Variable selection for the Gambia data

Chapter 5.3: Stochastic search variable selection

The *gambia* data in the *geoR* package includes data for 1332 children in the Gambia. The binary response Y_i is the indictor that child i tested positive for malaria. We use five covariates in X_{ij}:

1. Age: age of the child, in days
2. Netuse: indicator variable denoting whether (1) or not (0) the child regularly sleeps under a bed-net
3. Treated: indicator variable denoting whether (1) or not (0) the bed-net is treated (coded 0 if netuse=0)
4. Green: satellite-derived measure of the greenness of vegetation in the immediate vicinity of the village (arbitrary units)
5. PCH: indicator variable denoting the presence (1) or absence (0) of a health center in the village

We use the logit regression model

$$\text{logit}[\text{Prob}(Y_i = 1)) = \alpha + \sum_{j=1}^{p} X_{ij}\beta_j.$$

The spike-and-slab prior for β_j is $\beta_j = \gamma_j\delta_j$ where $\gamma_j \sim \text{Bernoulli}(0.5)$ and $\delta_j \sim \text{Normal}(0, \tau^2)$.

Load the data

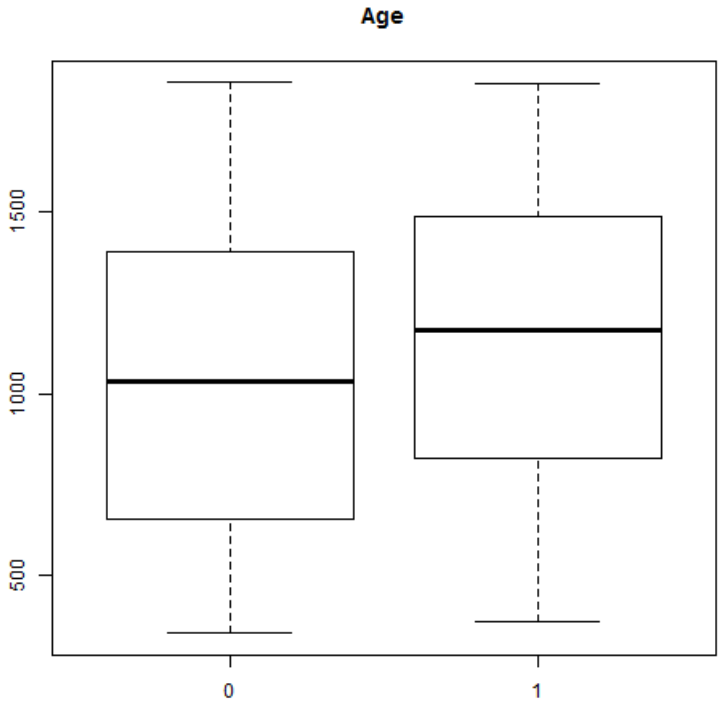
```
library(geoR)

Y <- gambia[,3]
X <- gambia[,4:8]

Y[1:5]
```

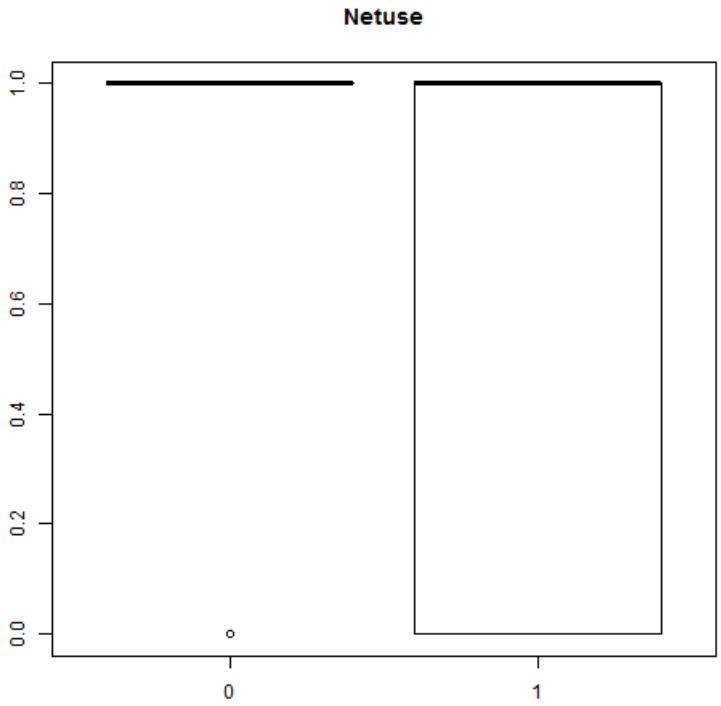
```
## [1] 1 0 0 1 0
```

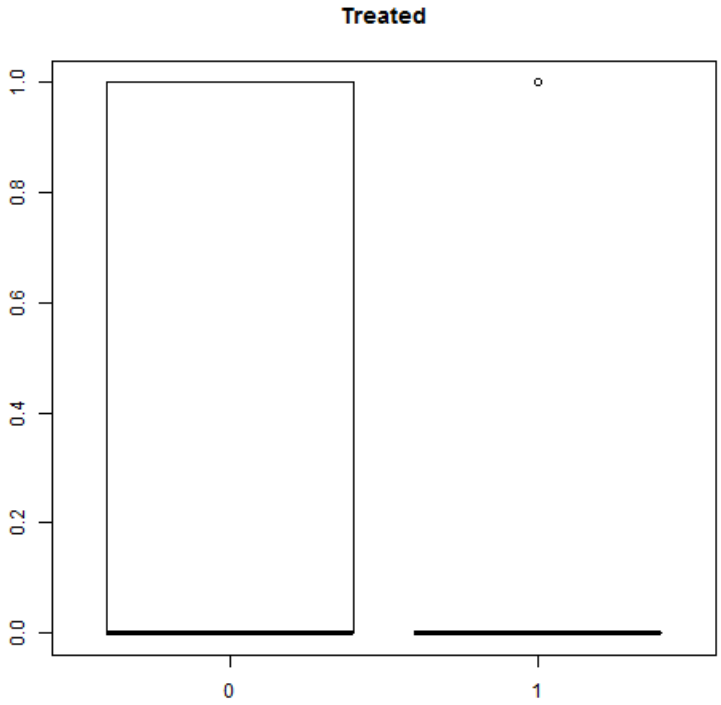
```
X[1:5,]
```

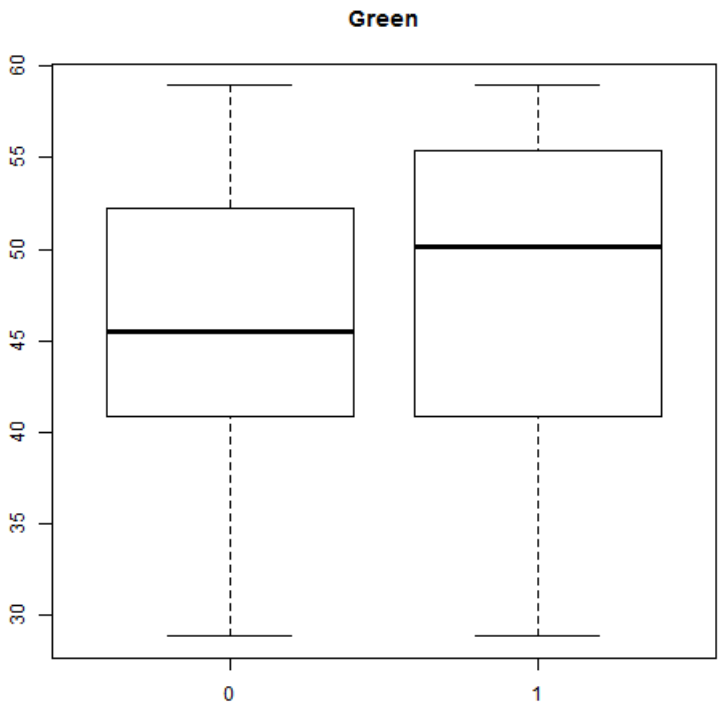
```
##       age netuse treated green phc
## 1850 1783      0       0 40.85   1
## 1851  404      1       0 40.85   1
## 1852  452      1       0 40.85   1
## 1853  566      1       0 40.85   1
## 1854  598      1       0 40.85   1
```

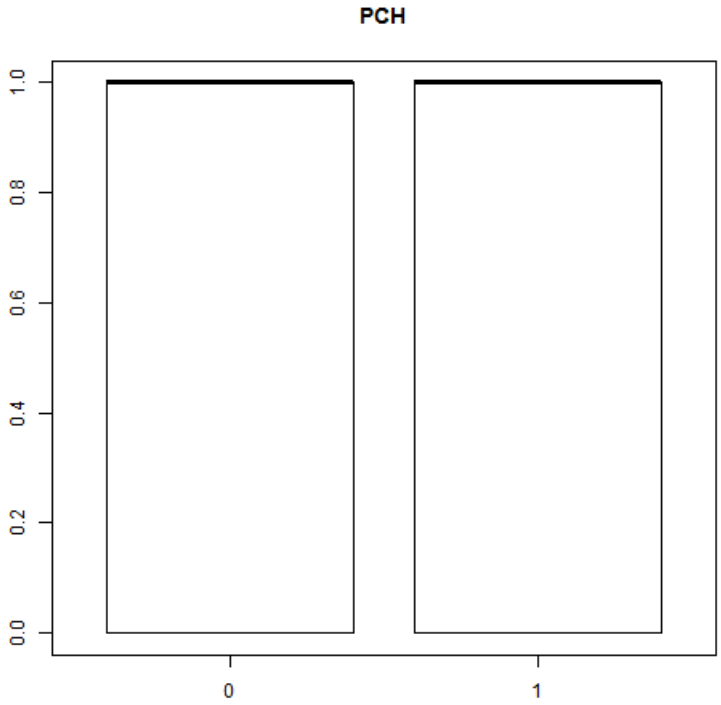
```
names <- c("Age","Netuse","Treated","Green","PCH")
for(j in 1:5){
  boxplot(X[,j]~Y,main=names[j])
}
```


Age
1500
1000
500
0
1


Netuse
1.0
0.8
0.6
0.4
0.2
0.0
0
1


Treated
0.0
0.2
0.4
0.6
0.8
1.0
0
1


Green
30
35
40
45
50
55
60
0
1




```
# Standardize X
X <- scale(X)
X[1:5,]
```

```
##            age     netuse    treated      green       phc
## 1850  1.650148 -1.5683351 -0.6167739 -0.8462609 0.6802564
## 1851 -1.588791  0.6373055 -0.6167739 -0.8462609 0.6802564
## 1852 -1.476050  0.6373055 -0.6167739 -0.8462609 0.6802564
## 1853 -1.208292  0.6373055 -0.6167739 -0.8462609 0.6802564
## 1854 -1.133132  0.6373055 -0.6167739 -0.8462609 0.6802564
```

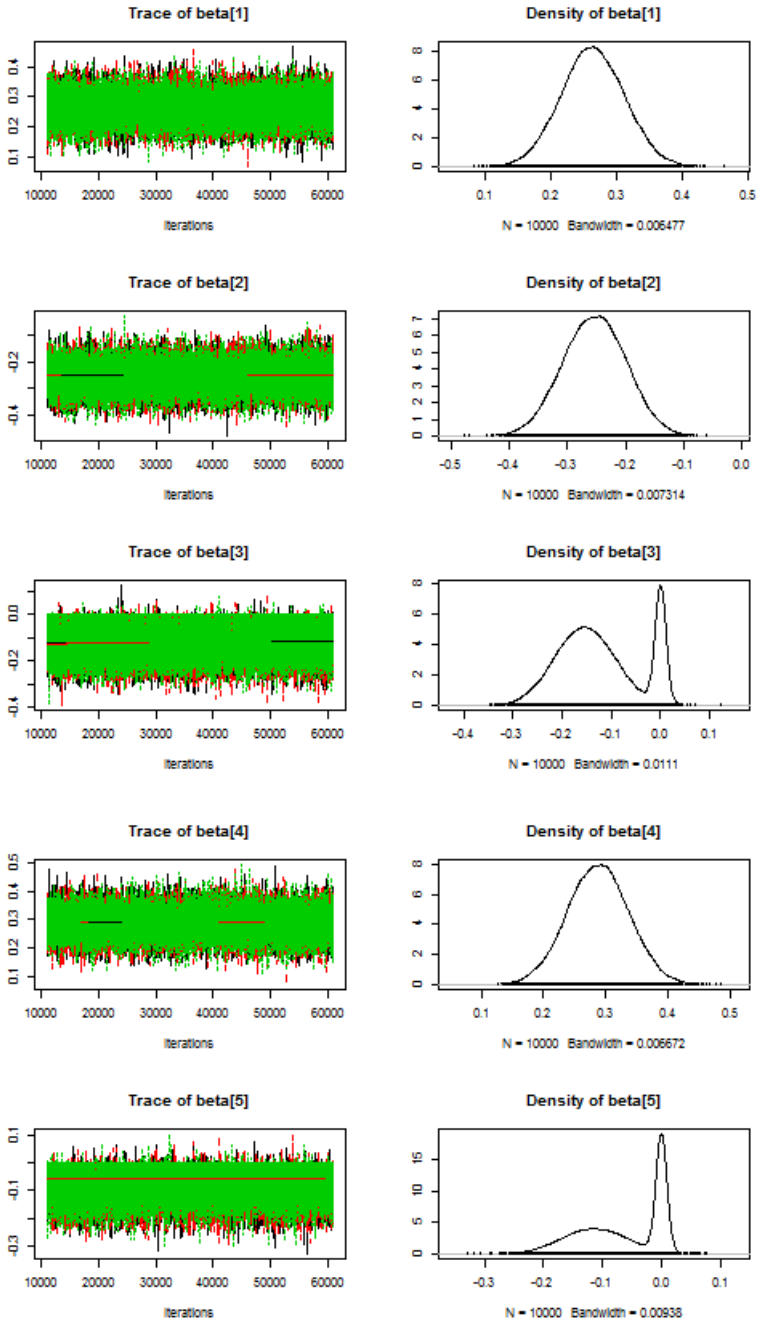
```
n <- length(Y)
p <- ncol(X)
```

Define the models in JAGS

```
  library(rjags)

  m <- textConnection("model{
    for(i in 1:n){
      Y[i]          ~ dbern(pi[i])
      logit(pi[i]) <- alpha          + X[i,1]*beta[1] + X[i,2]*beta[2] +
                      X[i,3]*beta[3] + X[i,4]*beta[4] + X[i,5]*beta[5]
    }
    for(j in 1:5){
       beta[j] <- gamma[j]*delta[j]
       gamma[j] ~ dbern(0.5)
       delta[j] ~ dnorm(0,tau)
    }
    alpha ~ dnorm(0,0.01)
    tau   ~ dgamma(0.1,0.1)
  }")
```

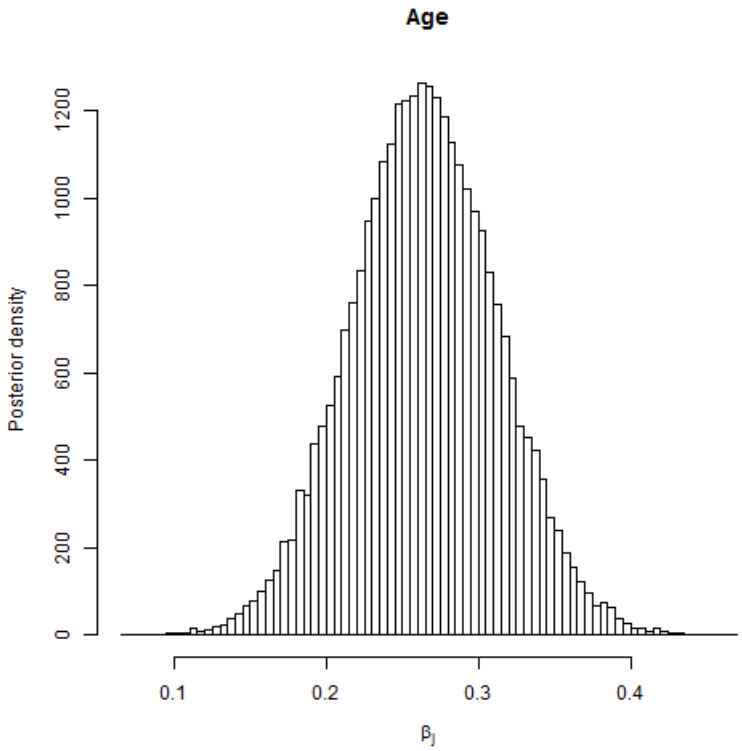
Fit the model

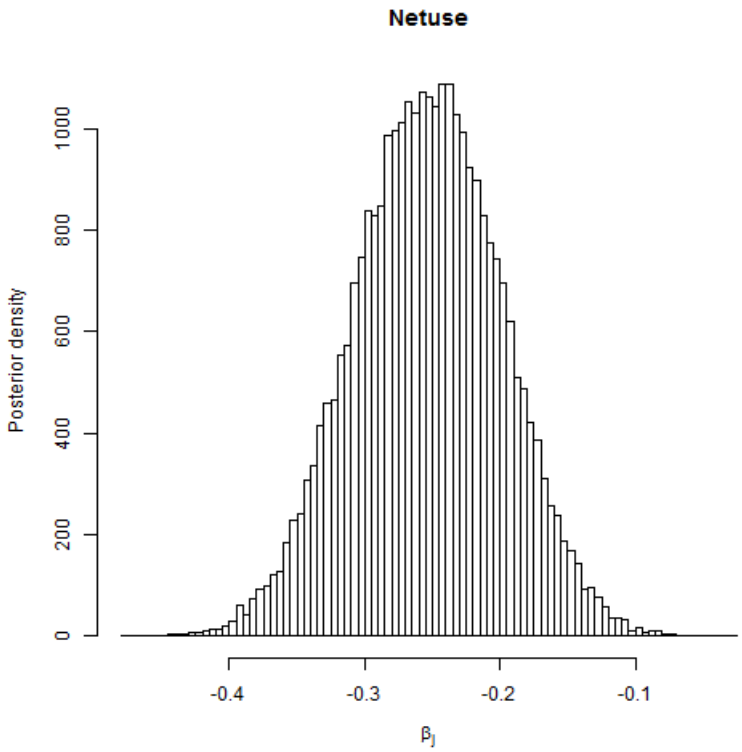
```
data   <- list(Y=Y,X=X,n=n)
burn   <- 10000
iters  <- 50000
chains <- 3
model  <- jags.model(m,data = data, n.chains=chains,quiet=TRUE)
update(model, burn, progress.bar="none")
samps  <- coda.samples(model, variable.names=c("beta"),
                       thin=5, n.iter=iters, progress.bar="none")
plot(samps)
```

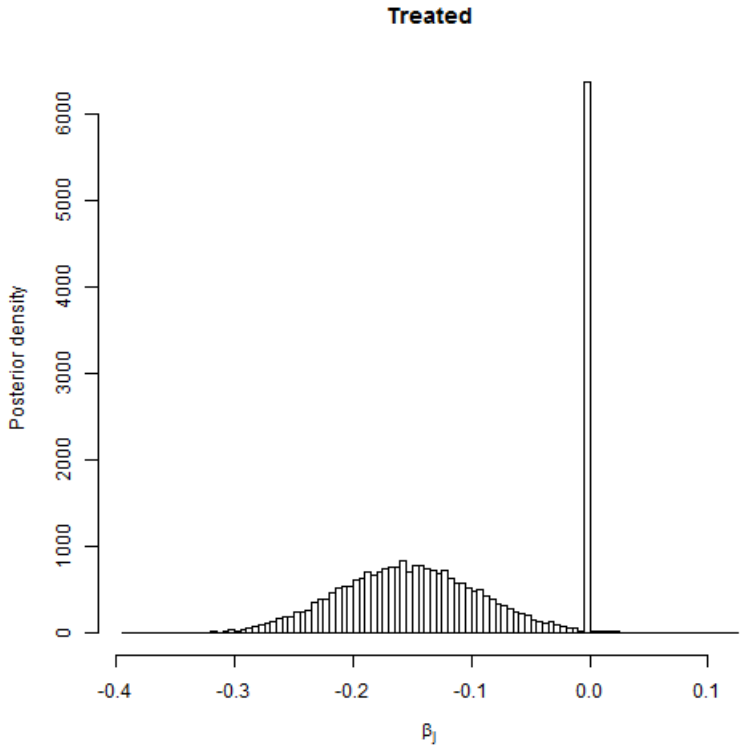


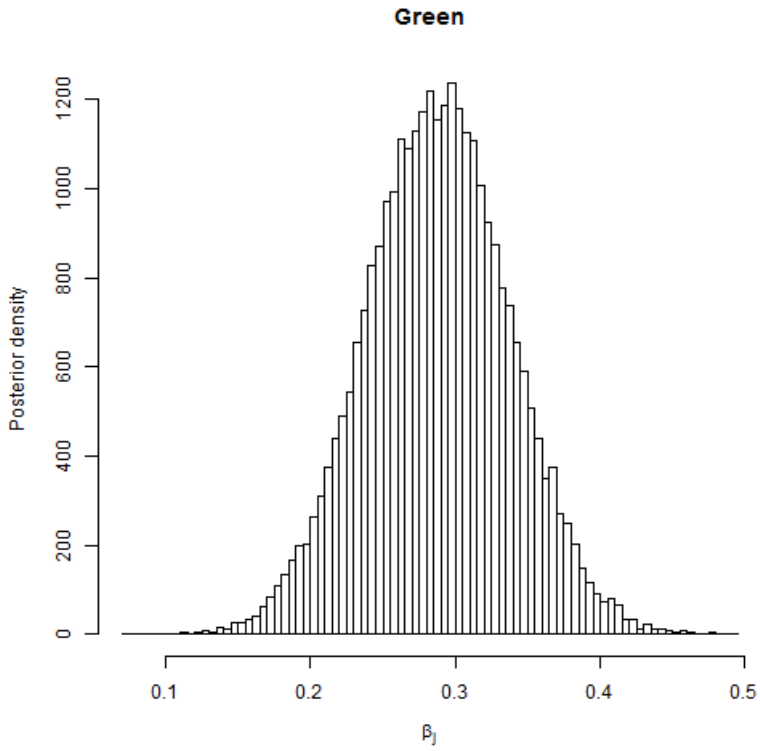
Summarize the marginal distributions of the β_j

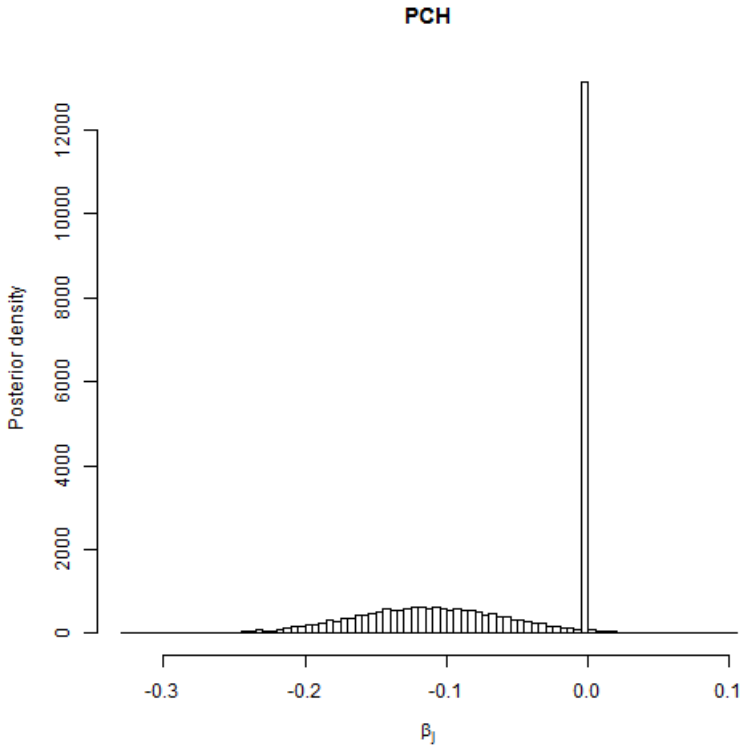
```
beta    <- NULL
for(l in 1:chains){
  beta <- rbind(beta,samps[[l]])
}
colnames(beta) <- names

for(j in 1:5){
  hist(beta[,j],xlab=expression(beta[j]),ylab="Posterior density",
       breaks=100,main=names[j])
}
```






Treated
Posterior density
0
1000
2000
3000
4000
5000
6000
-0.4
-0.3
-0.2
-0.1
0.0
0.1
βj


Green
Posterior density
0
200
400
600
800
1000
1200
0.1
0.2
0.3
0.4
0.5
βj




```
Inc_Prob <- apply(beta!=0,2,mean)
Q        <- t(apply(beta,2,quantile,c(0.5,0.05,0.95)))
out      <- cbind(Inc_Prob,Q)

kable(round(out,2))
```

	Inc_Prob	50%	5%	95%
Age	1.00	0.26	0.19	0.34
Netuse	1.00	-0.25	-0.34	-0.17
Treated	0.79	-0.13	-0.24	0.00
Green	1.00	0.29	0.21	0.37
PCH	0.56	-0.05	-0.19	0.00

Summary: Age, bed-net use and greenness are included with posterior probability one and are thus clearly important predictors of malaria. Treatment of the bed net and proximity to a health center are included with posterior probability more than a half and so there is moderate evidence that these variables are important predictors of malaria prevalence. The posterior distribution of these parameters has an unusual shape: they are a combination of a Gaussian curve for samples that include the variable and a spike at zero for samples that exclude the variable.

Compute the posterior probability of each model

```
model <- "Intercept"
for(j in 1:5){
  model <- paste(model,ifelse(beta[,j]==0,"","+"))
  model <- paste(model,ifelse(beta[,j]==0,"",names[j]))
}
model[1:5]
```

```
## [1] "Intercept + Age + Netuse + Treated + Green + PCH"
## [2] "Intercept + Age + Netuse + Treated + Green  "
## [3] "Intercept + Age + Netuse + Treated + Green + PCH"
## [4] "Intercept + Age + Netuse + Treated + Green  "
## [5] "Intercept + Age + Netuse + Treated + Green + PCH"
```

```
beta[1:5,]
```

```
##            Age     Netuse    Treated     Green         PCH
## [1,] 0.2527252 -0.3024030 -0.1315871 0.2947381 -0.01603794
## [2,] 0.1660592 -0.2622006 -0.1285444 0.2221916  0.00000000
## [3,] 0.2250195 -0.1569258 -0.1485445 0.2938200 -0.12117986
## [4,] 0.2628377 -0.2609074 -0.1929870 0.3536249  0.00000000
## [5,] 0.2372177 -0.2419001 -0.1116356 0.2404865 -0.16442993
```

```
  model_probs <- table(model)/length(model)
  model_probs <- sort(model_probs,dec=T)
  round(model_probs,3)
```

```
## model
##     Intercept + Age + Netuse + Treated + Green
##                                           0.420
## Intercept + Age + Netuse + Treated + Green + PCH
##                                           0.370
##         Intercept + Age + Netuse   + Green + PCH
##                                           0.195
##             Intercept + Age + Netuse   + Green
##                                           0.015
```

Summary: Three models dominate the posterior probability:

1. Intercept + Age + Netuse + Green + Treated
2. Intercept + Age + Netuse + Green + Treated + PCH
3. Intercept + Age + Netuse + Green + PCH

Therefore it is clear that age, bed net use and greeness should be included in the model, but uncertainty about whether one or both of the remaining two variables should be included.