Assignment 2-Group11

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Exercise 1

1. Because the given λ from an interval [0.01,0.1], we need to test each possible value from this interval. Therefore, except for the standard bootstrap test code, we need to apply a loop from 0.01 to 0.1 with the step of 0.0001 to calculate the p-value for each value.
   The code is shown as Fig.1. The final output "p" means the biggest p-value of the test and the "lamadaflag" means the corresponding value of λ.

```
> bill <- scan("telephone.txt",skip=1)
Read 200 items
> B=1000
> t=max(bill)
> tstar=numeric(B)
> n=length(bill)
> lamada=0.01
> p=0
> lamadaflag=0
>
> for(count in 1:900){
+   lamada=lamada+0.0001;
+   for (i in 1:B){
+     xstar=rexp(n,lamada)
+     tstar[i]=max(xstar)
+   }
+   pl=sum(tstar<t)/B
+   pr=sum(tstar>t)/B
+   ptemp=2*min(pl,pr)
+   if(ptemp>p){
+     p=ptemp
+     lamadaflag=lamada
+   }
+ }
> p
[1] 0.998
> lamadaflag
[1] 0.0471
```

Figure1: Bootstrap test

We could know that when λ is 0.0471, the p-value reaches the max value of 0.998, which is not less than 5%. So we will not reject the H_0, thus the data in telephone.txt stems from the exponential distribution $Exp(\lambda)$ with some λ from [0:01; 0:1]

2. We plot the histogram of bill to see the distribution of the original data set. The code is shown in Fig.2 and the Histogram is shown in Fig.3.

```
> bill <- scan("telephone.txt",skip=1)
Read 200 items
> B=1000
> hist(bill,prob=T)
```

Figure2: Histogram code
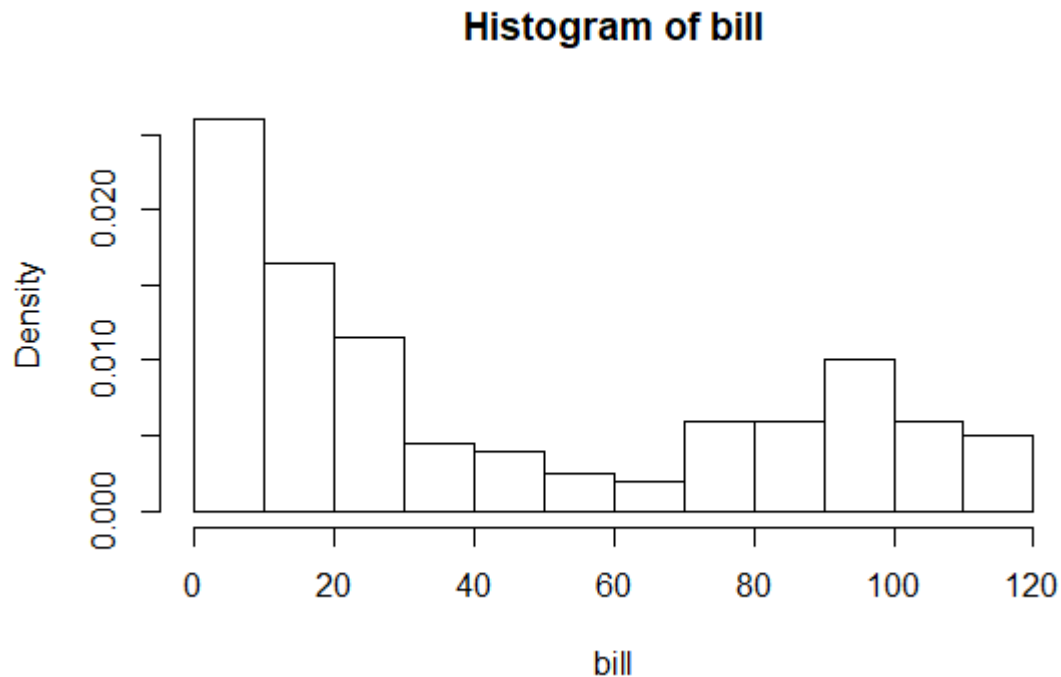
Histogram of bill

Figure3: Histogram of bill

From Fig.3 we could know there is many bills around 0 so we need to check it. We use the summary function to check the statistical results as shown in Fig.4.

```
> summary(bill)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  0.000   9.385  26.905  43.588  84.828 119.630
```

Figure4: Statistical results

It shows the min value is 0 so the company need to check if all the survey is useful. From the histogram we could know that there may be two main group of customers, one is lower than 30 and the other is around 100. The company should reconsider the different bills' plan for different groups for better market competitiveness.

Exercise 2

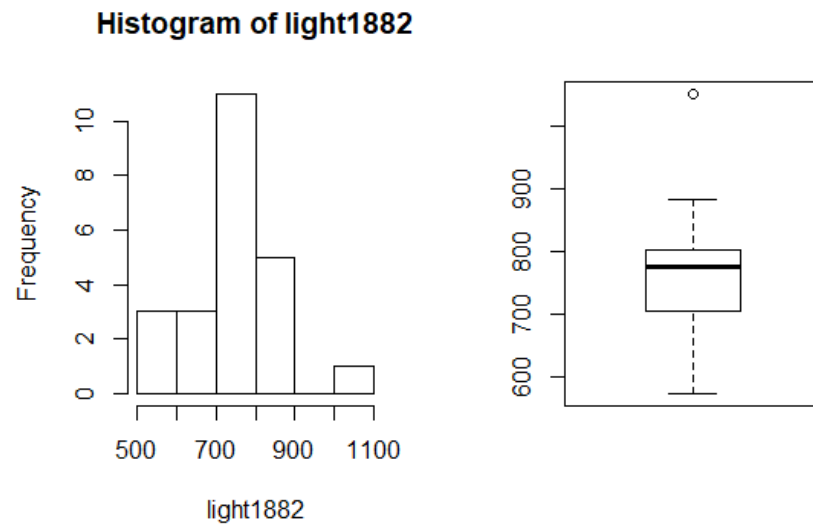1. The histograms and box plots of each dataset is shown in Fig.5, Fig.6 and Fig.7.
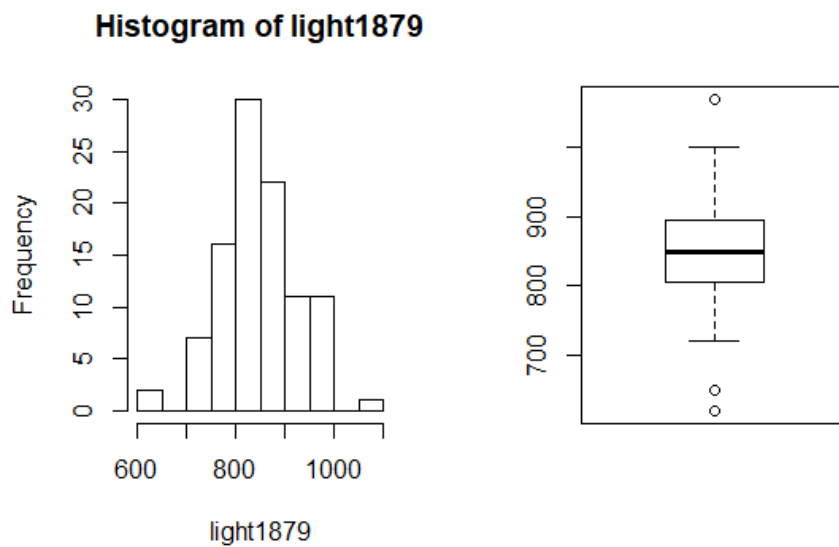
Histogram of light1882

Figure5: Histogram and boxplot of "light1879.txt"

Histogram of light1879

Figure6: Histogram and boxplot of "light1882.txt"
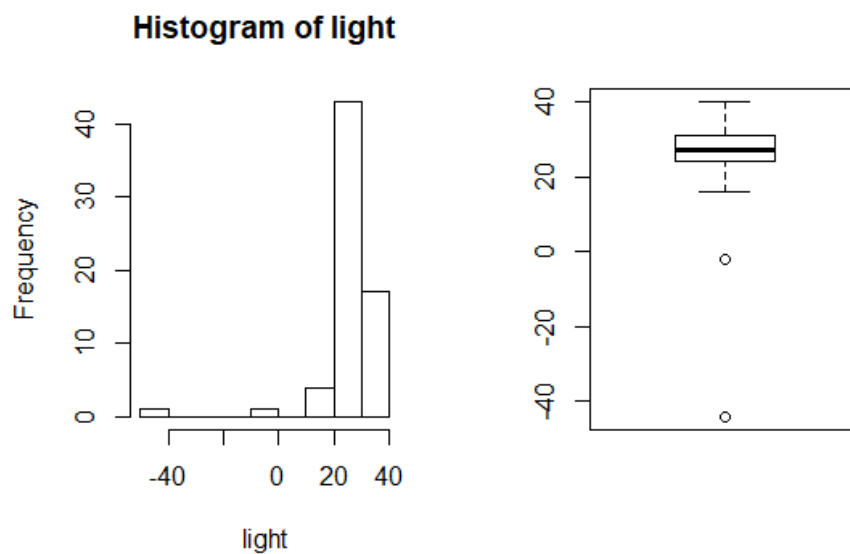

Histogram of light

Figure7: Histogram and boxplot of "light.txt"

From the histograms and box plots we could know that there is always a peak value of frequency in the given data set and there always are some too high/low values (outliers) in the given dataset. In Michelson's data the peak value is around 800 and the Newcomb's dataset is around 20, which all of them show the measurement of velocity of light.

2. We first pre-preprocess the given data to make the data represent the speed of light. Then we use the processed data to calculate the confidence interval. The code is shown as follows.

```
> light1879 <- scan("light1879.txt")
Read 100 items
> light1882 <- scan("light1882.txt")
Read 23 items
> light <- scan("light.txt")
Read 66 items
>
> value1=light1879+299000
> value2=light1882+299000
> value3=7442000000/(light+24800)
>
> M1=mean(value1)
> T1=median(value1)
> M2=mean(value2)
> T2=median(value2)
> M3=mean(value3)
> T3=median(value3)
>
> B=1000
> Tstar1=numeric(B)
> Tstar2=numeric(B)
> Tstar3=numeric(B)
>
> for(i in 1:B)
+ {
+    Xstar1=sample(value1,replace=TRUE)
+    Xstar2=sample(value2,replace=TRUE)
+    Xstar3=sample(value3,replace=TRUE)
+    Tstar1[i]=mean(Xstar1)
+    Tstar2[i]=mean(Xstar2)
+    Tstar3[i]=mean(Xstar3)
+ }
> Tstar125=quantile(Tstar1,0.025)
> Tstar1975=quantile(Tstar1,0.975)
> Tstar225=quantile(Tstar2,0.025)
> Tstar2975=quantile(Tstar2,0.975)
> Tstar325=quantile(Tstar3,0.025)
> Tstar3975=quantile(Tstar3,0.975)
>
> c11=c(2*M1-Tstar1975,2*M1-Tstar125)
> c12=c(2*T1-Tstar1975,2*T1-Tstar125)
> c21=c(2*M2-Tstar2975,2*M2-Tstar225)
> c22=c(2*T2-Tstar2975,2*T2-Tstar225)
> c31=c(2*M3-Tstar3975,2*M3-Tstar325)
> c32=c(2*T3-Tstar3975,2*T3-Tstar325)
```

Figure8: Code for three data set

The confidence interval results are shown in Fig.9.

```
> c11
   97.5%     2.5%
299837.8 299867.7
> c12
   97.5%     2.5%
299833.0 299862.9
> c21
   97.5%     2.5%
299714.5 299799.6
> c22
   97.5%     2.5%
299750.1 299835.2
> c31
   97.5%     2.5%
299728.1 299791.0
> c32
   97.5%     2.5%
299708.9 299771.8
```

Figure9: Confidence interval results

We could know for Michelson in 1879, when mean is used, the confidence interval is [299837.8, 299867.7] as c11. When median is used, the confidence interval is [299833.0, 299862.9] as c12.

We could know for Michelson in 1882, when mean is used, the confidence interval is [299714.5,299799.6] as c21. When median is used, the confidence interval is [299750.1 299835.2] as c22.

We could know for Newcomb, when mean is used, the confidence interval is [299728.1,299791.0] as c31. When median is used, the confidence interval is [299708.9,299771.8] as c32.

3. From the results we could know that we get shorter confidence intervals when using popular medians other than popular means, which means it is tend to be more accurate confidence intervals when the median is applied. Because the mean is highly influenced by the high/low values while the median is more robust and stable in such cases.

4. From the internet, the speed of light is 299792458m / s, which is 299792.458km/s It is consistent with the measurements of Michelson and Newcomb in 1882. Because the actual value exists in the confidence intervals of the dataset.

Exercise 3

1. Make the following assumptions based on the question：
H_0: the median duration μ is smaller or equal to 31 days
H_1: median is greater than 31 days
Because of the small sample size, we are not sure about normality and whether it is from a symmetric population with a certain median. So we choose to use sign

test to check whether we should reject H_0 or not. The code and results are shown below as figure 10:

```
> binom.test(sum(klm<=31),length(klm),p=0.5)

        Exact binomial test

data:  sum(klm <= 31) and length(klm)
number of successes = 20, number of trials = 60, p-value = 0.01349
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.2168694 0.4668727
sample estimates:
probability of success
             0.3333333

>|
```

Figure 10: Code and results of KLM median test

Conclusion: As the p-value is 0.01349<0.05. So we reject H_0, which means that the median duration μ is greater than 31 days.

2. Make the following assumptions based on the question：
    H_0: the criterium is met.
    H_1: the criterium is not met.

```
> binom.test(sum(klm>72),length(klm),p=0.1)

        Exact binomial test

data:  sum(klm > 72) and length(klm)
number of successes = 13, number of trials = 60, p-value = 0.007478
alternative hypothesis: true probability of success is not equal to 0.1
95 percent confidence interval:
 0.1207160 0.3419562
sample estimates:
probability of success
             0.2166667
```

Figure 11: Code and results of criterium sign test

As the p-value of this sign test is 0.007478<0.05. So we reject H_0, which means the criterium is not met.

Exercise 4

1. According to the question, this experiment has been carried out on different clouds and each cloud generate one numerical outcome and there are two groups of experimental units: the seeded and unseeded ones, so the data are not paired and we choose two sample t-test. We can make the following assumption:

H_0: silver nitrate has an effect on rain fall

H_1: silver nitrate do not have effect on rain fall

1.1 two samples t-test

```
> t.test(clouds[,1],clouds[,2])

        Welch Two Sample t-test

data:  clouds[, 1] and clouds[, 2]
t = 1.9984, df = 33.856, p-value = 0.05375
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
  -4.740491 559.585876
sample estimates:
mean of x mean of y
 441.9846  164.5619
```

Figure 12: two samples t-test for clouds

As p-value is 0.05375>0.05, H_0 of is not rejected. Which means that silver nitrate has an effect on rain falls. And from the mean of seeded and unseeded clouds we can see that the seeded clouds have more rain fall than the unseeded ones.

1.2 Mann-Whitney test

```
> wilcox.test(clouds[,1],clouds[,2])

        Wilcoxon rank sum test with continuity correction

data:  clouds[, 1] and clouds[, 2]
W = 473, p-value = 0.01383
alternative hypothesis: true location shift is not equal to 0
```

Figure 13: Mann-Whitney test for clouds

The null hypothesis is that the rain fall data of seeded and unseeded are identical populations. To test the hypothesis, we apply the wilcox.test function to compare the two independent samples. As the p-value turns out to be 0.01383, and is less than the 0.05 significance level, we reject the null hypothesis. And T is large, which indicate that clouds[,1] is shifted towards the right from clouds[,2], i.e. that seeded rain fall values are bigger than unseeded rain fall values.

1.3 Kolmogorov-Smirnov test

```
> ks.test(clouds[,1],clouds[,2])

        Two-sample Kolmogorov-Smirnov test

data:  clouds[, 1] and clouds[, 2]
D = 0.42308, p-value = 0.01905
alternative hypothesis: two-sided
```

Figure 14: Kolmogorov-Smirnov test for clouds

As p-value = 0.01905<0.05, H_0 of equal means is rejected. The mean of clouds[,1] is larger, which indicates that the seeded clouds have more rain fall than the unseeded ones and silver nitrate has an positive influence on rain falls.

2.   First we process the data to the square root values.

　 2.1 two samples t-test

```
> clouds2=sqrt(clouds)
> clouds2[,1]
 [1] 11.384200  5.603570 52.398473 22.115605 20.736441 17.401149
 [7] 10.908712  2.024846  9.612492  4.183300 14.166863 16.574076
[13] 16.574076  2.774887 40.693980 31.272992 14.092551 26.521689
[19] 41.204369 18.278403 10.876580 15.968719 10.737784 15.572412
[25]  5.718391  6.371813
> clouds2[,2]
 [1]  5.108816  5.128353  9.327379  9.746794 19.297668  0.100000
 [7]  4.159327  4.939636  3.391165 17.922053  8.276473  9.027735
[13]  6.877500  5.347897 28.811456 18.587630 34.678524  6.049793
[19]  2.213594  2.213594  6.410928  5.385165 12.767145 15.630099
[25] 12.157302  4.658326
> t.test(clouds2[,1],clouds2[,2])

        Welch Two Sample t-test

data:  clouds2[, 1] and clouds2[, 2]
t = 2.4246, df = 43.363, p-value = 0.01956
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
  1.202087 13.071300
sample estimates:
mean of x mean of y
17.068014  9.931321
```

Figure 15: Two sample t-test for $\sqrt{clouds}$

As p-value is 0.01956<0.05 and less than the former one (0.05375) which is not square rooted, H_0 is rejected. Because after the square root calculation, the differences of data between the two samples have been narrowed, which indicates that the square root values of seeded and unseeded clouds have no significant difference.

2.2 Mann- Whitney test

```
> wilcox.test(clouds2[,1],clouds2[,2])

        Wilcoxon rank sum test with continuity correction

data:  clouds2[, 1] and clouds2[, 2]
W = 473, p-value = 0.01383
alternative hypothesis: true location shift is not equal to 0
```

Figure 16: Mann- Whitney test for $\sqrt{clouds}$

We can see that the p-value here is exactly same as the result of Mann-Whitney test for clouds, because MW test works by bringing the data of two independent samples into a single space, in which data is globally ranked. Because the distribution of samples after square root has not changed, so the p-value is same as the former result.

2.3 Kolmogorov-Smirnov test

```
> ks.test(clouds2[,1],clouds2[,2])

        Two-sample Kolmogorov-Smirnov test

data:  clouds2[, 1] and clouds2[, 2]
D = 0.42308, p-value = 0.01905
alternative hypothesis: two-sided
```

Figure 17: Kolmogorov-Smirnov test for $\sqrt{clouds}$

We can see that the p-value here is exactly same as the result of Kolmogorov-Smirnov test on the sample "clouds". Because this test the distribution of samples after square root has not changed, so the p-value is same as the former result.

3. First we process the data to square root of the square root values.

3.1 two samples t-test

```
> clouds3 = sqrt(clouds2)
> clouds3[,1]
 [1] 3.374048 2.367186 7.238679 4.702723 4.553728 4.171468 3.302834
 [8] 1.422971 3.100402 2.045312 3.763889 4.071127 4.071127 1.665799
[15] 6.379183 5.592226 3.754005 5.149921 6.419063 4.275325 3.297966
[22] 3.996088 3.276856 3.946189 2.391316 2.524245
> clouds3[,2]
 [1] 2.2602690 2.2645866 3.0540758 3.1219856 4.3929111 0.3162278
 [7] 2.0394428 2.2225291 1.8415116 4.2334446 2.8768859 3.0046190
[13] 2.6224987 2.3125520 5.3676304 4.3113374 5.8888474 2.4596328
[19] 1.4878153 1.4878153 2.5319811 2.3205958 3.5731142 3.9534920
[25] 3.4867323 2.1583155
> t.test(clouds3[,1],clouds3[,2])

        Welch Two Sample t-test

data:  clouds3[, 1] and clouds3[, 2]
t = 2.5968, df = 48.826, p-value = 0.0124
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.2196477 1.7236468
sample estimates:
mean of x mean of y
 3.878988  2.907340
```

Figure 18: Two sample t-test for $\sqrt{\sqrt{clouds}}$

As p-value is 0.0124<0.05 and less than the former ones, H_0 is rejected. The reasons are same as the former one (2.1).

3.2 Mann-Whitney test

```
> wilcox.test(clouds3[,1],clouds3[,2])

        Wilcoxon rank sum test with continuity correction

data:  clouds3[, 1] and clouds3[, 2]
W = 473, p-value = 0.01383
alternative hypothesis: true location shift is not equal to 0
```

Figure 19: Mann-Whitney test for $\sqrt{\sqrt{clouds}}$

The reason of p-value did not change is as same as 2.2 had shown.

3.3 Kolmogorov-Smirnov test

```
> ks.test(clouds3[,1],clouds3[,2])

        Two-sample Kolmogorov-Smirnov test

data:  clouds3[, 1] and clouds3[, 2]
D = 0.42308, p-value = 0.01905
alternative hypothesis: two-sided
```

Figure 20: Kolmogorov-Smirnov test for $\sqrt{\sqrt{clouds}}$

The reason of p-value did not change is as same as 2.3 had shown.

Exercise 5

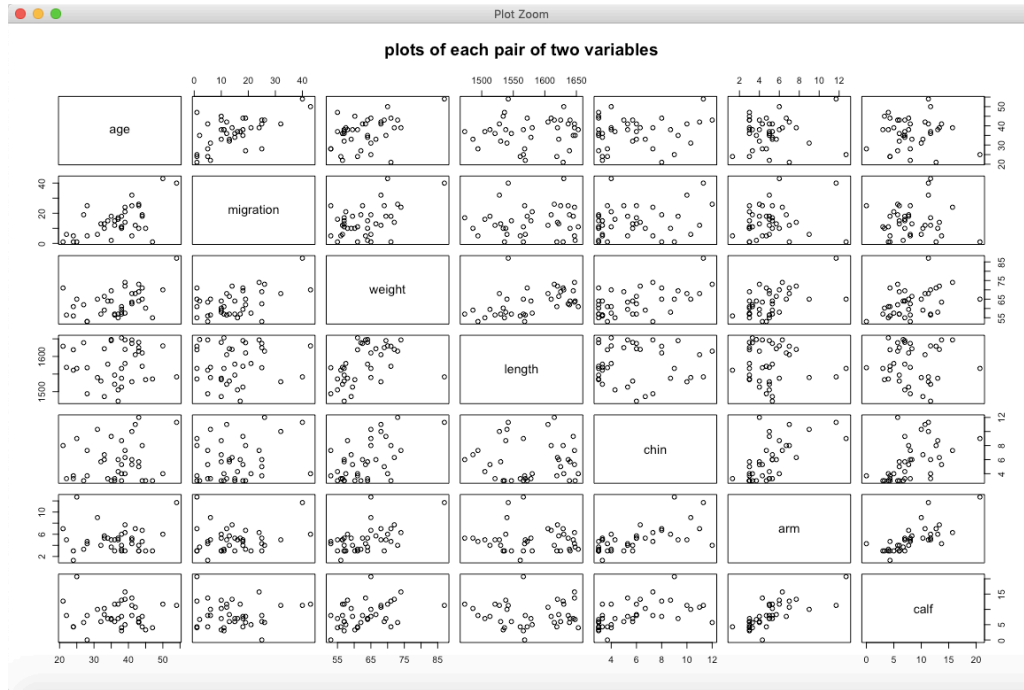1. Using the code pairs(peruvians[1:7]) we get plots of each pair of two variables as below:

Figure 21: plots of each pair of two variables

2. QQ-plots show that normality is not plausible for the migration sample. Hence, we choose to use the rank correlation test of Spearman to test the correlation between migration and other variables .
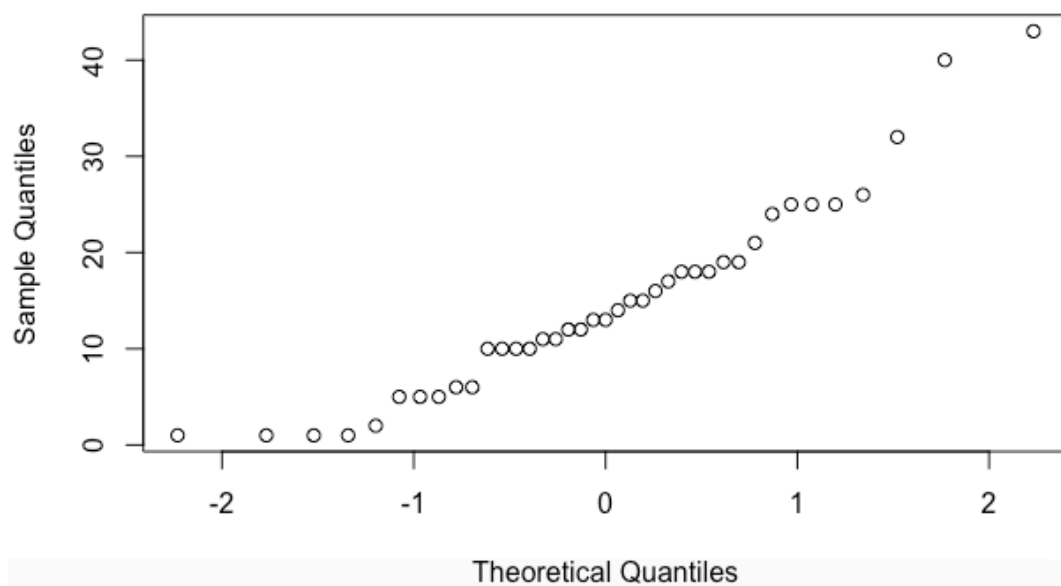

Figure 22: Q-Q plot migration

2.1 The rank correlation test between migration and age

```
> cor.test(migration,age,method="spearman")

        Spearman's rank correlation rho

data:  migration and age
S = 5176.6, p-value = 0.002189
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.4760575
```

Figure 23: rank correlation test of Spearman between migration and age

We can see that p-value is 0.002189<0.05. So there is correlation between migration and age, if normality is assumed.

2.2 The rank correlation test between migration and weight

```
> cor.test(migration,weight,method="spearman")

        Spearman's rank correlation rho

data:  migration and weight
S = 6415.1, p-value = 0.02861
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.3506956
```

Figure 24: rank correlation test of Spearman between migration and weight

We can see that p-value is 0.02861<0.05. So there is correlation between migration and weight. But the correlation is not too big. If normality is assumed.

2.3 The rank correlation test between migration and length

```
> cor.test(migration,length,method="spearman")

        Spearman's rank correlation rho

data:  migration and length
S = 9044.3, p-value = 0.6087
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.08458432
```

Figure 25: rank correlation test of Spearman between migration and length

We can see that p-value is 0.6807>0.05. So there is no correlation between migration and length, if normality is assumed.

2.4 The rank correlation test between migration and wrist

```
> cor.test(migration,wrist,method="spearman")

        Spearman's rank correlation rho

data:  migration and wrist
S = 7712.8, p-value = 0.1797
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.2193498
```

Figure 26: rank correlation test of Spearman between migration and wrist

We can see that p-value is 0.1797>0.05. So there is no correlation between migration and wrist, if normality is assumed.

2.5 The rank correlation test between migration and systolic

```
> cor.test(migration,systolic,method="spearman")

        Spearman's rank correlation rho

data:  migration and systolic
S = 11544, p-value = 0.3054
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.1684286
```

Figure 27: rank correlation test of Spearman between migration and systolic

We can see that p-value is 0.3054>0.05. So there is no correlation between migration and systolic, if normality is assumed.

2.6 The rank correlation test between migration and diastolic

```
> cor.test(migration,diastolic,method="spearman")

        Spearman's rank correlation rho

data:  migration and diastolic
S = 9137.6, p-value = 0.6494
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.07514098
```

Figure 28: rank correlation test of Spearman between migration and diastolic

We can see that p-value is 0.6494>0.05. So there is no correlation between migration and diastolic, if normality is assumed.

EXERCISE 6

1. data and graphical

(1) Study the data:

As shown on the Table 1, we compute the mean and standard deviation of running time (lemo and energy drink). Specifically, the "lemo_difference" = "running time before (lemo)" – "running time after (lemo)".
We can find two basic results:

a. Energy drink group seems run faster after drinking the energy drink, because the time of "energy_after" is shorter than the time of "energy_before. Similarly, softdrink group seems run slower after drinking the softdrink, because the time of "lemo_after" is longer than the time of "lemo_before.

b. From the standard deviation, we can find that energy drink group has lower standard deviation than softdrink group. Therefore, the energy drink group's data tend to be close to the mean of the set.

Table 1 The mean and Standard Deviation of lemo and energy

	mean	standard deviation
lemo_before	7.554	0.5471157
lemo_after	7.699	0.8339551
lemo_difference	-0.145	0.6232248
energy_before	7.733	0.2971417
energy_after	7.578	0.4585319
energy_difference	0.154	0.3229258

(2) Graphical representations:

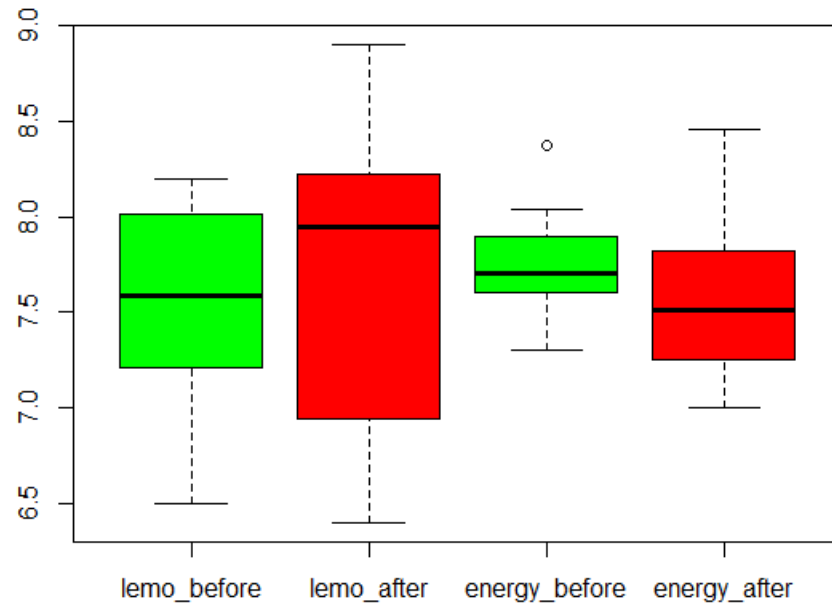As shown on the figure29 and figure30, we can see the distribution of energy drink group is more concentrated.

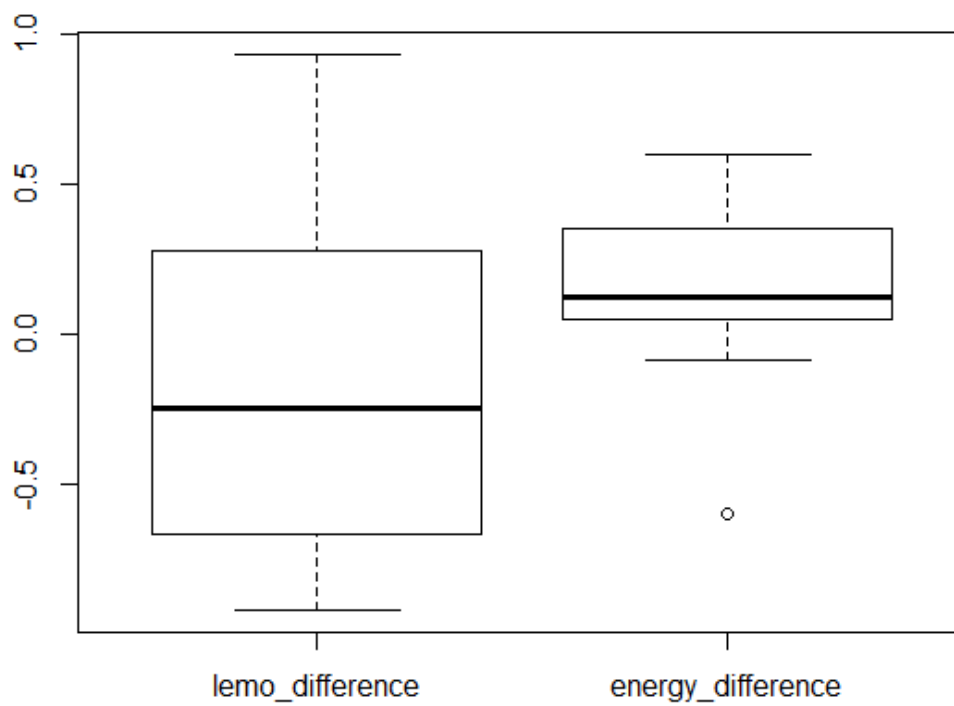**Figure29: boxplots of soft drink and energy drink (before and after)**

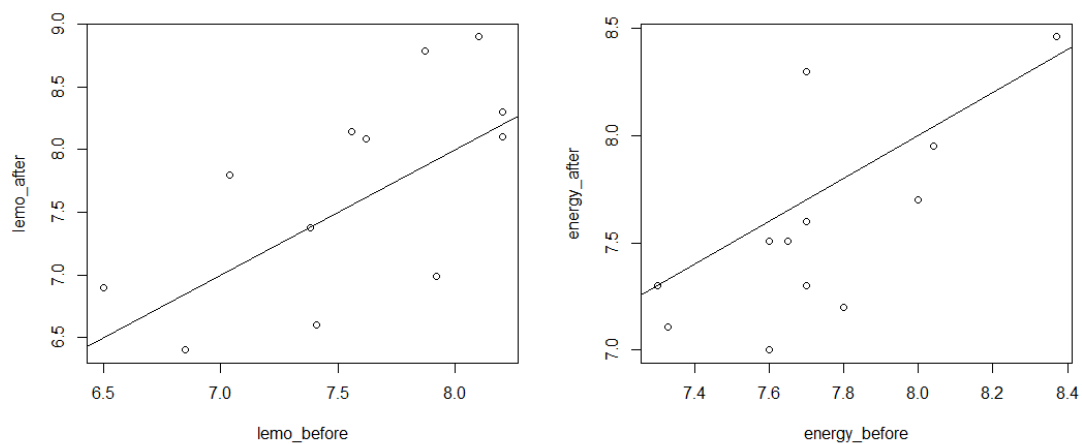**Figure30:   boxplots of soft drink and energy drink (difference)**

Figure31 plot of before and after

code of (1):

```r
alldata = read.table("run.txt")

lemo_before = alldata[which(alldata$drink=="lemo"),"before"]
lemo_after = alldata[which(alldata$drink=="lemo"),"after"]
lemo_difference = lemo_before - lemo_after
energy_before =
alldata[which(alldata$drink=="energy"),"before"]
energy_after = alldata[which(alldata$drink=="energy"),"after"]
energy_difference = energy_before - energy_after
mydiff = c(lemo_difference,energy_difference)
alldata$difference = mydiff

mean(lemo_before)
mean(lemo_after)
mean(lemo_difference)
mean(energy_before)
mean(energy_after)
mean(energy_difference)

sd(lemo_before)
sd(lemo_after)
sd(lemo_difference)
sd(energy_before)
sd(energy_after)
sd(energy_difference)

par(mfrow=c(1,2))
plot(lemo_before,lemo_after); abline(0,1)
plot(energy_before,energy_after); abline(0,1)
```

```
boxplot(lemo_before,lemo_after,energy_before,energy_after,
names=c("lemo_before","lemo_after","energy_before","energy_aft
er"),col=c('green','red',"green","red"))
boxplot(lemo_difference,energy_difference,names=c("lemo_differ
ence","energy_difference"))
```

2. Test separately

We can use paired t-test, because each group contains two numerical outcomes per experimental unit and our interest is in a possible difference between the two outcomes.

H0 = there is not a significant difference in speed in the two running tasks.

For softdrink group, the p-value = 0.4373 > 0.05. Therefore, we cannot reject H0, which means there is not a significant difference in speed in the two running tasks after drinking softdrink.

result of paired t-test on softdrink:

```
> t.test(lemo_before,lemo_after,paired = TRUE)


        Paired t-test

data:  lemo_before and lemo_after
t = -0.80596, df = 11, p-value = 0.4373
alternative hypothesis: true difference in means is not eq
ual to 0
95 percent confidence interval:
 -0.5409781  0.2509781
sample estimates:
mean of the differences
              -0.145
```

For energy drink group, the p-value = 0.1246 > 0.05. Therefore, we cannot reject H0, which means there is not significant a difference in speed in the two running tasks after drinking energy drink.

result of paired t-test on energy drink:

```
> t.test(energy_before,energy_after, paired=TRUE)


        Paired t-test

data:  energy_before and energy_after
t = 1.6538, df = 11, p-value = 0.1264
alternative hypothesis: true difference in means is not eq
ual to 0
```

```
95 percent confidence interval:
 -0.05101059  0.35934392
sample estimates:
mean of the differences
          0.1541667
```

Finally, we check the normality assumption on the differences.

Q-Q Plot lemo before   **Q-Q Plot lemo after**

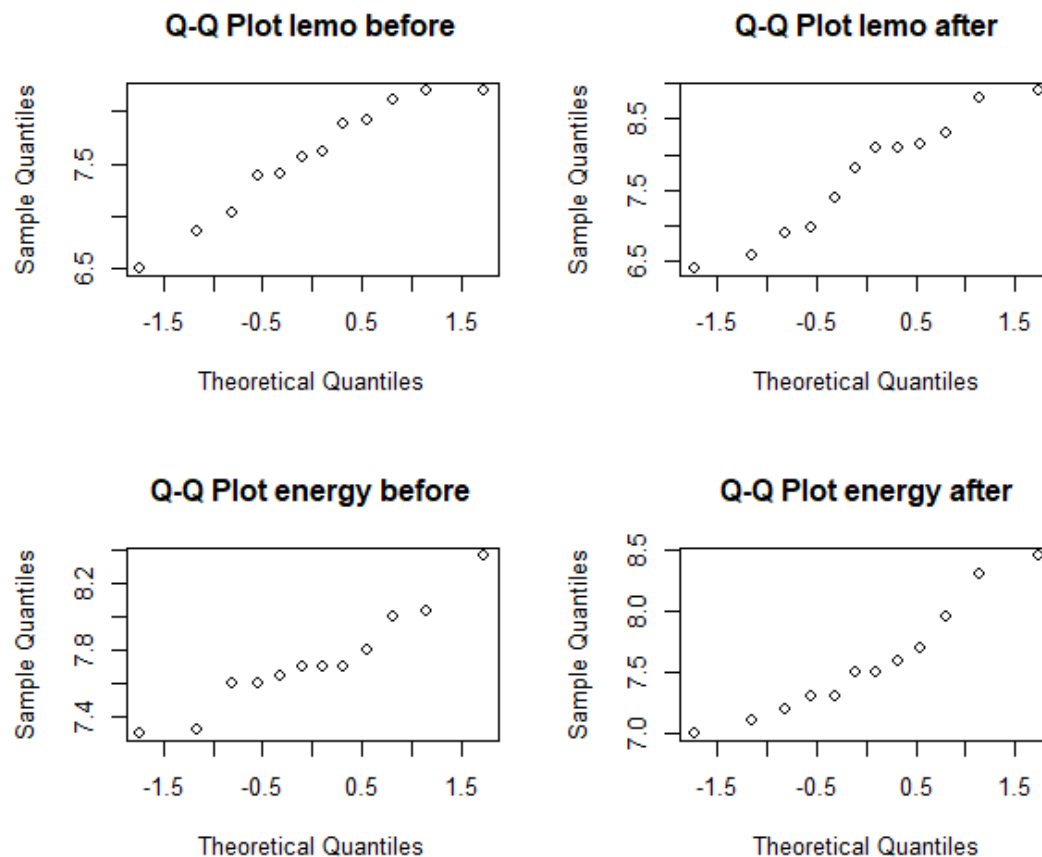**Q-Q Plot energy before**   **Q-Q Plot energy after**

Figure 32, Q-Q plots of energy drink and softdrink group

After Shapiro-Wilk normality test, there is no reason to suspect that the running time sample are not taken from a normal population.

result of Shapiro-Wilk normality test on soft drink:

```
> shapiro.test(lemo_before)

    Shapiro-Wilk normality test

data:  lemo_before
W = 0.93899, p-value = 0.485


> shapiro.test(lemo_after)

    Shapiro-Wilk normality test
```

```
    data:  lemo_after
    W = 0.94117, p-value = 0.5133


    > shapiro.test(energy_before)

        Shapiro-Wilk normality test

    data:  energy_before
    W = 0.93334, p-value = 0.4169


    > shapiro.test(energy_after)

        Shapiro-Wilk normality test

    data:  energy_after
    W = 0.92444, p-value = 0.3249
```

code of (2)

```
t.test(lemo_before,lemo_after,paired = TRUE)
t.test(energy_before,energy_after, paired=TRUE)

par(mfrow=c(2,2))
qqnorm(lemo_before,main="Q-Q Plot lemo before")
qqnorm(lemo_after,main="Q-Q Plot lemo after")
qqnorm(energy_before,main="Q-Q Plot energy before")
qqnorm(energy_after,main="Q-Q Plot energy after")

shapiro.test(lemo_before)
shapiro.test(lemo_after)
shapiro.test(energy_before)
shapiro.test(energy_after)
```

3. Test whether these time differences

As the table 2 shows, we can find the time difference of soft drink and energy drink.

Table 2. The time difference of soft drink and energy drink

time difference of soft drink	time difference of energy drink
0. 93	0. 22
−0. 58	−0. 60
−0. 47	−0. 09
0. 45	0. 10
−0. 92	0. 60
0. 81	0. 09

0.00	0.40
−0.76	0.60
−0.80	0.30
−0.40	0.14
0.10	0.09
−0.10	0.00

Because there are two groups of student, one drinking softdrink and anther one drinking energy drink respectively, they are two independent samples. We use two samples t-test.

results of t-test of time difference:

```
> t.test(lemo_difference,energy_difference)

	Welch Two Sample t-test

data:  lemo_difference and energy_difference
t = -1.4764, df = 16.509, p-value = 0.1586
alternative hypothesis: true difference in means is not
 equal to 0
 95 percent confidence interval:
 -0.7276409  0.1293076
sample estimates:
 mean of x  mean of y
-0.1450000  0.1541667
```

The p-value=0.1586 > 0.05. Therefore, we cannot reject H0, which means there is not a time difference between soft drink and energy drink.

Finally, we check the normality assumption. Figure 33 shows the Q-Q plot of soft drink and energy drink time difference.
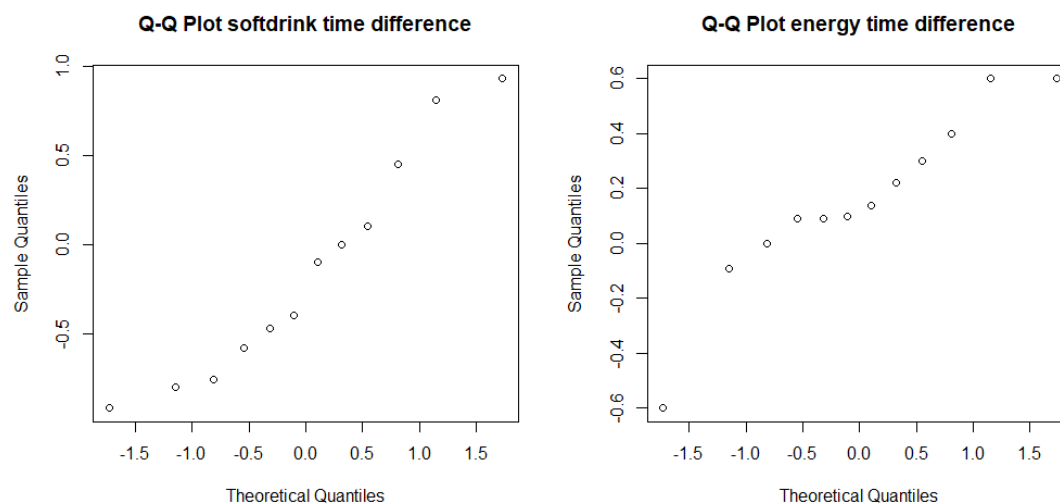

Figure33. Q-Q plot of soft drink and energy drink time difference

After Shapiro-Wilk normality test, there is no reason to suspect that the differences are not taken from a normal population. The reason is that p-value of soft drink = 0.3723 > 0.05, and the p-value of energy drink = 0.2788 > 0.05.

result of Shapiro-Wilk normality test on soft drink:

```
> shapiro.test(lemo_before-lemo_after)

	Shapiro-Wilk normality test

data:  lemo_before - lemo_after
W = 0.92927, p-value = 0.3725
```

result of Shapiro-Wilk normality test on energy drink:

```
> shapiro.test(energy_before-energy_after)

	Shapiro-Wilk normality test

data:  energy_before - energy_after
W = 0.91913, p-value = 0.2788
```

code of (3):

```
lemo_before = alldata[which(alldata$drink=="lemo"),"before"]
lemo_after = alldata[which(alldata$drink=="lemo"),"after"]
lemo_difference = lemo_before - lemo_after
energy_before =
alldata[which(alldata$drink=="energy"),"before"]
energy_after = alldata[which(alldata$drink=="energy"),"after"]
energy_difference = energy_before - energy_after

t.test(lemo_difference,energy_difference)

shapiro.test(lemo_difference-energy_difference)

qqnorm(lemo_difference,main="Q-Q Plot softdrink time
difference")
qqnorm(energy_difference,main="Q-Q Plot energy time
difference")
shapiro.test(lemo_before-lemo_after)
shapiro.test(energy_before-energy_after)
```

4. plausible objection

The original design is testing on two different group of students, which is 12 pupils for each. However, we think different student may influence the results. Also, the 60 meters is too short to find the time difference.
We suggest the new design of the experiment:

(1) test on the same pupils, randomized and double-blind for drinking softdirnk and energy drink.

(2) running on 500 meters

5. **Yes, because the t-test result of   3)   also cannot reject H0.**

6. **normal distribution assumption** on these differences is needed for the analysis in 3).

The vector into 24 residuals to investigate this assumption in QQ-plot is shown on the figure 34.
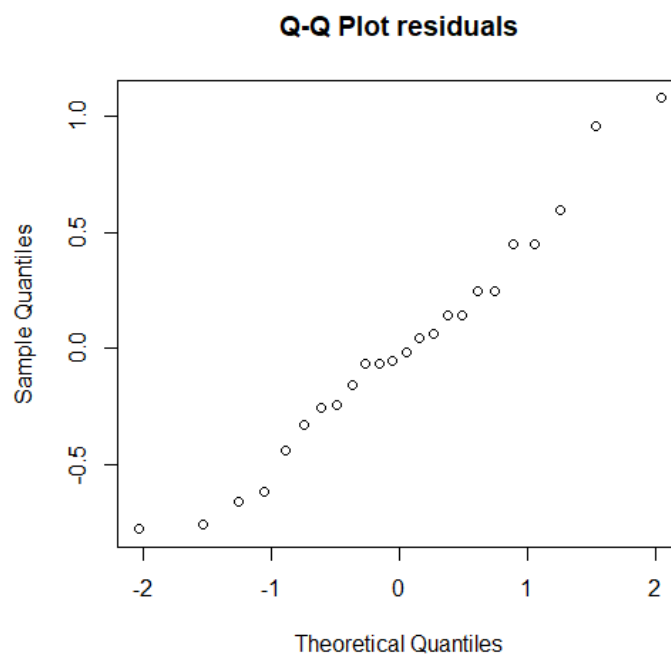

Figure 34. Q-Q Plot residuals

code of (6):

```
diff =
data.frame(lemo_diff=lemo_difference,energy_diff=energy_differ
ence)
diff_frame=
data.frame(yield=as.vector(as.matrix(diff)),variety=factor(rep
(1:2,each=12)))
diff_frame[1:12,]
timeonaov= lm(yield~variety,data=diff_frame)
anova(timeonaov)
par(mfrow=c(1,1)); qqnorm(residuals(timeonaov),main="Q-Q Plot
residuals")
```

EXERCISE 7

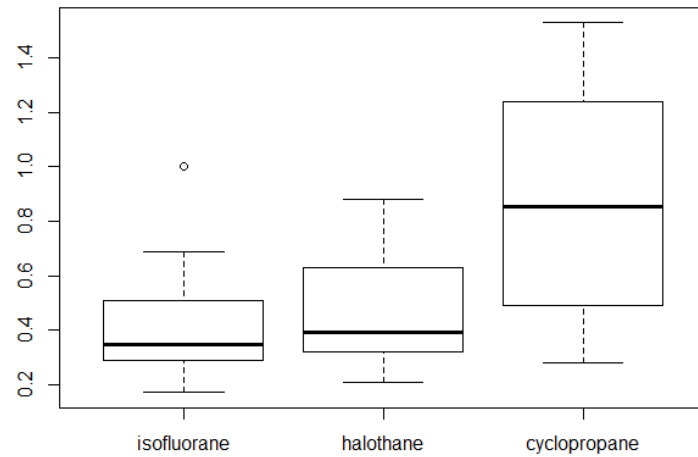**1.** As the figure 35 shows, the boxplots of 3 samples.

Figure 35. Boxplots of 3 samples

As the figure shows, the Q-Q plots of 3 samples. There is no reason to suspect that the two samples are not taken from a normal population.
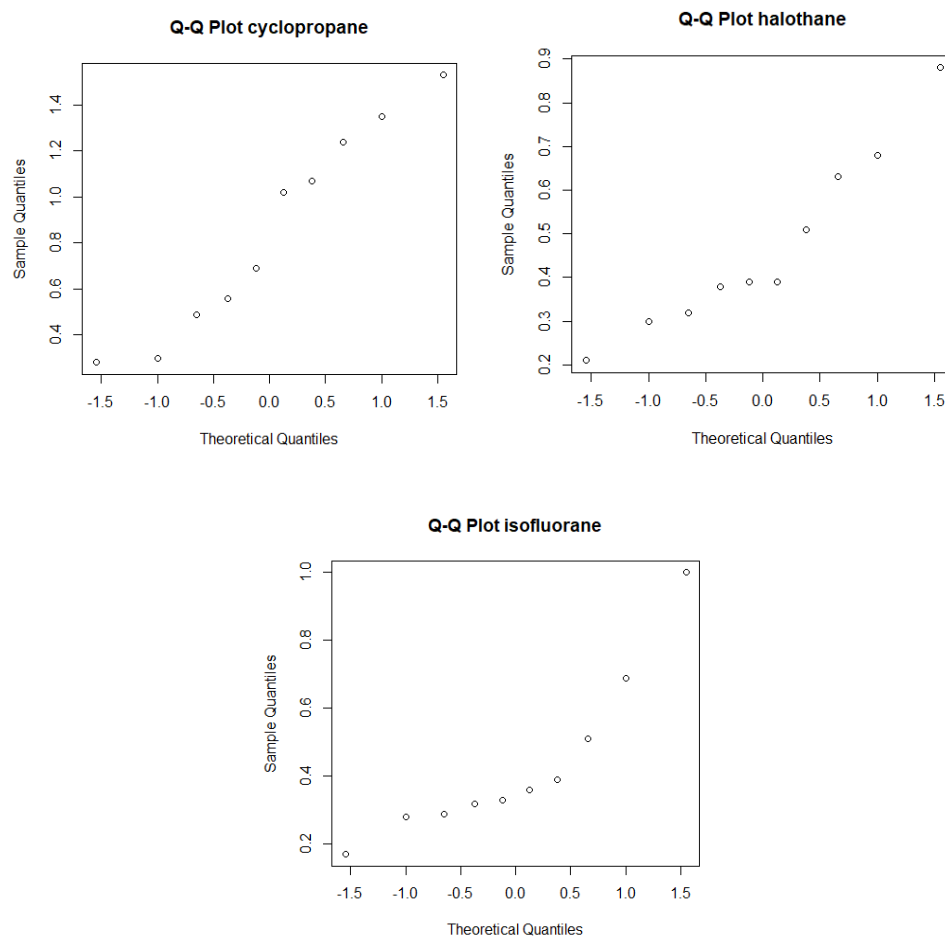

Figure 36. Q-Q plots of 3 samples

code of (1):

```
dogs = read.table("dogs.txt", header=TRUE)
isofl = dogs$isofluorane
haloe = dogs$halothane
cyclo = dogs$cyclopropane
boxplot(dogs)
qqnorm(isofl,main="Q-Q Plot isofluorane")
qqnorm(haloe,main="Q-Q Plot halothane")
qqnorm(cyclo,main="Q-Q Plot cyclopropane")
```

2. We use one-way ANOVA to test.

The p-value=0.011< 0.05, so we reject H0. 1-way ANOVA yield significant differences among the three drugs.

result of ANOVA:

```
> anova(dogsonaov)
Analysis of Variance Table

Response: yield
          Df Sum Sq Mean Sq F value Pr(>F)
variety    2 1.0808 0.54040   5.355  0.011 *
Residuals 27 2.7247 0.10092
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1
```

We takes "isofluorane" as a base level and compares the other levels to it. The estimates:

$\hat{\mu}1 = 0.4340$; $\hat{\mu}2 - \hat{\mu}1 = 0.0350$; $\hat{\mu}3 - \hat{\mu}1 = 0.4190$;

Therefor, estimate of "isofluorane" is 0.4340; estimate of "halothane" is 0.4690; estimate of "cyclopropane" is 0.8530.

result of summary:

```
> summary(dogsonaov)

Call:
lm(formula = yield ~ variety, data = dogs_frame)

Residuals:
    Min      1Q  Median      3Q     Max
-0.5730 -0.1608 -0.0790  0.2000  0.6770

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.4340     0.1005   4.320 0.000189 ***
variety2      0.0350     0.1421   0.246 0.807266
variety3      0.4190     0.1421   2.949 0.006504 **
```

```
   ---
   Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
 ' ' 1

Residual standard error: 0.3177 on 27 degrees of freedom
Multiple R-squared:  0.284,    Adjusted R-squared:  0.231
F-statistic: 5.355 on 2 and 27 DF,  p-value: 0.011
```

Diagnostics:
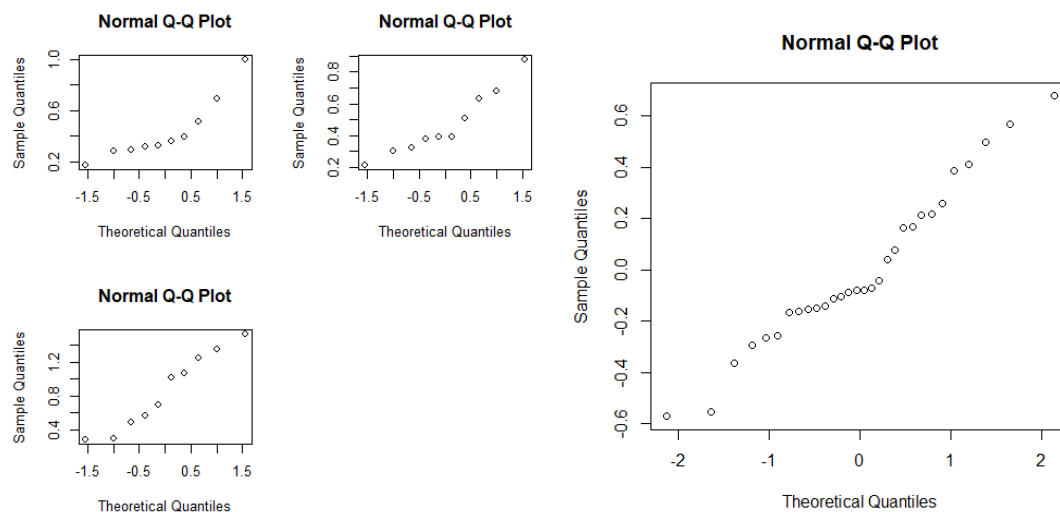
The Q-Q plot is shown on the figure 37.

Figure 37. Q-Q plots of three drugs

Because the 3 samples are small, separate QQ-plots are not so useful. The second plot, using residuals, uses all 30 points, but corrected for being sampled from different populations. The residuals don't seem to deviate significantly from normal.

code of (2):

```
dogs_frame =
data.frame(yield=as.vector(as.matrix(dogs)),variety=factor(rep
(1:3,each=10)))
dogsonaov=lm(yield~variety,data=dogs_frame)
anova(dogsonaov)
summary(dogsonaov)
confint(dogsonaov)

par(mfrow=c(2,2)); for (i in 1:3) qqnorm(dogs[,i])
par(mfrow=c(1,1)); qqnorm(residuals(dogsonaov))
```

3. Kruskal-Wallis test

As the Kruskal-Wallis test shows, the p-value=0.05948>0.05, we cannot reject H0. There is not a significant difference among the three drugs.

```
   > kruskal.test(worms,group)
```

```
      Kruskal-Wallis rank sum test

data:  worms and group
Kruskal-Wallis chi-squared = 5.6442, df = 2, p-value =
0.05948
```

The reason why there is a difference between the two test is that ANOVA is value-based, but Kruskal-Wallis is rank based. ANOVA can analyze normal distribution, but Kruskal-Wallis is suitable for non-normal distribution.

From Shapiro-Wilk normality test, "halothane" and "cyclopropane" samples are normal distribution. However, "isofluorane" is non-normal distribution.

```
> shapiro.test(isofl)

    Shapiro-Wilk normality test

data:  isofl
W = 0.83093, p-value = 0.03434


> shapiro.test(haloe)

    Shapiro-Wilk normality test

data:  haloe
W = 0.9234, p-value = 0.3862


> shapiro.test(cyclo)

    Shapiro-Wilk normality test

data:  cyclo
W = 0.93334, p-value = 0.4815
```

code of (3):

```
dogframe=data.frame(worms=as.vector(as.matrix(dogs)),group=as.
factor(rep(1:3,each=10)))
attach(dogframe)
kruskal.test(worms,group)

shapiro.test(isofl)
shapiro.test(haloe)
shapiro.test(cyclo)
```