# Statistics using R

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### T-test in statistics

### One sample t-test & two sample t-test

#### To check the normal distribution;

to check the normality distribution we can perform Shapiro Wilk test and Kolmogrov Simirnov Test, or we can draw a histogram and qqnorm plot,

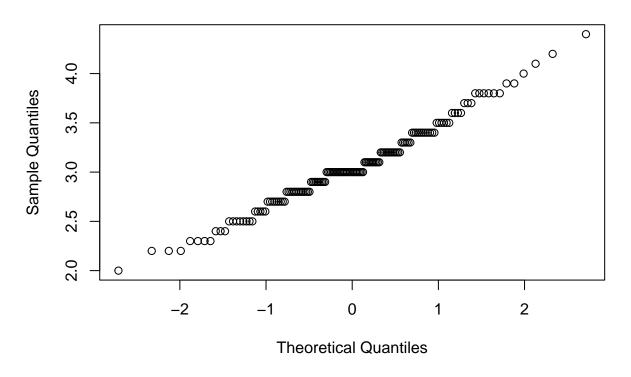
```
df <- iris
shapiro.test(df$Sepal.Width)</pre>
```

```
##
## Shapiro-Wilk normality test
##
## data: df$Sepal.Width
## W = 0.98492, p-value = 0.1012
```

so based upon the above result we can say that Sepal. Width in iris is normal.

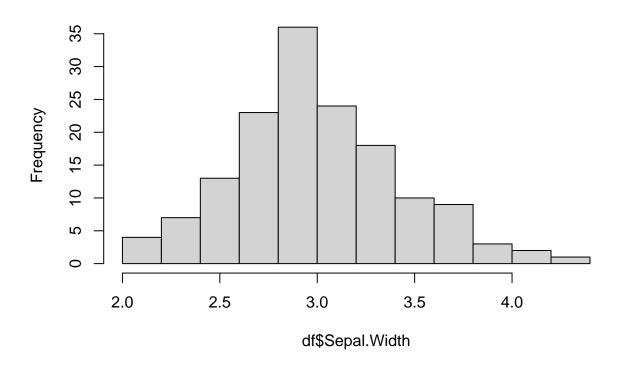
```
qqnorm(df$Sepal.Width)
```

## Normal Q-Q Plot



hist(df\$Sepal.Width)

## Histogram of df\$Sepal.Width



#### To check the composition of data;

we can perform Leven's Test to check the composition of variable

```
library(car)

## Loading required package: carData

leveneTest(df$Sepal.Width ~ df$Species , data=df)

## Levene's Test for Homogeneity of Variance (center = median)

## Df F value Pr(>F)

## group 2 0.5902 0.5555

## 147
```

### One sample T-test on Sepal Width Data

```
t.test(df$Sepal.Width , mu=5)

##
## One Sample t-test
```

```
##
## data: df$Sepal.Width
## t = -54.587, df = 149, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 5
## 95 percent confidence interval:
## 2.987010 3.127656
## sample estimates:
## mean of x
## 3.057333</pre>
```

#### Two sample T-test

There two types of two sample t-test - Unpaired T-test - Paired T-test

#### Unpaired T-test

```
library(tidyverse)
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr
             1.1.4
                       v readr
                                    2.1.5
## v forcats 1.0.0
                                    1.5.1
                        v stringr
## v ggplot2 3.5.1
                        v tibble
                                    3.2.1
## v lubridate 1.9.3
                        v tidyr
                                    1.3.1
## v purrr
              1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                    masks stats::lag()
## x dplyr::recode() masks car::recode()
## x purrr::some() masks car::some()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become error
t.test(df$Sepal.Width ~ df$Species=="setosa" |df$Species=="versicolor")
##
## Welch Two Sample t-test
## data: df$Sepal.Width by df$Species == "setosa" | df$Species == "versicolor"
## t = -1.8905, df = 135.22, p-value = 0.06083
## alternative hypothesis: true difference in means between group FALSE and group TRUE is not equal to
## 95 percent confidence interval:
## -0.255765152 0.005765152
## sample estimates:
```

The above result indicates that these two variable has no significant difference.

## mean in group FALSE mean in group TRUE
## 2.974 3.099

```
library(tidyverse)
t.test(df$Sepal.Width ~ df$Species=="versicolor" |df$Species=="virginica")
```

```
##
## Welch Two Sample t-test
##
## data: df$Sepal.Width by df$Species == "versicolor" | df$Species == "virginica"
## t = 8.8121, df = 87.596, p-value = 1.035e-13
## alternative hypothesis: true difference in means between group FALSE and group TRUE is not equal to ## 95 percent confidence interval:
## 0.4306031 0.6813969
## sample estimates:
## mean in group FALSE mean in group TRUE
## 3.428 2.872
```

According to above the result the variables are significantly different from each other.

#### Paired T-test

For this test we have randomly created a data set having two thousand observations, with a standard deviation of ten.

```
pre_treatment <- c(rnorm(2000, mean = 140, sd=10 ))</pre>
tibble(pre_treatment)
## # A tibble: 2,000 x 1
##
      pre_treatment
##
               <dbl>
##
   1
                142.
## 2
                132.
##
  3
                145.
##
   4
                147.
##
  5
                133.
##
  6
                142.
##
  7
                157.
##
    8
                144.
##
  9
                144.
## 10
               126.
## # i 1,990 more rows
post_treatment <- c(rnorm(2000, mean = 170, sd=10))</pre>
```

```
## # A tibble: 2,000 x 1
##
      post_treatment
##
               <dbl>
##
                161.
   1
##
                159.
##
  3
                166.
##
   4
                169.
## 5
                182.
##
   6
                187.
##
  7
                153.
## 8
                175.
                169.
##
   9
```

tibble(post\_treatment)

```
## 10    163.
## # i 1,990 more rows

t.test(pre_treatment, post_treatment, paired = TRUE)

##
## Paired t-test
##
## data: pre_treatment and post_treatment
## t = -95.981, df = 1999, p-value < 2.2e-16
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -30.28099 -29.06832
## sample estimates:
## mean difference</pre>
```

The result indicates that the averages of pre\_treatment and post\_treatment data differ significantly from each other.

-29.67466

##