EDDA - Assignment 1

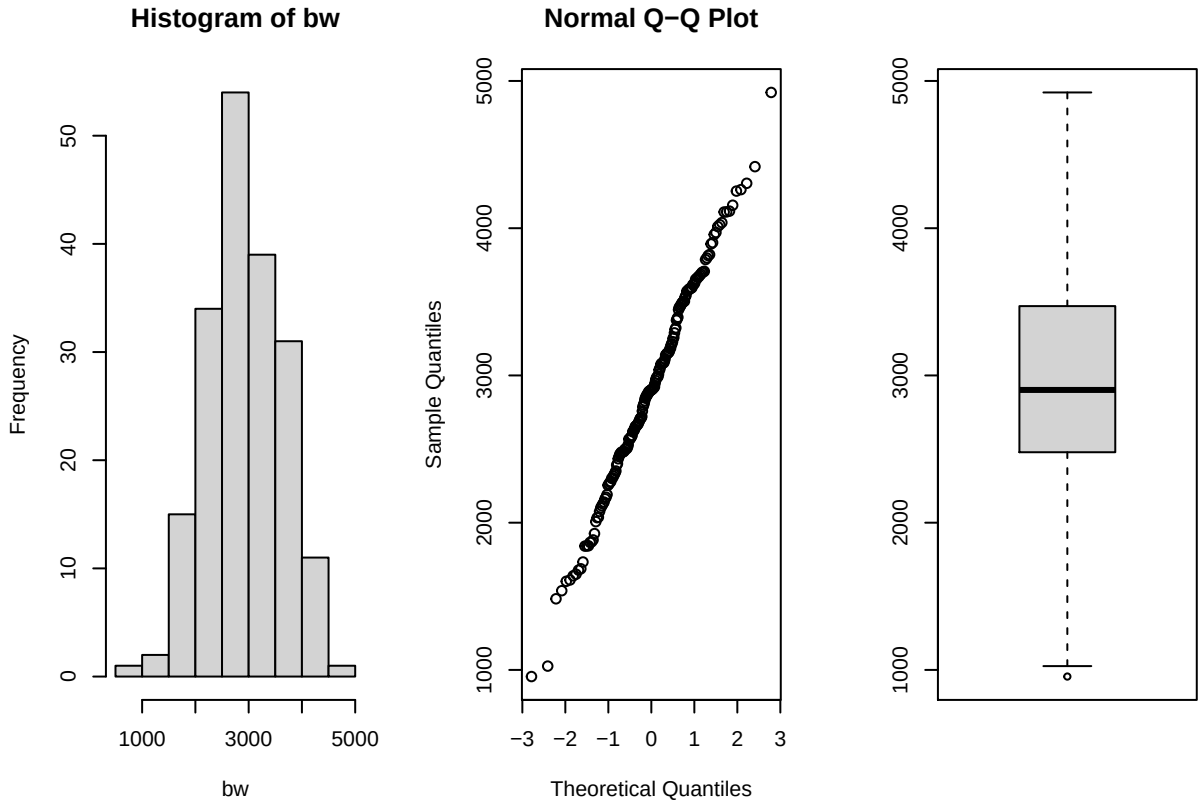
Exercise 1

The data set birthweight.txt contains the birthweights of 188 newborn babies. We are interested in finding the underlying (population) mean mu of birthweights.

a) Check normality of the data. Compute a point estimate for mu. Derive, assuming normality (irrespective of your conclusion about normality od the data), a bounded 90% confidence interval for mu.

To check normality for the data we use a qqplot, historgram, box plot and shapiro-wilks test.

```
par(mfrow=c(1,3))
data=read.table(file="data/birthweight.txt",header=TRUE)

bw = data$birthweight
hist(bw)
qqnorm(bw)
boxplot(bw)
```



```
shapiro.test(bw)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  bw
## W = 0.99595, p-value = 0.8995
```

The graphical methods show that the data is normal. The Shapiro-Wilk test reinforces this assumption as it shows a p-value of 0.8995, meaning that the H0 is not rejected and therefore the data is normal. Furthermore, a point estimate for mu is conducted along side a 90% confidence interval.

```
m = mean(bw)
sd = sd(bw)
n = length(bw)
error = qnorm(0.95)*sd/sqrt(n)
ci = c(m-error, m+error)
m
```

```
## [1] 2913.293
```

```
ci
```

```
## [1] 2829.618 2996.967
```

b) An expert claims that the mean birthweight is bigger than 2800, verify this claim by using at-test.What is the outcome of the test if you take alpha = 0.1? And other values of alpha?

A t-test is performed to verify the claim that the mean birthweight is bigger than 2800. The t-test shows a p-value of 0.014. This means that this claim is significant for an alpha of 0.1. The claim is significant for all alpha's above 0.014 and insignificant for alpha's below 0.014.

```
t.test(bw, mu=2800, alternative = "greater", conf.level = 0.95)
```

```
##
##  One Sample t-test
##
## data:  bw
## t = 2.2271, df = 187, p-value = 0.01357
## alternative hypothesis: true mean is greater than 2800
## 95 percent confidence interval:
##  2829.202      Inf
## sample estimates:
## mean of x
##  2913.293
```

c) In the R-output of the test from b), also a confidence interval is given, but why is it different from theconfidence interval found in a) and why is it one-sided?

The confidence interval interval is different because the one-sample t-test returns a 95% confidence interval while a 90% confidence interval is conducted in 1b). The confidence interval is one sided because the critical area of the weight distribution is compared to a mean where it is greater than 2800, but not both greater and less than 2800.

Exercise 2

a)

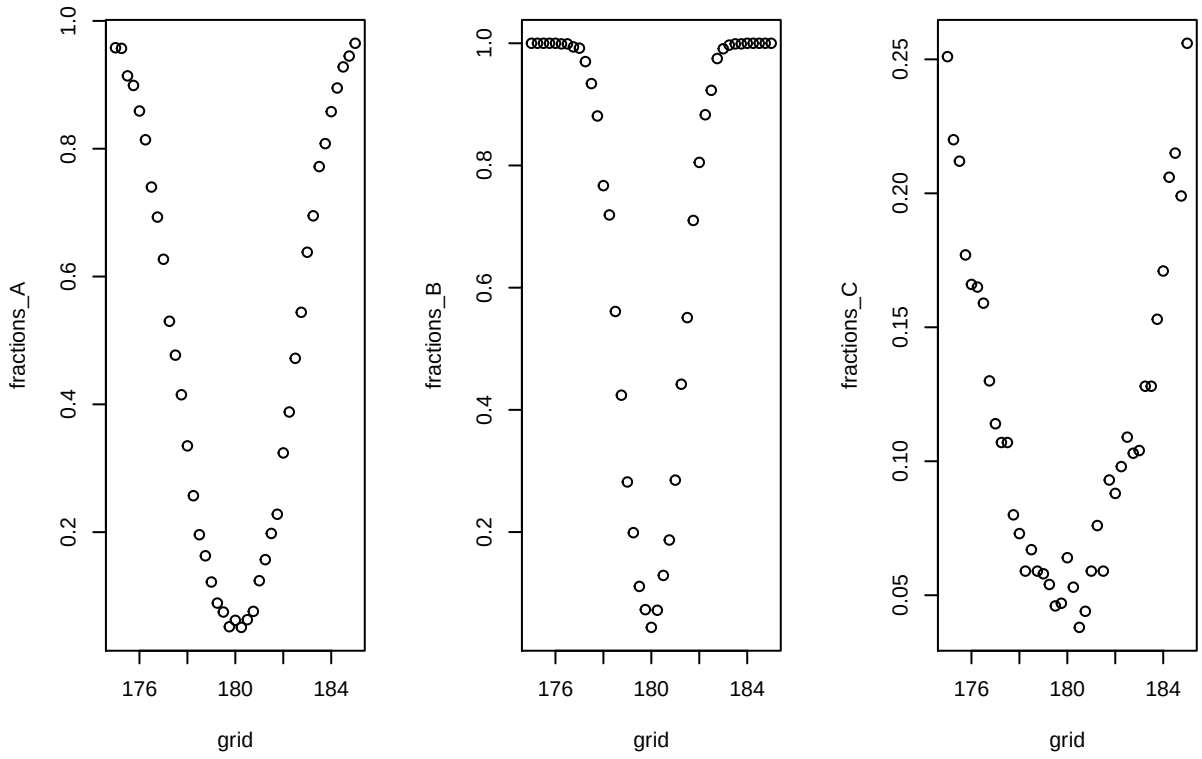
```
n <- m <- 30
mu <- 180
nu <- 175
sd <- 5
grid <- seq(175,185, by=0.25)

power_function<-function(grid,n,m,mu,sd) {
  B <- 1000
  p <- numeric(B)
  G <- length(grid)
  fractions <- numeric(G)
  for (grid_nu in 1:G){
    p <- numeric(B)
    for (b in 1:B){
      x <- rnorm(n,mu,sd)
      y <- rnorm(m,grid[grid_nu],sd)
      p[b] <- t.test(x,y, var.equal = TRUE)[[3]]
    }
    fractions[grid_nu] <- mean(p<0.05)
  }
  return(fractions)
}

fractions_A <- power_function(grid,n,m,mu,sd)
```

b)

```
n <- m <- 100
mu <- 180
sd <- 5

fractions_B <- power_function(grid,n,m,mu,sd)
```

c)

```
n <- m <- 30
mu <- 180
sd <- 15

fractions_C <- power_function(grid,n,m,mu,sd)
par(mfrow=c(1,3))
plot(grid,fractions_A)
plot(grid,fractions_B)
plot(grid,fractions_C)
```



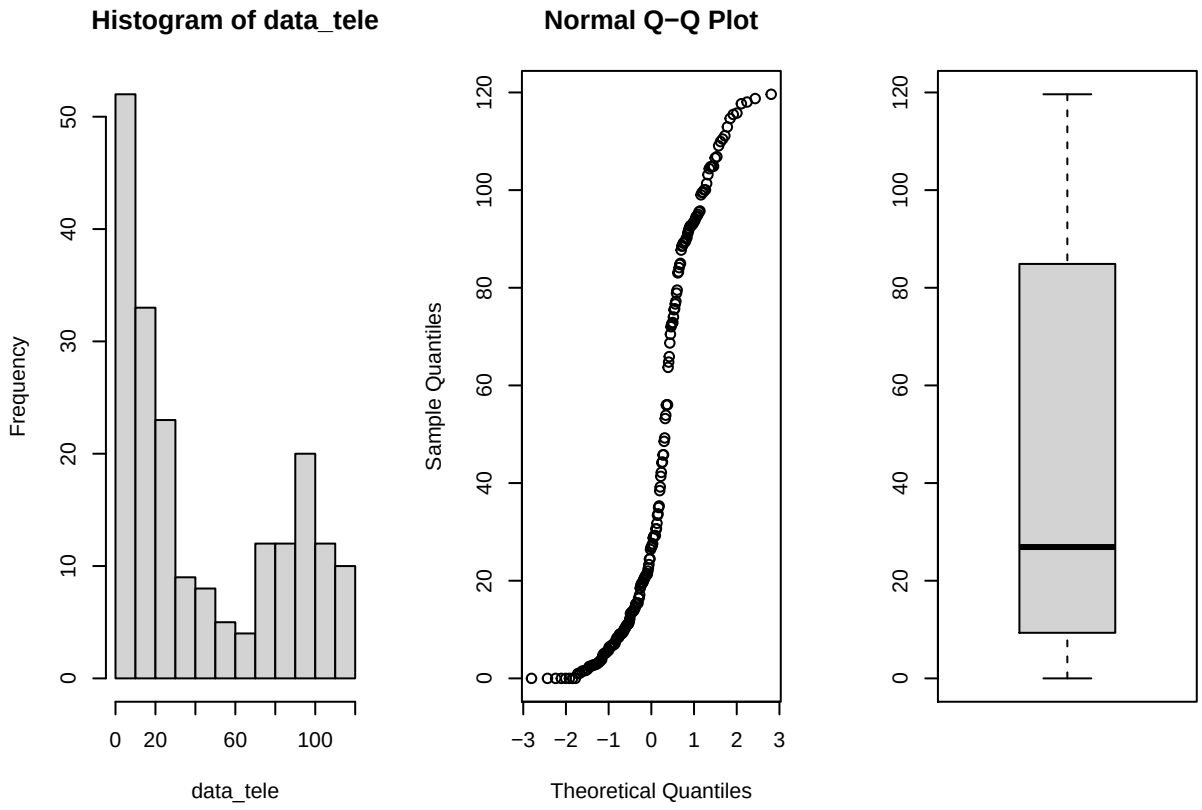
d)

The more datapoints seems to have an influence on the narrowness of the plot. Furthermore, a bigger std gives a more wider distribution of fractions as presented in the plot of C.

Exercise 3

a)

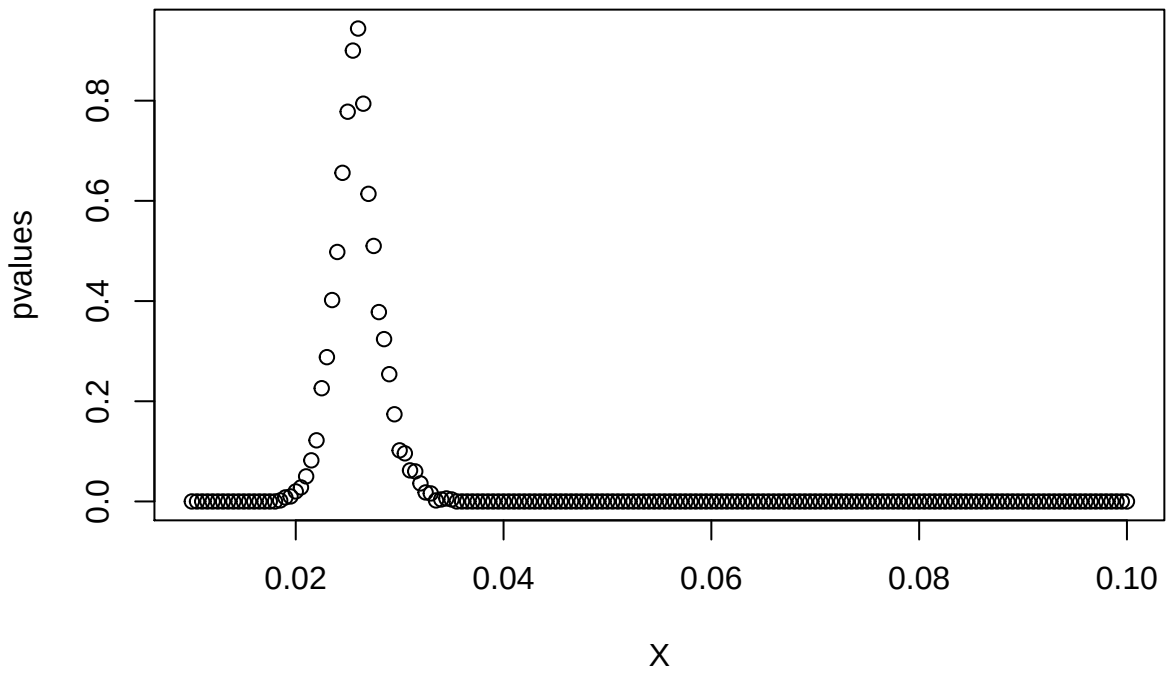
```
data<-read.table(file="data/telephone.txt",header=TRUE)
data_tele <- data$Bills
par(mfrow=c(1,3))
hist(data_tele)
qqnorm(data_tele)
boxplot(data_tele)
```



The data seems oddly distributed with two subpeaks, would have expected a more normally distributed set. Therefore perhaps a good idea if the manager arranges the prices better.

b)

```
X <- seq(0.01, 0.1, 0.0005)
pvalues <- c()
t <- median(data_tele)
for (x in X){
  B <- 1000
  tstar <- numeric(B)
  n <- length(data_tele)

  for (i in 1:B){
    xstar <- rexp(n,x)
    tstar[i] <- median(xstar)
  }
  pl<-sum(tstar<t)/B
  pr<-sum(tstar>t)/B
  p<-2*min(pl,pr)
  pl;pr;p
  pvalues <- c(pvalues,p)
}
#pvalues
plot(X, pvalues)
```



There exist an Exp function that fits the hypothesis

c)

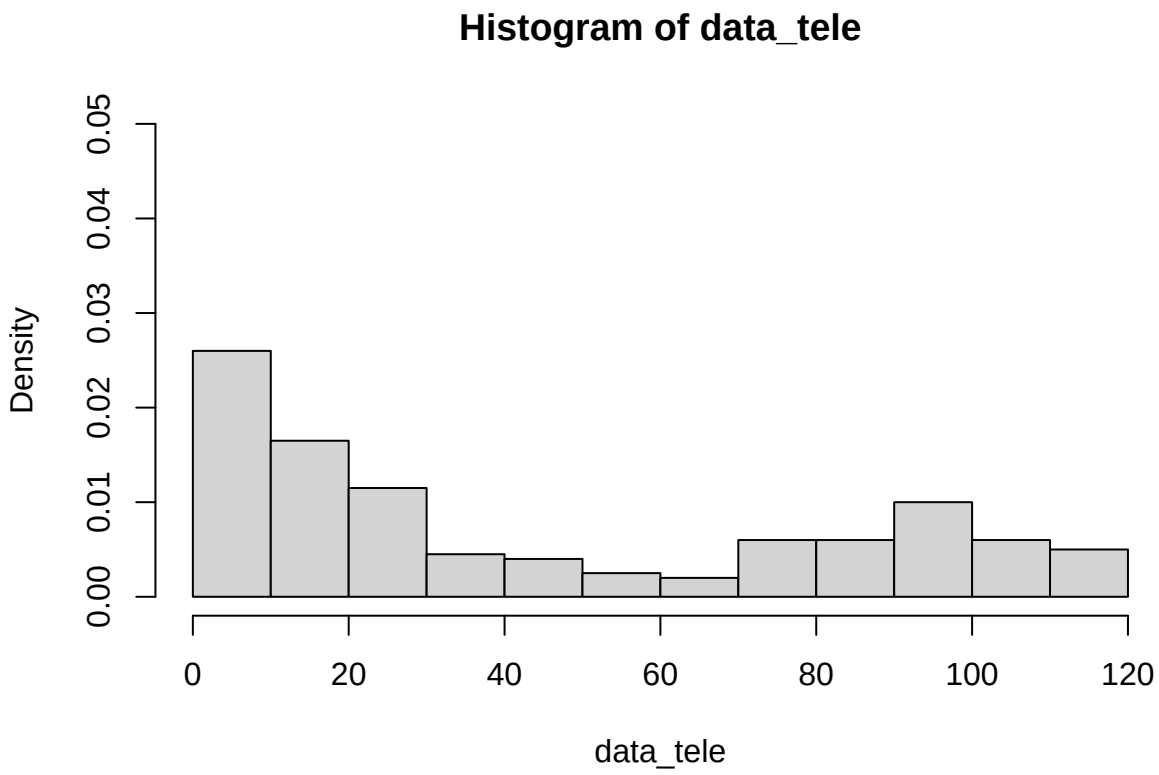
```
B <- 1000
T1 <- median(data_tele)
Tstar <- numeric(B)
for (i in 1:B){
  Xstar <- sample(data_tele,replace=TRUE)
  Tstar[i] <- median(Xstar)
}
Tstar25 <- quantile(Tstar,0.025)
Tstar975 <- quantile(Tstar, 0.975)

T1
```

```
## [1] 26.905
```

```
c(2*T1-Tstar975, 2*T1-Tstar25)
```

```
## 97.5%  2.5%
## 18.65 33.34
```

```r
hist(data_tele, prob=T, ylim=c(0,0.05))
x<-seq(0,max(data_tele),length=1000)
lines(x,exp(x),type="l",col="blue",lwd=2)
```



d)

```r
max_index <- which.max(pvalues)

opt_Lambda <- X[max_index]
```

The variable opt_Lambda is the optimal lambda value with the highest P-value.

e)

```r
bill_bigeq40 <- sum(data_tele>=40)
bill_smal40 <- sum(data_tele<40)

binom.test(bill_bigeq40, length(data_tele),p=0.5)
```

```
##
```

```
##  Exact binomial test
##
## data:  bill_bigeq40 and length(data_tele)
## number of successes = 83, number of trials = 200, p-value = 0.0194
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.3459337 0.4866247
## sample estimates:
## probability of success
##                  0.415
```

```
binom.test(bill_smal40, length(data_tele),p=0.5)
```

```
##
##  Exact binomial test
##
## data:  bill_smal40 and length(data_tele)
## number of successes = 117, number of trials = 200, p-value = 0.0194
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.5133753 0.6540663
## sample estimates:
## probability of success
##                  0.585
```

```
bill_less10 <- sum(data_tele < 10)
bill_less10/length(data_tele)
```

```
## [1] 0.26
```

Exercise 4

a)

Disregarding the type of drink, test whether the run times before drink and after are correlated.

```
data <- read.table(file="data/run.txt",header=TRUE)
cor(data$before, data$after)
```

```
## [1] 0.638803
```

Run times before and after the drink seem to be positively correlated.

b)

```r
# calculate differences
data <- data %>%
  mutate(diff = before - after)

# filter for lemo

lemo <- data %>%
  filter(drink == "lemo")

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 equal to 0
## 95 percent confidence interval:
##  -0.5409781  0.2509781
## sample estimates:
## mean of the differences
##                  -0.145
```

```r
# filter for energy

energy <- data %>%
  filter(drink == "energy")

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 equal to 0
## 95 percent confidence interval:
##  -0.05101059  0.35934392
## sample estimates:
## mean of the differences
##               0.1541667
```

For both energy and soft-drink groups there does not seem to be a significant difference in running times.

c)

For each pupil compute the time difference between the two running tasks. Test whether these time differences are effected by the type of drink.

```r
# perform t-test

t.test(lemo$diff, energy$diff)
```

```
##
##  Welch Two Sample t-test
##
## data:  lemo$diff and energy$diff
## 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 is > 0.05 therefore the means of the two populations are not significantly different.

d)

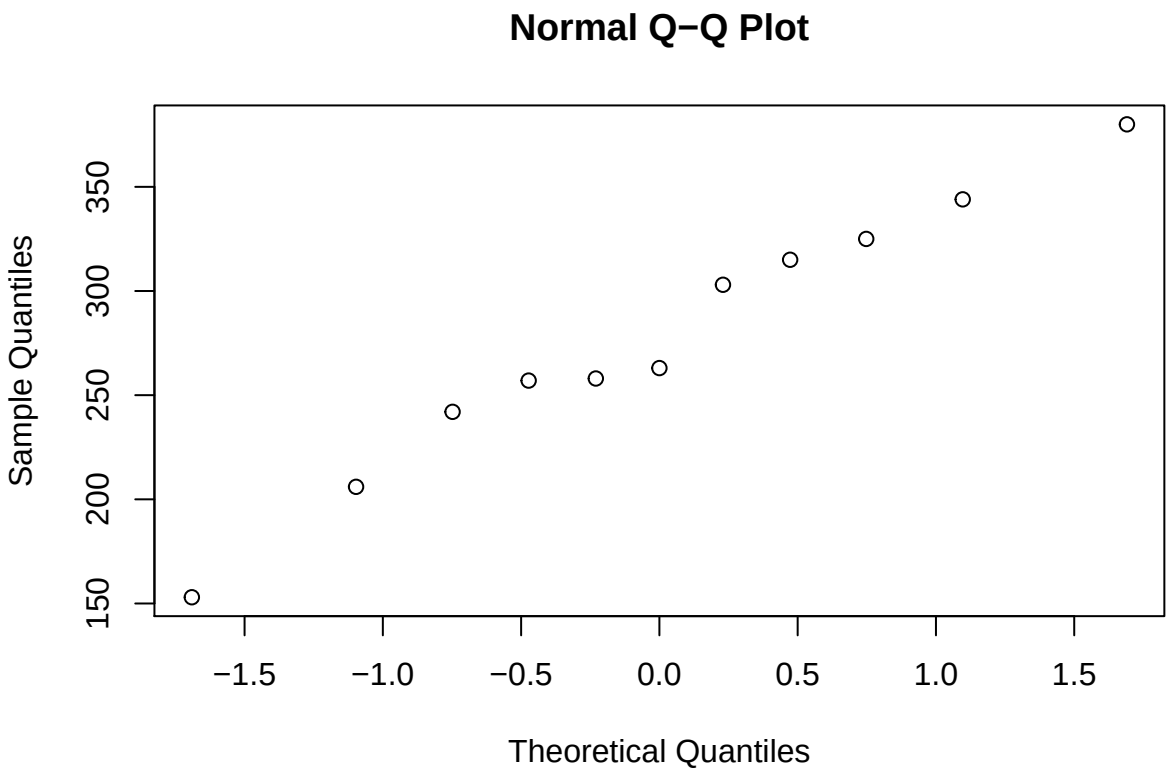
Can you think of a plausible objection to the design of the experiment in b) if the main aim was to test whether drinking the energy drink speeds up the running? Is there a similar objection to the design of the experiment in c)? Comment on all your fndings in this exercise.

Exercise 5

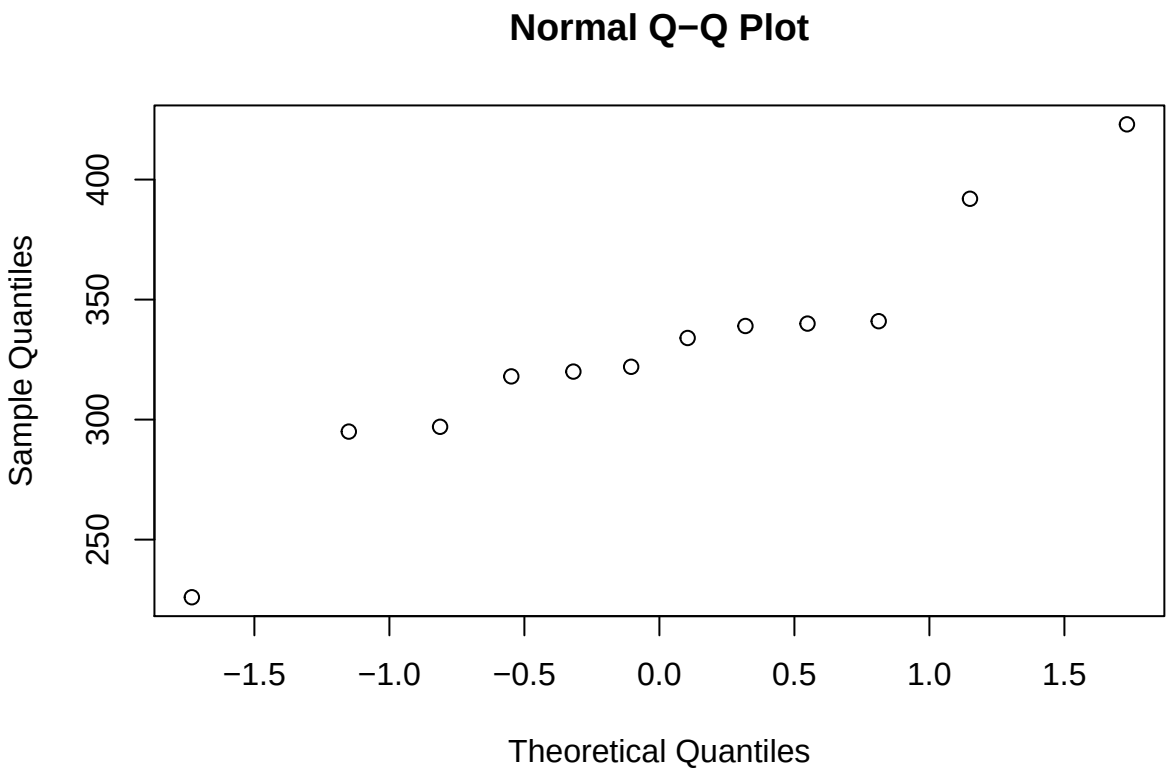
a)

Test whether the distributions of the chicken weights for meatmeal and sunflower groups are different by performing three tests: the two samples t-test (argue whether the data are paired or not), the Mann-Whitney test and the Kolmogorov-Smirnov test. Comment on your fndings.

```r
# filter for meatmeal

meatmeal <- chickwts %>%
  filter(feed == "meatmeal") %>%
  select(weight)

# filter for sunflower

sunflower <- chickwts %>%
  filter(feed == "sunflower") %>%
  select(weight)

# check for data normality

qqnorm(meatmeal$weight)
```




```
qqnorm(sunflower$weight)
```




```
# perform t-test, the data is not paired

t.test(meatmeal, sunflower)
```

```
##
##  Welch Two Sample t-test
##
## data:  meatmeal and sunflower
## t = -2.1564, df = 18.535, p-value = 0.04441
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -102.572435   -1.442716
## sample estimates:
## mean of x mean of y
##  276.9091  328.9167
```

```
# Mann-Whitney test

wilcox.test(meatmeal$weight, sunflower$weight)
```

```
##
##  Wilcoxon rank sum exact test
##
## data:  meatmeal$weight and sunflower$weight
## W = 36, p-value = 0.06882
## alternative hypothesis: true location shift is not equal to 0
```

```r
# Kolmogorov-Smirnov test

ks.test(meatmeal$weight, sunflower$weight)
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  meatmeal$weight and sunflower$weight
## D = 0.47727, p-value = 0.1085
## alternative hypothesis: two-sided
```

Data in chickwts is not paired as the "treatment" of different feed was applied to different newly-hatched chicks not the same chick. From t-test we can see that the p-values <0.05, therefore the means between the two groups are significantly different. From Mann-Whitney test we can see that p-value is >0.05 therefore we can not conclude that the medians of the two datasets are different. From Kolgomorov-Smirnov test we can not conclude that the means are different.

b)

Conduct a one-way ANOVA to determine whether the type of feed supplement has an effect on the weight of the chicks. Give the estimated chick weights for each of the six feed supplements. What is the best feed supplement?

```r
chickaov <- lm(weight~feed, data = chickwts)
# performing one-way ANOVA
anova(chickaov)
```

```
## Analysis of Variance Table
##
## Response: weight
##           Df Sum Sq Mean Sq F value    Pr(>F)
## feed       5 231129   46226  15.365 5.936e-10 ***
## Residuals 65 195556    3009
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#extracting more information
summary_table <- summary(chickaov)
knitr::kable(data.frame(summary_table$coefficients), "latex")
```

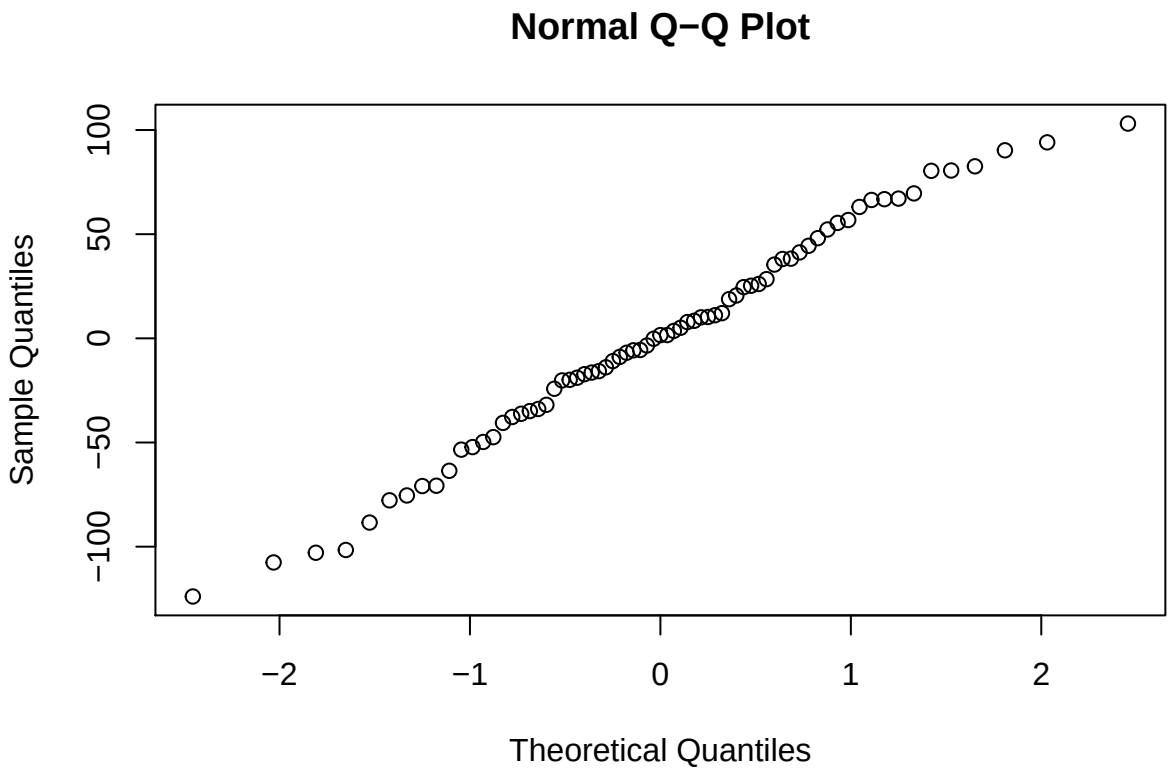
	Estimate	Std..Error	t.value	Pr...t..
(Intercept)	323.583333	15.83391	20.4360920	0.0000000
feedhorsebean	-163.383333	23.48549	-6.9567776	0.0000000
feedlinseed	-104.833333	22.39254	-4.6816194	0.0000149
feedmeatmeal	-46.674242	22.89580	-2.0385502	0.0455667
feedsoybean	-77.154762	21.57799	-3.5756235	0.0006654
feedsunflower	5.333333	22.39254	0.2381746	0.8124949

From the results of one-way ANOVA we can see that the p-values is <0.05 therefore we can conclude that the means between all of the feed varieties are significantly different. From summary statistics it seems that "sunflower" feed is the feed resulting in highest weight. therefore it is the best.

c)

Check the ANOVA model assumptions by using relevant diagnostic tools.

```
# check for normality
qqnorm(chickaov$residuals)
```




```
# check if the variances are equal
chickwts %>%
  group_by(feed) %>%
  summarise(variance = var(weight))
```

```
## # A tibble: 6 x 2
##   feed      variance
## * <fct>        <dbl>
## 1 casein       4152.
## 2 horsebean    1492.
## 3 linseed      2729.
## 4 meatmeal     4212.
## 5 soybean      2930.
## 6 sunflower    2385.
```

From qqplot assumption of normality holds. However the assumption of equal variances does not hold.

d)

Does the Kruskal-Wallis test arrive at the same conclusion about the effect of feed supplement as the test in b)? Explain possible differences between conclusions of the Kruskal-Wallis and ANOVA tests.

```
kruskal.test(weight~feed, data = chickwts)
```

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

With Kruskal-Wallis test we arrive to the same conclusion as with ANOVA.