MED4 AAU CPH

Design and analysis of experiments

May 29, 2018

I'll be making these assignments with R instead of matlab, so the syntax and plots will look different. I really feel like the course is too tool dependent, and R really should be taught in tandem with matlab.

1

1.a

I load in the mat file, and put it into a data frame called data. This mean that chinese\$x.ch is now data\$ch and us is data\$us.

```
chinese <- readMat('ChineseEnglish.mat')
data <- data.frame(ch=chinese$x.ch, us=chinese$x.us)
```

To calculate the standard error of the mean I made this function based on the mathematical formula:

$$\sigma_M = \frac{\sigma}{\sqrt{N}}$$

```
sem <- function(x){
sd(x)/sqrt(length(x))
}</pre>
```

This is the output of calling mean() and se() on both the chinese and american dataset.

```
1 [1] "Chinese mean and standard error"
2 [1] 12.28588
3 [1] 0.4274665
4
5 [1] "American mean and standard error"
6 [1] 10.49732
7 [1] 0.4584607
```

Histogram of data\$ch and data\$us

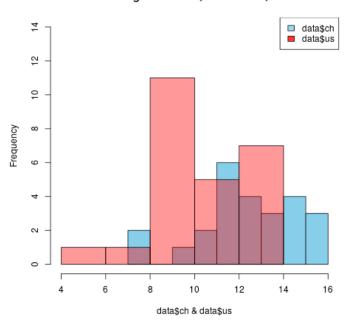
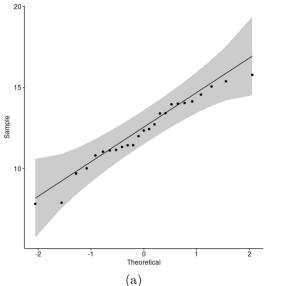
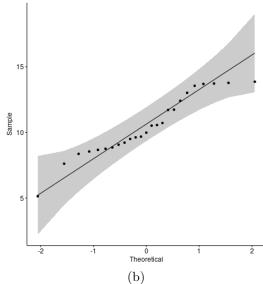


Figure 1

1.b

Ordinal level of measurement.





To test for normality I did the Shapiro-Wilk normality test, and with a p-value above 0.05, one can be confident that these samples are drawn from a normal distribution, something that is also shown in the two qqplots above.

```
data: data$ch
W = 0.9636, p-value = 0.4907
data: data$us
W = 0.93656, p-value = 0.1233
```

1.c

 $H_0 = Chinese$ speaking are as good singers on average as american speaking $H_1 = Chinese$ speaking are better on average than american speaking I use a two sample independent test, and from running the later snippet, with a significance level of 1%, I get t = 2.8533 and p-value = 0.006377. From this we can reject H0

ttest <- t.test(data\$ch, data\$us, conf.level=0.99)

1.d

The effect size, can be calculated with Cohen's d, which goes as follows:

$$d = \frac{MeanDifference}{PooledsampleSD}$$

The pooled sampled Standard Deviation is calculated like this:

$$psd = \sqrt{\frac{S_1^2 + S_2^2}{2}}$$

And accomplishing this in R, I made this function

```
cohens_d <- function(x, y) {
    lenX <- length(x) - 1
    lenY <- length(y) - 1
    meanDiff <- abs(mean(x) - mean(y))
    pssd <- lenX * var(x) + lenY * var(y)
    pssd <- pssd/(lenX + lenY)
    pssd <- sqrt(pssd)
    print("Cohen's D")
    print(cd <- meanDiff/pssd)
}</pre>
```

When running the function, I get a d value of 0.8070461, which is a big effect.

1.e

1.f

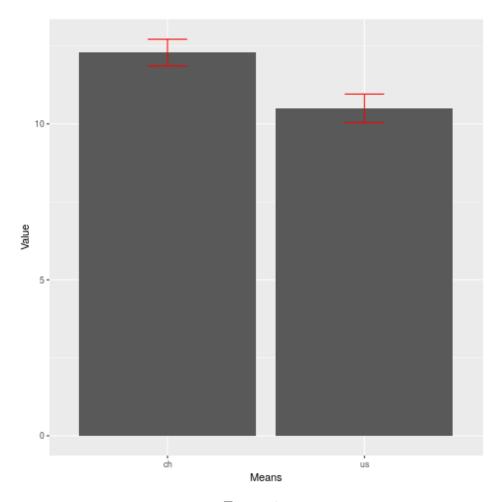


Figure 2

2

I load in the .mat file, and save it in weights, I then make a data frame called weights, with the variables save as after and before inside.

```
weights <- readMat('weights.mat')
weights <- data.frame(before = weights$w.before, after = weights$w.after)</pre>
```

2.a

The mean and standard deviation of before is: 92.42223 & 10.61654The mean and standard deviation of after is: 93.82223 & 11.64763

Histogram of weights\$before and weights\$after

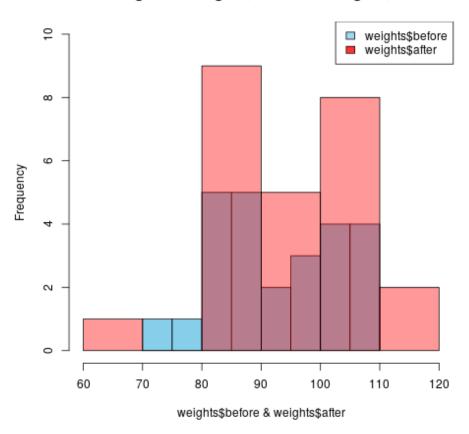
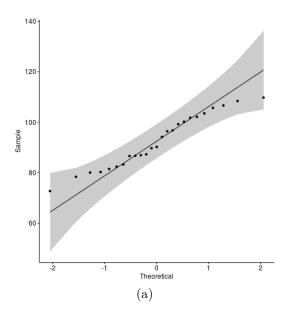
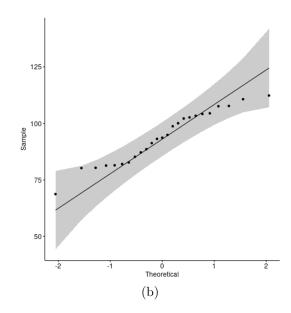


Figure 3

2.b

Interval data.





Both when looking at the above qqplots and the results from the Shapiro-Wilk test, it can confidently say that the data are from normally distributed samples.

```
data: weights$before
W = 0.95608, p-value = 0.3419
data: weights$after
W = 0.95425, p-value = 0.3119
```

2.c

 $H_0 = The weights will not have changed$

 $H_1 = The weights will have decreased$

To run the two sample paired t-test, we use the R function t.test(), with pair=T to tell the function that this is a paired t-test, and a conf.level=.9995 to tell it that the significance level is $\alpha = 0.0005$. The test is dependent.

```
t.test(weights$before, weights$after, pair=T, alternative='less', conf.level=.9995)
```

The result is t = -2.1433, df = 24, p-value = 0.02122, which mean that we can reject the null hypothesis, but since the mean of the of the weights have gone from 92.42 to 93.82, which means that weights, on average has gone up, so the alternative hypothesis is also wrong.

2.d

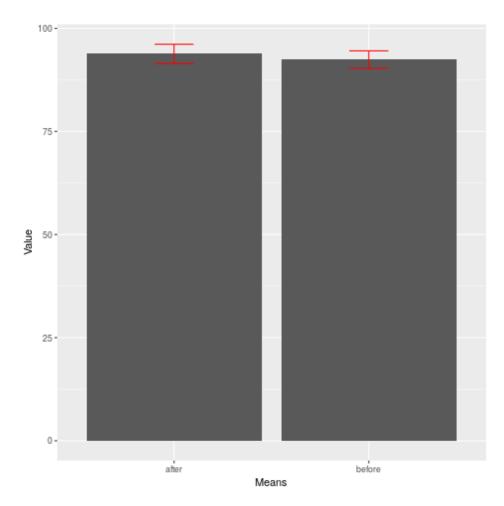


Figure 4

3

```
heights <- readMat('Dutchdanish.mat')
heights <- data.frame(du = heights$x.du, da = heights$x.da)</pre>
```

3.a

The means and Standard errors were calculated the same way as the previous section. The mean and standard deviation of du is: 182.6718~&~0.8439

The mean and standard deviation of da is: 180.0995 & 0.7247

Histogram of heights\$du and heights\$da

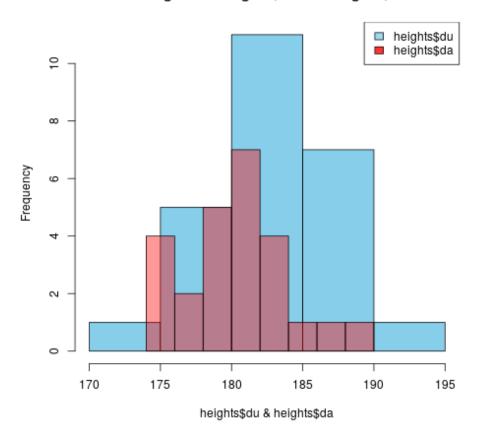
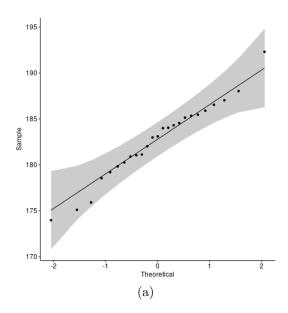
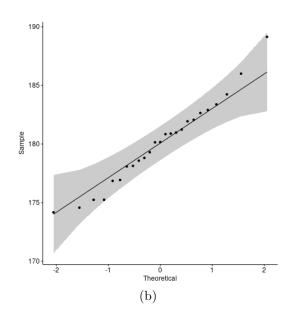


Figure 5

3.b

Ratio level of measurement.





From the above qqplots and the Shapiro-Wilk test, I can with confidence say the the data is from a normal distribution.

```
data: heights$du
W = 0.97796, p-value = 0.8418
data: heights$da
W = 0.97478, p-value = 0.7664
```

Doing an F test, shows the samples don't come from a distribution with the same variance.

```
F = 1.356, num df = 24, denom df = 24, p-value = 0.4612
```

3.c

 $H_0 = Danish \ and \ Dutch \ males \ aged \ 20-25 \ dont' \ differ \ in \ height \ on \ average$ $H_1 = Danish \ and \ Dutch \ males \ aged \ 20-25 \ differ \ in \ height \ on \ average$ Two sample independent t-test. With t as 2.3117 and the p-value at 0.02523, the H_0 is easily rejected.

```
t = 2.3117, df = 46.928, p-value = 0.02523
```

3.d

Doing the Cohen's D calculation from earlier, gives a d value of 0.6538, which is slightly above medium effect.

3.e

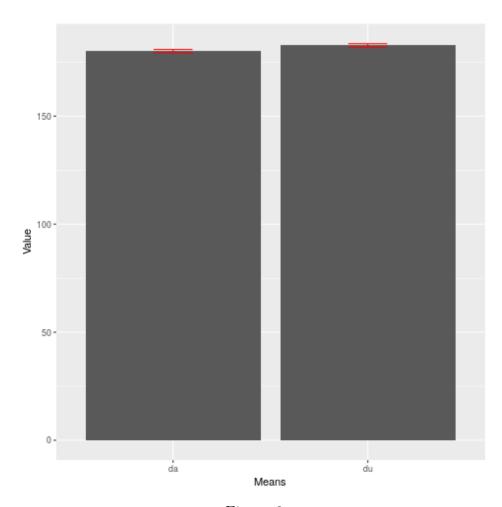


Figure 6