Solution to computer exam in Bayesian learning

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First load all the data into memory by running the R-file given at the exam

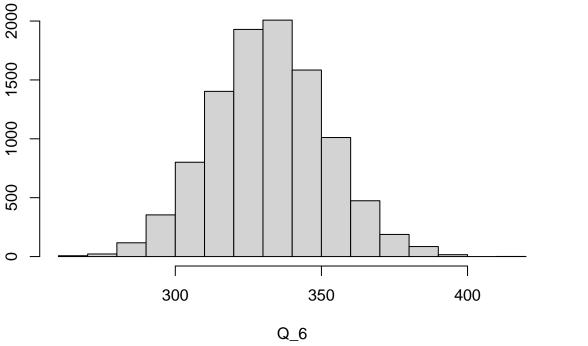
```
rm(list=ls())
source("ExamData.R")
set.seed(1)
```

Problem 1

1b

```
alpha_n <- 2326
beta_n <- 7
theta <- rgamma(1e4,shape = alpha_n,rate = beta_n)
Q_6 <- rpois(1e4,theta)
hist(Q_6,main="Posterior distribution",xlab="Q_6",ylab="")</pre>
```

Posterior distribution

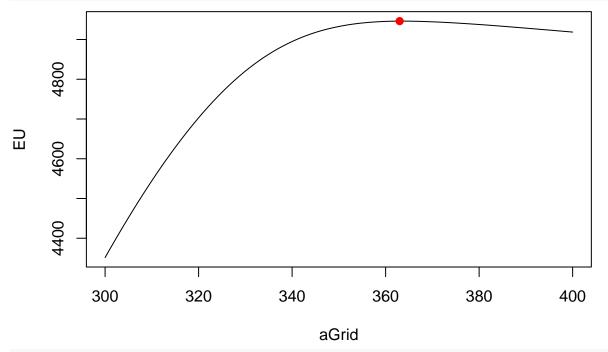


```
mean(Q_6 > 350)
## [1] 0.1775
```

The posterior probability is 0.178. The posterior distribution is plotted above.

1c

```
aGrid <- seq(300,400,by=1)
EU <- rep(NA,length(aGrid),1)
count <- 0
for (a in aGrid){
    count <- count + 1
    EU[count] <- mean(utility_func(a,Q_6))
}
plot(aGrid, EU, type = "l")
aOpt = aGrid[which.max(EU)] # This is the optimal a
points(aOpt,mean(utility_func(a=aOpt, Q_6)), col = "red",pch=19)</pre>
```



a0pt

[1] 363

The optimal number of products in stock (a) is 363.

Problem 2

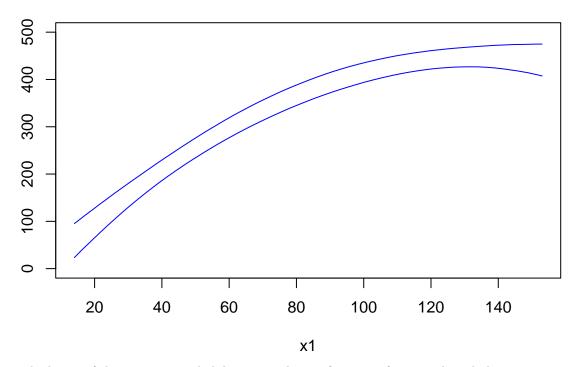
2a

```
mu_0 <- as.vector(rep(0,6))
Omega_0 <- (1/100)*diag(6)
v_0 <- 1
sigma2_0 <- 100**2
nIter <- 10000

PostDraws <- BayesLinReg(y, X, mu_0, Omega_0, v_0, sigma2_0, nIter)</pre>
```

```
Betas <- PostDraws$betaSample</pre>
Means <- colMeans(Betas)</pre>
CredInt \leftarrow matrix(0,6,2)
for (j in 1:6){
  CredInt[j,] <- quantile(Betas[,j],probs=c(0.005,0.995))</pre>
PostRes \leftarrow matrix(0,6,3)
PostRes[,1] <- t(Means)</pre>
PostRes[,2:3] <- CredInt</pre>
PostRes
                                 [,2]
##
                 [,1]
                                               [,3]
## [1,] -490.4249992 -1.486995e+03 498.94407149
          10.7268860 5.704980e+00 15.81988500
## [2,]
## [3,]
          -0.0260867 -3.647196e-02 -0.01578911
## [4,]
        33.3430410 -3.809424e+01 108.06775472
         -0.6092026 -2.024708e+00
## [5,]
                                       0.75924254
## [6,]
          -0.1344050 -3.121198e-01
                                        0.03562525
It is 99 % posterior probability that beta_1 is on the interval (5.7,15.8).
2b
Sigma2 <- PostDraws$sigma2Sample</pre>
mean(sqrt(Sigma2))
## [1] 40.05494
median(sqrt(Sigma2))
## [1] 39.63477
2c
x1_grid \leftarrow seq(min(X[,2]),max(X[,2]),0.1)
Mu_draws <- matrix(0,length(x1_grid),2)</pre>
for (ii in 1:length(x1_grid)){
  Curr_x <- c(1,x1_grid[ii],x1_grid[ii]**2,27,27**2,x1_grid[ii]*27)</pre>
  CurrMu <- Betas %*% Curr_x
  Mu_draws[ii,] <- quantile(CurrMu,probs=c(0.025,0.975))</pre>
plot(x1_grid,Mu_draws[,1],"n",main="95 % posterior probability intervals as a function of x1",
     xlab="x1", ylab="",ylim=c(0,500))
lines(x1 grid,Mu draws[,1],col="blue")
lines(x1_grid,Mu_draws[,2],col="blue")
```

95 % posterior probability intervals as a function of x1

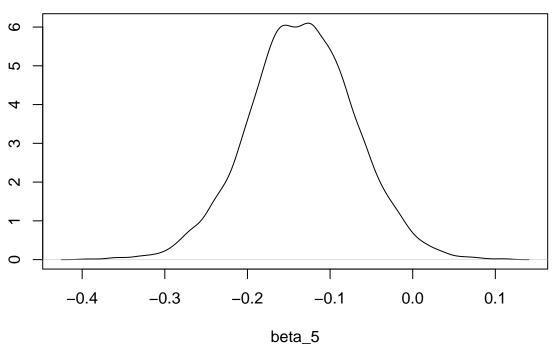


The limits of the posterior probability intervals as a function of x1 are plotted above.

2d

```
Effect_x1x2 <- Betas[,6]
plot(density(Effect_x1x2),main="Posterior distribution",xlab="beta_5", ylab="")</pre>
```

Posterior distribution



```
quantile(Effect_x1x2,probs=c(0.025,0.975))
```

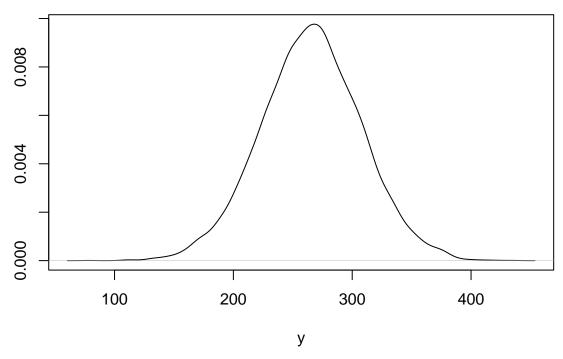
```
## 2.5% 97.5%
## -0.265031107 -0.007967831
```

There is substantial probability mass that the effect on y from x1 depends on x2, where the slope for x1 decreases (becomes more negative) as the value of x2 increases. This is also supported by the 95 % equal tail credible interval for beta_5 with only negative values.

2e

```
Mu <- Betas[,1] + Betas[,2]*50 + Betas[,3]*50**2 + Betas[,4]*25 + Betas[,5]*25**2 + Betas[,6]*50*25
Sigma <- sqrt(Sigma2)
y_Vals <- rnorm(10000,Mu,Sigma)
plot(density(y_Vals),main="Posterior predictive distribution of y",xlab="y", ylab="")</pre>
```

Posterior predictive distribution of y



The posterior predictive distribution of y is plotted above.

2f

```
T_y <- max(y)
T_y_rep <- matrix(0,nIter,1)
Mu <- Betas %*% t(X)
for (ii in 1:nIter){
   y_Vals <- rnorm(length(y),Mu[ii,],Sigma[ii])
   T_y_rep[ii,1] <- max(y_Vals)
}
mean(T_y_rep >= T_y)
```

[1] 0.9885

The posterior predictive p-value is 0.989, which is far away from 0.5. Hence, the model can not replicate the length of the largest mollusc in the data in a good way.

Problem 3

3d

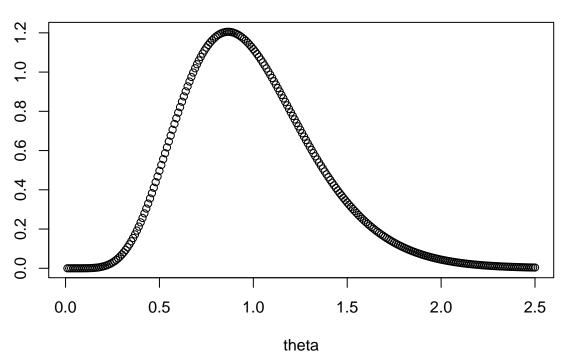
```
LogPost <- function(theta,n,Sumx3){
  logLik <- n*log(theta) - Sumx3*theta;
  logPrior <- 2*log(theta) - 4*theta;
  return(logLik + logPrior)
}
theta_grid <- seq(0.01,2.5,0.01)</pre>
```

```
PostDens_propto <- exp(LogPost(theta_grid,5,4.084))

PostDens <- PostDens_propto/(0.01*sum(PostDens_propto))

plot(theta_grid,PostDens,main="Posterior distribution",xlab="theta", ylab="")
```

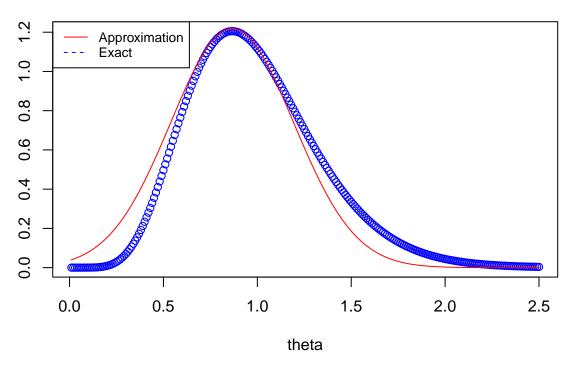
Posterior distribution



The posterior distribution is given above.

3e

Posterior distribution



The posterior approximation is not that accurate because the exact posterior distribution is skewed to the right.