DSCI/MATH 530 RLab Five

Overview

This lab will illustrate the concept of power of a hypothesis test. Although the computation s can sometimes get involved the idea is straightforward. We know if the null hypothesis is true and the level is .05 then we will only reject H_0 5 percent of time. This is our error rate. But we are also interested in how often we reject the null when it is false. Ideally this should be with high probability. A power computation will allow us to see if this is the case.

Submission

Please submit through gradescope. Complete this assignment using R Markdown and converting to pdf. Make sure each problem is on a separate page. Use \newpage before each problem to insert a page break.

You can also refer to the .Rmd file for this assignment to have an example of this markdown document. Note however, that this version is setup to also use Latex for some math and conversion directly to pdf.

```
1.
```

```
(a) H_0: \mu = 55
H_1: \mu \neq 55
```

(b)

```
sigma<- 2/3
alpha<- .01
beta<- .05
mu0<- 55
delta<- .5
Za2<- qnorm(alpha/2, lower.tail=FALSE)
Zb<- qnorm(beta, lower.tail=FALSE)
n=27.9
n</pre>
```

[1] 27.9

(c)

```
t=.2/(.8/sqrt(28))
t=2.89
2*pt(-abs(t),df=27)
```

[1] 0.00751064

Since the p value is less than the significance level we rejected the null hypothesis. (\mathbf{d})

```
n=50
t=2.58+(.5*sqrt(50)/.8-1.645)
power = 1 - pt(t,df=49)
power = .554
power
```

[1] 0.554

2 Extra questions related to Problem 7.10

```
pt( abs(t), df= n, lower.tail=FALSE)*2

## [1] 2.16262e-06

pnorm( abs(t) , lower.tail=FALSE)*2

## [1] 8.583253e-08
```

P values change when n is small. t is skewed. These are similar values.

3 Power curves

From the previous problem and the text (see equ. 7.9) we have the following computation for the power at any true mean μ and any sample size n assuming a normal approximation.

The goal in this problem is create a figure similar to 7.4 but specifically for this speedometer testing context.

Now consider a sequence of 75 μ values

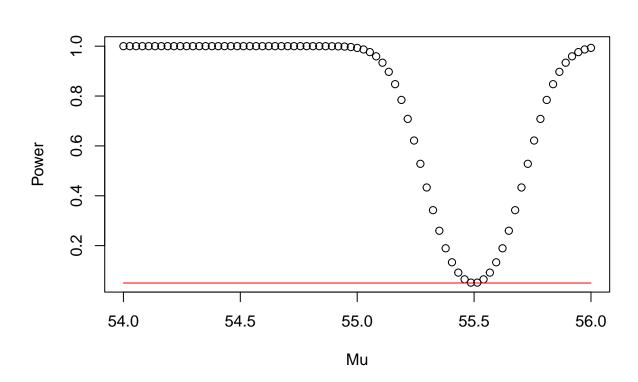
```
muGrid<- seq( 54, 56, length.out= 75)
```

3(a)

Use a **for** loop in R to compute the power at each of this mean values and for a sample size of 30 and 50. Be sure to create empty arrays of length 75 before the loop so you will have space to save the power values.

Plot both power curves with μ on the X axis and the power on the Y. Be sure to label the figure completely and add a vertical line at 55 and a horizonal line at .05. Explain why the power curve is exactly equal to .05 when $\mu = 55$. Modest use of color in a figure is always encouraged! To see the available colors in R type colors () in the console

To add more than one line on a plot draw one of the curves using the plot function and then the lines function to add the second curve.



This is exactly .05 at 55.5 because the difference between mu1 and mu0. ## 3(b) Find the interval for the μ grid so that the power for each case is .8 or less.

Here is a trick in R to find the range of an array (i.e. power) that is less than or equal to some target (.8 in this case). Make sure you understand why this works!

```
ind<- power <= .8
range( muGrid[ind])</pre>
```

[1] 55.18919 55.81081

4 Testing the value of a variance.

From the text there is a Chi-squared test to determine if a variance, σ^2 (or its square root, σ) are different than a null hypothesis. The test for the variance being larger than a set value is

$$H_0: \sigma^2 \leq \sigma_0^2$$
 and $H_a: \sigma^2 > \sigma_0^2$

Let

$$W = (n-1)s^2/\sigma_0^2$$

and the α level test is reject H_0 if W exceeds the quantile based on a chi squared distribution. Note that this quantile is easily found in R as

```
qchisq( alpha, n, lower.tail= FALSE)
```

4 (a)

From problem 1 setup the hypothesis test that the variance is greater than $.8^2 = .64$ and for n = 30. Determine the quantile for level .05.

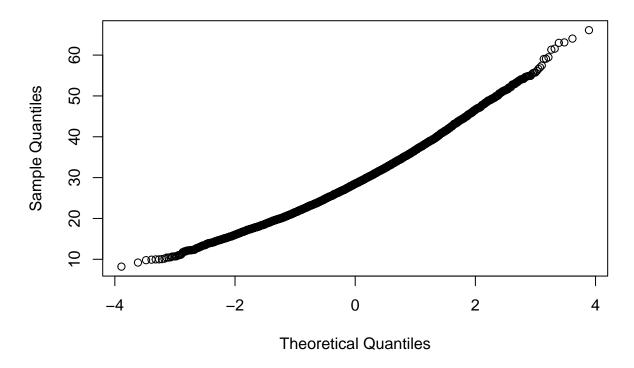
Now estimate this quantile by simulation here we generate 1000 realizations of the test statistic under the null hypothesis. Note that the results do not depend on the choice of μ but we just use 55 to avoid confusion.

```
M<- 10000
n<- 30
mu<- 55
sigma0<- .8
W<- rep( NA, 10000)
set.seed( 111)
for( k in 1:M ){
   ySample<- rnorm( n, mu, sigma0)
   W[k]<- (n-1)* var( ySample)/ sigma0^2
}</pre>
```

The relevant quantile is approximated by finding the .95 sample quantile for W. Use the code above to find it and compare to the exact expression. Now crank up the Monte Carlo size to 10000. Does the result become more accurate? This result becomes tighter when we increase type size of the sample. ## 4(b) Make a qqplot (e.g. qqnorm of the distribution from (a) and comment on its similarity to a normal. (The sample variance is sum so it is not unreasonable to expect the central limit theorem might apply.)

```
qqnorm(W)
```

Normal Q-Q Plot



This is very normal. Notice that there are no signicant outliers. ## 4(c) EXTRA CREDIT For a data set , Y the MAD(Y) (median absolute deviation) is an alternative estimate for σ and, unlike the sample variance, is not influenced by a few outliers in the data. The MAD has a simple form. Find the median of the data, find the absolute differences between each data point and the median, and find the median of those differences. The final step is to multiply by the constant 1.4826 so that the MAD is unbaised for σ when the data is normal. In R code we have the simple code line

```
absDiff<- abs( ySample - median(ySample) )
mad<- 1.4826 * median ( absDiff )</pre>
```

and there is also the handy function mad to find this in R. Now consider the same hypothesis test in 3(a) but use the test statistic WMAD = $\text{MAD}(y)/\sigma_0$ Adapt the Monte Carlo code from (a) to find the quantile to test the hypothesis (n = 30, $\alpha = .05$) using this test statistic.

```
M<- 10000
n<- 30
mu<- 55
sigma0<- .8
W<- rep( NA, 10000)
set.seed( 111)
for( k in 1:M ){
   ySample<- rnorm( n, mu, sigma0)
   absDiff<- abs( ySample - median(ySample) )
   mad<- 1.4826 * median ( absDiff )
   W[k]<-mad
}
qqnorm(W)</pre>
```

Normal Q-Q Plot

