Assignment 1

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Exercise 1

First, we construct a simple function that will return the power of the t-test using the given parameters (n,m,mu,nu,sd).

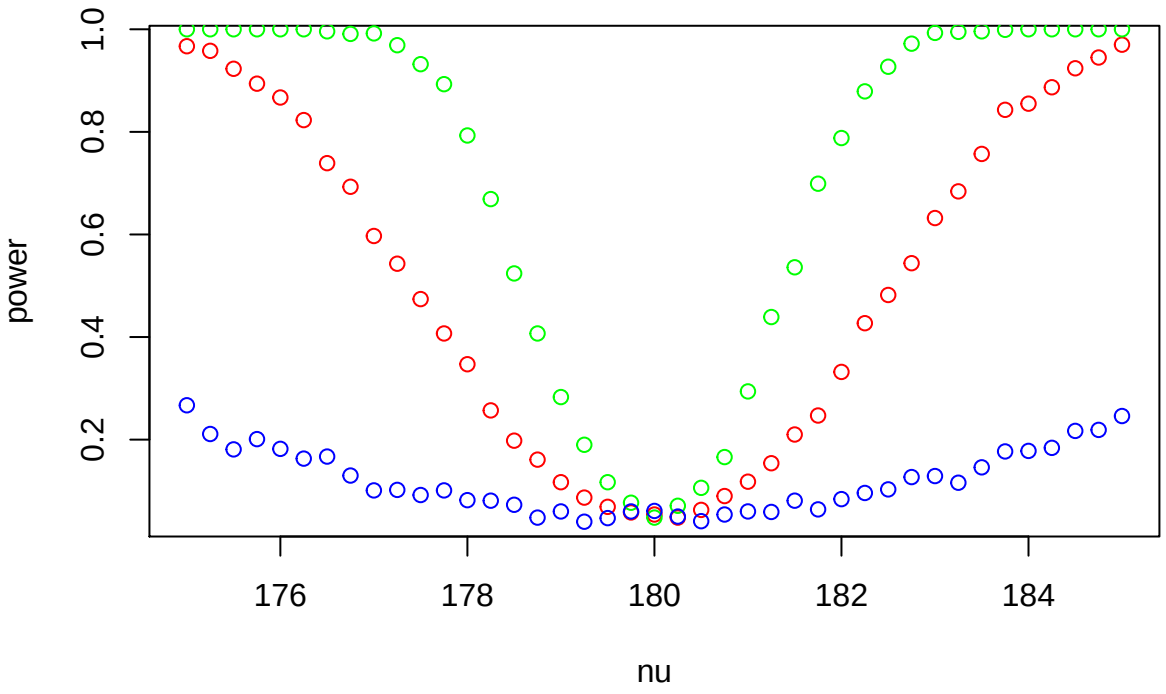
```
powerOfTtest <- function(n, m, mu, nu, sd)
{
  B = 1000; p = numeric(B); power = numeric(length(nu))
  for (i in 1:length(nu))
  {
    for (b in 1:B)
    {
      x = rnorm(n, mu,sd); y = rnorm(m, nu[i],sd)
      p[b] = t.test(x,y,var.equal=TRUE)[[3]]
    }
    power[i] = mean(p<0.05)
  }
  power
}
```

a) & **b)** &**c)** Using the above function, we can now easily calculate the power of the t-test with the given parameters. This is plotted for all sets of parameters, with red for subquestion a, green for subquestion b, and blue for subquestion c.

```
nu = seq(175,185,by=0.25); mu = 180 # these parameters stay equal in all sets
# compute and plot power function with parametrs : n = m = 30, and sd = 5
n = m = 30; sd = 5
power = powerOfTtest(n, m, mu, nu, sd)
plot(nu, power, col = 'red')

# compute and plot power function with parametrs : n = m = 100,and sd = 5.
n = m = 100; sd = 5
power = powerOfTtest(n, m, mu, nu, sd)
points(nu, power, col = 'green')

# compute power function with parametrs : n = m = 30, and sd = 15.
n = m = 30; sd = 15
power = powerOfTtest(n, m, mu, nu, sd)
points(nu, power, col = 'blue')
```

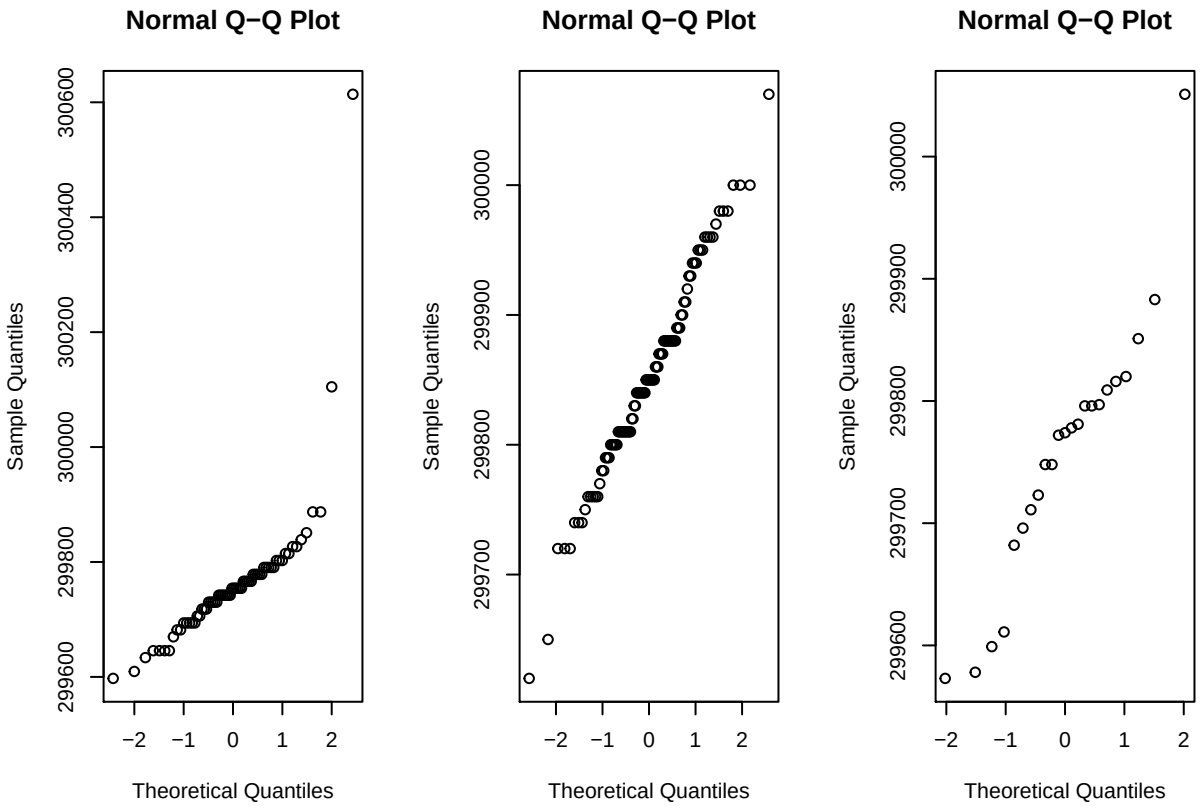


d) First, with fixed n,m,sd and mu. As the second sample's mean of the sampling distribution (nu) goes closer to mu, the power of p-value could be rather low which suggests t-test tends to NOT rejects the null hypothesis and gives the right result. Second, comparing plot from problem a and b, b's up-side-down bell-shaped plot is thinner than a's plot, indicating as sample size increase t-test becomes more strict, t-test will NOT reject null hypothesis only when two means fairly close to each other. The third conclusion comes from problem c, when standard deviation becomes larger, its plot became less smooth and t-test's performance became unstable. Because higher sample sizes yield higher power, increasing sample size may solve this problem.

Exercise 2

a) To investigate the normality for all three data sets, we choose to use Shapiro-Wilk normality test with an alpha level of 0.05. The null-hypothesis of this test is that the population is normally distributed.

```
light = 7.442 / ((scan('light.txt', quiet=TRUE) / 1000 + 24.8) / 10^6)
light1879 = scan('light1879.txt', quiet=TRUE) + 299000
light1882 = scan('light1882.txt', quiet=TRUE) + 299000
par(mfrow=c(1,3))
qqnorm(light); qqnorm(light1879); qqnorm(light1882)
```




```
shapiro.test(light)[[2]]
```

```
## [1] 2.72356e-12
```

```
shapiro.test(light1879)[[2]]
```

```
## [1] 0.5137039
```

```
shapiro.test(light1882)[[2]]
```

```
## [1] 0.1111188
```

We drew QQ-plot and computed all three data sets' Shapiro test p-value. We got the data from light1879 and light1882 are nearly in a line in QQ-plot have Shapiro test p-values greater than 0.05, which means these two data sets' data are normally distributed. Besides, the data from light has a Shapiro test's p-value lower than 0.05, and the data values are not distribued in a line in QQ-plot, which means this data set does not have nomality.

In conclusion it can be deduced that 'light1879' and 'light1882' are both normally distributed, and the data set 'light' is not normally distributed.

b) We can use t-distribution to calculate distribution confidence intervals even the distribution is not a normal distribution. t.test in R would give me confidence intervals directly.

```
lightCi = t.test(light)[[4]]
light1879Ci = t.test(light1879)[[4]]
light1882Ci = t.test(light1882)[[4]]
c(lightCi[1], lightCi[2])
```

```
## [1] 299731.9 299795.8
```

```
c(light1879Ci[1], light1879Ci[2])
```

```
## [1] 299836.7 299868.1
```

```
c(light1882Ci[1], light1882Ci[2])
```

```
## [1] 299709.9 299802.5
```

A 95% confidence interval tells us that the true mean of the population is contained by this interval, with 95% certainty. However, the three confidence intervals don't all overlap (only light and light1882 overlap), even though in theory the data of all three datasets should be sampled from the same population (the true mean in this case would be the true speed of light). Therefore it is hard to try to pin down the true mean by this data alone. **c)** The current most accurate value for the speed of light is 299792.458. To see if our data is consistent with this value, our true population mean, we will test it. For the normal distributed data we will use a t-test. A t-test will perform less accurately when the distribution is not normal, so we choose Wilcoxon signed rank test to find the first sample's p-value (as the first sample, light.txt, is not normally distributed. In this test, the null hypothesis is that the mean of the data is the true speed of light, 299792.458.

```
lightSpeed = 299792.458
p = wilcox.test(light,mu=lightSpeed)[[3]]
p1879 = t.test(light1879, mu=lightSpeed)[[3]]
p1882 = t.test(light1882,mu=lightSpeed)[[3]]
p; p1879; p1882;
```

```
## [1] 4.450593e-06
```

```
## [1] 1.823745e-11
```

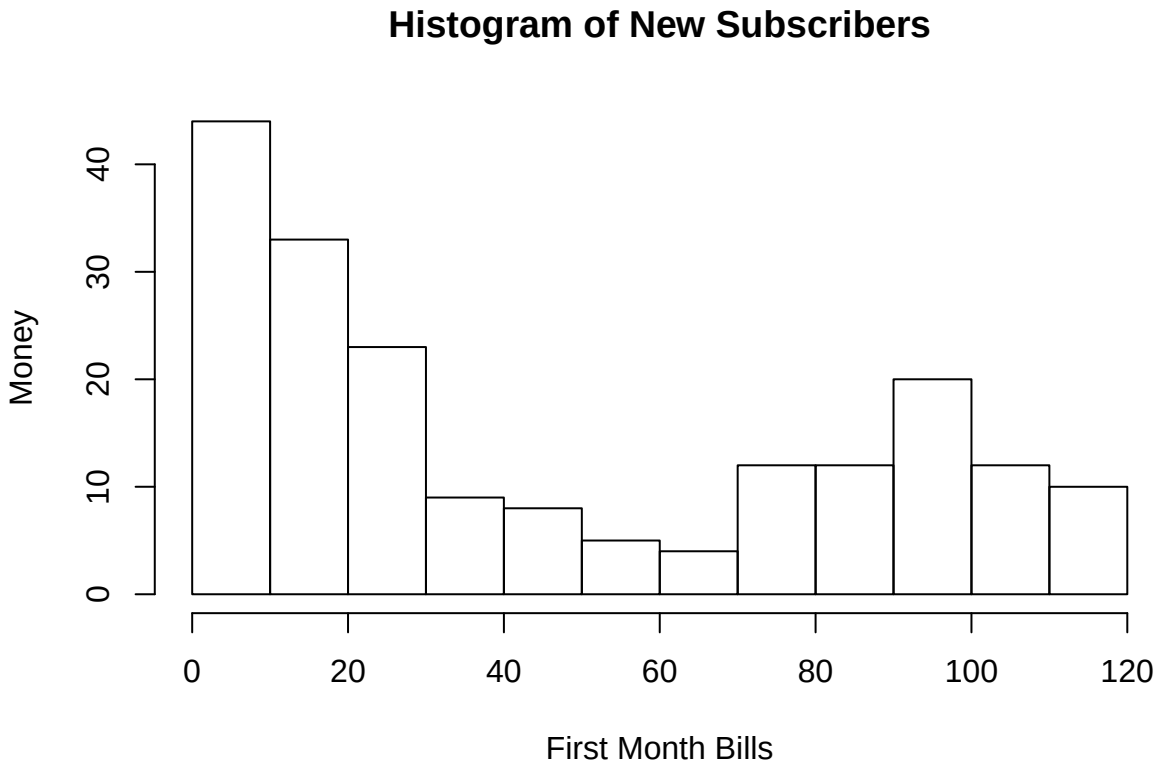
```
## [1] 0.1189198
```

As one can see, only light1882's p-valuee (0.1189198) > 0.05, which makes it most accurate sample we have; furthermore, it seems that most data from the measurements of Michelson and Newcomb are not consistent with the true speed of light.

Exercise 3

a)

```
telephoneBills = read.table('telephone.txt', header=TRUE)
telephone =  telephoneBills[telephoneBills$Bills!=0, ]
hist(telephone, xlab='First Month Bills', ylab='Money', main='Histogram of New Subscribers')
```



The best plot to represent the distribution of subscribers is a histogram. The strategy that the manager should adopt is to increase the preferential activities in the price range of 30-70, in order to promote low consumption users to increase consumption, and ultimately increase users in this price range. There is one inconsistency in the data. It contains zero values, which is inappropriate since the survey should only target customers who have already spent money on their services. Hence zero-cost subscribers shouldn't be included.

b) With lambda in the range between 0.01 and 0.1, we construct a sequence consist of 20 elements. And we use bootstrap-test to test every single one of them to evaluate whether the data fit an exponential distribution.

```
lambdas=seq(0.01, 0.1, by=0.005)
B=1000
t=median(telephone)
n=length(telephone)
p=numeric(length(lambdas))
for (i in 1:length(lambdas)) {
  tstar=numeric(B)
  for (b in 1:B) {
    xstar=rexp(n, lambdas[i])
    tstar[b]=median(xstar)
  }
  pl=sum(tstar<t)/B
  pr=sum(tstar>t)/B
  p[i]=2*min(pl,pr)
}
p
```

```
##  [1] 0.000 0.000 0.084 0.708 0.028 0.000 0.000 0.000 0.000 0.000 0.000
## [12] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
```

As result, when lambda equals 0.025, p-value $= 0.692 > 0.05$, so the data fits Exp(0.025).

c) To construct a 95% bootstrap confidence interval, first we should do bootstrap simulation to generate

1000 groups $(X_1^*, \ldots, X_N^*)$ and compute $T_i^* = median\,(X_1^*, \ldots, X_N^*)$. With the formula for the bootstrap confidence interval with confidence $1 - 2\alpha$: $\left[2T - T^*_{(1-\alpha)}, 2T - T^*_{(\alpha)}\right]$, I can now construct a 95% bootstrap confidence interval.

```
B = 1000
medians = numeric(B)
for (b in 1:B) {
  xstar=sample(telephone, size=length(telephone), replace=TRUE)
  medians[b] = median(xstar)
}
Tstar25 = quantile(medians, 0.025)
Tstar975 = quantile(medians, 0.975)
T1 = median(telephone)
c(2*T1-Tstar975,2*T1-Tstar25)
```

```
##  97.5%   2.5%
## 17.110 36.745
```

d) For an exponential distribution, we have $E[X] = \frac{1}{\lambda}$. When applying bootstrap to simulate central limit theorem to an exponential distribution, we could expect $\hat{\lambda} = \frac{1}{\bar{X}}$.

```
B = 1000
sample_means = numeric(B)
medians = numeric(B)
for (b in 1:B) {
  xstar = sample(telephone, size=length(telephone), replace=TRUE)
  sample_means[b] = mean(xstar)
  medians[b] = median(xstar)
}
central = mean(sample_means)
lambda = 1 / central
lambda
```

```
## [1] 0.02210621
```

```
Tstar25 = quantile(medians, 0.025)
Tstar975 = quantile(medians, 0.975)
T1 = median(telephone)
c(2*T1-Tstar975,2*T1-Tstar25)
```

```
##    97.5%     2.5%
## 17.88550 36.71025
```

Finally we got $\lambda = 0.022$, and CI for population median is [17.88550, 36.71025]. In conlusion the λ of c) and d) are quite same(0.025 vs 0.022), and CI c) and d) are nearly the same.

e) We have chosen a sign test to verify wheter the median is bigger or equal to 40, and wheter the probability less than 10 is at most 25%.

```
binom.test(sum(telephone>=40),length(telephone),p=0.5)[[3]]
```

```
## [1] 0.07091956
```

```
binom.test(sum(telephone<10),length(telephone),p=0.25, alternative='greater')[[3]]
```

```
## [1] 0.7714992
```

The p-value of first test $0.0709 > 0.05$. Conclusion: H0 is not rejected, median bill is bigger or equal to 40 euro. The p-value of first test $0.7715 > 0.05$. Conclusion: H0 is not rejected, the fraction of bills less than 10

euro is at most 25%.

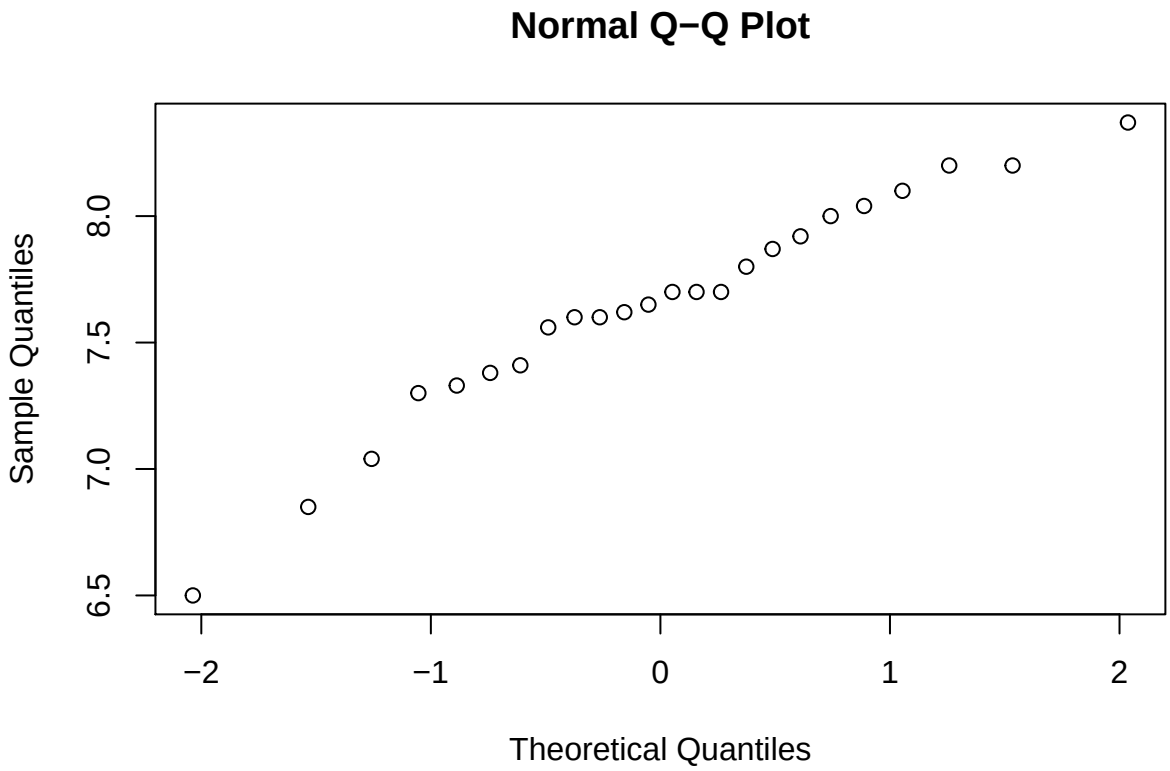
Exercise 4

a)

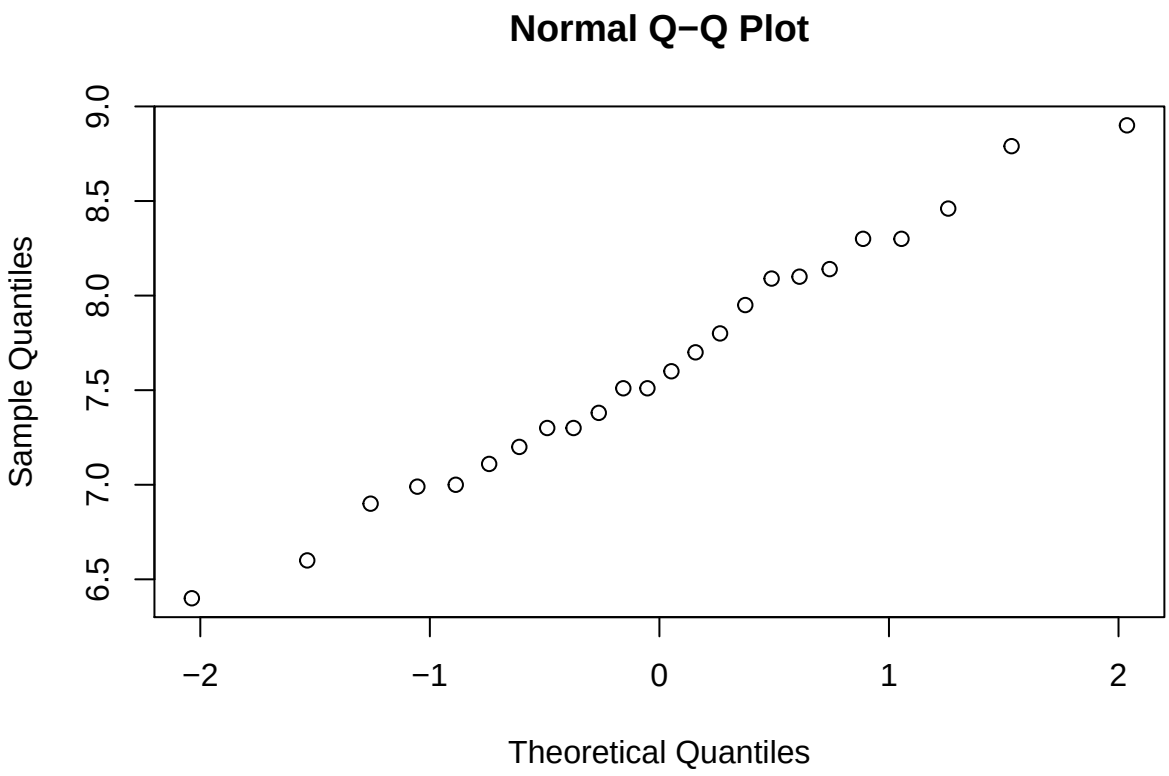
```
run = read.table('run.txt')
cor.test(run$before, run$after)
```

```
##
##  Pearson's product-moment correlation
##
## data:  run$before and run$after
## t = 3.8944, df = 22, p-value = 0.00078
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.3171271 0.8286612
## sample estimates:
##      cor
## 0.638803
```

```
qqnorm(run$before)
```




```
qqnorm(run$after)
```




```
shapiro.test(run$before)[[2]]
```

```
## [1] 0.4168152
```

```
shapiro.test(run$after)[[2]]
```

```
## [1] 0.9463846
```

For both two columns' data are nomally distributed, we could use Pearon's to test whether run times before drink and after are correlated, and finally we got p-value = 0.00078, which is much smaller than 0.05.

Moreover, we ran Shapiro-Wilk normality test and drew QQ-Plot to check both the "before runing data" and the "after running data"'s normlity.

As both data Shapiro test p-value results are bigger than 0.05 and QQ-Plots' dots are both nearly in a line, both tow columns' data are normally distributed.

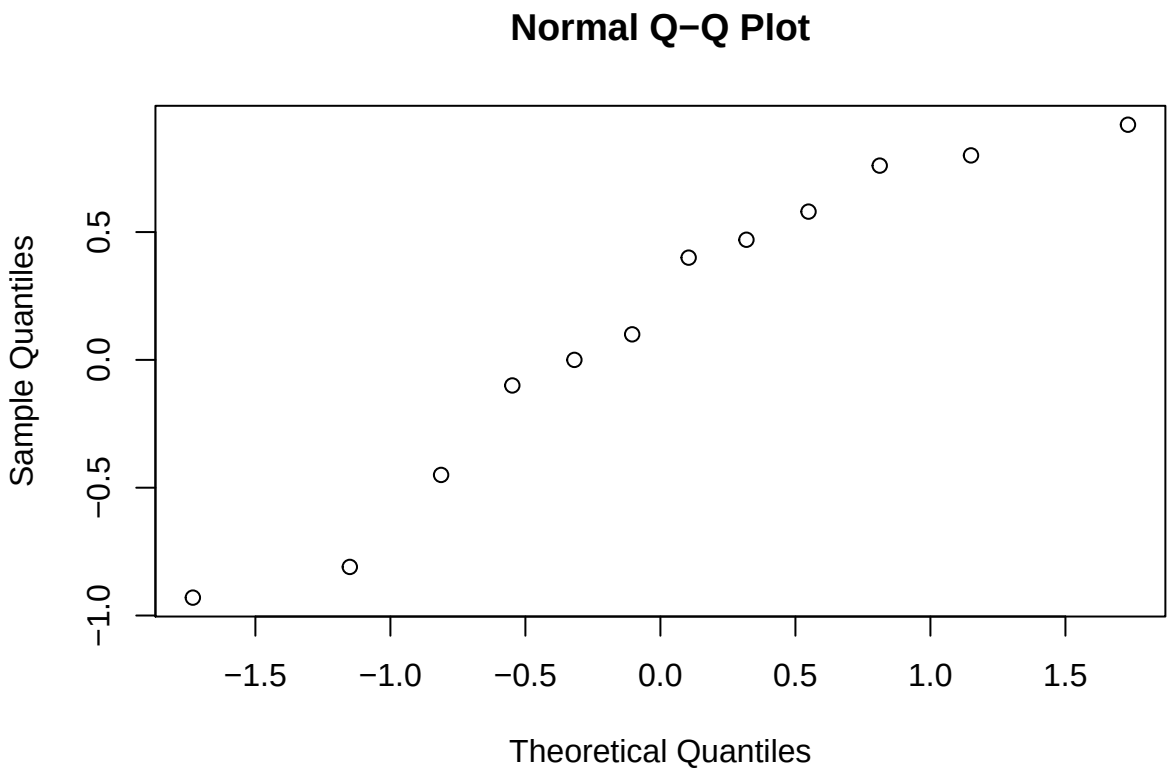
Conclusion: there is significant correlation, given dataset's normality.

b) For difference in speed test we will use t-tset in both softdrink and the energy drink conditions. The test null hypothesis: $H_0 : \mu_{before} = \mu_{after}$, and alternative hypothesis: $\mu_{before} \neq \mu_{after}$.

```
lemo = run[run$drink=='lemo', ]
t.test(lemo$before, lemo$after, paired = TRUE)[[3]]
```

```
## [1] 0.4373423
```

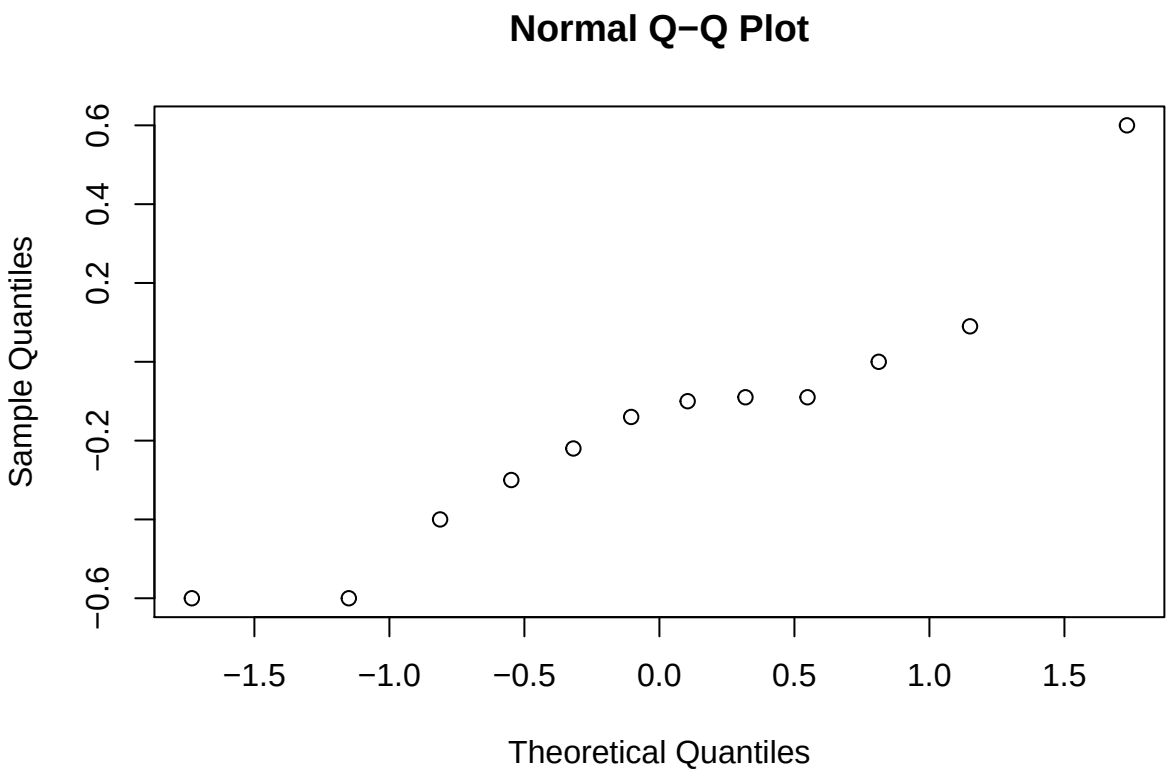
```r
qqnorm(lemo$after - lemo$before)
```




```r
energy = run[run$drink=='energy', ]
t.test(energy$before, energy$after, paired = TRUE)[[3]]
```

```
## [1] 0.1263962
```

```r
qqnorm(energy$after - energy$before)
```



From the paired t-test's requirement, difference between run before and run after should be normally distributed, however from the QQ-plot it shows that neither soft drink' nor energy drink's differences are normally distributed. So we will try to use permutation tests, which normality of data differencee is not required.

```
 mystat=function(x,y) {mean(x-y)}
B=1000
tstar=numeric(B)
for (i in 1:B)
{
 lemonstar=t(apply(cbind(lemo$before,lemo$after),1,sample))
 tstar[i]=mystat(lemonstar[,1],lemonstar[,2])
}
 myt=mystat(lemo$before,lemo$after)
 pl=sum(tstar<myt)/B
 pr=sum(tstar>myt)/B
 p=2*min(pl,pr)
 p
```

```
## [1] 0.406
```

```
mystat=function(x,y) {mean(x-y)}
B=1000
tstar=numeric(B)
for (i in 1:B)
{
 lemonstar=t(apply(cbind(energy$before,energy$after),1,sample))
 tstar[i]=mystat(lemonstar[,1],lemonstar[,2])
}
 myt=mystat(energy$before,energy$after)
 pl=sum(tstar<myt)/B
 pr=sum(tstar>myt)/B
```

```
p=2*min(pl,pr)
p
```

```
## [1] 0.112
```

Both two permutation tests results (softdrink: 0.406 and energy: 0.112) are bigger than 0.05, which means there are no big speed difference before drink and and after, no matter we test on which drink.

A more interesing outcome is t.test of softdrink's p-value = 0.4373423 > 0.05 and t.test of energy's p-value = 0.1263962 > 0.05, which means t-test results also show no big speed difference before drink and and after, both in softdrink condition and energy drink condition.

c) We chose permutation test and $T_i^* = mean(X^* - Y^*)$ to test whether these time differences are effected by the type of drink.

```
lemo$difference = lemo$before - lemo$after
energy$difference = energy$before - energy$after
mystat=function(x,y) {mean(x-y)}
B=1000
tstar=numeric(B)
for (i in 1:B) {
  adiffstar=t(apply(cbind(lemo$difference,energy$difference),1,sample))
  tstar[i]=mystat(adiffstar[,1],adiffstar[,2])
}
myt=mystat(lemo$difference,energy$difference)
pl=sum(tstar<myt)/B
pr=sum(tstar>myt)/B
p=2*min(pl,pr)
p
```

```
## [1] 0.158
```

p-value = 0.158 > 0.05, hence the is no difference between the two types of drinks.

d) Whether drinking the energy drink speeds up the running have another important attribute, that is the test time after drinking. Maybe energy drink will have great influence just in a very short time, may be 5 min, after it drinked. So more test cases on test time are needed. This is the similar objection to the the experiment design in c).

Exercise 5

a)

```
meatmeal = chickwts[chickwts$feed == 'meatmeal', ]$weight
sunflower = chickwts[chickwts$feed == 'sunflower', ]$weight
t.test(meatmeal, sunflower)[[3]]
```

```
## [1] 0.04441462
```

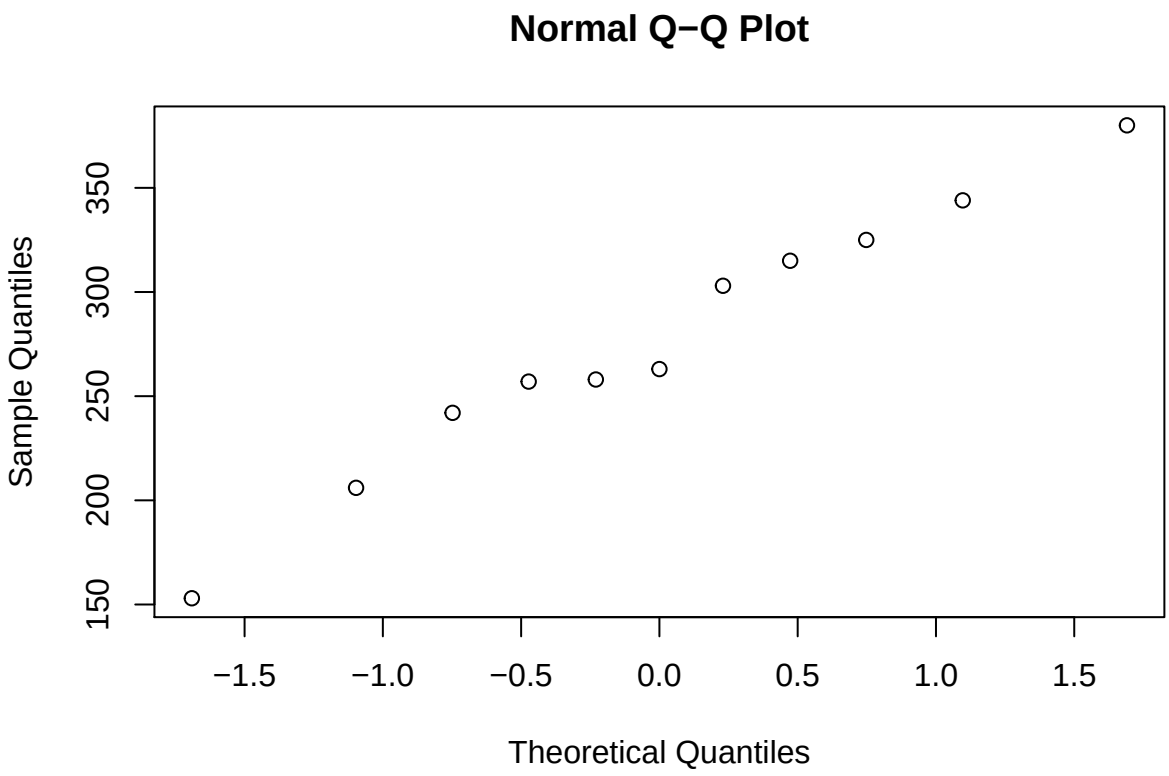
```
wilcox.test(meatmeal, sunflower)[[3]]
```

```
## [1] 0.06881704
```

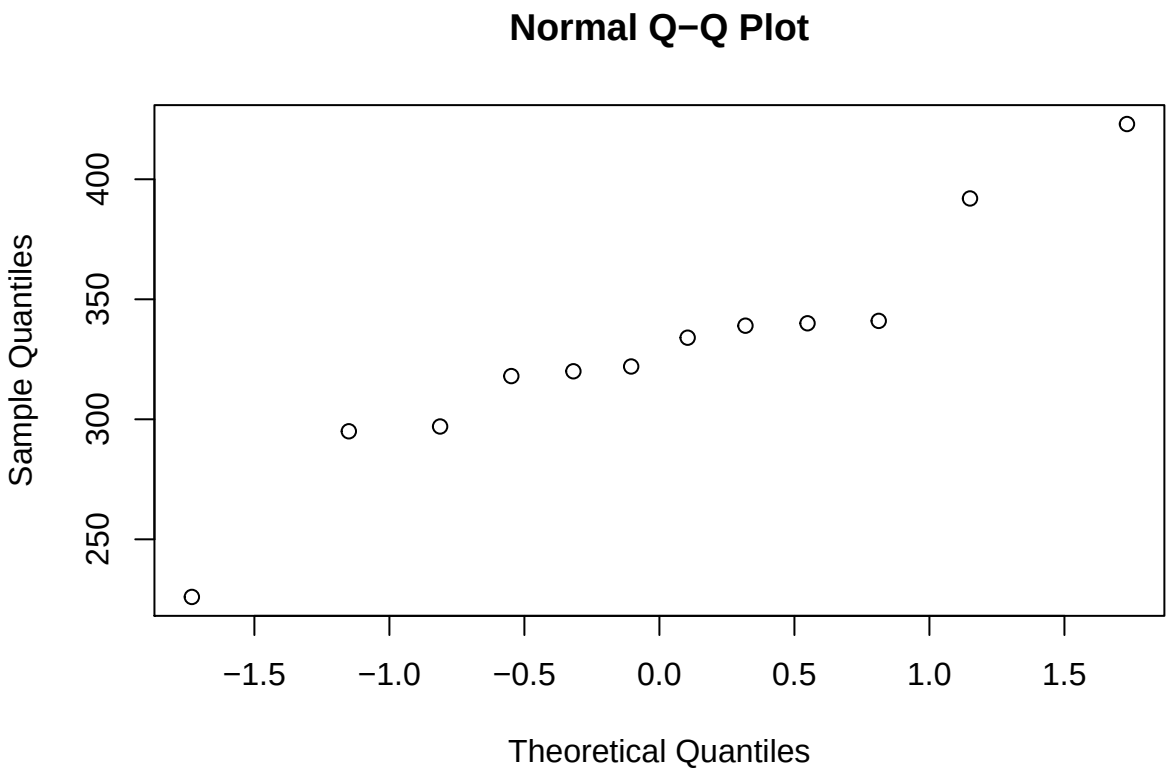
```
ks.test(meatmeal, sunflower)[[2]]
```

```
## [1] 0.108496
```

```
qqnorm(meatmeal)
```




```
qqnorm(sunflower)
```



For paired t-test argues that the two outcomes are measured on the same experimental unit, but it is not in this case, so the data is not paired.

After we ran the tests, we got t-test reulst: 0.04441462, Mann-Whitney test result: 0.06881704, Kolmogorov-

Smirnov test result: 0.108496.

From, t-test result, we can assume that meatmeal condition and sunflower condition has great difference of mean weight, but this assumption is not correct. This is becuase from QQ-plot of sunflower we can find that the data is not normally distributed.

Both Mann-Whitney test and Kolmogorov-Smirnov test show that there are no big difference between meatmeal condition and sunflower condition.

But why MW got bigger p-value than KS's p-value?The KS test is sensitive to any differences in the two distributions. Substantial differences in shape, spread or median will result in a small P value. In contrast, the MW test is mostly sensitive to changes in the median. This means in this question we'd better take MW's p-value.

b)

```
chickwtsaov=lm(weight~feed,data=chickwts)
anova(chickwtsaov)[[5]][1]
```

```
## [1] 5.93642e-10
```

```
summary(chickwtsaov)
```

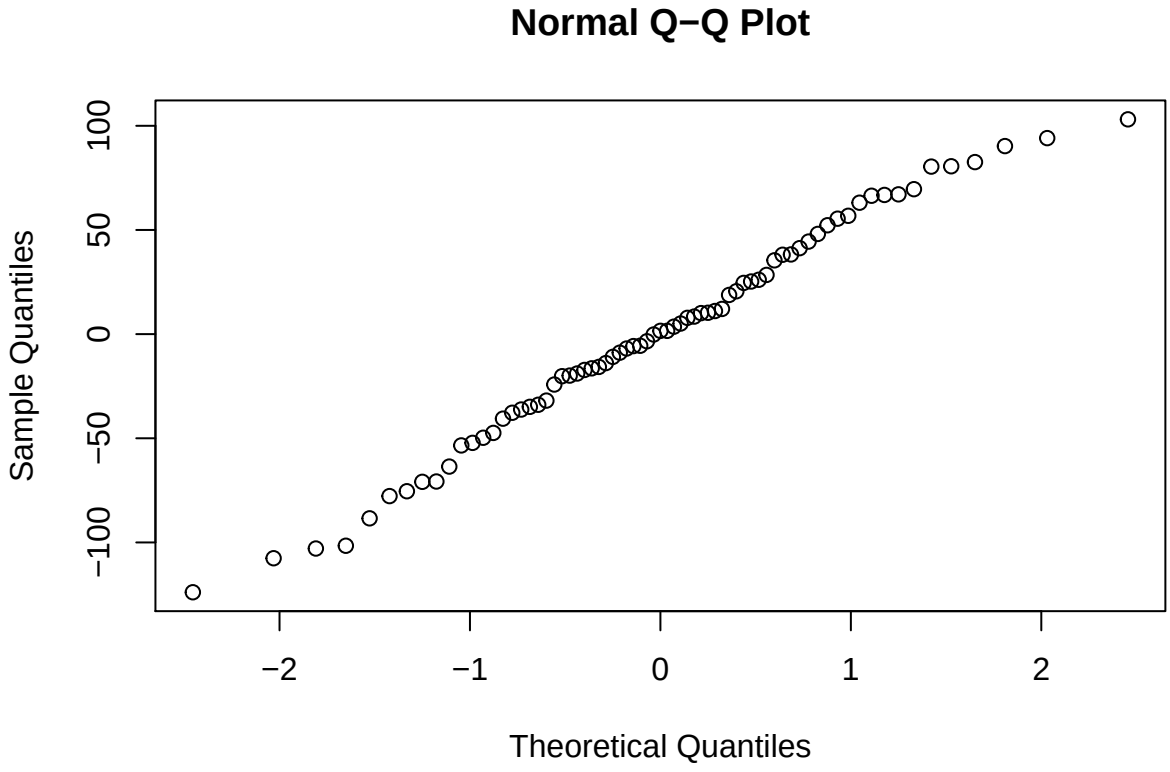
```
##
## Call:
## lm(formula = weight ~ feed, data = chickwts)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -123.909  -34.413    1.571   38.170  103.091
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    323.583     15.834  20.436  < 2e-16 ***
## feedhorsebean -163.383     23.485  -6.957 2.07e-09 ***
## feedlinseed   -104.833     22.393  -4.682 1.49e-05 ***
## feedmeatmeal   -46.674     22.896  -2.039 0.045567 *
## feedsoybean    -77.155     21.578  -3.576 0.000665 ***
## feedsunflower    5.333     22.393   0.238 0.812495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.85 on 65 degrees of freedom
## Multiple R-squared:  0.5417, Adjusted R-squared:  0.5064
## F-statistic: 15.36 on 5 and 65 DF,  p-value: 5.936e-10
```

After ran the script, we got one-way ANOVA's p-value=5.93642e-10 < 0.05, so we can reach a conclusion that there do have difference between each group.

The summary of ANOVA shows estimated chick weights for each feed supplements are 323.583(casein), -163.383+323.583=160.2(horsebean), 218.75(linseed), 276.909(meatmeal), 246.428(soybean) and 328.916(sunflower).

In conclusion sunflower is the best feed supplement.

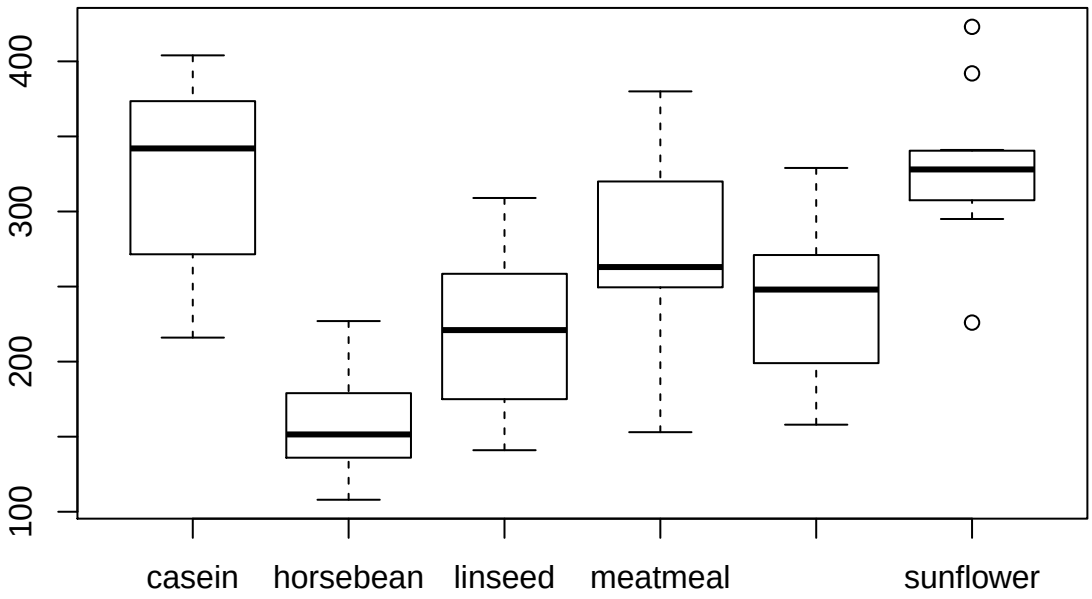
```
par(mfrow=c(1,1)); qqnorm(residuals(chickwtsaov))
```



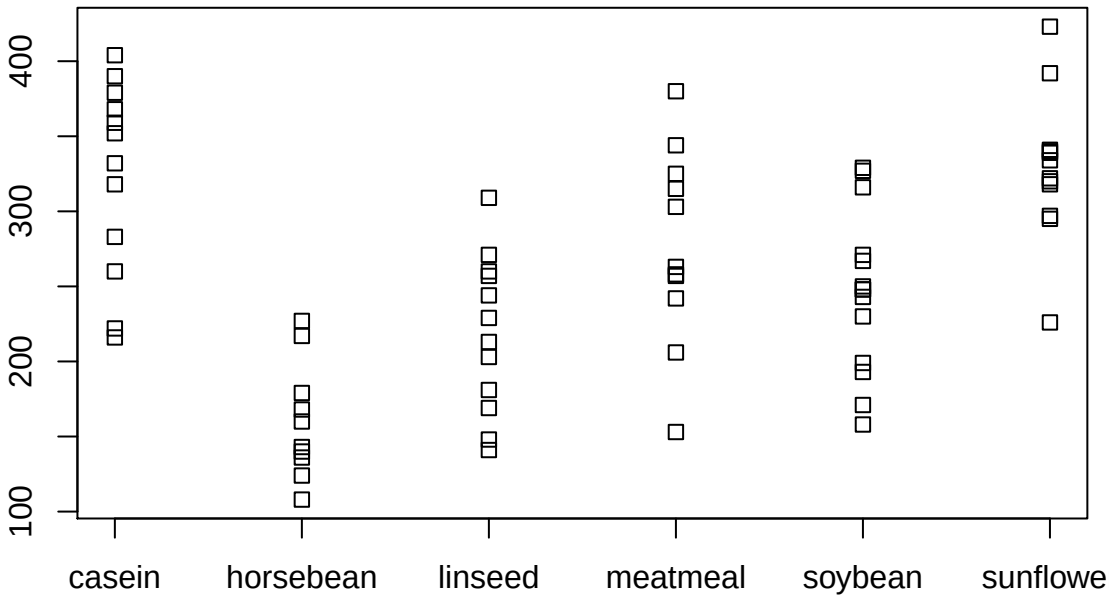
Finally we need to check the assumption of normality of the populations. We used residuals data to draw QQ-plots, and all data are in a line, which is normality.

c)

```
X <- split(chickwts$weight, chickwts$feed)
boxplot(X)
```




```
stripchart(X,vertical=TRUE)
```



I choose boxplot and strip to check the ANOVA model assumptions. In boxplot graph both casein and sunflower condition got the highest middian. From the strip chart we found that casein condition distributed more widely, in contranst sunflower condition's data is more concentrated. These mean out conclusion in b) is correct.

d)

```
attach(chickwts)
kruskal.test(weight,feed)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  weight and feed
## Kruskal-Wallis chi-squared = 37.343, df = 5, p-value = 5.113e-07
```

The Kruskal-Wallis test p-value is 5.113e-07$<$ 0.05, so we can reach a conclusion that there do have difference between each group. Furthermore, this conclusion is the same as b).