King Saud University

College of Computer and Information Sciences

Information Technology department

IT 326: Data Mining

Course Project

Water quality

Project Report: Data Summarization and Preprocessing

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[Pick the date]

1 Problem

in our project we chose water quality dataset, it is an imaginary dataset in an urban environment, this dataset provide a set of elements (e.g. alumunium,ammonia,barium..etc) that can determine whether the water is safe of not.

Water is the most important natural resource on earth specially clean water which is the core to any community's success, we recognize the essential role of healthy water as the key to human growth and vitality. Globally, at least 2 billion people use a contaminated drinking water source, our goal is to bring knowledge to people and make this dataset a reference for people who wants to know if water is safe or not.

2 Data Mining Task

We will use classification and clustering as data mining task, for classification it is a binary classification , the class label is (is_safe) which has two possible values : 1 which indicates that water is safe , 0 which indicates that water is not safe ,The goal of classification in our case is to predict the water class label easier and faster and determining whether water is safe or not based in a set of elements(eg.Ammonia, Barium, Arsenic) provided in the dataset.

In clustering we will study and analyze water based on the elements which in turn represents the quality of the water, our goal is to find the similarity to identify distinct groups and clusters and what are the elements that distinguishes the water to be safe or not .

3 Data

Source: We chose the dataset from kaggle website (https://www.kaggle.com/mssmartypants/water-quality)

Number of objects is 7999(figure1), Number of attributes 21(figure2), with 3 missing values for all attribute(figure3) in row 7552 , 7569 and 7891 all in attribute ammonia .

```
> nrow(waterQuality)
[1] 7999
```

figure(1)

```
> ncol(waterQuality)
[1] 21
```

figure(2)

```
> sum(is.na(waterQuality))
[1] 3
```
figure(3)

Attributes information:

Attribute name	*Description*	*Data Type*	*Possible values*
aluminum	*Level of aluminum per liter*	*Numeric*	*0~5.5*
ammonia	*Level of ammonia per liter*	*Numeric*	*-2~30*
arsenic	*Level of arsenic per liter*	*Numeric*	*0~1.1*
barium	*Level of barium per liter*	*Numeric*	*0~5*
cadmium	*Level of cadmium per liter*	*Numeric*	*0~0.13*
chloramine	*Level of chloramine per liter*	*Numeric*	*0~9*
chromium	*Level of chromium per liter*	*Numeric*	*0~0.9*
copper	*Level of copper in water per liter.*	*Numeric*	*0~2*
fluoride	*Level of fluoride in water per liter.*	*Numeric*	*0~1.5*
bacteria	*Level of bacteria in water per liter.*	*Numeric*	*0~1*
viruses	*Level of viruses in water per liter.*	*Numeric*	*0~1*
lead	*Level of lead in water per liter.*	*Numeric*	*0~0.2*

nitrates	*Level of nitrates in water per liter.*	*Numeric*	*0~20*
nitrites	*Level of nitrites in water per liter.*	*Numeric*	*0~3*
mercury	Level of mercury in water per liter.	*Numeric*	*0~0.01*
perchlorate	Level of perchlorate in water per liter.	*Numeric*	*0~65*
radium	Level of radium in water per liter.	*Numeric*	*0~8*
selenium	Level of selenium in water per liter.	*Numeric*	*0~0.1*
silver	Level of silver in water per liter.	*Numeric*	*0~0.5*
uranium	Level of uranium in water per liter.	*Numeric*	*0~0.09*
is_safe	Level of is_safe in water per liter.	*Binary*	*0: not safe* *1:safe*

Five number summary:

```
> summary(waterQuality)
   aluminium         ammonia             arsenic
 Min.   :0.0000   Length:7999        Min.   :0.0000
 1st Qu.:0.0400   Class :character   1st Qu.:0.0300
 Median :0.0700   Mode  :character   Median :0.0500
 Mean   :0.6662                      Mean   :0.1614
 3rd Qu.:0.2800                      3rd Qu.:0.1000
 Max.   :5.0500                      Max.   :1.0500
     barium           cadmium           chloramine
 Min.   :0.000   Min.   :0.00000   Min.   :0.000
 1st Qu.:0.560   1st Qu.:0.00800   1st Qu.:0.100
 Median :1.190   Median :0.04000   Median :0.530
 Mean   :1.568   Mean   :0.04281   Mean   :2.177
 3rd Qu.:2.480   3rd Qu.:0.07000   3rd Qu.:4.240
 Max.   :4.940   Max.   :0.13000   Max.   :8.680
    chromium          copper          flouride
 Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
 1st Qu.:0.0500   1st Qu.:0.0900   1st Qu.:0.4050
 Median :0.0900   Median :0.7500   Median :0.7700
 Mean   :0.2472   Mean   :0.8059   Mean   :0.7716
 3rd Qu.:0.4400   3rd Qu.:1.3900   3rd Qu.:1.1600
 Max.   :0.9000   Max.   :2.0000   Max.   :1.5000

    silver           uranium          is_safe
Min.   :0.0000   Min.   :0.00000   Length:7999
1st Qu.:0.0400   1st Qu.:0.02000   Class :character
Median :0.0800   Median :0.05000   Mode  :character
Mean   :0.1478   Mean   :0.04467
3rd Qu.:0.2400   3rd Qu.:0.07000
Max.   :0.5000   Max.   :0.09000
```

```
    bacteria          viruses             lead
Min.   :0.0000   Min.   :0.0000   Min.   :0.00000
1st Qu.:0.0000   1st Qu.:0.0020   1st Qu.:0.04800
Median :0.2200   Median :0.0080   Median :0.10200
Mean   :0.3197   Mean   :0.3286   Mean   :0.09945
3rd Qu.:0.6100   3rd Qu.:0.7000   3rd Qu.:0.15100
Max.   :1.0000   Max.   :1.0000   Max.   :0.20000
   nitrates          nitrites          mercury
Min.   : 0.000   Min.   :0.00   Min.   :0.000000
1st Qu.: 5.000   1st Qu.:1.00   1st Qu.:0.003000
Median : 9.930   Median :1.42   Median :0.005000
Mean   : 9.819   Mean   :1.33   Mean   :0.005194
3rd Qu.:14.610   3rd Qu.:1.76   3rd Qu.:0.008000
Max.   :19.830   Max.   :2.93   Max.   :0.010000
 perchlorate         radium          selenium
Min.   : 0.00   Min.   :0.000   Min.   :0.00000
1st Qu.: 2.17   1st Qu.:0.820   1st Qu.:0.02000
Median : 7.74   Median :2.410   Median :0.05000
Mean   :16.46   Mean   :2.921   Mean   :0.04968
3rd Qu.:29.48   3rd Qu.:4.670   3rd Qu.:0.07000
Max.   :60.01   Max.   :7.990   Max.   :0.10000
```

after we implement the code to show the five number summary (above) we noticed that Ammonia data type is character which is not helpful in our study

	aluminium	ammonia	arsenic	barium	cadmium	chloramine
1	1.65	9.08	column 2: character 40	2.85	0.007	
2	2.32	21.16	0.010	3.31	0.002	
3	1.01	14.02	0.040	0.58	0.008	
4	1.36	11.33	0.040	2.96	0.001	
5	0.92	24.33	0.030	0.20	0.006	
6	0.94	14.47	0.030	2.88	0.003	
7	2.36	5.6	0.010	1.35	0.004	

we think it is a mistake that happened while data entry process, so we decided to convert Ammonia data type from character to numeric so that we can analyse the five number summary .

```
> waterQuality$ammonia=as.numeric(waterQuality$ammonia)
```

Our dataset after the conversion

```
> summary(waterQuality)
   aluminium          ammonia
 Min.   :0.0000   Min.   :-0.080
 1st Qu.:0.0400   1st Qu.: 6.577
 Median :0.0700   Median :14.130
 Mean   :0.6662   Mean   :14.278
 3rd Qu.:0.2800   3rd Qu.:22.133
 Max.   :5.0500   Max.   :29.840
                  NA's   :3
    arsenic            barium
 Min.   :0.0000   Min.   :0.000
 1st Qu.:0.0300   1st Qu.:0.560
 Median :0.0500   Median :1.190
 Mean   :0.1614   Mean   :1.568
 3rd Qu.:0.1000   3rd Qu.:2.480
 Max.   :1.0500   Max.   :4.940
```

```
     viruses             lead
 Min.   :0.0000   Min.   :0.00000
 1st Qu.:0.0020   1st Qu.:0.04800
 Median :0.0080   Median :0.10200
 Mean   :0.3286   Mean   :0.09945
 3rd Qu.:0.7000   3rd Qu.:0.15100
 Max.   :1.0000   Max.   :0.20000

    nitrates          nitrites
 Min.   : 0.000   Min.   :0.00
 1st Qu.: 5.000   1st Qu.:1.00
 Median : 9.930   Median :1.42
 Mean   : 9.819   Mean   :1.33
 3rd Qu.:14.610   3rd Qu.:1.76
 Max.   :19.830   Max.   :2.93

    mercury           perchlorate
 Min.   :0.000000   Min.   : 0.00
 1st Qu.:0.003000   1st Qu.: 2.17
 Median :0.005000   Median : 7.74
 Mean   :0.005194   Mean   :16.46
 3rd Qu.:0.008000   3rd Qu.:29.48
 Max.   :0.010000   Max.   :60.01
```

```
    cadmium           chloramine
 Min.   :0.00000   Min.   :0.000
 1st Qu.:0.00800   1st Qu.:0.100
 Median :0.04000   Median :0.530
 Mean   :0.04281   Mean   :2.177
 3rd Qu.:0.07000   3rd Qu.:4.240
 Max.   :0.13000   Max.   :8.680

    chromium           copper
 Min.   :0.0000   Min.   :0.0000
 1st Qu.:0.0500   1st Qu.:0.0900
 Median :0.0900   Median :0.7500
 Mean   :0.2472   Mean   :0.8059
 3rd Qu.:0.4400   3rd Qu.:1.3900
 Max.   :0.9000   Max.   :2.0000

    flouride           bacteria
 Min.   :0.0000   Min.   :0.0000
 1st Qu.:0.4050   1st Qu.:0.0000
 Median :0.7700   Median :0.2200
 Mean   :0.7716   Mean   :0.3197
 3rd Qu.:1.1600   3rd Qu.:0.6100
 Max.   :1.5000   Max.   :1.0000
```

```
     radium           selenium
 Min.   :0.000   Min.   :0.00000
 1st Qu.:0.820   1st Qu.:0.02000
 Median :2.410   Median :0.05000
 Mean   :2.921   Mean   :0.04968
 3rd Qu.:4.670   3rd Qu.:0.07000
 Max.   :7.990   Max.   :0.10000

     silver           uranium
 Min.   :0.0000   Min.   :0.00000
 1st Qu.:0.0400   1st Qu.:0.02000
 Median :0.0800   Median :0.05000
 Mean   :0.1478   Mean   :0.04467
 3rd Qu.:0.2400   3rd Qu.:0.07000
 Max.   :0.5000   Max.   :0.09000

   is_safe
 Length:7999
 Class :character
 Mode  :character
```

Outliers:

```
> OutlierAl = outlier(waterQuality$aluminium, logical=TRUE)
> sum(OutlierAl)
[1] 1
> OutlierAmm = outlier(waterQuality$ammonia, logical=TRUE)
> sum(OutlierAmm)
[1] NA
> OutlierArs = outlier(waterQuality$arsenic, logical=TRUE)
> sum(OutlierArs)
[1] 2
> OutlierBar = outlier(waterQuality$barium, logical=TRUE)
> sum(OutlierBar)
[1] 1
> OutlierCad = outlier(waterQuality$cadmium, logical=TRUE)
> sum(OutlierCad)
[1] 62
> OutlierChlo = outlier(waterQuality$chloramine, logical=TRUE)
> sum(OutlierChlo)
[1] 1
> OutlierChrom = outlier(waterQuality$chromium, logical=TRUE)
> sum(OutlierChrom)
[1] 12
> OutlierCo <- outlier(waterQuality$copper, logical=TRUE)
> sum(OutlierCo)
[1] 6
> OutlierFl <- outlier(waterQuality$flouride, logical=TRUE)
> sum(OutlierFl)
[1] 25
> OutlierBa <- outlier(waterQuality$bacteria, logical=TRUE)
> sum(OutlierBa)
[1] 45
> OutlierVi <- outlier(waterQuality$viruses, logical=TRUE)
> sum(OutlierVi)
[1] 62
> OutlierLe <- outlier(waterQuality$lead, logical=TRUE)
> sum(OutlierLe)
[1] 16
> OutlierNi1 <- outlier(waterQuality$nitrates, logical=TRUE)
> sum(OutlierNi1)
[1] 1
> OutlierNi2 <- outlier(waterQuality$nitrites, logical=TRUE)
> sum(OutlierNi2)
[1] 1
```

```
> OutlierMe <- outlier(waterQuality$mercury, logical=TRUE)
> sum(OutlierMe)
[1] 371
> OutlierPe <- outlier(waterQuality$perchlorate, logical=TRUE)
> sum(OutlierPe)
[1] 1
> OutlierRa <- outlier(waterQuality$radium, logical=TRUE)
> sum(OutlierRa)
[1] 4
> OutlierSe <- outlier(waterQuality$selenium, logical=TRUE)
> sum(OutlierSe)
[1] 400
> OutlierSi <- outlier(waterQuality$silver, logical=TRUE)
> sum(OutlierSi)
[1] 36
> OutlierUr <- outlier(waterQuality$uranium, logical=TRUE)
> sum(OutlierUr)
[1] 447
>
```

Correlation analysis:

We used correlation analysis to determine the relationship between two different attributes in our dataset and how strongly one attribute implies the other, and if they are dependant or independent of each other. Since our dataset attributes is all of numeric type, then the right method to be applied is correlation coeffiecent. Each two attributes will be postively correlated if the correlation coefficient value is larger than 0, and they will be negatively correlated if the value is negative which is smaller than 0, also the two values will be totally independent if the value is equal to 0.

```
> cor(waterQuality$lead, waterQuality$arsenic)
[1] -0.08775631
> cor(waterQuality$aluminium, waterQuality$silver)
[1] 0.3349928
> cor(waterQuality$bacteria, waterQuality$viruses)
[1] 0.6184804
> cor(waterQuality$selenium, waterQuality$arsenic)
[1] -0.007009078
```

Negatively correlated

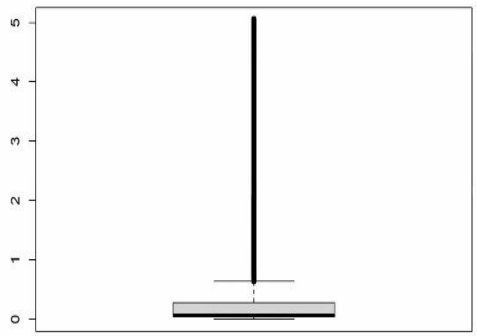
Positively correlated

Positively correlated

Negatively correlated

Boxplots :

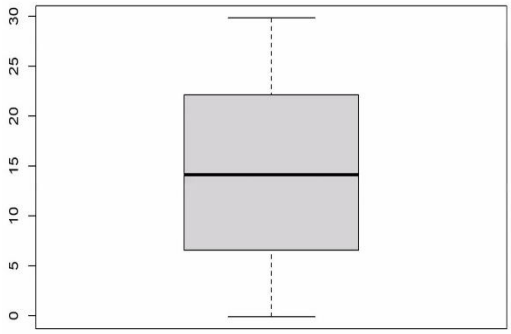
Aluminium




```
> boxplot(waterQuality$aluminium, data = waterQuality)
```

the boxplot show the values of the attribute Aluminium,with min 0 and max 5.05 it show that there are outliers Above The value 0.8.

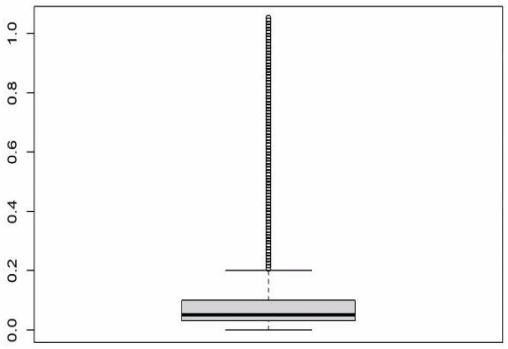
Ammonia




```
> boxplot(waterQuality$ammonia, data = waterQuality)
```

the boxplot show the values of the attribute ammonia, with min -2 and max 30, there is no outliers.

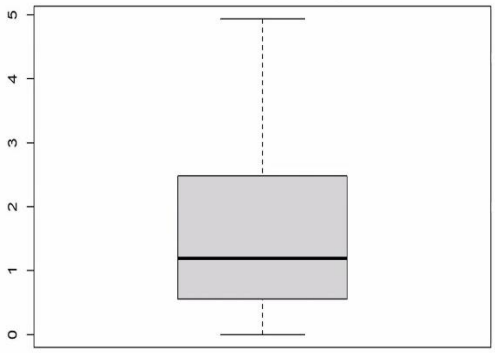
Arsenic




```
> boxplot(waterQuality$arsenic, data = waterQuality)
```

the boxplot show the values of the attribute aresenic,with min 0 and max 1.1, it show that there are outliers Above The value 0.2

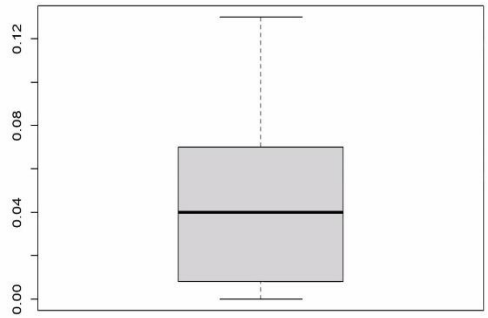
Barium




```
> boxplot(waterQuality$barium, data = waterQuality)
```

the boxplot show the values of the attribute Barium,with min 0 and max 5 there is no outliers.

Cadmium

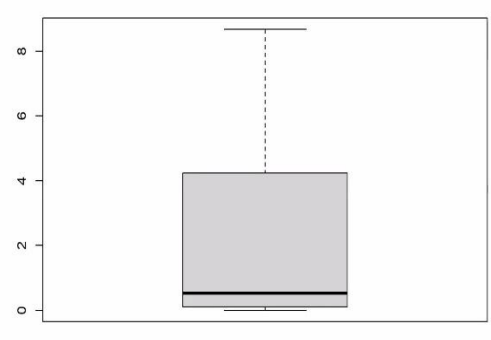



```
> boxplot(waterQuality$cadmium, data = waterQuality)
```

the boxplot show the values of the attribute

Cadmium,with min 0 and max 0.13 there is outliers.

Chloramine

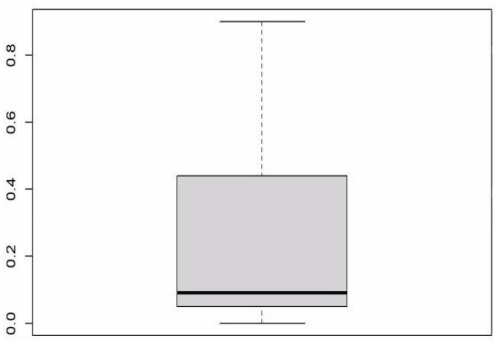



```
> boxplot(waterQuality$chloramine, data = waterQuality)
```

the boxplot show the values of the attribute

Chloramine,with min 0 and max 9 there is no no outliers.

Chromium

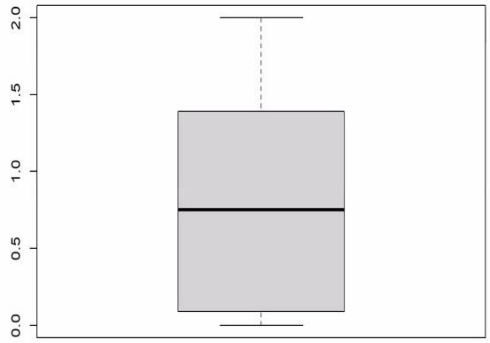



```
> boxplot(waterQuality$chromium, data = waterQuality)
```

the boxplot show the values of the attribute

Chromium,with min 0 and max 0.9 there is no outliers.

Copper

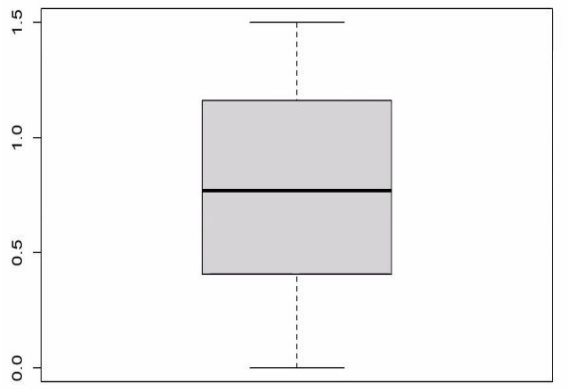



```
> boxplot(waterQuality$copper, data = waterQuality)
```

the boxplot show the values of the attribute

Copper,with min 0 and max 2 there is no outliers.

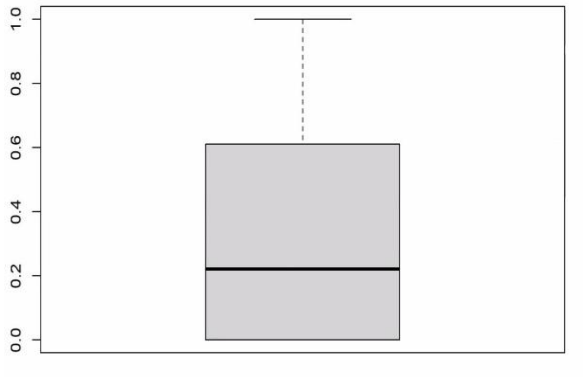
Fluoride




```
> boxplot(waterQuality$flouride, data = waterQuality)
```

the boxplot show the values of the attribute flouride,with min 0 and max 1.5 there is no outliers.

Bacteria




```
> boxplot(waterQuality$bacteria, data = waterQuality)
```

the boxplot show the values of the attribute bacteria,with min 0 and max 1 there is no outliers.

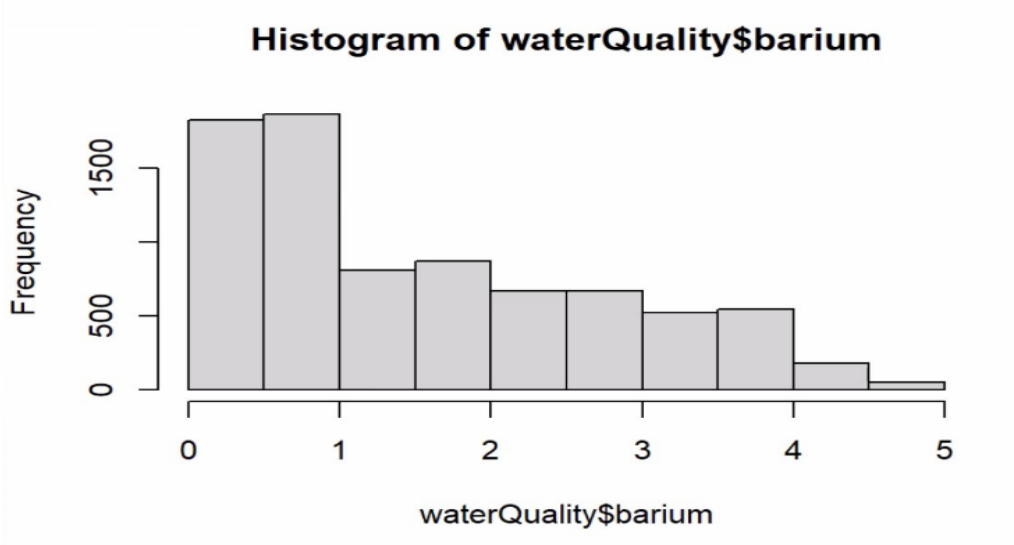
Plotting methods :

Histogram

The histogram shows the frequency of the baruim , it shows that most water have baruim concentration between 0-1.1 which is the normal concentration in a liter of water , also there are a few water which have between 4-5.1 .

As you can see there is water that contain 0 baruim , which is not normal because when baruim is combined with other chemicals it effects water well .

```
> hist(waterQuality$barium)
```

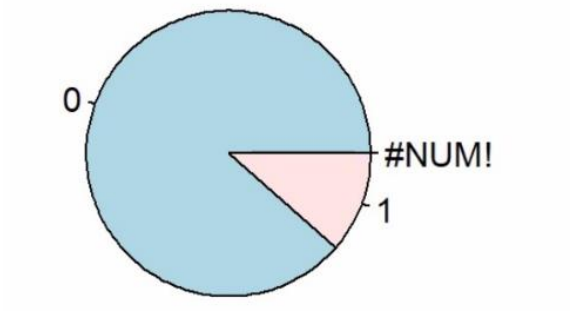


Pie chart

The pie chart shows that the data are not equally distributed between (0 not safe , 1 safe)

Based on class label (is_safe) , cleaning needed since there are missing value . here we noticed that ("#Num!") is not one of the possible values (this problem is handled in preprocessing) .

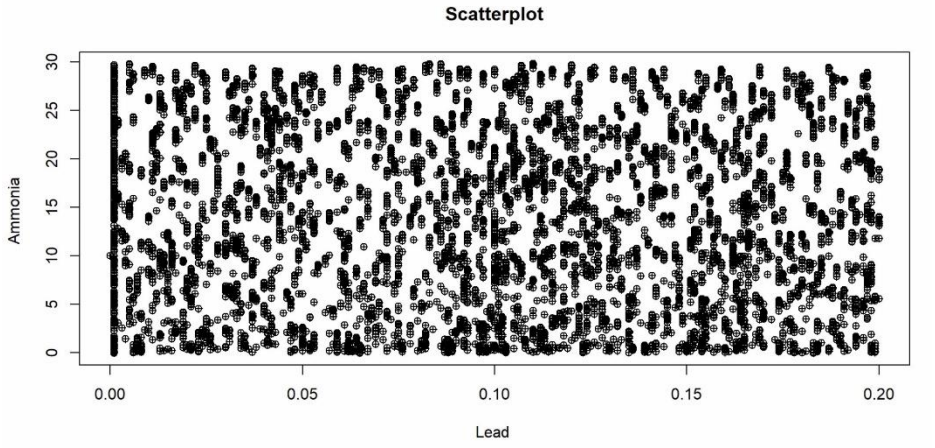
```
> pie(table(waterQuality$is_safe))
```



Scatterplot

This scatter plot shows that there is no correlation between ammonia and lead because there is huge dispersion between the points and there is no specific patteren .

```
> plot(waterQuality$lead,waterQuality$ammonia, main="Scatterplot",xlab="Lead",ylab="Ammonia")
```



4 Data preprocessing

1- Cleaning data for missing values :

Since dealing with missing values is an important step in data cleaning , in our case we have 3 missing values to deal with .

```
> sum(is.na(waterQuality))
[1] 3
```

By this command we locate the missing values .

```
> is.na(waterQuality$ammonia)
```

Output :

```
[7753] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7765] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7777] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7789] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7801] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7813] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7825] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7837] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7849] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7861] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7873] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7885] FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE
[7897] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7909] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7921] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7933] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7945] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7957] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7969] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7981] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7993] FALSE FALSE FALSE FALSE FALSE FALSE FALSE
>
```

```
[7549] FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7561] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE
[7573] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7585] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7597] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7609] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7621] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7633] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7645] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7657] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7669] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7681] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7693] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7705] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7717] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7729] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7741] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7753] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7765] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7777] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7789] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7801] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[7813] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

We decide to deal with missing values by replacing them with the average of Ammonia with this code.

```
> waterQuality$ammonia=ifelse(is.na(waterQuality$ammonia),a
ve(waterQuality$ammonia,FUN=function(x) mean(x,na.rm=TRU
E)),waterQuality$ammonia)
>
```

Output : (rows with missing values after cleaning)

First row that was containing missing value

	aluminium	ammonia	arsenic	barium	cadmium	chloramine
7890	0.10	4.79000	0.04	0.70	0.03	0
7891	0.01	14.27821	0.08	0.49	0.00	0
7892	0.05	16.61000	0.09	0.20	0.00	0
7893	0.08	3.25000	0.10	0.32	0.05	0
7894	0.05	0.05000	0.01	0.29	0.06	0

Second row that was containing missing value

	aluminium	ammonia	arsenic	barium	cadmium	chloramine
7551	0.01	0.13000	0.05	0.28	0.04	0
7552	0.03	14.27821	0.08	0.79	0.07	0
7553	0.10	8.76000	0.10	0.66	0.07	0
7554	0.04	0.26000	0.08	1.58	0.08	0
7555	0.07	0.52000	0.01	0.31	0.04	0

Third row that was containing missing value

	aluminium	ammonia	arsenic	barium	cadmium	chloramine
7568	0.06	8.84000	0.04	3.47	0.02	0
7569	0.06	14.27821	0.07	1.72	0.08	0
7570	0.09	0.26000	0.09	0.45	0.01	0
7571	0.00	8.57000	0.05	0.82	0.03	0
7572	0.08	14.23000	0.02	0.98	0.05	0

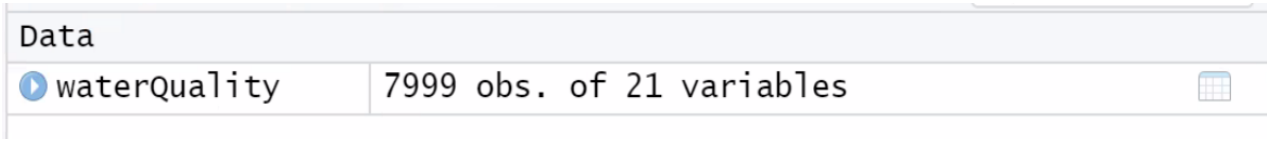
2- Detecting and removing outliers :

Outliers are values that are not usual in the dataset, excluding outliers can make the dataset statistically significant . We decide to deal with outliers to improve the dataset quality and make it more accurate.

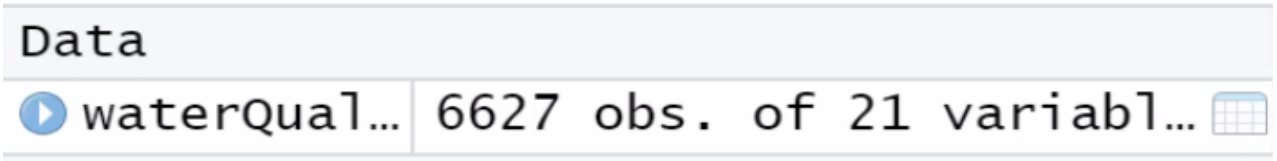
We used this code to remove the outliers (the rest of the code are in appendix page below)

```
> library(outliers)
> OutlierUran=outlier(waterQuality$uranium,logical=TRUE)
> Find_outlier=which(OutlierUran==TRUE,arr.ind=TRUE)
> waterQuality= waterQuality[-Find_outlier,]
```

Dataset before removing outliers :



Dataset after removing outliers :



3- Encoding :

In our dataset we have one nominal attribute(binary) which is (is_safe) containg two possible values which is 0 indicating that water is not safe , 1 indicating water is safe.

We used this code on the class label (is_safe) to do the encoding process from (0,1) to(No,Yes) to make our data set more understandable .

```
> waterQuality$is_safe = factor(waterQuality$is_safe,levels = c
("0","1"), labels = c("No","Yes"))
```

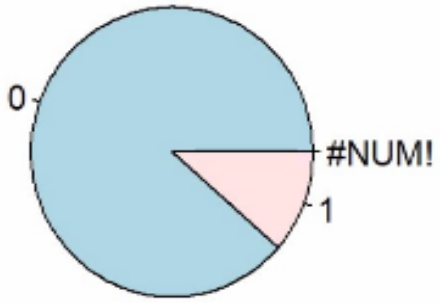
attribute(is_safe) before encoding :

nitrites	mercury	perchlorate	radium	selenium	silver	uranium	is_safe
1.13	0.007	37.75	6.78	0.08	0.34	0.02	1
1.93	0.003	32.26	3.21	0.08	0.27	0.05	1
1.11	0.006	50.28	7.07	0.07	0.44	0.01	0
1.29	0.004	9.12	1.72	0.02	0.45	0.05	1
1.11	0.003	16.90	2.41	0.02	0.06	0.02	1
1.89	0.006	27.17	5.42	0.08	0.19	0.02	1
1.81	0.001	53.35	7.24	0.08	0.08	0.07	0
1.84	0.004	23.43	4.99	0.08	0.25	0.08	1
1.46	0.010	30.42	0.08	0.03	0.31	0.01	1
1.25	0.006	55.40	7.80	0.05	0.33	0.06	0

attribute(is_safe) after encoding :

nitrites	mercury	perchlorate	radium	selenium	silver	uranium	is_safe
1.13	0.007	37.75	6.78	0.08	0.34	0.02	Yes
1.93	0.003	32.26	3.21	0.08	0.27	0.05	Yes
1.11	0.006	50.28	7.07	0.07	0.44	0.01	No
1.29	0.004	9.12	1.72	0.02	0.45	0.05	Yes
1.11	0.003	16.90	2.41	0.02	0.06	0.02	Yes
1.89	0.006	27.17	5.42	0.08	0.19	0.02	Yes
1.81	0.001	53.35	7.24	0.08	0.08	0.07	No
1.84	0.004	23.43	4.99	0.08	0.25	0.08	Yes
1.46	0.010	30.42	0.08	0.03	0.31	0.01	Yes

We noticed that after we created the pie chart it shows that the class label is_safe have three values which are (0 , 1, "#Num!") as shown .



"#Num!" is unknown value and ambiguous and not acceptable in our dataset.

when we encoded the class label (is_safe) we realized the "#Num!" becomes a null value so we used this code to delete the null rows and clean our data set from unaccepted values.

```
waterQuality <- na.omit(waterQuality)
```

Here is our dataset before deleting the null values :

waterQua…	6627 obs. of 21 varia…

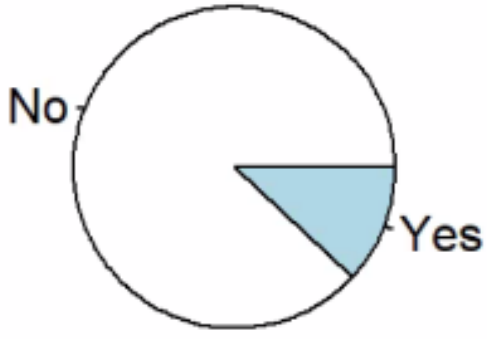
Here is our dataset after deleting the null values :

waterQuality	6624 obs. of 21 variables

Then we used this code to show the pie chart without null values :

```
pie(table(waterQuality$is_safe))
```

then The pie chart appears without the unknown value ("#Num!"):



4- Normalization :

Normalization is where the attribute data are scaled so as to fall in a smaller range , we apply min-max normalization for the highest 3 attributes in range which are (Ammonia , Nitrates, Perchlorate).

We used this code to do normalization process :

```
##Normlize amonia
normlize<- function(x){
  return((x-min(x)) / (max(x)-min(x)))
}
waterQuality$ammonia<-normlize(waterQuality$ammonia)
##Normlize perchlorate
normlize<- function(x){
  return((x-min(x)) / (max(x)-min(x)))
}
waterQuality$perchlorate<-normlize(waterQuality$perchlorate)
##Normlize nitrates
normlize<- function(x){
  return((x-min(x)) / (max(x)-min(x)))
}
waterQuality$nitrates<-normlize(waterQuality$nitrates)
```

Nitrates before normalization :

acteria	viruses	lead	nitrates	nitrites	mercury	perchlorate	radium	selenium
0.20	0.000	0.054	16.08	1.13	0.007	0.63032226	6.78	
0.65	0.650	0.100	2.01	1.93	0.003	0.53865420	3.21	
0.05	0.003	0.078	14.16	1.11	0.006	0.83953916	7.07	
0.71	0.710	0.016	1.41	1.29	0.004	0.15227918	1.72	
0.13	0.001	0.117	6.74	1.11	0.003	0.28218400	2.41	
0.67	0.670	0.135	9.75	1.89	0.006	0.45366505	5.42	
0.16	0.005	0.197	13.65	1.81	0.001	0.89079980	7.24	

Nitrates after normalization :

opper	flouride	bacteria	viruses	lead	nitrates	nitrites	mercury	perchlorate
0.17	0.05	0.20	0.000	0.054	0.81120646	1.13	0.007	0.630
0.66	0.90	0.65	0.650	0.100	0.10095911	1.93	0.003	0.538
0.02	0.99	0.05	0.003	0.078	0.71428571	1.11	0.006	0.839
1.66	1.08	0.71	0.710	0.016	0.07067138	1.29	0.004	0.152
0.57	0.61	0.13	0.001	0.117	0.33972741	1.11	0.003	0.282
1.38	0.11	0.67	0.670	0.135	0.49167087	1.89	0.006	0.453
1.86	0.86	0.16	0.005	0.197	0.68854114	1.81	0.001	0.890

Ammonia before normalization :

	aluminium	ammonia	arsenic	barium	cadmium	chloramine
1	1.65	9.08	0.040	2.85	0.007	
2	2.32	21.16	0.010	3.31	0.002	
3	1.01	14.02	0.040	0.58	0.008	
4	1.36	11.33	0.040	2.96	0.001	
5	0.92	24.33	0.030	0.20	0.006	
6	0.94	14.47	0.030	2.88	0.003	
8	3.93	19.87	0.040	0.66	0.001	
9	0.60	24.58	0.010	0.71	0.005	
10	0.22	16.76	0.020	1.37	0.007	
11	3.27	3.60	0.001	2.69	0.005	
12	1.35	21.96	0.040	0.84	0.002	
13	1.88	19.26	0.020	2.78	0.008	

Ammonia after normalization :

	aluminium	ammonia	arsenic	barium	cadmium	chloramine	chromium	cop
1	1.65	0.305917753	0.040	2.85	0.007	0.35	0.83	
2	2.32	0.709796055	0.010	3.31	0.002	5.28	0.68	
3	1.01	0.471079906	0.040	0.58	0.008	4.24	0.53	
4	1.36	0.381143430	0.040	2.96	0.001	7.23	0.03	
5	0.92	0.815780675	0.030	0.20	0.006	2.67	0.69	
6	0.94	0.486125042	0.030	2.88	0.003	0.80	0.43	
8	3.93	0.666666667	0.040	0.66	0.001	6.22	0.10	
9	0.60	0.824139084	0.010	0.71	0.005	3.14	0.77	
10	0.22	0.562688064	0.020	1.37	0.007	6.40	0.49	

Perchlorate before normalization :

	nitrates	nitrites	mercury	perchlorate	radium	selenium	si
16	1.41	1.29	0.004	9.12	1.72	0.02	
17	6.74	1.11	0.003	16.90	2.41	0.02	
35	9.75	1.89	0.006	27.17	5.42	0.08	
97	13.65	1.81	0.001	53.35	7.24	0.08	
57	14.66	1.84	0.004	23.43	4.99	0.08	
09	4.79	1.46	0.010	30.42	0.08	0.03	
45	8.47	1.25	0.006	55.40	7.80	0.05	
11	18.40	1.49	0.009	21.52	1.30	0.08	
03	4.37	1.95	0.006	22.12	1.97	0.03	
01	1.16	1.11	0.008	26.80	5.58	0.09	
17	1.99	1.08	0.007	11.16	0.98	0.01	
30	1.91	1.20	0.008	0.18	6.89	0.06	

Perchlorate after normalization :

	nitrites	mercury	perchlorate	radium	selenium	silver	uranium	is_safe
08	1.13	0.007	0.63032226	6.78	0.08	0.34	0.02	Yes
01	1.93	0.003	0.53865420	3.21	0.08	0.27	0.05	Yes
6	1.11	0.006	0.83953916	7.07	0.07	0.44	0.01	No
41	1.29	0.004	0.15227918	1.72	0.02	0.45	0.05	Yes
74	1.11	0.003	0.28218400	2.41	0.02	0.06	0.02	Yes
75	1.89	0.006	0.45366505	5.42	0.08	0.19	0.02	Yes
55	1.81	0.001	0.89079980	7.24	0.08	0.08	0.07	No

Dataset before :

waterQuality

Filter

	aluminium	ammonia	arsenic	barium	cadmium	chloramine	chromium	copper	flouride	bacteria	viruses	lead	nitrates	nitrites	mercury	perchlorate	radium	selenium	silver	uranium	is_safe
1	1.65	9.08	0.040	2.85	0.007	0.35	0.83	0.17	0.05	0.20	0.000	0.054	16.08	1.13	0.007	37.75	6.78	0.08	0.34	0.02	1
2	2.32	21.16	0.010	3.31	0.002	5.28	0.68	0.66	0.90	0.65	0.650	0.100	2.01	1.93	0.003	32.26	3.21	0.08	0.27	0.05	1
3	1.01	14.02	0.040	0.58	0.008	4.24	0.53	0.02	0.99	0.05	0.003	0.078	14.16	1.11	0.006	50.28	7.07	0.07	0.44	0.01	0
4	1.36	11.33	0.040	2.96	0.001	7.23	0.03	1.66	1.08	0.71	0.710	0.016	1.41	1.29	0.004	9.12	1.72	0.02	0.45	0.05	1
5	0.92	24.33	0.030	0.20	0.006	2.67	0.69	0.57	0.61	0.13	0.001	0.117	6.74	1.11	0.003	16.90	2.41	0.02	0.06	0.02	1
6	0.94	14.47	0.030	2.88	0.003	0.80	0.43	1.38	0.11	0.67	0.670	0.135	9.75	1.89	0.006	27.17	5.42	0.08	0.19	0.02	1
7	2.36	5.6	0.010	1.35	0.004	1.28	0.62	1.88	0.33	0.13	0.007	0.021	18.60	1.78	0.007	45.34	2.84	0.10	0.24	0.08	0
8	3.93	19.87	0.040	0.66	0.001	6.22	0.10	1.86	0.86	0.16	0.005	0.197	13.65	1.81	0.001	53.35	7.24	0.08	0.08	0.07	0
9	0.60	24.58	0.010	0.71	0.005	3.14	0.77	1.45	0.98	0.35	0.002	0.167	14.66	1.84	0.004	23.43	4.99	0.08	0.25	0.08	1
10	0.22	16.76	0.020	1.37	0.007	6.40	0.49	0.82	1.24	0.83	0.830	0.109	4.79	1.46	0.010	30.42	0.08	0.03	0.31	0.01	1
11	3.27	3.6	0.001	2.69	0.005	5.75	0.15	0.60	1.29	0.04	0.008	0.145	8.47	1.25	0.006	55.40	7.80	0.05	0.33	0.06	0
12	1.35	21.96	0.040	0.84	0.002	0.10	0.76	0.17	0.58	0.52	0.520	0.011	18.40	1.49	0.009	21.52	1.30	0.08	0.48	0.08	1
13	1.88	19.26	0.020	2.78	0.008	0.05	0.42	1.00	0.09	0.91	0.910	0.103	4.37	1.95	0.006	22.12	1.97	0.03	0.06	0.05	1
14	4.93	23.98	0.040	3.05	0.008	0.70	0.51	1.35	1.07	0.70	0.700	0.101	1.16	1.11	0.008	26.80	5.58	0.09	0.38	0.03	1
15	2.89	18.82	0.050	3.77	0.008	5.99	0.54	0.79	0.54	0.20	0.009	0.126	17.56	1.82	0.009	17.54	4.33	0.10	0.05	0.02	1
16	0.61	2.41	0.030	0.59	0.002	1.94	0.77	1.54	0.62	0.23	0.001	0.017	1.99	1.08	0.007	11.16	0.98	0.01	0.47	0.03	1
17	3.47	15.84	0.020	0.06	0.001	5.29	0.47	1.08	1.43	0.89	0.890	0.080	1.91	1.20	0.008	0.18	6.89	0.06	0.12	0.08	1
18	2.11	17.03	0.020	0.88	0.009	7.78	0.88	1.15	0.34	0.85	0.850	0.065	17.86	1.53	0.003	19.40	1.14	0.10	0.40	0.01	1
19	4.88	26.94	0.020	0.36	0.001	1.21	0.68	0.71	0.99	0.75	0.750	0.071	0.31	1.22	0.002	56.70	1.00	0.00	0.41	0.05	0
20	4.12	17.99	0.020	3.43	0.006	0.01	0.41	1.82	0.22	0.99	0.990	0.108	8.06	1.76	0.005	24.29	0.88	0.10	0.10	0.07	1
21	0.68	18.99	0.001	0.04	0.006	4.57	0.20	1.18	1.00	0.92	0.920	0.086	9.46	1.41	0.007	21.79	3.05	0.03	0.13	0.08	1
22	1.15	8.12	0.020	0.97	0.007	3.47	0.65	1.51	1.46	0.58	0.580	0.061	8.96	1.50	0.004	14.60	1.74	0.03	0.01	0.06	1
23	0.27	10.67	0.020	0.55	0.001	3.74	0.12	1.77	0.43	0.80	0.800	0.114	12.69	1.18	0.008	34.64	0.90	0.02	0.16	0.06	1
24	4.32	20.64	0.030	2.60	0.008	7.24	0.61	1.23	1.44	0.56	0.560	0.012	9.42	1.74	0.004	36.23	3.22	0.07	0.18	0.08	0
25	2.36	27.05	0.010	0.68	0.003	4.07	0.13	1.34	0.29	0.96	0.960	0.167	15.05	1.92	0.002	56.32	7.99	0.06	0.50	0.06	0
26	3.31	22.07	0.030	0.46	0.001	7.22	0.73	1.05	1.00	0.25	0.007	0.109	1.92	1.07	0.001	39.40	0.49	0.04	0.47	0.05	1
27	1.82	6.81	0.010	0.85	0.006	2.55	0.25	1.09	1.35	0.16	0.002	0.031	16.99	1.70	0.007	44.76	1.15	0.08	0.26	0.08	1
28	3.42	2.4	0.001	2.80	0.003	2.87	0.73	0.27	0.53	0.44	0.002	0.110	13.73	1.69	0.009	55.27	3.29	0.04	0.17	0.00	0
29	4.41	15.14	0.030	1.76	0.007	6.63	0.62	1.57	0.26	0.69	0.690	0.182	1.49	1.81	0.008	24.91	2.39	0.01	0.20	0.05	1
30	4.57	25.84	0.010	3.04	0.002	2.78	0.72	0.46	1.41	0.08	0.006	0.049	9.64	1.43	0.006	36.57	4.55	0.03	0.19	0.00	0
31	1.69	22.8	0.001	2.01	0.002	5.87	0.78	1.53	0.87	0.13	0.008	0.079	8.64	1.19	0.007	24.61	7.77	0.06	0.11	0.05	1
32	1.87	6.1	0.050	3.74	0.008	2.86	0.52	1.03	0.51	0.77	0.770	0.012	1.11	1.55	0.008	20.32	2.21	0.02	0.48	0.04	1
33	2.71	26.19	0.040	3.02	0.006	4.00	0.17	1.56	0.91	0.38	0.005	0.013	11.00	1.00	0.006	14.16	6.16	0.05	0.05	0.08	1
34	1.63	15.75	0.030	2.54	0.008	4.25	0.74	1.35	1.24	0.12	0.006	0.193	17.29	1.27	0.001	58.15	1.71	0.09	0.44	0.05	0
35	0.01	29.29	0.001	2.93	0.007	7.75	0.68	1.09	0.00	0.80	0.800	0.091	17.33	1.86	0.001	43.09	3.76	0.09	0.30	0.00	0
36	4.49	4.07	0.050	1.87	0.005	4.55	0.32	0.90	0.55	0.30	0.002	0.135	5.23	1.43	0.004	36.52	6.15	0.04	0.16	0.04	1
37	3.52	23.19	0.030	2.69	0.006	4.94	0.76	1.85	1.24	0.75	0.750	0.124	1.91	1.00	0.008	24.84	3.19	0.08	0.37	0.06	1
38	4.35	26.85	0.020	0.88	0.004	0.64	0.61	0.91	0.42	0.44	0.006	0.107	13.24	1.19	0.009	0.73	0.50	0.04	0.35	0.00	1
39	2.51	13.08	0.040	1.58	0.002	2.86	0.87	1.88	0.40	0.13	0.004	0.085	11.96	1.35	0.008	46.30	4.70	0.10	0.04	0.05	0
40	2.34	19.9	0.030	2.67	0.006	4.30	0.26	0.08	0.34	0.26	0.003	0.146	7.96	1.56	0.006	51.39	2.41	0.09	0.12	0.05	0
41	1.71	9.49	0.050	3.63	0.006	2.24	0.90	0.22	0.68	0.63	0.630	0.162	11.40	1.83	0.005	42.64	6.14	0.09	0.44	0.06	0

Dataset after :

Filter

	aluminium	ammonia	arsenic	barium	cadmium	chloramine	chromium	copper	flouride	bacteria	viruses	lead	nitrates	nitrites	mercury	perchlorate	radium	selenium	silver	uranium	is_safe
1	1.65	0.305917753	0.040	2.85	0.007	0.35	0.83	0.17	0.05	0.20	0.000	0.054	0.811206461	1.13	0.007	0.630322257	6.78	0.08	0.34	0.02	Yes
2	2.32	0.709796055	0.010	3.31	0.002	5.28	0.68	0.66	0.90	0.65	0.650	0.100	0.100959112	1.93	0.003	0.538654199	3.21	0.08	0.27	0.05	Yes
3	1.01	0.471079906	0.040	0.58	0.008	4.24	0.53	0.02	0.99	0.05	0.003	0.078	0.714285714	1.11	0.006	0.839539155	7.07	0.07	0.44	0.01	No
4	1.36	0.381143430	0.040	2.96	0.001	7.23	0.03	1.66	1.08	0.71	0.710	0.016	0.070671378	1.29	0.004	0.152279178	1.72	0.02	0.45	0.05	Yes
5	0.92	0.815780675	0.030	0.20	0.006	2.67	0.69	0.57	0.61	0.13	0.001	0.117	0.339727410	1.11	0.003	0.282184004	2.41	0.02	0.06	0.02	Yes
6	0.94	0.486125042	0.030	2.88	0.003	0.80	0.43	1.38	0.11	0.67	0.670	0.135	0.491670873	1.89	0.006	0.453665053	5.42	0.08	0.19	0.02	Yes
8	3.93	0.666666667	0.040	0.66	0.001	6.22	0.10	1.86	0.86	0.16	0.005	0.197	0.688541141	1.81	0.001	0.890799800	7.24	0.08	0.08	0.07	No
9	0.60	0.824139084	0.010	0.71	0.005	3.14	0.77	1.45	0.98	0.35	0.002	0.167	0.739525492	1.84	0.004	0.391217232	4.99	0.08	0.25	0.08	Yes
10	0.22	0.562688064	0.020	1.37	0.007	6.40	0.49	0.82	1.24	0.83	0.830	0.109	0.241292277	1.46	0.010	0.507931207	0.08	0.03	0.31	0.01	Yes
11	3.27	0.122701438	0.001	2.69	0.005	5.75	0.15	0.60	1.29	0.04	0.008	0.145	0.427057042	1.25	0.006	0.925029220	7.80	0.05	0.33	0.06	No
12	1.35	0.736542962	0.040	0.84	0.002	0.10	0.76	0.17	0.58	0.52	0.520	0.011	0.928319031	1.49	0.009	0.359325430	1.30	0.08	0.48	0.08	Yes
13	1.88	0.646272150	0.020	2.78	0.008	0.05	0.42	1.00	0.09	0.91	0.910	0.103	0.220090863	1.95	0.006	0.369343797	1.97	0.03	0.06	0.05	Yes
14	4.93	0.804078903	0.040	3.05	0.008	0.70	0.51	1.35	1.07	0.70	0.700	0.101	0.058051489	1.11	0.008	0.447487060	5.58	0.09	0.38	0.03	Yes
16	0.61	0.082915413	0.030	0.59	0.002	1.94	0.77	1.54	0.62	0.23	0.001	0.017	0.099949520	1.08	0.007	0.186341626	0.98	0.01	0.47	0.03	Yes
17	3.47	0.531929121	0.020	0.06	0.001	5.29	0.47	1.08	1.43	0.89	0.890	0.080	0.095911156	1.20	0.008	0.003005510	6.89	0.06	0.12	0.08	Yes
19	4.88	0.903042461	0.020	0.36	0.001	1.21	0.68	0.71	0.99	0.75	0.750	0.071	0.015143867	1.22	0.002	0.946735682	1.00	0.00	0.41	0.05	No
21	0.68	0.637245069	0.001	0.04	0.006	4.57	0.20	1.18	1.00	0.92	0.920	0.086	0.477031802	1.41	0.007	0.363833695	3.05	0.03	0.13	0.08	Yes
22	1.15	0.273821464	0.020	0.97	0.007	3.47	0.65	1.51	1.46	0.58	0.580	0.061	0.451792024	1.50	0.004	0.243780264	1.74	0.03	0.01	0.06	Yes
23	0.27	0.359077232	0.020	0.55	0.001	3.74	0.12	1.77	0.43	0.80	0.800	0.114	0.640080767	1.18	0.008	0.578393722	0.90	0.02	0.16	0.06	Yes
24	4.32	0.692410565	0.030	2.60	0.008	7.24	0.61	1.23	1.44	0.56	0.560	0.012	0.475012620	1.74	0.004	0.604942394	3.22	0.07	0.18	0.08	No
26	3.31	0.740220662	0.030	0.46	0.001	7.22	0.73	1.05	1.00	0.25	0.007	0.109	0.096415952	1.07	0.001	0.657872767	0.49	0.04	0.47	0.05	Yes
27	1.82	0.230023404	0.010	0.85	0.006	2.55	0.25	1.09	1.35	0.16	0.002	0.031	0.857142857	1.70	0.007	0.747370179	1.15	0.08	0.26	0.08	Yes
28	3.42	0.082581077	0.001	2.80	0.003	2.87	0.73	0.27	0.53	0.44	0.002	0.110	0.692579505	1.69	0.009	0.922858574	3.29	0.04	0.17	0.00	No
29	4.41	0.508525577	0.030	1.76	0.007	6.63	0.62	1.57	0.26	0.69	0.690	0.182	0.074709743	1.81	0.008	0.415929204	2.39	0.01	0.20	0.05	Yes
30	4.57	0.866265463	0.010	3.04	0.002	2.78	0.72	0.46	1.41	0.08	0.006	0.049	0.486118122	1.43	0.006	0.610619469	4.55	0.03	0.19	0.00	No
31	1.69	0.764627215	0.001	2.01	0.002	5.87	0.78	1.53	0.87	0.13	0.008	0.079	0.435638566	1.19	0.007	0.410920020	7.77	0.06	0.11	0.05	Yes
32	1.87	0.206285523	0.050	3.74	0.008	2.86	0.52	1.03	0.51	0.77	0.770	0.012	0.055527511	1.55	0.008	0.339288696	2.21	0.02	0.48	0.04	Yes
33	2.71	0.877967235	0.040	3.02	0.006	4.00	0.17	1.56	0.91	0.38	0.005	0.013	0.554770318	1.00	0.006	0.236433461	6.16	0.05	0.05	0.08	Yes
34	1.63	0.528920094	0.030	2.54	0.008	4.25	0.74	1.35	1.24	0.12	0.006	0.193	0.872286724	1.27	0.001	0.970946736	1.71	0.09	0.44	0.05	No
36	4.49	0.138415246	0.050	1.87	0.005	4.55	0.32	0.90	0.55	0.30	0.002	0.135	0.263503281	1.43	0.004	0.609784605	6.15	0.04	0.16	0.04	Yes
37	3.52	0.777666332	0.030	2.69	0.006	4.94	0.76	1.85	1.24	0.75	0.750	0.124	0.095911156	1.00	0.008	0.414760394	3.19	0.08	0.37	0.06	Yes
38	4.35	0.900033434	0.020	0.88	0.004	0.64	0.61	0.91	0.42	0.44	0.006	0.107	0.667844523	1.19	0.009	0.012189013	0.50	0.04	0.35	0.00	Yes

Appendix: this code show the outlier remove

```
library(outliers)
OutlierUran=outlier(waterQuality$uranium,logical=TRUE)
Find_outlier=which(OutlierUran==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierAl=outlier(waterQuality$aluminium,logical=TRUE)
Find_outlier=which(OutlierAl==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierArs=outlier(waterQuality$arsenic,logical=TRUE)
Find_outlier=which(OutlierArs==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierBar=outlier(waterQuality$barium,logical=TRUE)
Find_outlier=which(OutlierBar==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierCad=outlier(waterQuality$cadmium,logical=TRUE)
Find_outlier=which(OutlierCad==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierChlo=outlier(waterQuality$chloramine,logical=TRUE)
Find_outlier=which(OutlierChlo==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierChrom=outlier(waterQuality$chromium,logical=TRUE)
```

```
OutlierChrom=outlier(waterQuality$chromium,logical=TRUE)
Find_outlier=which(OutlierChrom==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierCo=outlier(waterQuality$copper,logical=TRUE)
 Find_outlier=which(OutlierCo==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierFl=outlier(waterQuality$flouride,logical=TRUE)
Find_outlier=which(OutlierFl==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierBa=outlier(waterQuality$bacteria,logical=TRUE)
Find_outlier=which(OutlierBa==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierVi=outlier(waterQuality$viruses,logical=TRUE)
Find_outlier=which(OutlierVi==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierLe=outlier(waterQuality$lead,logical=TRUE)
Find_outlier=which(OutlierLe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierNi1=outlier(waterQuality$nitrates,logical=TRUE)
Find_outlier=which(OutlierNi1==TRUE,arr.ind=TRUE)
```

```
Find_outlier=which(OutlierNi1==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierNi2=outlier(waterQuality$nitrites,logical=TRUE)
Find_outlier=which(OutlierNi2==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierMe=outlier(waterQuality$mercury,logical=TRUE)
Find_outlier=which(OutlierMe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierPe=outlier(waterQuality$perchlorate,logical=TRUE)
Find_outlier=which(OutlierPe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierRa=outlier(waterQuality$radium,logical=TRUE)
Find_outlier=which(OutlierRa==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierSe=outlier(waterQuality$selenium,logical=TRUE)
Find_outlier=which(OutlierSe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
OutlierSi=outlier(waterQuality$silver,logical=TRUE)
Find_outlier=which(OutlierSi==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
```

5 Data Mining Technique

For our dataset, we will use both classification and clustering.

We applied classification technique(supervised) because the class label (is_safe) is provided in our dataset which indicates whether water is safe or not by predicting the amount of elements(barium,ammonia..etc) for each liter of water.

We will divide our dataset to training and testing data by applying decision tree. We will use the training data set to construct the classification model, and the test data set to determine the accuracy of the classification model so we can predict the new data class labels accurately.

In order to apply the clustering technique(unsupervised), the class label (is_safe) must be removed from our dataset.

We used the K-means technique, which that each cluster is represented by the center of the cluster.

K-means assign each object to the cluster with the nearest center point based on euclidean distance.

The used packages for classification: party – caret

The used packages for clustering: factoextra – cluster – NbClust

The used methods for classification: set.seed() – nrow() – sample() – ctree() – table() – predict() – print() – plot()

confusionMatrix()

The used methods for clustering: set.seed() – subset() – scale() – kmeans() – fviz_cluster() – silhouette() – fviz_sillhouete() – fviz_NbClust() – lab() - dist() .

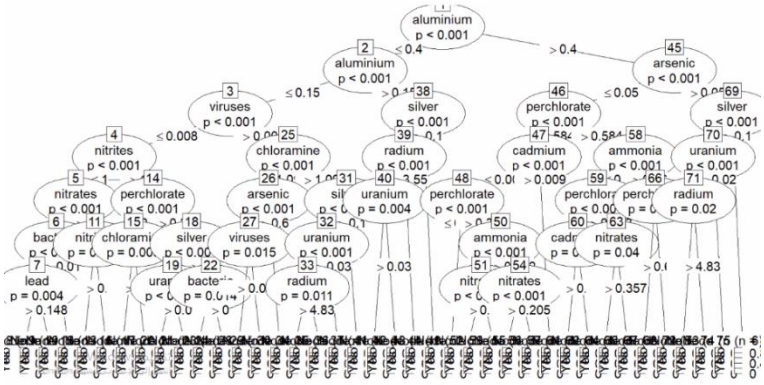
6 Evaluation and Comparison

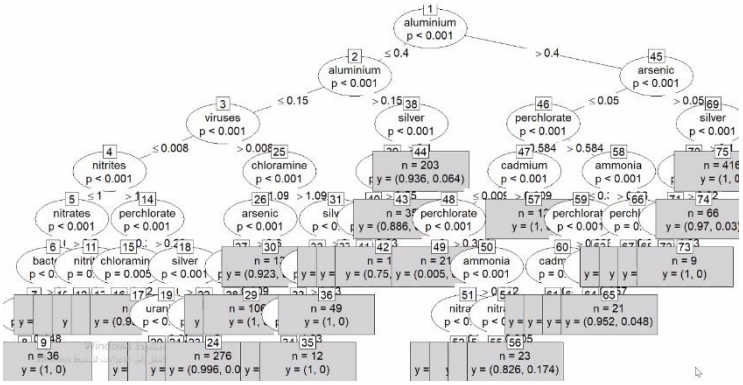
Classification:

Mining task	Comparison Criteria
Classification	– Decision Tree #1: 70% training 30% testing – Decision Tree #2: 50% training 50% testing – Decision Tree #3: 80% training 20% testing

	#1: 70% training 30% testing	#2: 50% training 50% testing	#3: 80% training 20% testing
Accuracy	95.50791%	96.25799%	96%
precision	96.02%	96.77%	96.35%
sensitivity	99.02%	99.07%	99.23%
specificity	69.26%	74.74%	71.61%
Preferred partition?	✗	✓	✗

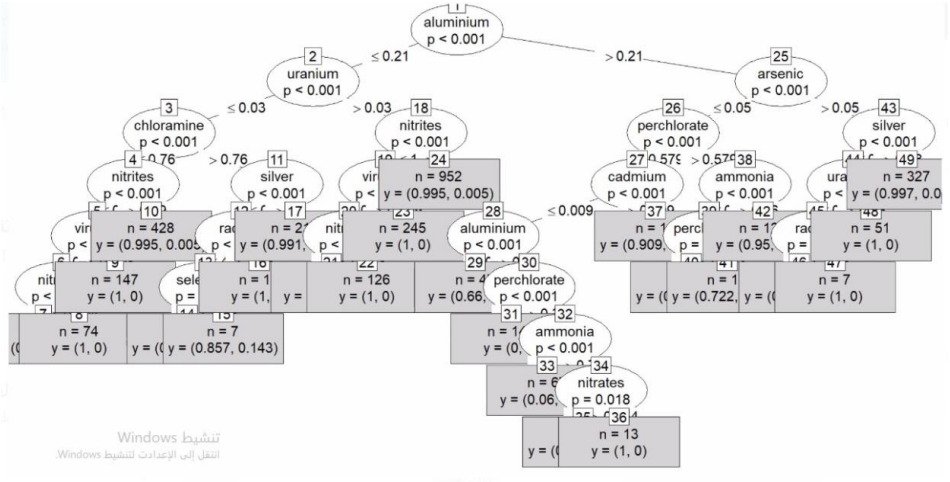
Decision Tree #1: 70%-30%

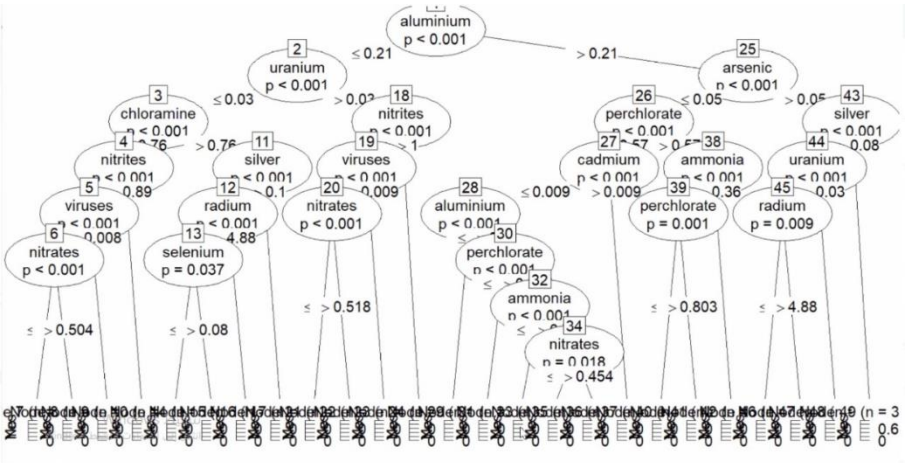




```
Confusion Matrix and Statistics

          Reference
Prediction   No  Yes
       No  1711   71
       Yes   17  160

               Accuracy : 0.9551
                 95% CI : (0.9449, 0.9638)
    No Information Rate : 0.8821
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.7597

 Mcnemar's Test P-Value : 1.606e-08

            Sensitivity : 0.9902
            Specificity : 0.6926
         Pos Pred Value : 0.9602
         Neg Pred Value : 0.9040
             Prevalence : 0.8821
         Detection Rate : 0.8734
   Detection Prevalence : 0.9096
      Balanced Accuracy : 0.8414

       'Positive' Class : No
```

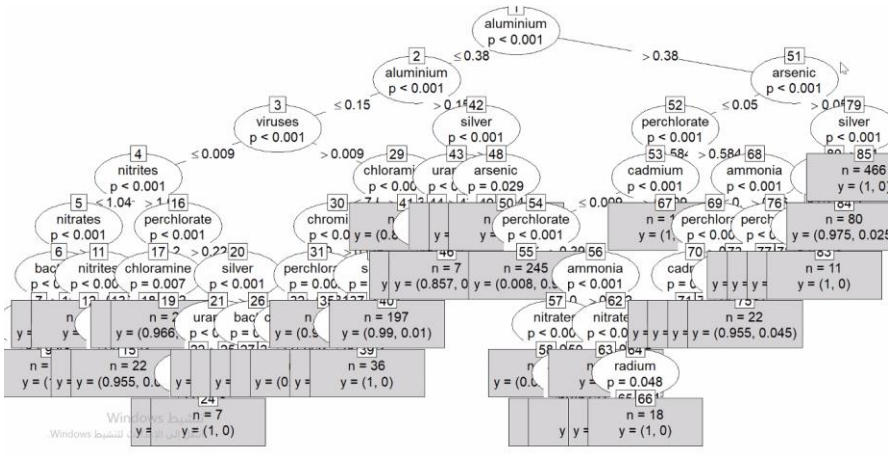

Decision Tree #2: 50%-50%

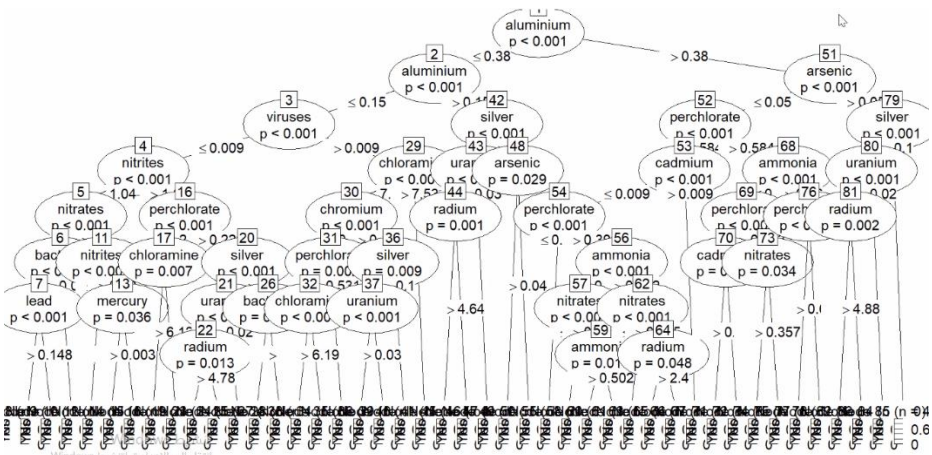




```
Confusion Matrix and Statistics

          Reference
Prediction   No  Yes
       No  2880   96
       Yes   27  284

               Accuracy : 0.9626
                 95% CI : (0.9555, 0.9688)
    No Information Rate : 0.8844
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.8013

 Mcnemar's Test P-Value : 8.713e-10

            Sensitivity : 0.9907
            Specificity : 0.7474
         Pos Pred Value : 0.9677
         Neg Pred Value : 0.9132
             Prevalence : 0.8844
         Detection Rate : 0.8762
   Detection Prevalence : 0.9054
      Balanced Accuracy : 0.8690

       'Positive' Class : No
```


Decision Tree #3: 80%-20%





```
Confusion Matrix and Statistics

          Reference
Prediction   No  Yes
       No  1161   44
       Yes    9  111

               Accuracy : 0.96
                 95% CI : (0.948, 0.9699)
    No Information Rate : 0.883
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.7854

 Mcnemar's Test P-Value : 3.008e-06

            Sensitivity : 0.9923
            Specificity : 0.7161
         Pos Pred Value : 0.9635
         Neg Pred Value : 0.9250
             Prevalence : 0.8830
         Detection Rate : 0.8762
   Detection Prevalence : 0.9094
      Balanced Accuracy : 0.8542

       'Positive' Class : No
```

Clustering:

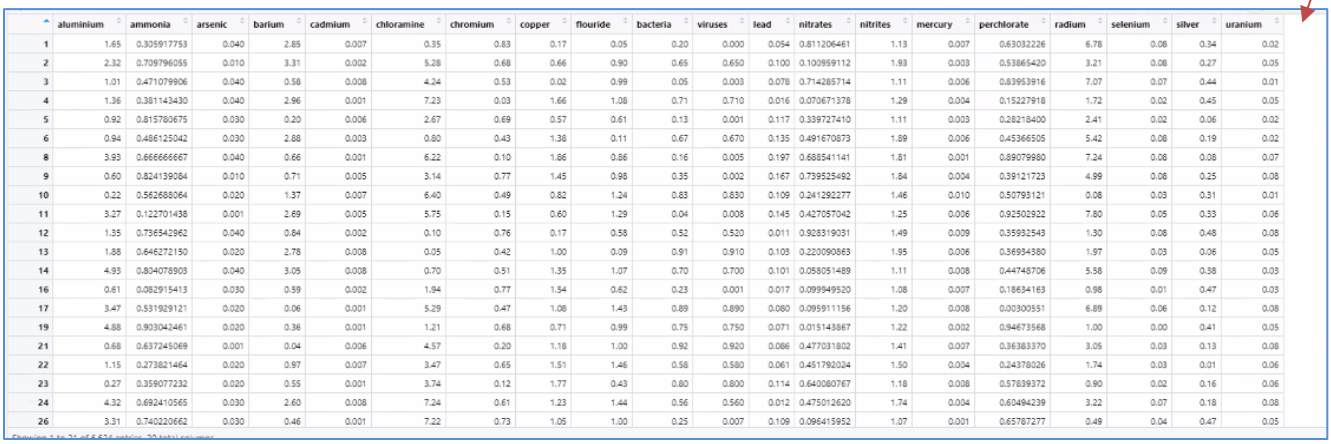
Now we will apply clustering to our dataset after removing the class label attribute

```
##Removing the class label for clustring technique
waterQuality<- subset( waterQuality, select = -is_safe )
```

Dataset after removing class label(is_safe)

Class label was here

waterQuality 6624 obs. of 20 variables



aluminium	ammonia	arsenic	barium	cadmium	chloramine	chromium	copper	flouride	bacteria	viruses	lead	nitrates	nitrites	mercury	perchlorate	radium	selenium	silver	uranium
1.65	0.305917753	0.040	2.85	0.007	0.35	0.83	0.17	0.05	0.20	0.000	0.054	0.811206461	1.13	0.007	0.63032226	6.78	0.08	0.34	0.02
2.32	0.709796055	0.010	3.31	0.002	5.28	0.68	0.66	0.90	0.65	0.650	0.100	0.100959112	1.93	0.003	0.53865420	3.21	0.08	0.27	0.05
1.01	0.471079906	0.040	0.58	0.008	4.24	0.53	0.02	0.99	0.05	0.003	0.078	0.714285714	1.11	0.006	0.83953916	7.07	0.07	0.44	0.01
1.36	0.381143430	0.040	2.96	0.001	7.23	0.03	1.66	1.08	0.71	0.710	0.016	0.070671378	1.29	0.004	0.15227918	1.72	0.02	0.45	0.05
0.92	0.815780675	0.030	0.20	0.006	2.67	0.69	0.57	0.61	0.13	0.001	0.117	0.339727410	1.11	0.003	0.28218400	2.41	0.02	0.06	0.02
0.94	0.486125042	0.030	2.68	0.003	0.80	0.43	1.38	0.11	0.67	0.670	0.135	0.491670873	1.89	0.006	0.45366505	5.42	0.08	0.19	0.02
3.93	0.666666667	0.040	0.66	0.001	6.22	0.10	1.86	0.86	0.16	0.005	0.197	0.688541141	1.81	0.001	0.89079980	7.24	0.08	0.08	0.07
0.60	0.824139084	0.010	0.71	0.005	3.14	0.77	1.45	0.98	0.35	0.002	0.167	0.739525492	1.84	0.004	0.39121723	4.99	0.08	0.25	0.08
0.22	0.562688064	0.020	1.37	0.007	6.40	0.49	0.82	1.24	0.83	0.830	0.109	0.241292277	1.46	0.010	0.50793121	0.08	0.03	0.31	0.01
3.27	0.122701438	0.001	2.69	0.005	5.75	0.15	0.60	1.29	0.04	0.008	0.145	0.427057042	1.25	0.006	0.92502922	7.80	0.05	0.33	0.06
1.35	0.736542962	0.040	0.84	0.002	0.10	0.76	0.17	0.58	0.52	0.520	0.011	0.928319031	1.49	0.009	0.35932543	1.30	0.08	0.48	0.08
1.88	0.646272150	0.020	2.78	0.008	0.05	0.42	1.00	0.09	0.91	0.910	0.103	0.220090863	1.95	0.006	0.36934380	1.97	0.03	0.06	0.05
4.93	0.804078903	0.040	3.05	0.008	0.70	0.51	1.35	1.07	0.70	0.700	0.101	0.058051489	1.11	0.008	0.44748706	5.58	0.09	0.38	0.03
0.61	0.082915413	0.030	0.59	0.002	1.94	0.77	1.54	0.62	0.23	0.001	0.017	0.099949520	1.08	0.007	0.18634163	0.98	0.01	0.47	0.03
3.47	0.531929121	0.020	0.06	0.001	5.29	0.47	1.08	1.43	0.89	0.890	0.080	0.095911156	1.20	0.008	0.00300551	6.89	0.06	0.12	0.08
4.88	0.903042461	0.020	0.36	0.001	1.21	0.68	0.71	0.99	0.75	0.750	0.071	0.015143867	1.22	0.002	0.94673568	1.00	0.00	0.41	0.05
0.68	0.637245069	0.001	0.04	0.006	4.57	0.20	1.18	1.00	0.92	0.920	0.086	0.477031802	1.41	0.007	0.36383370	3.05	0.03	0.13	0.08
1.15	0.273821464	0.020	0.97	0.007	3.47	0.65	1.51	1.46	0.58	0.580	0.061	0.451792024	1.50	0.004	0.24378026	1.74	0.03	0.01	0.06
0.27	0.359077232	0.020	0.55	0.001	3.74	0.12	1.77	0.43	0.80	0.800	0.114	0.640080767	1.18	0.008	0.57839372	0.90	0.02	0.16	0.06
4.32	0.692410565	0.030	2.60	0.008	7.24	0.61	1.23	1.44	0.56	0.560	0.012	0.475012620	1.74	0.004	0.60494239	3.22	0.07	0.18	0.08
3.31	0.740220662	0.030	0.46	0.001	7.22	0.73	1.05	1.00	0.25	0.007	0.109	0.096415952	1.07	0.001	0.65787277	0.49	0.04	0.47	0.05

Clustering

- K=2
- K=3
- K=5

	K=2	K=3	K=5
Silhouette width for each cluster	cluster size ave.sil.width 1 1 3168 0.07 2 2 3456 0.26	cluster size ave.sil.width 1 1 1072 0.11 2 2 2951 0.05 3 3 2601 0.13	cluster size ave.sil.width 1 1 918 0.08 2 2 1855 0.07 3 3 1121 0.04 4 4 1174 0.08 5 5 1556 0.13
Silhouette width for all clusters	0.17	0.09	0.08
Visualization	Figure 1	Figure 2	Figure 3
Preferred partition?	✓	✗	✗

Figure 1


Cluster plot
Dim2 (8.4%)
Dim1 (20.5%)
cluster
1
2
Windows تنشيط
انتقل إلى الإعدادات لتنشيط Windows.

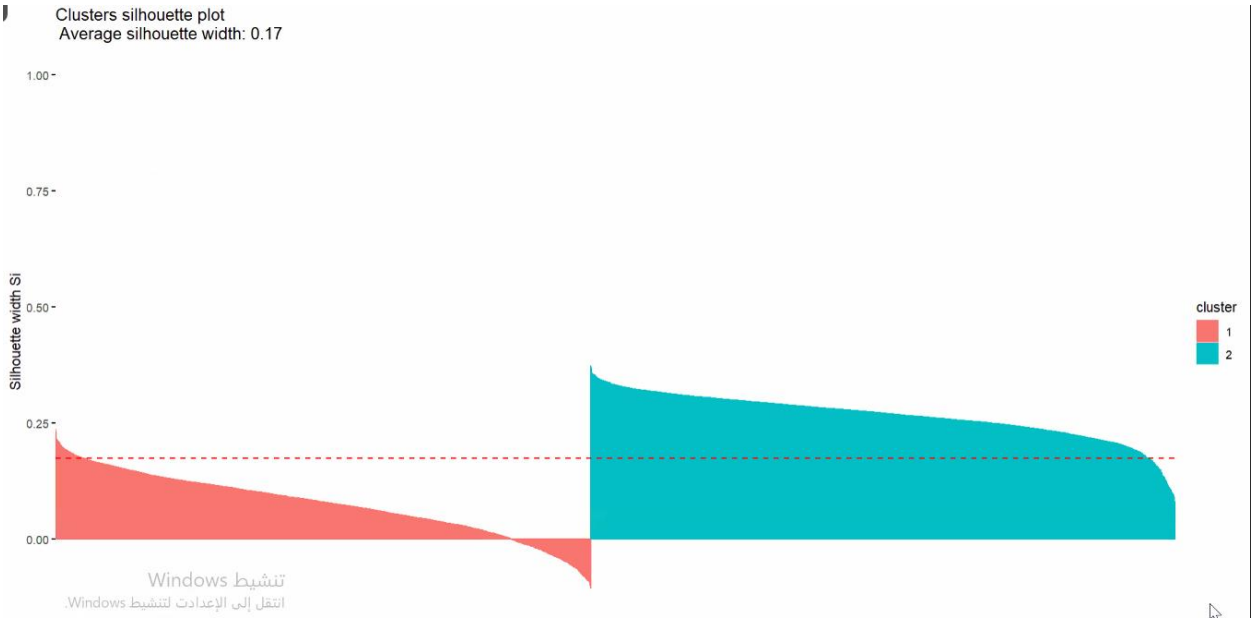
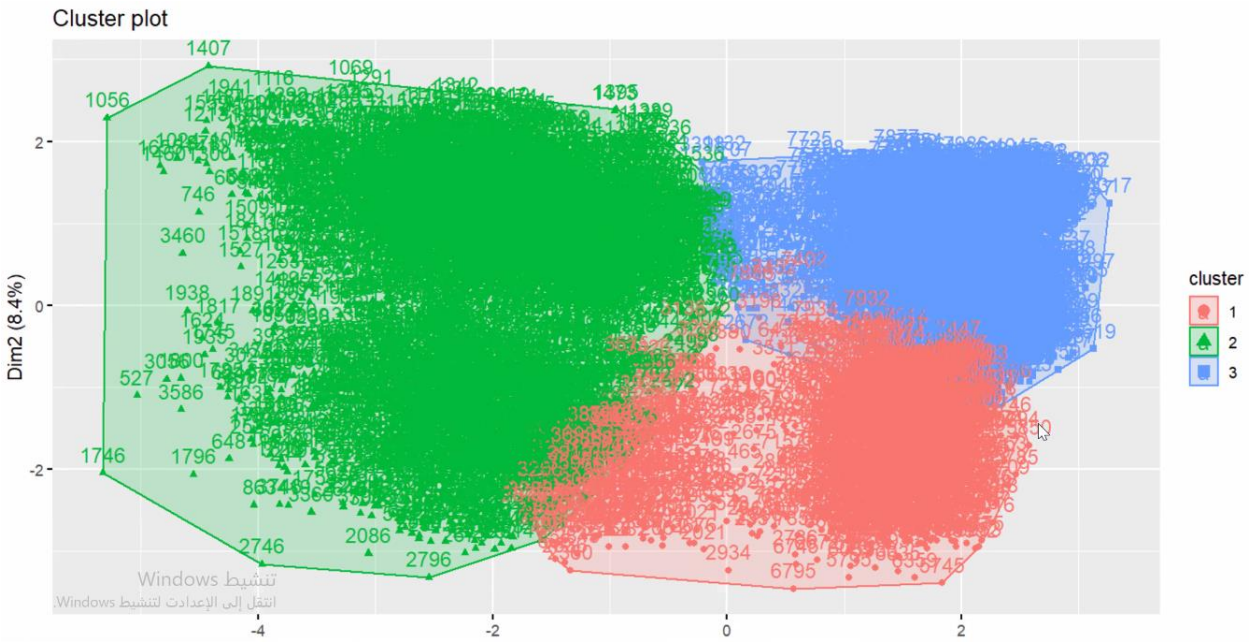

Clusters silhouette plot
Average silhouette width: 0.17
Silhouette width Si
1.00
0.75
0.50
0.25
0.00
cluster
1
2
Windows تنشيط
انتقل إلى الإعدادات لتنشيط Windows.

Figure 2


Cluster plot
Dim2 (8.4%)
cluster
1
2
3

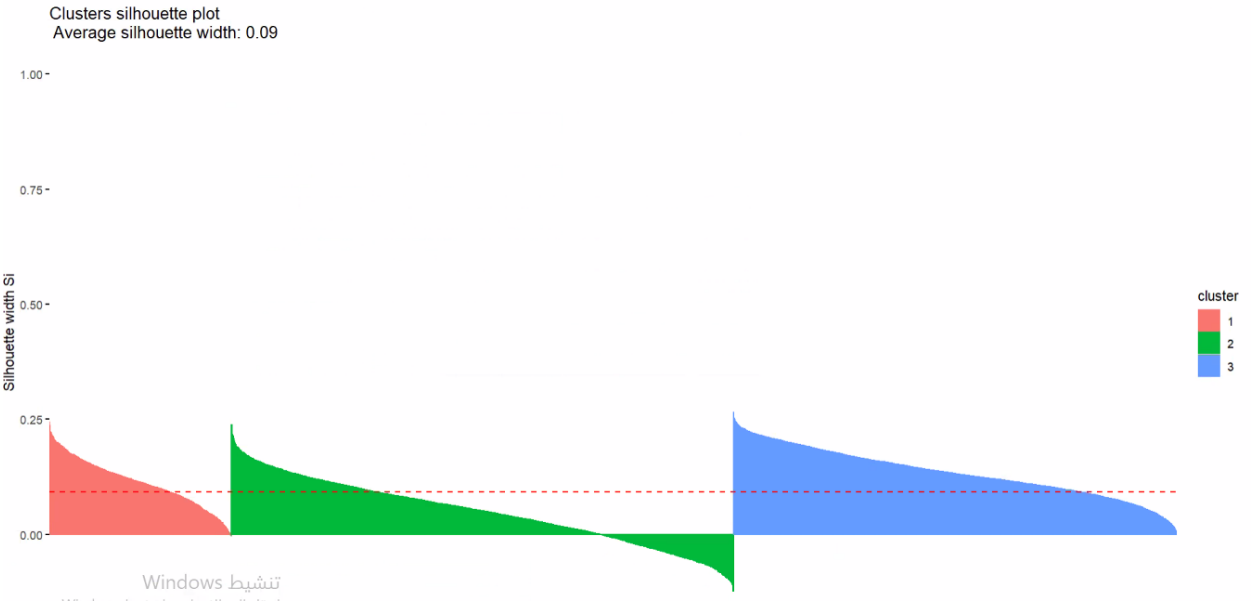
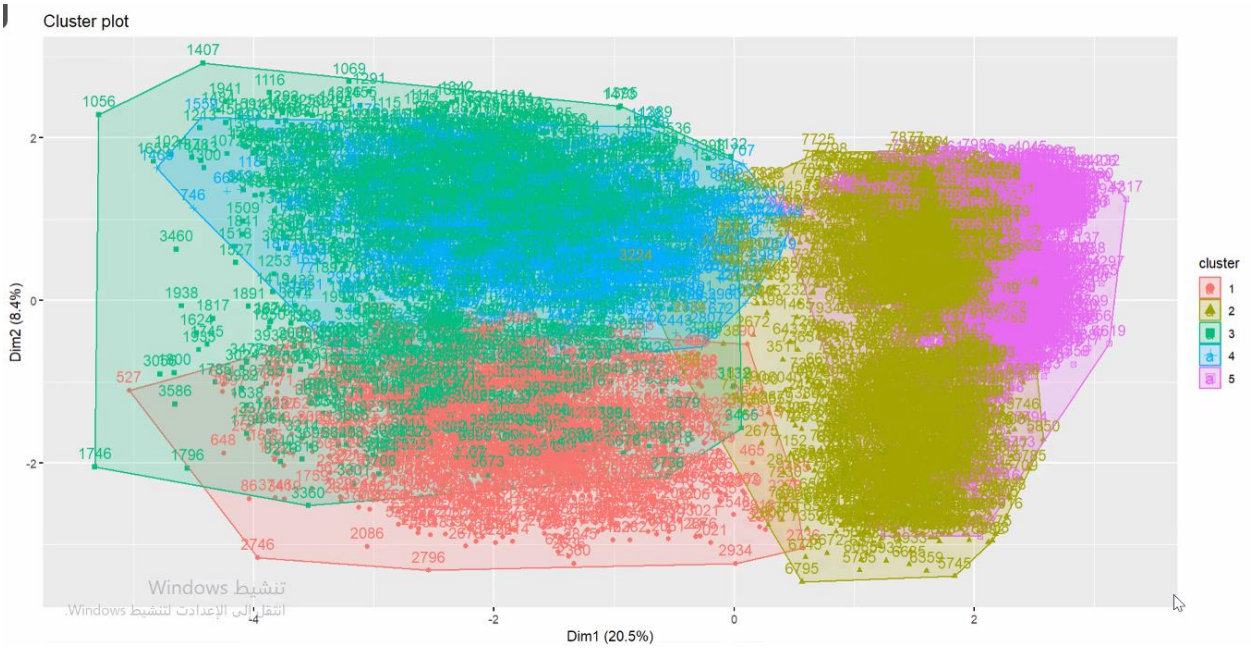
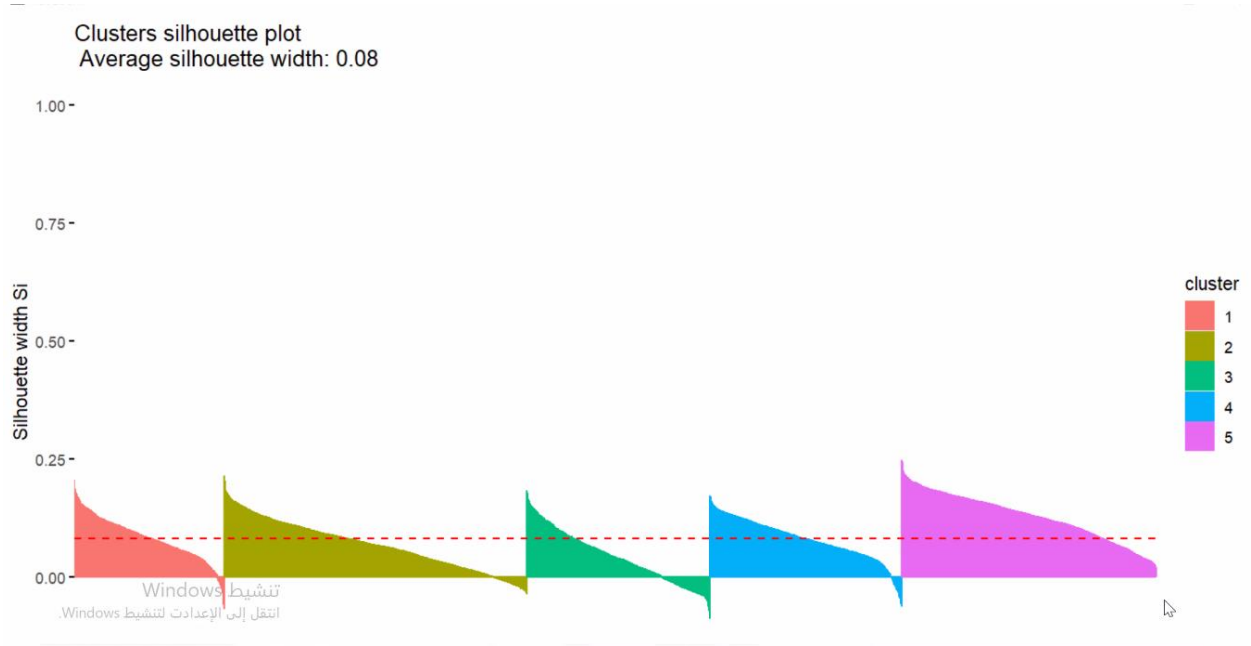
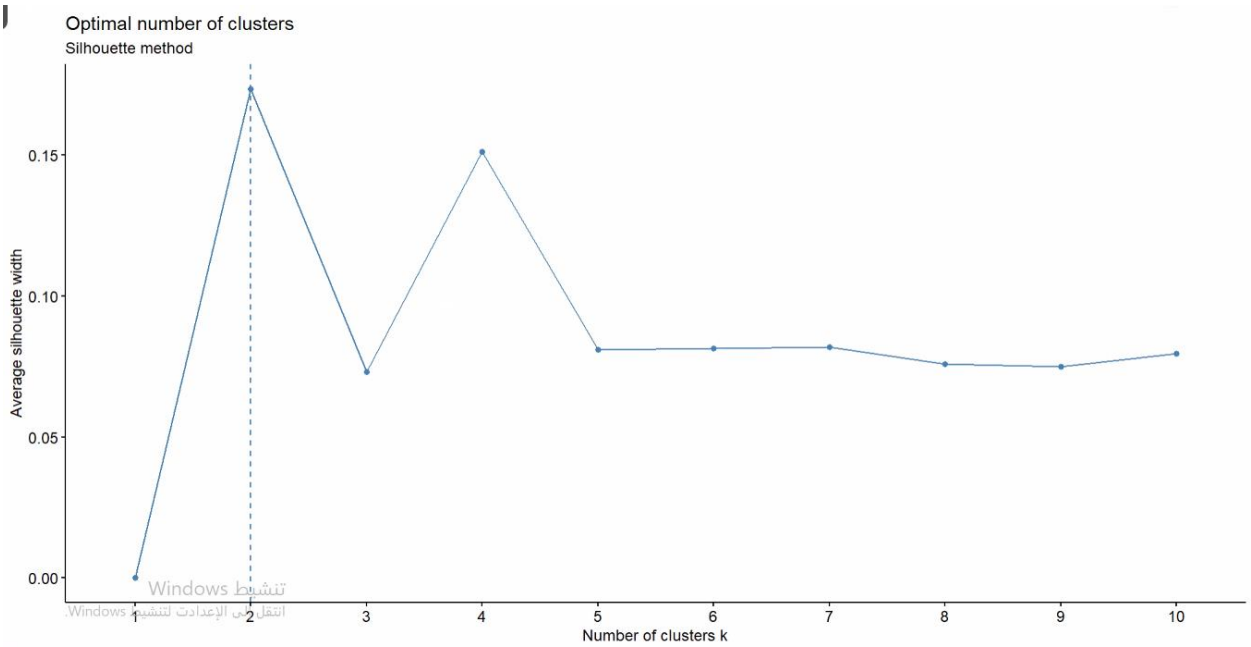

Clusters silhouette plot
Average silhouette width: 0.09
Silhouette width Si
cluster
1
2
3

Figure 3


Cluster plot
Dim2 (8.4%)
Dim1 (20.5%)
cluster
1
2
3
4
5


Clusters silhouette plot
Average silhouette width: 0.08
Silhouette width Si
1.00
0.75
0.50
0.25
0.00
cluster
1
2
3
4
5



7 Findings

After studying the water quality dataset, from determining what each attribute do and how the attribute will effect each other, we apply some preprocessing methods such as cleaning, transformation to prepare our dataset for data mining process.

For classification we studied different cases by dividing our dataset by using Ctree method and then we came up with these results:

-70% training 30% testing , Accuracy=95.50791%

-50% training 50% testing , Accuracy=96.25799%

-80% training 20% testing , Accuracy=96%

We noticed that almost all accuracies are the same, but these results lead to determine the best model for classification technique which is (50%,50%) because it has the highest accuracy which means the class label (is_safe) is affected by all attributes.

(ammonia , barium , arsenic…etc) , that means the evaluation model we considered to be the best classify most of the tuples that are covered by the rule and it correctly classified by class label (is_safe), also this

model lead to determine the correct class_label for each object faster than the others . after analyzing the decision trees we noticed that (80%,20%) and (70%,30%) first splitting point was aluminum and the second level of the tree include aluminum and we think that what makes both two cases accuracies lower than (50%,50%), in (50%,50%) case the second level exchanged the aluminum with uranium.

We noticed that some of our dataset attributes has no affect in the decision tree and has not appeared as a decision node to determine the leaf node (decision) , and these attribute are barium , chromium , copper , fluoride , bacteria , lead and mercury .

As a result, we think analyzing and studying the decision tree is interesting for individuals because they can use this tree to determine that the water they use and drink is safe or not, and for companies to end up selling water that is good for people and the environment. We can also extract some rules from this tree such as:

if the aluminum > 0.21 and the arsenic > 0.05 and the silver < 0.08 and the uranium > 0.03 then n=51 and y=(1,0)

For clustering we studied different cases by changing the number of clusters k and using k-means method and then we came up with these results:

-k=2 , Silhouette width for all clusters: 0.17

-k=3 , Silhouette width for all clusters: 0.09

-k=5 , Silhouette width for all clusters:0.08

These results lead to determine the best model for clustering technique is k=2 because it has the highest Silhouette width (0.17) for all clusters, (0.07) for the first cluster and (0.26) for the second cluster, since the value is approaching 1 ,that means the objects within a cluster are closer to each other than to the objects in the other cluster.

After analyzing the plots, we configure what supports the quality of k=2, that the clusters are not overlapping in figure 1 above, unlike k=3 and k=5, the clusters are overlapping pointedly, in k=3, we can

see that cluster 1,3 and cluster 1,2 are intertwined with each other in figure 2 above, as well as in k=5, we can see for example that cluster 2,5 and cluster 3,4 and other clusters are highly overlapped in figure 3 above, which can make k=5 the worst case in choosing number of clusters.

To capitalize, what makes k=3 and k=5 not in consideration is that because of the overlapping that result in inability when observing where each object belong to the right cluster, but k=2 the Silhouette width is 0.17 which is optimal because k-means method consider the number approach to 1 is better than the others, and what increased our confidence with k=2 is that it is not overlapping, to enhance our analyzing we validated which number of clusters is the best using fviz_nbclus() method , that came up with 2 clusters.

8 Code

```r
#Data minning project
dataset=read.csv('/Users/admin/Desktop/WATER QUALITY/waterQuality.txt')

nrow(waterQuality)
ncol(waterQuality)
sum(is.na(waterQuality))
summary(waterQuality)
waterQuality$ammonia<-as.numeric(waterQuality$ammonia)

boxplot(waterQuality$aluminium , data=waterQuality)
boxplot(waterQuality$ammonia , data=waterQuality)
boxplot(waterQuality$arsenic , data=waterQuality)
boxplot(waterQuality$cadmium , data=waterQuality)
boxplot(waterQuality$chloramine,data=waterQulaity)
boxplot(waterQuality$Chromium,data=waterQulaity)
boxplot(waterQuality$Copper,data=waterQulaity)
boxplot(waterQuality$flouride,data=waterQulaity)
boxplot(waterQuality$bacteria,data=waterQulaity)
hist(waterQuality$barium)
pie(table(waterQuality$is_safe))
plot(waterQuality$lead,waterQuality$ammonia , main="Scatterplot", xlab="Lead", ylab="Ammonia")

is.na(waterQuality&ammonia)
waterQuality$ammonia=ifelse(is.na(waterQuality$ammonia),ave(waterQuality$ammonia,FUN=function(x) mean(x,na.rm=TRUE))
```

```r
#install.packeges("outliers")
library(outliers)
OutlierUran=outlier(waterQuality$uranium,logical=TRUE)
sum(OutlierUran)
Find_outlier=which(OutlierUran==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierAl=outlier(waterQuality$aluminium,logical=TRUE)
sum(OutlierAl)
Find_outlier=which(OutlierAl==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierArs=outlier(waterQuality$arsenic,logical=TRUE)
sum(OutlierArs)
Find_outlier=which(OutlierArs==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierBar=outlier(waterQuality$barium,logical=TRUE)
sum(OutlierBar)
Find_outlier=which(OutlierBar==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierCad=outlier(waterQuality$cadmium,logical=TRUE)
sum(OutlierCad)
Find_outlier=which(OutlierCad==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
```

```r
OutlierChlo=outlier(waterQuality$chloramine,logical=TRUE)
sum(OutlierChlo)
Find_outlier=which(OutlierChlo==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierChrom=outlier(waterQuality$chromium,logical=TRUE)
sum(OutlierChrom)
Find_outlier=which(OutlierChrom==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierCo=outlier(waterQuality$copper,logical=TRUE)
sum(OutlierCo)
Find_outlier=which(OutlierCo==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierFl=outlier(waterQuality$flouride,logical=TRUE)
sum(OutlierFl)
Find_outlier=which(OutlierFl==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierBa=outlier(waterQuality$bacteria,logical=TRUE)
sum(OutlierBa)
Find_outlier=which(OutlierBa==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]
```

```r
OutlierVi=outlier(waterQuality$viruses,logical=TRUE)
sum(OutlierVi)
Find_outlier=which(OutlierVi==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierLe=outlier(waterQuality$lead,logical=TRUE)
sum(OutlierLe)
Find_outlier=which(OutlierLe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierNi1=outlier(waterQuality$nitrates,logical=TRUE)
sum(OutlierNi1)
Find_outlier=which(OutlierNi1==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierNi2=outlier(waterQuality$nitrites,logical=TRUE)
sum(OutlierNi2)
Find_outlier=which(OutlierNi2==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierMe=outlier(waterQuality$mercury,logical=TRUE)
sum(OutlierMe)
Find_outlier=which(OutlierMe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierPe=outlier(waterQuality$perchlorate,logical=TRUE)
```

```r
OutlierPe=outlier(waterQuality$perchlorate,logical=TRUE)
sum(OutlierPe)
Find_outlier=which(OutlierPe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierRa=outlier(waterQuality$radium,logical=TRUE)
sum(OutlierRa)
Find_outlier=which(OutlierRa==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierSe=outlier(waterQuality$selenium,logical=TRUE)
sum(OutlierSe)
Find_outlier=which(OutlierSe==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

OutlierSi=outlier(waterQuality$silver,logical=TRUE)
sum(OutlierSi)
Find_outlier=which(OutlierSi==TRUE,arr.ind=TRUE)
waterQuality= waterQuality[-Find_outlier,]

#Encoding:
waterQuality$is_safe = factor(waterQuality$is_safe,levels = c("0","1"), labels = c("No","Yes"))
```

```r
##Normlize amonia
normlize<- function(x){
  return((x-min(x)) / (max(x)-min(x)))
}
waterQuality$ammonia<-normlize(waterQuality$ammonia)
##Normlize perchlorate
normlize<- function(x){
  return((x-min(x)) / (max(x)-min(x)))
}
waterQuality$perchlorate<-normlize(waterQuality$perchlorate)
##Normlize nitrates
normlize<- function(x){
  return((x-min(x)) / (max(x)-min(x)))
}
waterQuality$nitrates<-normlize(waterQuality$nitrates)


View(waterQuality)

waterQuality <- na.omit(waterQuality)
pie(table(waterQuality$is_safe))

##Classification/30,70
set.seed(1234)
firstP <- sample(2, nrow(waterQuality), replace=TRUE, prob=c(0.7, 0.3))
trainData <- waterQuality[firstP==1,]
testData <- waterQuality[firstP==2,]
install.packages('party')
library(party)
myFormula <- is_safe ~ aluminium + ammonia + arsenic + barium + cadmium + chloramine+ chromium + copper + flouride +

waterQuality_ctree <- ctree(myFormula, data=trainData)
table(predict(waterQuality_ctree), trainData$is_safe)
print(waterQuality_ctree)
plot(waterQuality_ctree,type="simple")
plot(waterQuality_ctree)

testPred <- predict(waterQuality_ctree, newdata = testData)

#Evaluate the model
#Create the confusion matrix
table(testPred, testData$is_safe)

install.packages('caret')
library(caret)
results <- confusionMatrix(testPred, testData$is_safe)
acc <- results$overall["Accuracy"]*100
acc
results
```

```r
##Classifation/50,50
set.seed(1234)
firstP <- sample(2, nrow(waterQuality), replace=TRUE, prob=c(0.5, 0.5))
trainData <- waterQuality[firstP==1,]
testData <- waterQuality[firstP==2,]

myFormula <- is_safe ~ aluminium + ammonia + arsenic + barium + cadmium + chloramine+ chromium + copper + flouride +

waterQuality_ctree <- ctree(myFormula, data=trainData)
table(predict(waterQuality_ctree), trainData$is_safe)
print(waterQuality_ctree)
plot(waterQuality_ctree,type="simple")
plot(waterQuality_ctree)

testPred <- predict(waterQuality_ctree, newdata = testData)

#Evaluate the model
#Create the confusion matrix
table(testPred, testData$is_safe)

results <- confusionMatrix(testPred, testData$is_safe)
acc <- results$overall["Accuracy"]*100
acc
results

##Classifation/80,20
```

```r
##Classifation/80,20
set.seed(1234)
firstP <- sample(2, nrow(waterQuality), replace=TRUE, prob=c(0.8, 0.2))
trainData <- waterQuality[firstP==1,]
testData <- waterQuality[firstP==2,]

myFormula <- is_safe ~ aluminium + ammonia + arsenic + barium + cadmium + chloramine+ chromium + copper + flouride +

waterQuality_ctree <- ctree(myFormula, data=trainData)
table(predict(waterQuality_ctree), trainData$is_safe)
print(waterQuality_ctree)
plot(waterQuality_ctree,type="simple")
plot(waterQuality_ctree)

testPred <- predict(waterQuality_ctree, newdata = testData)

#Evaluate the model
#Create the confusion matrix
table(testPred, testData$is_safe)

results <- confusionMatrix(testPred, testData$is_safe)
acc <- results$overall["Accuracy"]*100
acc
results
```

```r
##Removing the class label for clustring technique
waterQuality<- subset( waterQuality, select = -is_safe )

# k-means clustering
set.seed(8953)

waterQuality <- scale(waterQuality)
#First clustring K=2:
kmeans.result1 <- kmeans(waterQuality, 2)
kmeans.result1

install.packages("factoextra")
library(factoextra)
fviz_cluster(kmeans.result1, data = waterQuality)

###Cluster Validation
install.packages("cluster")
library(cluster)
#average for each cluster
avg_sil <- silhouette(kmeans.result1$cluster,dist(waterQuality))
fviz_silhouette(avg_sil)

##############################
#Second clustring K=3:
kmeans.result2 <- kmeans(waterQuality,3)
kmeans.result2
```

```r
fviz_cluster(kmeans.result2, data = waterQuality)

###Cluster Validation

#average for each cluster
avg_sil <- silhouette(kmeans.result2$cluster,dist(waterQuality))
fviz_silhouette(avg_sil)

##############################
#Third clustring K=5:
kmeans.result3 <- kmeans(waterQuality,5)
kmeans.result3


fviz_cluster(kmeans.result3, data = waterQuality)

###Cluster Validation

#average for each cluster
avg_sil <- silhouette(kmeans.result3$cluster,dist(waterQuality))
fviz_silhouette(avg_sil)

install.packages("NbClust")
library(NbClust)
fviz_nbclust(waterQuality, kmeans, method = "silhouette")+labs(subtitle = "Silhouette method")

```

9 References

https://www.kaggle.com/mssmartypants/water-quality

10 Tasks Distribution

ID	Name	Responsibilities
Jumanah aldawsari	441201034	All project parts .
Lama alshaya	441201236	All project parts .
Nouf alsadhan	441201104	All project parts .
Aljawharah alzamil	441201203	All project parts .