Bayesian Learning Lab2

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QUESTION 1

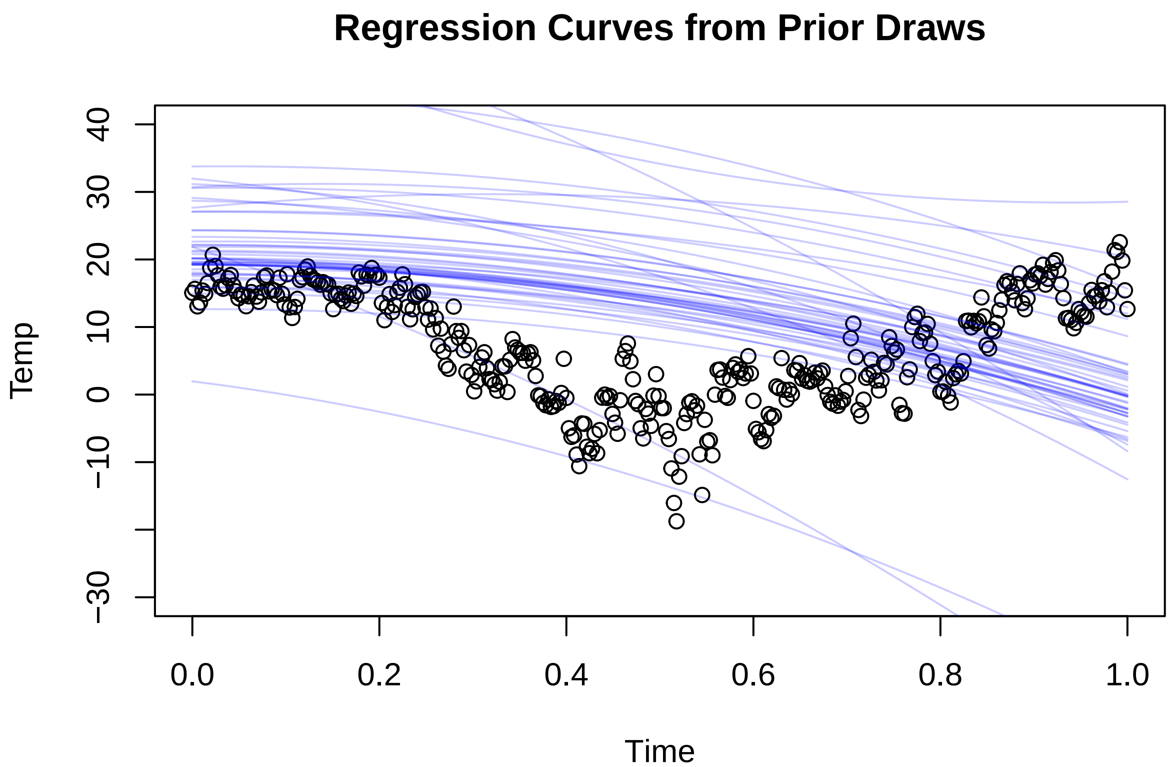
Part A)

```r
###### Bayesian Learning Lab 2 ######
############ Question 1 #############

# Libraries Used
library(MASS)
library(mvtnorm)
```

```
## Warning: package 'mvtnorm' was built under R version 4.4.2
```

```r
#### PART A)

# loading dataset
data <- read.csv("C:/Users/Dell/OneDrive - Linköpings universitet/732A73 Bayesian Learning/Labs/Lab2/te

data$time2 <- data$time^2
x <- as.matrix(cbind(1, data$time, data$time2))
y <- data$temp
n <- length(y)

# Given Prior Hyperparamters
# mu0 <- c(0, 100, -100)
#omega0 <- 0.01* diag(3)
mu0 <- c(20, 0, -20) # modified
omega0 <- diag(c(0.1, 1, 1)) # modified
nu0 <- 1
sigma02 <- 1

# Evaluate time points
time_seq <- seq(0, 1, length.out = 100)
X_plot <- cbind(1, time_seq, time_seq^2)

# Number of prior draws
S <- 50

# Simulating prior draws, beta and plot
beta_prior_draws <- matrix(0, S, 3)
```

```r
sigma2_prior_draws <- (nu0*sigma02)/rchisq(S,df = nu0)

plot(data$time, data$temp, xlab = "Time", ylab = "Temp", ylim = c(-30,40),
     main = "Regression Curves from Prior Draws")

for(s in 1:S){

  cov_beta <- sigma2_prior_draws[s] * solve(omega0)
  beta_prior <- rmvnorm(1, mu0, cov_beta)
  beta_prior_draws[s,] <- beta_prior

  y_pred <- X_plot %*% t(beta_prior)
  lines(time_seq, y_pred, col = rgb(0, 0, 1, alpha = 0.2))
}
```



Observation -

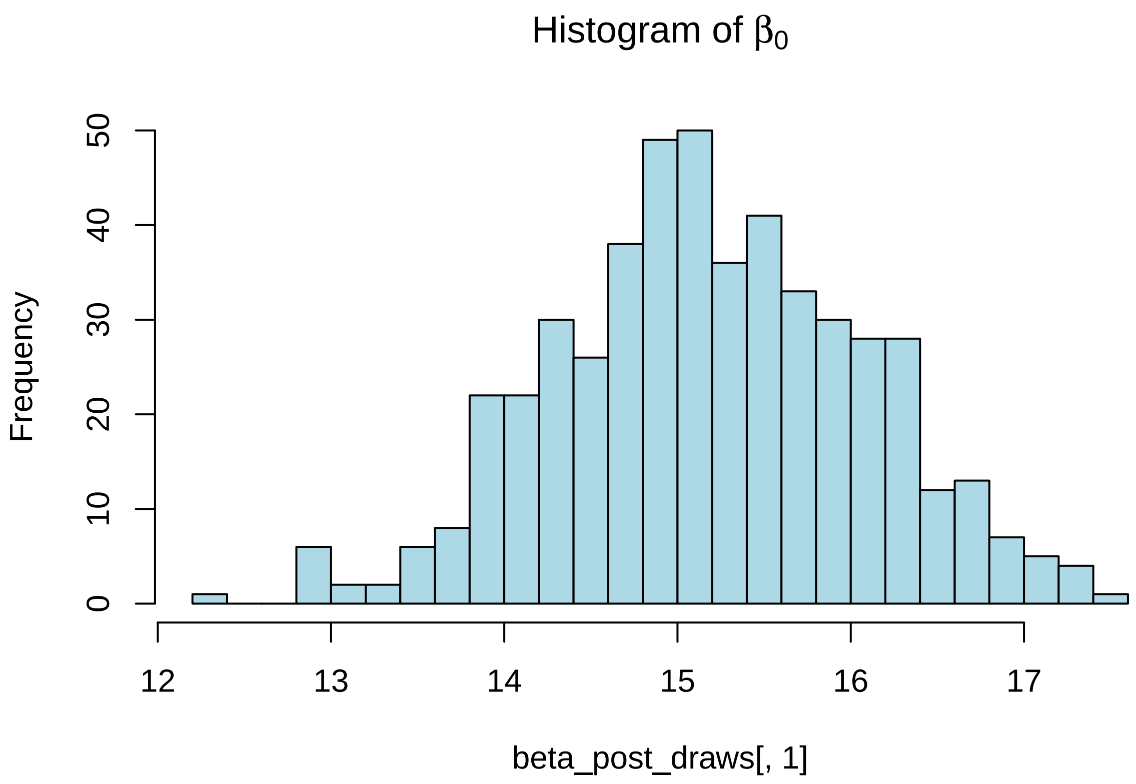
The given dataset is related to temperature in Linkoping city at different point of time. Since, the temperature varies seasonally so the prior might have $\mu 0$ = c(-20, 0, 20) and moderate uncertainty that is, $\Omega 0$ = c(0.1, 1, 1). The regression curves look reasonable because they fall within the range of plausable temperature value of [-20, 20]

PART B)

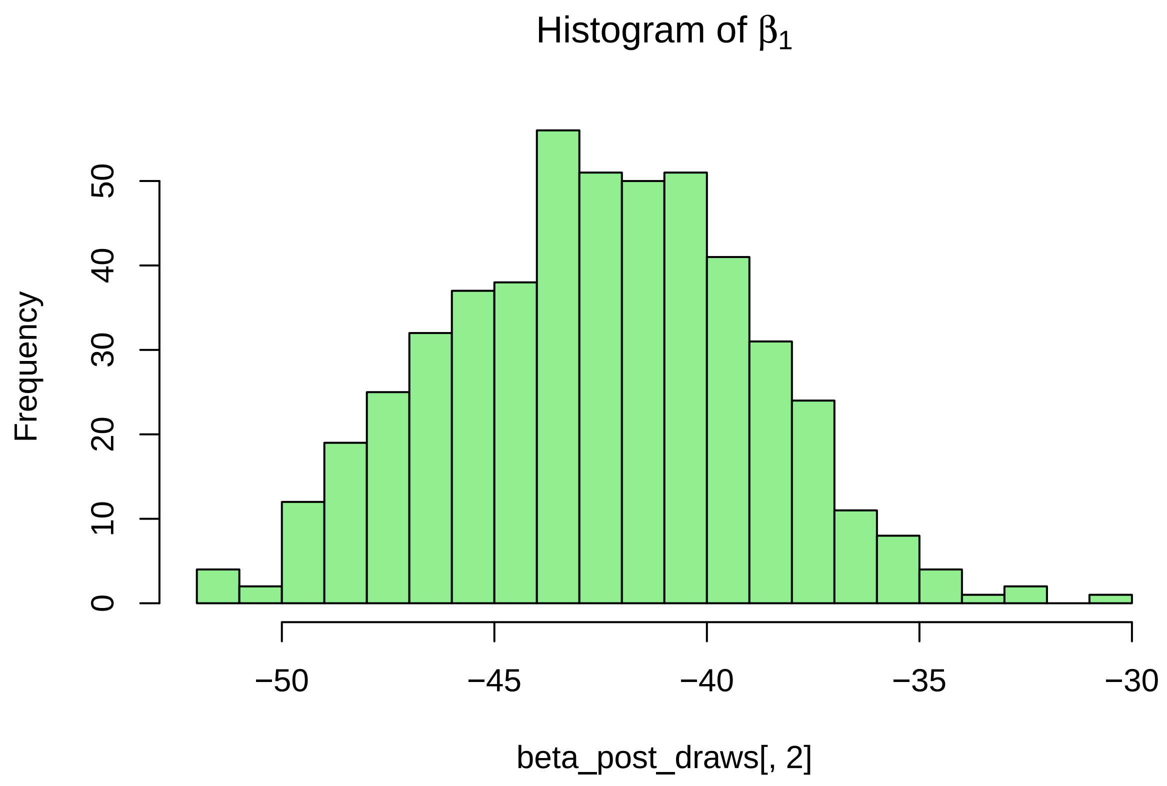
```
#### PART B)

xtx <- t(x) %*% x
xty <- t(x) %*% y

# Posterior Parameters
mu_n <- solve(xtx + omega0) %*% (xty + omega0 %*% mu0)
omega_n <- xtx + omega0
nu_n <- nu0 + n
sigma_n2 <- (nu0*sigma02 + sum(y^2) + t(mu0) %*% omega0 %*% mu0 - t(mu_n)
             %*% omega_n %*% mu_n)/ nu_n

# Simulate Posterior Samples
N <- 500
sigma2_post_draws <- c((nu_n*sigma_n2)/rchisq(N,df = nu_n))
```

```
## Warning in (nu_n * sigma_n2)/rchisq(N, df = nu_n): Recycling array of length 1 in array-vector arithm
##   Use c() or as.vector() instead.
```

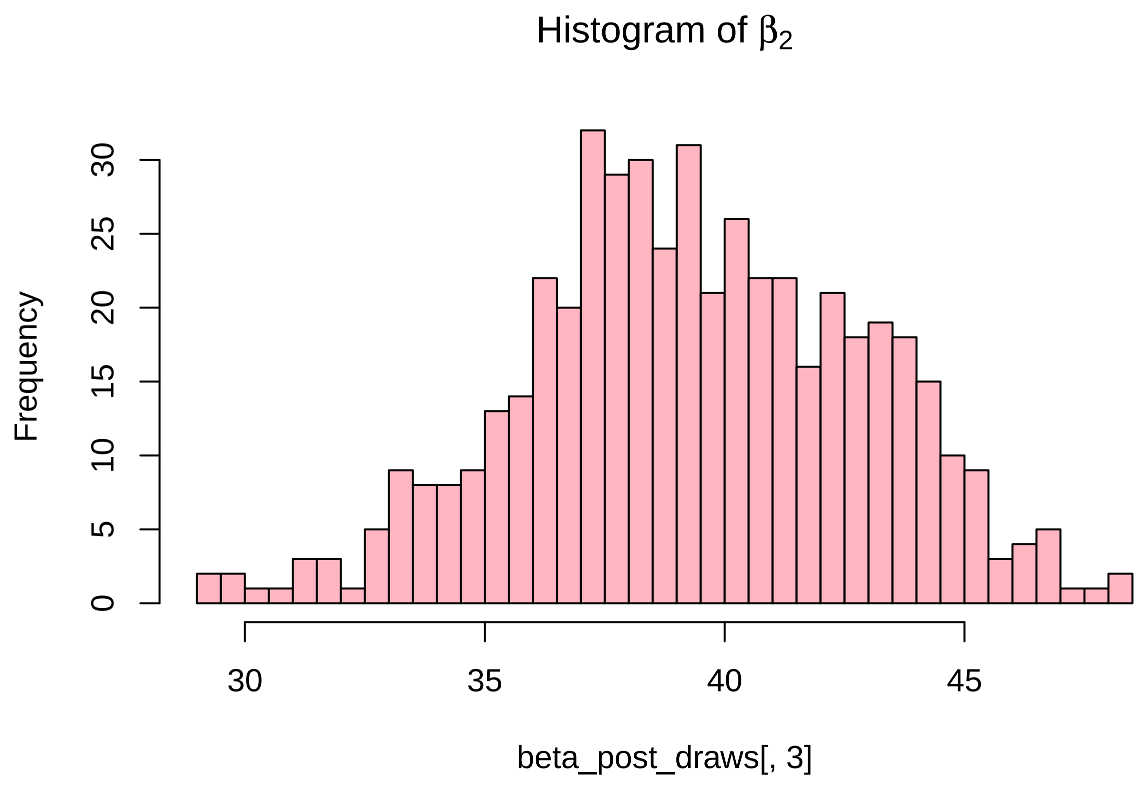
```
beta_post_draws <- matrix(0, N, 3)

for (i in 1:N){
  beta_post_draws[i,] <- rmvnorm(1, mu_n, sigma2_post_draws[i] * solve(omega_n))
}

# Plot Posterior Histogram
hist(beta_post_draws[,1], main = expression("Histogram of " * beta[0]),
     breaks = 30, col = "lightblue")
```



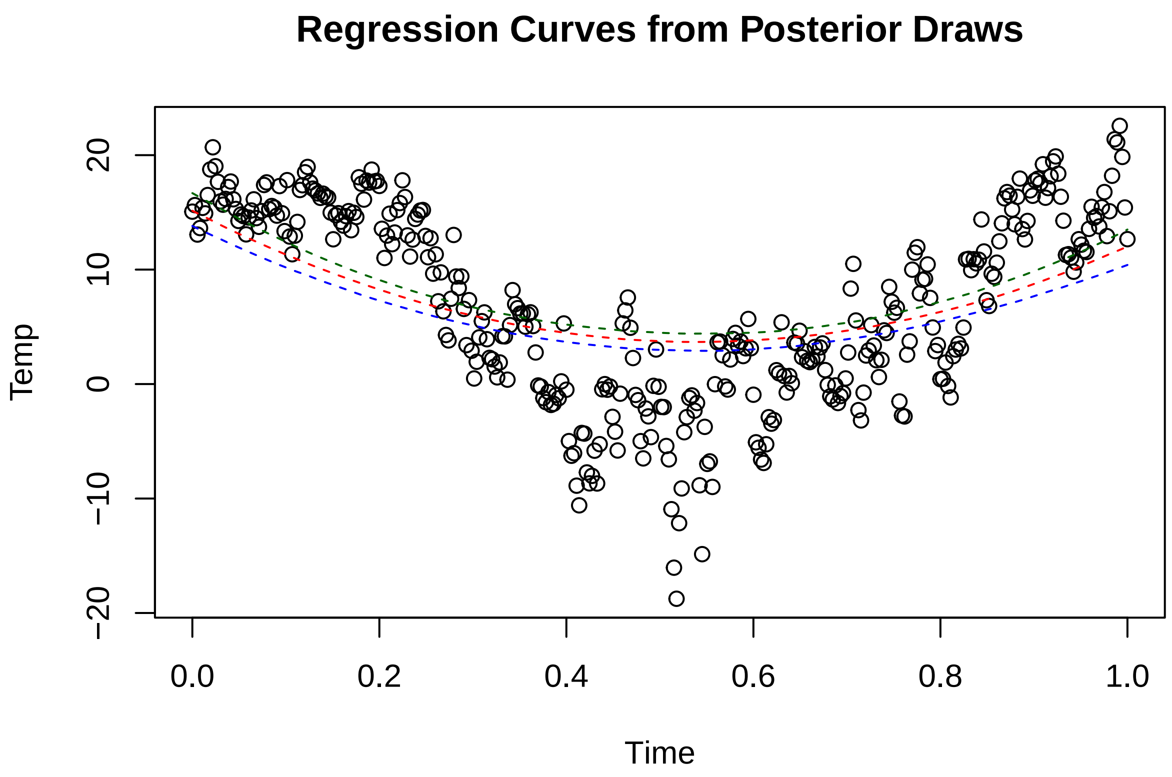
```r
hist(beta_post_draws[,2], main = expression("Histogram of " * beta[1]),
     breaks = 30, col = "lightgreen")
```



```r
hist(beta_post_draws[,3], main = expression("Histogram of " * beta[2]),
     breaks = 30, col = "lightpink")
```



```r
# For each time, compute posterior predictive curve
f_post <- apply(beta_post_draws, 1, function(b) X_plot %*% b)

# Compute pointwise statistics
f_median <- apply(f_post, 1, median)
f_lower <- apply(f_post, 1, quantile, probs = 0.05)
f_upper <- apply(f_post, 1, quantile, probs = 0.95)

# Plot
plot(data$time, data$temp, xlab = "Time", ylab = "Temp",
     main = "Regression Curves from Posterior Draws")
lines(time_seq, f_lower, col = "blue", lty = 2)
lines(time_seq, f_upper, col = "darkgreen", lty = 2)
lines(time_seq, f_median, col = "red", lty = 2)
```



Observation-

The posterior probability interval does not contain most of the data points. The actual data points also contain noise $\epsilon \sim$ N(0, σ^2). So, to get the full dataset in the given range, variance(σ^2) is to be included in the prediction interval.

PART C)

Computing time with lowest temperature -

$$f(t) = \beta 0 + \beta 1 * t + \beta 2 * t^2$$

and

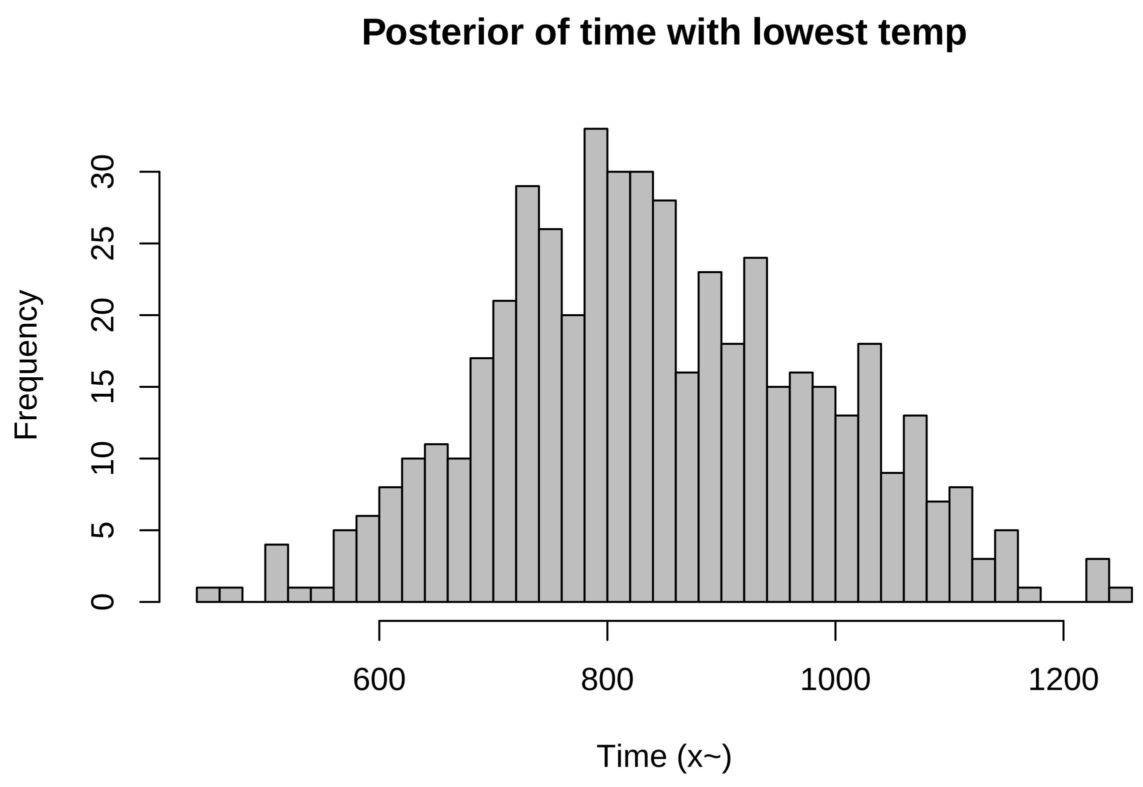
$$f'(t) = \beta 1 + 2 * \beta 2 * t$$

Now, putting f'(t) = 0 will give the minimum value for t. Because $\beta 2 > 0$ Thus,

$$t = -\beta 1/(2 * \beta 2)$$

```
### Part C)

# Computing time with lowest temperature -
# f(t) = \beta0 + \beta1*t + \beta2*t^2
# f'(t) = \beta1 + 2*\beta2*t
# putting f'(t) = 0 will give the minimum value for t. Because \beta2 > 0
```

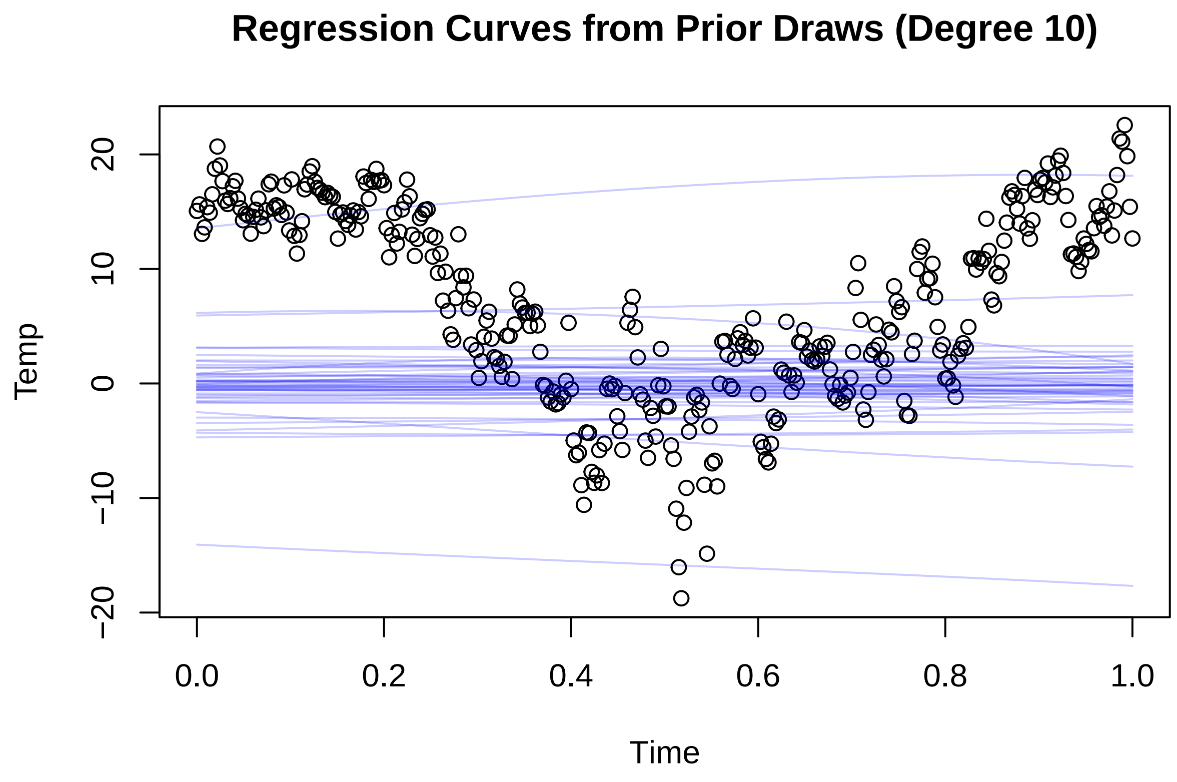
```r
# Thus,     t = - \beta1 / (2*\beta2)
x_min <- -beta_post_draws[,2] / 2* beta_post_draws[,3]

# Plot the posterior distribution
hist(x_min,  breaks = 30, col = "gray",
     main = "Posterior of time with lowest temp",
     xlab = "Time (x̃)" )
```



PART D)

```r
### Part D)

# Build X matrix with polynomial terms up to degree 10
X10 <- sapply(0:10, function(i) data$time^i)
X10 <- as.matrix(X10)

# Prior mean and precision
mu0_10 <- rep(0, 11)
lambda <- 5
omega0_10 <- diag(lambda^(0:10))

# For prediction
# time_seq <- seq(0, 1, length.out = 100)
```

```r
X_plot_10 <- sapply(0:10, function(j) time_seq^j)
X_plot_10 <- as.matrix(X_plot_10)

# Prior predictive draws
# S <- 50
beta_prior_draws_10 <- matrix(0, S, 10 + 1)
# sigma2_prior_draws <- (nu0 * sigma02) / rchisq(S, df = nu0)

# Plot prior predictive regression curves
plot(data$time, data$temp, xlab = "Time", ylab = "Temp",
     main = "Regression Curves from Prior Draws (Degree 10)")

for(s in 1:S){

  cov_beta_10 <- sigma2_prior_draws[s] * solve(omega0_10)
  beta_prior_10 <- rmvnorm(1, mu0_10, cov_beta_10)
  beta_prior_draws_10[s,] <- beta_prior_10

  y_pred_10 <- X_plot_10 %*% t(beta_prior_10)
  lines(time_seq, y_pred_10, col = rgb(0, 0, 1, alpha = 0.2))
}
```



Observation -

The suitable prior mean should be $\mu 0 = 0$ as it expresses no strong belief in any specific shape for the curve. The suitable prior precision could be a diagonal matrix with increasing values for higher degree as higher degree terms would be heavily shrunk towards zero preventing overfitting unless data strongly supports them. Thus, $\mu 0 = \text{rep}(0, 11)$ and $\Omega 0 = \text{diag}(\lambda\hat{}(0{:}10))$ where $\lambda = 5$

Question 2

PART A)

```r
###### QUESTION 2 ##############
######## 1ST PART #############
#Consider the logistic regression model: Pr(y = 1|x ,beta)= (exp (x^T beta)/
# 1+exp(x^T beta)) where y equals 1 if the person has a disease and 0 if not.
# x is a 6-dimensional vector containing five features and a column of
# 1's to include an intercept in the model.
# The values of the variables Age, Duration_of_symptoms, and White_blood in
# x need to be standardized to mean 0 and variance 1. For each of these
# variables xj, calculate the standardized value for each observation
# i by using the formula (x ij-(xj bar)/s xj)  where (xj bar )and s xj are
# the sample mean and standard deviation of xj, respectively.
# The goal is to approximate the posterior distribution of the parameter vector
# beta  with a multivariate normal distribution
# (beta|y,x~N(beta tilda,j^-1y(beta tilda))) where beta tilda is the posterior
# mode and J( beta tilda) is the negative of the observed Hessian evaluated at
# the posterior mode.
# Load required package
library(mvtnorm)

# Load the dataset
disease_data <- read.csv("C:/Users/Dell/OneDrive - Linköpings universitet/732A73 Bayesian Learning/Githu

set.seed(12345)
standardize <- function(x, mean_val = NULL, sd_val = NULL) {
  if (is.null(mean_val)) mean_val <- mean(x, na.rm = TRUE)
  if (is.null(sd_val)) sd_val <- sd(x, na.rm = TRUE)

  (x - mean_val) / sd_val
}




# Prepare the response variable (using 'class_of_diagnosis' as outcome)
y <- disease_data$class_of_diagnosis  # Assuming 1 = has disease, 0 = healthy
# Calculate standardization parameters (must do this FIRST)
age_mean <- mean(disease_data$age)
age_sd <- sd(disease_data$age)
symptoms_mean <- mean(disease_data$duration_of_symptoms)
symptoms_sd <- sd(disease_data$duration_of_symptoms)
whiteblood_mean <- mean(disease_data$white_blood)
whiteblood_sd <- sd(disease_data$white_blood)
```

```r
set.seed(12345)
means <- list(
  age = age_mean,
  duration = symptoms_mean,
  white_blood = whiteblood_mean
)
set.seed(12345)
sds <- list(
  age = age_sd,
  duration = symptoms_sd,
  white_blood = whiteblood_sd
)
# Prepare predictors with standardization where needed
X <- cbind(# C binder means column-wise into a matrix or data frame.
  Intercept = 1,
  Age = (disease_data$age - age_mean)/age_sd,
  Gender = disease_data$gender,
  Symptoms = (disease_data$duration_of_symptoms - symptoms_mean)/symptoms_sd,
  Breathing = disease_data$dyspnoea,
  WhiteCells = (disease_data$white_blood - whiteblood_mean)/whiteblood_sd
)

# Convert to X is stored as a numeric matrix
X <- as.matrix(X)

#(A)Calculate both beta tilda and J(beta_tilda) by using the optim function in
# R.Use the prior beta~ N(0, tau^2I), where tau=2.

# Define log-posterior function with N(0, tau²I) prior (tau=2)
log_posterior <- function(beta, X, y) {
  eta <- X %*% beta #here it computes linear predictor
  prob <- plogis(eta)  # Logistic function or equal to 1/(1+exp(eta)) which is same as logistic express
  log_lik <- sum(y * log(prob) + (1-y) * log(1-prob)) # log-likelihood is been applies on the above log
  log_prior <- sum(dnorm(beta, mean=0, sd=2, log=TRUE))  # Prior N(0,4)# here we calculate log-prior fo
  log_lik + log_prior
}
set.seed(12345)
# Find posterior mode (beta_tilde) and Hessian (J)
optim_result <- optim(#optim function here is general optimization function
  par = rep(0, ncol(X)),#It is the starting point for optimization,,it createsa vector of zeros,in logi
  fn = log_posterior,# this is the function that needs to be maximized
  X = X, y = y,
  method = "BFGS",
  control = list(fnscale=-1),  # Maximize
  hessian = TRUE  # it calculates the Hessian matrix(ie the second derivative )at the solution
)# why second derivative , the first derivate tells the direction of the
#gradient steep increase
#the second derivative or the hessian tells about the curvature of the slope
#(ie how fast the slope is changing)

# Extract results
beta_tilde <- optim_result$par  # Posterior mode
J_beta_tilde <- -optim_result$hessian  # Negative Hessian
```

```
# (B) Present the numerical values of beta tilda and J^-1y(beta tilda )for
# the Disease data.
# Name the coefficients
names(beta_tilde) <- colnames(X)
rownames(J_beta_tilde) <- colnames(X)
colnames(J_beta_tilde) <- colnames(X)

# Print results
cat("(B) Posterior Mode (beta_tilde):\n")
```

```
## (B) Posterior Mode (beta_tilde):
```

```
print(beta_tilde)
```

```
##   Intercept         Age      Gender    Symptoms   Breathing  WhiteCells
## -0.38824219 -0.26614789 -0.64238957  0.19312998 -0.13752407 -0.04498936
```

```
cat("\n(B) Inverse Negative Hessian (J^-1(beta_tilde)):\n")
```

```
##
## (B) Inverse Negative Hessian (J^-1(beta_tilde)):
```

```
print(solve(J_beta_tilde))  # Posterior covariance matrix
```

```
##               Intercept           Age       Gender      Symptoms     Breathing
## Intercept   0.097747237 -0.0005446210 -0.034623004 -0.0029000657 -0.0797576510
## Age        -0.000544621  0.0163896960  0.002484340 -0.0001408962  0.0009300174
## Gender     -0.034623004  0.0024843401  0.063183813  0.0028488970  0.0027926987
## Symptoms   -0.002900066 -0.0001408962  0.002848897  0.0149912622  0.0006546427
## Breathing  -0.079757651  0.0009300174  0.002792699  0.0006546427  0.0975458776
## WhiteCells  0.001504192 -0.0010567361 -0.001338187 -0.0006455806 -0.0006531182
##               WhiteCells
## Intercept   0.0015041923
## Age        -0.0010567361
## Gender     -0.0013381871
## Symptoms   -0.0006455806
## Breathing  -0.0006531182
## WhiteCells  0.0163250544
```

```
post_cov <- solve(J_beta_tilde)
# (C) Compute an approximate 95% equal tail posterior probability interval
# for the regression coeffcient to the variable Age.

# Get Age coefficient index
age_index <- which(names(beta_tilde) == "Age")#IT IS MENTIONS IN THE QUESTION
# that we find the postirio mode and returns the coefficient of the age

# Calculate posterior standard deviation for Age
age_sd <- sqrt(solve(J_beta_tilde)[age_index, age_index])
```

```r
# 95% equal-tailed credible interval
age_ci <- beta_tilde[age_index] + c(-1.96, 1.96) * age_sd

cat("\n(C) 95% Posterior Interval for Age coefficient:\n")
```

```
##
## (C) 95% Posterior Interval for Age coefficient:
```

```r
cat(sprintf("[%.4f, %.4f]\n", age_ci[1], age_ci[2]))
```

```
## [-0.5171, -0.0152]
```

```r
# Interpretation
if (prod(age_ci) > 0) {  # Both limits have same sign
  cat("Age is statistically significant (95% CI doesn't contain 0)\n")
  if (age_ci[1] > 0) {
    cat("Older age increases disease probability\n")
  } else {
    cat("Older age decreases disease probability\n")
  }
} else {
  cat("Age is not statistically significant (95% CI contains 0)\n")
}
```

```
## Age is statistically significant (95% CI doesn't contain 0)
## Older age decreases disease probability
```

```r
#(D) verify that estimation results reasonable by comparing the posterior
# means tomaximum likelihood estimates given by:glmModel

# Optional: Compare with frequentist approach
cat("\nComparison with standard glm() results:\n")
```

```
##
## Comparison with standard glm() results:
```

```r
glm_fit <- glm(y ~ Age + Gender + Symptoms + Breathing + WhiteCells,
               data = as.data.frame(X[,-1]),  # Remove intercept
               family = binomial)
print(summary(glm_fit))
```

```
##
## Call:
## glm(formula = y ~ Age + Gender + Symptoms + Breathing + WhiteCells,
##     family = binomial, data = as.data.frame(X[, -1]))
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.38961    0.31999  -1.218   0.2234
## Age         -0.26762    0.12839  -2.084   0.0371 *
## Gender      -0.64938    0.25415  -2.555   0.0106 *
## Symptoms     0.19367    0.12270   1.578   0.1145
## Breathing   -0.13348    0.31924  -0.418   0.6759
## WhiteCells  -0.04504    0.12813  -0.352   0.7252
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 384.25  on 312  degrees of freedom
## Residual deviance: 369.86  on 307  degrees of freedom
## AIC: 381.86
##
## Number of Fisher Scoring iterations: 4
```

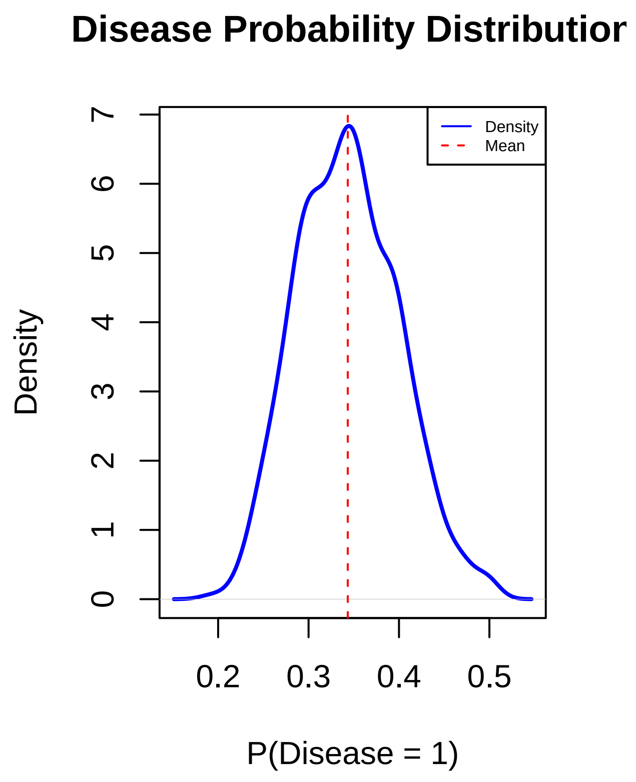
Observation -

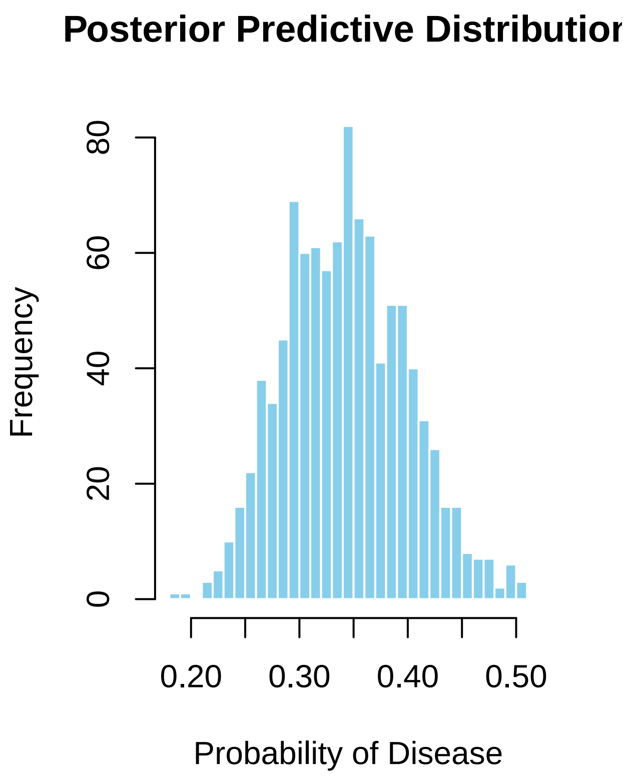
Age is statistically significantly important in predicting disease status in the given dataset. Based on both Bayesian and glm results, older individulas(with standardized Age) are less likely to have the disease. The value is almost the same ,which means that the approximation might be resonable.

Part B)

```r
############################################################################
#2ND PART
set.seed(12345)
# 1. Define the simulation function (improved version)
simulate_predictive <- function(age, gender, symptoms, breathing, whiteblood,
                                n_sim = 10000) {
  # Standardize the continuous variables using the same scaling as before
  age_std <- (age - age_mean) / age_sd
  symptoms_std <- (symptoms - symptoms_mean) / symptoms_sd
  whiteblood_std <- (whiteblood - whiteblood_mean) / whiteblood_sd

  # Create the feature vector for this patient
  x_patient <- c(1, age_std, gender, symptoms_std, breathing, whiteblood_std)

  # Simulate beta draws from posterior normal approximation
  beta_draws <- rmvnorm(n_sim, mean = beta_tilde, sigma = post_cov)

  # Calculate Pr(y=1|x) for each draw
  prob_draws <- plogis(beta_draws %*% x_patient)

  return(prob_draws)
}

# 2. Simulate for our specific patient:
# 38-year-old woman (gender=1), 10 days symptoms, no labored breathing (0),
# 11000 white blood
library(ggplot2)
# 1. Define core functions
```

```r
sigmoid <- function(z) 1 / (1 + exp(-z))
set.seed(12345)
predict_prob <- function(beta_mean, beta_cov, new_x, n_samples = 1000) {
  beta_samples <- rmvnorm(n_samples, beta_mean, beta_cov)
  apply(beta_samples, 1, function(beta) sigmoid(sum(new_x * beta)))
}

new_patient <- c(
  1,  # Intercept
  standardize(38, means$age, sds$age),  # Age
  standardize(10, means$duration, sds$duration),  # Symptoms
  standardize(11000, means$white_blood, sds$white_blood),  # WhiteBlood
  1,  # Gender (1 = female)
  0   # Dyspnoea (0 = no)
)
set.seed(12345)
probs <- predict_prob(beta_tilde, post_cov, new_patient)

# 5. Visualization (clean and simple)
par(mfrow = c(1, 2))

# Density plot
plot(density(probs), main = "Disease Probability Distribution",
     xlab = "P(Disease = 1)", col = "blue", lwd = 2)
abline(v = mean(probs), col = "red", lty = 2)
legend("topright", legend = c("Density", "Mean"),
       col = c("blue", "red"), lty = c(1, 2), cex = 0.5)

# Histogram
hist(probs, breaks = 30, col = "skyblue", border = "white",
     main = "Posterior Predictive Distribution",
     xlab = "Probability of Disease")
```





```r
par(mfrow = c(1, 1))

# 6. Print results
cat("\nPrediction Summary for 38yo Female Patient:\n")
```

```
##
## Prediction Summary for 38yo Female Patient:
```

```r
cat(sprintf("Mean probability: %.3f\n", mean(probs)))
```

```
## Mean probability: 0.343
```

```r
cat(sprintf("95%% Credible Interval: [%.3f, %.3f]\n",
            quantile(probs, 0.025), quantile(probs, 0.975)))
```

```
## 95% Credible Interval: [0.245, 0.460]
```