Mini Project # 5

Qingyu Lan, Lakshmi Priyanka Selvaraj

Contribution of each group member:

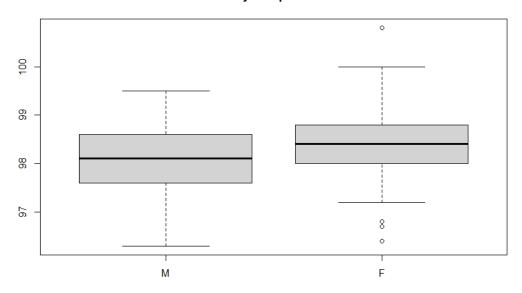
Both members worked on the questions together.

Section 1. Answers to the specific questions asked

1. Question 1

a.

Body Temperature



From the exploratory data analysis it seems like there is a difference between male and female body temperature, since the range of the two have differences between them.

Null hypothesis: Difference between means of male and female = 0
Alternative hypothesis: Difference between means of male and female != 0

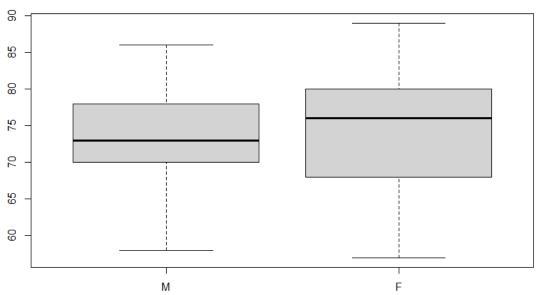
```
Welch Two Sample t-test
```

```
data: male$body_temperature and female$body_temperature
t = -2.2854, df = 127.51, p-value = 0.02394
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
    -0.53964856 -0.03881298
sample estimates:
mean of x mean of y
98.10462 98.39385
```

From the t test, we have a low p-value of 0.02394, and the 95% confidence interval does not contain 0, therefore we have to reject our null hypothesis, and take the alternative hypothesis that there is a difference between the mean of male and female body temperature.

b.





From the exploratory analysis it seems male and female have around the same heart rate, although the median is different by a bit, the quartiles and minimum and maximum seems to center around the same area.

Null hypothesis: Difference between means of male and female = 0
Alternative hypothesis: Difference between means of male and female != 0

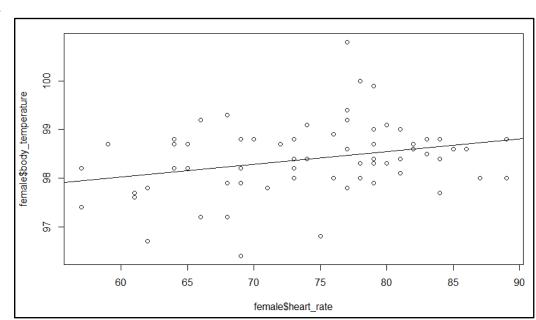
> t.test(male\$heart_rate, female\$heart_rate, alterantive = "two.sided", var.equal = F)

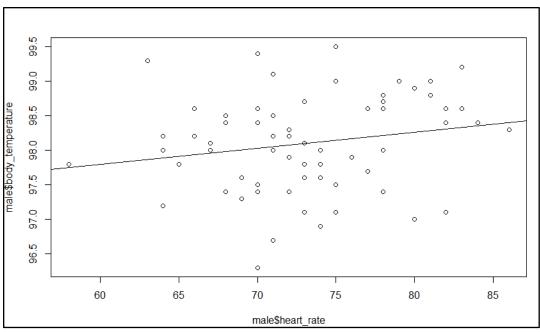
```
Welch Two Sample t-test
```

```
data: male$heart_rate and female$heart_rate
t = -0.63191, df = 116.7, p-value = 0.5287
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
    -3.243732    1.674501
sample estimates:
mean of x mean of y
73.36923    74.15385
```

From the t test, we have a p-value of 0.5287, and the 95% confidence interval does contain 0, therefore we keep our null hypothesis, there is no difference between male and female heart rate

C.

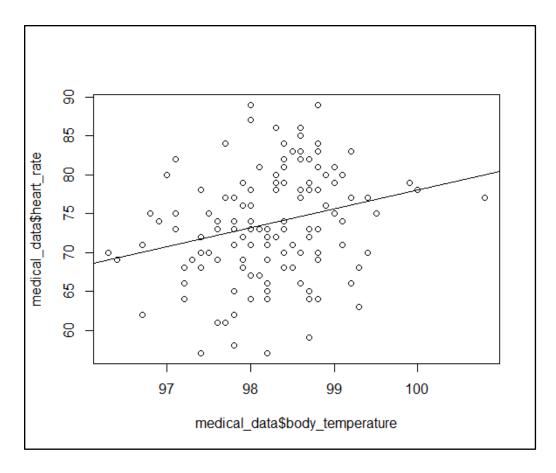




From the exploratory analysis, we can see that both male and female have a positive relationship between body temperature and heart rate.

```
> cor(male$body_temperature, male$heart_rate)
[1] 0.1955894
> cor(female$body_temperature, female$heart_rate)
[1] 0.2869312
```

From the correlation results, we can see that there is a weak positive relationship between body temperature and heart rate for both male and female, with the female having a bit stronger correlation than male.



On comparing the correlation between the heart rate and body temperature, irrespective of the gender, we find there is a very weak positive correlation of 0.2536.

> cor(medical_data\$body_temperature,medical_data\$heart_rate)
[1] 0.2536564

```
> temp = coverageProb(0.01,5,0.05)
> cp1 <- c(cp1,temp[1])
> cp2 <- c(cp2,temp[2])
> print(temp)
[1] 0.8130 0.7902
```

Our first monte carlo run to find the coverage probability of the confidence intervals using lambda = 0.01, n = 5

b.

Coverage probability for confidence interval using the z-interval method:

```
n = 5 n = 10 n = 30 n = 100

lambda = 0.01 0.8086 0.8594 0.9166 0.9382

lambda = 0.1 0.8062 0.8688 0.9126 0.9338

lambda = 1 0.8006 0.8678 0.9138 0.9370

lambda = 10 0.8086 0.8684 0.9222 0.9374
```

Coverage probability for confidence interval using the bootstrap percentile interval method:

```
n = 5 n = 10 n = 30 n = 100

lambda = 0.01 0.7814 0.8530 0.9182 0.9380

lambda = 0.1 0.7816 0.8650 0.9110 0.9356

lambda = 1 0.7772 0.8624 0.9136 0.9374

lambda = 10 0.7818 0.8624 0.9242 0.9380
```

C.

From our result, the larger the n value is, the more accurate is the intervals for both the z-interval method and the percentile method. At n =100, both the z-interval and bootstrap percentile method have around 0.93 coverage probability. The answer does not seem to be dependent on lambda as the result is fairly similar with different lambdas but the same n value for both types of intervals. Although the z-interval method is more accurate when n = 5, the accuracy between the two becomes almost the same for n = 10 and above. I would recommend the z-interval method because it performs better at n = 5, but there is no significant difference at higher n values.

d.

No, it does not depend on the specific values of lambda that were fixed in advance, since the result improves across all values of lambda as n increases.

Section 2: R code.

R code for question 1

make sure to have the file bodytemp-heartrate.csv in the working directory # we did it by having it pasted in the working directory getwd()

```
# read from the csv file
bodytemp heartrate = read.csv("bodytemp-heartrate.csv", header = T)
# print the reading variable to check
print(bodytemp heartrate)
# divide the variables into male and female
male = subset(bodytemp heartrate, bodytemp heartrate$gender == 1)
female = subset(bodytemp heartrate, bodytemp heartrate$gender == 2)
# box plot for a and b
boxplot(male$body temperature, female$body temperature, names = c("M","F"), main = "Body
Temperature")
boxplot(male$heart rate, female$heart rate, names = c("M","F"), main = "Heart Rate")
# t test for question a and b
t.test(male$body_temperature, female$body_temperature, alternative = 'two.sided', var.equal =
t.test(male$heart_rate, female$heart_rate, alternative = "two.sided", var.equal = F)
# correlation values
cor(male$body temperature, male$heart rate)
cor(female$body temperature, female$heart rate)
# scatter plot with regression line
plot(male$heart rate, male$body temperature, pch = 1)
abline(lm(male$body temperature~male$heart rate))
plot(female$heart rate, female$body temperature, pch = 1)
abline(lm(female$body temperature~female$heart rate))
#scatterplot for entire data
cor(bodytemp heartrate$body temperature,bodytemp heartrate$heart rate)
plot(bodytemp heartrate$body temperature,bodytemp heartrate$heart rate,pch=1)
abline(Im(bodytemp heartrate$heart rate~bodytemp heartrate$body temperature))
R code for question 2
library(boot)
# make a function for boottrap to use for finding the mean
mean.npar <- function(data, indices){
 return(mean(data[indices]))
```

```
# make a function to generate both confidence interval based on
# lambda, n, and alpha
conf.fun <- function(lambda, n, alpha){</pre>
 # generate the data
 x= rexp(n,lambda)
 # find ci with z
 ci=mean(x) + c(-1, 1) * qnorm(1-alpha/2) * sd(x)/sqrt(n)
 #print(ci)
 # find ci with boottraps
 mean.npar.boot = boot(x, mean.npar, R=999, sim="ordinary", stype = "i")
 ci2 = sort(mean.npar.boot$t)[c(25, 975)]
 #print(ci2)
 return(c(ci,ci2))
#test
\#cic = conf.fun(0.01,5,0.05)
#print(cic)
#print(cic[3])
# make a function to do replication and find out the coverage probability
coverageProb <- function(lambda,n,alpha){</pre>
 ci collection = replicate(10, conf.fun(lambda, n, alpha))
 # find the conditional probablity of both ci with z and ci with bootstrap
 p1 = mean(((1/lambda)>=ci collection[1,])*((1/lambda)<=ci collection[2,]))
 p2 = mean(((1/lambda)>=ci collection[3,])*((1/lambda)<=ci collection[4,]))
 return(c(p1,p2))
}
# make list to store coverage probability
cp = c(coverageProb(0.01,5,0.05),
   coverageProb(0.01,10,0.05),
    coverageProb(0.01,30,0.05),
   coverageProb(0.01,100,0.05),
   coverageProb(0.1,5,0.05),
   coverageProb(0.1,10,0.05),
   coverageProb(0.1,30,0.05),
    coverageProb(0.1,100,0.05),
   coverageProb(1,5,0.05),
   coverageProb(1,10,0.05),
```

}

```
coverageProb(1,30,0.05),
   coverageProb(1,100,0.05),
   coverageProb(10,5,0.05),
   coverageProb(10,10,0.05),
   coverageProb(10,30,0.05),
   coverageProb(10,100,0.05)
   )
print(cp)
# break apart the cp into cp for z and cp for percentage ci method
cp1 = c()
cp2 = c()
odd = T
for(i in cp){
 if (odd == T){
  odd = F
  cp1 = c(cp1,i)
 }else{
  odd = T
  cp2 = c(cp2,i)
}
}
# test codes
#print(cp1)
#print(cp2)
# make table for z-interval
cptable <- matrix(cp1,ncol=4,byrow=TRUE)
colnames(cptable) <- c("n = 5","n = 10","n = 30", "n = 100")
rownames(cptable) <- c("lambda = 0.01","lambda = 0.1","lambda = 1", "lambda = 10")
cptable <- as.table(cptable)
cptable
# make table for percentile method
cptable1 <- matrix(cp2,ncol=4,byrow=TRUE)
colnames(cptable1) <- c("n = 5","n = 10","n = 30", "n = 100")
rownames(cptable1) <- c("lambda = 0.01","lambda = 0.1","lambda = 1", "lambda = 10")
cptable1 <- as.table(cptable1)</pre>
cptable1
```