# Assignment Part III

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set.seed(980824)

## Summary

## Task 1

### Approach :

To calculate the AIC, the formula

$2 * k - 2 * l(\hat{\theta_{ml}})$

was applied where k is the number of parameters in the theta. To calculate the leave-one-out cross-validation, the formula

$\frac{\sum_{i=1}^{n} l_i(\hat{theta_i})}{n}$

was applied where $\hat{\theta_i}$ is $\hat{\theta_{ml}}(X_{-i})$, $(X_{-i})$ is one observation $(X_i)$ left out of X, $l_i(\hat{theta_i})$ is the log likelihood for the i-th left out observation and n is the total number of observations. These values were then compared with the AIC from R in the provided summary.

### Code :

```
# ---- Task_1 ----

# Compute AIC = 2k - 2l(theta_ml)
n <- nrow(X)
theta0 = rep(0, ncol(X))
k <- length(theta0)
theta_estimate <- NR(theta0, 3, y, X)
log_likelihood <- l(theta_estimate, y, X)
aic_computed <- 2*k - 2*log_likelihood

#AIC output from R summary
r_summary_aic <- summary(modell)$aic

# Compute k_cv =sum(l_i(theta_i))/n
# Here, theta_i = theta_ml(X_-i)
nk_cv <- 0
for(i in 1:n) {
  X_minus_i <- X[-i, , drop=FALSE]
  y_minus_i <- y[-i, , drop=FALSE]
  X_i <- X[i, , drop=FALSE]
```

```
  y_i <- y[i, , drop=FALSE]
  theta_i <- NR(theta0, 3, y_minus_i, X_minus_i)
  # log likelihood for i-th observation
  log_likelihood_theta_i <- l(theta_i, y_i, X_i)
  nk_cv <- nk_cv + log_likelihood_theta_i
}

k_cv <- nk_cv/n

# Creating a comparison data frame
comparison_aic_values <- data.frame(
  "AIC_R_model" = r_summary_aic,
  "AIC_computed" = aic_computed,
  "2*nK_CV_computed" = 2*nk_cv
)
```

### Output :

```
comparison_aic_values
```

```
##   AIC_R_model AIC_computed X2.nK_CV_computed
## 1    1302.397     1302.397         -1302.367
```

### Observation :

The computed AIC value and the AIC value from the R summary coincide in value. The computed K_CV is in the same magnitude as $AIC/(-2n)$ as expected.

## Task 2

### Approach :

The a posteriori density combines the a priori and the likelihood of the data. For the logistic regression, we have y data, X and the parameter vector $\theta$. so the a posteriori density is proportional to: $P(\theta|y,X) \propto P(y|X,\theta)P(\theta)$ where $P(\theta)$ is the a prior density and $P(y|X,\theta)$ is. the likelihood from the logistic regression model.

for a binary outcome, the likelihood for the logistic regression is given by the following equation:

$P(y_i|X_i,\theta) = \frac{1}{(1+\exp(-X_i\theta)}$

The a priori is Gaussian: $\theta$ $N(0,100I)$ so the a prior density is the following: $P(\theta) \propto exp(-\frac{1}{2}\theta^T(100I)^{-1}\theta)$

### Code :

```
# ---- Task_2 ----
post <- function(theta, y, X) {
  eta <- X %*% theta # Logistic regression likelihood
  likelihood <- prod(plogis(eta)^y * (1 - plogis(eta))^(1 - y))
  prior <- exp(-0.5 * sum(theta^2 / 100)) # a priori with theta ~ N(0, 100 * I)
  posterior <- likelihood * prior # posteriori is proportional to a priori * likelihood
  return(posterior)
}
```

### Output :

```
Xtest <- cbind(1, 18:25, rep(c(0, 1), 4), rep(c(1, 1, 0, 0), 2))
ytest <- c(rep(TRUE, 4), rep(FALSE, 4))
testing<-post(c(260, -10, 10, -20), ytest, Xtest) / post(c(270, -15, 15, -25), ytest , Xtest)
testing
```

```
## [1] 3.707556e+25
```

### Observation :

Given the results obtained by the test the function works correctly.

## Task 3

### Approach :

### Code :

```
# ---- Task_3 ----

mh_algo <- function(theta_estimate, y, X) {
  N <- 10000
  theta <- matrix(nrow = N, ncol = 4)
  # initial value as the calculated theta_estimate
  theta[1,] <- theta_estimate
  # here, suggested sigma as standard error from part II
  sigma <- standard_error(theta_estimate, y, X)
  for (i in 2:N) {
    theta_star <- theta[i-1,] + rnorm(4) * sigma
    # check if the acceptance probability is greater than the acceptance ratio
    posterior_theta_star <- post(theta_star, y, X)
    posterior_theta <- post(theta[i-1,], y, X)
    ratio <- runif(1)
    if (posterior_theta_star/ posterior_theta > ratio) {
      theta[i,] <- theta_star  # Accept the proposal
    } else {
      theta[i,] <- theta[i-1,]  # Reject the proposal
    }
  }
  return(theta)
}

theta_sample <- mh_algo(theta_estimate, y, X)
```

### Output :

Parameter Plots

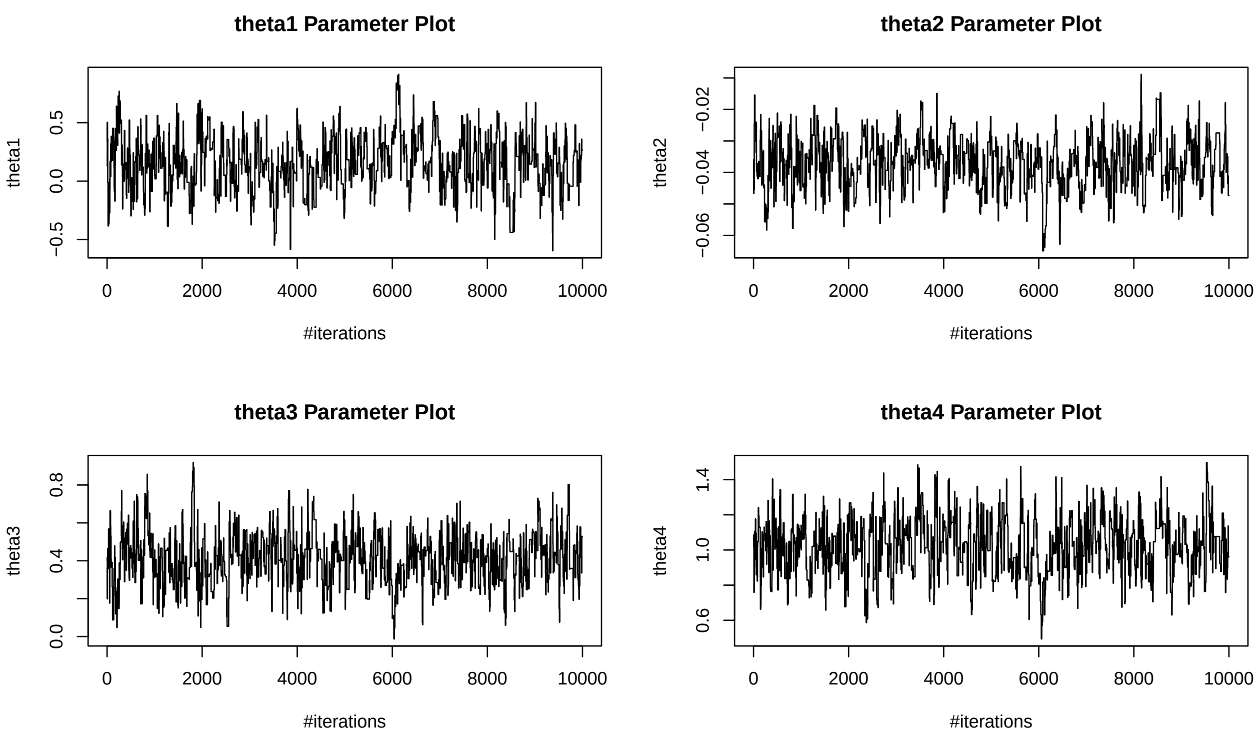
```
par(mfrow=c(2,2))
plot(x = c(1:10000), y = theta_sample[,1], type = "l", col = "black",
main="theta1 Parameter Plot", xlab= "#iterations", ylab = "theta1")

plot(x = c(1:10000), y = theta_sample[,2], type = "l", col = "black",
```

```
main="theta2 Parameter Plot", xlab= "#iterations", ylab = "theta2")

plot(x = c(1:10000), y = theta_sample[,3], type = "l", col = "black",
main="theta3 Parameter Plot", xlab= "#iterations", ylab = "theta3")

plot(x = c(1:10000), y = theta_sample[,4], type = "l", col = "black",
main="theta4 Parameter Plot", xlab= "#iterations", ylab = "theta4")
```



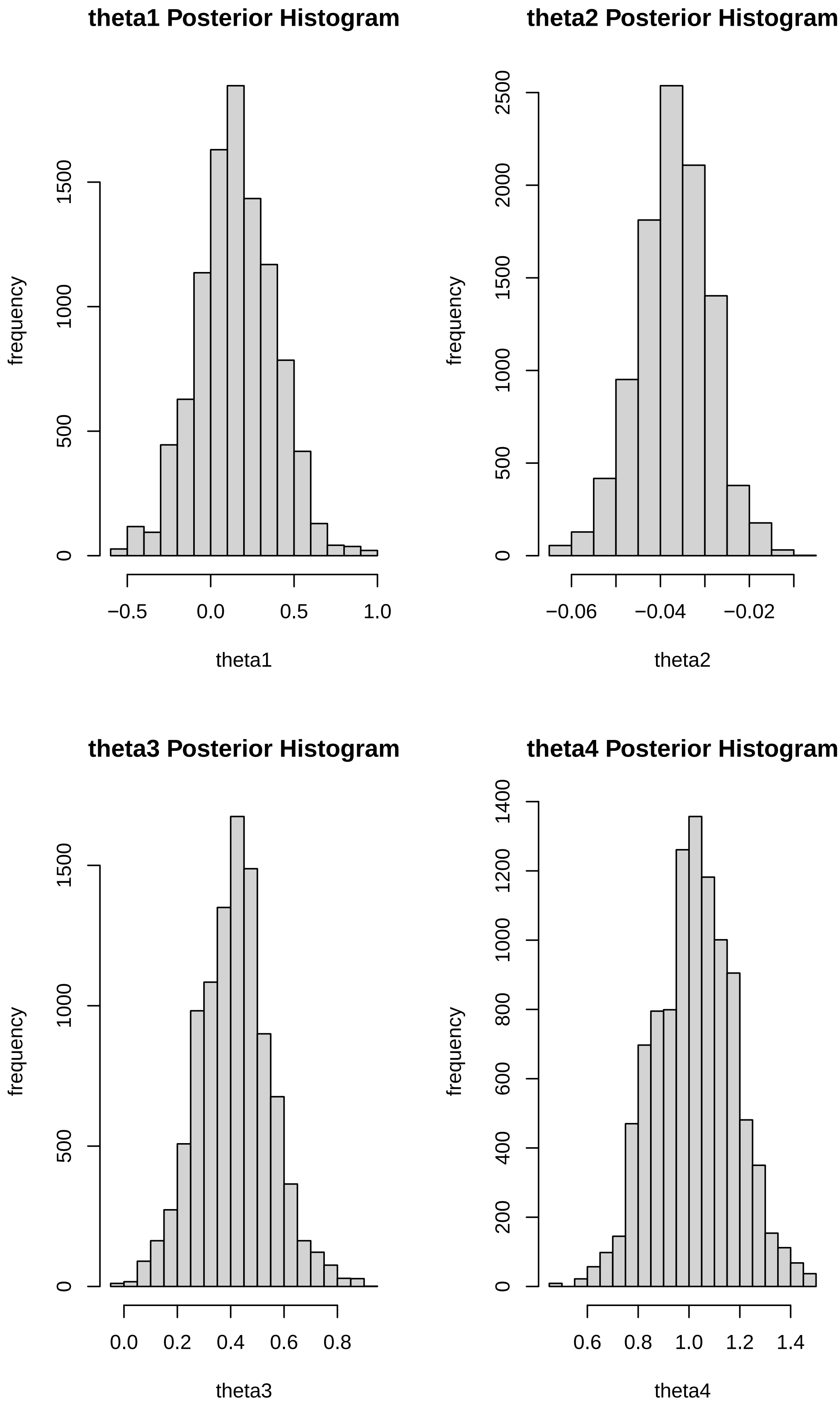

Parameter Posteriors Histograms

```
par(mfrow=c(2,2))
hist(x = theta_sample[(1:10000), 1], col = "lightgray",
main="theta1 Posterior Histogram", xlab= "theta1", ylab = "frequency")

hist(x = theta_sample[(1:10000), 2],  col = "lightgray",
main="theta2 Posterior Histogram", xlab= "theta2", ylab = "frequency")

hist(x = theta_sample[(1:10000), 3], col = "lightgray",
main="theta3 Posterior Histogram", xlab= "theta3", ylab = "frequency")

hist(x = theta_sample[(1:10000), 4], col = "lightgray",
main="theta4 Posterior Histogram", xlab= "theta4", ylab = "frequency")
```


theta1 Posterior Histogram
frequency
0
500
1000
1500
−0.5
0.0
0.5
1.0
theta1
theta2 Posterior Histogram
frequency
0
500
1000
1500
2000
2500
−0.06
−0.04
−0.02
theta2
theta3 Posterior Histogram
frequency
0
500
1000
1500
0.0
0.2
0.4
0.6
0.8
theta3
theta4 Posterior Histogram
frequency
0
200
400
600
800
1000
1200
1400
0.6
0.8
1.0
1.2
1.4
theta4

**Observation :**