HW4- Stats Josh Miltier

THEORETICAL PORTION

PROBLEM #1.

Type I Error is when the null hypothesis is rejected even though it shouldn't have been.

Type II Error is accepting the null hypothesis even though it was in fact false.

A Type I Error is more relevant to reduce in probability and can be reduced by having a lower significance level. By doing this, it broadens the span of certainty and reduces the change that the true data value is outside of that span.

A Type II Error probability is also important and can be reduced from increasing the sample size. A larger sample size will be more beneficial and accurate than a smaller sample size.

PROBLEM #2.

a. H_0 : $p = p_0$, H_a : $p \neq p_0$, $\alpha = 0.01$, Z-score = 2.5758 (with $\alpha/2$), $p_0 = 39\%$ $\hat{p} = 72/150 = 0.48$

$$Z = \frac{\widehat{p} - p_0}{\sqrt{\frac{p_0(1 - p_0)}{n}}}$$

$$Z = \frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1 - p_0)}{n}}} \qquad Z = \frac{0.48 - 0.39}{\sqrt{\frac{0.39 * (1 - 0.39)}{150}}}$$

Z = 2.2599

Z is not greater than or equal to $Z_{\alpha/2}$ and Z is not less than or equal to $-Z_{\alpha/2}$

Conclusion: Fail to Reject Ho: There is not enough evidence to support that the actual percentage of the population has type A blood at the $\alpha = 0.01$ significant level.

b. H_0 : $p = p_0$, H_a : $p \neq p_0$, $\alpha = 0.05$, Z-score = 1.96 (with $\alpha/2$) Z = 2.2599

Z is greater than or equal to $Z_{\alpha/2}$ and Z is not less than or equal to $-Z_{\alpha/2}$

Conclusion: Reject H_0 ; there is sufficient evidence at the $\alpha = 0.05$ significant level to support that the actual percentage of the population has type A blood.

PROBLEM #3.

a. n = 20, x = 52 minutes, $\sigma = 7$, $\alpha = 0.05$

$$H_0$$
: $\mu = \mu_0$, H_a : $\mu < \mu_0$

$$z = \frac{\overline{x} - \mu_0}{\sigma / \sqrt{n}} \qquad z = \frac{52 - 55}{\frac{7}{\sqrt{20}}}$$

z = -1.9166

Using $\Phi^{-1}(0.972) = 1.917$ gives the area up to the upper bound of the positive Z-score of 1.917. Thus 1 - 0.972 gives the p-value of 0.028. Since $p < \alpha$, we reject H_0 because there is sufficient evidence to support the average drying time is not equal to the normal drying time.

- b. The probability of type I error is equivalent to the significant level of .05, thus the probably of a Type I Error is 5%.
- In order to find the type II error, the critical value of Z is calculated by Z_{α} when $\alpha = 0.05$ which is -1.645 ($\Phi^{-1}(0.95) = 1.645$) using multiplied by the standard deviation of 7 and adding the μ_0 of 55. This equates to $Z_{critical} = 43.4857$. The probability of a type two error is $P(Z > (Z_{critical} - \mu)/\sigma)$. Performing a CDF for P(Z > -1.3592) = 0.08704 [in R: pnorm(43.4857, 53, 7)]. The probably of a Type II Error is 8.7%.

PROBLEM #4.

- a. H_0 : $\lambda = 15$, H_a : $\lambda > 15$, to reject the null hypothesis, the value of c using a Poisson distribution and an type I error probability to 0.10 is 20. Concluding that X > 20.
- b. The probability of a type II error using the cut off point of 20 from [#4,a] (since X must be 20 or greater) code:

$$x_{critical}_1 = (qnorm(.1) * (sqrt(20)) + 20)$$

 $type_{II}_10 = ((x_{critical}_1 - 25) / (sqrt(20)));pnorm(type_{II}_10)$

outcome:

Type II Error probability: 0.8207%

PROBLEM #5.

$$\begin{split} &H_0: \, \mu = 5, \, H_a: \, \mu > 5 \\ a. \quad &n\bar{X} \sim N(n\mu, \, n\sigma^2) \\ &E(n\bar{X}) = nE(\bar{X}) = n\mu \\ &Var(n\bar{X}) = n^2 Var(\bar{X}) = n^2 \, \sigma^2/n = n\sigma^2 \end{split}$$

b. For determining the if the null hypothesis should be rejected, a Z-score will be used since we are assuming n > 30.

Thus

$$Z = \frac{\sum X_i - n\mu}{n\sigma^2}$$

c. $\alpha = 0.10$, n = 40, $\Sigma_i X_i = 251.04$, and s = 5.69

$$Z = \frac{251.04 - 40(5)}{40(5.69)^2}$$

Z = 0.03941

d. p-value = 0.4843

Since the p-value is greater than the significant level (0.10), I **Fail to Reject H**₀. There is not sufficient evidence to support that the company's lightbulb lifetime is comparable to the leading brands 3 year lifetime, as at 10% significant level.

e. Power of test:

code:

$$\begin{array}{l} x_critical_.1 = (qnorm(.1)*(5.69/sqrt(40))) + 5 \\ type_II_.10 = ((x_critical_.1 - 6) / (5.69); 1-pnorm(type_II_.10) \\ x_critical_.1 = (qnorm(.1)*(5.69/sqrt(40))) + 5 \\ type_II_.10 = ((x_critical_.1 - 7) / (5.69); 1-pnorm(type_II_.10) \\ x_critical_.1 = (qnorm(.1)*(5.69/sqrt(40))) + 5 \\ type_II_.10 = ((x_critical_.1 - 8) / (5.69); 1-pnorm(type_II_.10) \\ \end{array}$$

outcome:

True mean 6, power = 0.6474 True mean 7, power = 0.7103 True mean 8, power = 0.7673

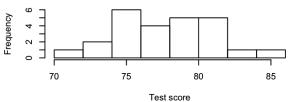
COMPUTATIONAL PORTION

Code and graphs included with each part, not indexed.

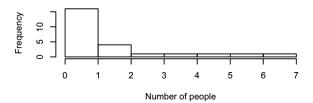
PROBLEM #1 - COMPUTATIONAL

```
#1, part a.
           code:
                      IIN <- read.table("isitnormal", header=T)</pre>
                      ###FOR HISTOGRAMS###
                      par(mfrow=c(3,2))
                      hist(IIN[,1], main="Calc I final scores", xlab="Test score")
                      hist(IIN[,2], main="Store: amount of people before first purchase", xlab="Number of people")
                      hist(IIN[,3], main="Walked to work", xlab="Number of people")
                      hist(IIN[,4], main="Amount of time to finish first problem on test",xlab="Time (minutes)")
                      hist(IIN[,5], main="Error measurements on a well calibrated device", xlab="Error amount (mm)")
                      hist(IIN[,6], main="Rainfall in September", xlab="Amount of rainfall (inches)")
                      ##FOR BOXPLOTS###
                      par(mfrow=c(1,6))
                      boxplot(IIN[,1], ylab="Calc I final scores - Test score")
                      boxplot(IIN[,2], ylab="Store: amount of people before first purchase - Number of people")
                      boxplot(IIN[,3], ylab="Walked to work - Number of people")
                      boxplot(IIN[,4], ylab="Amount of time to finish first problem on test - Time (minutes)")
                      boxplot(IIN[,5], ylab="Error measurements on a well calibrated device - Error amount (mm)")
                      boxplot(IIN[,6], ylab="Rainfall in September - Amount of rainfall (inches)")
                      ##FOR NORMALITY###
                      par(mfrow=c(3,2))
                      ggplot() + gqnorm(IIN[,1], main="Calc I final scores", xlab="Normal")#; gqline(IIN[,1])
                      qqnorm(IIN[,2], main="Store: amount of people before first purchase", xlab="Normal"); qqline(IIN[,2])
                      qqnorm(IIN[,3], main="Walked to work", xlab="Normal"); qqline(IIN[,3])
                      qqnorm(IIN[,4], main="Amount of time to finish first problem on test", xlab="Normal"); qqline(IIN[,4])
                      qqnorm(IIN[,5], main="Error measurements on a well calibrated device", xlab="Normal"); qqline(IIN[,5])
                      ggnorm(IIN[,6], main="Rainfall in September", xlab="Normal"); ggline(IIN[,6])
           output:
                      (ON NEXT PAGE)
```

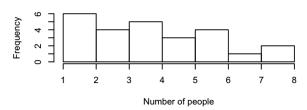




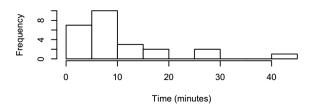
Store: amount of people before first purchase



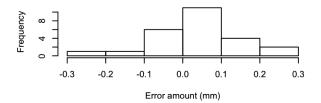
Walked to work



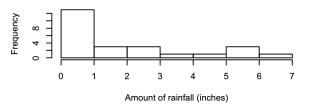
Amount of time to finish first problem on test

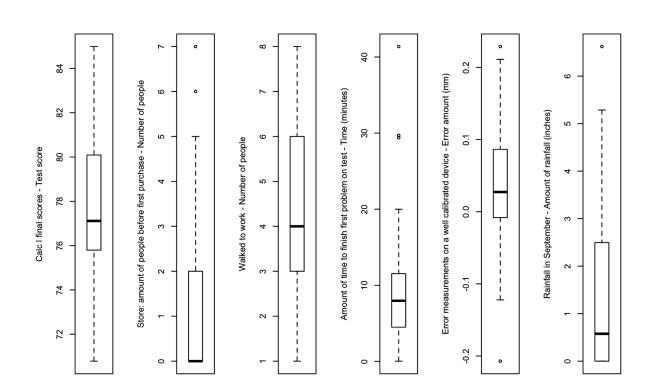


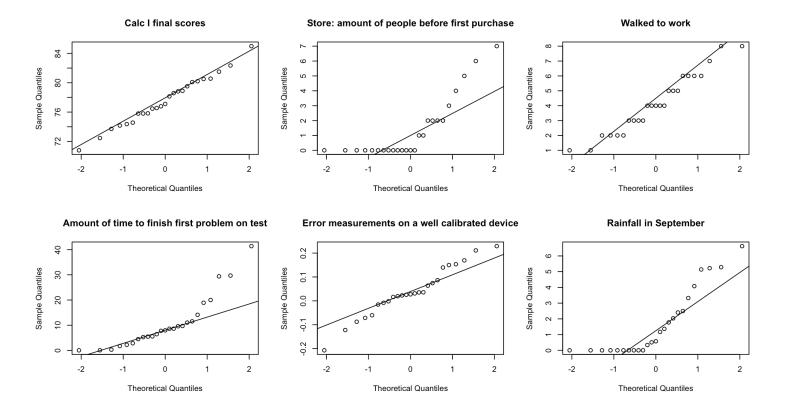
Error measurements on a well calibrated device



Rainfall in September







<u>Conclusion</u>: The only column that appears to my normally distributed is the first column from comparing all three graphs above. Column 2 and 6 appear to come from an Geometric distribution OR Exponential distribution. Though column 6 could also come from a Weibull distribution. Columns 3 and 4 look to be from a Poisson distribution while the remaining column 5 looks to come from a Binomial distribution. These assumptions are all based on above graphical analysis.

PROBLEM #2 - COMPUTATIONAL

```
#2, part a.

code:

ALD <- read.table("ALD Data", header=FALSE)

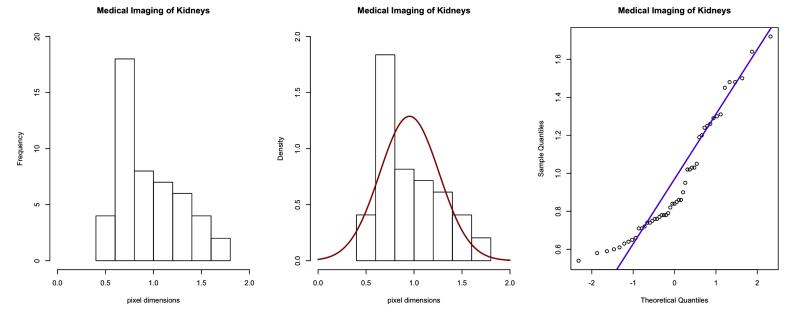
par(mfrow=c(1,3))

hist(ALD[,1], xlim=c(0,2), ylim=c(0,20),xlab="pixel dimensions", main="Medical Imaging of Kidneys")

hist(ALD[,1], xlim=c(0,2), ylim=c(0,2), xlab="pixel dimensions", main="Medical Imaging of Kidneys", freq=FALSE)
```

curve(dnorm(x,mean(ALD[,1]),sd(ALD[,1])), lwd=2,col="firebrick", add=TRUE)
qqnorm(ALD[,1], main="Medical Imaging of Kidneys"); qqline(ALD[,1], col="blueviolet", lwd=2)

output:



<u>Conclusion:</u> Based on the third graph, the ALD data does not seem plausible to represent a normal distribution. Normality must be assumed in order to accurately calculate the confidence interval for the true mean ALD.

```
#2, part b. H_0: \ \mu = 1.0, \ H_a: \ \mu \neq 1.0, \ \alpha = 0.05 \\ \underline{code:} \\ z_value = (mean(ALD[,1])-1)/(sd(ALD[,1])/(sqrt(length(ALD[,1])))) \\ z_value \\ ALD_LB <- qnorm(.025,mean(ALD[,1],sd(ALD[,1]))) \\ ALD_UB <- qnorm(.975,mean(ALD[,1],sd(ALD[,1]))) \\ ALD_LB \\ ALD_UB \\ \underline{output:} \\ > z_value \\ [1] -1.075003 \\ > ALD_LB \\ [1] -1.094701 \\ > ALD_UB \\ [1] 2.825227
```

<u>Conclusion:</u> Since the z-value is greater than the lower bound, I **Fail to Reject H** $_{0}$. There is insufficient evidence to support the true average mean ALD is different than 1.0 at a 5% significance level.

Conclusion:

Since the p-value is greater than the significant level, it supports the conclusive statement from part b.

PROBLEM #3 - COMPUTATIONAL

```
#3, part a.
```

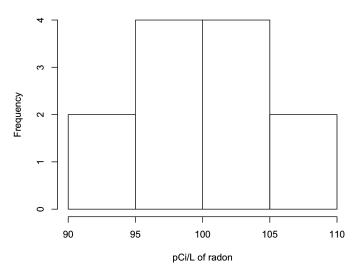
```
code:
```

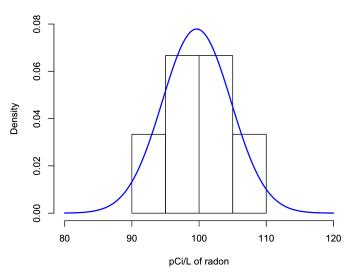
```
rad_dat <- scan("radon data")
par(mfrow=c(1,2))
hist(rad_dat, xlim=c(90,110), xlab="pCi/L of radon", main="Radon Detectors @ 100 pCi/L radon")
hist(rad_dat, xlim=c(80,120), ylim=c(0,.08), xlab="pCi/L of radon", main="Radon Detectors @ 100 pCi/L radon", freq=FALSE)
curve(dnorm(x,mean(rad_dat),sd(rad_dat)), lwd=2,col="blue", add=TRUE)
```

output:

Radon Detectors @ 100 pCi/L radon

Radon Detectors @ 100 pCi/L radon





#3, part b.

 H_0 : μ = 100, H_a : μ ≠ 100, α = 0.05, degrees of freedom = 11

The data appears to be normal with the average of means closely resembling the population mean of 100 pCi/L. However, changing the number of breaks of the histogram to 6 or greater shows that it isn't as normally distributed. Also the sample size is less than 31 and the standard deviation of the population isn't know.

#3, part c.

Carrying out a t-test for calculating the p-value of the hypotheses with R coding: code:

[1] 0.8206974

Conclusion: The first values show the rejection regions, the second as the test statistic, and the 3rd as the p-value. Since the p-value (0.8207) is greater than the significant level (.05), then there isn't significant evidence that the population mean reading under these conditions differs from 100 pCi/L, after being exposed to 100 pCi/L. Thus, **fail to reject Ho.**

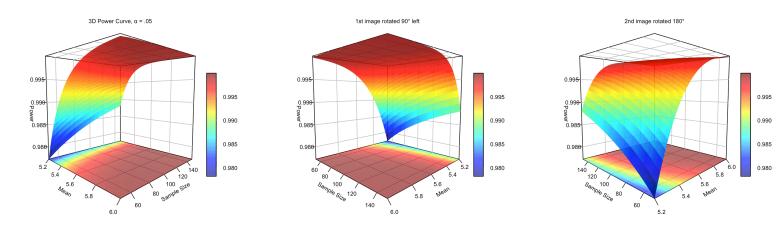
PROBLEM #4 - COMPUTATIONAL

#4, part *a combined with b.* code:

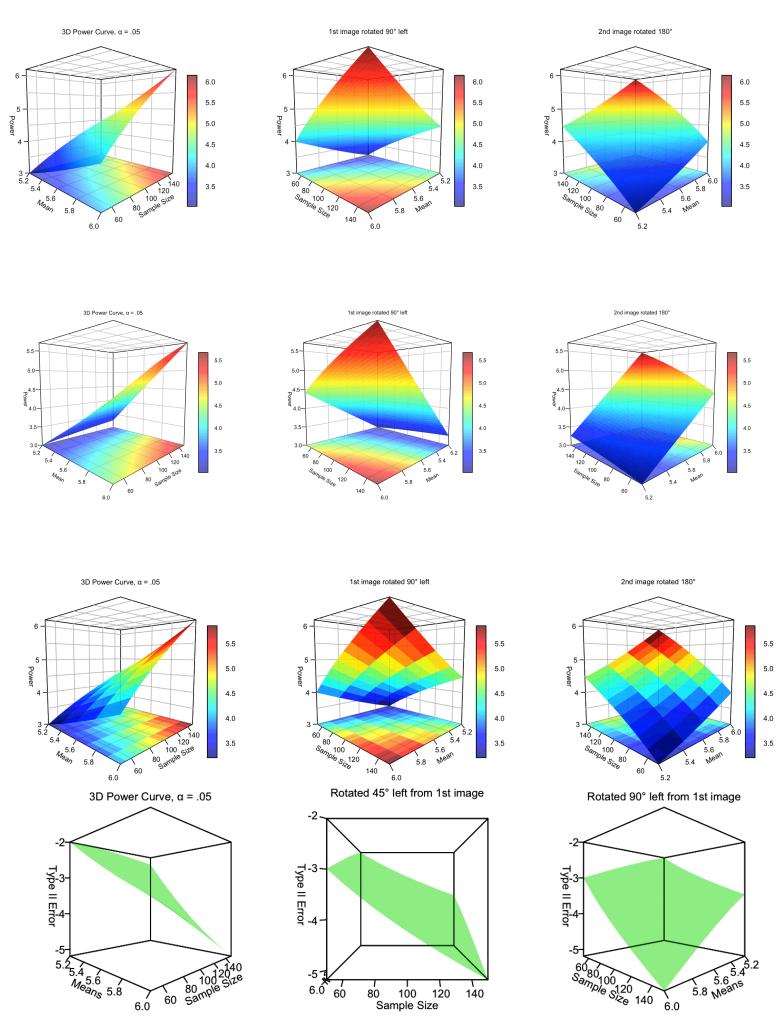
```
n = seq(50, 150, 10)
glueMeans = seq(5.2,6,.2)
x_{critical}.05 = (qnorm(.05) * (4/sqrt(n))) + 5
type_II_.05=matrix(0,nrow=5,ncol=11)
for (i in 1:5){
  for (j in 1:11){
     type_{II}_{0} = ((x_{critical}_{0} - 05[i] - glueMeans[i]) / (4/sqrt(n[j])))
  }
tAngle=45
pAngle=5
par(mfrow=c(1,3))
persp3D(glueMeans,n,1-pnorm(type_II_.05), theta=tAngle, phi=pAngle, xlab="Mean", ylab="Sample Size", zlab="Power",
           axes=TRUE, alpha=.7, bty="b2", colkey = list(length = 0.3, shift=-.02, col.ticks="white", width=1.2), image=TRUE,
           ticktype="detailed")
text(0,.6,"3D Power Curve, \alpha = .05")
persp3D(glueMeans,n,1-pnorm(type_II_.05), theta=tAngle+90, phi=pAngle, xlab="Mean", ylab="Sample Size", zlab="Power",
           axes=TRUE, alpha=.7,bty="b2",colkey = list(length = 0.3,shift=-.02,col.ticks="white", width=1.2), image=TRUE,
           ticktype="detailed")
text(0,.6,"1st image rotated 90° left")
persp3D(glueMeans,n,1-pnorm(type_II_.05), theta=tAngle+270, phi=pAngle, xlab="Mean", ylab="Sample Size", zlab="Power",
           axes=TRUE, alpha=.7, bty="b2",colkey = list(length = 0.3,shift=-.02,col.ticks="white", width=1.2), image=TRUE,
           ticktype="detailed")
```

output:

text(0,.6,"2nd image rotated 180°")



HW4- Stats Josh Miltier



60

6.0

100

Sample Size

120

140

۲ 6.0