

Stat 361 - Recitation 10

MC Methods for Statistical Inference

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Monte Carlo Hypothesis Testing

1. Using an available random sample of size n from the population of interest, calculate the observed value of the test statistic, let's say t_0 .
2. Decide on a pseudo-population that reflects the characteristics of the true population under the null hypothesis.
3. Obtain a random sample of size n from the pseudo-population.
4. Calculate the value of the test statistic using the random sample in step 3 and record it.
5. Repeat steps 3 and 4 for M trials. We now have values, t_1, t_2, \dots, t_M , that serve as an estimate of the distribution of the test statistic, T , when the null hypothesis is true.

A. Critical Value Approach

- Obtain the critical value by using the quantiles of estimated empirical distribution of the test statistic for the given significance level α .
- Lower tail test: get the α th sample quantile, \hat{q}_α from the t_1, t_2, \dots, t_M .
- Upper tail test: get the $(1-\alpha)$ -th sample quantile $\hat{q}_{1-\alpha}$, from the t_1, t_2, \dots, t_M .
- Two tail test: get the α -th sample quantile $\hat{q}_{\frac{\alpha}{2}}$ and $\hat{q}_{1-\frac{\alpha}{2}}$ from the t_1, t_2, \dots, t_M .
- If t_0 falls in the critical region, then reject the null hypothesis.

Question 1:

The “data” dataset contains 60 observations. We are interested in using the data to test the following null and alternative hypothesis;

$$H_0 : \mu \leq 14.5$$

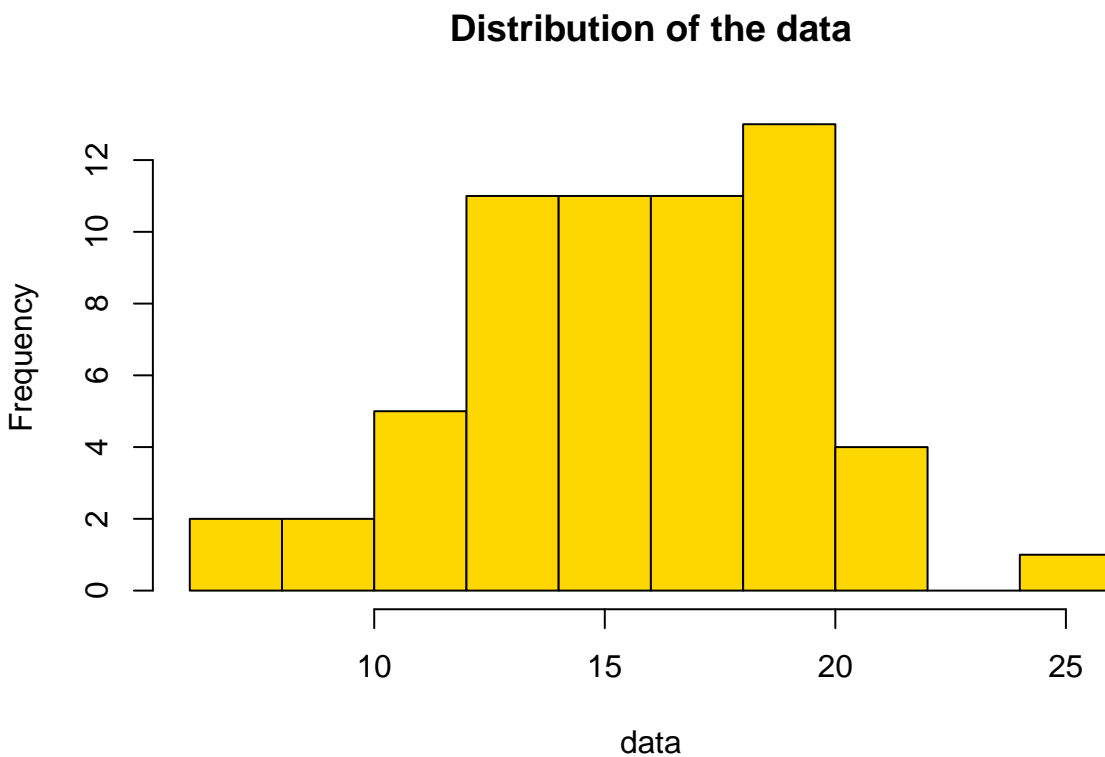
$$H_1 : \mu > 14.5$$

Assume that population variance is known and it is 9. ($\sigma^2 = 9$)

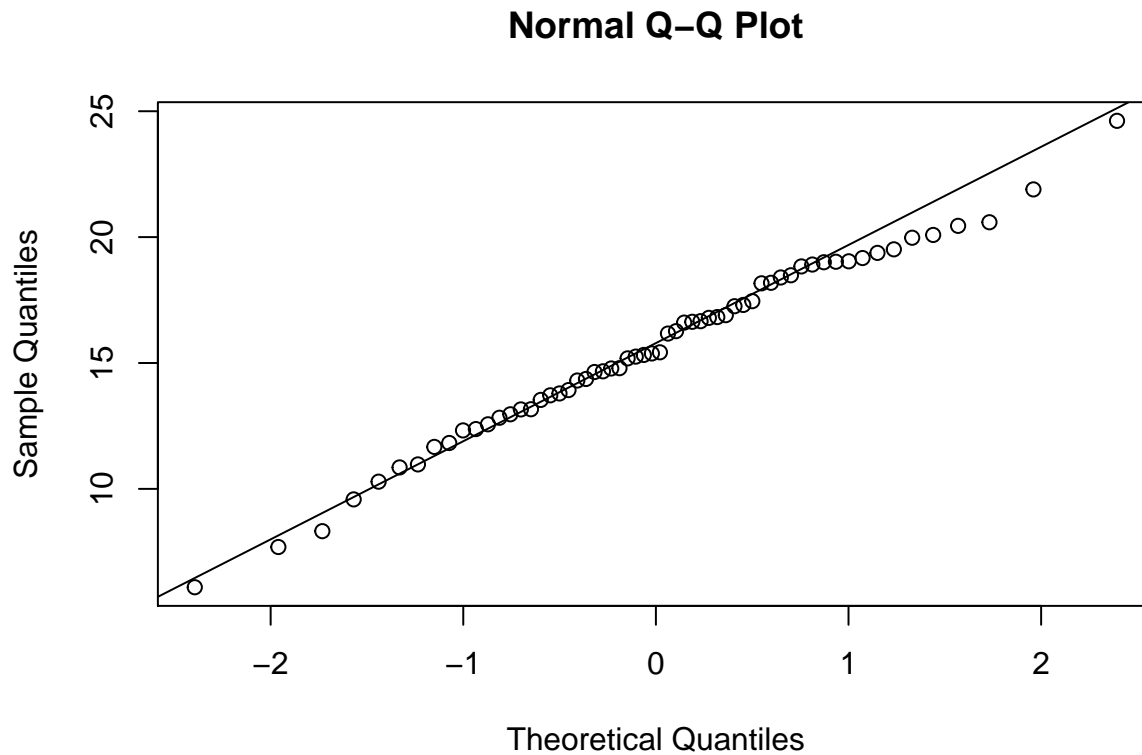
We will perform our hypothesis test using simulation to get the critical value. Our test statistic is

$$z_{test} = \frac{\bar{x} - \mu_0}{\sigma / \sqrt{n}}$$

```
#read data into R.  
data <- as.vector(read.table("data.txt",header = T)$X)  
  
#check its distributional properties  
hist(data, main = "Distribution of the data", col = "Gold")
```



```
#it looks symmetric  
qqnorm(data);qqline(data)
```



```
shapiro.test(data)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: data  
## W = 0.98914, p-value = 0.8719
```

```
# We can conclude that the data comes from Normal
```

```
data <- as.vector(read.table("data.txt",header = T)$X)
```

```
q1.function <- function(data, Mu0, sig, M=104, alpha = 0.05){
```

```
  n <- length(data)  
  S.Error <- (sig / sqrt(n))  
  test.stat <- (mean(data) - Mu0) / S.Error
```

```
  TestScores <- numeric(M)
```

```

for(i in 1:M){
  x <- rnorm(n, Mu0, sig) # generate random sample under H0
  TestScores[i] <- (mean(x) - Mu0) / S.Error
}
# Get the critical value for alpha
Critical.Value <- quantile(TestScores,1-alpha)

if(abs(test.stat) > abs(Critical.Value)){
  cat("From MC Simulation we get an estimated Critical Value of",
      round(Critical.Value,3),"\n", "Test Statistic is",
      round(test.stat,3),"\n","\n",
      "Therefore, we have enough evidence to reject the null hypothesis",
      "\n","\n")
}else{
  cat("From MC Simulation we get an estimated Critical Value of",
      round(Critical.Value,3),"\n", "Test Statistic is",
      round(test.stat,3),"\n",
      "Therefore, we do not have enough evidence to reject the null hypothesis",
      "\n","\n")
}

a <- seq(-3,3,0.01)
plot(a, dnorm(a), type = "l",lwd = 2.5, ylab = "", xlab = "")
abline(h=0, lwd = 2.5)
abline(v = Critical.Value, col = "Red")
abline(v = test.stat, col = "Dark Blue")
points(x = Critical.Value, y = 0, pch = 1, cex = 2, col = "Red")
points(x = test.stat, y = 0, pch = 2, cex = 2, col = "Dark Blue")
legend("topright",legend = c("Critical Value","Test Stat"),
      col = c("Red","Dark Blue"), pch = 1:2)

return(list(test_stat = test.stat,
            Critical_Value = as.numeric(Critical.Value)))
}

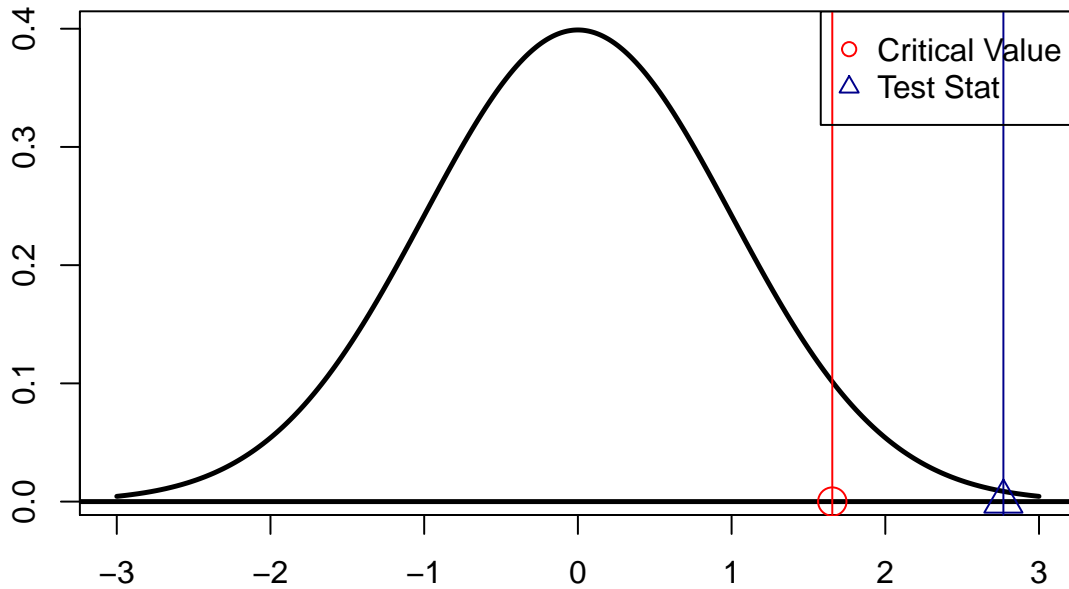
q1.function(data, 14.5, 3)

```

```

## From MC Simulation we get an estimated Critical Value of 1.655
## Test Statistic is 2.768
##
## Therefore, we have enough evidence to reject the null hypothesis
##

```



```
## $test_stat
## [1] 2.768279
##
## $Critical_Value
## [1] 1.655014
```

B. P-Value Approach

Estimate the p-value by using the distribution found in step 5, using the following.

- Lower Tail Test:

$$\hat{p} = \frac{\#(t_i \leq t_0)}{M}; \quad i = 1, 2, \dots, M$$

- Upper Tail Test:

$$\hat{p} = \frac{\#(t_i \geq t_0)}{M}; \quad i = 1, 2, \dots, M$$

If $\hat{p} \leq \alpha$, then reject the null hypothesis.

Question 2:

Now, consider the same hypothesis in Question 4 this time apply Monte Carlo Simulation to test the hypothesis using P-Value approach.

```

data <- as.vector(read.table("data.txt",header = T)$X)

q2.function <- function(data, Mu0, sig, M=10^4, alpha = 0.05){

  n <- length(data)
  S.Error <- (sig / sqrt(n))
  test.stat <- (mean(data) - Mu0) / S.Error

  TestScores <- numeric(M)

  for(i in 1:M){
    x <- rnorm(n, Mu0, sig) # generate random sample under H0
    TestScores[i] <- (mean(x) - Mu0) / S.Error
  }

  pvalue <- length(which(TestScores >= test.stat))/M

  if(pvalue < alpha){
    cat("Since P-value",pvalue,"which is less than the significance level",
        alpha, "\n",
        "Therefore, we can reject the null hypothesis.", "\n", "\n")
  }else{
    cat("Since P-value",pvalue,
        "which is greater than the significance level",
        alpha, "\n",
        "Therefore, we can not reject the null hypothesis.",
        "\n", "\n")
  }
  return(list(P_Value = pvalue))
}

q2.function(data, 14.5, 3)

```

```

## Since P-value 0.0025 which is less than the significance level 0.05
## Therefore, we can reject the null hypothesis.
##

## $P_Value
## [1] 0.0025

```

Power Calculations:

Question 3:

Use simulation to estimate empirical power and plot the curve for the test statistic.

Power = $P(\text{Rej. null hyp.} \mid \text{null hyp. is false})$

```
M <- 10^4
mu0 <- 14.5
sig <- 3
n <- length(data)

mu <- c(seq(12.5, 16.5, 0.1)) #alternatives
m <- length(mu)

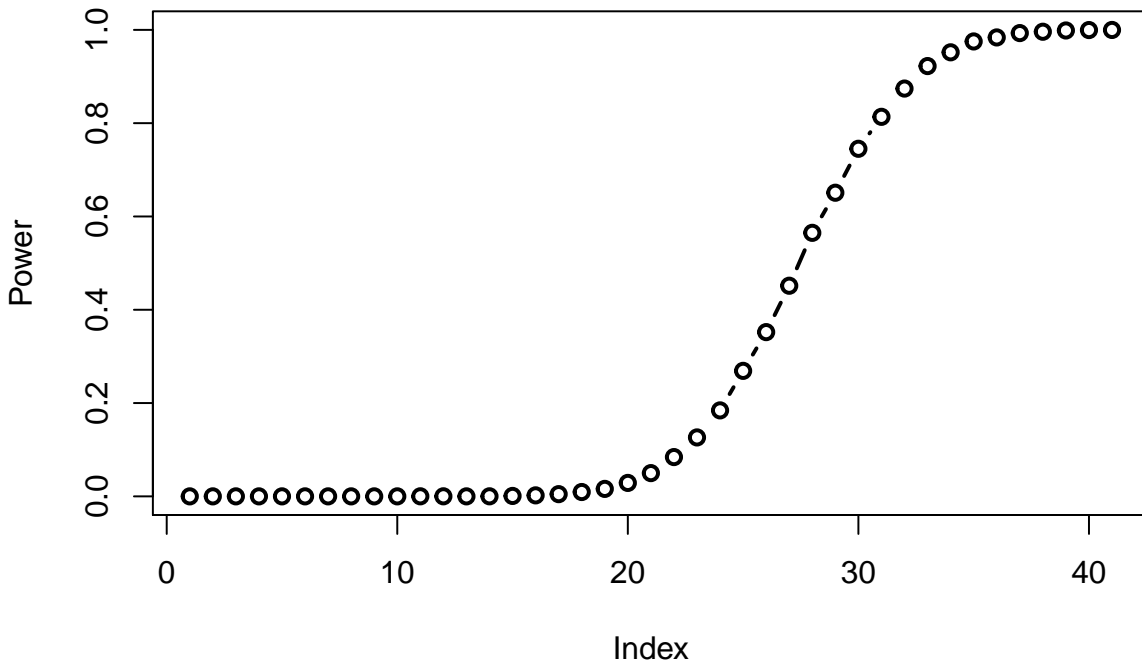
Beta <- numeric(m)
for(j in 1:m){

  pval <- numeric(M)

  for(i in 1:M){
    x <- rnorm(n, mu[j], sig)
    test.stat <- t.test(x, alternative = "greater", mu = mu0)
    pval[i] <- test.stat$p.value
  }

  Beta[j] <- mean(pval <= 0.05)
}

plot(Beta, type = "b", lwd = 2, ylab = "Power")
```



Count Five Test:

The two sample “Count Five” test for equality of variance introduced by [McGrath and Yeh](#) counts the number of extreme points of each sample relative to the range of the other sample. Suppose the means of the two samples are equal and the sample sizes are equal. An observation in one sample is considered extreme if it is not within the range of the other sample. If either sample has five or more extreme points, the hypothesis of equal variance is rejected.

Question 4:

Use Count Five Test to find the power of the hypothesis for the equality of variances of two iid random samples.

Generate X and Y using this code.

```
x <- rnorm(100, 20, 7)
```

```
y <- rnorm(100, 30, 5)
```


$$H_0 : \sigma_x^2 = \sigma_y^2$$

$$H_1 : \sigma_x^2 \neq \sigma_y^2$$

```
count5test <- function(x,y){
  X <- x-mean(x)
  Y <- y-mean(y)
  outX <- sum(X > max(Y)) + sum(X < min(Y))
  outY <- sum(Y > max(X)) + sum(Y < min(X))
  return(as.integer(max(c(outX,outY)) > 5))
}

M <- 10^4
C5Result <- 0

for(i in 1:M){

  x <- rnorm(100, 20, 7)
  y <- rnorm(100, 30, 5)
  # return 1 (reject) or 0 (do not reject H0)
  # for count5test(x,y)
  C5Result <- C5Result + count5test(x,y)

}

power <- C5Result / M
power

## [1] 0.723
```