Assignment Covering Chapters 2 & 3 of *Bayesian Computation with R*

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1. **Chapter 2: Introduction to Bayesian Thinking** Write your own code for the following:
   (a) Simulating a sample from a posterior distribution when you have a histogram prior.
   (b) Prior predictive density function, `pdiscp()`.
   (c) Prior predictive density function, `pbetap()`.
   (d) Discrete credible interval, `discint`.

Solution:

(a) Let's start by defining a function to generate the values for the histogram prior:

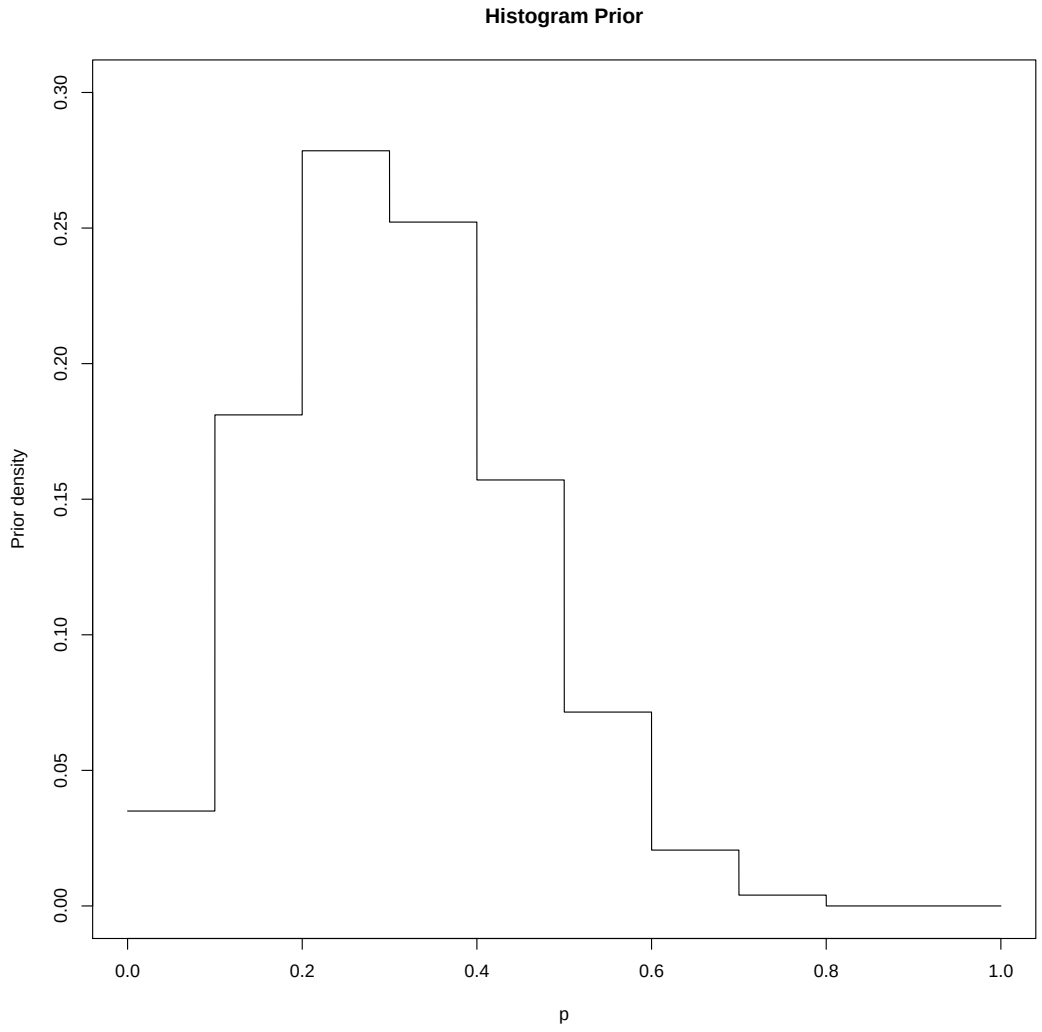
```
#Function to generate prior values for each value in x
get_histprior_value <- function(x, histprior){
  vec <- rep(NA, length=length(x))
  for(i in 1:length(vec)){
    new_vec <- histprior[histprior[,1]>=x[i],]

    #Check if new_vec is matrix or vector and index accordingly
    if(!is.null(ncol(new_vec))){
      vec[i] <- new_vec[1,2]
    } else{
      vec[i] <- new_vec[2]
    }
  }

  return(vec)
}
```

Now let's prepare the data for input into our new `get_histprior_value` function:

```
#Generate points for interval
interval <- seq(0.1, 1, by = 0.1)

#Prior probability
prior <- c(1, 5.2, 8, 7.2, 4.6, 2.1, 0.7, 0.1, 0, 0)
prior <- prior/sum(prior)

#Create the histogram prior
histprior <- sample(interval, 10000, replace=TRUE, prob = prior)
histprior <- table(histprior)/sum(table(histprior))
histprior <- as.matrix(histprior)
names <- rownames(histprior)
rownames(histprior) <- NULL
histprior <- cbind(as.numeric(names),as.numeric(histprior))
histprior <- rbind(histprior, c(0.9, 0))
histprior <- rbind(histprior, c(1.0, 0))
```

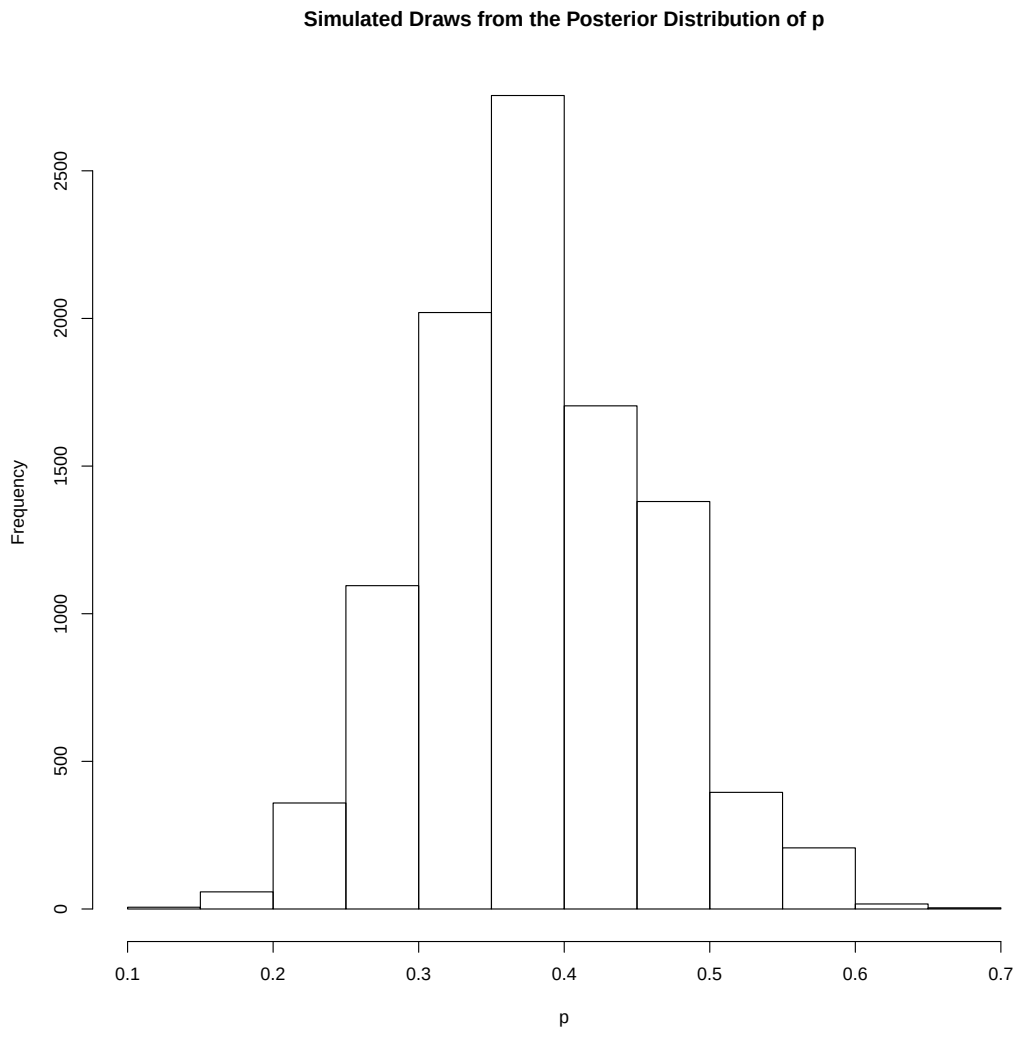
Now let's plot the prior:

```
#Output histogram of prior
curve(get_histprior_value(x, histprior), from=0, to = 1,
      ylim = c(0, 0.3), n = 10000,
      xlab="p", ylab = "Prior density", main = "Histogram Prior")
```



Finally, let's generate and plot the posterior:

```
s <- 11
f <- 16

p <- seq(0, 1, length = 10000)

post <- get_histprior_value(p, histprior) * dbeta(p, s+1, f+1)

post <- post/sum(post)

ps <- sample(p, replace = TRUE, prob = post)

hist(ps, xlab="p", main="Simulated Draws from the Posterior Distribution of p")
```



(b) Let's start with `pdiscp()`:

```
pdiscp <- function(p, prior, m, ys){
  pred <- rep(NA, length = length(ys))

  #Loop through possible y values
  for(i in 1:length(ys)){
    val <- 0
    #Loop through possible proportions in discrete prior
    for(j in 1:length(p)){
      f <- choose(m, ys[i]) * (p[j])^(ys[i]) * (1-p[j])^(m-ys[i])
      g <- prior[j]
      val <- val + (f*g)
    }
    pred[i] <- val
  }

  #Return vector of probabilities for each y value
  return(pred)
}
```

```r
#Test run
p <- seq(0.05, 0.95, by=0.1)
prior <- c(1, 5.2, 8, 7.2, 4.6, 2.1, 0.7, 0.1, 0, 0)
prior <- prior/sum(prior)
m <- 20
ys <- 0:20
pred <- pdiscp(p, prior, m, ys)

round(cbind(0:20, pred), 3)
```

```
##           pred
##  [1,]  0 0.020
##  [2,]  1 0.044
##  [3,]  2 0.069
##  [4,]  3 0.092
##  [5,]  4 0.106
##  [6,]  5 0.112
##  [7,]  6 0.110
##  [8,]  7 0.102
##  [9,]  8 0.089
## [10,]  9 0.074
## [11,] 10 0.059
## [12,] 11 0.044
## [13,] 12 0.031
## [14,] 13 0.021
## [15,] 14 0.013
## [16,] 15 0.007
## [17,] 16 0.004
## [18,] 17 0.002
## [19,] 18 0.001
## [20,] 19 0.000
## [21,] 20 0.000
```

(c) Now let's try `pbetap()`:

```
pbetap <- function(ab, m, ys){
  pred <- rep(NA, length = length(ys))

  for(i in 1:length(ys)){
    choose <- choose(m, ys[i])

    beta_num <- beta(ab[1] + ys[i], ab[2] + m - ys[i])

    beta_denom <- beta(ab[1], ab[2])

    pred[i] <- choose*(beta_num/beta_denom)
  }

  #Return vector of probabilities for each y value
  return(pred)
}
```

```
#Test run
ab <- c(3.26, 7.19)
m <- 20
ys <- 0:20
pred <- pbetap(ab, m, ys)
round(cbind(0:20, pred), 3)
```

```
##           pred
##  [1,]  0 0.018
##  [2,]  1 0.045
##  [3,]  2 0.072
##  [4,]  3 0.095
##  [5,]  4 0.108
##  [6,]  5 0.114
##  [7,]  6 0.111
##  [8,]  7 0.102
##  [9,]  8 0.088
## [10,]  9 0.073
## [11,] 10 0.057
## [12,] 11 0.043
## [13,] 12 0.030
## [14,] 13 0.020
## [15,] 14 0.012
## [16,] 15 0.007
## [17,] 16 0.004
## [18,] 17 0.002
## [19,] 18 0.001
## [20,] 19 0.000
## [21,] 20 0.000
```

(d) Finally, here's `discint`:

```
discint <- function(dist, covprob){
  total_prob <- 0
  y_list <- c()

  #Find max probability value
  #Centers credible interval around y value with max probability
  i <- which.is.max(dist[,2])
  total_prob <- total_prob + dist[i,2]
  y_list <- c(y_list, dist[i,1])

  i_prev <- i-1
  i_next <- i+1

  while(total_prob < covprob){
    #Check if previous row is within range of matrix
    if(i_prev >= 1 & i_prev <= nrow(dist)){
      prev_val <- dist[i_prev,2]
    } else{
      prev_val <- -1
    }

    #Check if next row is within range of matrix
    if(i_next >= 1 & i_next <= nrow(dist)){
      next_val <- dist[i_next,2]
    } else{
      next_val <- -1
    }

    #Compare values for i_next and i_prev
    if(dist[i_next,2] >= dist[i_prev,2]){
      total_prob <- total_prob + dist[i_next, 2]
      y_list <- c(y_list, dist[i_next, 1])
      i_next <- i_next + 1
    } else{
      total_prob <- total_prob + dist[i_prev, 2]
      y_list <- c(y_list, dist[i_prev, 1])
      i_prev <- i_prev - 1
    }
  }

  output <- list(prob = total_prob, set = sort(y_list))

  return(output)
}
```

```r
#Test run
p <- rbeta(1000, 3.26, 7.19)
y <- rbinom(1000, 20, p)
freq <- table(y)
ys <- as.integer(names(freq))
predprob <- freq/sum(freq)

dist <- cbind(ys, predprob)
covprob <- 0.9

discint(dist, covprob)
```

```
## $prob
## [1] 0.911
##
## $set
##  [1]  1  2  3  4  5  6  7  8  9 10 11
```

2. **Chapter 2: Introduction to Bayesian Thinking** Show how the author derived the predictive density formula below with a $beta(a, b)$ prior (pg. 31 of book):

$$\begin{aligned} f(\tilde{y}) &= \int f_B(\tilde{y}|m,p)g(p)dp \\ &= \binom{m}{\tilde{y}} \frac{B(a+\tilde{y}, b+m-\tilde{y})}{B(a,b)} \end{aligned}$$

where $\tilde{y} = 0, \ldots, m$.

Solution:

$$\begin{aligned} f(\tilde{y}) &= \int f_B(\tilde{y}|m,p)g(p)dp \\ &= \int_0^1 \binom{m}{\tilde{y}} p^{\tilde{y}}(1-p)^{m-\tilde{y}} \left(\frac{1}{B(a,b)} p^{a-1}(1-p)^{b-1} \right) dp \\ &= \binom{m}{\tilde{y}} \frac{1}{B(a,b)} \int_0^1 p^{\tilde{y}}(1-p)^{m-\tilde{y}} \left(p^{a-1}(1-p)^{b-1} \right) dp \\ &= \binom{m}{\tilde{y}} \frac{1}{B(a,b)} \int_0^1 p^{\tilde{y}+a-1}(1-p)^{m-\tilde{y}+b-1} dp \\ &= \binom{m}{\tilde{y}} \frac{1}{B(a,b)} B(a+\tilde{y}, b+m-\tilde{y}) \\ &= \binom{m}{\tilde{y}} \frac{B(a+\tilde{y}, b+m-\tilde{y})}{B(a,b)} \end{aligned}$$

3. **Chapter 2: Introduction to Bayesian Thinking** Exercise 5.

Solution:

```
#a)
mu <- c(20, 30, 40, 50, 60, 70)
prior <- c(.1, .15, .25, .25, .15, .1)
prior <- prior/sum(prior)

#b)
y <- c(38.6, 42.4, 57.5, 40.5, 51.7, 67.1, 33.4, 60.9, 64.1, 40.1, 40.7, 6.4)
ybar <- mean(y)

#c)
n <- length(y)
sigma_squared <- var(y)

like <- exp(-(n/(2*sigma_squared))*(mu - ybar)^2)

#d)
post <- prior*like/sum(prior*like)

#e)
dist <- cbind(mu, post)
discint(dist, 0.8)

## $prob
##      post
## 0.9921244
##
## $set
## mu mu
## 40 50
```

4. **Chapter 2: Introduction to Bayesian Thinking** Exercise 6.

Solution:

```
#a)
lambda <- c(0.5, 1, 1.5, 2, 2.5, 3)
prior <- c(0.1, 0.2, 0.3, 0.2, 0.15, 0.05)
prior <- prior/sum(prior)

pred <- rep(NA, length = length(lambda))
y <- 12

for(i in 1:length(lambda)){
  pred[i] <- prior[i]*exp(-6*lambda[i])*(6*lambda[i])^12
}
pred <- pred/sum(pred)
pred <- cbind(lambda, pred)
print(round(pred,5))

##      lambda    pred
## [1,]    0.5 0.00009
## [2,]    1.0 0.03679
## [3,]    1.5 0.35652
## [4,]    2.0 0.37357
## [5,]    2.5 0.20299
## [6,]    3.0 0.03004

#b)
predictive_prob <- rep(NA, length = length(lambda))
for(i in 1:length(lambda)){
  predictive_prob[i] <- exp(-7*lambda[i])*pred[i]
}

sum(predictive_prob)

## [1] 0.01605361
```

5. **Chapter 3: Single-Parameter Models** Write your own versions of the functions `binomial.beta.mix()` and `pbetat()`.

Solution:

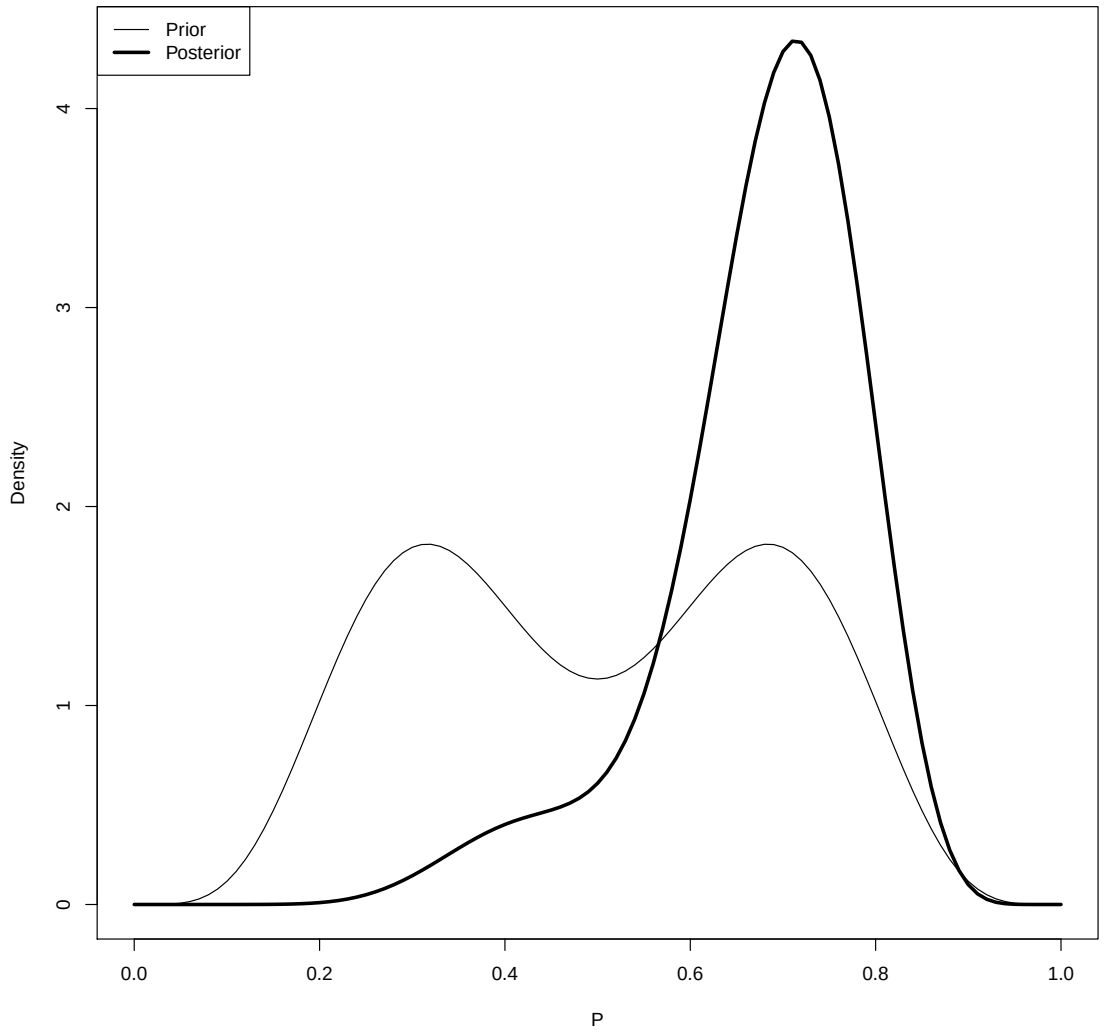
```
binomial.beta.mix <- function(probs, betpar, data){
  m = data[1] + data[2]

  lambda_data <- (probs[1] * pbetap(betpar[1,], m, data[1]))/
    (probs[1] * pbetap(betpar[1,], m, data[1]) +
       probs[2] * pbetap(betpar[2,], m, data[1]))

  posterior <- c()
  posterior$probs <- matrix(c(lambda_data, (1-lambda_data)), nrow=1, ncol=2)
  colnames(posterior$probs) <- c("beta.par1", "beta.par2")

  posterior$betapar <- rbind(c(betapar[1,1] + data[1], betapar[1,2] + data[2]),
                             c(betapar[2,1] + data[1], betapar[2,2] + data[2]))
  rownames(posterior$betapar) <- c("beta.par1", "beta.par2")
  colnames(posterior$betapar) <- c("", "")

  return(posterior)
}
```

Here is an example run using the values from the book (p. 51-52):

```
#Example run
probs <- c(.5, .5)
beta.par1 <- c(6, 14)
beta.par2 <- c(14, 6)
betapar <- rbind(beta.par1, beta.par2)
data <- c(7,3)

post <- binomial.beta.mix(probs, betapar, data)

post$probs

##       beta.par1 beta.par2
## [1,] 0.09269663 0.9073034

post$betapar

##
## beta.par1 13 17
## beta.par2 21  9
```

Now let's plot the posterior and the prior:

```
curve(post$probs[1]*dbeta(x,13,17) + post$probs[2]*dbeta(x,21,9),
      from = 0, to = 1, lwd=3, xlab = "P", ylab = "Density")
curve(0.5*dbeta(x,6,12)+0.5*dbeta(x,12,6),0,1,add=TRUE)
legend("topleft", legend=c("Prior", "Posterior"), lwd=c(1,3))
```



6. **Chapter 3: Single-Parameter Models** On pg. 55, Albert writes, "One can show that the posterior probability that the coin is fair is given by:"

$$\lambda(y) = \frac{0.5P_0(Y \leq 5)}{0.5P_0(Y \leq 5) + 0.5P_1(Y \leq 5)}.$$

Show this.

Solution: On pg. 54, Albert shows that the posterior density of the model where the coin is fair ($p = 0.5$) is given by:

$$\lambda(y) = \frac{.5p(y|.5)}{.5p(y|.5) + .5m_1(y)}$$

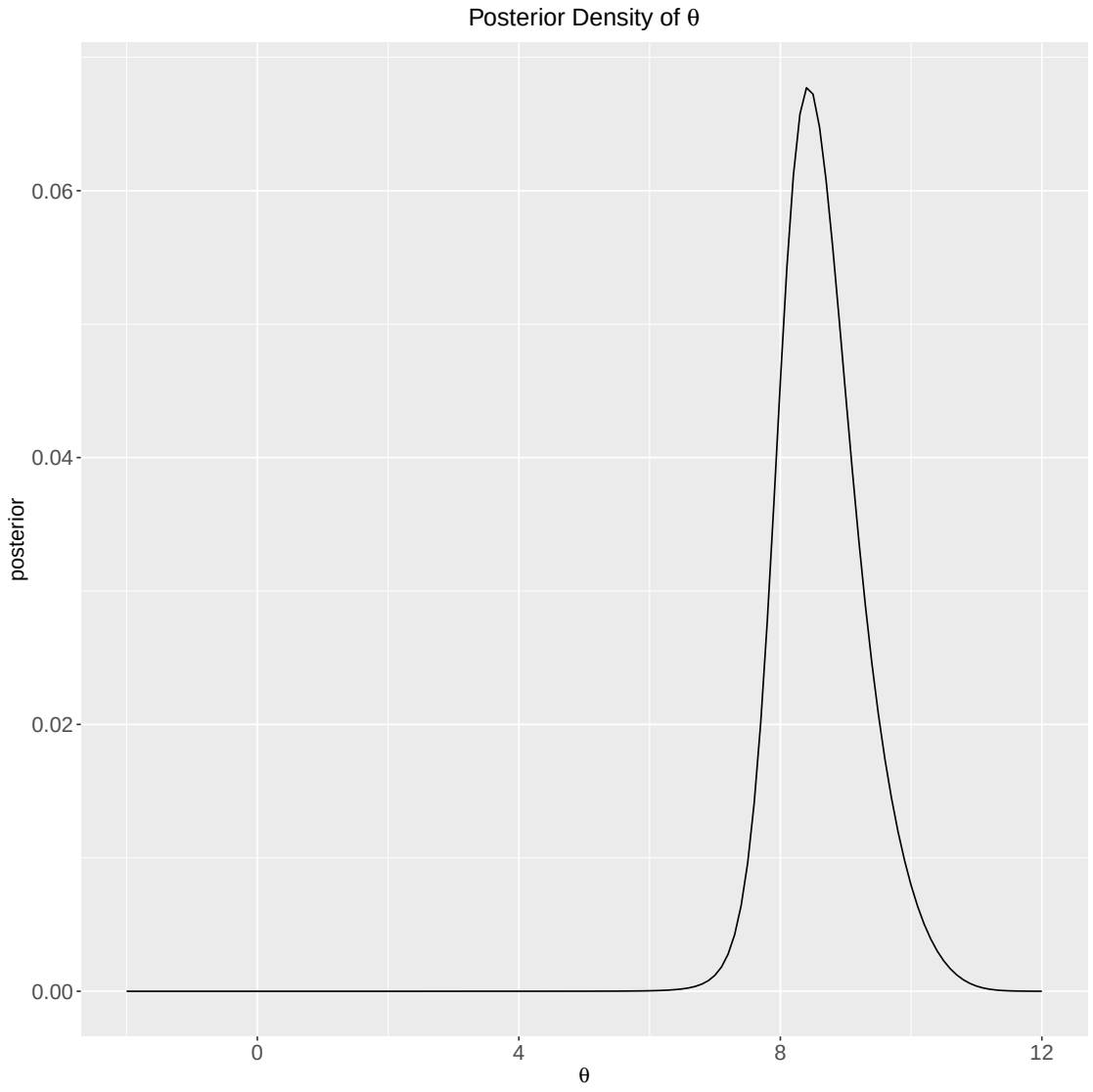
where $p(y|.5)$ is the binomial density for y when $p = .5$ and $m_1(y)$ is the (prior) predictive density for y using the beta density.

The equation on pg. 55 essentially takes the above equation and sums over the probability of $y = 0, 1, 2, 3, 4, 5$.

7. **Chapter 3: Single-Parameter Models** Do all Exercises at the end of the chapter.

Solution:

1.
```r
#a)
data <- c(0, 10, 9, 8, 11, 3, 3, 8, 8, 11)

theta <- seq(from = -2, to = 12, by = 0.1)

#b)
posterior_density <- rep(1, length(theta))

for(i in 1:length(theta)){
  for(j in 1:length(data)){
    posterior_density[i] <- posterior_density[i] * (1/(1+((data[j] - theta[i])^2)))
  }
}

posterior_density <- posterior_density/sum(posterior_density)

#c)
df <- data.frame(theta = theta, posterior = posterior_density)

ggplot(df, aes(x = theta, y = posterior)) +
  geom_line() +
  xlab(TeX('$\\theta$')) +
  ggtitle(TeX('Posterior Density of $\\theta$')) +
  theme.info
```




```r
#d)
samples <- sample(theta, 100000, replace = TRUE, prob = posterior_density)

#Posterior mean
mean(samples)
```

```
## [1] 8.629352
```

```r
#Posterior standard deviation
sd(samples)
```

```
## [1] 0.6469175
```

2. Let $\theta = 1/\lambda = \lambda^{-1}$. Then we have $\lambda = \theta^{-1}$ and:

$$\begin{aligned}\lambda^{-n-1}e^{-s/\lambda} &= (\theta^{-1})^{-n-1}e^{-s/(\theta^{-1})} \\ &= \theta^{-1(-n-1)}e^{-s\theta} \\ &= \theta^{n+1}e^{-s\theta}\end{aligned}$$

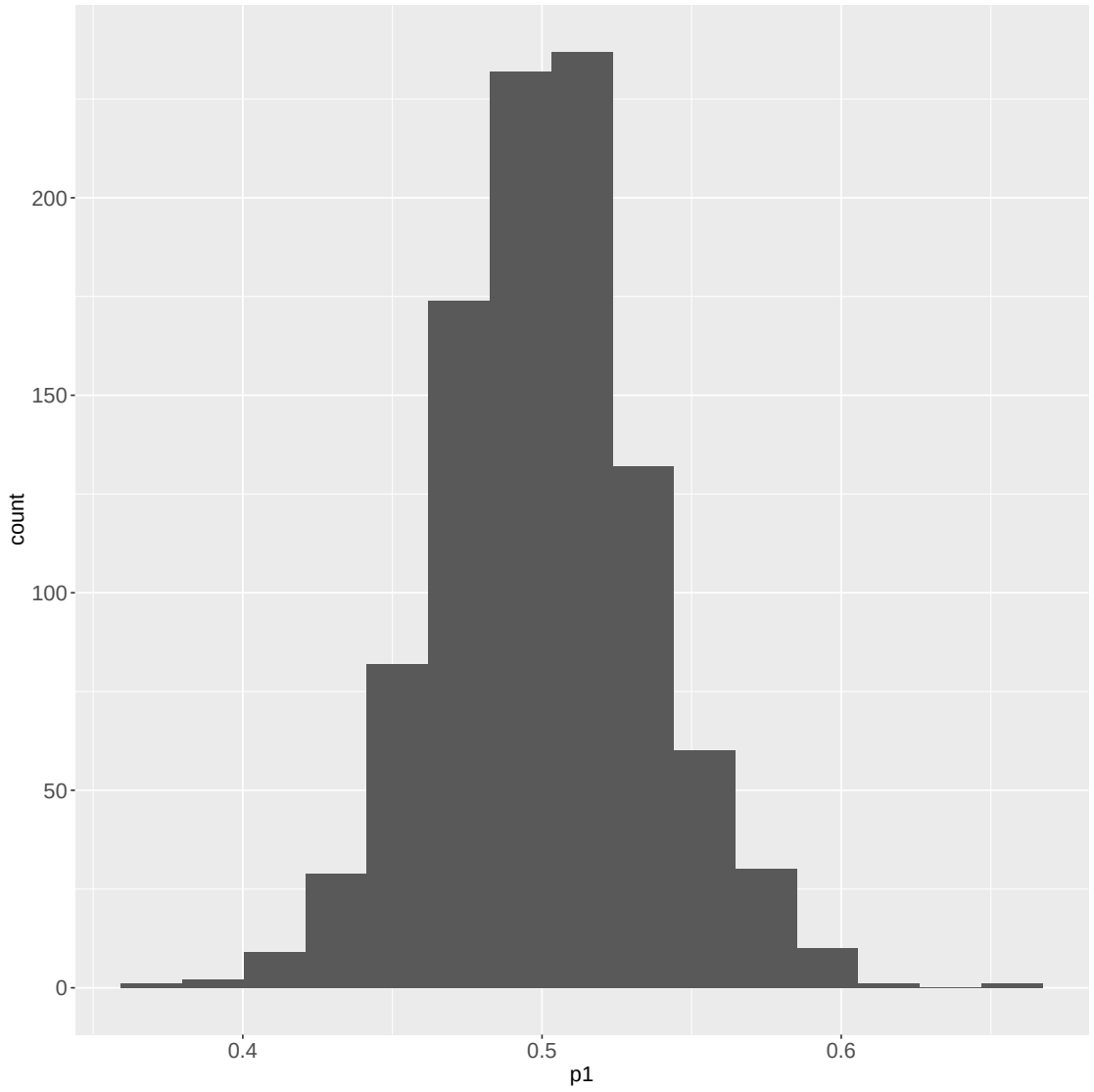
So, θ has a gamma density with shape parameter $n+2$ and rate parameters s.

```
#b)
burn_times <- c(751, 594, 1213, 1126, 819)

n <- length(burn_times)
s <- sum(burn_times)

theta_draws <- rgamma(1000, shape = n+2, rate = s)

#c)
lambda_draws <- 1/theta_draws

#d)
greater_than_1000 <- sum(lambda_draws > 1000)

posterior_prob_greater_than_1000 <- greater_than_1000/length(lambda_draws)

print(posterior_prob_greater_than_1000)


## [1] 0.156
```

3. We know $100 \leq N \leq 200$. So,

```
N <- seq(from = 100, to = 200, by = 1)
post <- rep(0, length = length(N))

n <- length(y)

for(i in 1:length(post)){
  post[i] <- 1/(N[i]^n)
}

samples <- sample(N, 100000, replace = TRUE, prob = post)

#Posterior mean
mean(samples)


## [1] 144.2164


#Posterior standard deviation
sd(samples)


## [1] 29.00468
```

4.
```r
#a)
p1 <- rbeta(1000, shape1 = 100, shape2 = 100)

df1 <- data.frame(p1 = p1)

ggplot(data = df1, aes(x=p1)) + geom_histogram(bins = 15) + theme.info
```



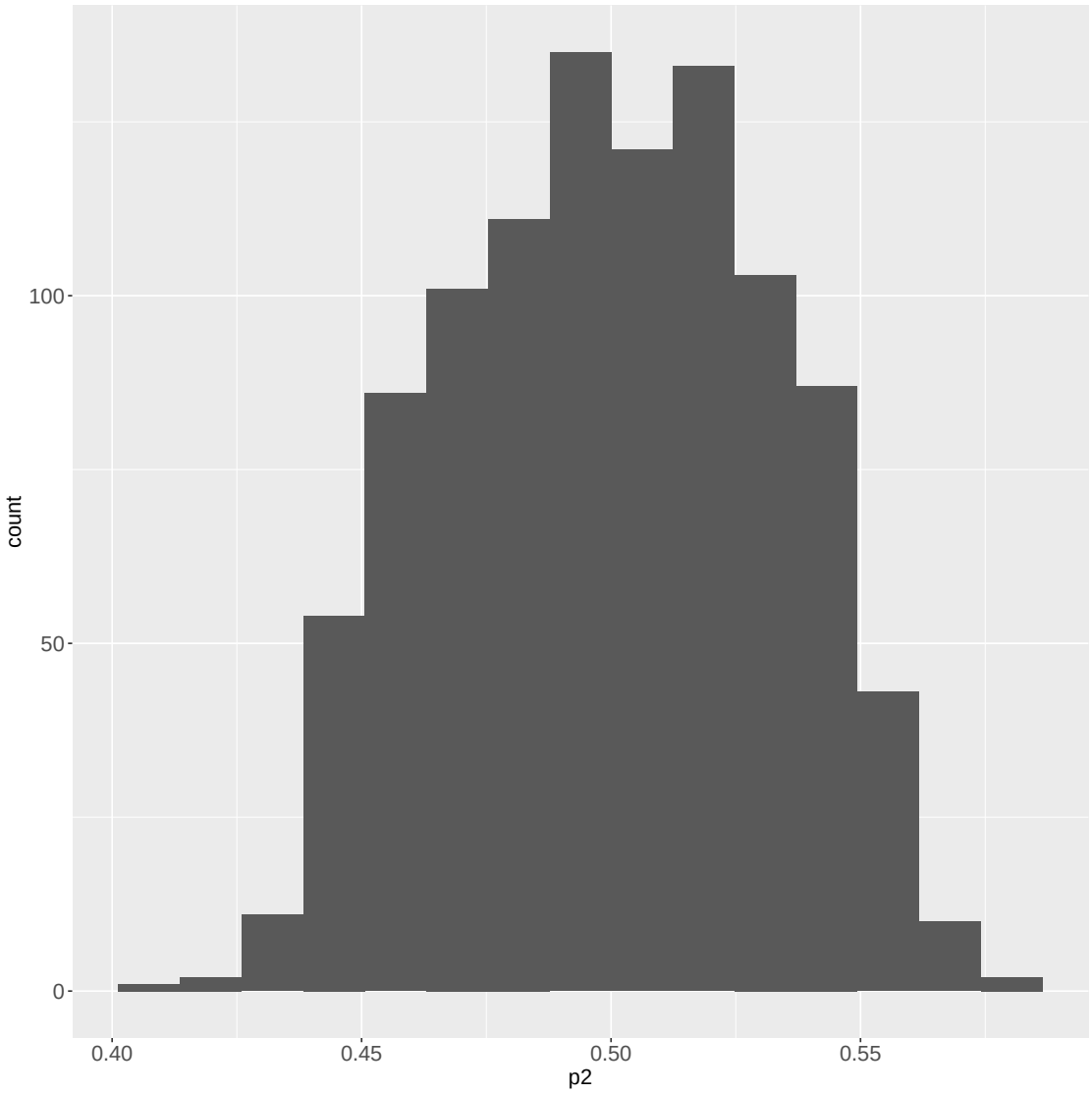
```r
#Mean of P1. Target is 0.5
mean(p1)
```

```
## [1] 0.5007184
```

```r
#Probability that 0.44 < p < 0.56. Target is a probability of 0.9
(sum(p1 < 0.56) - sum(p1 < 0.44))/length(p1)
```

```
## [1] 0.91
```

```r
p2 <- 0.9*rbeta(1000, 500, 500) + 0.1*rbeta(1000, 1, 1)

df2 <- data.frame(p2 = p2)

ggplot(data = df2, aes(x=p2)) + geom_histogram(bins = 15) + theme.info
```




```
#Mean of P2. Target is 0.5
mean(p2)
```

```
## [1] 0.4997092
```

```
#Probability that 0.44 < p < 0.56. Target is a probability of 0.9
(sum(p2 < 0.56) - sum(p2 < 0.44))/length(p2)
```

```
## [1] 0.965
```

```r
#b)
s <- 45
f <- 55

a1 <- 100
b1 <- 100

posterior1 <- rbeta(1000,a1+s, b1+f)

mean(posterior1)


## [1] 0.4829703


quantile(posterior1, c(0.05, 0.95))


##        5%       95%
## 0.4359717 0.5294894
```

```r
probs <- c(.9, .1)
beta.par1 <- c(500, 500)
beta.par2 <- c(1, 1)
betapar <- rbind(beta.par1, beta.par2)
data <- c(s,f)

post <- binomial.beta.mix(probs, betapar, data)

posterior2 <- post$probs[1] *
  rbeta(1000, post$betapar[1,1] +
          s, post$betapar[1,2] + f) +
  post$probs[2] *
  rbeta(1000, post$betapar[2,1] +
          s, post$betapar[2,2] + f)

mean(posterior2)


## [1] 0.4499606


quantile(posterior2, c(0.05, 0.95))


##        5%       95%
## 0.3944848 0.5083229
```

```r
#c)
s <- 30
f <- 70

s <- 45
f <- 55

a1 <- 100
b1 <- 100

posterior1 <- rbeta(1000,a1+s, b1+f)

mean(posterior1)


## [1] 0.4853572


quantile(posterior1, c(0.05, 0.95))


##        5%       95%
## 0.4375929 0.5313869


probs <- c(.9, .1)
beta.par1 <- c(500, 500)
beta.par2 <- c(1, 1)
betapar <- rbind(beta.par1, beta.par2)
data <- c(s,f)

post <- binomial.beta.mix(probs, betapar, data)

posterior2 <- post$probs[1] * rbeta(1000, post$betapar[1,1] +
                                      s, post$betapar[1,2] + f) +
  post$probs[2] *
  rbeta(1000, post$betapar[2,1] + s, post$betapar[2,2] + f)

mean(posterior2)


## [1] 0.450403


quantile(posterior2, c(0.05, 0.95))


##        5%       95%
## 0.3927499 0.5086557
```

In both cases, the means of the posteriors and the 90% confidence intervals are affected by the choice of prior. The difference is not overly drastic, but the means may differ by up to 0.04 depending upon the simulation.

5.
```r
#a)
p_value <- 2 * (1-pbinom(8, 20, 0.2))

print(p_value)


## [1] 0.01996357
```

This value is smaller than 0.05, so we can reject the hypothesis that the person does not have ESP.

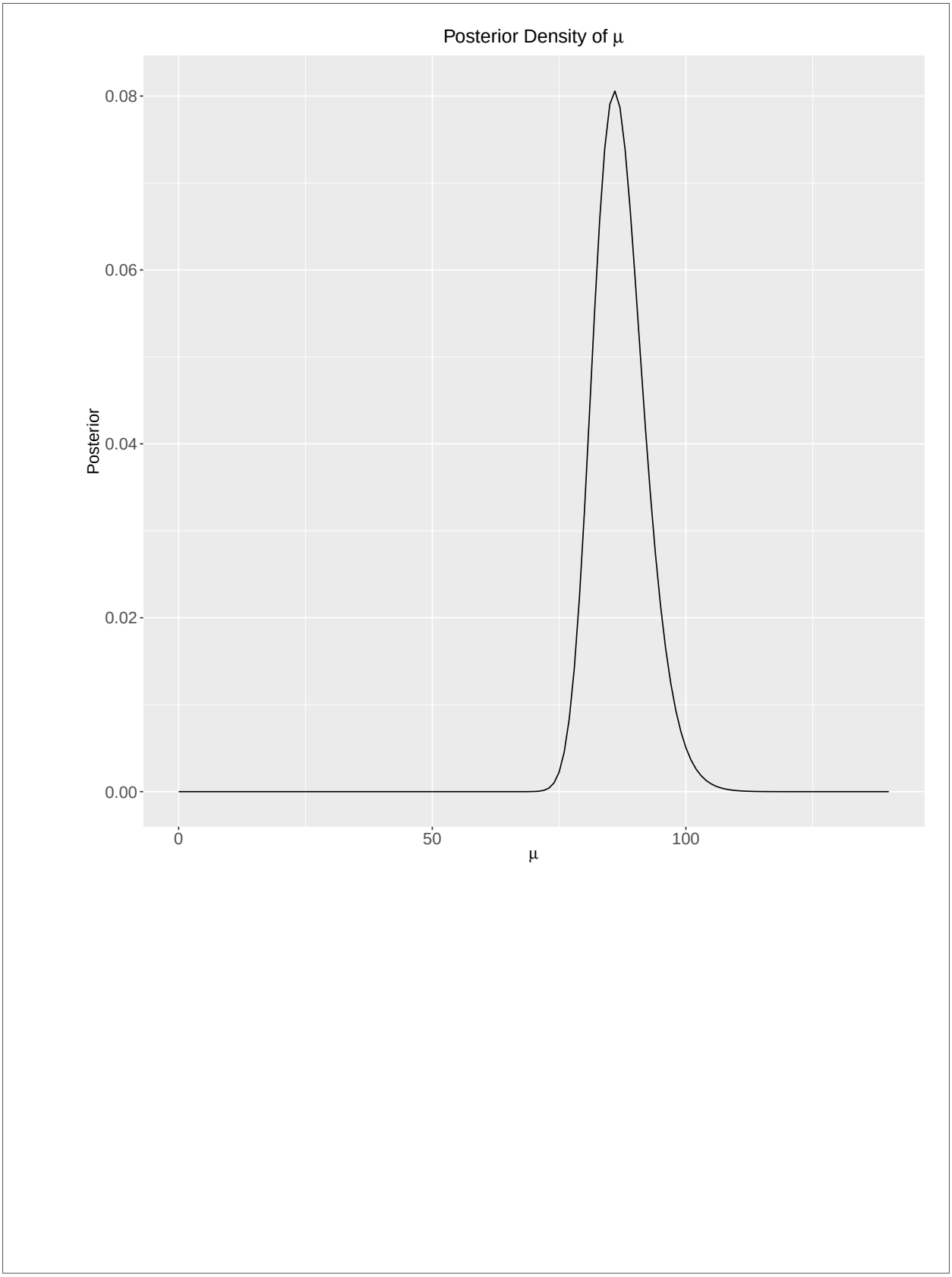
```r
pbetat <- function(p, prob, beta_params, data){
  y <- data[1]
  f <- data[2]
  a <- beta_params[1]
  b <- beta_params[2]

  m1 <- dbinom(y, n, p) * dbeta(p, a,b)/dbeta(p, a+y, b+n-y)

  #Lambda is the posterior probability that p = 0.2
  lambda <- dbinom(y,n,p)/(dbinom(y,n,p) + m1)

  return(lambda)
}

#b)
n <- 20
y <- 8
a <- 1
b <- 4
p <- 0.2
prob <- 0.5

#Lambda is the posterior probability that p = 0.2
lambda <- pbetat(p, prob, c(1, 4), c(y, n-y))

print(lambda)


## [1] 0.3410395
```

There is more evidence for the hypothesis that $p = 0.2$ than is suggested by the p-value above

```r
#c)
#Prior 1
print(pbetat(p, prob, c(.5, 2), c(y, n-y)))

## [1] 0.3900752

#Prior 2
print(pbetat(p, prob, c(2, 8), c(y, n-y)))

## [1] 0.328591

#Prior 3
print(pbetat(p, prob, c(8, 32), c(y, n-y)))

## [1] 0.3855337
```

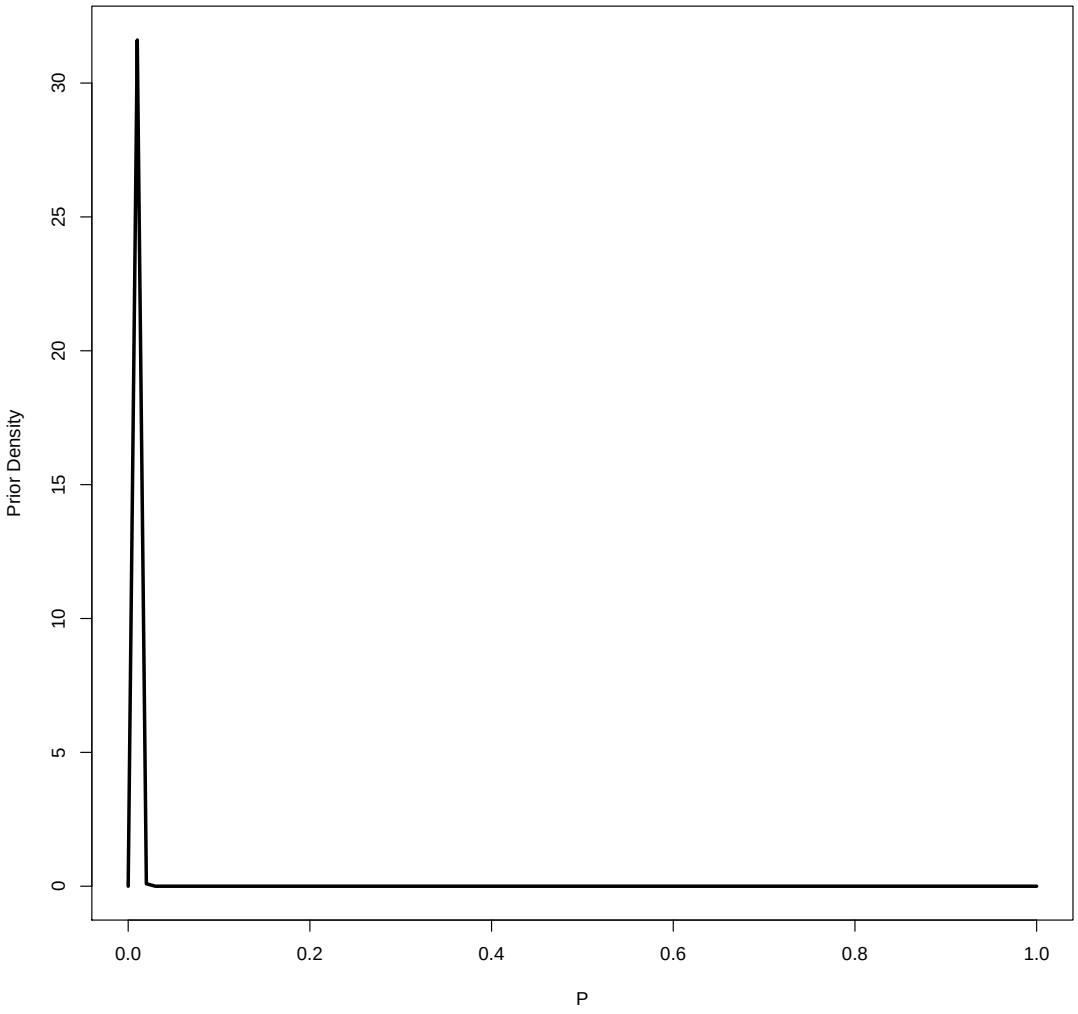
All four Bayesian computations assert that the posterior probability that $p = 2$ is between about 0.32 and 0.4. The range of posterior values is quite large and suggests a fairly sizeable probability that $p = 2$ is true. Since actual ESP is highly unlikely, we should not conclude that this person has ESP, which contradicts the analysis we performed using p-values.

6.
```r
#a)
mu <- seq(from = 0, to = 140, by = 1)
sigma <- 10
s <- 1
f <- 17

likelihood <- (pnorm(70, mu, sigma))^s * (1 - pnorm(70, mu, sigma))^f

likelihood <- likelihood/sum(likelihood)

data <- data.frame(mu = mu, likelihood = likelihood)

ggplot(data, aes(x= mu, y= likelihood)) +
  geom_line() +
  ggtitle(TeX("Posterior Density of $\\mu$")) +
  ylab("Posterior") +
  xlab(TeX("$\\mu$")) +
  theme.info
```


Posterior Density of μ
0.08
0.06
0.04
0.02
0.00
Posterior
0
50
100
μ

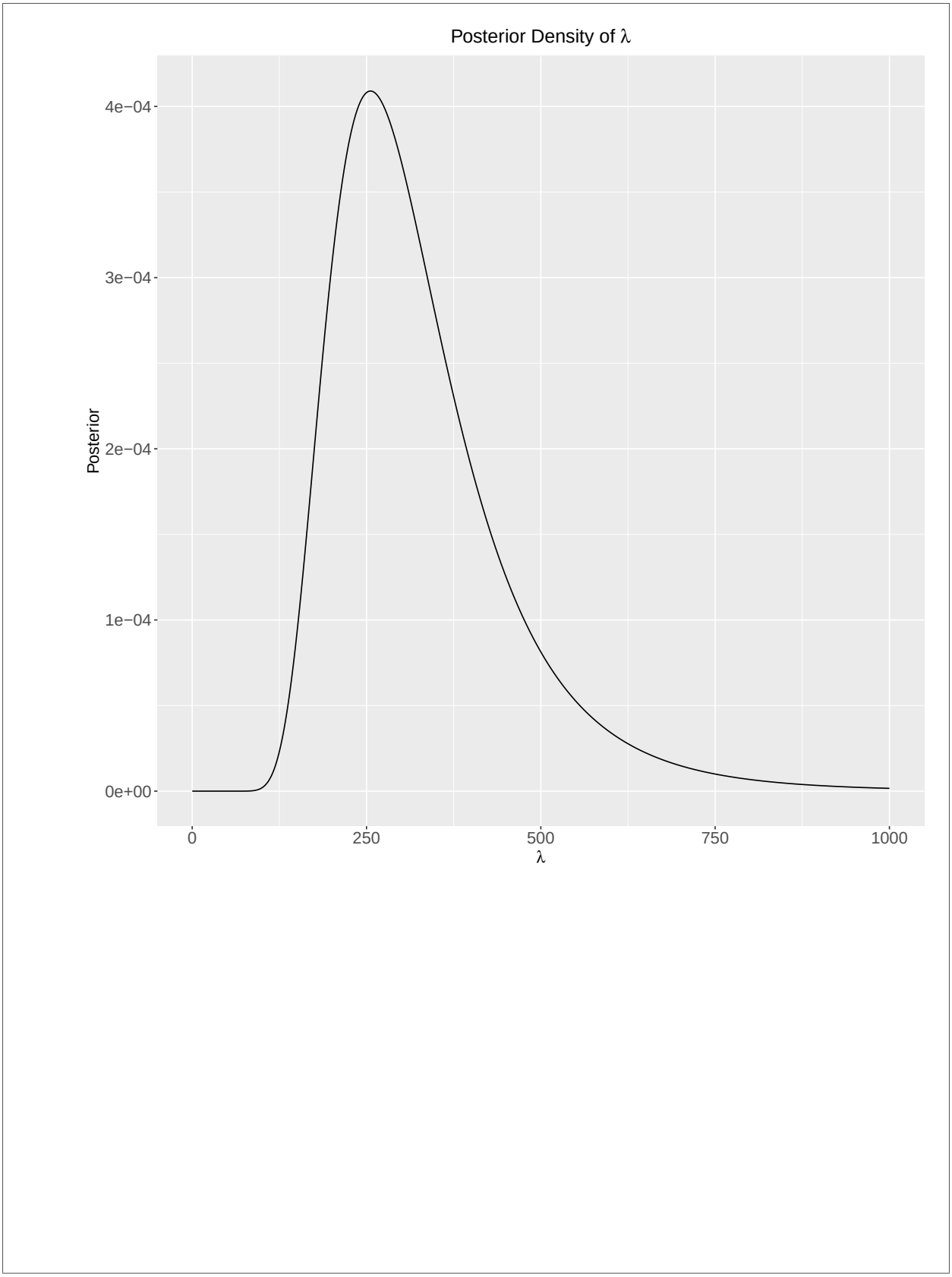
```r
#b)
posterior_mean <- likelihood * mu
posterior_mean <- sum(posterior_mean)

print(posterior_mean)


## [1] 87.11109


#c)
prob_greater_than_80 <- sum(likelihood[mu > 80])

print(prob_greater_than_80)


## [1] 0.9146066
```

7.
```r
suppressMessages(library(LearnBayes, quietly=TRUE,
                         warn.conflicts = FALSE,verbose = FALSE))


#a)
curve(0.5*dgamma(x, 1.5, 1000) + 0.5*dgamma(x,7,1000),
      from = 0, to = 1, lwd = 3,
      xlab = "P", ylab = "Prior Density")
```



```r
#b)
probs <- c(0.5, 0.5)
gamma.par1 <- c(1.5, 1000)
gamma.par2 <- c(7, 1000)
gammapar <- rbind(gamma.par1, gamma.par2)

#Data is supposed to contain a vector of counts and a vector of time intervals
#How to set this up?
data <- c()

#poisson.gamma.mix(probs, gammpar, data)

#Come back to this one
```

8.
```r
#a)
lambda <- seq(from = 0.1, to = 1000, by = 0.1)

prior <- 1/lambda

like <- pexp(100, 1/lambda)^3 * dexp(100,1/lambda)*
  (pexp(300, 1/lambda) - pexp(100,1/lambda))^3*
  dexp(300,1/lambda)*(1-pexp(300,1/lambda))^4

posterior <- like*prior

posterior <- posterior/sum(posterior)

data <- data.frame(lambda = lambda, posterior = posterior)

ggplot(data, aes(x= lambda, y= posterior)) +
  geom_line() +
  ggtitle(TeX("Posterior Density of $\\lambda$")) +
  ylab("Posterior") +
  xlab(TeX("$\\lambda$")) +
  theme.info
```


Posterior Density of λ
Posterior
4e−04
3e−04
2e−04
1e−04
0e+00
0
250
500
750
1000
λ

```r
#b)
mean_lambda <- lambda*posterior

mean_lambda <- sum(mean_lambda)

print(mean_lambda)

## [1] 327.2188

sample <- sample(lambda, size = 100000, replace = TRUE, prob = posterior)

print(sd(sample))

## [1] 127.6806

#c)
prob_between_300_and_500 <- sum(posterior[300 <= lambda & lambda <= 500])

print(prob_between_300_and_500)

## [1] 0.4059514
```