Breast Cancer Prediction Case Study - Bayesian Logistic Regression with Comparison of Frequentist and Bayesian Variable Selection Methods

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2025-03-14

```
library(readr)
library(dplyr)
library(ggplot2)
library(dplyr)
library(tidyr)
library(corrplot)
library(caret)
library(MCMCpack)
library(car)
library(boot)
library(gridExtra)
```

Introduction

This case study is based on the Breast Cancer Wisconsin (Diagnostic) Data Set (https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data). The data set contains 569 observations and 32 variables. The data set is available at the UCI Machine Learning Repository. The data set contains mean (and at times min and max) values of the patient for the following numeric (continious) variables:

a) radius (mean of distances from center to points on the perimeter)
b) texture (standard deviation of gray-scale values)
c) perimeter
d) area
e) smoothness (local variation in radius lengths)
f) compactness (perimeter^2 / area - 1.0)
g) concavity (severity of concave portions of the contour)
h) concave points (number of concave portions of the contour)
i) symmetry
j) fractal dimension ("coastline approximation" - 1)

The data set also contains the following Binary variables:

2) Diagnosis (M = malignant, B = benign)

Where Malignant (M) means the tumor is cancerous, while Benign (B): means that the tumor is non-cancerous.

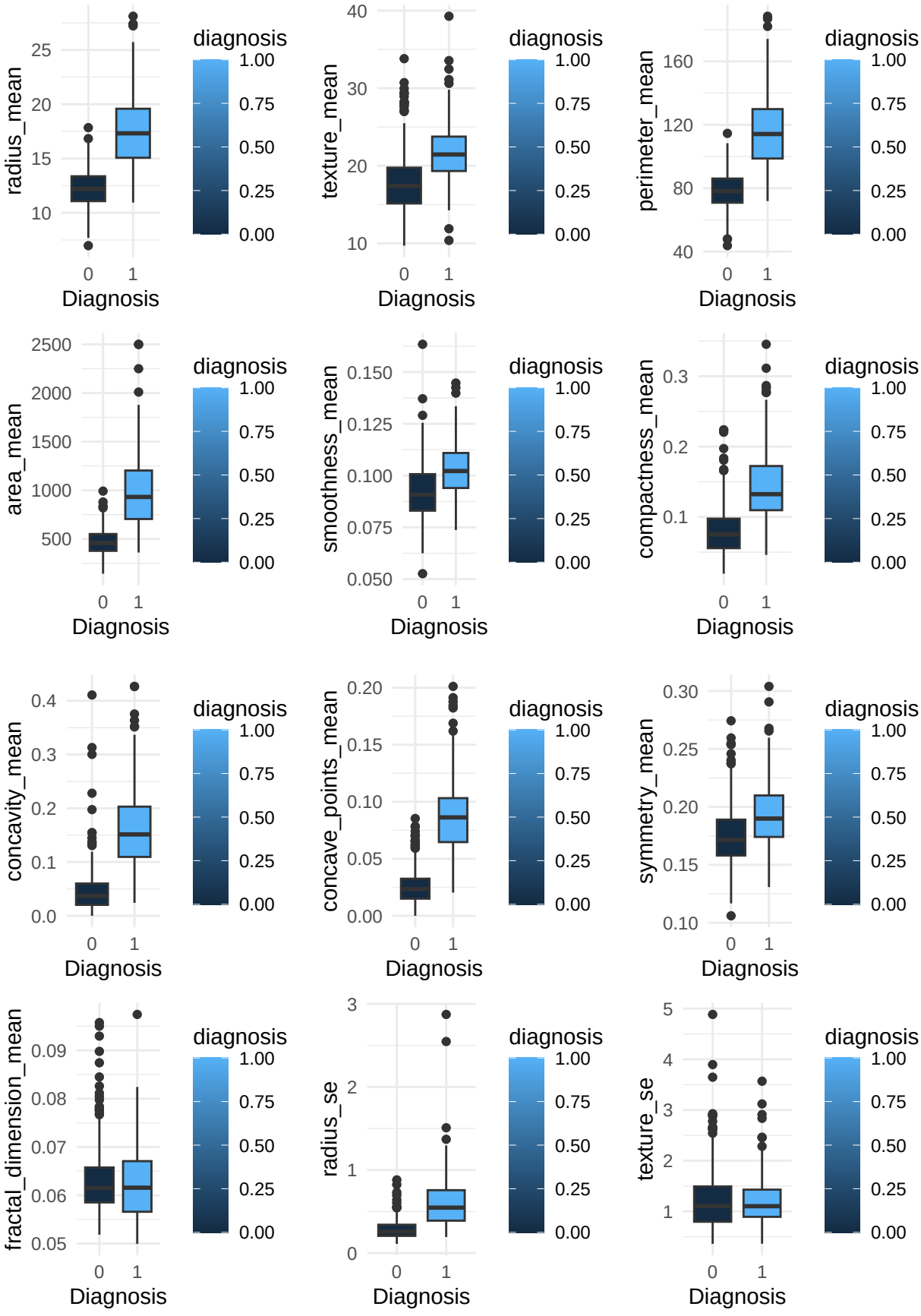
Read Data

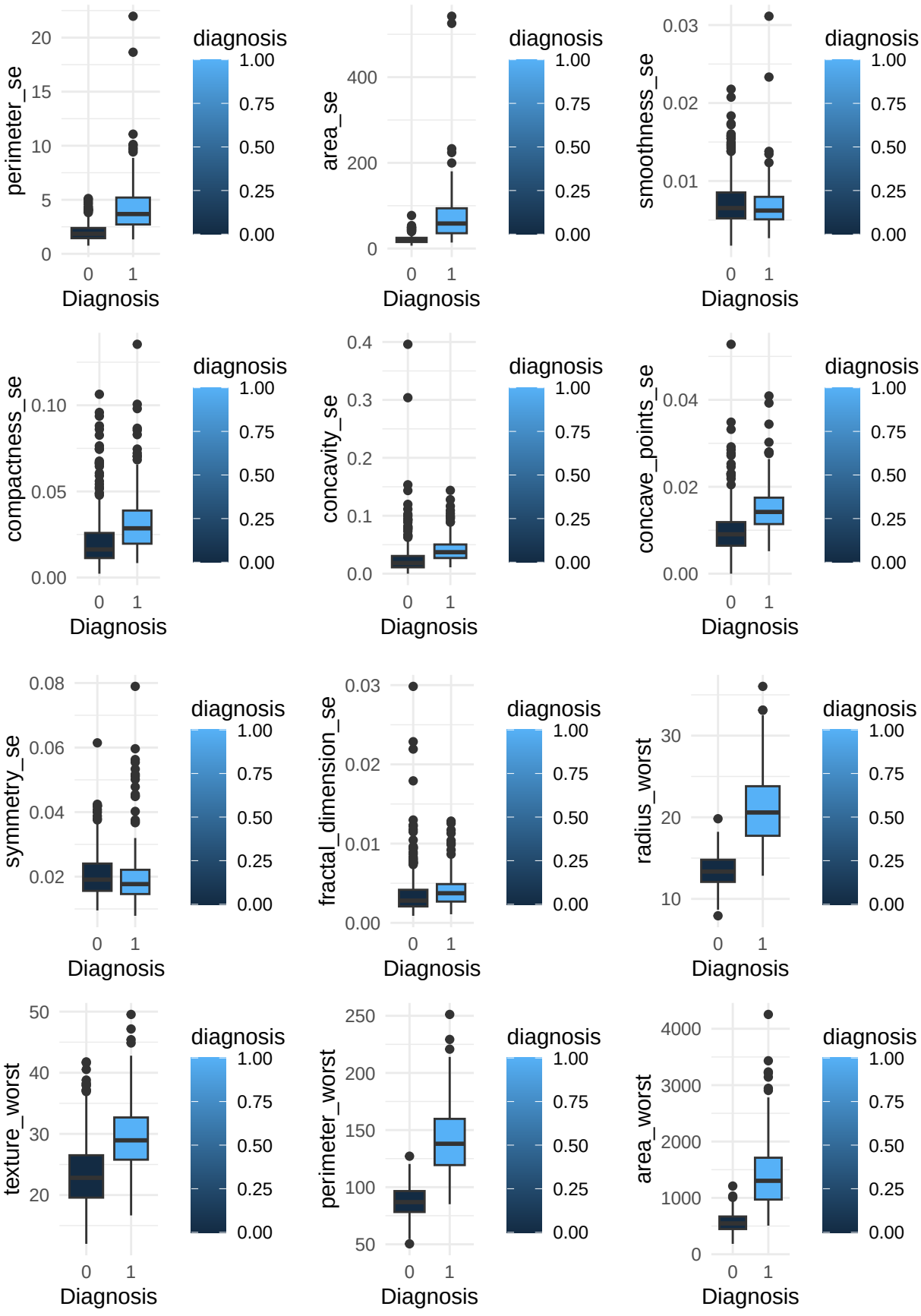
```
data <- read.csv("data.csv", header = TRUE, sep = ",")
data <- dplyr::select(data, -c(X,id))
names(data) <- gsub("\\.", "_", names(data))
data$diagnosis <- ifelse(data$diagnosis == "M", 1, 0)
```

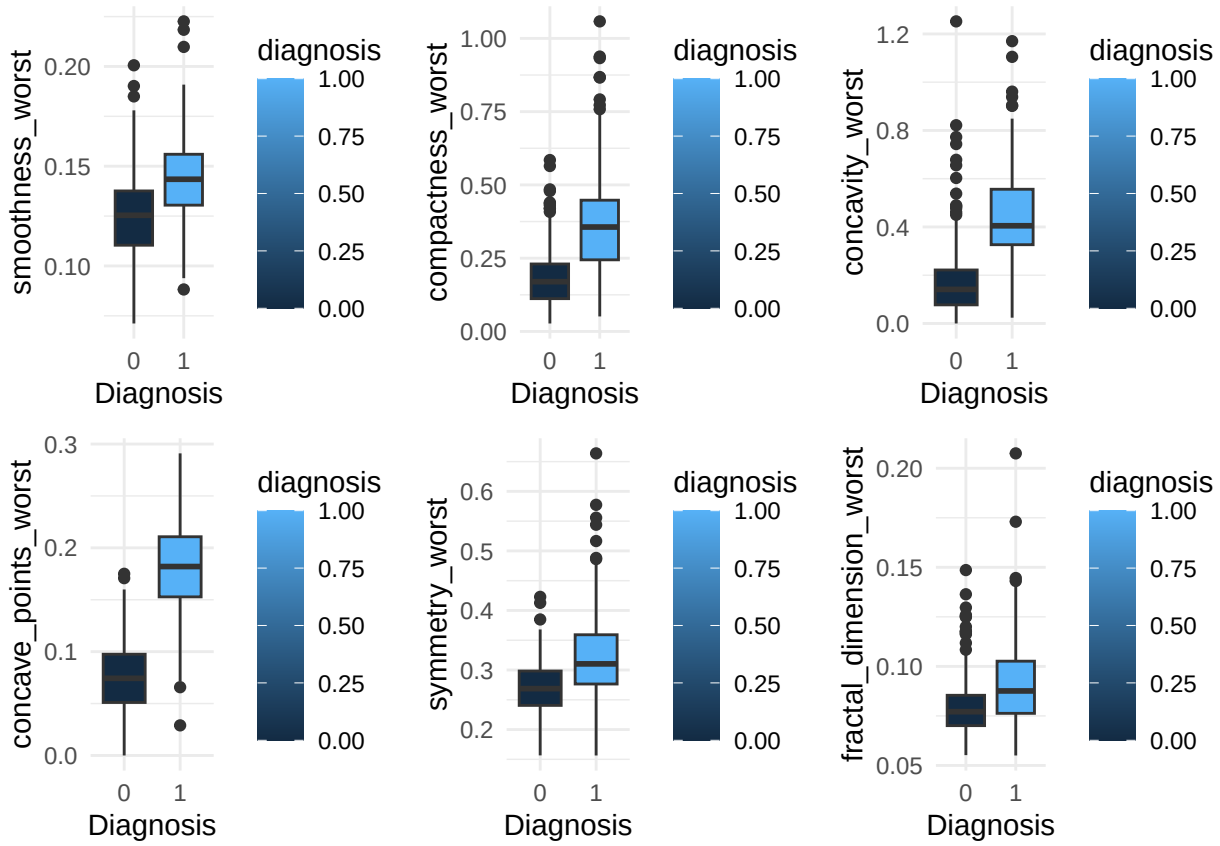
Exploratory Data Analysis

Relation with response var

```
numeric_vars <- data %>%select_if(is.numeric) %>% colnames()
numeric_vars <- setdiff(numeric_vars, "diagnosis")

plots <- lapply(numeric_vars, function(var) {
  ggplot(data, aes(x = factor(diagnosis), y = .data[[var]], fill = diagnosis)) +
    geom_boxplot() +
    labs(x = "Diagnosis", y = var) +
    theme_minimal()
})

# Print all plots

# Display plots in batches of 6 (2 rows × 3 columns)
num_plots <- length(plots)
batch_size <- 6

for(i in seq(1, num_plots, batch_size)) {
  end_idx <- min(i + batch_size - 1, num_plots)
  batch_plots <- plots[i:end_idx]
  grid.arrange(grobs = batch_plots, ncol = 3)
}
```


radius_mean
texture_mean
perimeter_mean
area_mean
smoothness_mean
compactness_mean
concavity_mean
concave_points_mean
symmetry_mean
fractal_dimension_mean
radius_se
texture_se
Diagnosis
diagnosis
1.00
0.75
0.50
0.25
0.00


perimeter_se
area_se
smoothness_se
compactness_se
concavity_se
concave_points_se
symmetry_se
fractal_dimension_se
radius_worst
texture_worst
perimeter_worst
area_worst
Diagnosis
diagnosis
1.00
0.75
0.50
0.25
0.00



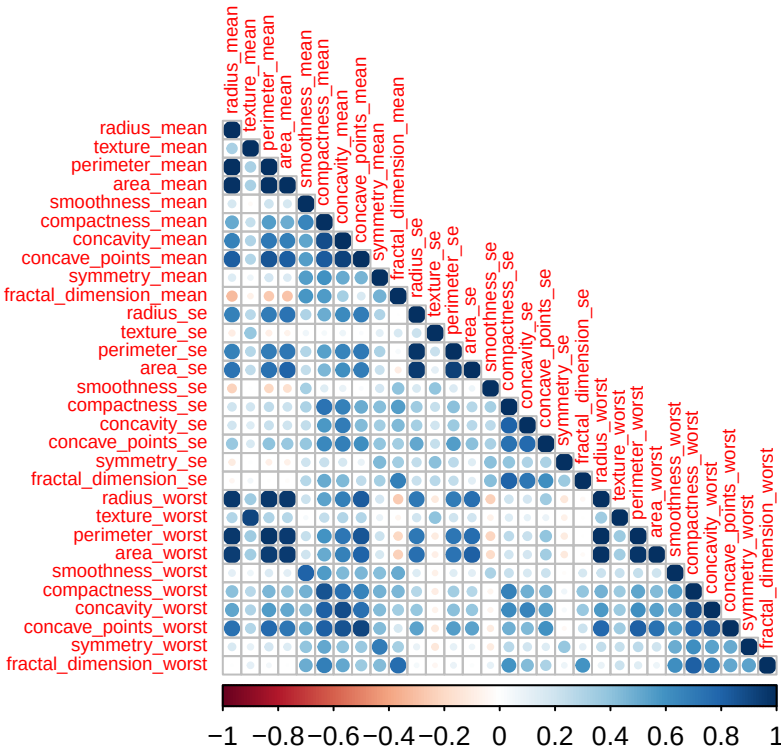

```
summary_stat <- data %>%
  group_by(factor(diagnosis)) %>%
  summarise(across(all_of(numeric_vars),
                   list(
                     mean = ~mean(.x, na.rm = TRUE),
                     sd = ~sd(.x, na.rm = TRUE),
                     median = ~median(.x, na.rm = TRUE),
                     min = ~min(.x, na.rm = TRUE),
                     max = ~max(.x, na.rm = TRUE)
                   )
            ))


# For easier viewing, you can pivot longer
summary_long <- summary_stat %>%
  pivot_longer(cols = -`factor(diagnosis)`,
               names_to = c("variable", "stat"),
               names_pattern = "(.*)_(.*)")

summary_long
```

```
## # A tibble: 300 x 4
##    `factor(diagnosis)` variable     stat   value
##    <fct>               <chr>        <chr>  <dbl>
##  1 0                   radius_mean  mean   12.1
##  2 0                   radius_mean  sd      1.78
```

```
##  3 0                    radius_mean  median 12.2
##  4 0                    radius_mean  min     6.98
##  5 0                    radius_mean  max    17.8
##  6 0                    texture_mean mean   17.9
##  7 0                    texture_mean sd      4.00
##  8 0                    texture_mean median 17.4
##  9 0                    texture_mean min     9.71
## 10 0                    texture_mean max    33.8
## # i 290 more rows
```

Correlation

```
# Check correlation between numeric variables
cor_matrix <- cor(data[, numeric_vars])
corrplot(cor_matrix, method = "circle",type="lower",tl.cex = 0.6)
```




```
# Or find highly correlated variables
high_cor <- findCorrelation(cor_matrix, cutoff = 0.8)
problematic_vars <- numeric_vars[high_cor]
print(problematic_vars)
```

```
##  [1] "concavity_mean"       "concave_points_mean"  "compactness_mean"
##  [4] "concave_points_worst" "concavity_worst"      "perimeter_worst"
##  [7] "radius_worst"         "perimeter_mean"       "compactness_worst"
## [10] "area_worst"           "radius_mean"          "perimeter_se"
## [13] "compactness_se"       "area_se"              "smoothness_mean"
## [16] "texture_mean"
```

Variable Selection

Frequentist Approach

Check VIF and remove variables with extremely high values

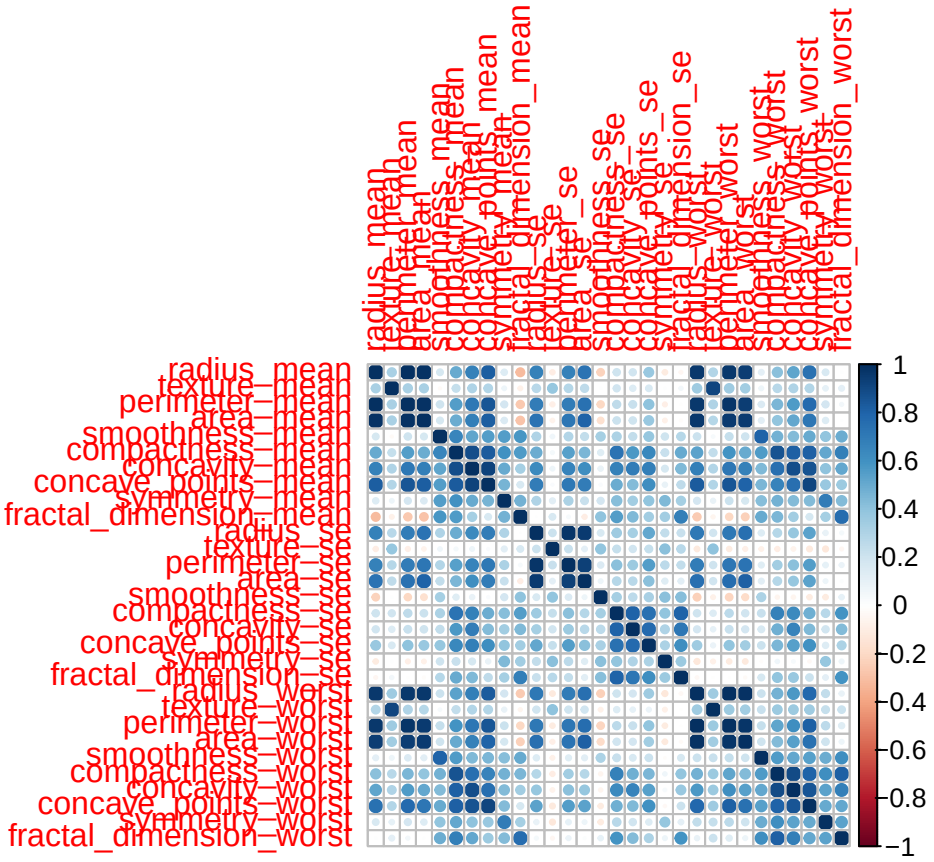
```
predictors <- setdiff(names(data), c("diagnosis"))
formula_str <- paste("diagnosis ~", paste(predictors, collapse = " + "))
formula <- as.formula(formula_str)

l_reg = lm(formula, data)
vif_values <- vif(l_reg)

vif_df <- data.frame(
  Variable = names(vif_values),
  VIF = vif_values
)
vif_df <- vif_df %>% arrange(desc(VIF))
print(vif_df)
```

```
##                                      Variable         VIF
## radius_mean                       radius_mean 3806.115296
## perimeter_mean                 perimeter_mean 3786.400419
## radius_worst                     radius_worst  799.105946
## perimeter_worst               perimeter_worst  405.023336
## area_mean                           area_mean  347.878657
## area_worst                         area_worst  337.221924
## radius_se                           radius_se   75.462027
## concavity_mean                 concavity_mean   70.767720
## perimeter_se                     perimeter_se   70.359695
## concave_points_mean       concave_points_mean   60.041733
## compactness_mean             compactness_mean   50.505168
## area_se                                 area_se   41.163091
## compactness_worst           compactness_worst   36.982755
## concave_points_worst     concave_points_worst   36.763714
## concavity_worst               concavity_worst   31.970723
## fractal_dimension_worst fractal_dimension_worst   18.861533
## texture_worst                   texture_worst   18.569966
## fractal_dimension_mean fractal_dimension_mean   15.756977
## concavity_se                     concavity_se   15.694833
## compactness_se                 compactness_se   15.366324
## texture_mean                     texture_mean   11.884048
## concave_points_se           concave_points_se   11.520796
## smoothness_worst             smoothness_worst   10.923061
## fractal_dimension_se     fractal_dimension_se    9.717987
## symmetry_worst                 symmetry_worst    9.520570
## smoothness_mean               smoothness_mean    8.194282
## symmetry_se                       symmetry_se    5.175426
## symmetry_mean                   symmetry_mean    4.220656
## texture_se                         texture_se    4.205423
## smoothness_se                   smoothness_se    4.027923
```

```
vars_to_exclude <- c(head(vif_df,15)$Variable)
# setdiff(problematic_vars , vars_to_exclude)
# setdiff(vars_to_exclude, problematic_vars)
```

Check correlations after excluding x VIF, variables to pay attention if something does not work.

```
# Check correlation between numeric variables
cor_matrix_f <- cor(data[, setdiff(numeric_vars, vars_to_exclude)])
corrplot(cor_matrix, method = "circle")
```




```
# Or find highly correlated variables
high_cor_f <- findCorrelation(cor_matrix_f, cutoff = 0.8)
problematic_vars_f <- setdiff(numeric_vars, vars_to_exclude)[high_cor_f]
print(problematic_vars_f)
```

```
## [1] "compactness_se"  "smoothness_mean" "texture_mean"
```

```
selected_freq <- setdiff(numeric_vars, vars_to_exclude)
```

Bayesian Approach

```r
library(BAS)
```

```
## Warning: package 'BAS' was built under R version 4.4.3
```

```r
# Fit a Bayesian logistic regression with variable selection
model_bas <- bas.glm(diagnosis ~ .,
                     data = data,
                     family = binomial(),
                     method = "MCMC", # or "BAS" for deterministic sampling
                     MCMC.iterations = 10000,
                     modelprior = uniform()) # Prior over model space

# Summary of results
summary(model_bas)
```

```
##                          P(B != 0 | Y)   model 1      model 2      model 3
## Intercept                       1.0000   1.00000   1.00000000   1.00000000
## radius_mean                     0.3158   1.00000   0.00000000   1.00000000
## texture_mean                    0.2038   0.00000   0.00000000   1.00000000
## perimeter_mean                  0.3528   0.00000   0.00000000   0.00000000
## area_mean                       0.2557   0.00000   0.00000000   0.00000000
## smoothness_mean                 0.2022   0.00000   0.00000000   0.00000000
## compactness_mean                0.4600   1.00000   0.00000000   0.00000000
## concavity_mean                  0.3770   0.00000   0.00000000   0.00000000
## concave_points_mean             0.6143   1.00000   0.00000000   0.00000000
## symmetry_mean                   0.1948   1.00000   0.00000000   0.00000000
## fractal_dimension_mean          0.1902   0.00000   0.00000000   0.00000000
## radius_se                       0.3274   1.00000   1.00000000   0.00000000
## texture_se                      0.2879   0.00000   0.00000000   0.00000000
## perimeter_se                    0.2975   0.00000   0.00000000   0.00000000
## area_se                         0.6860   0.00000   0.00000000   1.00000000
## smoothness_se                   0.3854   0.00000   1.00000000   0.00000000
## compactness_se                  0.4459   0.00000   0.00000000   0.00000000
## concavity_se                    0.3393   0.00000   0.00000000   0.00000000
## concave_points_se               0.5370   1.00000   0.00000000   0.00000000
## symmetry_se                     0.2209   0.00000   1.00000000   0.00000000
## fractal_dimension_se            0.5348   1.00000   1.00000000   1.00000000
## radius_worst                    0.3352   0.00000   0.00000000   1.00000000
## texture_worst                   0.9137   1.00000   1.00000000   0.00000000
## perimeter_worst                 0.2485   0.00000   1.00000000   0.00000000
## area_worst                      0.6157   1.00000   0.00000000   0.00000000
## smoothness_worst                0.3850   0.00000   0.00000000   1.00000000
## compactness_worst               0.2385   0.00000   1.00000000   1.00000000
## concavity_worst                 0.4227   0.00000   1.00000000   1.00000000
## concave_points_worst            0.3407   0.00000   1.00000000   1.00000000
## symmetry_worst                  0.6501   0.00000   0.00000000   1.00000000
## fractal_dimension_worst         0.4435   1.00000   1.00000000   0.00000000
## BF                                  NA   1.00000   0.02022016   0.01026313
## PostProbs                           NA   0.00420   0.00330000   0.00250000
## R2                                  NA   0.93270   0.92260000   0.92080000
## dim                                 NA  11.00000  11.00000000  11.00000000
## logmarg                             NA -51.63416 -55.53523034 -56.21335276
```

```
##                             model 4     model 5
## Intercept                 1.0000000   1.0000000
## radius_mean               0.0000000   1.0000000
## texture_mean              1.0000000   0.0000000
## perimeter_mean            1.0000000   0.0000000
## area_mean                 0.0000000   1.0000000
## smoothness_mean           1.0000000   0.0000000
## compactness_mean          0.0000000   1.0000000
## concavity_mean            0.0000000   0.0000000
## concave_points_mean       1.0000000   1.0000000
## symmetry_mean             0.0000000   0.0000000
## fractal_dimension_mean    0.0000000   0.0000000
## radius_se                 0.0000000   0.0000000
## texture_se                0.0000000   0.0000000
## perimeter_se              0.0000000   0.0000000
## area_se                   1.0000000   1.0000000
## smoothness_se             0.0000000   1.0000000
## compactness_se            0.0000000   0.0000000
## concavity_se              0.0000000   0.0000000
## concave_points_se         0.0000000   0.0000000
## symmetry_se               1.0000000   0.0000000
## fractal_dimension_se      0.0000000   1.0000000
## radius_worst              0.0000000   0.0000000
## texture_worst             0.0000000   1.0000000
## perimeter_worst           0.0000000   0.0000000
## area_worst                1.0000000   1.0000000
## smoothness_worst          1.0000000   0.0000000
## compactness_worst         0.0000000   0.0000000
## concavity_worst           0.0000000   1.0000000
## concave_points_worst      0.0000000   0.0000000
## symmetry_worst            1.0000000   1.0000000
## fractal_dimension_worst   1.0000000   1.0000000
## BF                        0.2013694   0.1143243
## PostProbs                 0.0024000   0.0022000
## R2                        0.9285000   0.9376000
## dim                      11.0000000  13.0000000
## logmarg                -53.2367695 -53.8028713
```

```r
# Posterior inclusion probabilities
pip <- model_bas$probne0
variable_names <- names(pip)
#pip_df <- data.frame(Variable = numeric_vars,
#                     InclusionProb = pip)
#pip_df <- pip_df[order(pip_df$InclusionProb, decreasing = TRUE),]
#print(pip_df)

selected_bayes <- c( "perimeter_mean", "concave_points_mean", "compactness_mean",
                     "concavity_mean", "area_se", "smoothness_se", "concave_points_se",
                     "fractal_dimension_se","radius_worst", "texture_worst",
                     "fractal_dimension_worst")
```

Logistic Models

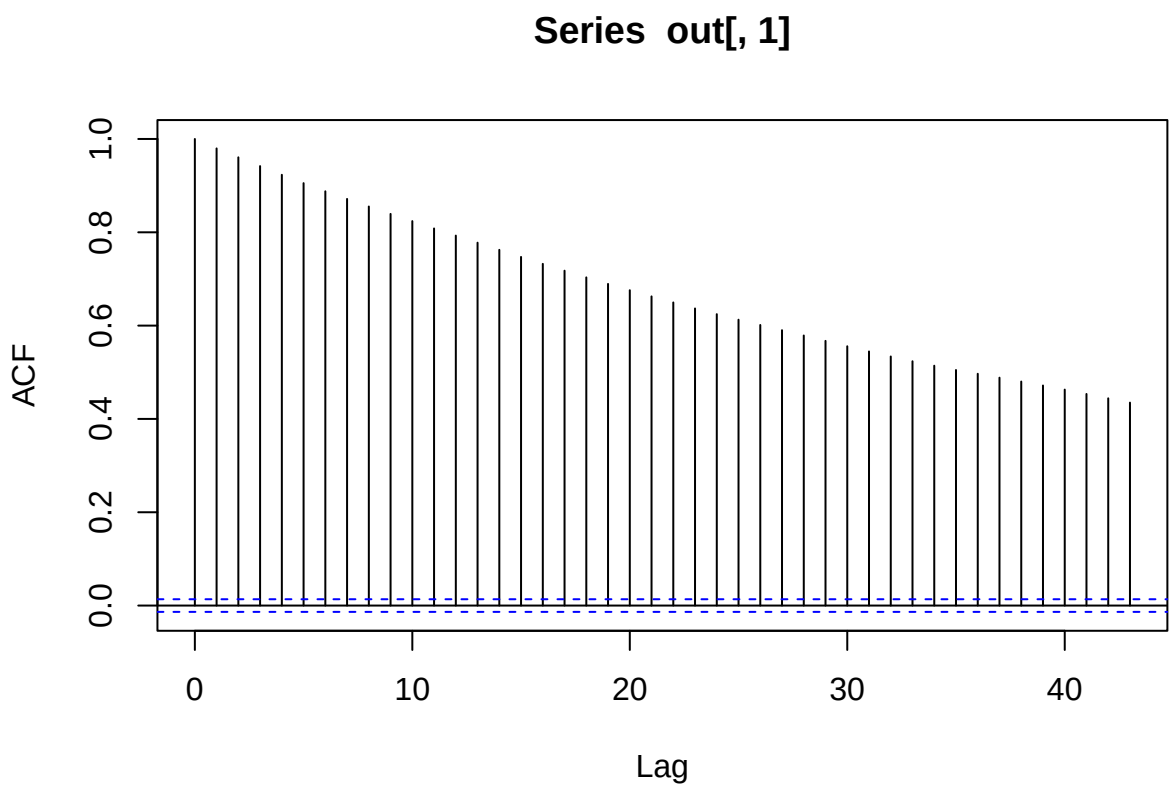
Freq var selection

```
formula_str <- paste("diagnosis ~", paste(selected_freq, collapse = " + "))
formula <- as.formula(formula_str)

freq_model1<-lm(formula, data = data)
beta.start1 <- coef(freq_model1)

out = MCMClogit(formula, data, burnin=1000, mcmc=21000, beta.start = beta.start1)
summary(out)
```

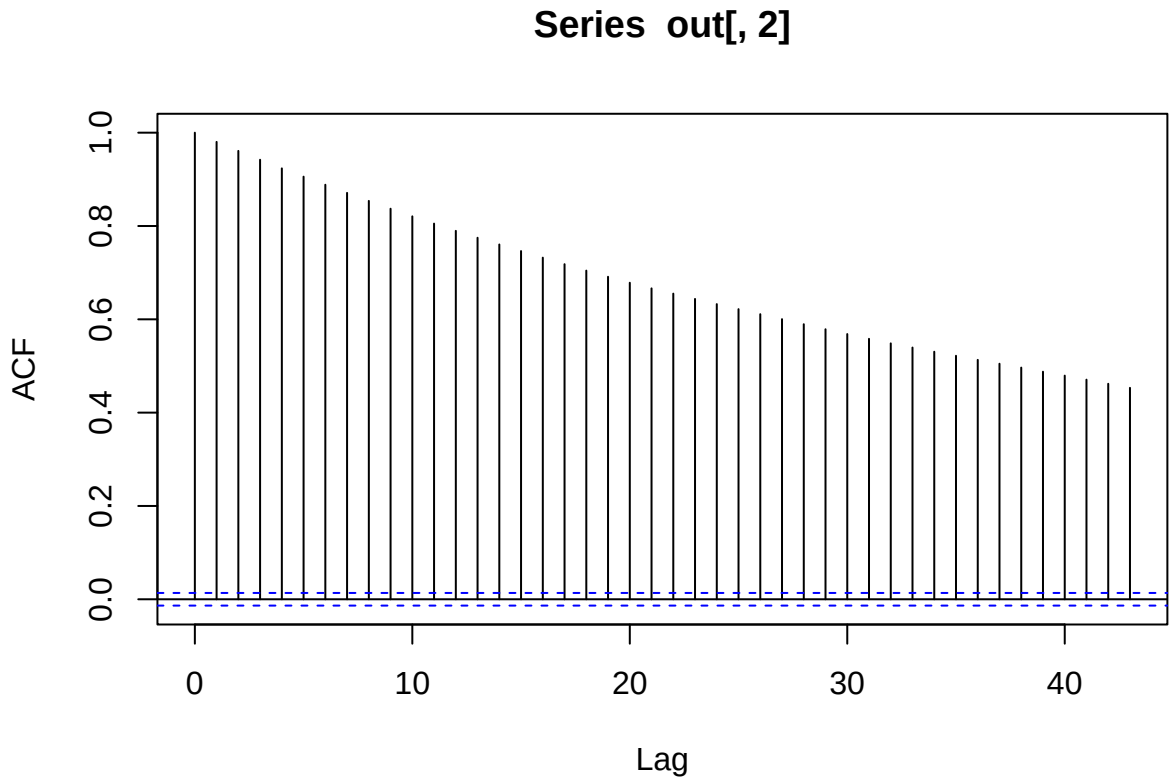
```
##
## Iterations = 1001:22000
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 21000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                              Mean       SD  Naive SE Time-series SE
## (Intercept)               -7.0448   2.7936 0.0192780       0.194235
## texture_mean               0.1402   0.1332 0.0009190       0.009217
## smoothness_mean          212.5324  39.8023 0.2746618       2.930954
## symmetry_mean              6.1214  13.6580 0.0942492       1.029750
## fractal_dimension_mean  -692.6680  86.5229 0.5970649       6.070409
## texture_se                -1.4180   0.7611 0.0052523       0.051882
## smoothness_se           -244.3942 113.0283 0.7799695       7.684728
## compactness_se            22.7986  27.5534 0.1901367       2.002600
## concavity_se              -1.5990  12.5088 0.0863193       0.973608
## concave_points_se        419.3653  67.1342 0.4632698       4.945145
## symmetry_se                0.1725  46.5293 0.3210826       3.015775
## fractal_dimension_se    -254.7769 237.3704 1.6380116      16.019617
## texture_worst              0.2644   0.1237 0.0008536       0.008767
## smoothness_worst          -0.7513  26.7957 0.1849080       1.771922
## symmetry_worst            12.2862   8.1680 0.0563646       0.596335
## fractal_dimension_worst  155.0970  37.1387 0.2562813       2.341975
##
## 2. Quantiles for each variable:
##
##                               2.5%        25%       50%       75%      97.5%
## (Intercept)              -12.45556   -8.79360   -7.0801   -5.1257   -1.54107
## texture_mean              -0.12287    0.04874    0.1382    0.2356    0.40810
## smoothness_mean          133.04711  188.72514  208.3203  240.4691  292.78315
## symmetry_mean            -20.78431   -2.58098    6.6107   15.3513   33.61856
## fractal_dimension_mean  -865.96422 -744.19734 -688.0979 -640.5828 -522.87375
## texture_se                -2.98513   -1.91367   -1.4060   -0.9046   -0.02046
## smoothness_se           -451.60599 -315.71718 -248.1793 -175.6460  -15.88348
## compactness_se           -30.94268    3.70100   23.7214   42.2483   72.24119
## concavity_se             -25.05991  -10.98320   -2.0636    7.6320   23.35489
```

```
## concave_points_se        285.73948  381.17421  414.5063  459.1587  565.12707
## symmetry_se              -90.66652  -27.98892    0.3550   29.4079   98.93149
## fractal_dimension_se    -735.58558 -423.48834 -261.8735  -89.4792  204.34667
## texture_worst              0.02234    0.18775    0.2620    0.3426    0.52044
## smoothness_worst         -55.15123  -18.34344    1.8441   17.3100   53.51026
## symmetry_worst            -2.53864    7.09859   11.6060   17.1774   30.02571
## fractal_dimension_worst   81.74641  131.53188  155.7603  178.0896  233.41108
```

```
acf(out[,1])
```




```
acf(out[,2])
```

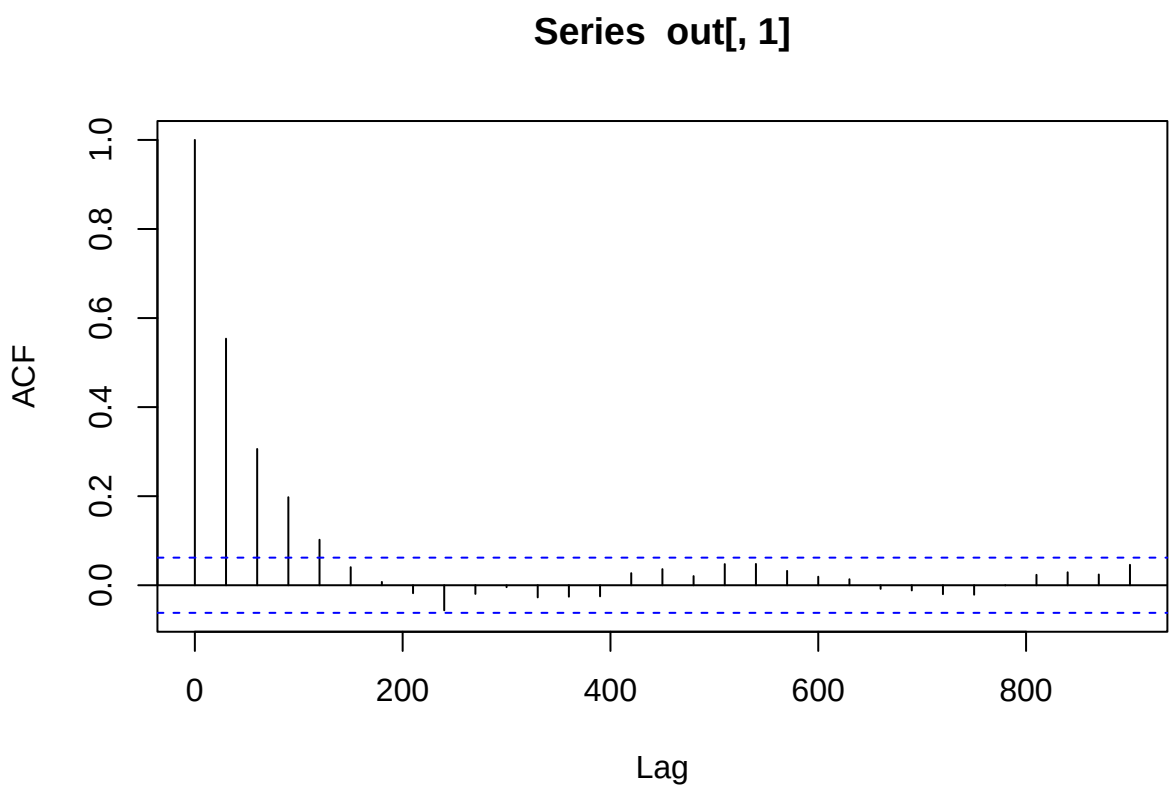



```
# Correct autocorrelation

out = MCMClogit(formula, data, burnin=5000, mcmc=30000, thin = 30,
                beta.start = beta.start1)
summary(out)
```

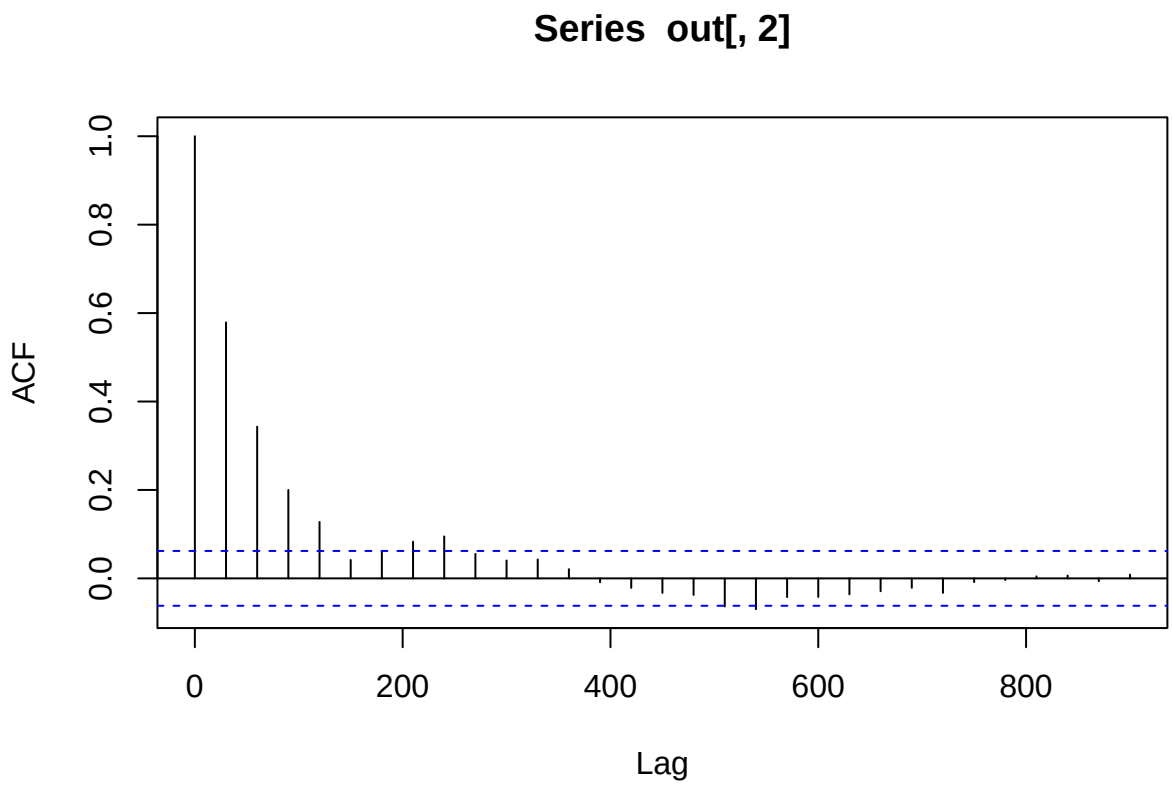
```
##
## Iterations = 5001:34971
## Thinning interval = 30
## Number of chains = 1
## Sample size per chain = 1000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                              Mean       SD Naive SE Time-series SE
## (Intercept)               -6.9619   2.9564 0.093488       0.174505
## texture_mean               0.1449   0.1338 0.004230       0.008603
## smoothness_mean          210.3856  38.8092 1.227254       2.364636
## symmetry_mean              6.7972  13.7695 0.435430       0.874829
## fractal_dimension_mean  -692.9451  85.9090 2.716683       5.109411
## texture_se                -1.4312   0.7698 0.024345       0.043598
## smoothness_se           -245.3894 120.4758 3.809779       6.431210
## compactness_se            20.8806  28.9179 0.914463       1.881365
## concavity_se              -2.1651  11.8429 0.374504       0.841066
## concave_points_se        419.8216  68.7222 2.173187       4.788362
## symmetry_se                2.8399  51.6192 1.632341       3.064199
## fractal_dimension_se    -235.3213 230.1363 7.277549      12.459032
```

```
## texture_worst              0.2585   0.1235 0.003904       0.008201
## smoothness_worst           0.4922  26.7191 0.844933       1.548509
## symmetry_worst            12.2236   8.5569 0.270594       0.595713
## fractal_dimension_worst  153.6350  38.6341 1.221717       2.154905
##
## 2. Quantiles for each variable:
##
##                                2.5%        25%       50%       75%      97.5%
## (Intercept)             -1.257e+01   -8.82359   -7.1256   -4.9263   -1.06303
## texture_mean            -1.264e-01    0.05609    0.1493    0.2347    0.42288
## smoothness_mean          1.346e+02  185.56985  207.4429  237.4691  285.25906
## symmetry_mean           -2.133e+01   -2.07081    7.2447   16.8415   33.46638
## fractal_dimension_mean  -8.685e+02 -748.06764 -687.5111 -638.0705 -535.08845
## texture_se              -3.011e+00   -1.90562   -1.3896   -0.9116   -0.01158
## smoothness_se           -4.695e+02 -329.76049 -253.4453 -166.7919    2.89369
## compactness_se          -3.356e+01    1.54953   21.3018   40.3877   76.28100
## concavity_se            -2.669e+01  -10.76965   -2.0245    6.0901   20.70983
## concave_points_se        2.861e+02  374.51992  416.7823  463.6432  566.28489
## symmetry_se             -1.014e+02  -29.30766    2.0131   37.1225   99.63610
## fractal_dimension_se    -7.050e+02 -385.97951 -235.5333  -66.6496  194.69516
## texture_worst            2.987e-03    0.17517    0.2570    0.3330    0.52035
## smoothness_worst        -5.199e+01  -17.05354   -0.2086   17.8640   54.16787
## symmetry_worst          -2.732e+00    6.80055   11.5672   17.4516   30.08029
## fractal_dimension_worst  7.957e+01  126.52236  155.9399  178.0914  231.92666
```

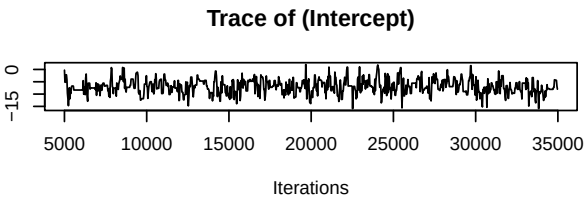
```
acf(out[,1])
```

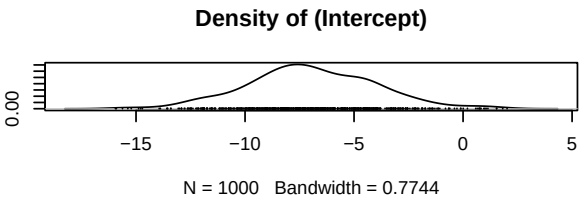


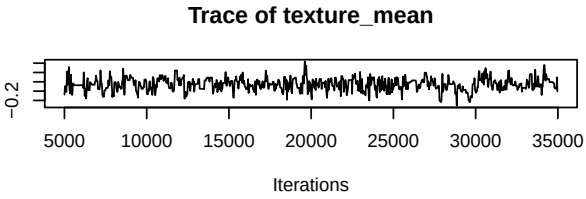
```r
acf(out[,2])
```

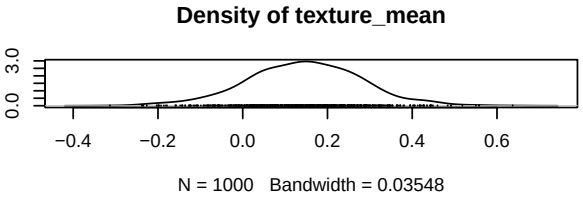


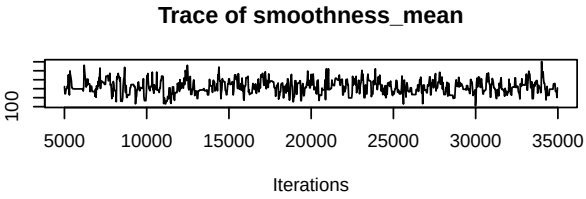

```r
plot(out)
```

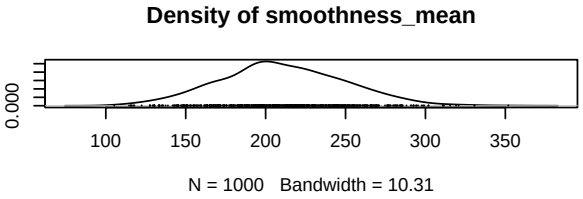

Trace of (Intercept)
−15
0
5000
10000
15000
20000
25000
30000
35000
Iterations

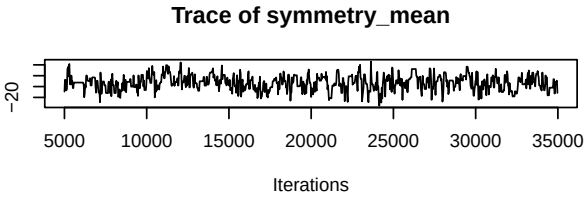

Density of (Intercept)
0.00
−15
−10
−5
0
5
N = 1000 Bandwidth = 0.7744

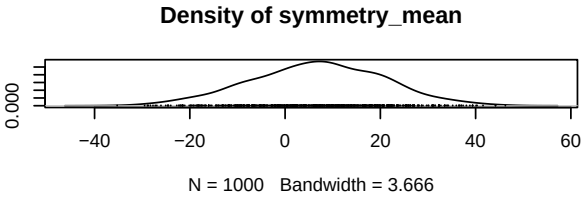

Trace of texture_mean
−0.2
5000
10000
15000
20000
25000
30000
35000
Iterations

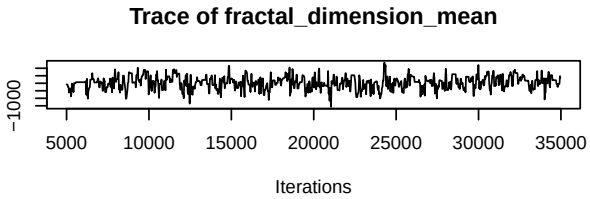

Density of texture_mean
0.0
3.0
−0.4
−0.2
0.0
0.2
0.4
0.6
N = 1000 Bandwidth = 0.03548

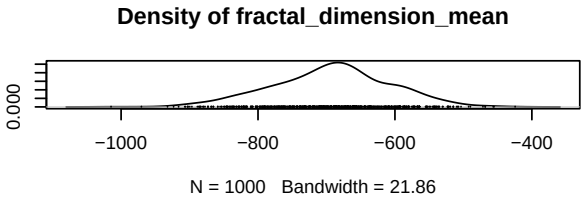

Trace of smoothness_mean
100
5000
10000
15000
20000
25000
30000
35000
Iterations

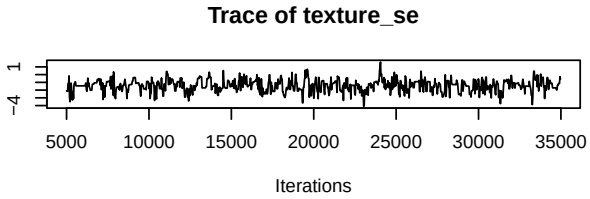

Density of smoothness_mean
0.000
100
150
200
250
300
350
N = 1000 Bandwidth = 10.31

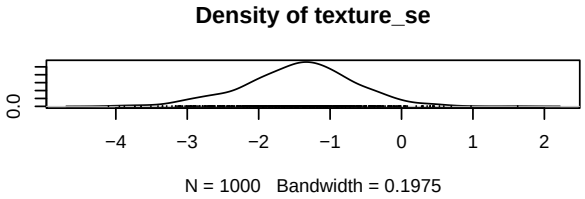

Trace of symmetry_mean
−20
5000
10000
15000
20000
25000
30000
35000
Iterations

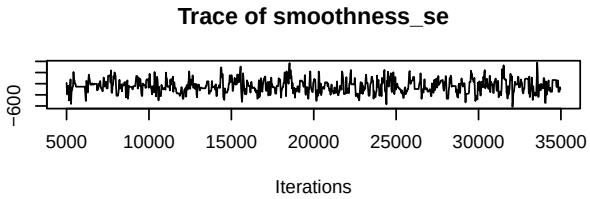

Density of symmetry_mean
0.000
−40
−20
0
20
40
60
N = 1000 Bandwidth = 3.666

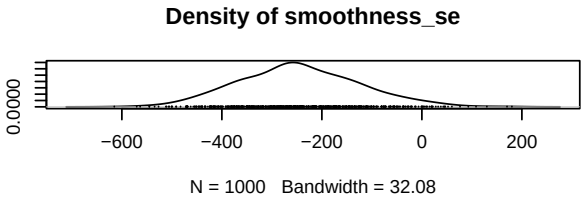

Trace of fractal_dimension_mean
−1000
5000
10000
15000
20000
25000
30000
35000
Iterations

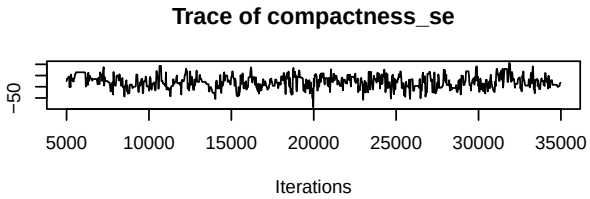

Density of fractal_dimension_mean
0.000
−1000
−800
−600
−400
N = 1000 Bandwidth = 21.86

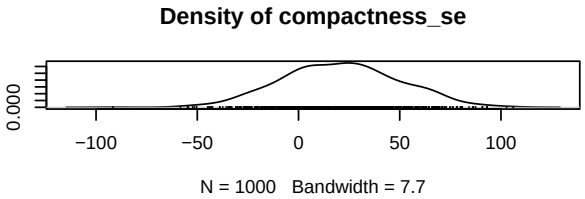

Trace of texture_se
−4
1
5000
10000
15000
20000
25000
30000
35000
Iterations

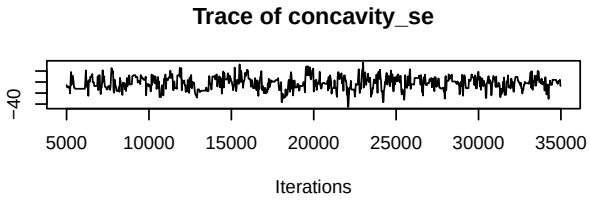

Density of texture_se
0.0
−4
−3
−2
−1
0
1
2
N = 1000 Bandwidth = 0.1975

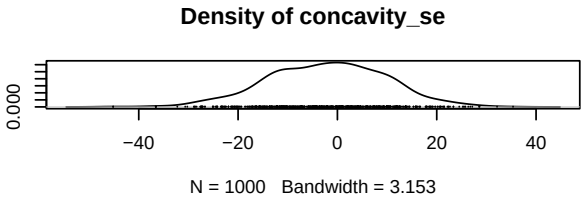

Trace of smoothness_se
−600
5000
10000
15000
20000
25000
30000
35000
Iterations

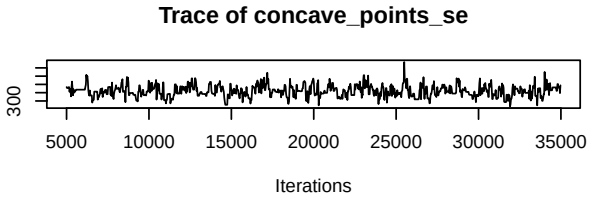

Density of smoothness_se
0.0000
−600
−400
−200
0
200
N = 1000 Bandwidth = 32.08

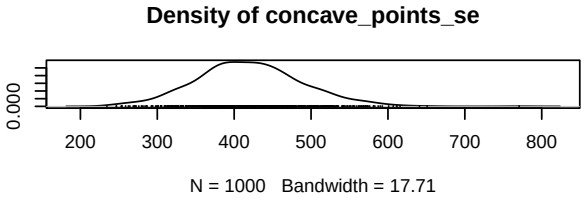

Trace of compactness_se
−50
5000
10000
15000
20000
25000
30000
35000
Iterations

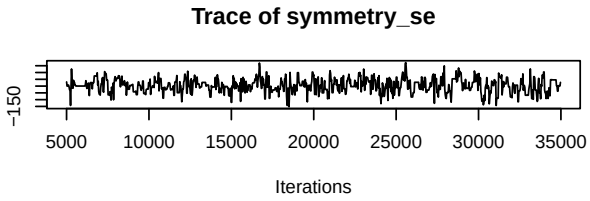

Density of compactness_se
0.000
−100
−50
0
50
100
N = 1000 Bandwidth = 7.7

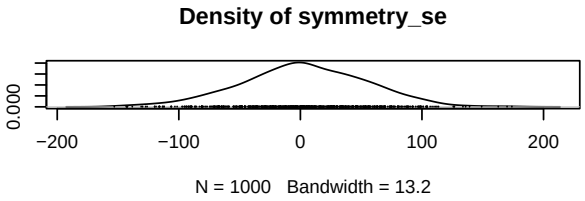

Trace of concavity_se
−40
5000
10000
15000
20000
25000
30000
35000
Iterations

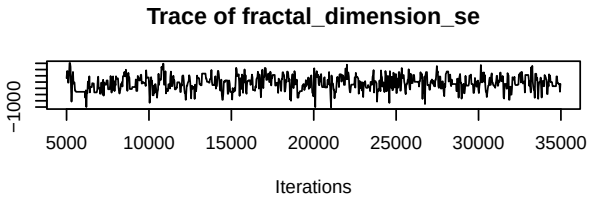

Density of concavity_se
0.000
−40
−20
0
20
40
N = 1000 Bandwidth = 3.153

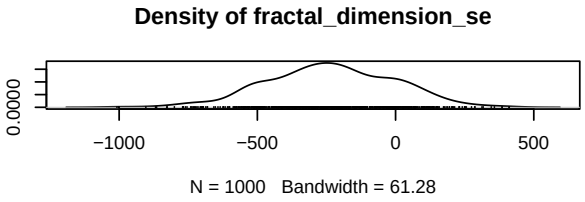

Trace of concave_points_se
300
5000
10000
15000
20000
25000
30000
35000
Iterations

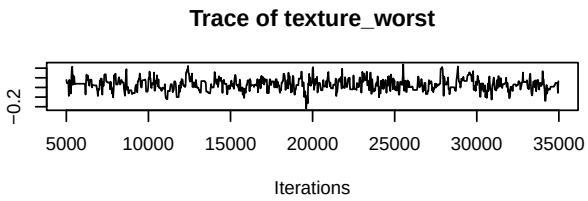

Density of concave_points_se
0.000
200
300
400
500
600
700
800
N = 1000 Bandwidth = 17.71

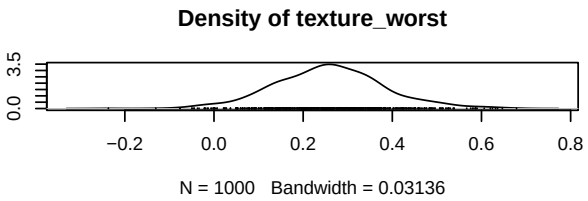

Trace of symmetry_se
−150
5000
10000
15000
20000
25000
30000
35000
Iterations

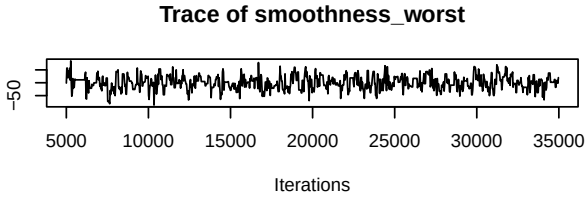

Density of symmetry_se
0.000
−200
−100
0
100
200
N = 1000 Bandwidth = 13.2

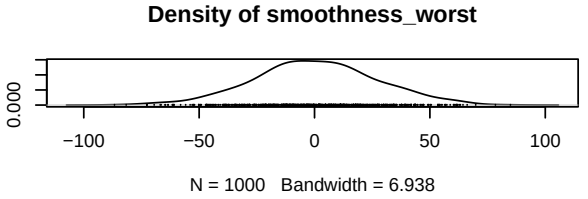

Trace of fractal_dimension_se
−1000
5000
10000
15000
20000
25000
30000
35000
Iterations

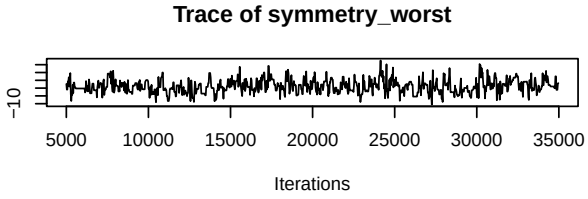

Density of fractal_dimension_se
0.0000
−1000
−500
0
500
N = 1000 Bandwidth = 61.28

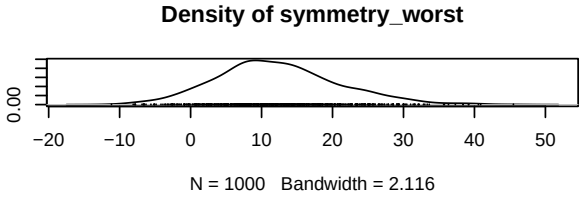


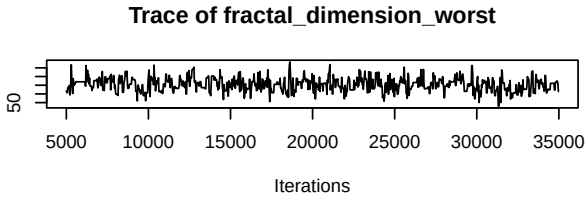


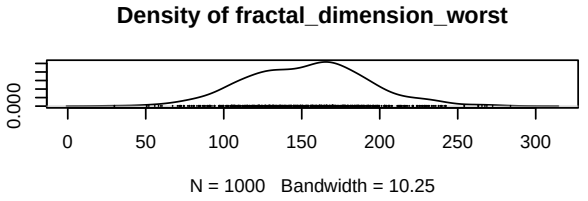












Bayes var selection

```
formula_str_b <- paste("diagnosis ~", paste(selected_bayes, collapse = " + "))
formula_b <- as.formula(formula_str_b)

# starting point
freq_model<-lm(formula_b, data = data)
beta.start <- coef(freq_model)

out_b = MCMClogit(formula_b, data, burnin=1000, mcmc=21000)
```

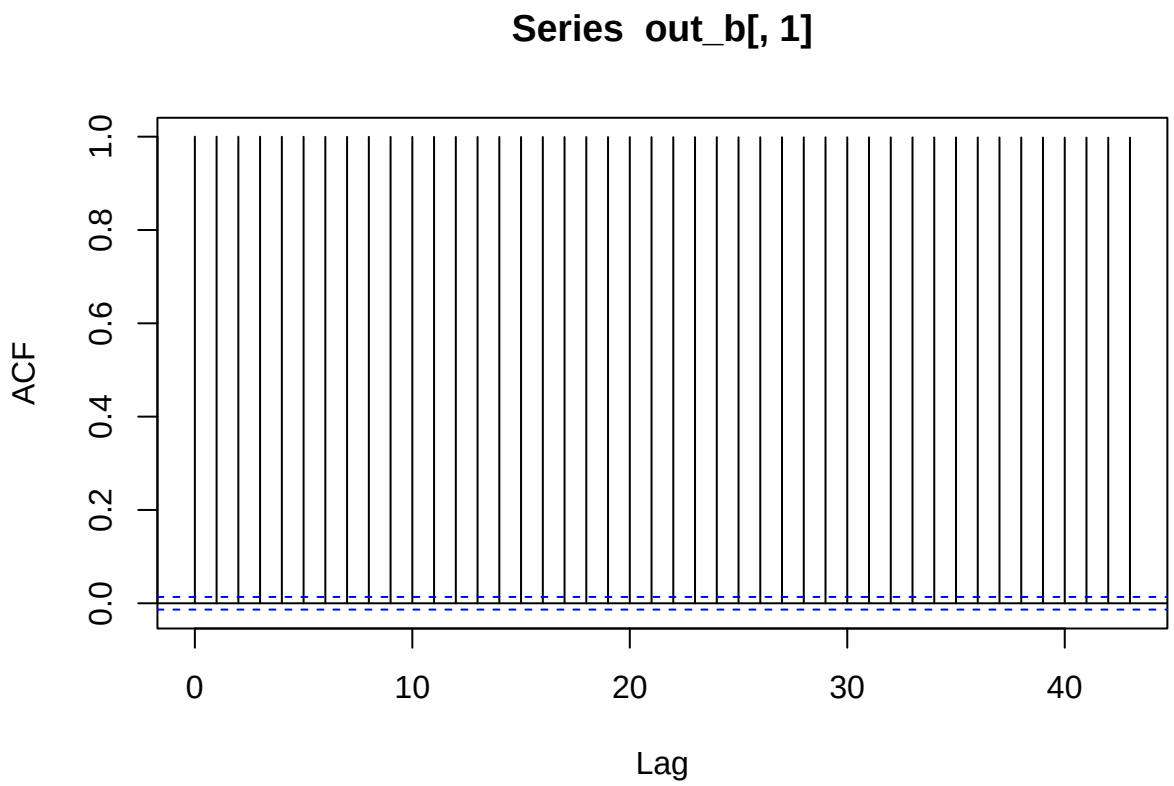
```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
summary(out_b)
```

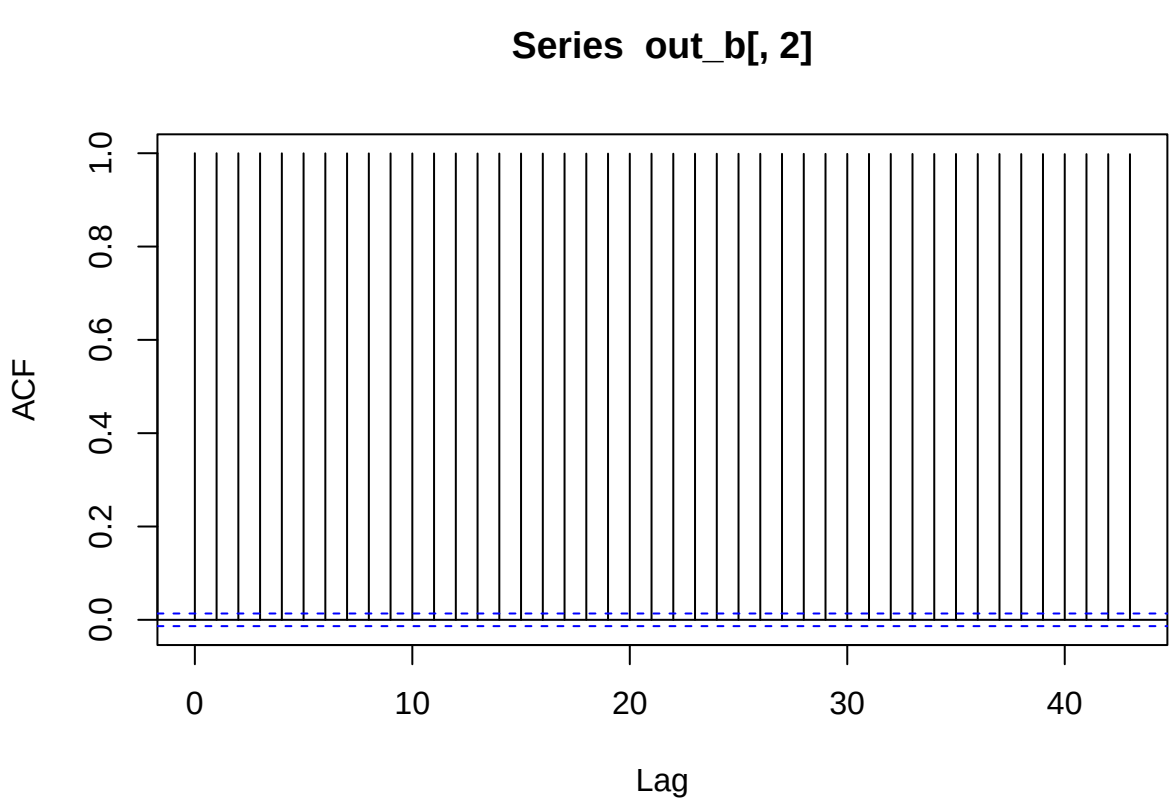
```
##
## Iterations = 1001:22000
## Thinning interval = 1
## Number of chains = 1
```

```
## Sample size per chain = 21000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                              Mean SD Naive SE Time-series SE
## (Intercept)               -66.8917  0        0              0
## perimeter_mean             -0.3481  0        0              0
## concave_points_mean       113.2543  0        0              0
## compactness_mean          -67.0638  0        0              0
## concavity_mean             36.5866  0        0              0
## area_se                     0.1428  0        0              0
## smoothness_se             433.2403  0        0              0
## concave_points_se         428.0355  0        0              0
## fractal_dimension_se    -2564.0379  0        0              0
## radius_worst                3.4530  0        0              0
## texture_worst               0.4372  0        0              0
## fractal_dimension_worst   318.5212  0        0              0
##
## 2. Quantiles for each variable:
##
##                              2.5%        25%        50%        75%      97.5%
## (Intercept)               -66.8917   -66.8917   -66.8917   -66.8917   -66.8917
## perimeter_mean             -0.3481    -0.3481    -0.3481    -0.3481    -0.3481
## concave_points_mean       113.2543   113.2543   113.2543   113.2543   113.2543
## compactness_mean          -67.0638   -67.0638   -67.0638   -67.0638   -67.0638
## concavity_mean             36.5866    36.5866    36.5866    36.5866    36.5866
## area_se                     0.1428     0.1428     0.1428     0.1428     0.1428
## smoothness_se             433.2403   433.2403   433.2403   433.2403   433.2403
## concave_points_se         428.0355   428.0355   428.0355   428.0355   428.0355
## fractal_dimension_se    -2564.0379 -2564.0379 -2564.0379 -2564.0379 -2564.0379
## radius_worst                3.4530     3.4530     3.4530     3.4530     3.4530
## texture_worst               0.4372     0.4372     0.4372     0.4372     0.4372
## fractal_dimension_worst   318.5212   318.5212   318.5212   318.5212   318.5212
```

```
acf(out_b[,1])
```


Series out_b[, 1]
ACF
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
Lag

```
acf(out_b[,2])
```


Series out_b[, 2]
ACF
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
Lag

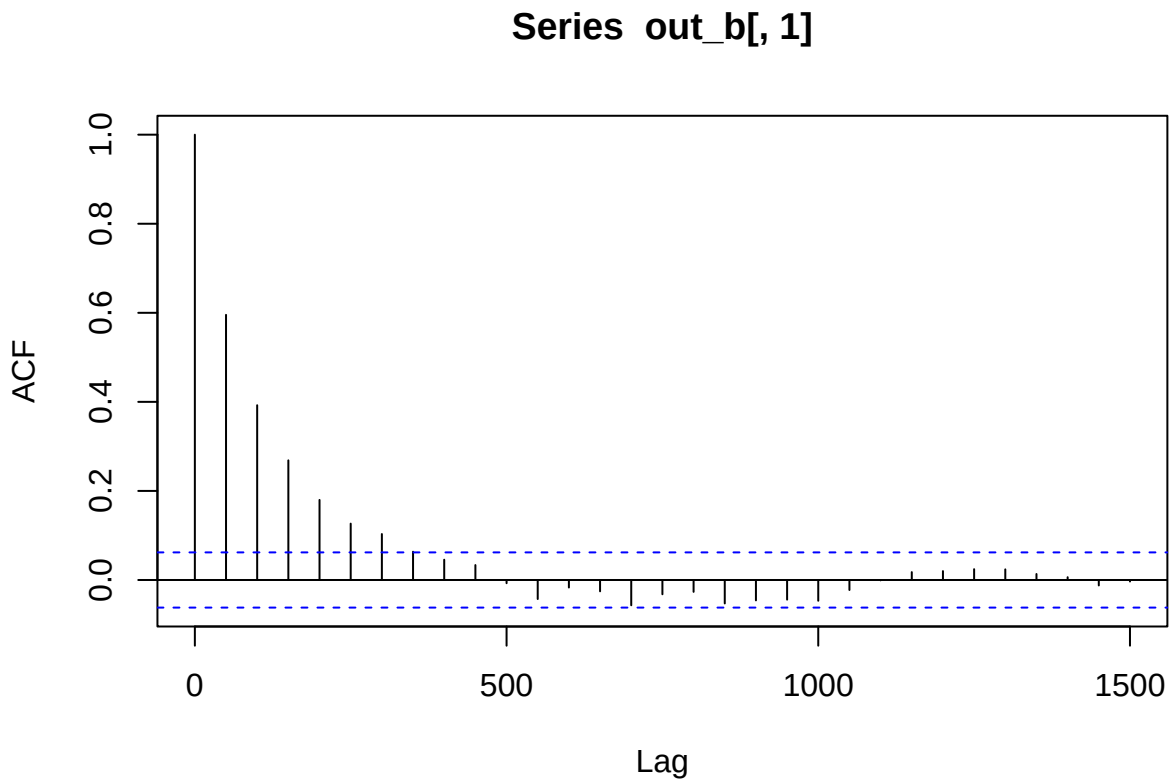
```
out_b = MCMClogit(formula_b, data, burnin=5000, mcmc=50000,
                  beta.start = beta.start, thin = 50, tune=0.5)
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

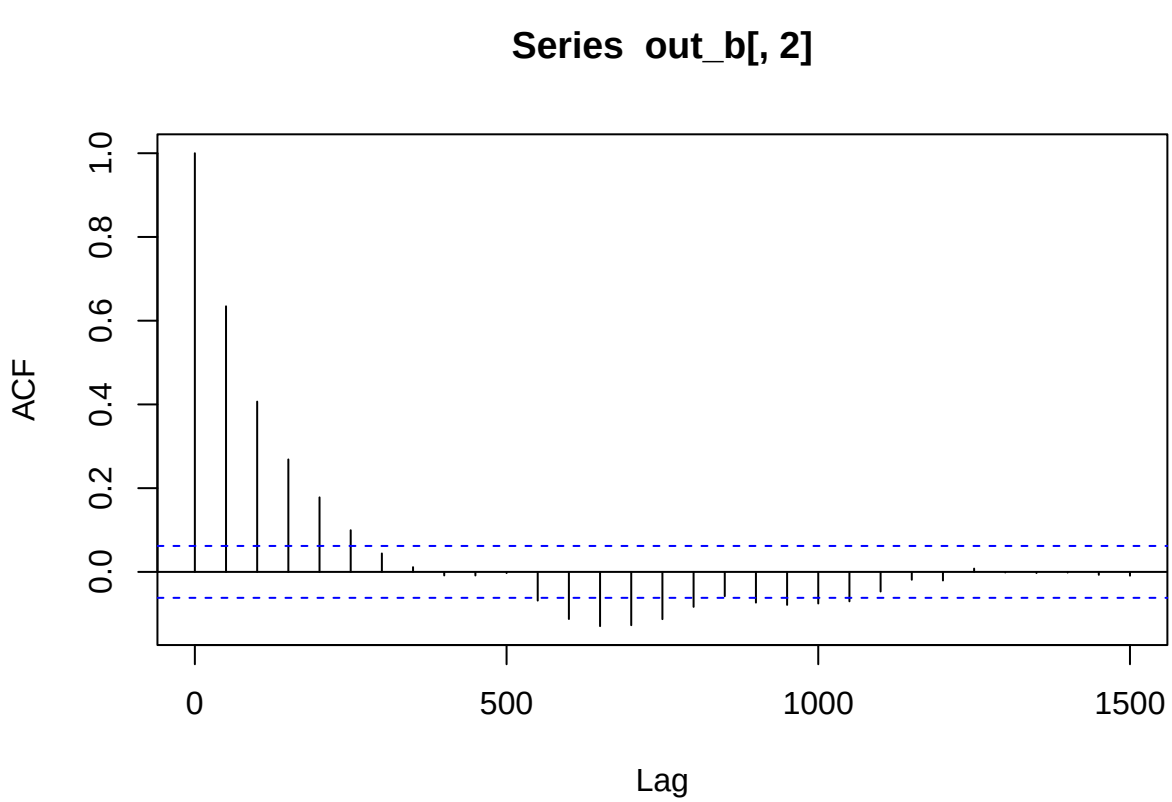
```
summary(out_b)
```

```
##
## Iterations = 5001:54951
## Thinning interval = 50
## Number of chains = 1
## Sample size per chain = 1000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                              Mean        SD  Naive SE Time-series SE
## (Intercept)             -4.089e+01   6.10325 1.930e-01      4.069e-01
## perimeter_mean          -8.767e-02   0.08165 2.582e-03      5.462e-03
## concave_points_mean      7.789e+01  33.64842 1.064e+00      2.578e+00
## compactness_mean        -4.411e+01  20.79019 6.574e-01      1.713e+00
## concavity_mean           1.849e+01  10.76886 3.405e-01      8.339e-01
## area_se                 -7.147e-03   0.01074 3.396e-04      5.185e-04
## smoothness_se            2.135e+02 150.05698 4.745e+00      1.353e+01
## concave_points_se        2.921e+02 101.48434 3.209e+00      5.821e+00
## fractal_dimension_se    -1.196e+03 340.24976 1.076e+01      1.952e+01
## radius_worst             1.662e+00   0.44882 1.419e-02      2.645e-02
## texture_worst            2.749e-01   0.05205 1.646e-03      3.775e-03
## fractal_dimension_worst  1.559e+02  46.60596 1.474e+00      3.093e+00
##
## 2. Quantiles for each variable:
##
##                              2.5%        25%        50%        75%      97.5%
## (Intercept)             -5.348e+01 -4.504e+01 -4.084e+01 -3.637e+01  -29.41492
## perimeter_mean          -2.363e-01 -1.449e-01 -9.337e-02 -3.226e-02    0.08183
## concave_points_mean      1.352e+01  5.524e+01  7.861e+01  1.017e+02  141.59098
## compactness_mean        -8.455e+01 -5.933e+01 -4.349e+01 -2.957e+01   -4.49315
## concavity_mean          -2.063e+00  1.172e+01  1.872e+01  2.589e+01   39.71891
## area_se                 -2.774e-02 -1.452e-02 -6.903e-03 -1.231e-04    0.01324
## smoothness_se           -8.381e+01  1.137e+02  2.063e+02  3.125e+02  512.29411
## concave_points_se        8.751e+01  2.252e+02  2.941e+02  3.573e+02  499.56987
## fractal_dimension_se    -1.905e+03 -1.411e+03 -1.177e+03 -9.488e+02 -589.19519
## radius_worst             7.393e-01  1.375e+00  1.711e+00  1.994e+00    2.41334
## texture_worst            1.752e-01  2.396e-01  2.744e-01  3.086e-01    0.37594
## fractal_dimension_worst  7.238e+01  1.237e+02  1.556e+02  1.866e+02  255.52220
```

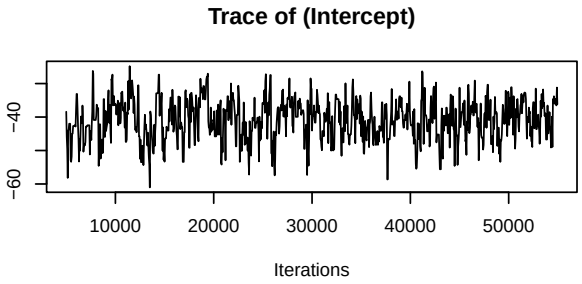
```
acf(out_b[,1])
```

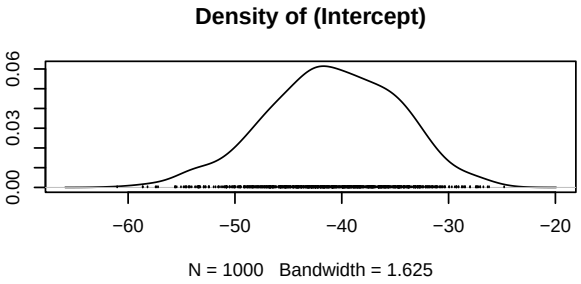

Series out_b[, 1]
ACF
0.0
0.2
0.4
0.6
0.8
1.0
0
500
1000
1500
Lag

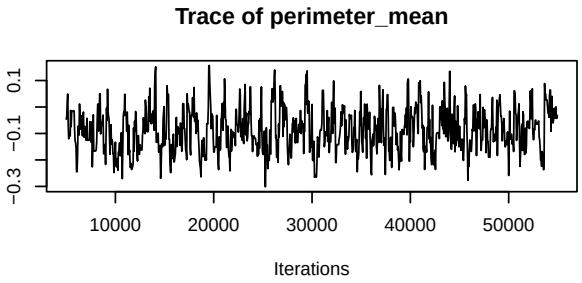
```
acf(out_b[,2])
```

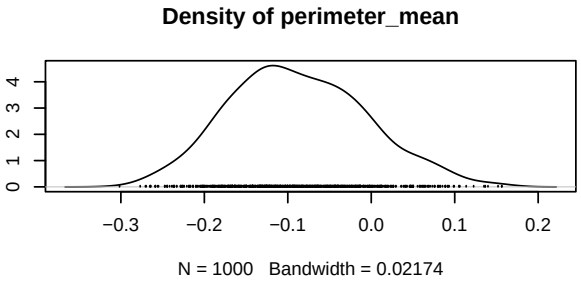

Series out_b[, 2]
ACF
0.0
0.2
0.4
0.6
0.8
1.0
0
500
1000
1500
Lag

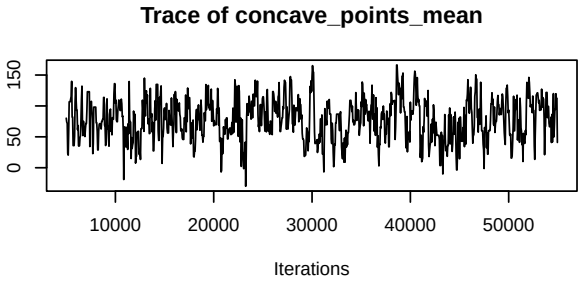
```
plot(out_b)
```

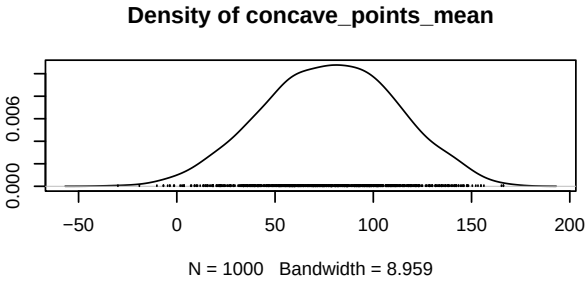

Trace of (Intercept)
−60
−40
10000
20000
30000
40000
50000
Iterations

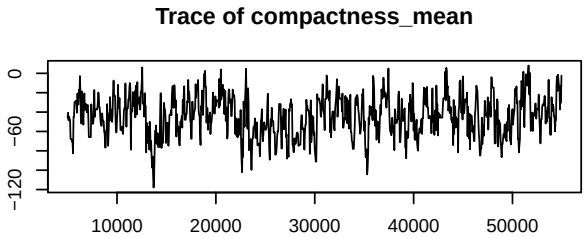

Density of (Intercept)
0.00
0.03
0.06
−60
−50
−40
−30
−20
N = 1000 Bandwidth = 1.625

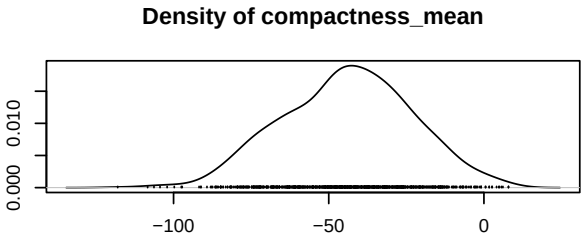

Trace of perimeter_mean
−0.3
−0.1
0.1
10000
20000
30000
40000
50000
Iterations

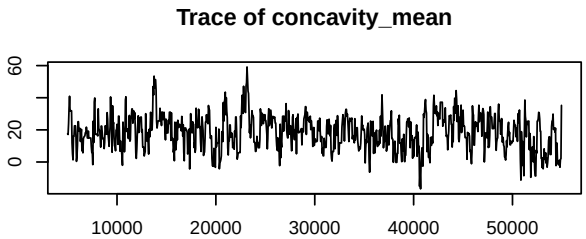

Density of perimeter_mean
0
1
2
3
4
−0.3
−0.2
−0.1
0.0
0.1
0.2
N = 1000 Bandwidth = 0.02174

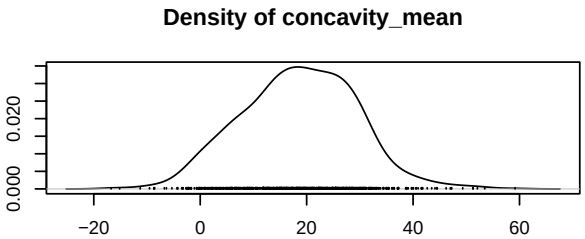

Trace of concave_points_mean
0
50
150
10000
20000
30000
40000
50000
Iterations

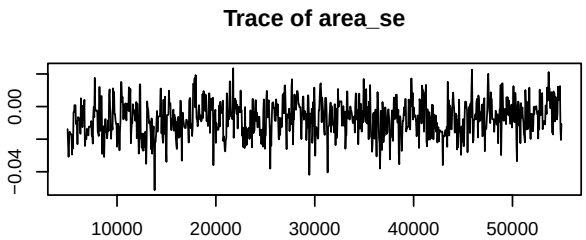

Density of concave_points_mean
0.000
0.006
−50
0
50
100
150
200
N = 1000 Bandwidth = 8.959

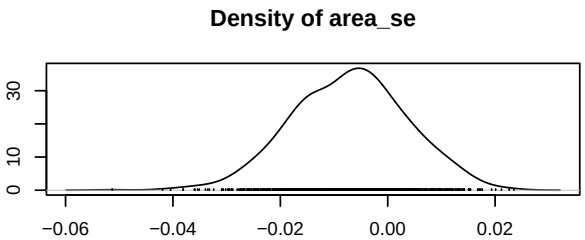

Trace of compactness_mean
0
−60
−120
10000
20000
30000
40000
50000
Iterations

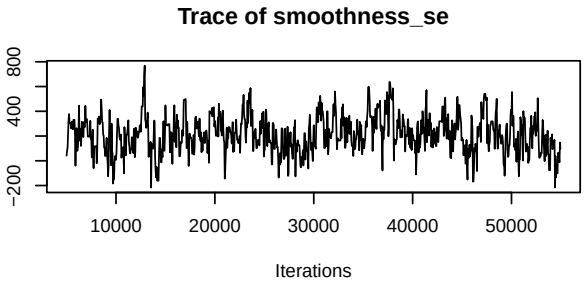

Density of compactness_mean
0.000
0.010
−100
−50
0
N = 1000 Bandwidth = 5.536

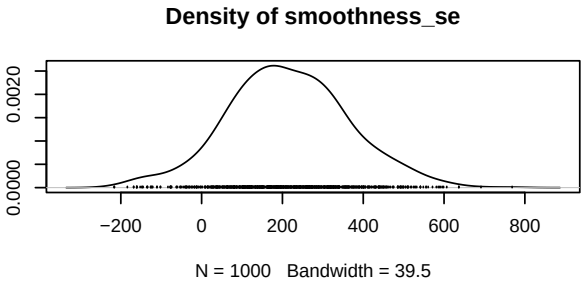

Trace of concavity_mean
60
20
0
10000
20000
30000
40000
50000
Iterations

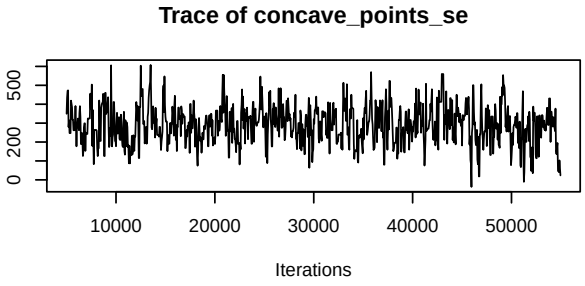

Density of concavity_mean
0.020
0.000
−20
0
20
40
60
N = 1000 Bandwidth = 2.816

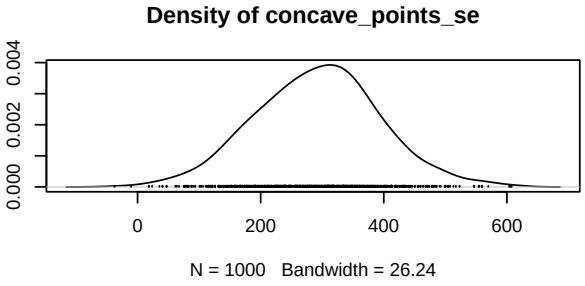

Trace of area_se
0.00
−0.04
10000
20000
30000
40000
50000
Iterations

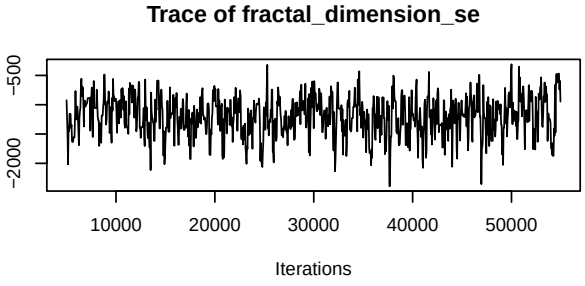

Density of area_se
30
10
0
−0.06
−0.04
−0.02
0.00
0.02
N = 1000 Bandwidth = 0.002859

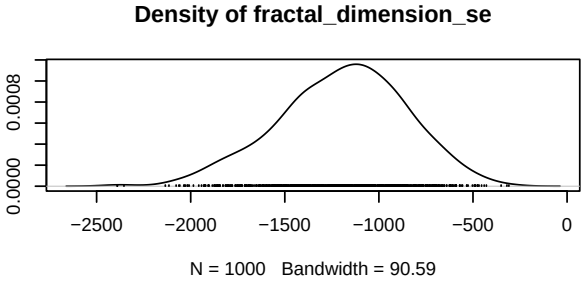

Trace of smoothness_se
−200
400
800
10000
20000
30000
40000
50000
Iterations

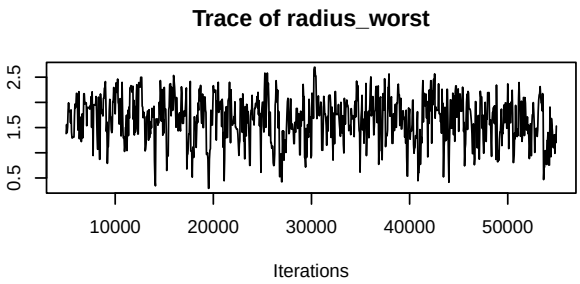

Density of smoothness_se
0.0000
0.0020
−200
0
200
400
600
800
N = 1000 Bandwidth = 39.5

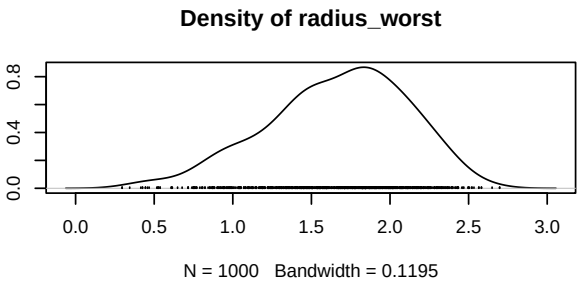

Trace of concave_points_se
0
200
500
10000
20000
30000
40000
50000
Iterations

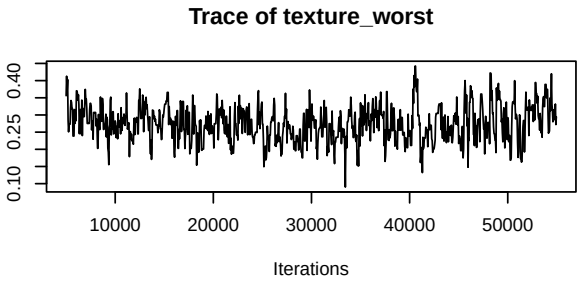

Density of concave_points_se
0.000
0.002
0.004
0
200
400
600
N = 1000 Bandwidth = 26.24

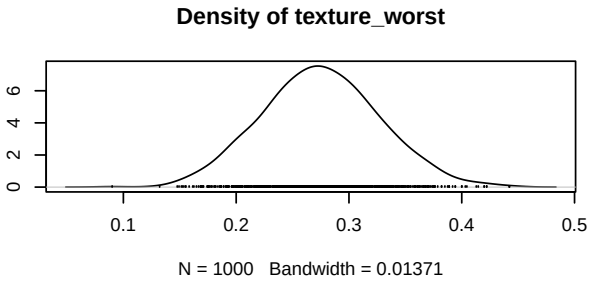

Trace of fractal_dimension_se
−2000
−500
10000
20000
30000
40000
50000
Iterations

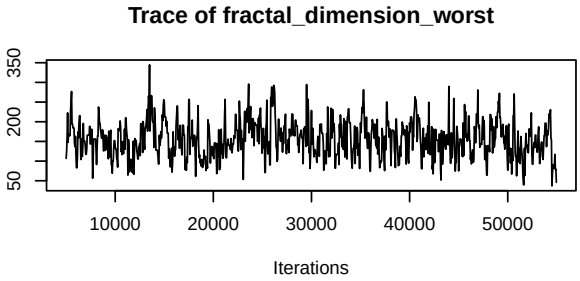

Density of fractal_dimension_se
0.0000
0.0008
−2500
−2000
−1500
−1000
−500
0
N = 1000 Bandwidth = 90.59

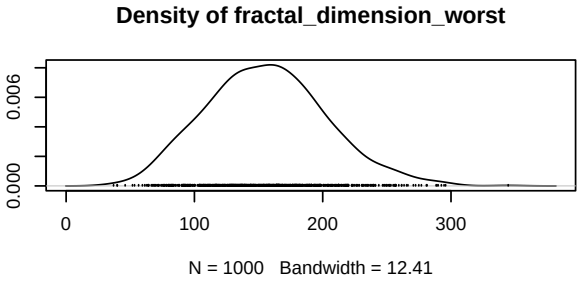













```
# Run Bayesian logistic regression with Spike-and-Slab priors (to variable selection)
set.seed(123)
model <- MCMClogit(formula, data = data, burnin = 5000, mcmc = 20000
                   , marginal.likelihood = "Laplace") # , thin = 10, b0 = 0, B0 = 0.1
```

```
## Warning in MCMClogit(formula, data = data, burnin = 5000, mcmc = 20000, : Cannot calculate marginal l
```

```
summary(model)
```

```
##
## Iterations = 5001:25000
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 20000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                              Mean       SD  Naive SE Time-series SE
## (Intercept)               -6.8170   2.9513 0.0208690       0.219795
## texture_mean               0.1294   0.1348 0.0009531       0.009661
## smoothness_mean          207.3107  41.2005 0.2913315       3.233150
```

```
## symmetry_mean              6.9549  13.6898 0.0968017       0.997838
## fractal_dimension_mean  -684.5427  91.4640 0.6467481       7.597434
## texture_se                -1.4813   0.7652 0.0054108       0.054139
## smoothness_se           -234.4591 126.4486 0.8941266       9.664144
## compactness_se            21.2337  26.1173 0.1846775       1.799246
## concavity_se              -1.4548  11.8178 0.0835642       0.846533
## concave_points_se        411.5040  64.7565 0.4578975       4.564841
## symmetry_se               -1.2348  53.9843 0.3817264       3.947217
## fractal_dimension_se    -193.6926 218.7169 1.5465618      12.937977
## texture_worst             0.2698   0.1255 0.0008877       0.009101
## smoothness_worst          0.9483  28.4640 0.2012712       2.053050
## symmetry_worst           12.2825   8.7408 0.0618070       0.658451
## fractal_dimension_worst  147.8957  37.6905 0.2665122       2.554404
##
## 2. Quantiles for each variable:
##
##                              2.5%        25%       50%       75%      97.5%
## (Intercept)              -12.51578   -8.78930   -6.8489   -4.7347   -0.98681
## texture_mean              -0.14451    0.03281    0.1240    0.2273    0.38854
## smoothness_mean          126.36954  181.04922  207.4663  233.5748  289.55512
## symmetry_mean            -20.77997   -1.01465    7.3981   15.9900   33.16468
## fractal_dimension_mean  -876.85892 -744.76209 -676.1047 -624.8130 -519.74380
## texture_se                -2.98677   -1.92703   -1.5112   -0.9390   -0.04385
## smoothness_se           -492.69637 -319.84949 -241.2256 -153.4581   38.46158
## compactness_se           -30.59198    5.34563   19.9356   38.9766   73.12934
## concavity_se             -25.61537   -8.41350   -1.4880    6.0837   21.32527
## concave_points_se        296.11128  368.03285  407.6404  450.6254  546.85401
## symmetry_se             -105.48846  -39.57962    1.0433   37.1174  108.12212
## fractal_dimension_se    -656.33024 -324.37467 -186.6719  -45.9750  200.42144
## texture_worst             0.04377    0.17585    0.2714    0.3511    0.53608
## smoothness_worst         -54.51081  -18.36763    0.8286   21.8650   56.01089
## symmetry_worst            -4.58397    6.13773   12.0131   18.5500   29.77524
## fractal_dimension_worst   82.79661  124.27778  144.7862  172.0666  233.27842
```

```
apply(model, 2, function(x) mean(x != 0))  # Approximate inclusion probability
```

```
##             (Intercept)            texture_mean         smoothness_mean
##                       1                       1                       1
##           symmetry_mean  fractal_dimension_mean              texture_se
##                       1                       1                       1
##           smoothness_se         compactness_se            concavity_se
##                       1                       1                       1
##       concave_points_se            symmetry_se    fractal_dimension_se
##                       1                       1                       1
##           texture_worst       smoothness_worst          symmetry_worst
##                       1                       1                       1
## fractal_dimension_worst
##                       1
```

Evaluate Models with Deviance Information Criterion (DIC)

In the following code, we will calculate the Deviance Information Criterion (DIC) for both the Frequentist and Bayesian models. The DIC is a measure of model fit that penalizes the complexity of the model. Lower

values of DIC indicate better model fit. The DIC is calculated as follows:

$$DIC = \bar{D} + p_D$$

where:
- $\bar{D}$ is the posterior mean deviance:

$$\bar{D} = \mathbb{E}[D(\theta) \mid \mathcal{D}]$$

with $D(\theta) = -2 \log p(\mathcal{D} \mid \theta)$, the deviance evaluated at parameter θ. - p_D a penalization term (effective number of parameters to penalize model complexity):

$$p_D = \bar{D} - D(\hat{\theta})$$

where $\hat{\theta}$ is the posterior mean of θ.

The R implementation of the DIC function is as follows and was developed with help of Prof Michael Wiper:

```
# DIC Code
DIC = function(model, X, data, target) {
  dev = 0
  # Calculate Average Deviance of MCMC
  for (i in 1:nrow(model)) {
    params <- model[i,]
    p = inv.logit(X %*% params)
    p[data[target] == 0] = 1-p[data[target] == 0]
    dev = dev - 2 * sum(log(p))  # Negative log-likelihood
  }
  D_bar = dev / nrow(model)

  # D_theta: Deviance at the posterior mean (using the average parameter values)
  posterior_means <- colMeans(model)
  linear_predictor <- X %*% posterior_means
  p_post <- inv.logit(linear_predictor)
  p_post[data[target] == 0] = 1-p_post[data[target] == 0]

  D_theta = -2 * sum(log(p_post)) # Deviance at the posterior mean

  # p_D: Posterior deviance penalty
  p_D = D_bar - D_theta

  # DIC
  DIC = D_bar + p_D

  return(list(DIC=DIC, D_bar=D_bar, p_D=p_D))
}
```

We now continue with applying the DIC Score to the model derived from frequentist variable selection and the model derived from Bayesian variable selection. The straight forward conclusion is that the DIC is significantly better (lower) for the model that was set up with the Bayesian Variable Selection approach. Based on this result, we conclude this to be the best model and will use it for further analysis.

```
# Frequentist
model = out
X <- model.matrix(~ texture_mean + smoothness_mean + symmetry_mean +
```

```
    fractal_dimension_mean + texture_se + smoothness_se + compactness_se +
    concavity_se + concave_points_se + symmetry_se + fractal_dimension_se +
    texture_worst + smoothness_worst + symmetry_worst + fractal_dimension_worst, data = data) # model m
target = "diagnosis"

print("Frequentist Variable Selection DIC Score")
```

```
## [1] "Frequentist Variable Selection DIC Score"
```

```
DIC(model, X, data, target)
```

```
## $DIC
## [1] 245.5246
##
## $D_bar
## [1] 229.9737
##
## $p_D
## [1] 15.5509
```

```
# Bayesian
model = out_b
X <- model.matrix(~ perimeter_mean + concave_points_mean + compactness_mean +
    concavity_mean + area_se + smoothness_se + concave_points_se +
    fractal_dimension_se + radius_worst + texture_worst + fractal_dimension_worst, data = data) # model
target = "diagnosis"

print("Bayesian Variable Selection DIC Score")
```

```
## [1] "Bayesian Variable Selection DIC Score"
```

```
DIC(model, X, data, target)
```

```
## $DIC
## [1] 89.86894
##
## $D_bar
## [1] 80.33019
##
## $p_D
## [1] 9.538756
```

Prediction

Since we already have our posterior coefficients from the MCMC samples, predicting is fairly straightforward. We will just have to turn the log odds back into probability space and choose a suitable threshold probability for the two classes (1 = malignant (cancer), 0 = benign)).

The standard threshold is 0.5. However, in the light of classifying cancer, one might choose this threshold more carefully. Assuming we are performing an initial cancer screening, we would prefer having a false

positive than a false negative. In simpler words, we would rather initially classify something as cancer that later turns out as no cancer than missing a cancer diagnosis that actually is one. By lowering the threshold, we reduce our exposure to false negatives and increase sensitivity.

```
# posterior mean coefficients from MCMC samples
posterior_means <- colMeans(out_b)

# linear preds is in log odds space
linear_preds <- X %*% posterior_means

# inverse logit to get probabilities
prob_preds <- 1 / (1 + exp(-linear_preds))

# turn proba into binary prediction
test_preds <- ifelse(prob_preds >= 0.4, 1, 0)
```

Now that we have our predictions, let's analyze the outcome

```
conf_matrix <- confusionMatrix(as.factor(test_preds),
                               as.factor(data$diagnosis),
                               positive = "1")
print(conf_matrix)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 351   5
##          1   6 207
##
##                Accuracy : 0.9807
##                  95% CI : (0.9657, 0.9903)
##     No Information Rate : 0.6274
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9587
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9764
##             Specificity : 0.9832
##          Pos Pred Value : 0.9718
##          Neg Pred Value : 0.9860
##              Prevalence : 0.3726
##          Detection Rate : 0.3638
##    Detection Prevalence : 0.3743
##       Balanced Accuracy : 0.9798
##
##        'Positive' Class : 1
##
```

Overall, the model performs very well accurately classifying 98% of both malignant and benign cases. Our goal of achieving a high sensitivity was reached by correctly detecting 207 cancer cases out of 212 overall

(97.6%). The specificity is also high with 98.3% of all benign cases correctly classified. Although false negatives might cause unnecessary medical procedures, we still prefer it this way. The model seems highly reliable as shown by the positive prediction value. When the model predicts cancer, it is correct 97.2% of the time. Overall, we have a more than solid classifier at hand.

Conclusion

This report applied bayesian logistic regression to predict breast cancer by using a breast mass cell dataset made available by the University of Irvine. The exploratory data analysis revealed significant correlations among predictors, which required variable selection. A comparison between frequentist and bayesian variable selection methods was conducted which proved the bayesian approach as far superior when assessed on the Deviance Information Criterion. The final model was evaluated via a confusion matrix which yielded a highly reliable classifier for cancer detection