
```

```
## Warning: NAs introduced by coercion
```

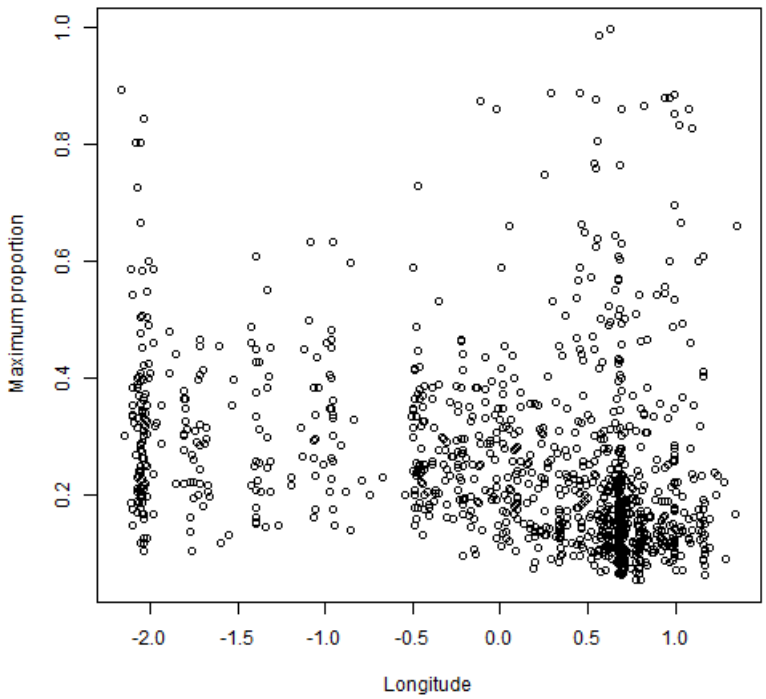
```
OTU      <- as.matrix(OTU)
Y        <- apply(OTU,1,max)/rowSums(OTU)
X        <- cbind(long,lat,temp,precip,NPP,elev,house,bedrooms)
names    <- c("Intercept","Longitude","Latitude",
              "Temperature","Precipitation","NPP",
              "Elevation","Single-family home",
              "Number of bedrooms")

# Remove observations with missing values
junk        <- is.na(rowSums(X))
Y           <- Y[!junk]
X           <- X[!junk,]
city        <- city[!junk]
state       <- state[!junk]

# Standardize the covariates
X           <- as.matrix(scale(X))

X           <- cbind(1,X) # add the intercept
colnames(X) <- names
n           <- length(Y)
p           <- ncol(X)
```

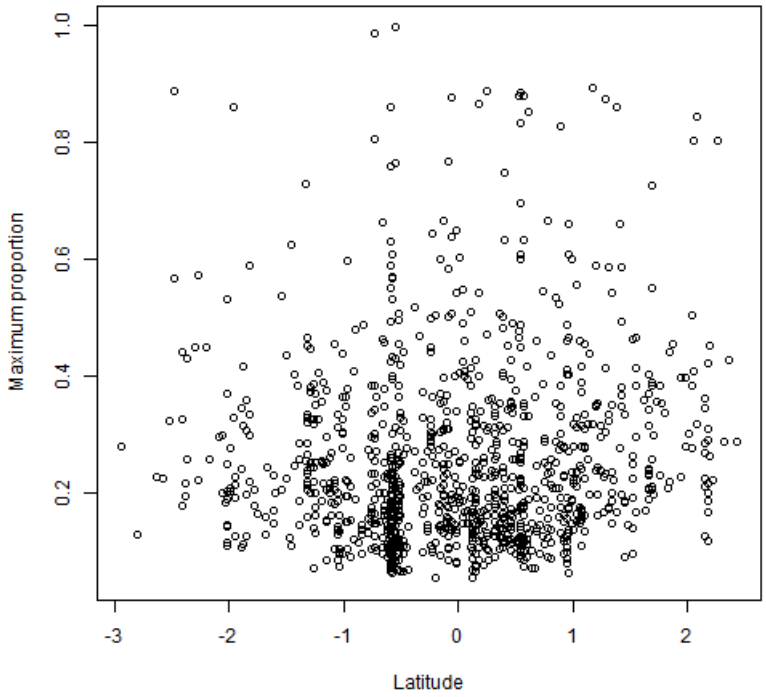
Plot the data

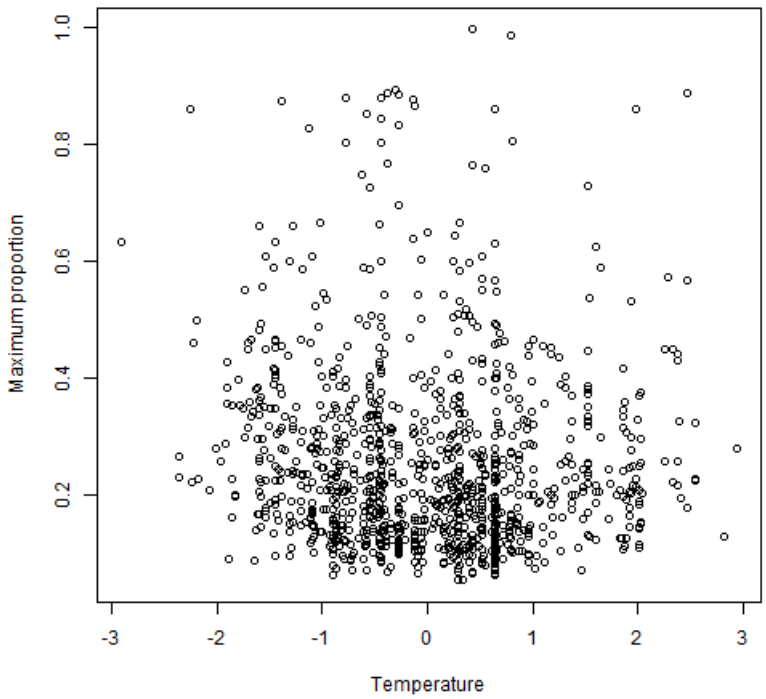
```
hist(Y,breaks=50,ylab="Maximum proportion")
```

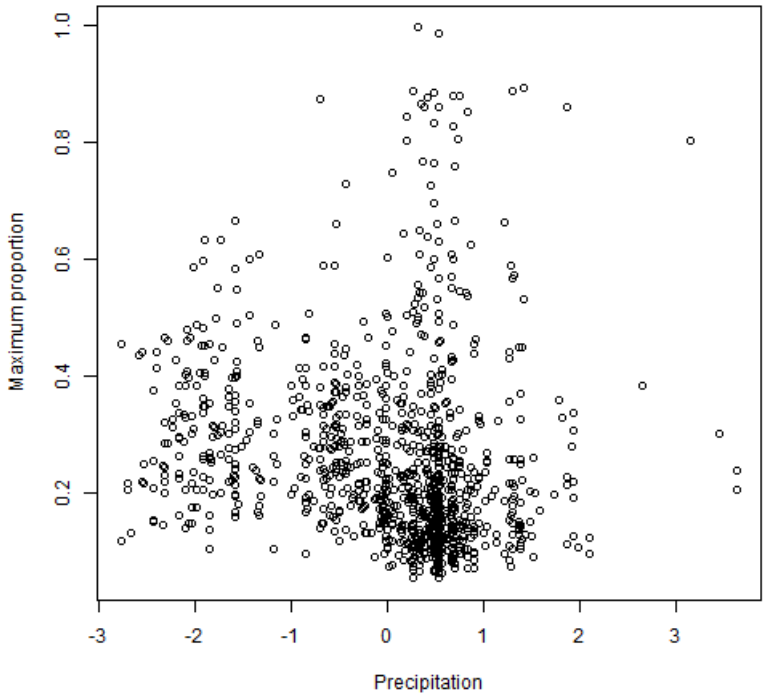


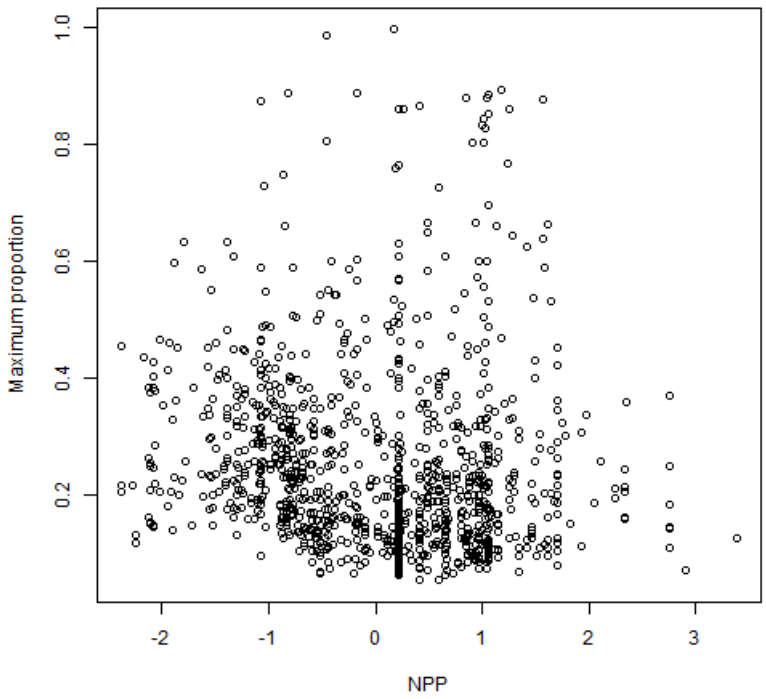

```
for(j in 2:p){
  plot(X[,j],Y,xlab=names[j],ylab="Maximum proportion")
}
```

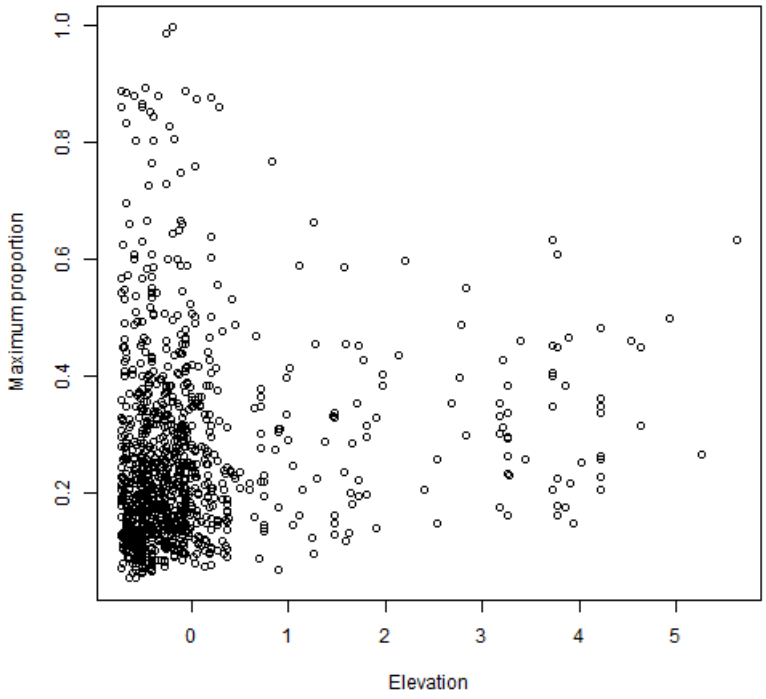

Maximum proportion
0.2
0.4
0.6
0.8
1.0
-2.0
-1.5
-1.0
-0.5
0.0
0.5
1.0
Longitude

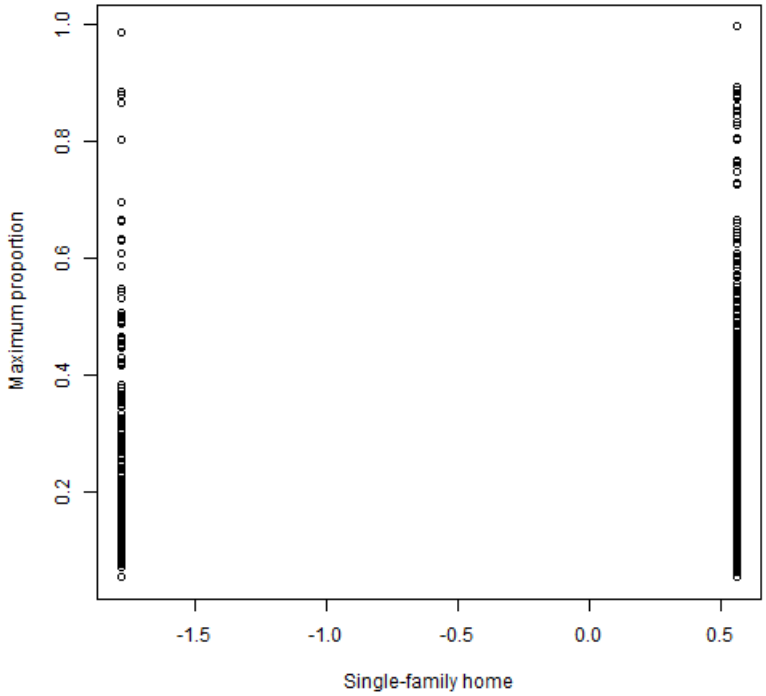

Maximum proportion
0.2
0.4
0.6
0.8
1.0
-3
-2
-1
0
1
2
Latitude

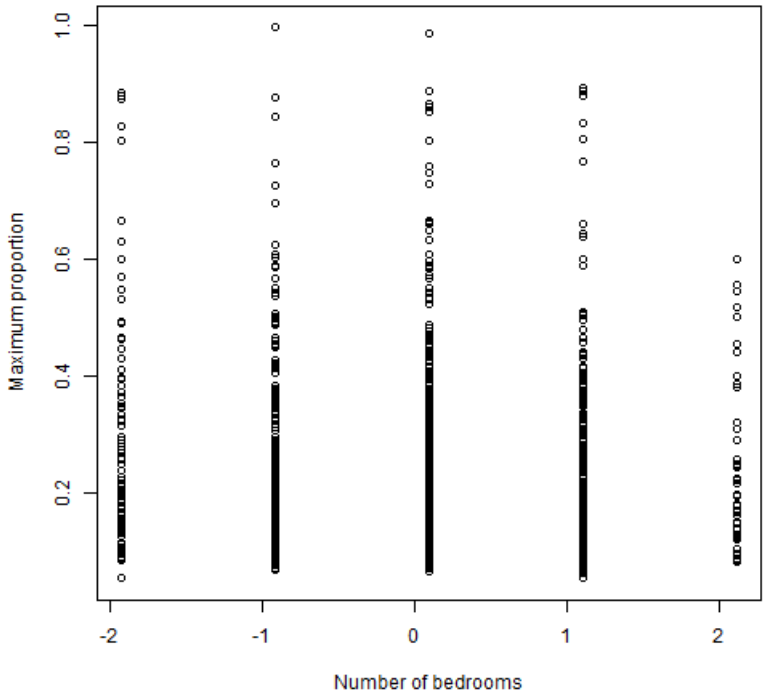

Maximum proportion
0.2
0.4
0.6
0.8
1.0
-3
-2
-1
0
1
2
3
Temperature


Maximum proportion
0.2
0.4
0.6
0.8
1.0
-3
-2
-1
0
1
2
3
Precipitation


Maximum proportion
0.2
0.4
0.6
0.8
1.0
-2
-1
0
1
2
3
NPP

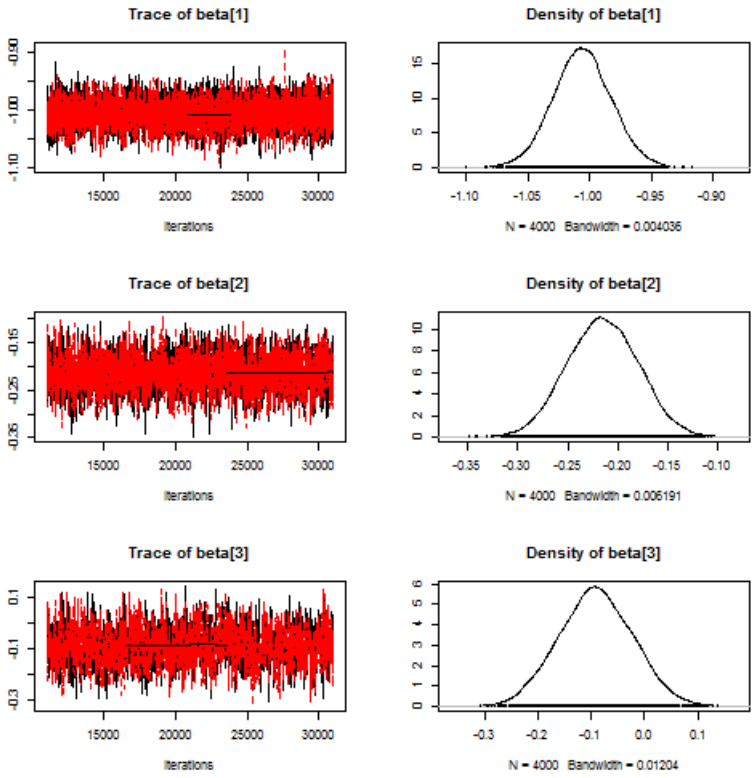

Maximum proportion
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
5
Elevation

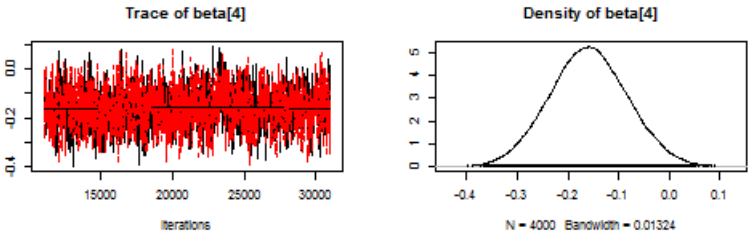




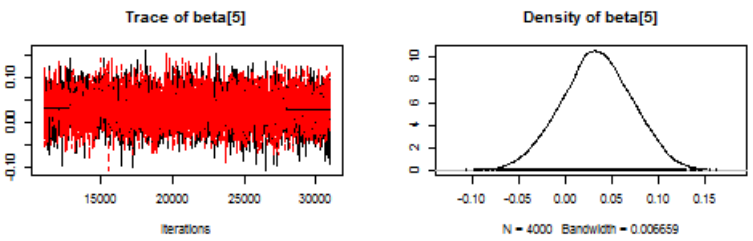
Fit the beta regression model in JAGS

```
library(rjags)

data   <- list(Y=Y,X=X,n=n,p=p)
params <- c("beta","r")

model_string <- textConnection("model{
   for(i in 1:n){
     Y[i]       ~ dbeta(r*mu[i],r*(1-mu[i]))
     logit(mu[i]) <- inprod(X[i,],beta[])
   }
   for(j in 1:p){beta[j] ~ dnorm(0,0.01)}
   r ~ dgamma(0.1,0.1)
}")

model <- jags.model(model_string,data = data, n.chains=2,quiet=TRUE)
update(model, 10000, progress.bar="none")
samples <- coda.samples(model, variable.names=params, thin=5, n.iter=20000, progress.bar="none")

plot(samples)
```

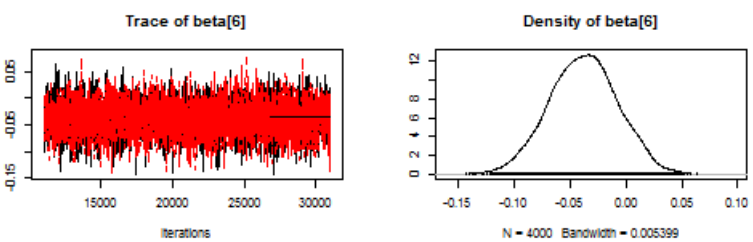



Trace of beta[4]
Iterations

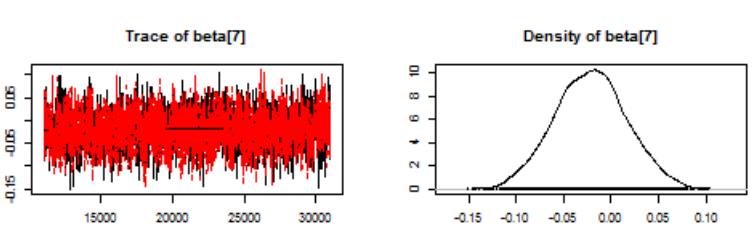
Density of beta[4]
N = 4000 Bandwidth = 0.01324


Trace of beta[5]
Iterations

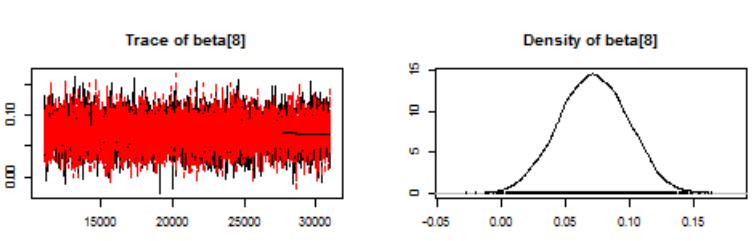
Density of beta[5]
N = 4000 Bandwidth = 0.006659


Trace of beta[6]
Iterations

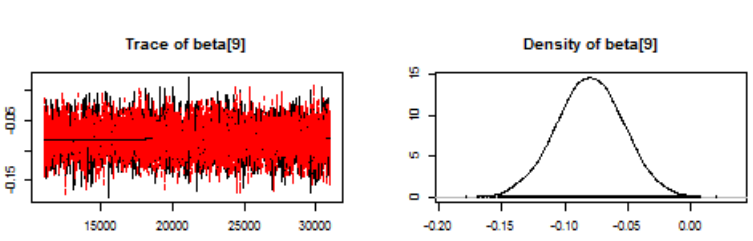
Density of beta[6]
N = 4000 Bandwidth = 0.005399


Trace of beta[7]
Iterations

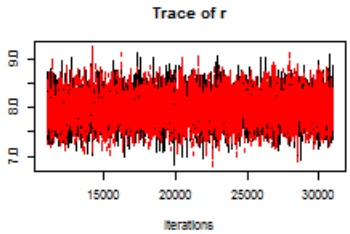
Density of beta[7]
N = 4000 Bandwidth = 0.006705

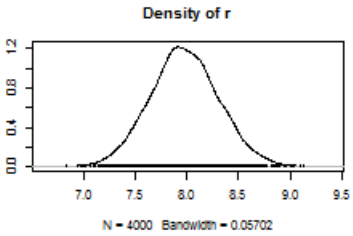

Trace of beta[8]
Iterations

Density of beta[8]
N = 4000 Bandwidth = 0.004692


Trace of beta[9]
Iterations

Density of beta[9]
N = 4000 Bandwidth = 0.004739






```
sum <- summary(samples)

rownames(sum$statistics) <- c(names,"r")
rownames(sum$quantiles)  <- c(names,"r")
sum$statistics           <- round(sum$statistics,3)
sum$quantiles            <- round(sum$quantiles,3)
sum
```

```
##
## Iterations = 11005:31000
## Thinning interval = 5
## Number of chains = 2
## Sample size per chain = 4000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                       Mean    SD Naive SE Time-series SE
## Intercept           -1.006 0.023    0.000          0.000
## Longitude           -0.215 0.035    0.000          0.001
## Latitude            -0.091 0.069    0.001          0.002
## Temperature         -0.159 0.075    0.001          0.002
## Precipitation        0.033 0.038    0.000          0.001
## NPP                 -0.038 0.031    0.000          0.000
## Elevation           -0.021 0.038    0.000          0.001
## Single-family home   0.072 0.027    0.000          0.000
## Number of bedrooms -0.080 0.027    0.000          0.000
## r                    7.977 0.330    0.004          0.004
##
## 2. Quantiles for each variable:
##
##                        2.5%    25%    50%    75%  97.5%
## Intercept           -1.052 -1.022 -1.006 -0.991 -0.960
## Longitude           -0.284 -0.239 -0.215 -0.191 -0.146
## Latitude            -0.224 -0.138 -0.091 -0.044  0.044
## Temperature         -0.306 -0.211 -0.160 -0.109 -0.010
## Precipitation       -0.043  0.008  0.033  0.059  0.106
## NPP                 -0.098 -0.059 -0.038 -0.017  0.020
## Elevation           -0.097 -0.047 -0.021  0.004  0.055
## Single-family home   0.020  0.054  0.072  0.090  0.123
## Number of bedrooms -0.134 -0.098 -0.080 -0.062 -0.027
## r                    7.336  7.758  7.972  8.193  8.638
```