Assignment 1

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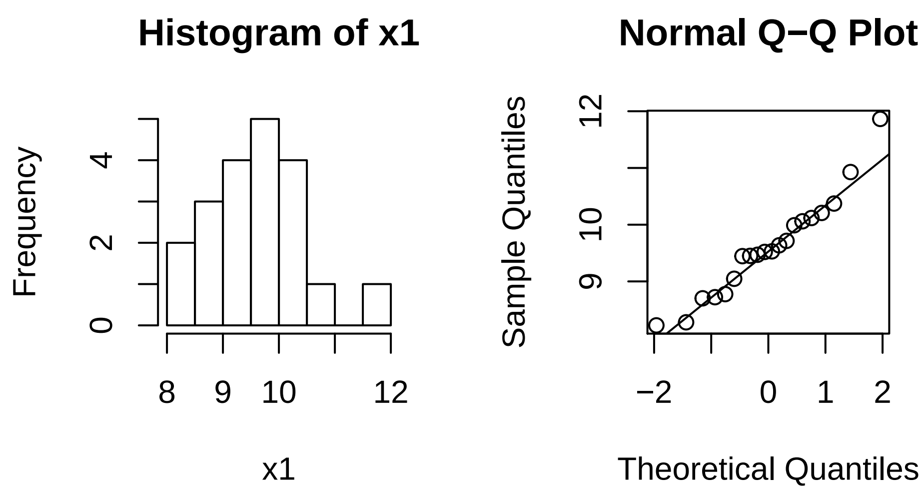
Exercise 1

We load the data from the data source.

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

Dataset x1

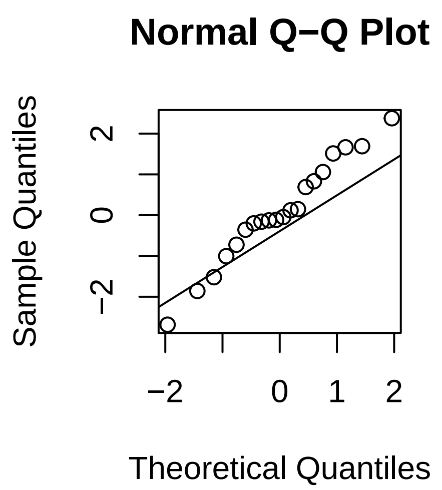
```
hist(x1);
qqnorm(x1);qqline(x1);
```



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.

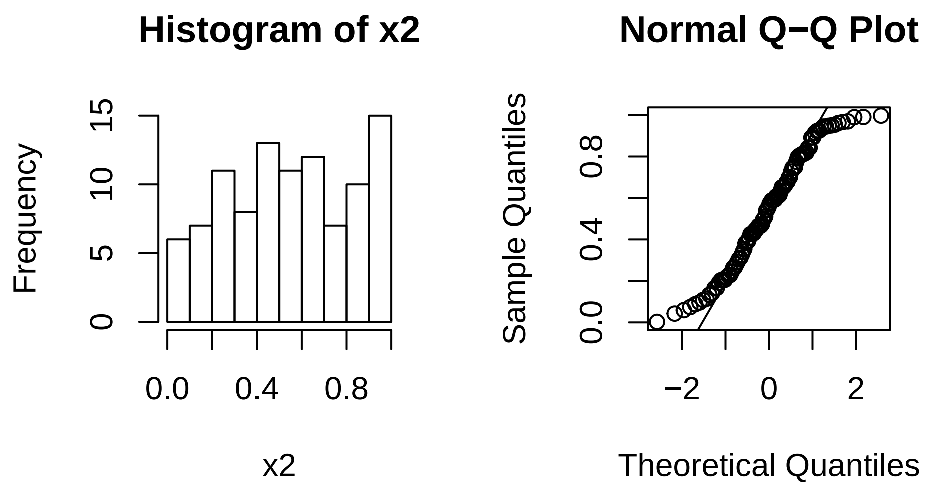
We can see the similarities with a QQ-plot of a normal distribution of the same size.

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



Dataset x2

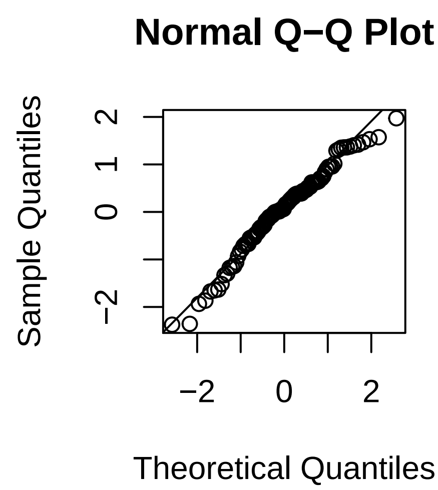
```r
hist(x2);
qqnorm(x2);qqline(x2)
```



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

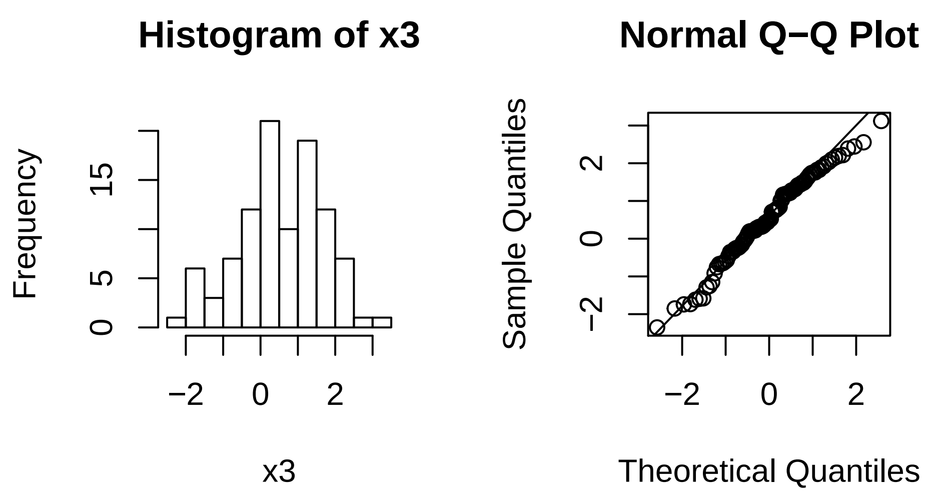
We can compare the QQ-plot to one representing a sample with normal distribution of the same size.

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



Dataset x3

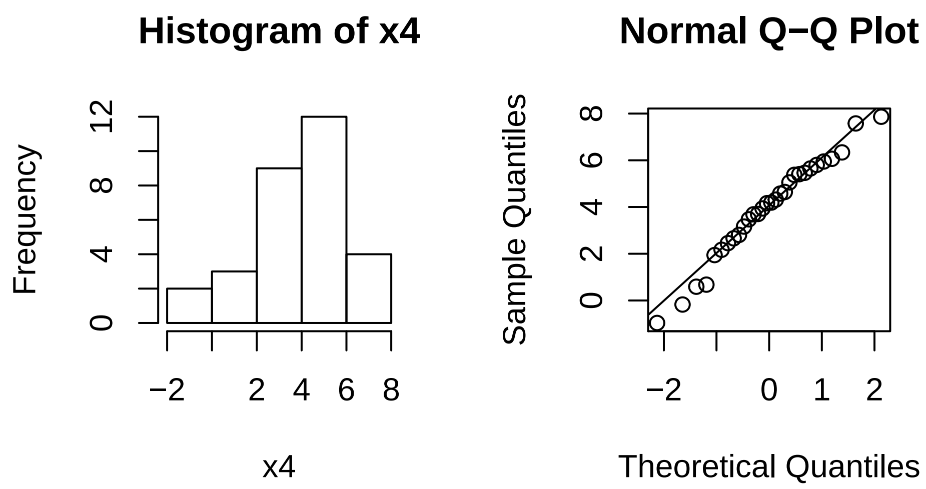
```r
hist(x3);
qqnorm(x3);qqline(x3)
```



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

Dataset x4

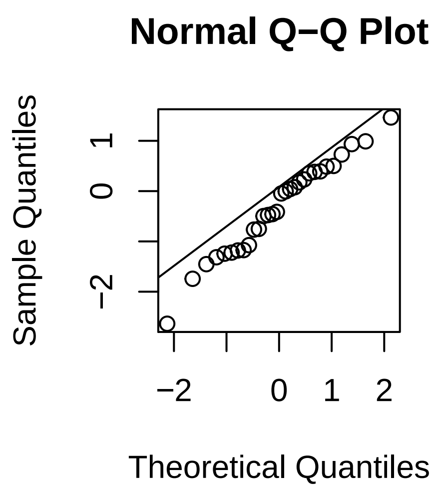
```r
hist(x4);
qqnorm(x4);qqline(x4)
```



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

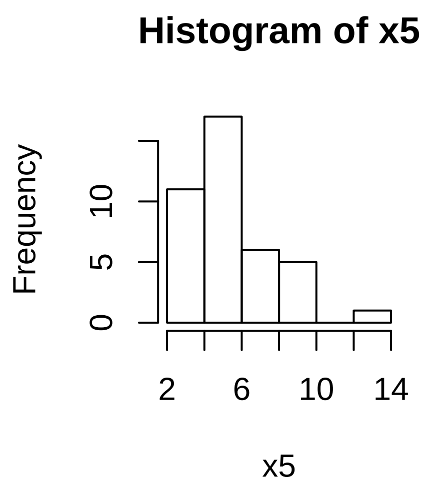
We can see the similarities with a QQ-plot of a normal distribution of the same size.

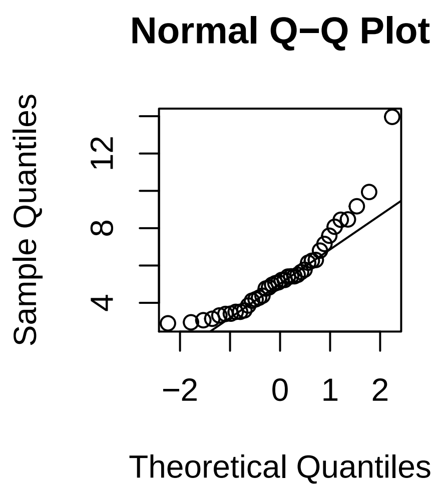
```r
qqnorm(rnorm(length(x4)));qqline(rnorm(length(x4)))
```



Dataset x5

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

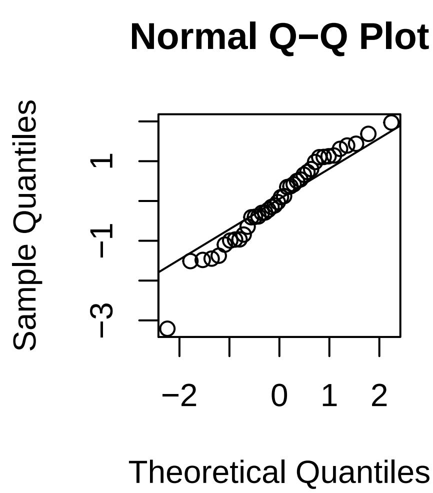




Neither the histogram nor the QQ-plot depìct a normal distribution.

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 than 5%

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

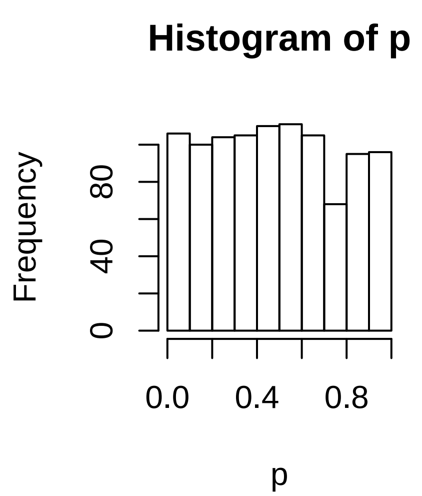
There are 45 values smaller than 5%. The power of the test is 0.045 with 95% confidence.

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

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

There are 106 values smaller than 10%. The power of the test is 0.106 with 90% confidence.

```
hist(p)
```



Findings: The statistical power of 0.045 and 0.106 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 we 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 than 5%

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

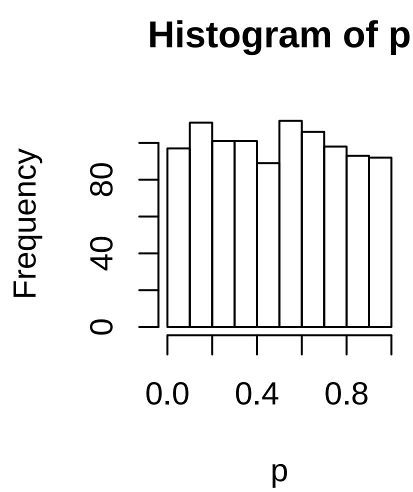
There are 48 values smaller than 5%. The power of the test is 0.048 with 95% confidence.

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

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

There are 97 values smaller than 10%. The power of the test is 0.097 with 90% confidence.

```
hist(p)
```



Findings: The statistical power of 0.048 and 0.097 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 we 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 than 5%

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

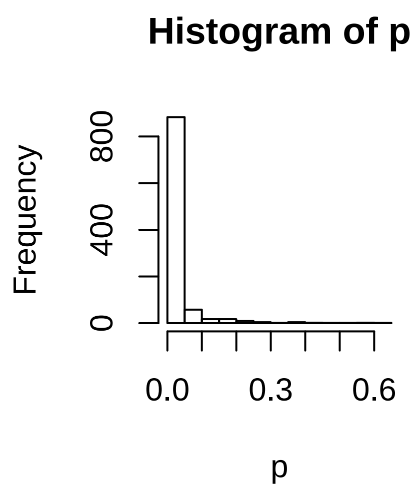
There are 883 values smaller than 5%. The power of the test is 0.883 with 95% confidence.

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

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

There are 941 values smaller than 10%. The power of the test is 0.941 with 90% confidence.

```
hist(p)
```



Findings: The statistical power of 0.883 and 0.941 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 we 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*.

```
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.

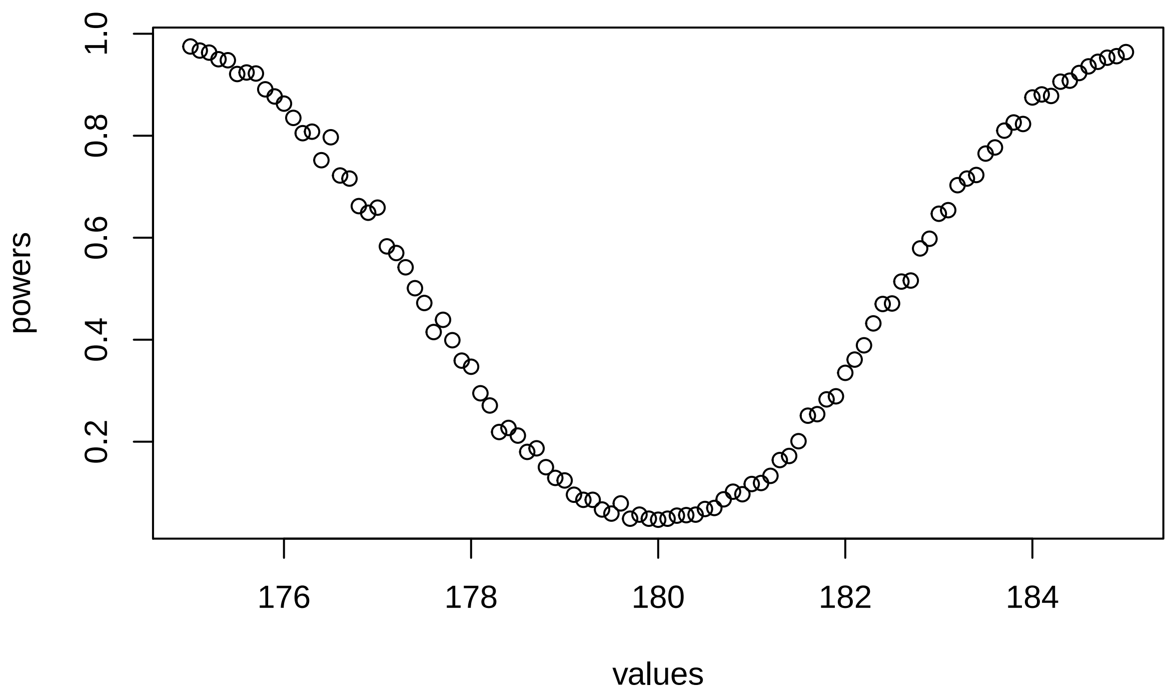
```
values = seq(175,185,by=0.1)
```

(1) Test values: mu=180, m=n=30 and sd=5. We calculate the powers for each value of *nu*.

```
powers=get_powers(30,30,180,5,values)
```

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

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

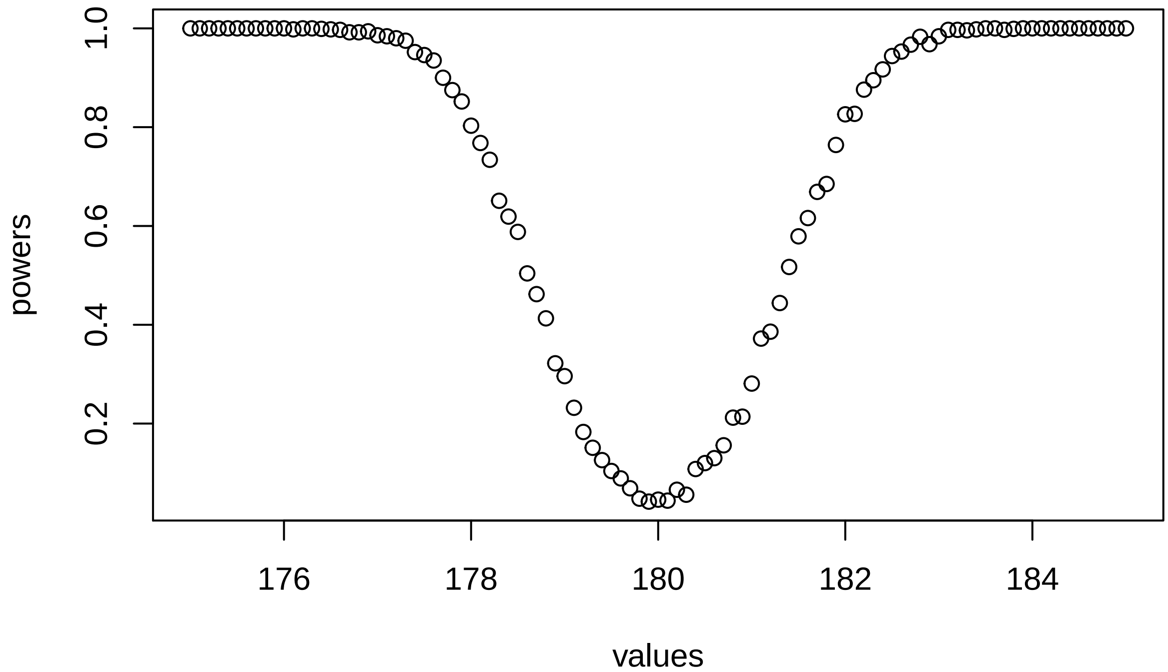


(2) Test values: mu=180, m=n=100 and sd=5. We calculate the powers for each value of *nu*.

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

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

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

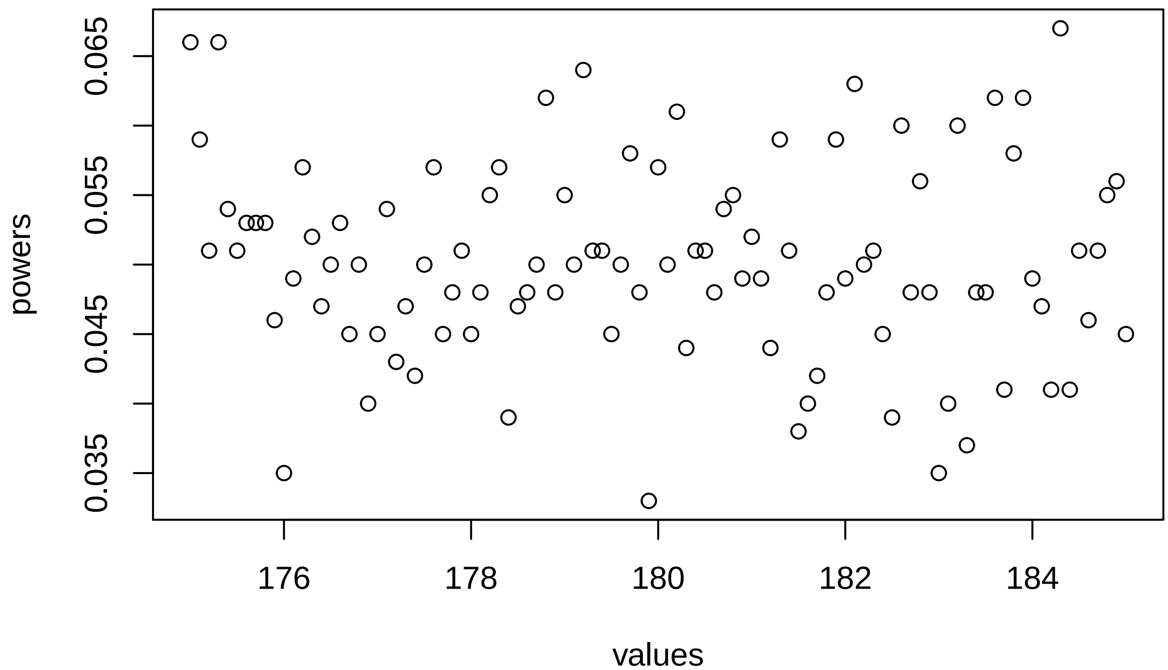


(3) Test values: mu=180, m=n=30 and sd=100. We calculate the powers for each value of *nu*.

```
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 when they get closer to *mu*.

Comparing the first and second plot, we see that when the population of the samples are bigger, the power obtained for the test are more precise. For example, in the first plot for *nu*=178 we get a power of 0.338 while in the second plot we get a power of 0.819 for the same value of *nu*.

In the last plot we see that, with the same population as in plot 1 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.