

Worksheet7

STAT414

2024-11-02

```
# 1. Consider the Introductory Example 1 of the Module07 slides.  
# (a) Test the Engineer's hypothesis. Clearly show all the seven steps of the testing of  
# hypothesis problem.
```

```
iron <- c(170, 167, 174, 179, 179, 156, 163, 156, 187, 156,  
183, 179, 174, 179, 170, 156, 187, 179, 183, 174, 187, 167, 159, 170, 179)  
  
sample_mean <- mean(iron)  
sample_sd <- sd(iron)  
n <- length(iron)  
n
```

```
## [1] 25
```

```
cat("  
1. Parameter of interest is the mean of the Brinell hardness of the iron  
2-3. H0: mu = 170  
    HA: mu > 170  
'the mean Brinell hardness of all such ductile iron pieces is greater than 170'  
Choose alpha = .05  
Use standard t-test because the sample size is less than 30  
")
```

```
##  
## 1. Parameter of interest is the mean of the Brinell hardness of the iron  
## 2-3. H0: mu = 170  
##    HA: mu > 170  
## 'the mean Brinell hardness of all such ductile iron pieces is greater than 170'  
## Choose alpha = .05  
## Use standard t-test because the sample size is less than 30
```

```
#4. test statistic for 1-sided t-test: xbar - mu0 / (s/sqrt(n))  
test_statistic <- (sample_mean - 170) / (sample_sd / sqrt(n))  
cat("4. Test statistic of data:", test_statistic)
```

```
## 4. Test statistic of data: 1.221843
```

```
#5-6 p-value of test statistic  
pvalue <- pt(test_statistic, n-1, lower.tail = FALSE)  
rejection <- qt(1 - .05, n-1)  
cat("5. The rejection region for an alpha of 0.05 is when the test statistic >", rejection)
```

```
## 5. The rejection region for an alpha of 0.05 is when the test statistic > 1.710882
```

```
cat("6. P-value of test statistic:", pvalue)
```

```
## 6. P-value of test statistic: 0.1168164
```

```
#Conclusion
```

```
cat("7. The p-value of the data is calculated to be", pvalue, "> .05, therefore we  
fail to reject the null hypothesis, and conclude that the mean Brinell hardness  
is equal to 170")
```

```
## 7. The p-value of the data is calculated to be 0.1168164 > .05, therefore we  
## fail to reject the null hypothesis, and conclude that the mean Brinell hardness  
## is equal to 170
```

```
# (b) Suppose we decided to use a different test: Reject H0 when Xbar > 174. (See page  
# 14 of the slide.). Compute the P(Type I Error) (= alpha for this test.)
```

```
# 1 - P(Xbar < 174)
```

```
#pnorm = probability that Xbar is less than 174 if the population mean is 170.
```

```
alpha <- 1 - pnorm(174,170,sample_sd/sqrt(n))
```

```
cat("Probability of a Type I Error for rejection rule Xbar > 174:", alpha)
```

```
## Probability of a Type I Error for rejection rule Xbar > 174: 0.0262243
```

```
# (c) Compute P(Type II Error) for this test, when mu = 172. (That is, compute Beta(172)).
```

```
#pnorm = probability that Xbar is less than or equal to 174 if the true mean is 172
```

```
beta <- pnorm(174,172,sample_sd/sqrt(n))
```

```
cat("The probability of type 2 error for rejection rule Xbar > 174, when mu=172:", beta)
```

```
## The probability of type 2 error for rejection rule Xbar > 174, when mu=172: 0.8339061
```

```
# (d) Compute the alpha and Beta(172) for the test used in part (a).
```

```
cat("The alpha of part a was defined to be .05, therefore the probability of a  
Type I error is simply 0.05.")
```

```
## The alpha of part a was defined to be .05, therefore the probability of a  
## Type I error is simply 0.05.
```

```
rejection_mean <- 170 + rejection * (sample_sd/sqrt(n))  
rejection_mean
```

```
## [1] 173.5286
```

```
A_beta <- pnorm(rejection_mean,172,sample_sd/sqrt(n))
```

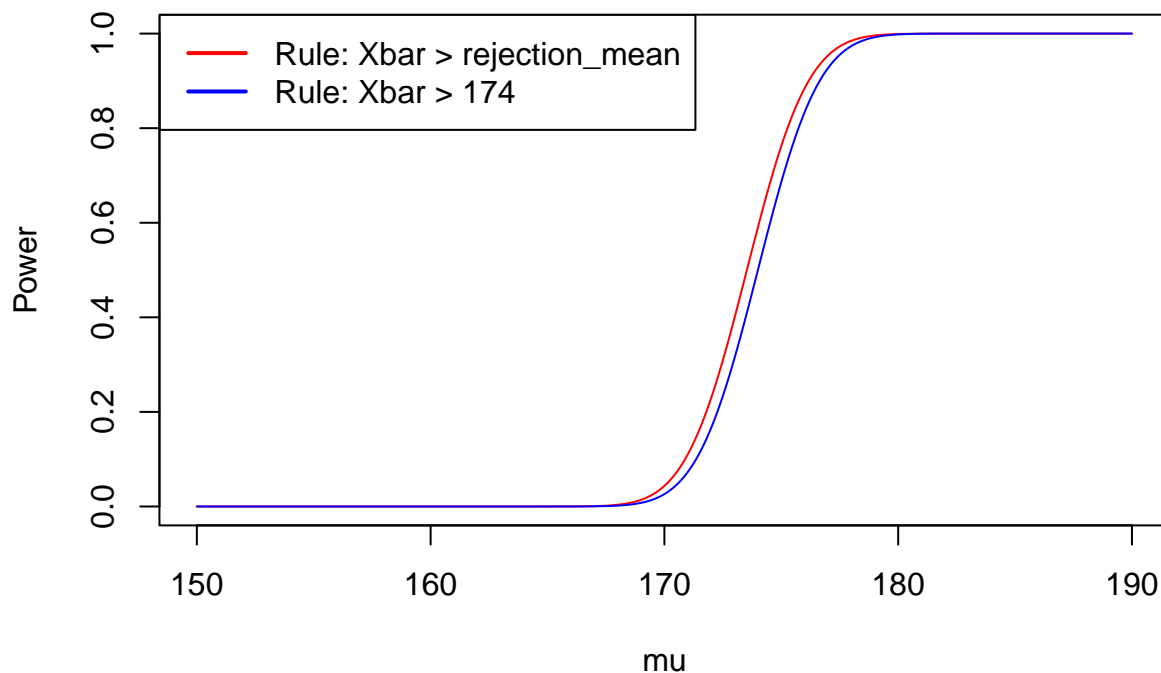
```
cat("The probability of type 2 error for rejection rule Xbar >",rejection_mean,"when mu=172:", A_beta)
```

```
## The probability of type 2 error for rejection rule Xbar > 173.5286 when mu=172: 0.7707034
```

```
# (e) Plot the power curves of the two testing procedures and compare.

#Power curve is plotted by plotting the values of Power(mu) vs various values of mu.
mu <- seq(150,190,0.1)
plot(mu, 1 - pnorm(rejection_mean, mu, sample_sd/sqrt(n)),
     type = "l", col = "red",
     xlab = "mu", ylab = "Power",
     main = "Power Curves for 2 procedures")
lines(mu, 1 - pnorm(174, mu, sample_sd/(sqrt(n))),
      col = "blue")
legend("topleft", legend = c("Rule: Xbar > rejection_mean", "Rule: Xbar > 174"),
      col = c("red", "blue"), lwd = 2)
```

Power Curves for 2 procedures



```
cat("Red is better because the power is higher at more instances of mu.")
```

```
## Red is better because the power is higher at more instances of mu.
```

```
# 2. Consider the Introductory Example 2 of the Module07 slides.
# (a) Test the Biologist's hypothesis. Clearly show all the seven steps of the testing of
# hypothesis problem.
```

```
heights <- c(11.5, 11.8, 15.7, 16.1, 14.1, 10.5, 15.2, 19.0, 12.8, 12.4, 19.2, 13.5,
16.5, 13.5, 14.4, 16.7, 10.9, 13.0, 15.1, 17.1, 13.3, 12.4, 8.50, 14.3,
12.9, 11.1, 15.0, 13.3, 15.8, 13.5, 9.30, 12.2, 10.3)
```

```

sample_mean <- mean(heights)
sample_sd <- sd(heights)
n <- length(heights)
mu <- 15.7

```

```

cat("
1. Parameter of interest is the mean height of the sunflower seedlings.
2-3. H0: mu = 15.7
    HA: mu < 15.7
Choose alpha = .05
Use standard t-test
")

```

```

##
## 1. Parameter of interest is the mean height of the sunflower seedlings.
## 2-3. H0: mu = 15.7
##    HA: mu < 15.7
## Choose alpha = .05
## Use standard t-test

```

```

#4. test statistic for 1-sided t-test: xbar - mu0 / (s/sqrt(n))
test_statistic <- (sample_mean - mu) / (sample_sd / sqrt(n))
cat("4. Test statistic:", test_statistic)

```

```

## 4. Test statistic: -4.599006

```

```

# Step 5-6: p-value and rejection region
p_value <- pt(test_statistic, df = n - 1)
rejection <- qt(0.05, df = n - 1)
cat("5. The rejection region for alpha = 0.05 is when the test statistic <", rejection)

```

```

## 5. The rejection region for alpha = 0.05 is when the test statistic < -1.693889

```

```

cat("6. P-value of test statistic:", p_value)

```

```

## 6. P-value of test statistic: 3.174244e-05

```

```

cat("7. the pvalue of 3.174244e-05 is much less than the chosen alpha of .05, therefore
    there is enough supporting evidence to reject the null hypothesis and suggest
    that the mean height of all sunflower seeds is less than 15.7cm")

```

```

## 7. the pvalue of 3.174244e-05 is much less than the chosen alpha of .05, therefore
##    there is enough supporting evidence to reject the null hypothesis and suggest
##    that the mean height of all sunflower seeds is less than 15.7cm

```

```

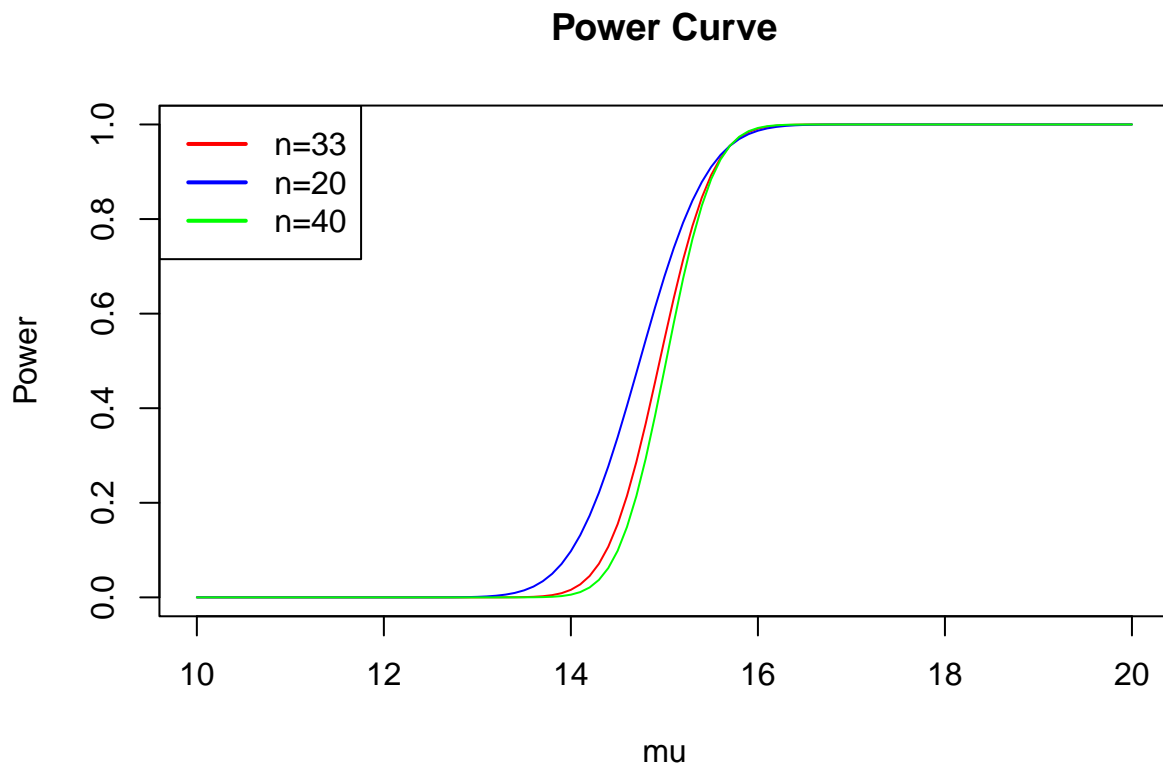
# (b) Plot the power curve.
mus <- seq(10, 20, by = 0.1)
rejection_mean <- mu + rejection * (sample_sd/sqrt(n))
rejection_mean_20 <- mu + rejection * sample_sd / sqrt(20)
rejection_mean_40 <- mu + rejection * sample_sd / sqrt(40)

```

```

plot(mus, 1 - pnorm(rejection_mean, mus, sample_sd/sqrt(n)),
     type = "l", col = "red",
     xlab = "mu", ylab = "Power",
     main = "Power Curve")
lines(mus, 1 - pnorm(rejection_mean_20, mus, sample_sd / sqrt(20)),
      col="blue")
lines(mus, 1 - pnorm(rejection_mean_40, mus, sample_sd / sqrt(40)),
      col="green")
legend("topleft", legend = c("n=33", "n=20", "n=40"),
      col = c("red", "blue", "green"), lwd = 2)

```



(c) Compare the above power curve to the power curves one would get for sample sizes 20 or 40.

```

cat("Green is the best, with the steepest slope that reaches max power the fastest.
     Which is a sample size = 40. has the highest power across the range of true
     means, higher sample size is better for power.")

```

```

## Green is the best, with the steepest slope that reaches max power the fastest.
##     Which is a sample size = 40. has the highest power across the range of true
##     means, higher sample size is better for power.

```