Assignment 1

Tanjina Islam and Miguel Morales Expósito, group 03

14 February 2018

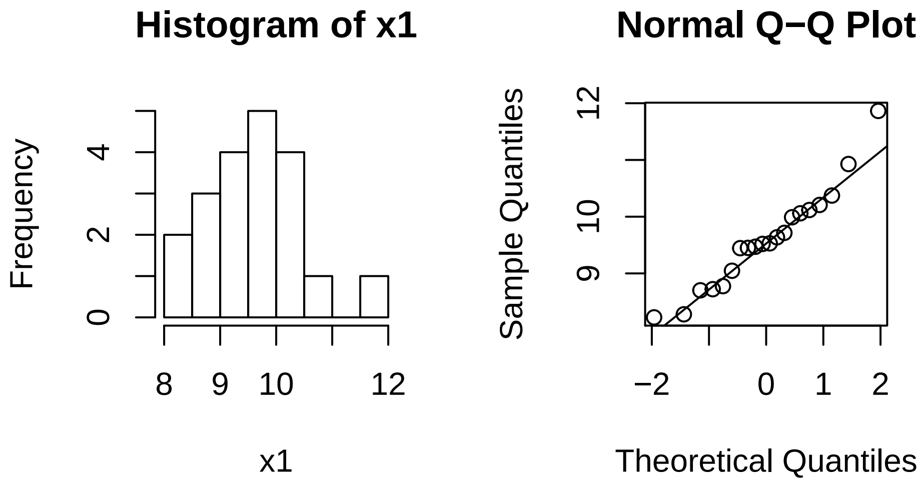
Exercise 1

We load the data from the data source and setup the size of the screen.

```
load(file="assign1.RData")
```

Dataset x1

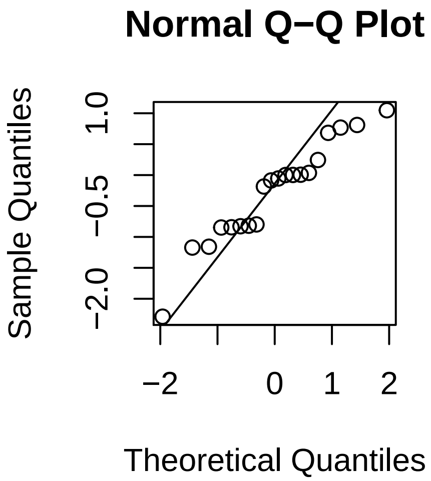
```

hist(x1);
qqnorm(x1);qqline(x1);
```



We can see that the histogram does not show a normal distribution but it is probably because the size of the sample is very small.However, the QQ-plot shows that the distribution is normal.

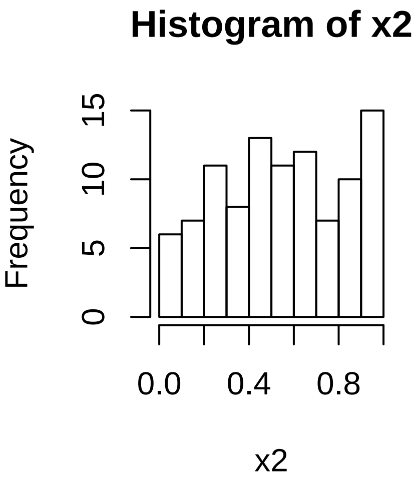
We can see the similarities with a QQ-plot of a normal distribution of the same size.

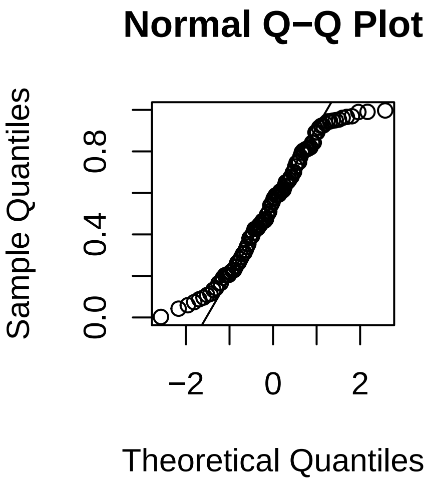
```
qqnorm(rnorm(length(x1)));qqline(rnorm(length(x1)))
```



Dataset x2

```
hist(x2);
qqnorm(x2);qqline(x2)
```

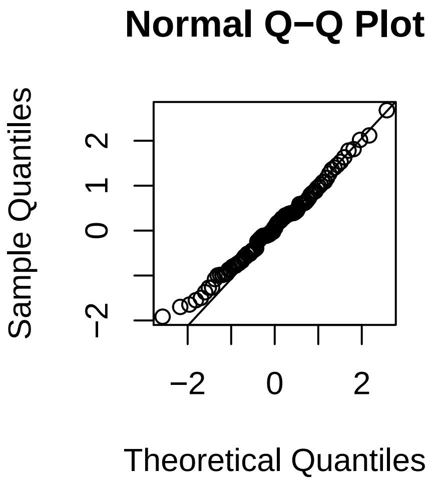




Both the histogram and QQ-plot do not show that the distribution is normal. The QQ-plot shows deviated tails.

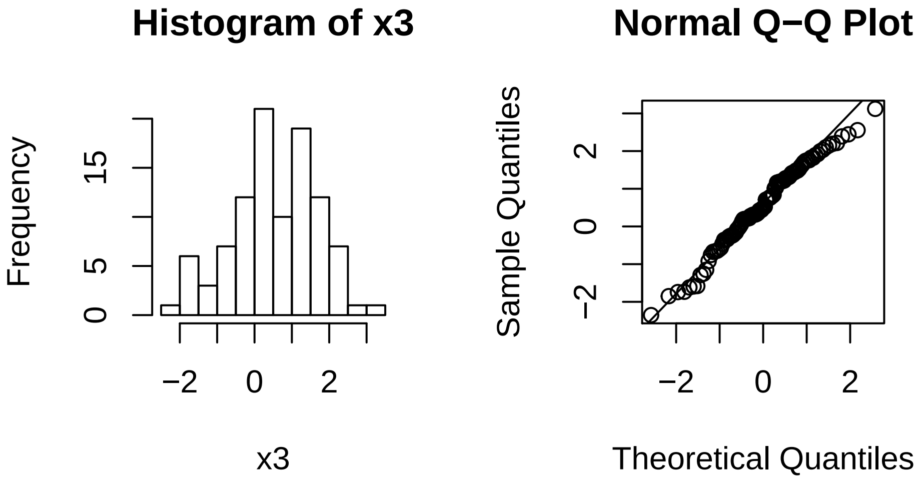
We can compare the QQ-plot to one representing a sample with normal distribution of the same size.

```
qqnorm(rnorm(length(x2)));qqline(rnorm(length(x2)))
```



Dataset x3

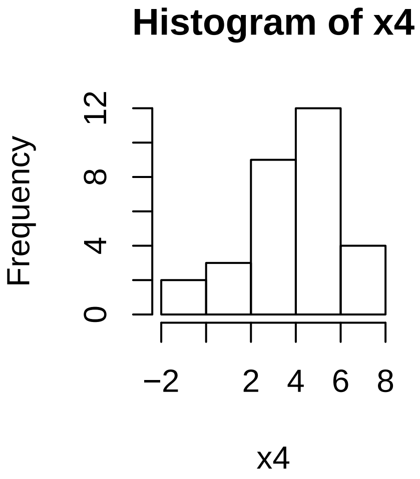
```
hist(x3);
qqnorm(x3);qqline(x3)
```

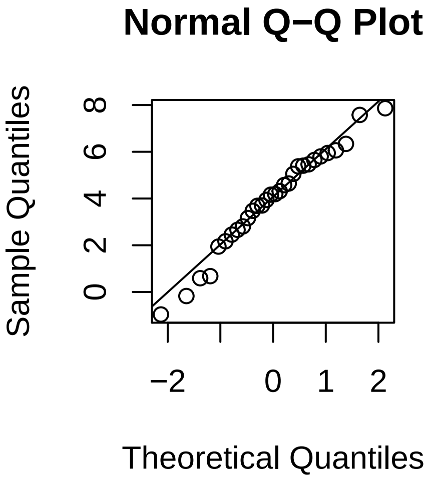


Both the histogram and QQ-plot show that the sample follows a normal distribution.

Dataset x4

```r
hist(x4);
qqnorm(x4);qqline(x4)
```

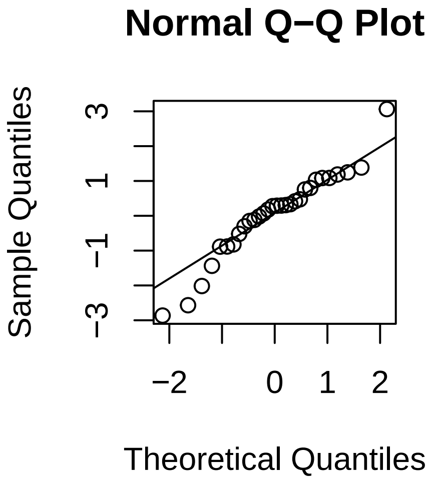




The histogram does not show a normal distribution but the QQ-plot does.

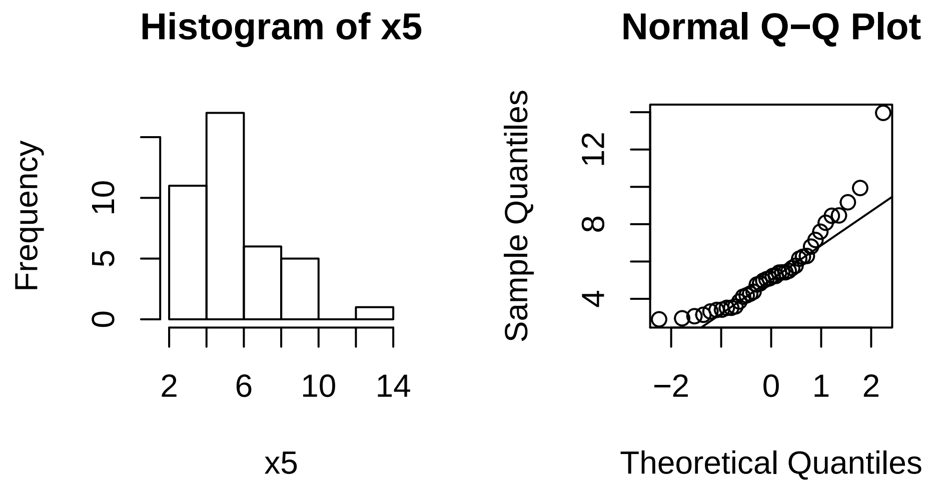
We can see the similarities with a QQ-plot of a normal distribution of the same size.

```r
qqnorm(rnorm(length(x4)));qqline(rnorm(length(x4)))
```



Dataset x5

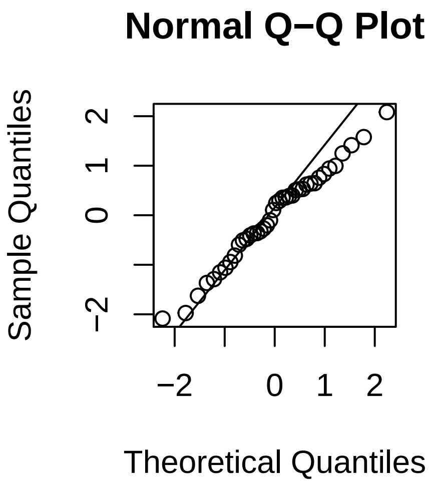
```r
hist(x5);
qqnorm(x5);qqline(x5)
```



Neither the histogram nor the QQ-plot depìct a normal distribution.

The QQ-plot is not similar to one of a normal distribution of the same size as x5.

```r
qqnorm(rnorm(length(x5)));qqline(rnorm(length(x5)))
```



Exercise 2

First we define a function to generate the list of p-values after running the tests 1000 times. The function takes by arguments *m*,*n*,*mu*,*nu* and *sd*.

```
get_p_values<-function(m,n,mu,nu,sd,iter=1000){
  B=iter
  p=numeric(B)

  for(b in 1:B){
    x=rnorm(m,mu,sd)
    y=rnorm(n,nu,sd)
    p[b]=t.test(x,y,var.equal = TRUE)[[3]]
  }
  return(p)
}
```

(1) Test values: mu=nu=180, m=n=30 and sd=10.

We obtain the number of p-values smaller that 5%

```
p=get_p_values(30,30,180,180,10)
p_amount=sum(p<0.05)
power95=mean(p<0.05)
```

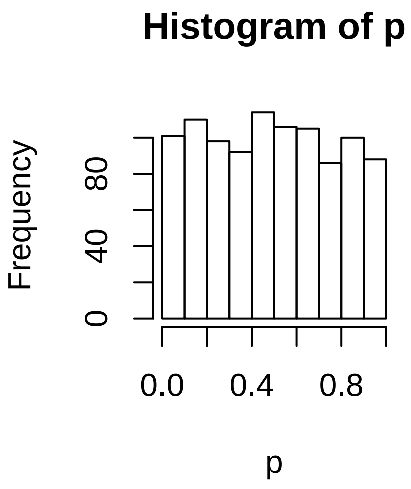
There are 45 values smaller than 5%. The power of the test is 0.045 with 95% confidence.

We obtain the number of p-values smaller that 10%

```
p_amount=sum(p<0.10)
power90=mean(p<0.10)
```

There are 101 values smaller than 10%. The power of the test is 0.101 with 90% confidence.

```
hist(p)
```



Findings: The statistical power of 0.045 and 0.101 indicate that the probability of correctly rejecting $H_0(mu == nu)$ is very low. This makes sense because in this test mu an nu are equal. Checking the histogram be see that the p-values follow a uniform distribution which indicates that H_0 is true.

(2) Test values: mu=nu=180, m=n=30 and sd=1.

We obtain the number of p-values smaller that 5%

```
p=get_p_values(30,30,180,180,1)
p_amount=sum(p<0.05)
power95=mean(p<0.05)
```

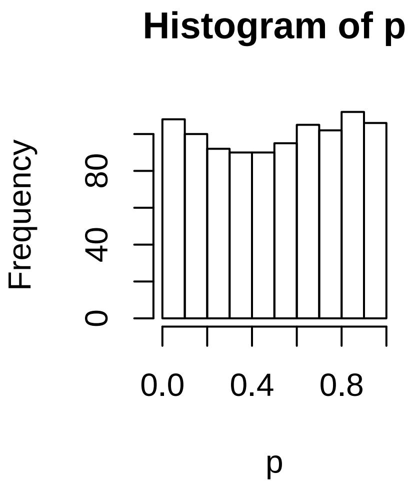
There are 61 values smaller than 5%. The power of the test is 0.061 with 95% confidence.

We obtain the number of p-values smaller that 10%

```
p_amount=sum(p<0.10)
power90=mean(p<0.10)
```

There are 108 values smaller than 10%. The power of the test is 0.108 with 90% confidence.

```
hist(p)
```



Findings: The statistical power of 0.061and 0.108 indicate that the probability of correctly rejecting $H_0(mu == nu)$ is very low. This makes sense because in this test mu an nu are equal. Checking the histogram be see that the p-values follow a uniform distribution which indicates that H_0 is true.

(3) Test values: mu=180, nu=175, m=n=30 and sd=6.

We obtain the number of p-values smaller that 5%

```
p=get_p_values(30,30,180,175,6)
p_amount=sum(p<0.05)
power95=mean(p<0.05)
```

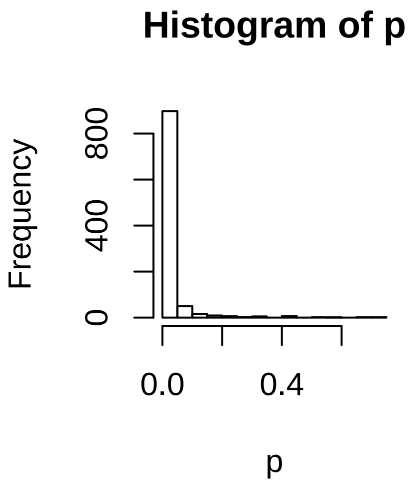
There are 897 values smaller than 5%. The power of the test is 0.897 with 95% confidence.

We obtain the number of p-values smaller that 10%

```r
p_amount=sum(p<0.10)
power90=mean(p<0.10)
```

There are 947 values smaller than 10%. The power of the test is 0.947 with 90% confidence.

```r
hist(p)
```



Findings: The statistical power of 0.897 and 0.947 indicate that the probability of correctly rejecting $H_0(mu == nu)$ is high. This makes sense because in this test mu an nu are different. Checking the histogram be see that the p-values do not follow a uniform distribution which they would if H_0 was true.

Exercise 3

First we define a function to get the powers for the t-test for every value in *values* as *nu*.

```r
get_powers<-function(m,n,mu,sd,values,iter=1000){
  powers = numeric(length(values))
  i=1
  for(nu in values){
    p=get_p_values(m,n,mu,nu,sd,iter=iter)
    powers[i]=mean(p<0.05)
    i=i+1
  }
  return(powers)
}
```

We define the values of nu.

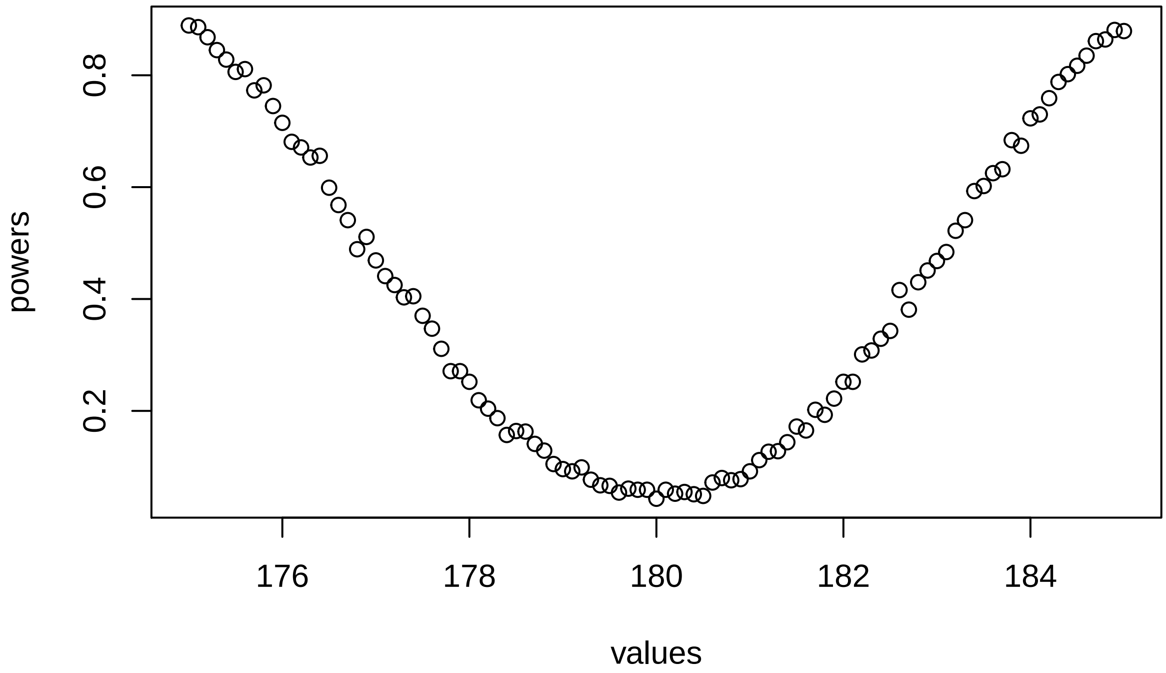
```r
values = seq(175,185,by=0.1)
```

(1) Test values: mu=180, m=n=30 and sd=6. We calculate the powers for each value of *nu*.

```
powers=get_powers(30,30,180,6,values)
```

We plot the power as a function of *nu*.

```
plot(values,powers)
```

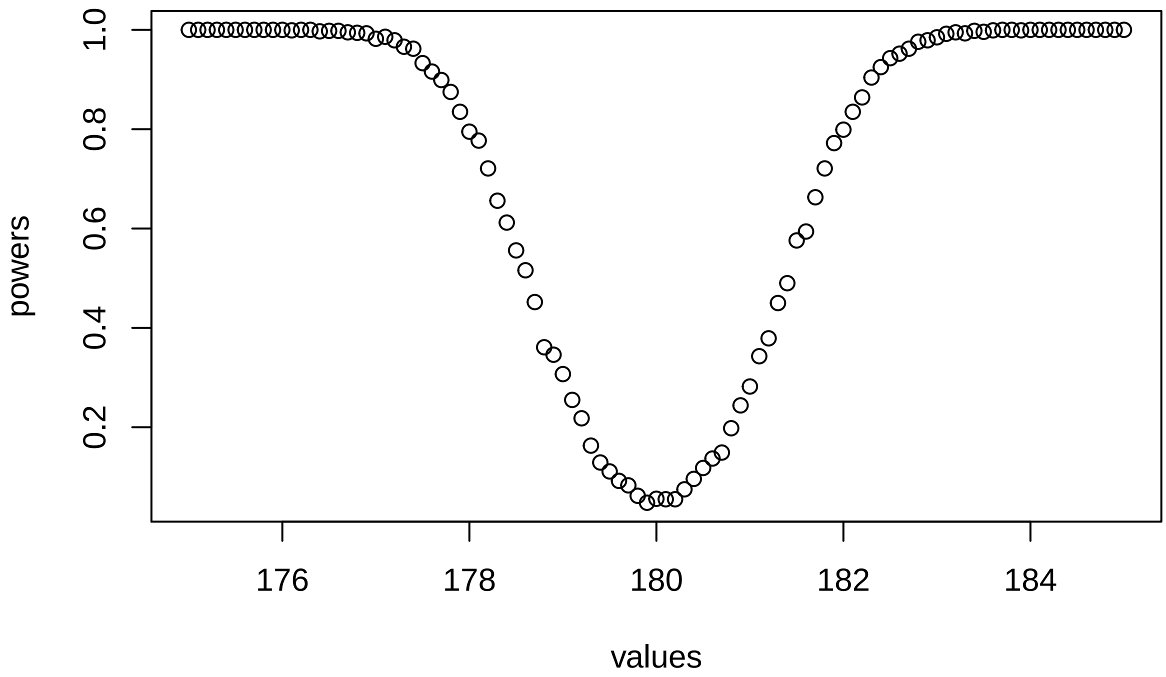


(2) Test values: mu=180, m=n=100 and sd=5. We calculate the powers for each value of *nu*.

```
powers=get_powers(100,100,180,5,values)
```

We plot the power as a function of *nu*.

```
plot(values,powers)
```

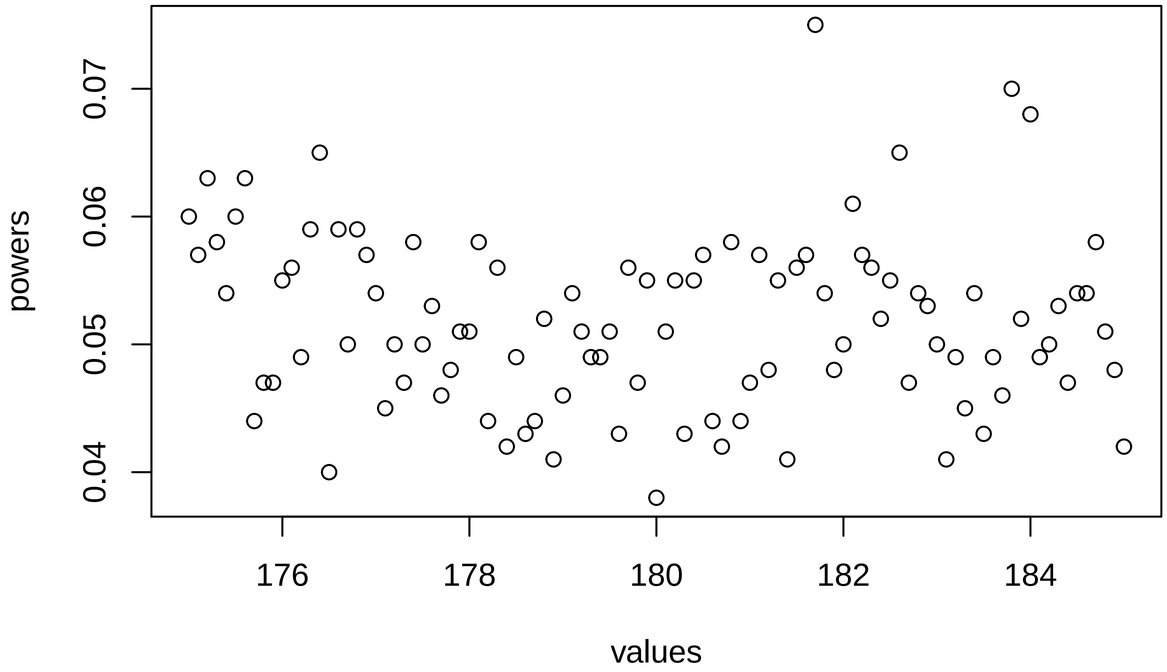


(3) Test values: mu=180, m=n=30 and sd=100. We calculate the powers for each value of *nu*.

```
powers=get_powers(30,30,180,100,values)
```

We plot the power as a function of *nu*.

```
plot(values,powers)
```



(4) Findings: With the first two plots we can see how the power of the test decreases when the *nu* values get closer to *mu* and it increases when *nu* values differ from *mu*. This indicates that the probability of correctly rejecting H_0 ($mu == nu$) is higher when *nu* values differ more from *mu* and it gets lower the closer the values get to *mu*.

We see that the bigger the population is, the easier it is to decide whether we should reject H_0 or not by looking at the power.

In the last plot we see that, with the same population but with a high standard deviation, we get low power values for any *nu* values while in the other plots we were getting high power values for the same nu values.