

QPM II - Problem Set 4

2024-11-13

1) The Negative Binomial Distribution

- a. Use the integrate function in R to find the Expected A Posteriori estimate of θ . Use a β distribution for the prior with parameters $\alpha = \beta = 1$.

```
# Given parameters
x <- c(23, 14, 24, 17, 4, 40, 17, 13, 31, 24)
s <- 1
alpha <- 1
beta <- 1

# Likelihood f(n)
likelihood <- function(theta) {
  suppressWarnings(prod(choose(x + s - 1, x) * theta^s * (1 - theta)^x))
}

# Integrals
num_posterior_integral <- integrate(function(theta) theta * dbeta(theta, alpha, beta) *
                                   likelihood(theta), 0, 1)
denom_posteriorintegral <- integrate(function(theta) dbeta(theta, alpha, beta) *
                                   likelihood(theta), 0, 1)

# EAP Estimate
E_theta <- num_posterior_integral$value / denom_posteriorintegral$value
cat("E(theta) =", E_theta, "\n")
```

```
## E(theta) = 0.5
```

- b. Now execute a similar method to find the posterior variance of θ .

The posterior variance is given by $\text{Var}(\theta) = E(\theta^2) - E(\theta)^2$. We have already calculated $E(\theta)$, therefore we need to calculate $E(\theta^2)$. The parameter is denoted by α .

```
# To calculate posterior variance, just square theta.
numerator <- integrate(function(theta) theta^2 *
                       dbeta(theta, alpha, beta) *
                       likelihood(theta), 0, 1)

# Denom is consistent
E_theta_squared <- numerator$value / denom_posteriorintegral$value

posterior_variance <- E_theta_squared - E_theta^2

cat("E(theta^2) =", E_theta_squared, "\n")
```

```
## E(theta^2) = 0.3333333
```

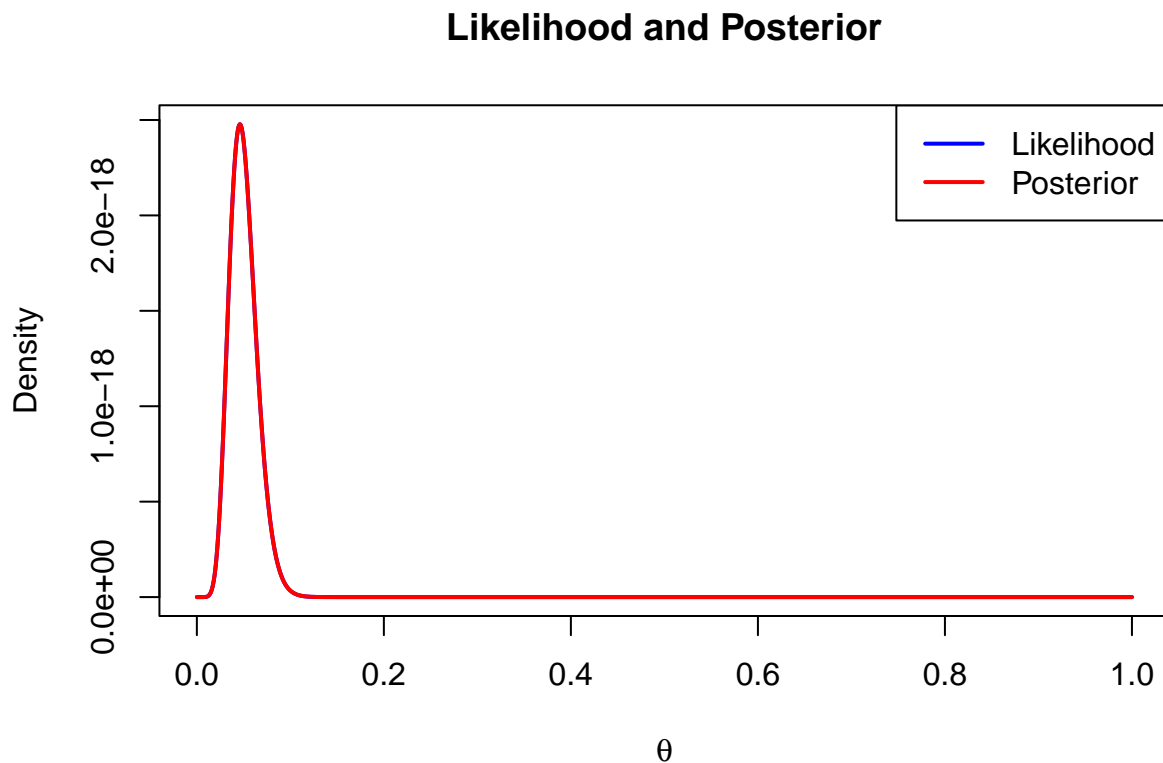
```
cat("Posterior Variance =", posterior_variance, "\n")
```

```
## Posterior Variance = 0.08333333
```

c. Now plot the likelihood function and the posterior and discuss how they differ.

```
theta_values <- seq(0, 1, length.out = 1000)
likelihood_values <- sapply(theta_values, likelihood)
posterior_values <- dbeta(theta_values, alpha, beta) * likelihood_values

plot(theta_values, likelihood_values, type = "l", col = "blue",
     lwd = 2, ylab = "Density", xlab = expression(theta),
     main = "Likelihood and Posterior")
lines(theta_values, posterior_values, col = "red", lwd = 2)
legend("topright", legend = c("Likelihood", "Posterior"), col = c("blue", "red"), lwd = 2)
```



The plot is overlapping. They do not differ.

d. Show that these results are sensitive to choices of α and β . Plot different posteriors, calculate the posterior mean using the numerical method above, and explain the changes.

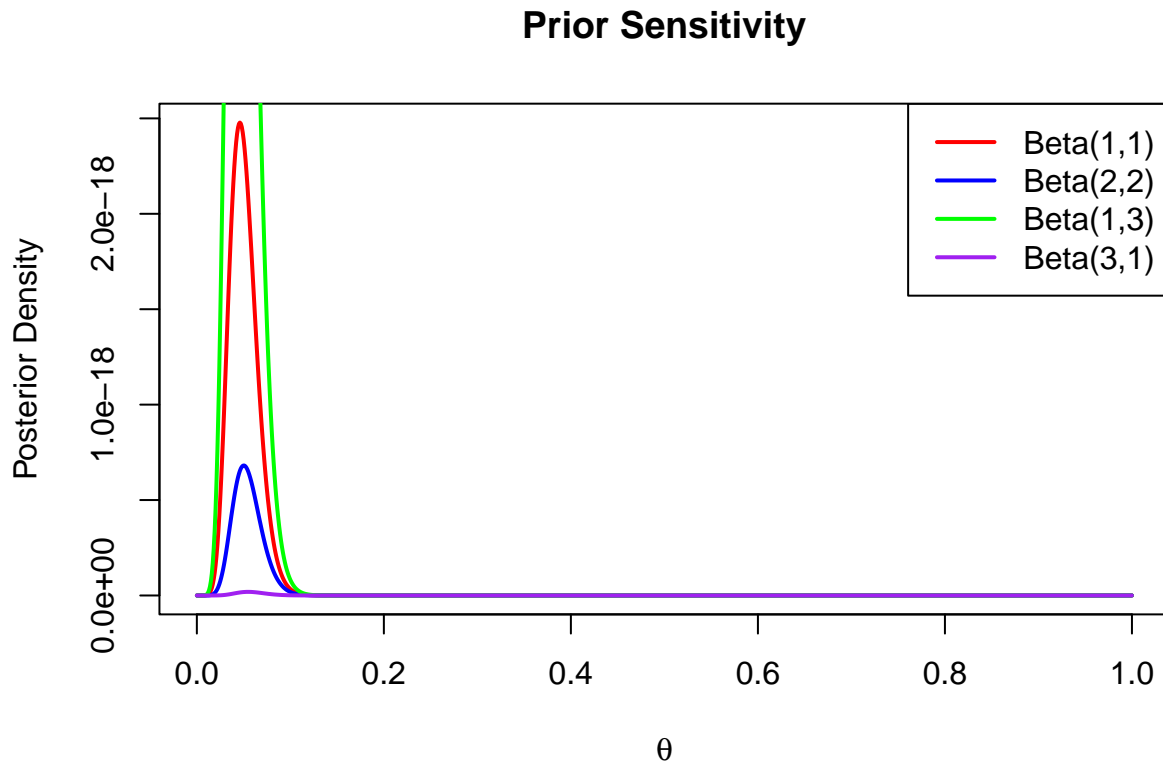
```

# Different priors
prior_params <- list(c(1, 1), c(2, 2), c(1, 3), c(3, 1))

plot(NULL, xlim = c(0, 1), ylim = c(0, max(posterior_values)),
     xlab = expression(theta), ylab = "Posterior Density", main = "Prior Sensitivity")

colors <- c("red", "blue", "green", "purple")
for (i in seq_along(prior_params)) {
  alpha_i <- prior_params[[i]][1]
  beta_i <- prior_params[[i]][2]
  posterior_i <- dbeta(theta_values, alpha_i, beta_i) * likelihood_values
  lines(theta_values, posterior_i, col = colors[i], lwd = 2)
}
legend("topright",
     legend = c("Beta(1,1)", "Beta(2,2)", "Beta(1,3)", "Beta(3,1)"),
     col = colors, lwd = 2)

```



Changes in the prior parameters shift the weight of the prior, affecting the posterior mean. A stronger prior like Beta(1,3) centers the distribution more along the mean of theta. Weaker distributions aren't as extremely tight around the mean.

- e. Perform a non-parametric bootstrap to find the standard error of the MLE

```

mle_theta <- function(data) {
  mean(data / (data + 1))
}

```

```

}

# Bootstrap
iterations <- 1000
bootstrap_mle <- replicate(iterations, mle_theta(sample(x, replace = TRUE)))

# SE of MLE
bootstrap_se <- sd(bootstrap_mle)
cat("Bootstrap Standard Error of MLE:", bootstrap_se)

```

```
## Bootstrap Standard Error of MLE: 0.01544707
```

2) One sample t-test

i. Conduct the likelihood ratio test for the null hypotheses using the results above

```

# Given data
data <- c(1, 3, 2, 4, -1, 7, 19, 3, -4, -5, -8)
n <- length(data)
theta0 <- 0
alpha <- 0.10

# T-statistic
x_bar <- mean(data)
S <- sd(data)
t_stat <- (x_bar - theta0) / (S / sqrt(n))

critical_value <- qt(1 - alpha, df = n - 1)

# Perform the hypothesis test
reject_null <- abs(t_stat) > critical_value
cat("Reject H0:", reject_null, "\n", "T-Statistic value:", abs(t_stat), "\n", "Critical Value:", critical_value, "\n")

## Reject H0: FALSE
## T-Statistic value: 0.8823841
## Critical Value: 1.372184

```

j. Find the power function for this test.

```

# power = Pr(rejecting H0 (t > critical value))
power_function <- function(theta, x_bar, S, n, critical_value) {
  non_central_t <- (x_bar - theta) / (S / sqrt(n))
  power <- pt(critical_value, df = n - 1, ncp = abs(non_central_t), lower.tail = FALSE)
  return(power)
}

```

k. Plot the power function for this test.

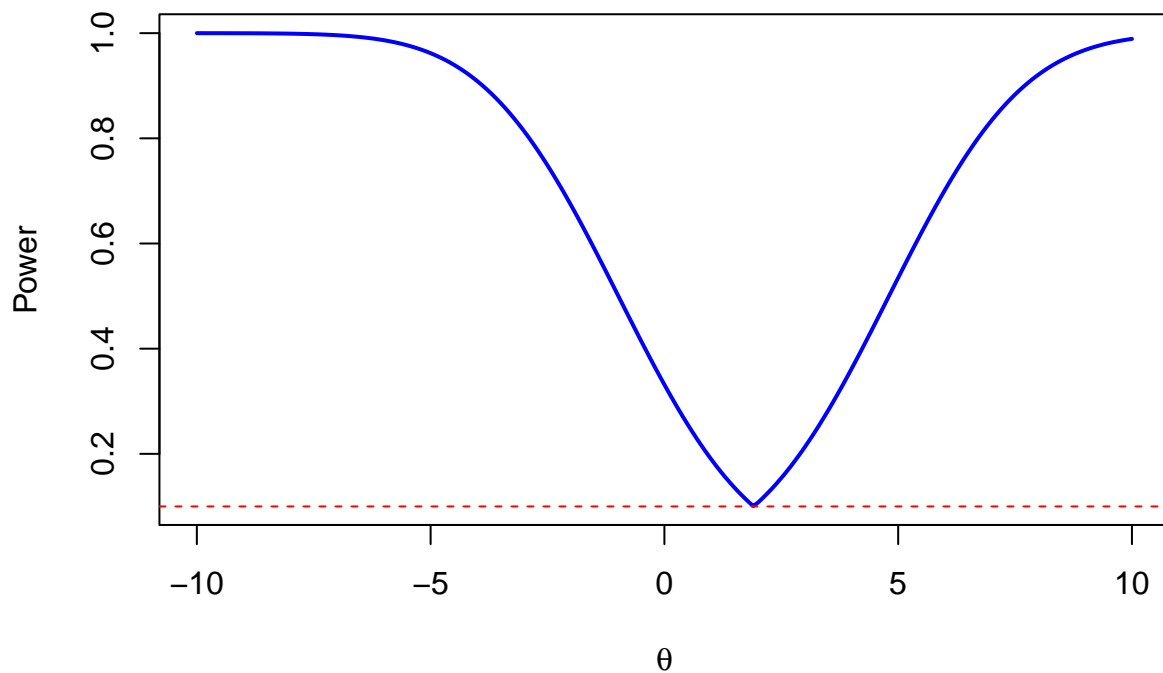
```

theta_values <- seq(-10, 10, by = 0.1) # Range of theta values
power_values <- sapply(theta_values, power_function,
                        x_bar = x_bar, S = S, n = n, critical_value = critical_value)

# Plotting of power function with the significance line == 2
plot(theta_values, power_values, type = "l", col = "blue", lwd = 2,
      xlab = expression(theta), ylab = "Power",
      main = "Power Function of the Likelihood Ratio Test")
abline(h = 0.10, col = "red", lty = 2)

```

Power Function of the Likelihood Ratio Test



3) Power Calculations

b + c

```

# Power Function Calculation for different mu_a values
mu_0 <- 7
mu_a_values <- c(7.5, 8, 8.5, 9)
n <- 20
critical_value <- 7.8225

power_function <- function(mu_a, critical_value, n) {
  z_score <- (critical_value - mu_a) / sqrt(5 / n)
  power <- 1 - pnorm(z_score)
  return(power)
}

```

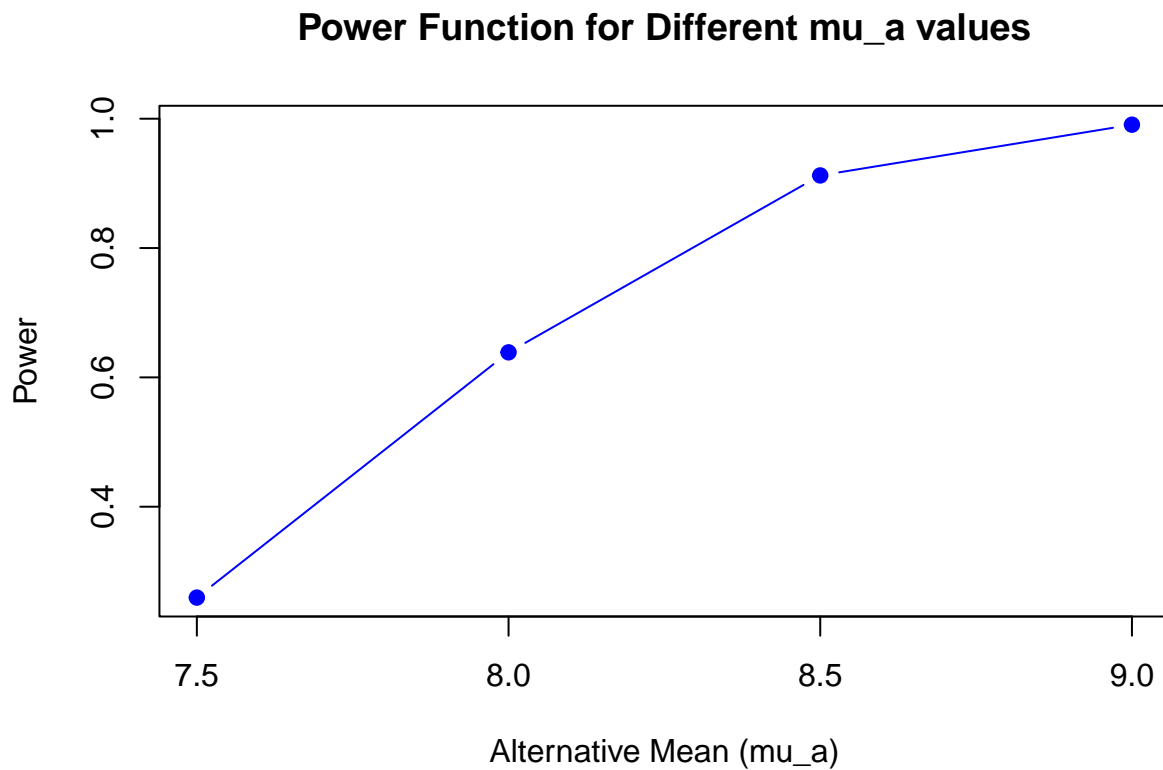
```

}

# Powers for i - iv
powers <- sapply(mu_a_values, power_function, critical_value = critical_value, n = n)

# Plot
plot(mu_a_values, powers, type = "b", pch = 19, col = "blue",
     xlab = "Alternative Mean (mu_a)", ylab = "Power",
     main = "Power Function for Different mu_a values")

```



d + e.

```

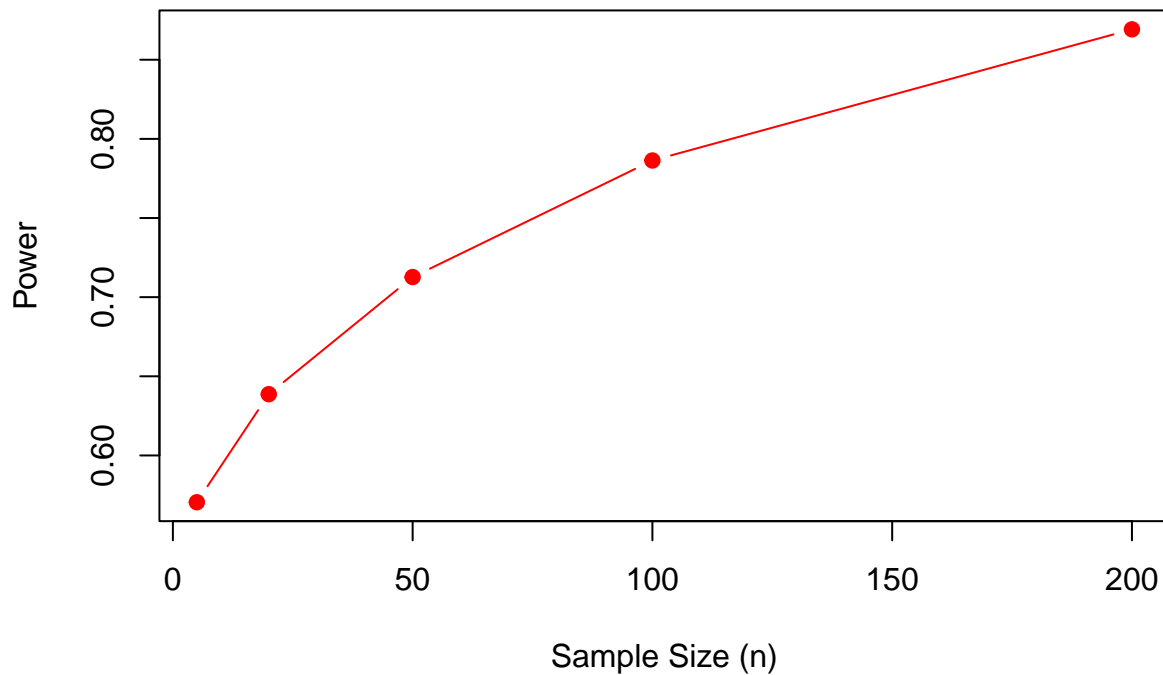
mu_a <- 8
sample_sizes <- c(5, 20, 50, 100, 200)

powers_size <- sapply(sample_sizes, power_function, mu_a = mu_a, critical_value = critical_value)

plot(sample_sizes, powers_size, type = "b", pch = 19, col = "red",
     xlab = "Sample Size (n)", ylab = "Power",
     main = "Power Function for Different Sample Sizes at mu = 8")

```

Power Function for Different Sample Sizes at $\mu = 8$



4) Simulation b - d.

```
alpha <- 0.05

false_discovery_rate_fn <- function(alpha, beta, phi) {
  false_discovery_rate <- (alpha * phi) / (alpha * phi + (1 - beta) * (1 - phi))
  return(false_discovery_rate)
}

false_discovery_rate_b <- false_discovery_rate_fn(alpha, beta = 0.75, phi = (1/6))
cat("b. False Discovery Rate:", false_discovery_rate_b, "\n")

## b. False Discovery Rate: 0.03846154

false_discovery_rate_c <- false_discovery_rate_fn(alpha, beta = 0.75, phi = (1/21) )
cat("c. False Discovery Rate:", false_discovery_rate_c, "\n")

## c. False Discovery Rate: 0.00990099

false_discovery_rate_d <- false_discovery_rate_fn(alpha, beta = 0.6, phi = (1/41))
cat("d. False Discovery Rate:", false_discovery_rate_d, "\n")

## d. False Discovery Rate: 0.003115265
```