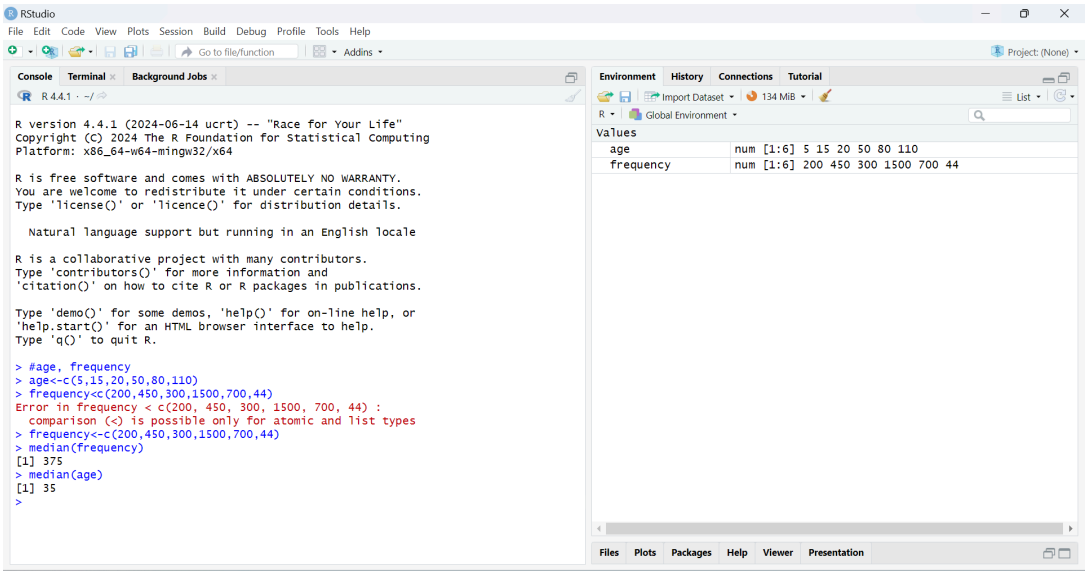
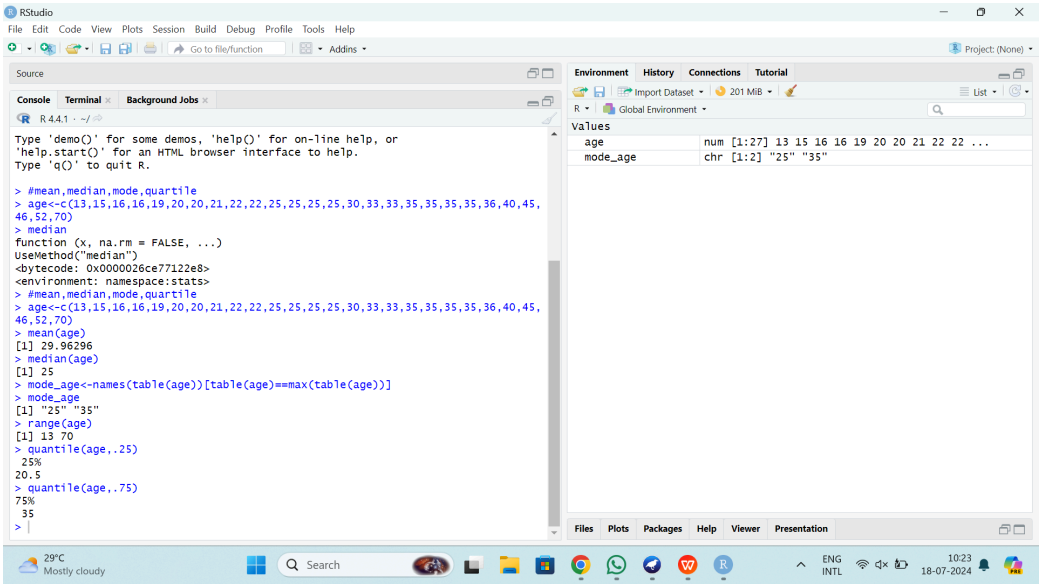
CSA1667-Data Warehousing And Data Mining

DAY-1

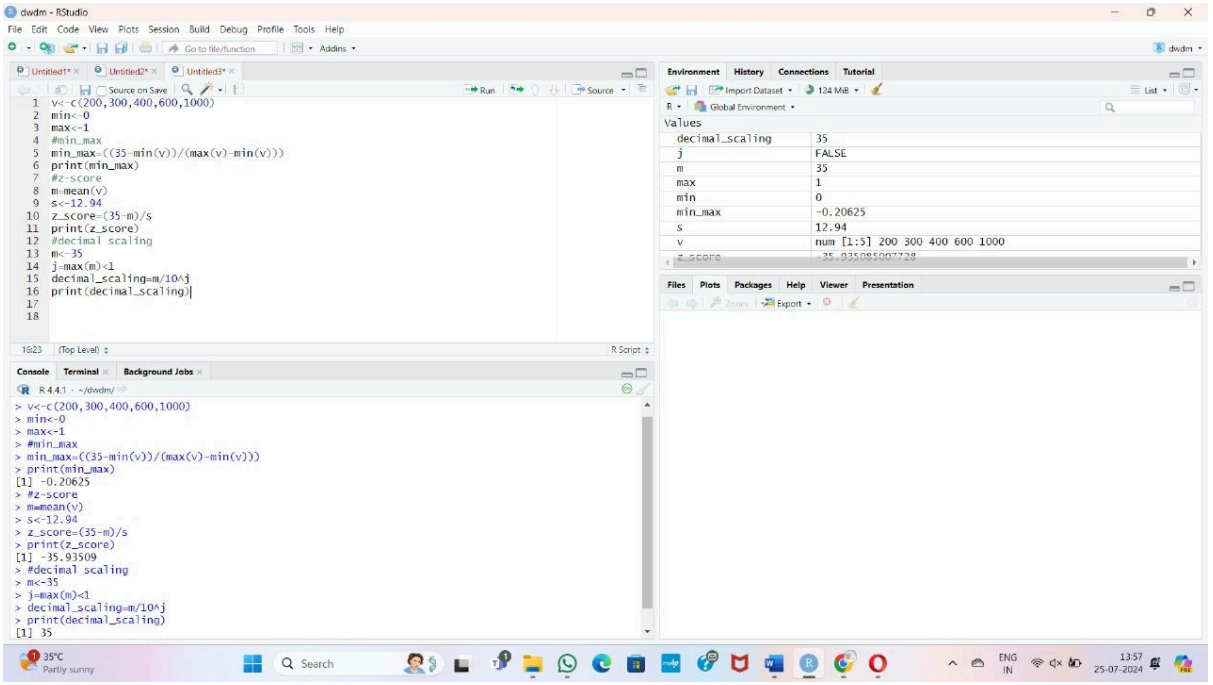
Q1:



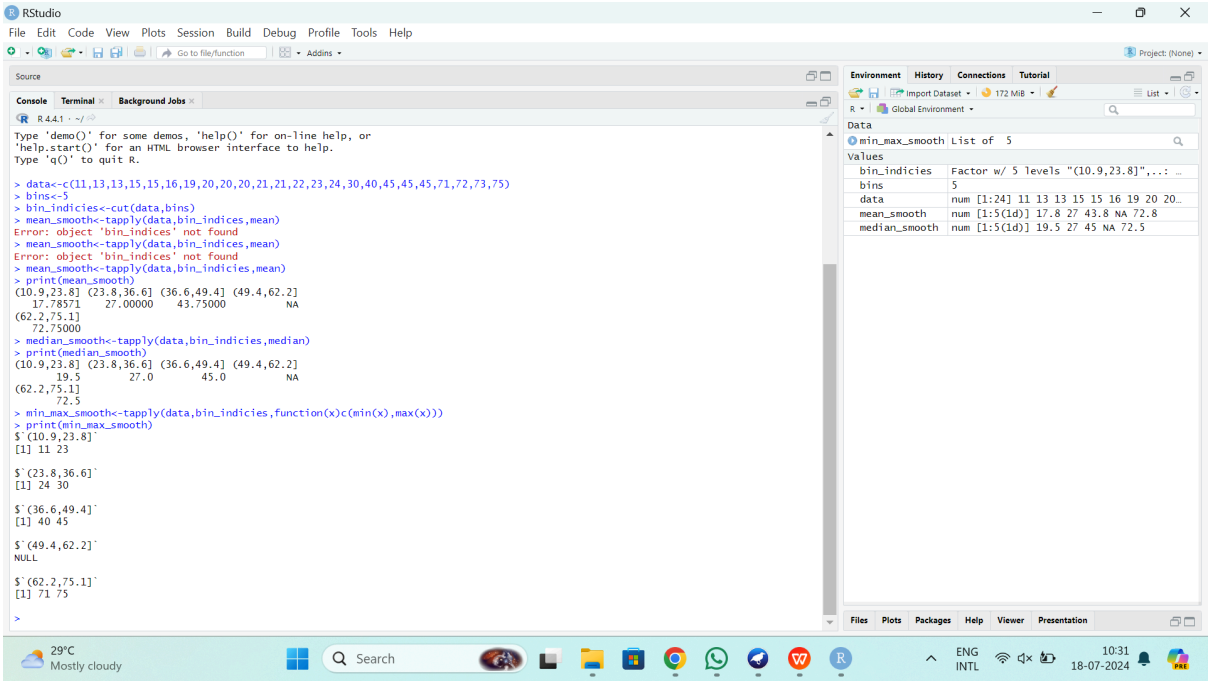
Q2:



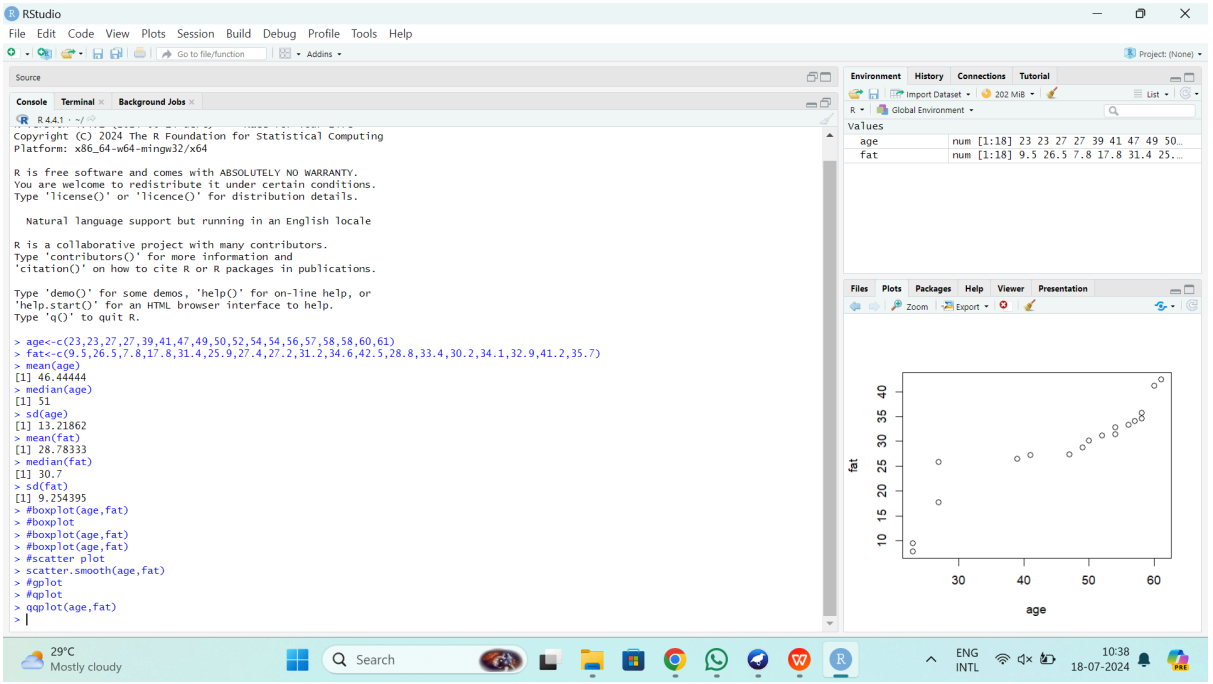
Q3:


dwdm - RStudio
v<-c(200,300,400,600,1000)
min<-0
max<-1
#min_max
min_max=((35-min(v))/(max(v)-min(v)))
print(min_max)
#z-score
m=mean(v)
s<-12.94
z_score=(35-m)/s
print(z_score)
#decimal scaling
m<-35
j=max(m)<1
decimal_scaling=m/10^j
print(decimal_scaling)
[1] -0.20625
[1] -35.93509
[1] 35

Q4:


RStudio
data<-c(11,13,13,15,15,16,19,20,20,20,21,21,22,23,24,30,40,45,45,45,71,72,73,75)
bins<-5
bin_indicies<-cut(data,bins)
mean_smooth<-tapply(data,bin_indicies,mean)
Error: object 'bin_indices' not found
median_smooth<-tapply(data,bin_indicies,median)
min_max_smooth<-tapply(data,bin_indicies,function(x)c(min(x),max(x)))
print(min_max_smooth)
[1] 11 23
[1] 24 30
[1] 40 45
NULL
[1] 71 75

Q5:


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Console Terminal Background Jobs
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Platform: x86_64-w64-mingw32/x64
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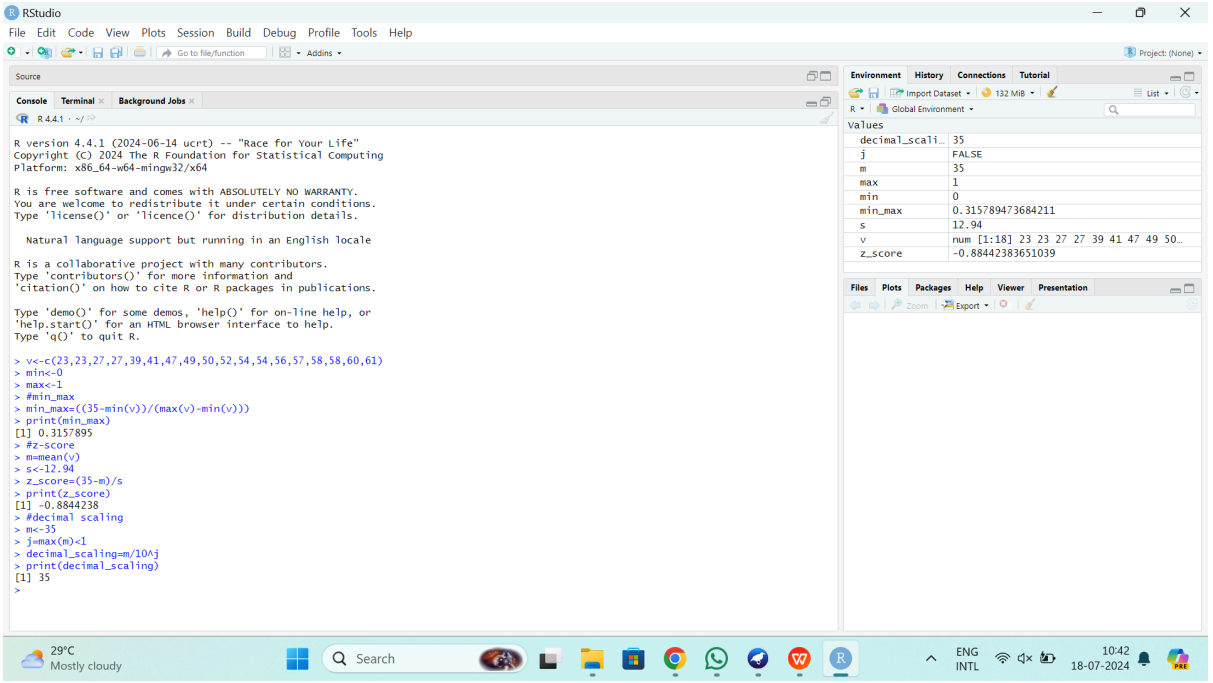
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> age<-c(23,23,27,27,39,41,47,49,50,52,54,54,56,57,58,58,60,61)
> fat<-c(9.5,26.5,7.8,17.8,31.4,25.9,27.4,27.2,31.2,34.6,42.5,28.8,33.4,30.2,34.1,32.9,41.2,35.7)
> mean(age)
[1] 46.44444
> median(age)
[1] 51
> sd(age)
[1] 13.21862
> mean(fat)
[1] 28.78333
> median(fat)
[1] 30.7
> sd(fat)
[1] 9.254395
> #boxplot(age,fat)
> #boxplot
> #boxplot(age,fat)
> #boxplot(age,fat)
> #scatter plot
> scatter.smooth(age,fat)
> #gplot
> #qplot
> qqplot(age,fat)
Environment History Connections Tutorial
Values
age num [1:18] 23 23 27 27 39 41 47 49 50...
fat num [1:18] 9.5 26.5 7.8 17.8 31.4 25...
Files Plots Packages Help Viewer Presentation
fat
age
10 15 20 25 30 35 40
30 40 50 60
29°C
Mostly cloudy
Search
ENG
INTL
10:38
18-07-2024

Q6:


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Console Terminal Background Jobs
R version 4.4.1 (2024-06-14 ucrt) -- "Race for Your Life"
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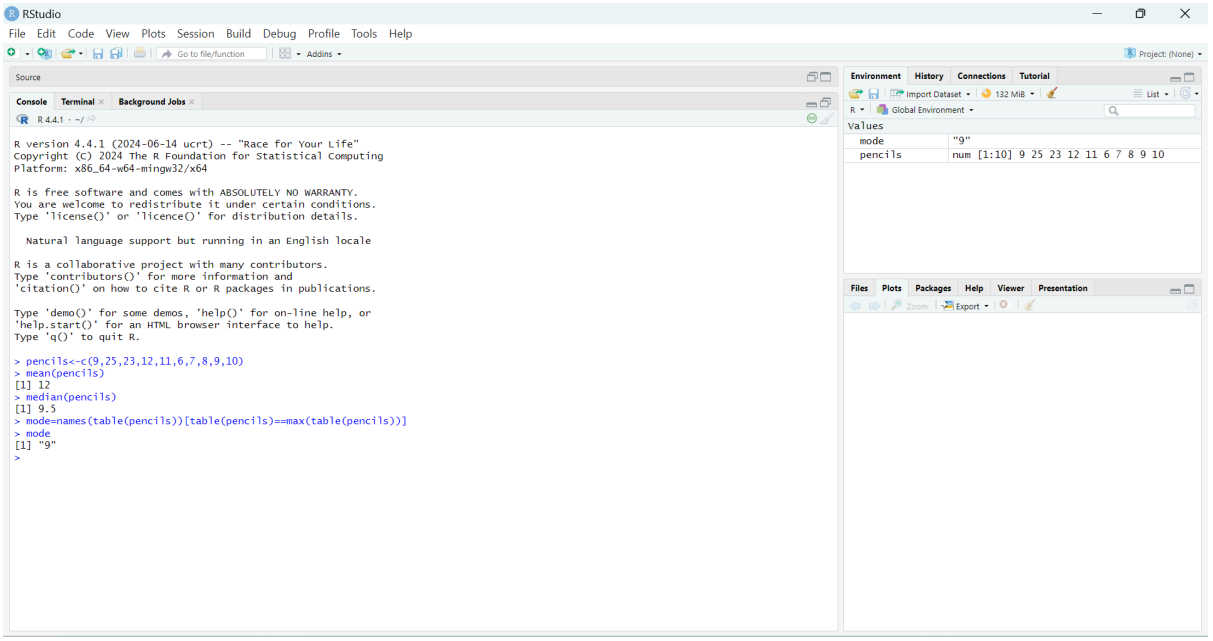
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> v<-c(23,23,27,27,39,41,47,49,50,52,54,54,56,57,58,58,60,61)
> min<-0
> max<-1
> #min_max
> min_max=((35-min(v))/(max(v)-min(v)))
> print(min_max)
[1] 0.3157895
> #z-score
> m=mean(v)
> s<-12.94
> z_score=(35-m)/s
> print(z_score)
[1] -0.8844238
> #decimal scaling
> m<-35
> j=max(m)<1
> decimal_scaling=m/10^j
> print(decimal_scaling)
[1] 35
Environment History Connections Tutorial
Values
decimal_scali... 35
j FALSE
m 35
max 1
min 0
min_max 0.315789473684211
s 12.94
v num [1:18] 23 23 27 27 39 41 47 49 50...
z_score -0.88442383651039
Files Plots Packages Help Viewer Presentation
29°C
Mostly cloudy
Search
ENG
INTL
10:42
18-07-2024

Q7:


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Source
Console Terminal Background Jobs
R 4.4.1 · ~/
R version 4.4.1 (2024-06-14 ucrt) -- "Race for Your Life"
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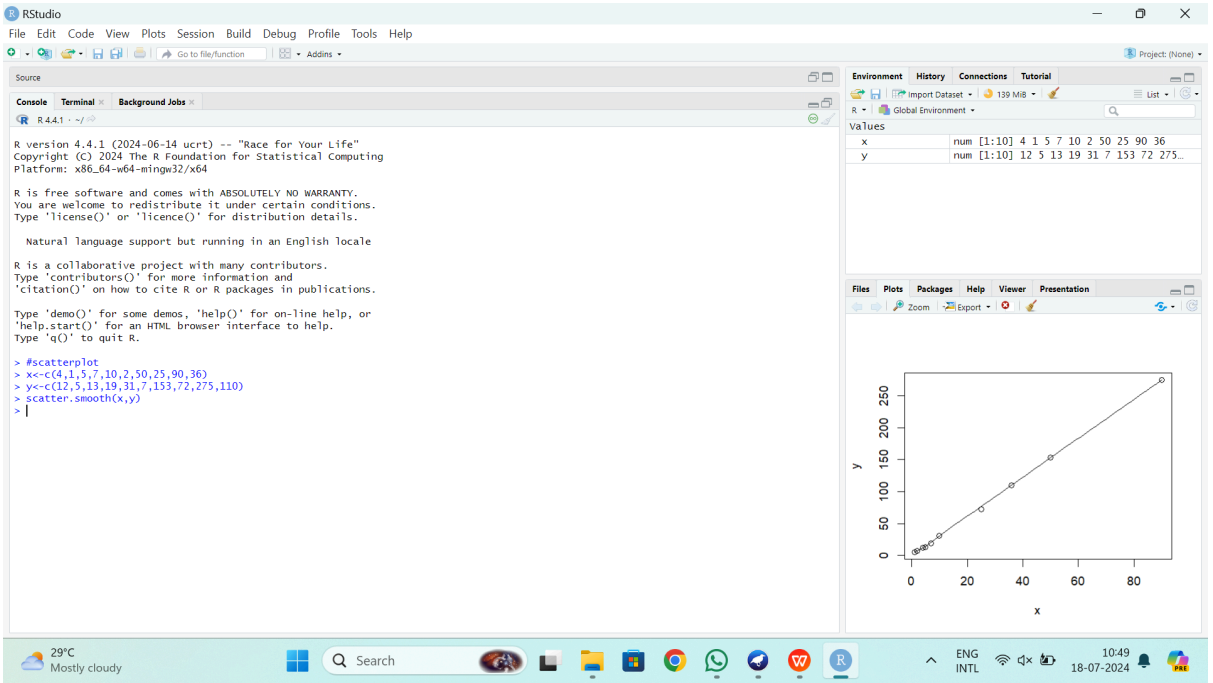
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> pencils<-c(9,25,23,12,11,6,7,8,9,10)
> mean(pencils)
[1] 12
> median(pencils)
[1] 9.5
> mode=names(table(pencils))[table(pencils)==max(table(pencils))]
> mode
[1] "9"
>
Environment History Connections Tutorial
Values
mode "9"
pencils num [1:10] 9 25 23 12 11 6 7 8 9 10
Files Plots Packages Help Viewer Presentation

Q8:


RStudio
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Source
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R 4.4.1 · ~/
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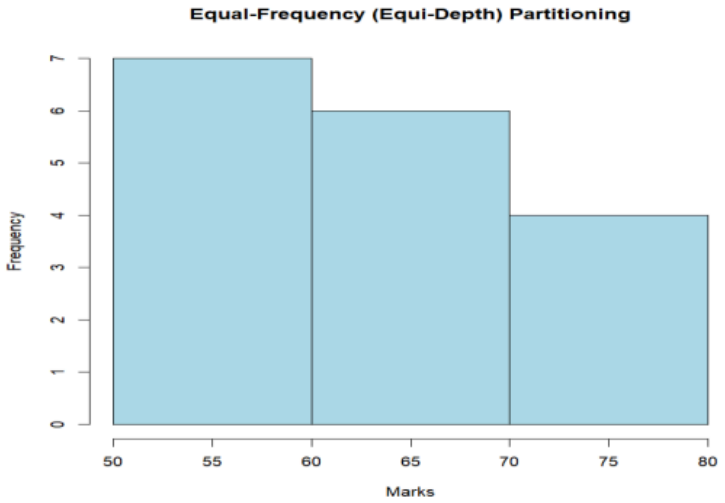
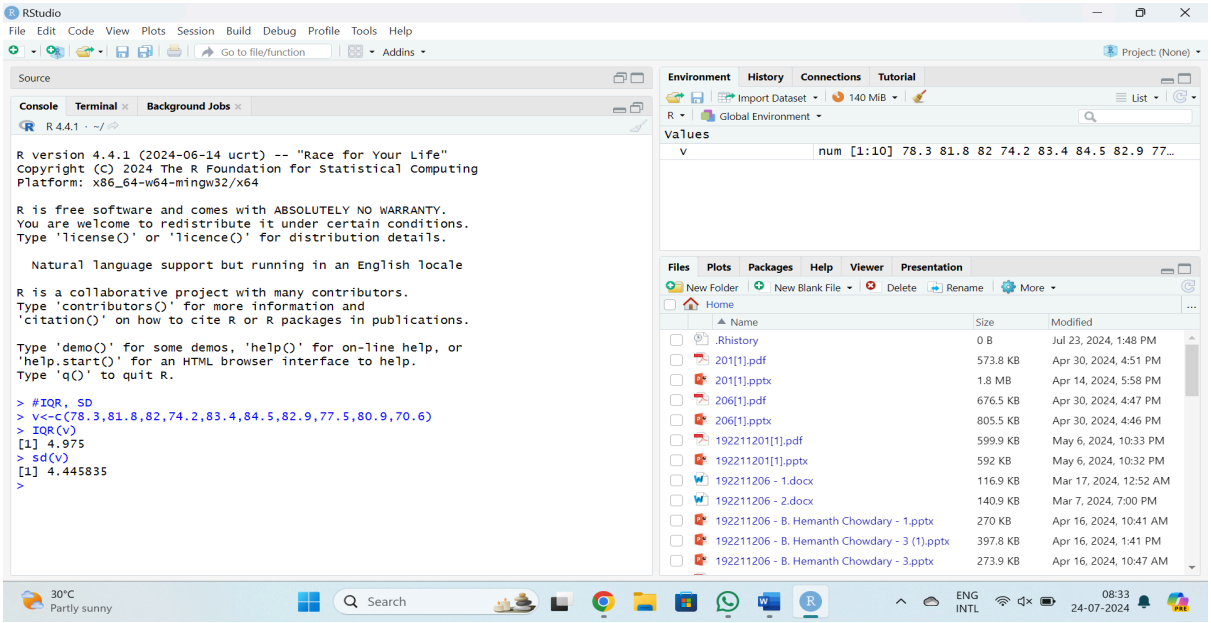
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> #scatterplot
> x<-c(4,1,5,7,10,2,50,25,90,36)
> y<-c(12,5,13,19,31,7,153,72,275,110)
> scatter.smooth(x,y)
Environment History Connections Tutorial
Values
x num [1:10] 4 1 5 7 10 2 50 25 90 36
y num [1:10] 12 5 13 19 31 7 153 72 275...
Files Plots Packages Help Viewer Presentation
y
0 50 100 150 200 250
x
0 20 40 60 80
29°C
Mostly cloudy
Search
ENG
INTL
10:49
18-07-2024

Q9:

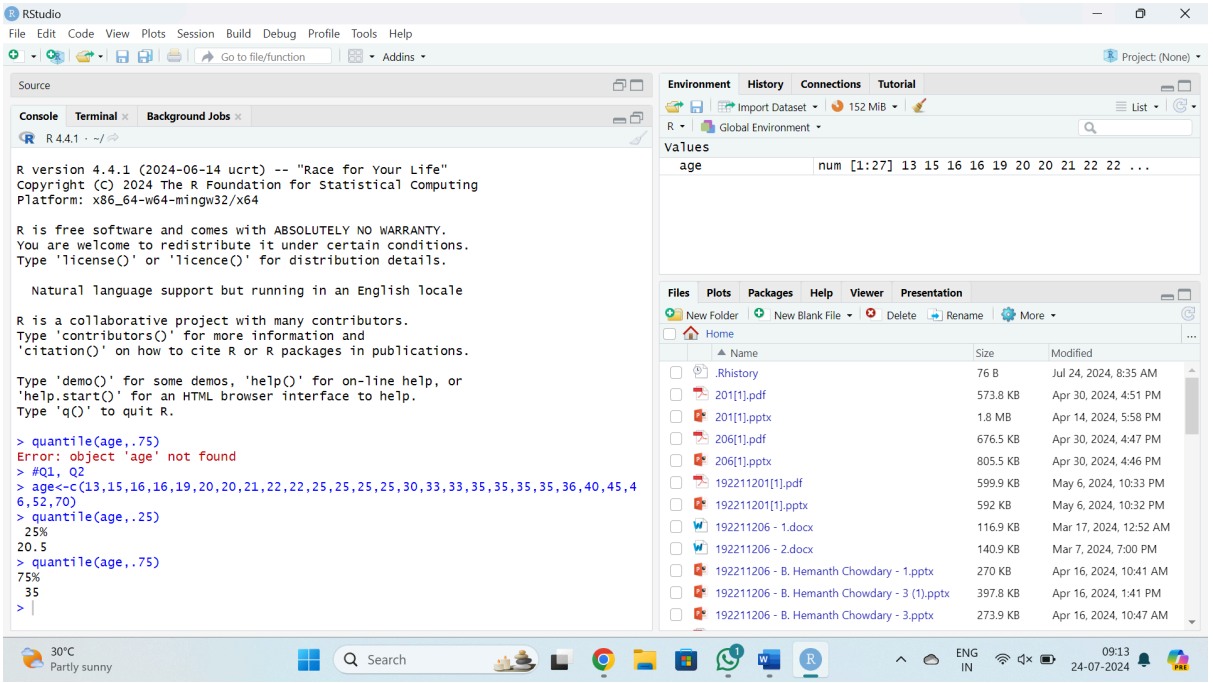
```
> print(smoothed_data_by_mean)
 [1] 18.9375 18.9375 18.9375 18.9375 18.9375 18.9375 18.9375 18.9375
 [9] 18.9375 18.9375 18.9375 18.9375 18.9375 18.9375 18.9375 18.9375
[17] 43.7500 43.7500 43.7500 43.7500 72.7500 72.7500 72.7500 72.7500
> print("Smoothed data by bin median:")
[1] "Smoothed data by bin median:"
> print(smoothed_data_by_median)
 [1] 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0
[14] 20.0 20.0 20.0 45.0 45.0 45.0 45.0 72.5 72.5 72.5 72.5
> print("Smoothed data by bin boundaries:")
[1] "Smoothed data by bin boundaries:"
> print(smoothed_data_by_boundaries)
(10.9,32.3]1 (10.9,32.3]2 (10.9,32.3]1 (10.9,32.3]2 (10.9,32.3]1
          11           30           11           30           11
(10.9,32.3]2 (10.9,32.3]1 (10.9,32.3]2 (10.9,32.3]1 (10.9,32.3]2
          30           11           30           11           30
(10.9,32.3]1 (10.9,32.3]2 (10.9,32.3]1 (10.9,32.3]2 (10.9,32.3]1
          11           30           11           30           11
(10.9,32.3]2 (10.9,32.3]1 (10.9,32.3]2 (10.9,32.3]1 (10.9,32.3]2
          30           11           30           11           30
```



Q10:



Q11:


RStudio
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Source
Console Terminal Background Jobs
R 4.4.1 · ~/
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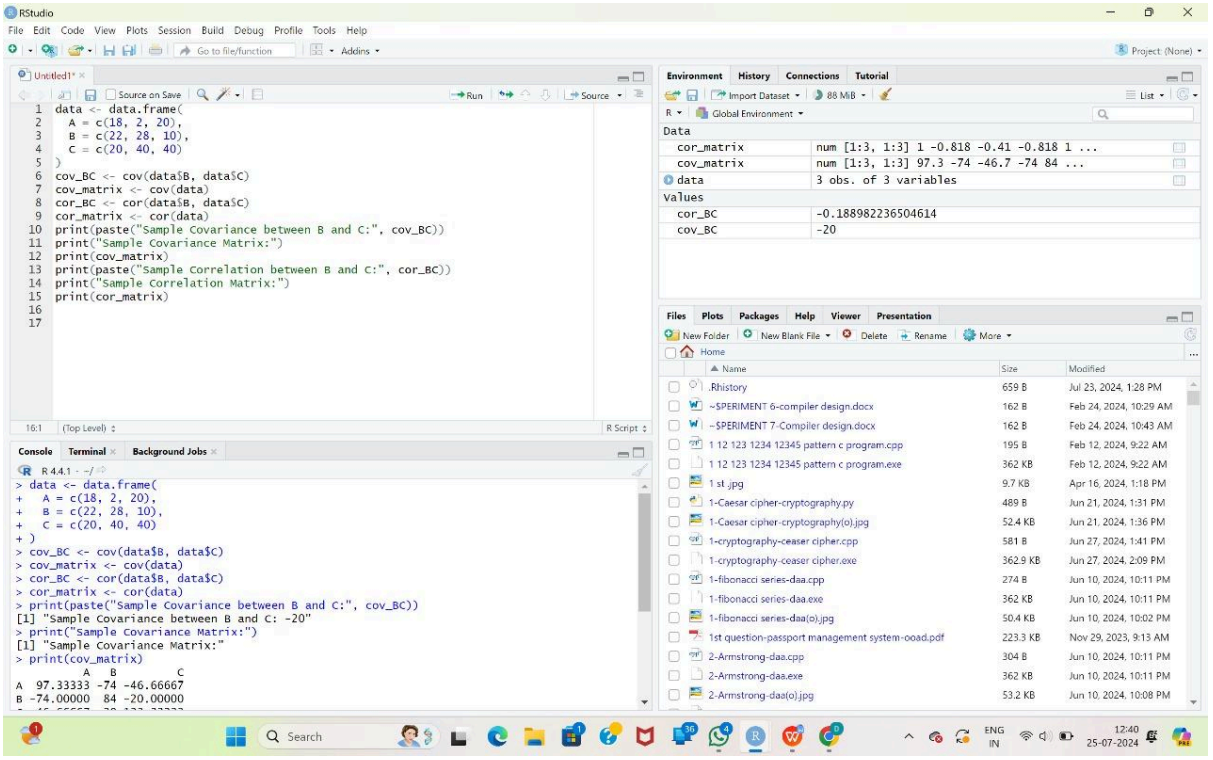
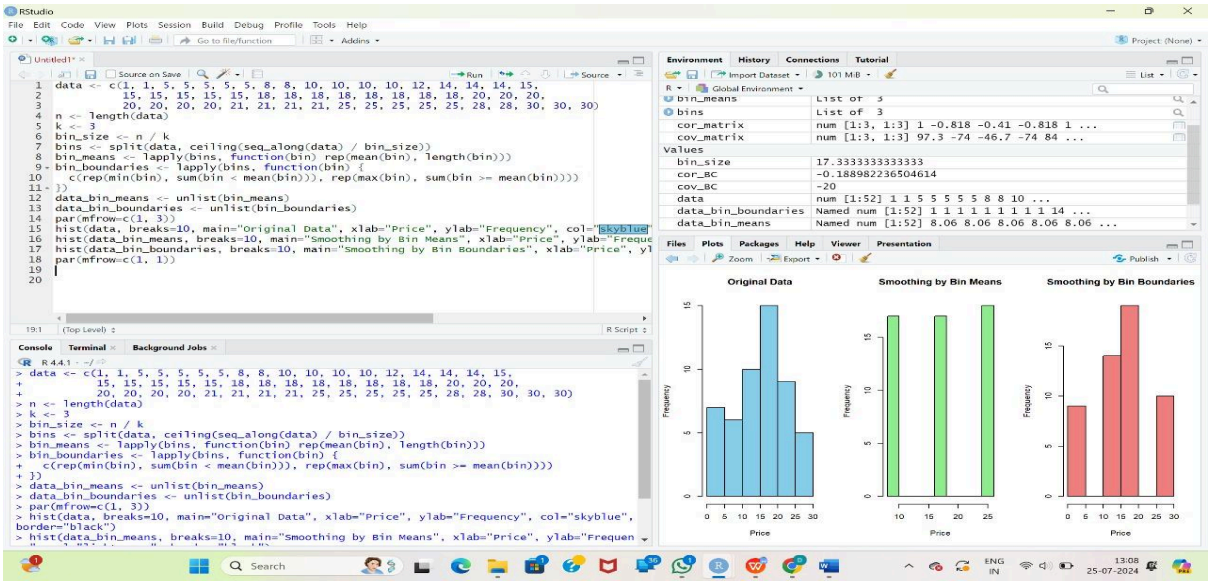
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> quantile(age,.75)
Error: object 'age' not found
> #Q1, Q2
> age<-c(13,15,16,16,19,20,20,21,22,22,25,25,25,25,30,33,33,35,35,35,35,36,40,45,46,52,70)
> quantile(age,.25)
25%
20.5
> quantile(age,.75)
75%
35
>
Environment History Connections Tutorial
Import Dataset 152 MiB
Global Environment
Values
age num [1:27] 13 15 16 16 19 20 20 21 22 22 ...
Files Plots Packages Help Viewer Presentation
New Folder New Blank File Delete Rename More
Home
Name Size Modified
.Rhistory 76 B Jul 24, 2024, 8:35 AM
201[1].pdf 573.8 KB Apr 30, 2024, 4:51 PM
201[1].pptx 1.8 MB Apr 14, 2024, 5:58 PM
206[1].pdf 676.5 KB Apr 30, 2024, 4:47 PM
206[1].pptx 805.5 KB Apr 30, 2024, 4:46 PM
192211201[1].pdf 599.9 KB May 6, 2024, 10:33 PM
192211201[1].pptx 592 KB May 6, 2024, 10:32 PM
192211206 - 1.docx 116.9 KB Mar 17, 2024, 12:52 AM
192211206 - 2.docx 140.9 KB Mar 7, 2024, 7:00 PM
192211206 - B. Hemanth Chowdary - 1.pptx 270 KB Apr 16, 2024, 10:41 AM
192211206 - B. Hemanth Chowdary - 3 (1).pptx 397.8 KB Apr 16, 2024, 1:41 PM
192211206 - B. Hemanth Chowdary - 3.pptx 273.9 KB Apr 16, 2024, 10:47 AM
30°C Partly sunny
Search
ENG IN
09:13 24-07-2024

DAY-2

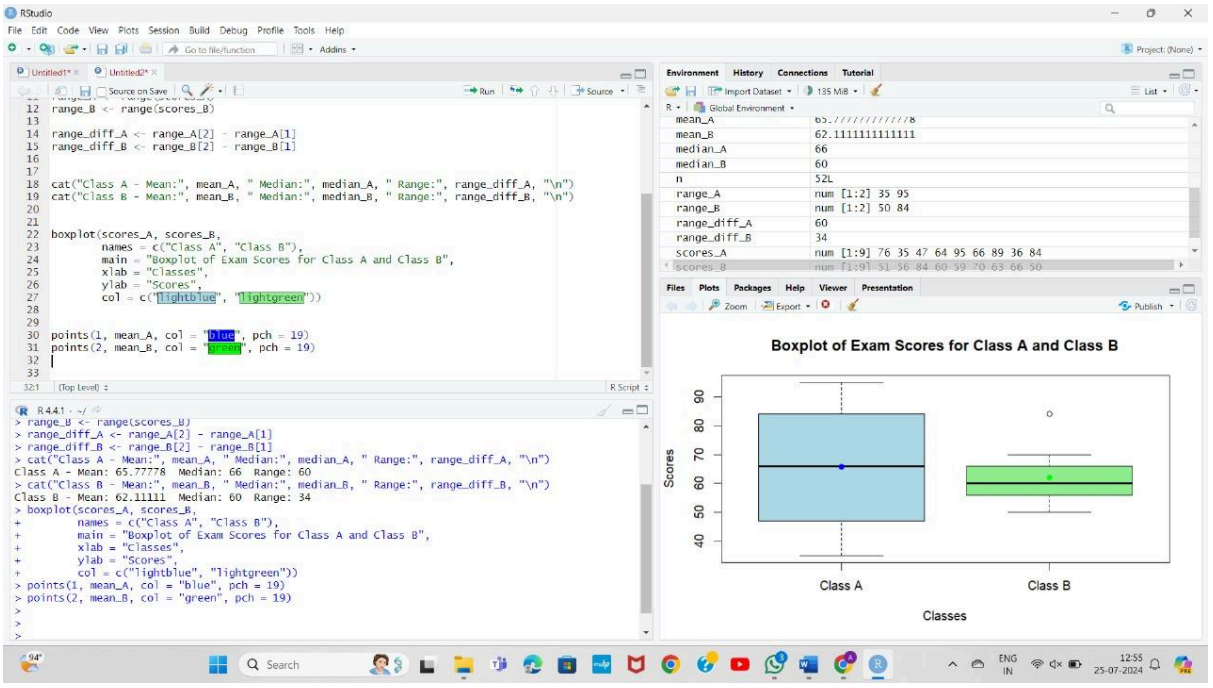
Q1:


data <- data.frame(
A = c(18, 2, 20),
B = c(22, 28, 10),
C = c(20, 40, 40)
)
cov_BC <- cov(data$B, data$C)
cov_matrix <- cov(data)
cor_BC <- cor(data$B, data$C)
cor_matrix <- cor(data)
print(paste("Sample Covariance between B and C:", cov_BC))
print("Sample Covariance Matrix:")
print(cov_matrix)
print(paste("Sample Correlation between B and C:", cor_BC))
print("Sample Correlation Matrix:")
print(cor_matrix)
[1] "Sample Covariance between B and C: -20"
[1] "Sample Covariance Matrix:"
A B C
A 97.33333 -74 -46.66667
B -74.00000 84 -20.00000

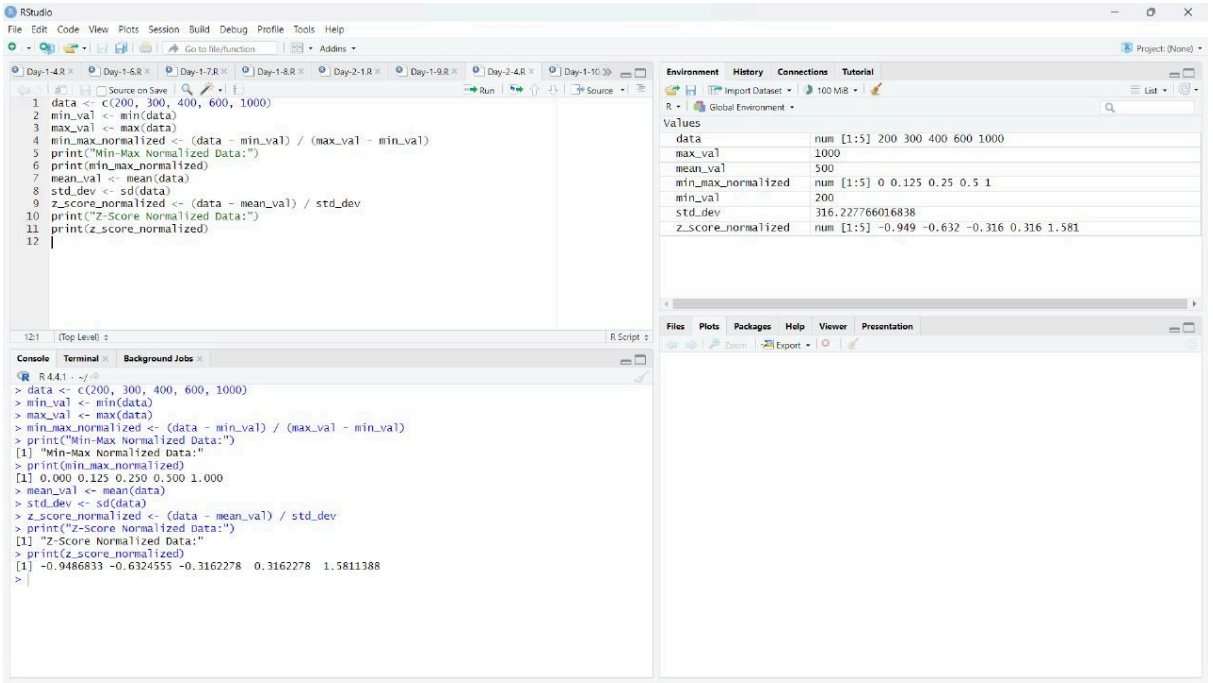
Q2:


data <- c(1, 1, 5, 5, 5, 5, 5, 8, 8, 10, 10, 10, 10, 12, 14, 14, 14, 15,
15, 15, 15, 15, 15, 18, 18, 18, 18, 18, 18, 18, 18, 20, 20, 20,
20, 20, 20, 20, 21, 21, 21, 21, 25, 25, 25, 25, 25, 28, 28, 30, 30, 30)
n <- length(data)
k <- 3
bin_size <- n / k
bins <- split(data, ceiling(seq_along(data) / bin_size))
bin_means <- lapply(bins, function(bin) rep(mean(bin), length(bin)))
bin_boundaries <- lapply(bins, function(bin) {
c(rep(min(bin), sum(bin < mean(bin))), rep(max(bin), sum(bin >= mean(bin))))
})
data_bin_means <- unlist(bin_means)
data_bin_boundaries <- unlist(bin_boundaries)
par(mfrow=c(1, 3))
hist(data, breaks=10, main="Original Data", xlab="Price", ylab="Frequency", col="skyblue",
hist(data_bin_means, breaks=10, main="Smoothing by Bin Means", xlab="Price", ylab="Freque
hist(data_bin_boundaries, breaks=10, main="Smoothing by Bin Boundaries", xlab="Price", yl
par(mfrow=c(1, 1))
Original Data
Smoothing by Bin Means
Smoothing by Bin Boundaries
Frequency
Price

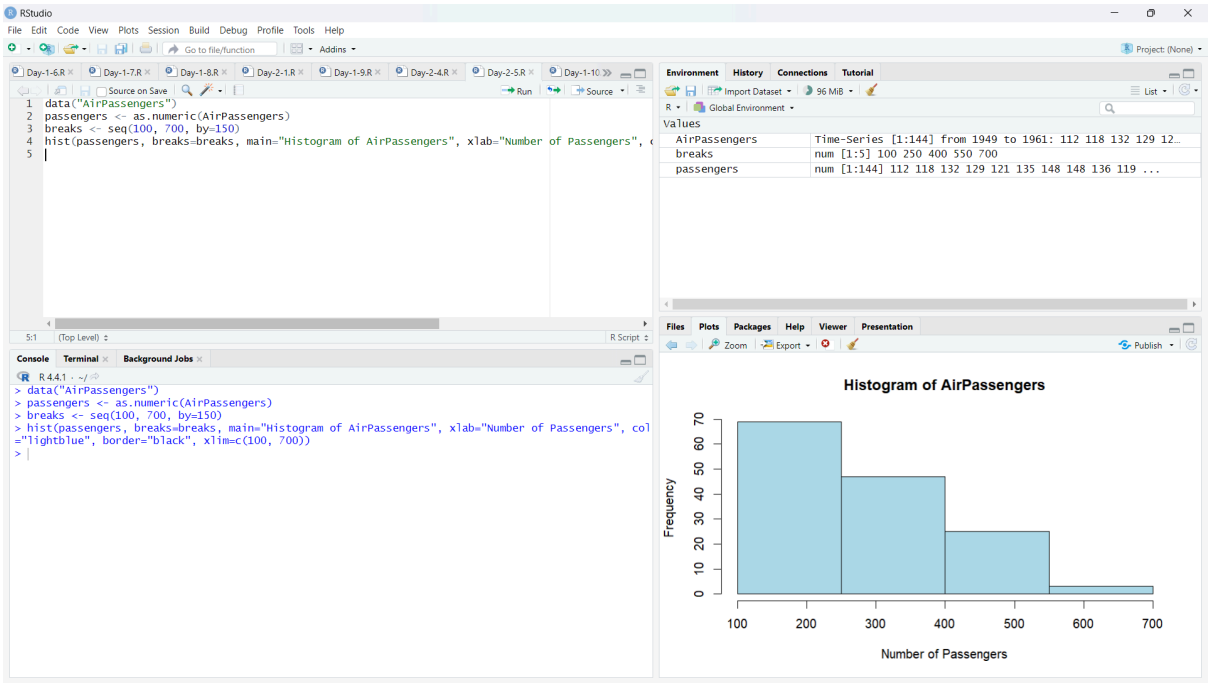
Q3:


RStudio
range_B <- range(scores_B)
range_diff_A <- range_A[2] - range_A[1]
range_diff_B <- range_B[2] - range_B[1]
cat("Class A - Mean:", mean_A, " Median:", median_A, " Range:", range_diff_A, "\n")
cat("Class B - Mean:", mean_B, " Median:", median_B, " Range:", range_diff_B, "\n")
boxplot(scores_A, scores_B,
names = c("Class A", "Class B"),
main = "Boxplot of Exam Scores for Class A and Class B",
xlab = "Classes",
ylab = "Scores",
col = c("lightblue", "lightgreen"))
points(1, mean_A, col = "blue", pch = 19)
points(2, mean_B, col = "green", pch = 19)
mean_B 62.1111111111111
median_A 66
median_B 60
n 52L
range_A num [1:2] 35 95
range_B num [1:2] 50 84
range_diff_A 60
range_diff_B 34
scores_A num [1:9] 76 35 47 64 95 66 89 36 84
Boxplot of Exam Scores for Class A and Class B
Scores
Class A
Class B
Classes

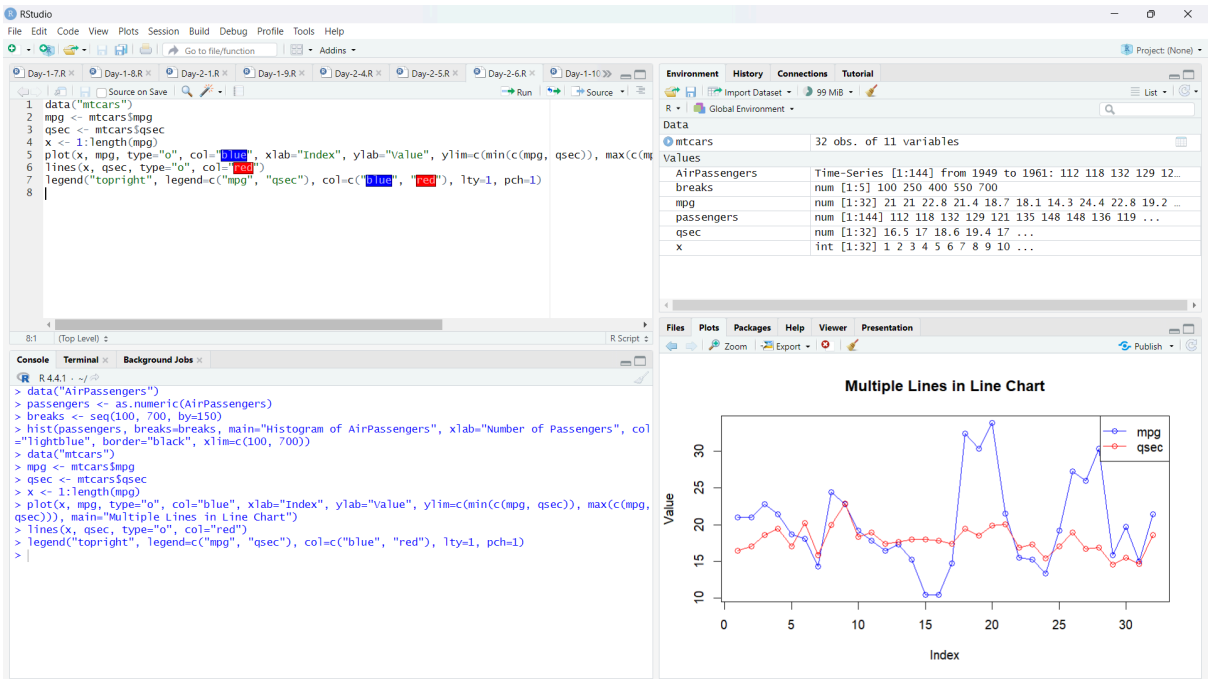
Q4:


RStudio
data <- c(200, 300, 400, 600, 1000)
min_val <- min(data)
max_val <- max(data)
min_max_normalized <- (data - min_val) / (max_val - min_val)
print("Min-Max Normalized Data:")
print(min_max_normalized)
mean_val <- mean(data)
std_dev <- sd(data)
z_score_normalized <- (data - mean_val) / std_dev
print("Z-Score Normalized Data:")
print(z_score_normalized)
[1] "Min-Max Normalized Data:"
[1] 0.000 0.125 0.250 0.500 1.000
[1] "Z-Score Normalized Data:"
[1] -0.9486833 -0.6324555 -0.3162278 0.3162278 1.5811388
data num [1:5] 200 300 400 600 1000
max_val 1000
mean_val 500
min_max_normalized num [1:5] 0 0.125 0.25 0.5 1
min_val 200
std_dev 316.227766016838
z_score_normalized num [1:5] -0.949 -0.632 -0.316 0.316 1.581

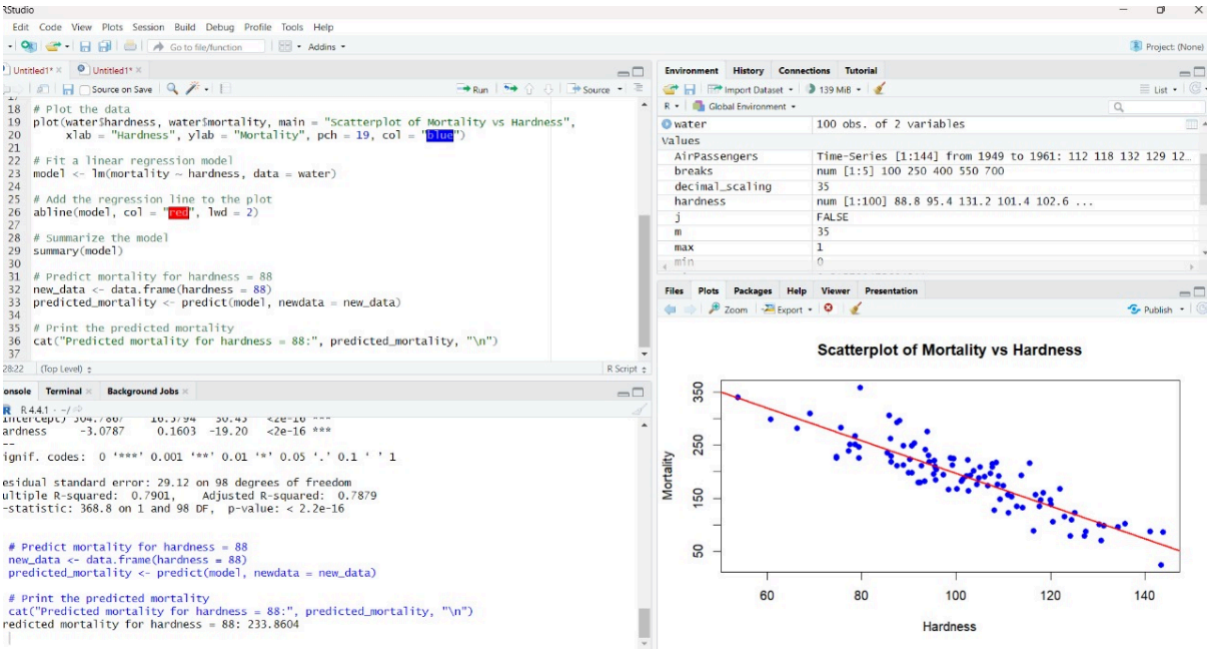
Q5:


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Day-1-6.R Day-1-7.R Day-1-8.R Day-2-1.R Day-1-9.R Day-2-4.R Day-2-5.R Day-1-10
Source on Save Run Source
1 data("AirPassengers")
2 passengers <- as.numeric(AirPassengers)
3 breaks <- seq(100, 700, by=150)
4 hist(passengers, breaks=breaks, main="Histogram of AirPassengers", xlab="Number of Passengers", c
5
5:1 (Top Level) R Script
Console Terminal Background Jobs
R 4.4.1 · ~/
> data("AirPassengers")
> passengers <- as.numeric(AirPassengers)
> breaks <- seq(100, 700, by=150)
> hist(passengers, breaks=breaks, main="Histogram of AirPassengers", xlab="Number of Passengers", col
="lightblue", border="black", xlim=c(100, 700))
>
Environment History Connections Tutorial
Import Dataset 96 MiB List
R Global Environment
Values
AirPassengers Time-Series [1:144] from 1949 to 1961: 112 118 132 129 12…
breaks num [1:5] 100 250 400 550 700
passengers num [1:144] 112 118 132 129 121 135 148 148 136 119 ...
Files Plots Packages Help Viewer Presentation
Zoom Export Publish
Histogram of AirPassengers
Frequency
0 10 20 30 40 50 60 70
100 200 300 400 500 600 700
Number of Passengers

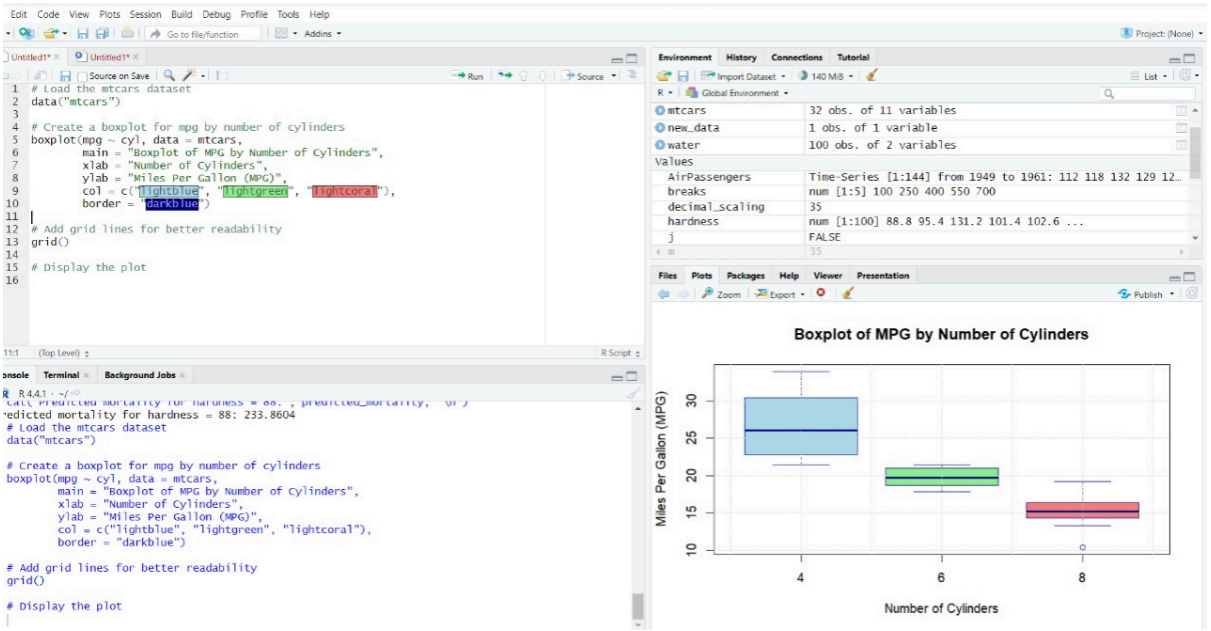
Q6:


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Day-1-7.R Day-1-8.R Day-2-1.R Day-1-9.R Day-2-4.R Day-2-5.R Day-2-6.R Day-1-10
Source on Save Run Source
1 data("mtcars")
2 mpg <- mtcars$mpg
3 qsec <- mtcars$qsec
4 x <- 1:length(mpg)
5 plot(x, mpg, type="o", col="blue", xlab="Index", ylab="Value", ylim=c(min(c(mpg, qsec)), max(c(mp
6 lines(x, qsec, type="o", col="red")
7 legend("topright", legend=c("mpg", "qsec"), col=c("blue", "red"), lty=1, pch=1)
8
8:1 (Top Level) R Script
Console Terminal Background Jobs
R 4.4.1 · ~/
> data("AirPassengers")
> passengers <- as.numeric(AirPassengers)
> breaks <- seq(100, 700, by=150)
> hist(passengers, breaks=breaks, main="Histogram of AirPassengers", xlab="Number of Passengers", col
="lightblue", border="black", xlim=c(100, 700))
> data("mtcars")
> mpg <- mtcars$mpg
> qsec <- mtcars$qsec
> x <- 1:length(mpg)
> plot(x, mpg, type="o", col="blue", xlab="Index", ylab="Value", ylim=c(min(c(mpg, qsec)), max(c(mpg,
qsec))), main="Multiple Lines in Line Chart")
> lines(x, qsec, type="o", col="red")
> legend("topright", legend=c("mpg", "qsec"), col=c("blue", "red"), lty=1, pch=1)
>
Environment History Connections Tutorial
Import Dataset 99 MiB List
R Global Environment
Data
mtcars 32 obs. of 11 variables
Values
AirPassengers Time-Series [1:144] from 1949 to 1961: 112 118 132 129 12…
breaks num [1:5] 100 250 400 550 700
mpg num [1:32] 21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 …
passengers num [1:144] 112 118 132 129 121 135 148 148 136 119 ...
qsec num [1:32] 16.5 17 18.6 19.4 17 ...
x int [1:32] 1 2 3 4 5 6 7 8 9 10 ...
Files Plots Packages Help Viewer Presentation
Zoom Export Publish
Multiple Lines in Line Chart
mpg
qsec
Value
10 15 20 25 30
0 5 10 15 20 25 30
Index

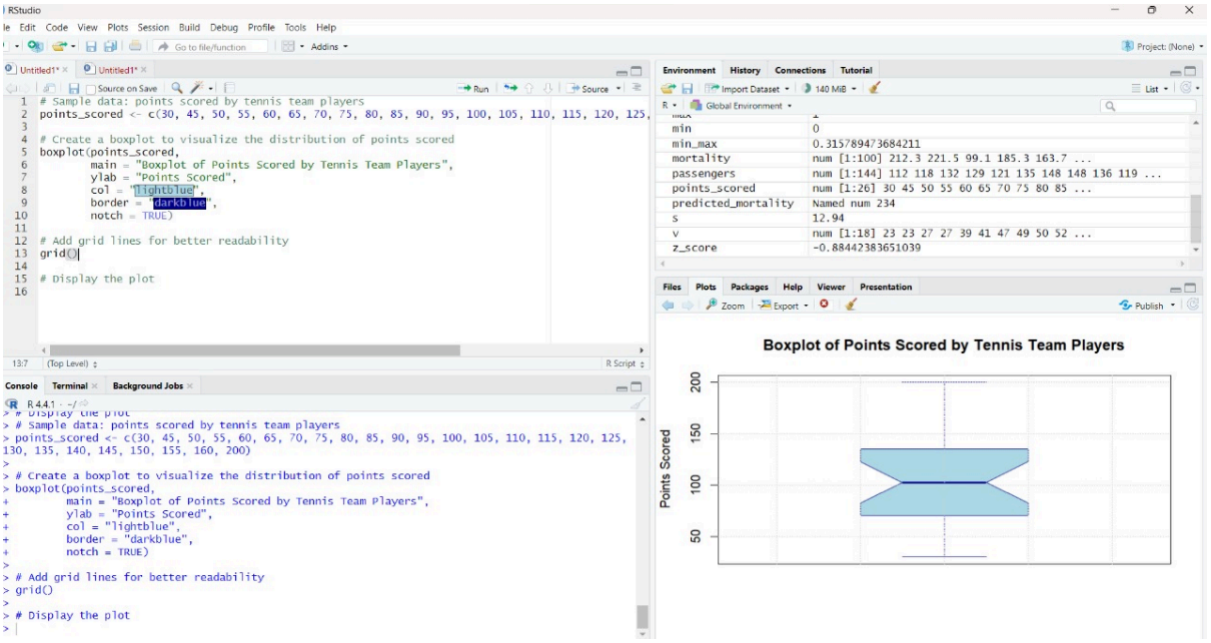
Q7:


Scatterplot of Mortality vs Hardness
Mortality
Hardness
50
150
250
350
60
80
100
120
140

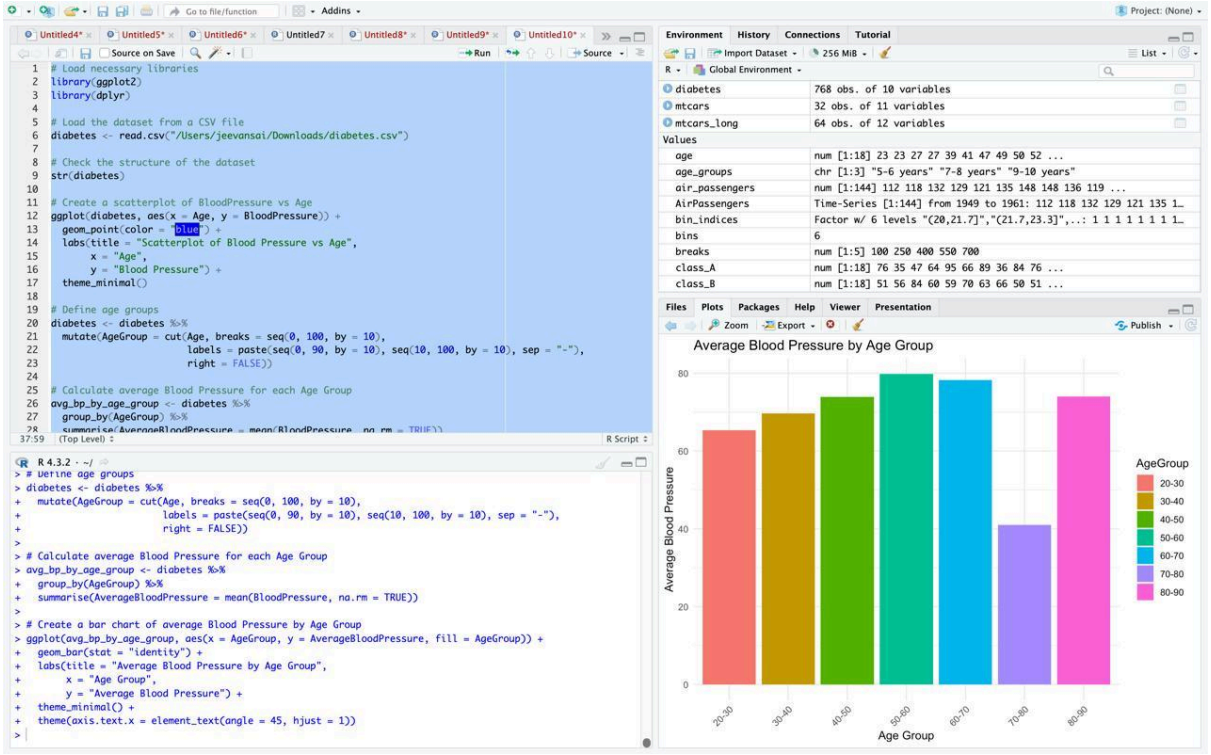
Q8:


Boxplot of MPG by Number of Cylinders
Miles Per Gallon (MPG)
Number of Cylinders
10
15
20
25
30
4
6
8

Q9:

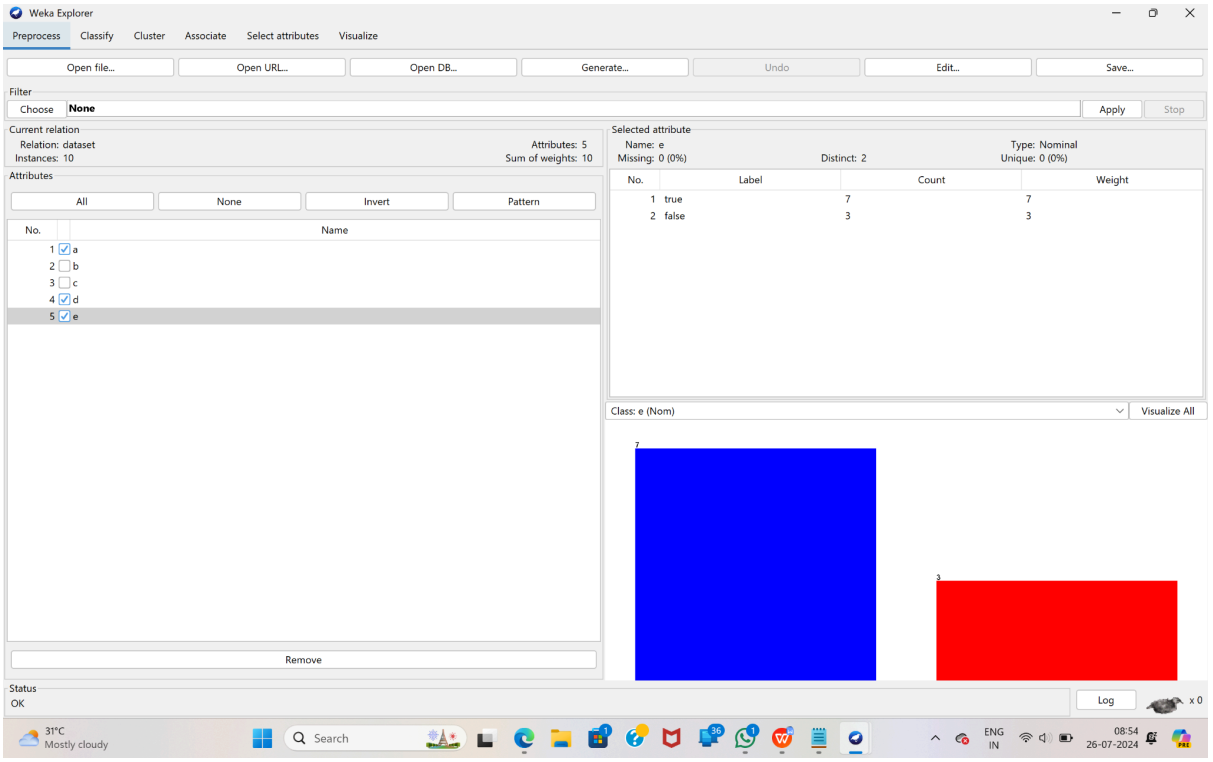

Boxplot of Points Scored by Tennis Team Players
Points Scored
200
150
100
50

Q10:

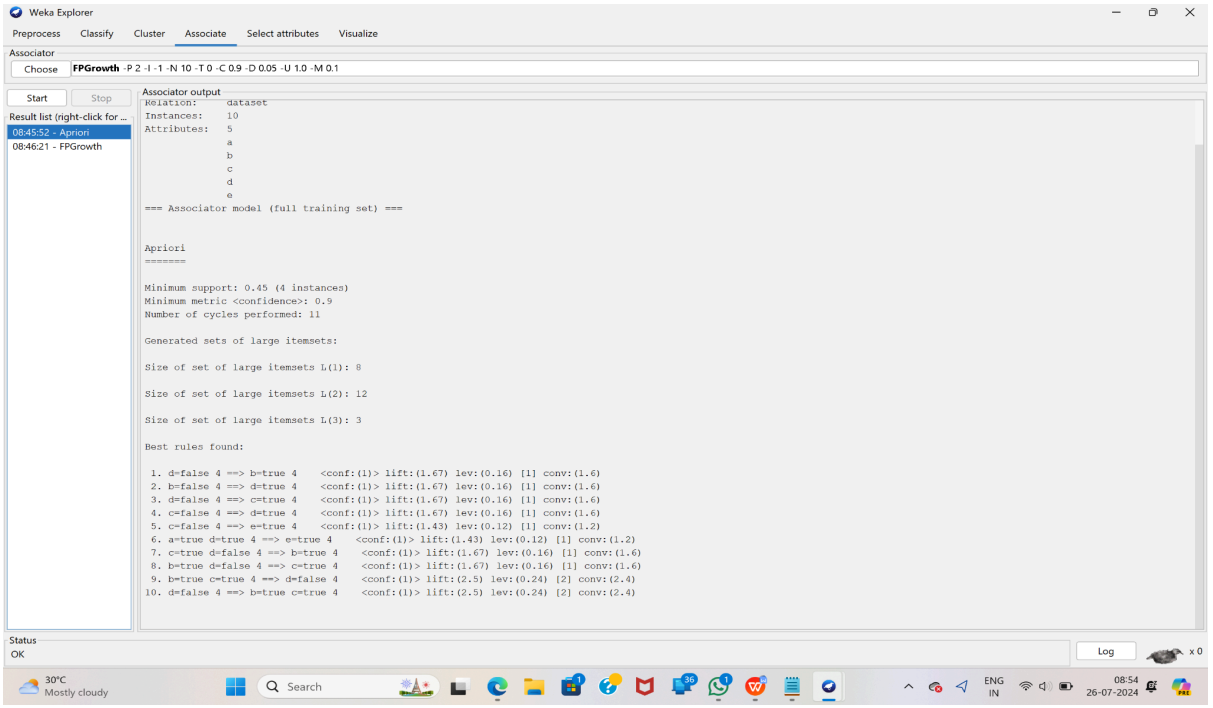

Average Blood Pressure by Age Group
Average Blood Pressure
Age Group
AgeGroup
20-30
30-40
40-50
50-60
60-70
70-80
80-90

DAY-3

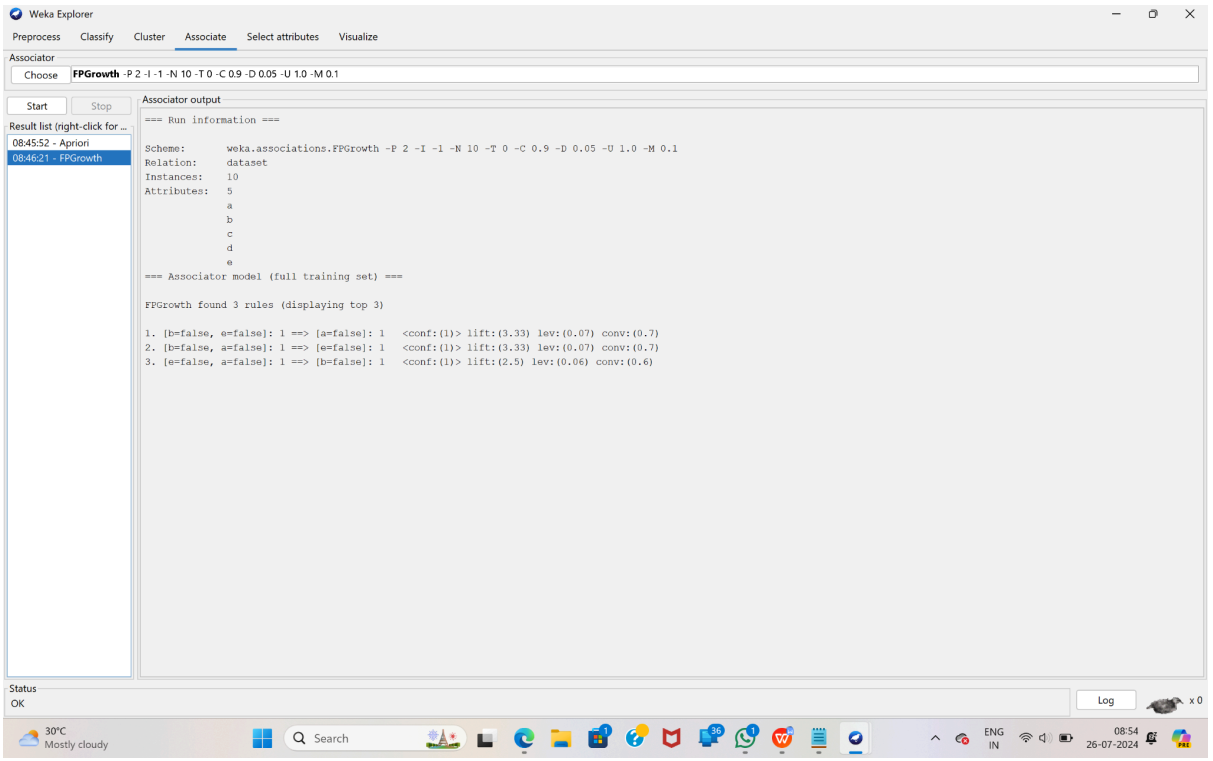
Q1:



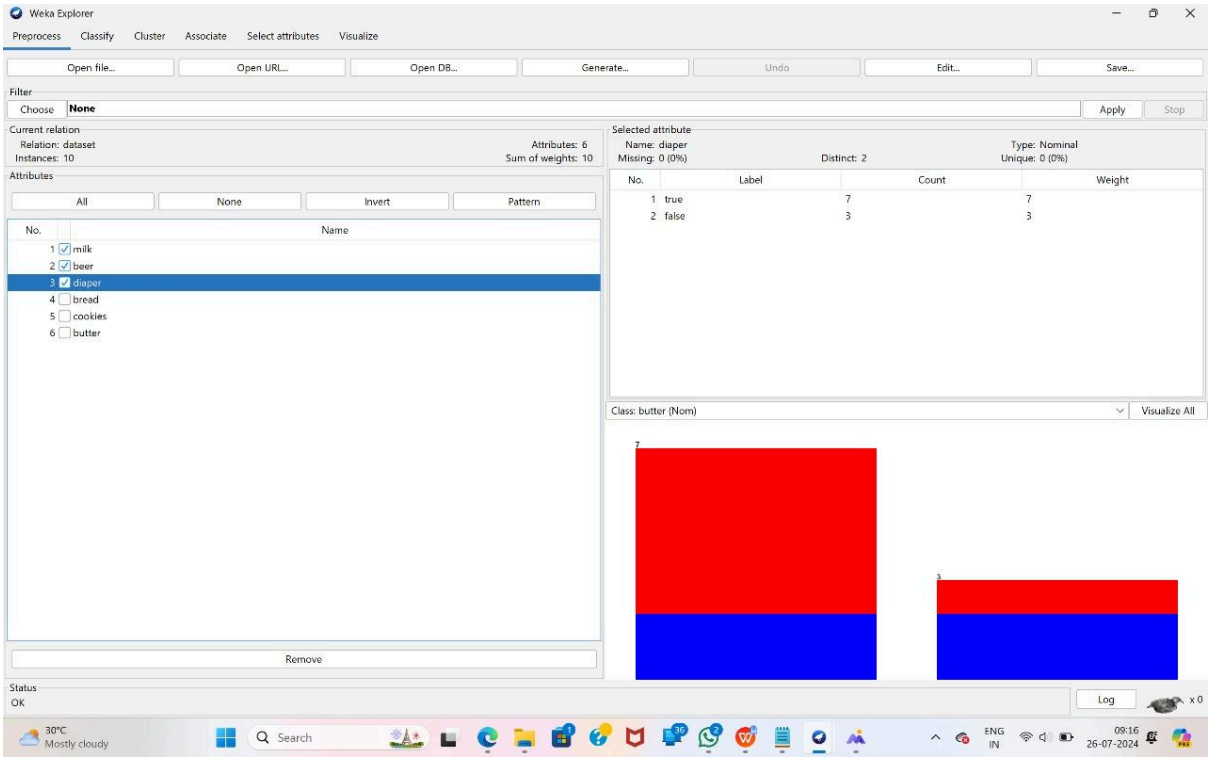
Apriori Algorithm:



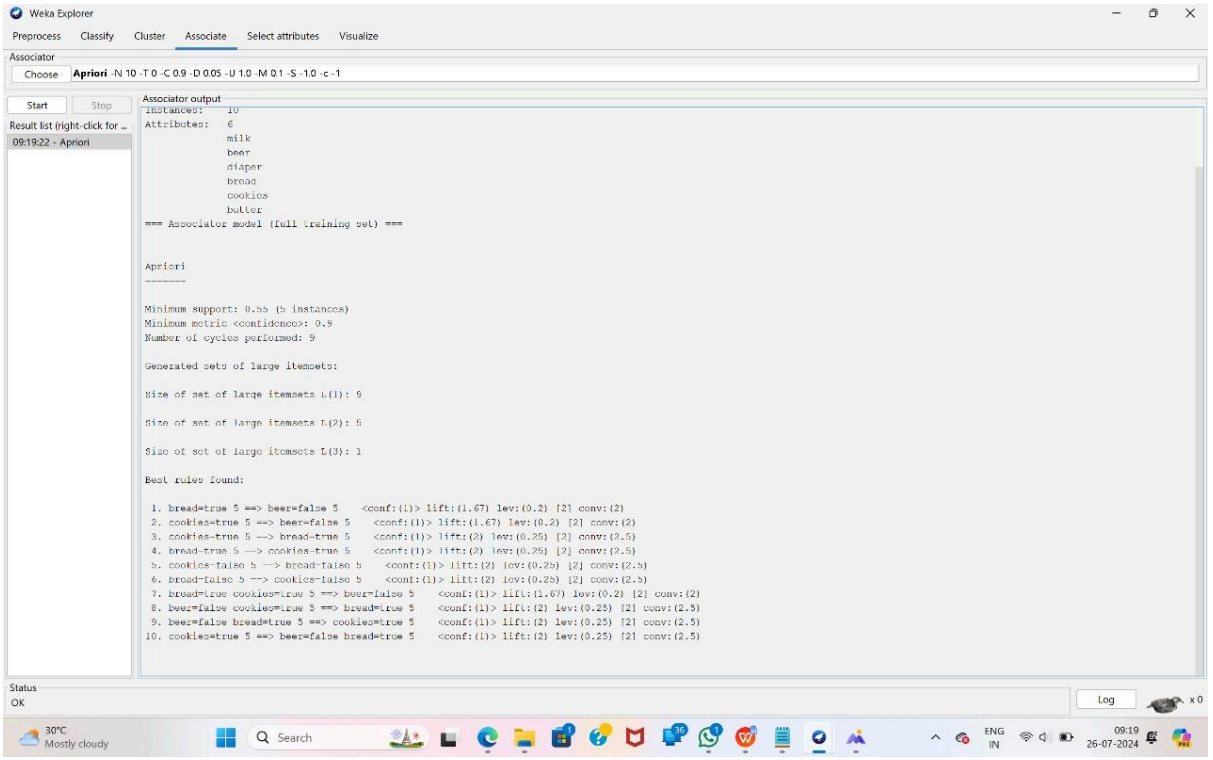
FP GROWTH:


Weka Explorer
Preprocess Classify Cluster Associate Select attributes Visualize
Associator
Choose FPGrowth -P 2 -I -1 -N 10 -T 0 -C 0.9 -D 0.05 -U 1.0 -M 0.1
Start Stop
Result list (right-click for ...
08:45:52 - Apriori
08:46:21 - FPGrowth
Associator output
=== Run information ===
Scheme: weka.associations.FPGrowth -P 2 -I -1 -N 10 -T 0 -C 0.9 -D 0.05 -U 1.0 -M 0.1
Relation: dataset
Instances: 10
Attributes: 5
a
b
c
d
e
=== Associator model (full training set) ===
FPGrowth found 3 rules (displaying top 3)
1. [b=false, e=false]: 1 ==> [a=false]: 1 <conf:(1)> lift:(3.33) lev:(0.07) conv:(0.7)
2. [b=false, a=false]: 1 ==> [e=false]: 1 <conf:(1)> lift:(3.33) lev:(0.07) conv:(0.7)
3. [e=false, a=false]: 1 ==> [b=false]: 1 <conf:(1)> lift:(2.5) lev:(0.06) conv:(0.6)
Status
OK
Log
x 0
30°C
Mostly cloudy
Search
ENG
IN
08:54
26-07-2024

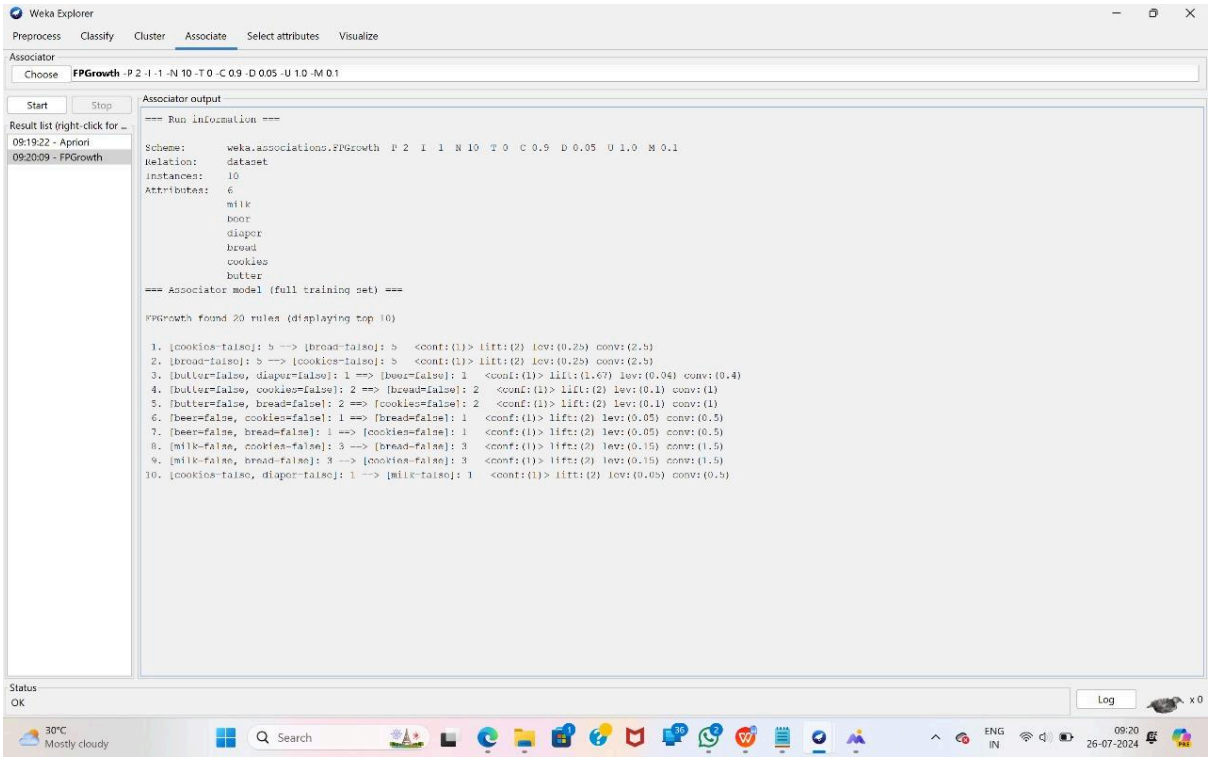
Q2:


Weka Explorer
Preprocess Classify Cluster Associate Select attributes Visualize
Open file... Open URL... Open DB... Generate... Undo Edit... Save...
Filter
Choose None Apply Stop
Current relation
Relation: dataset
Instances: 10
Attributes: 6
Sum of weights: 10
Selected attribute
Name: diaper
Missing: 0 (0%)
Distinct: 2
Type: Nominal
Unique: 0 (0%)
Attributes
All None Invert Pattern
No. Name
1 milk
2 beer
3 diaper
4 bread
5 cookies
6 butter
No. Label Count Weight
1 true 7 7
2 false 3 3
Class: butter (Nom)
Visualize All
Remove
Status
OK
Log
x 0
30°C
Mostly cloudy
Search
ENG
IN
09:16
26-07-2024

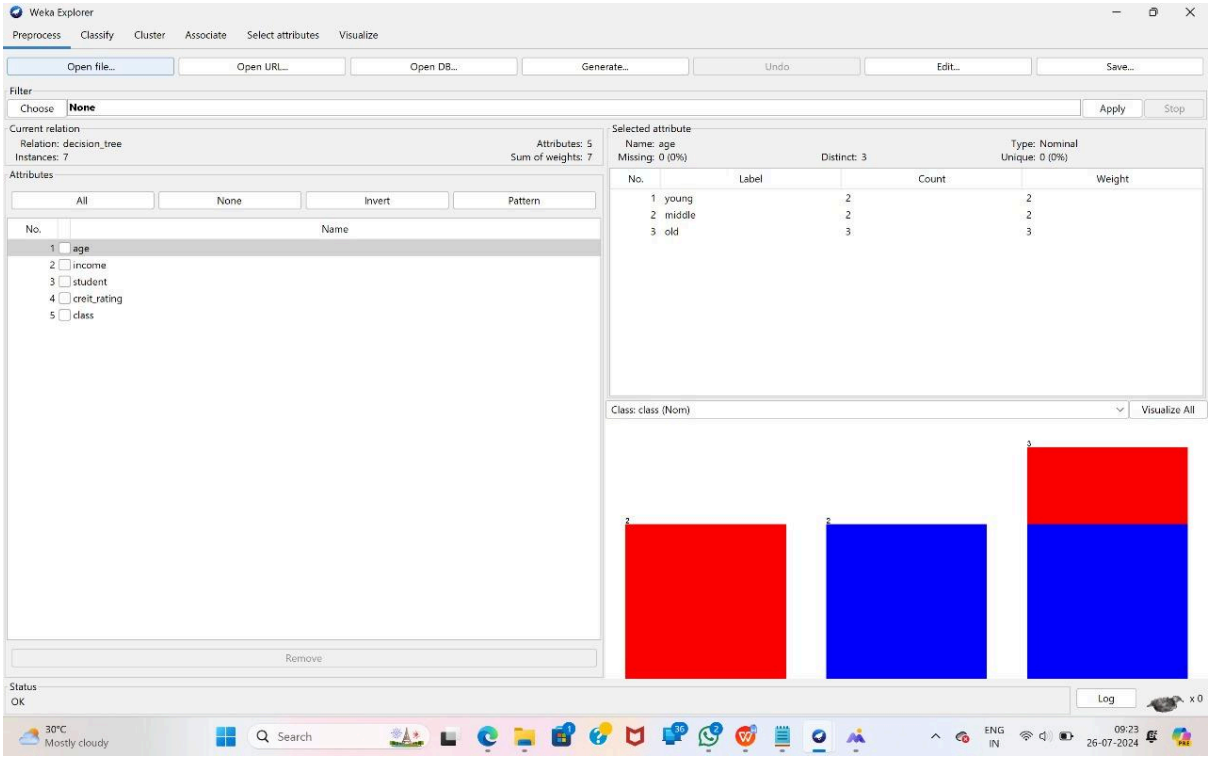
Apriori Algorithm:



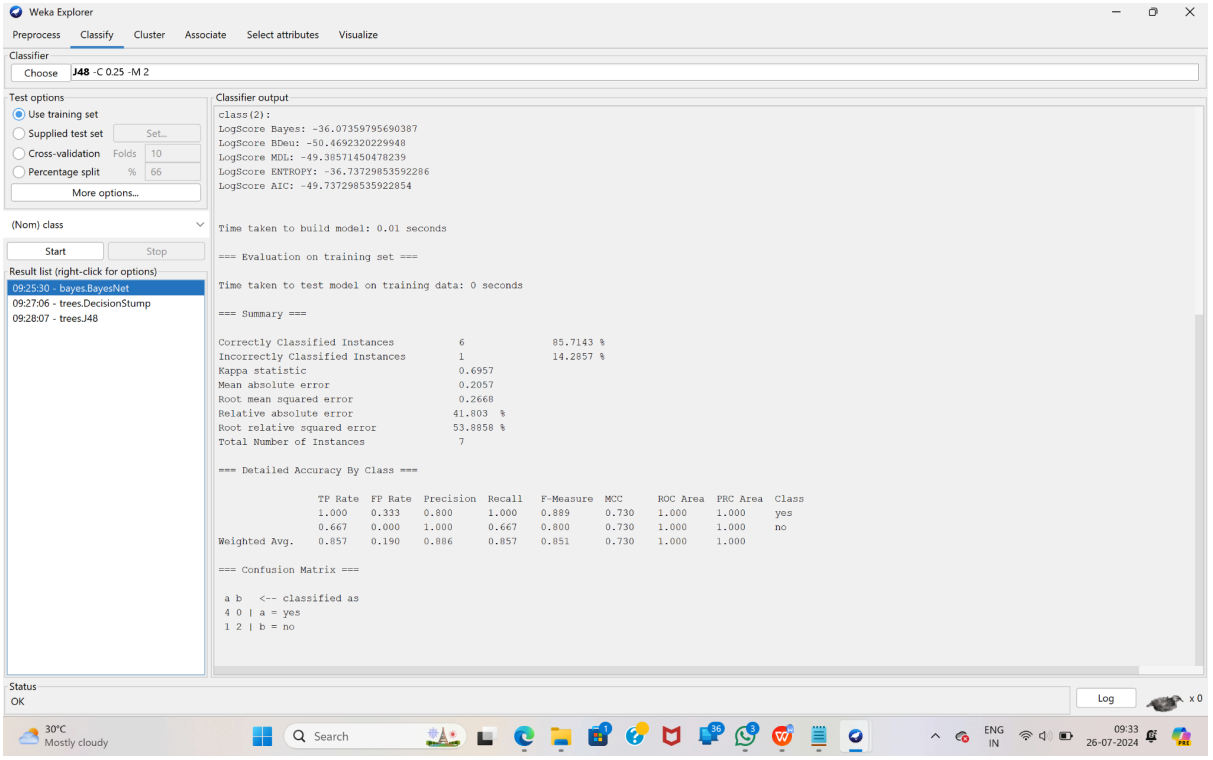
FP GROWTH:



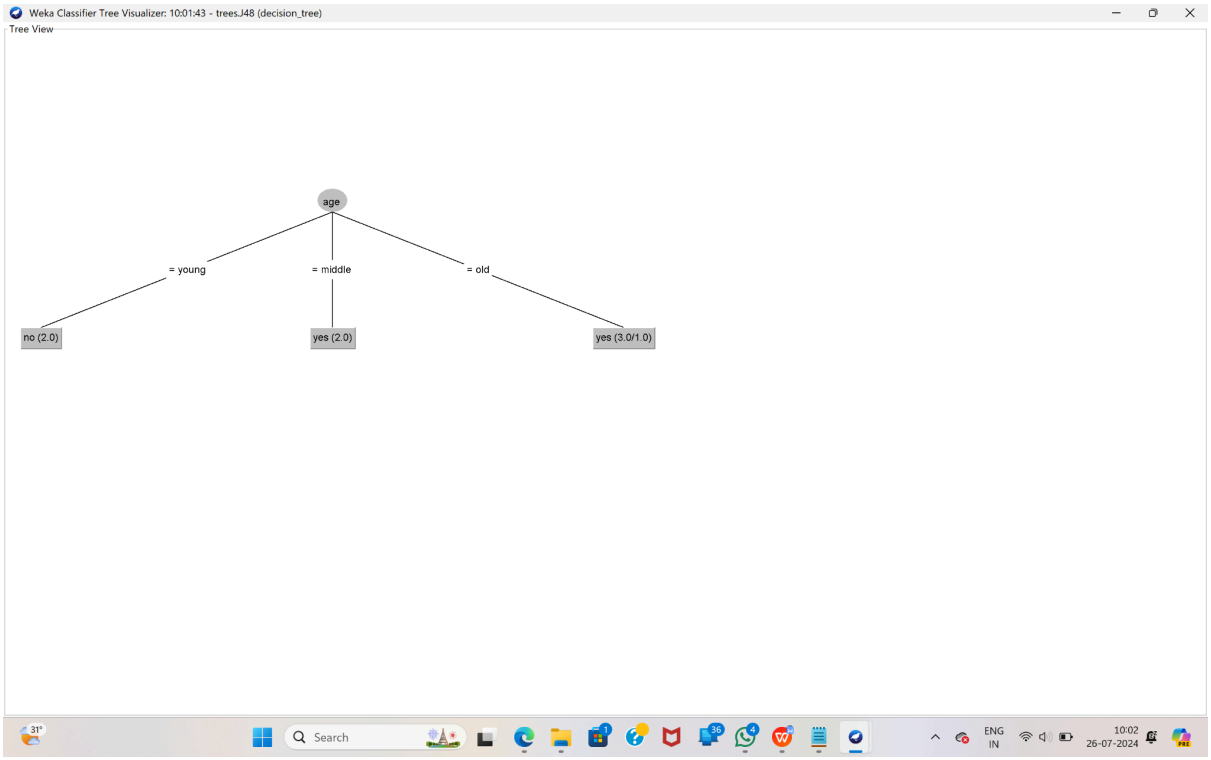
Q3:



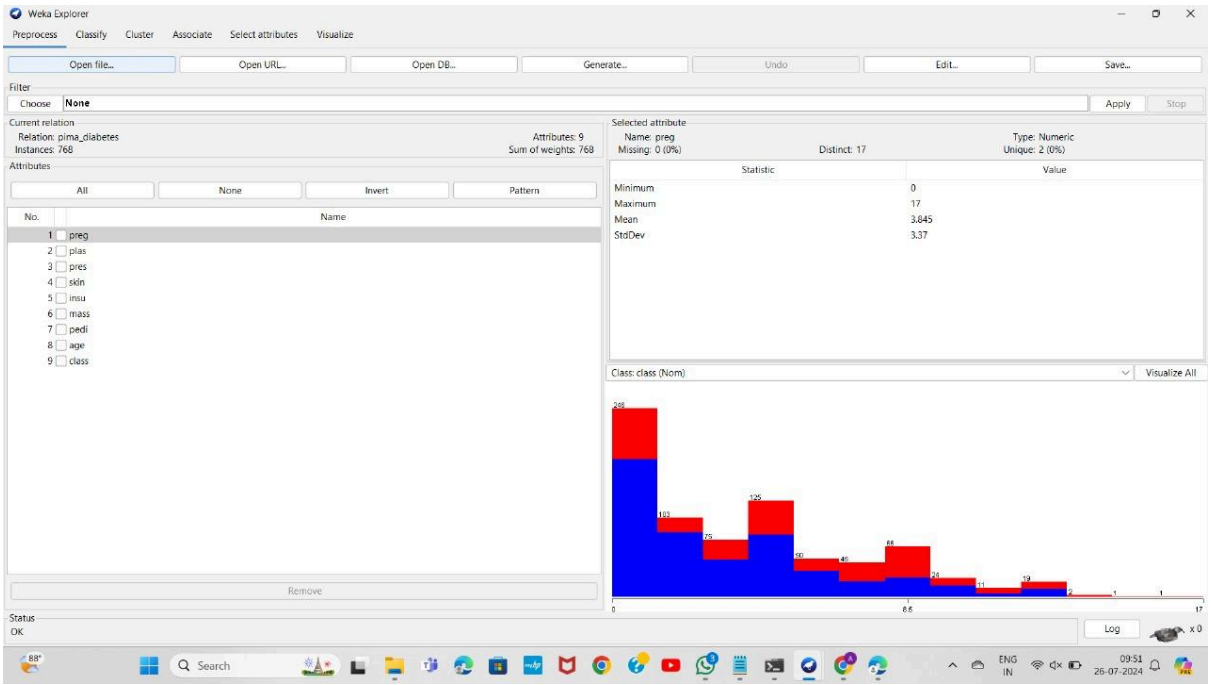
Bayes classification:



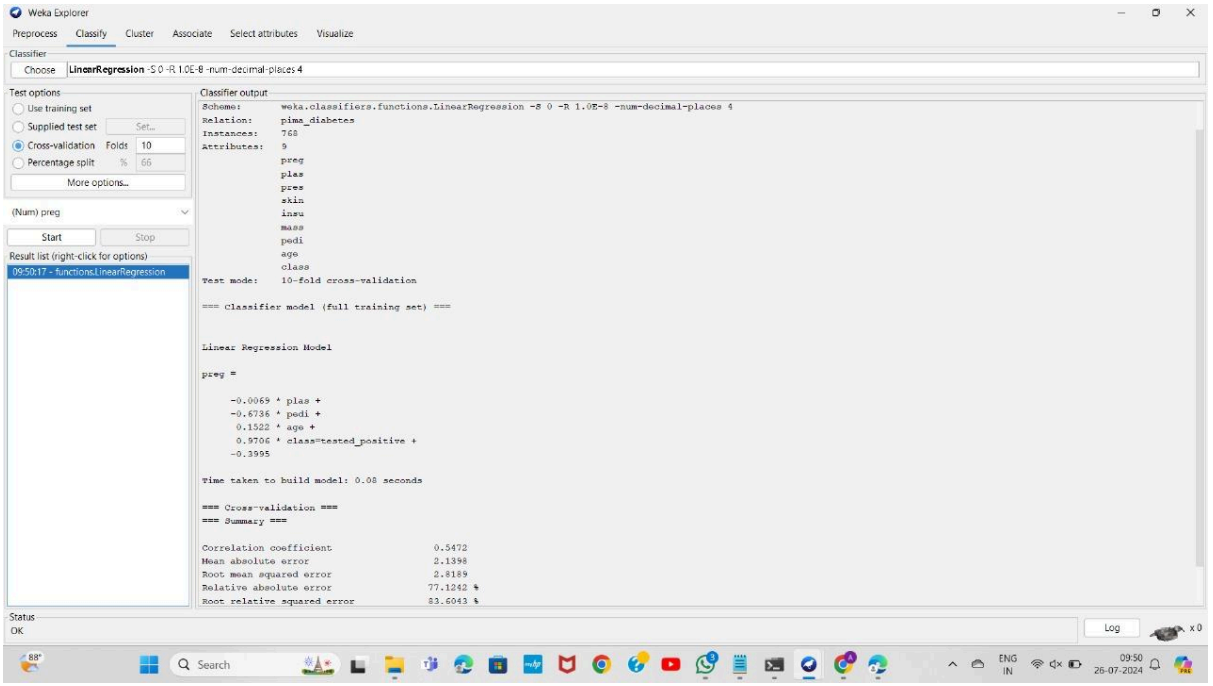
Descion tree:



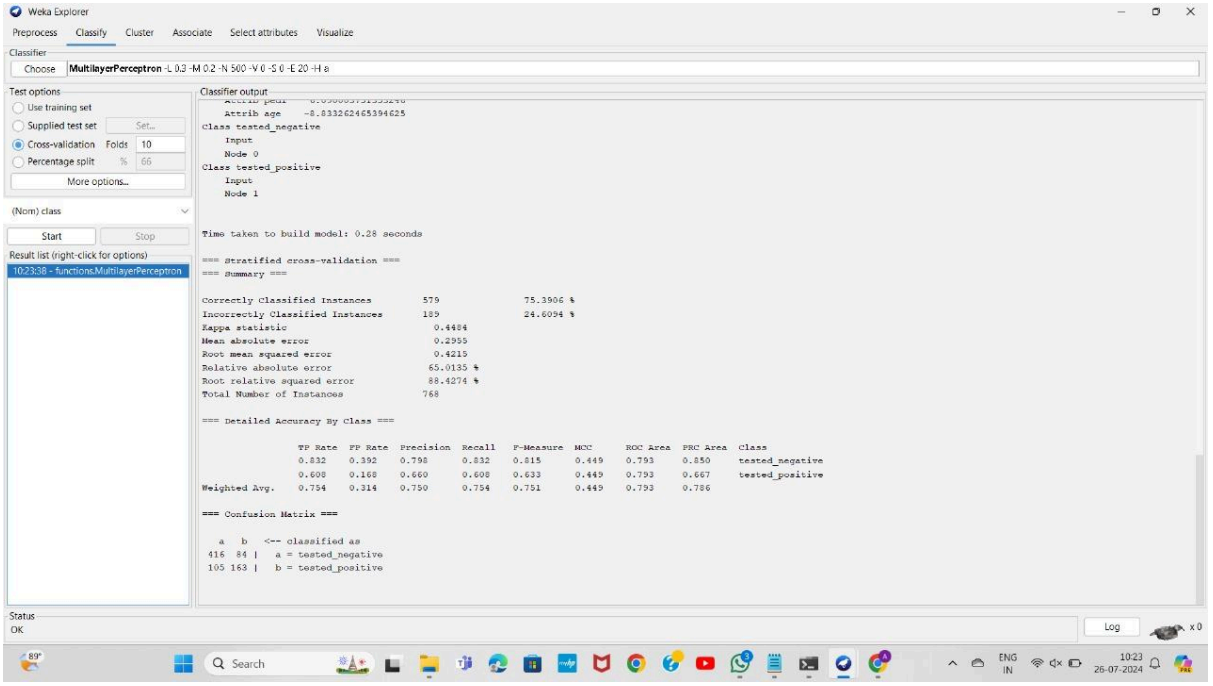
Q4:



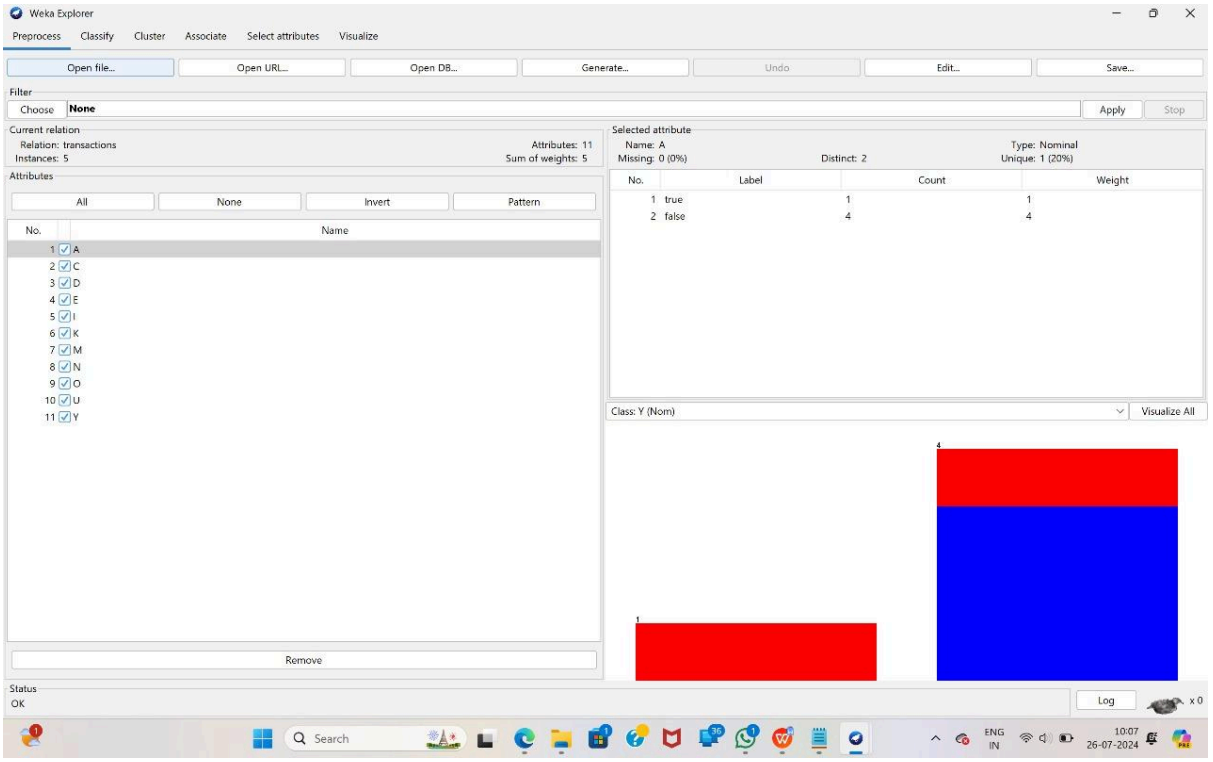
Linear regression:



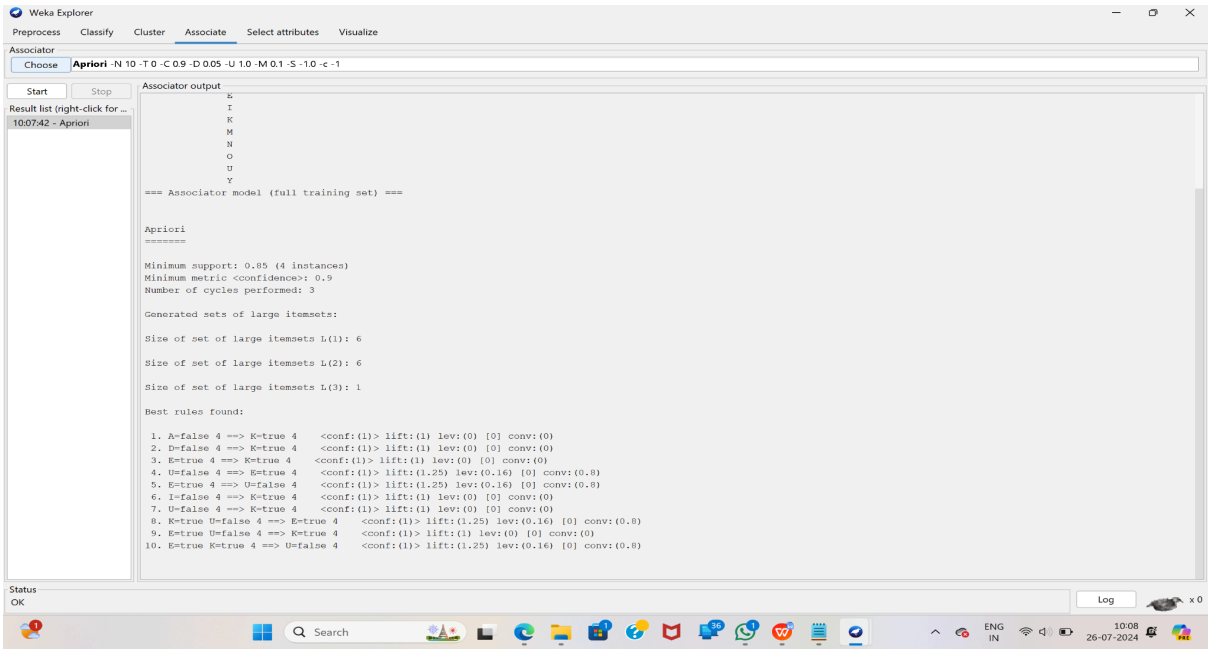
Multiple regression:



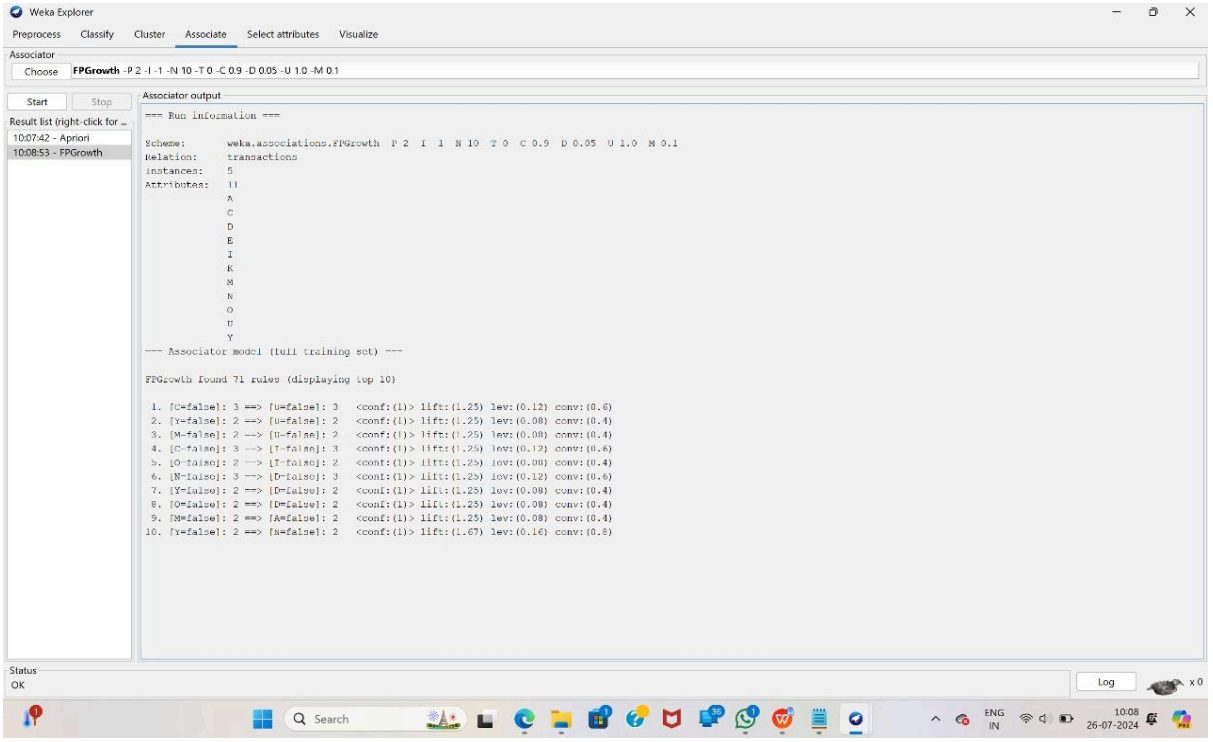
Q5:



Apriori Algorithm:

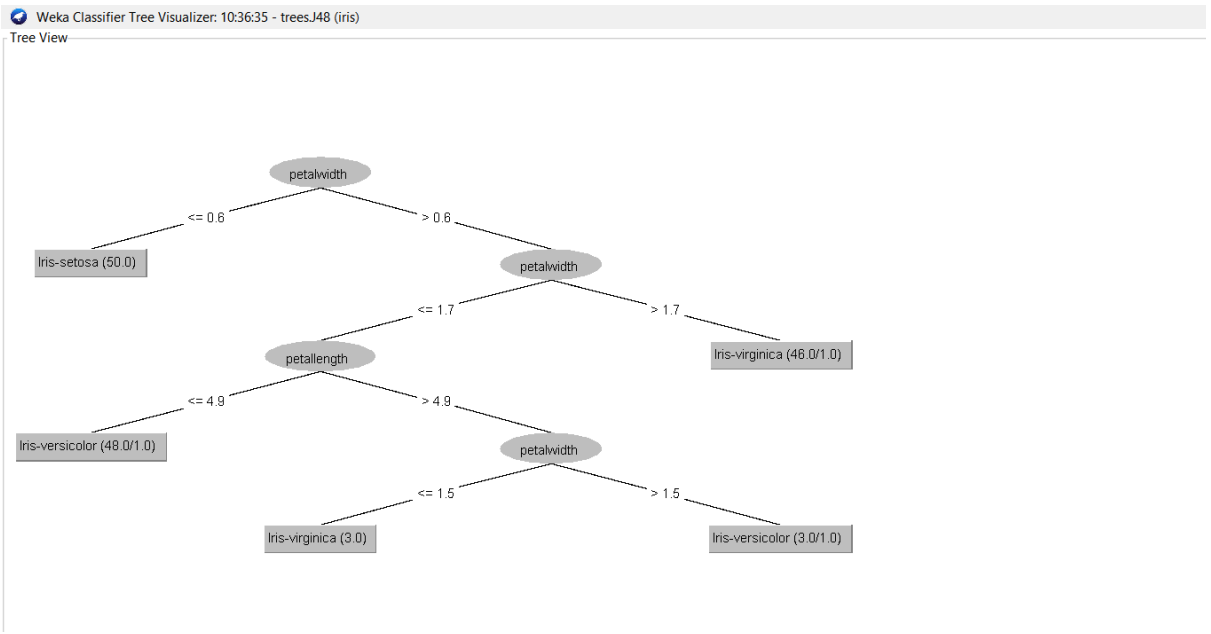


FP GROWTH:

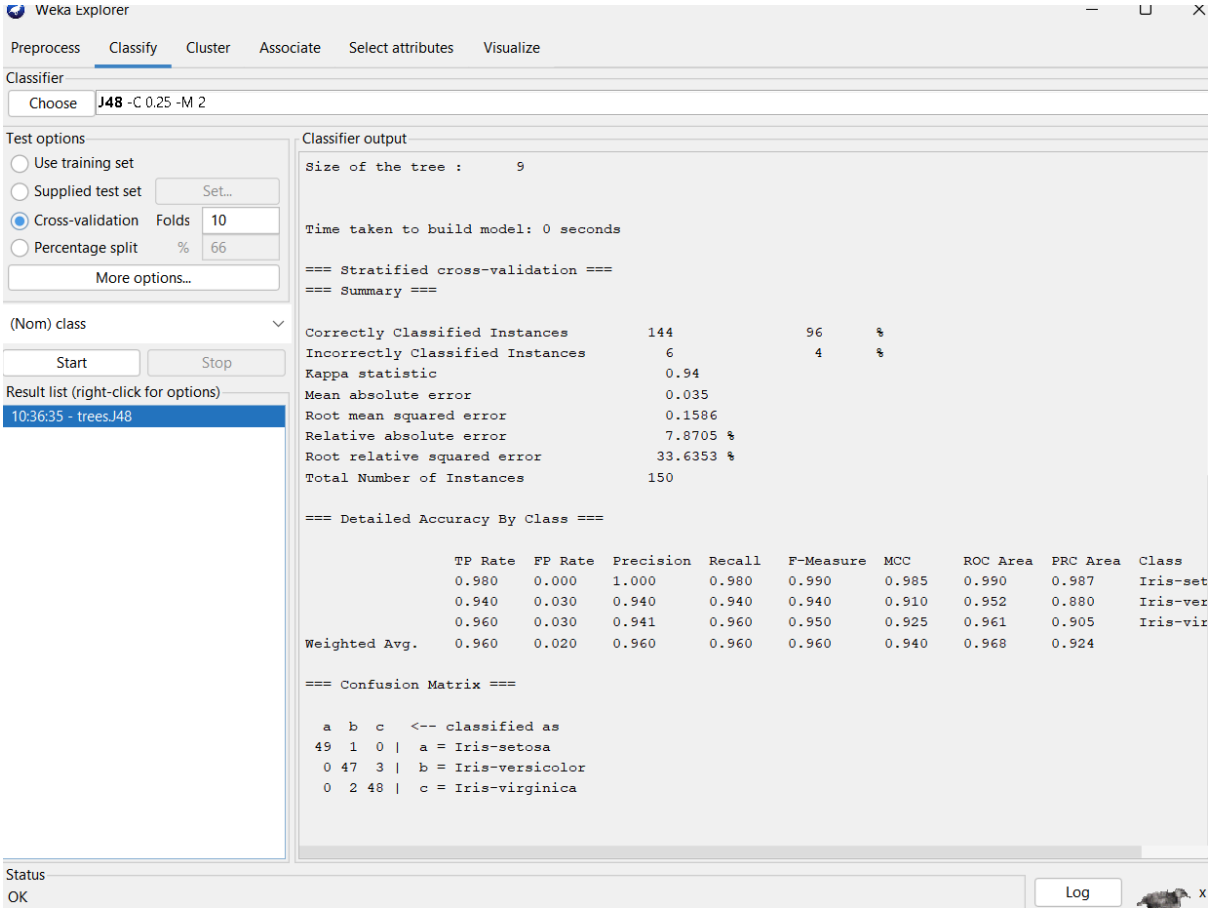


Q6:

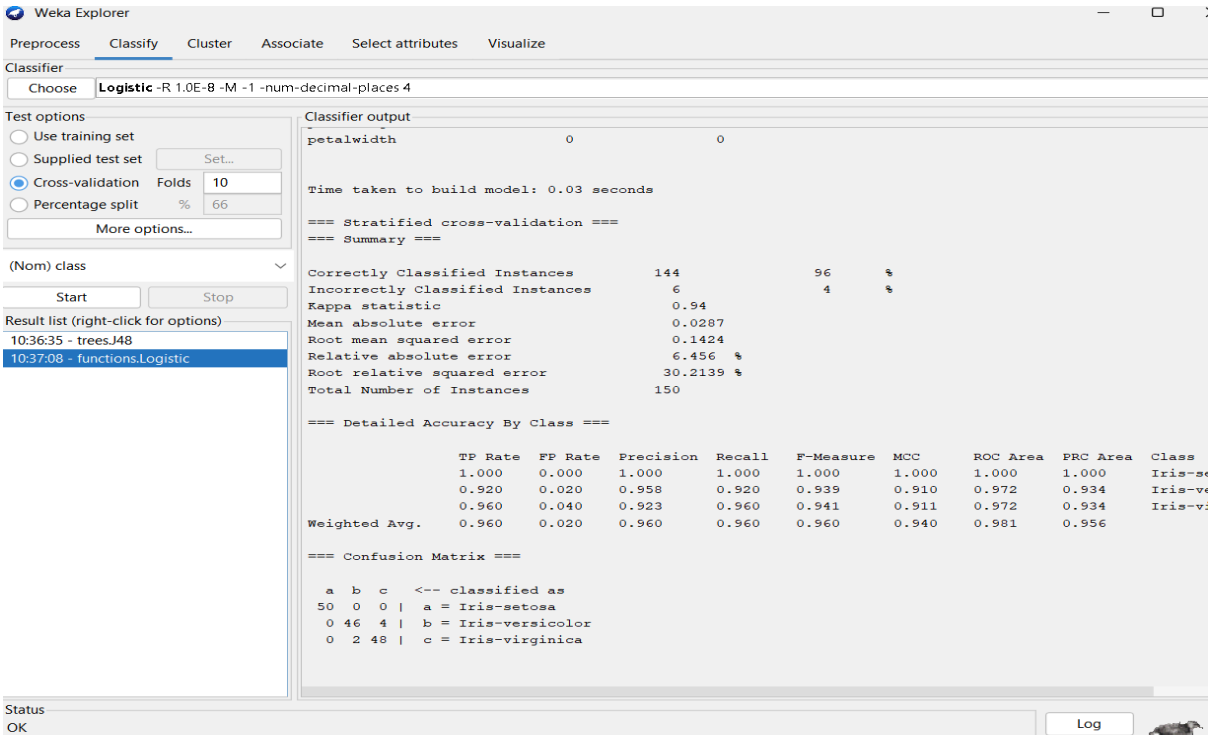
TREE:



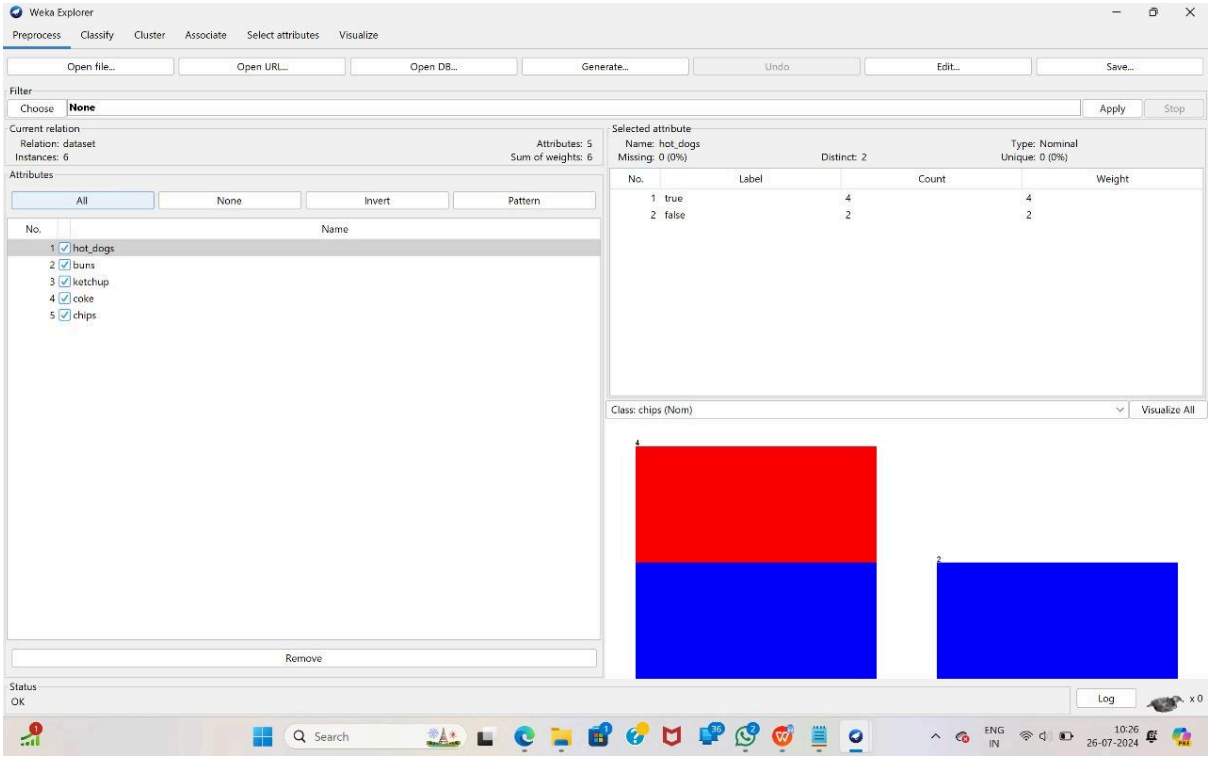
PREPROCESS:



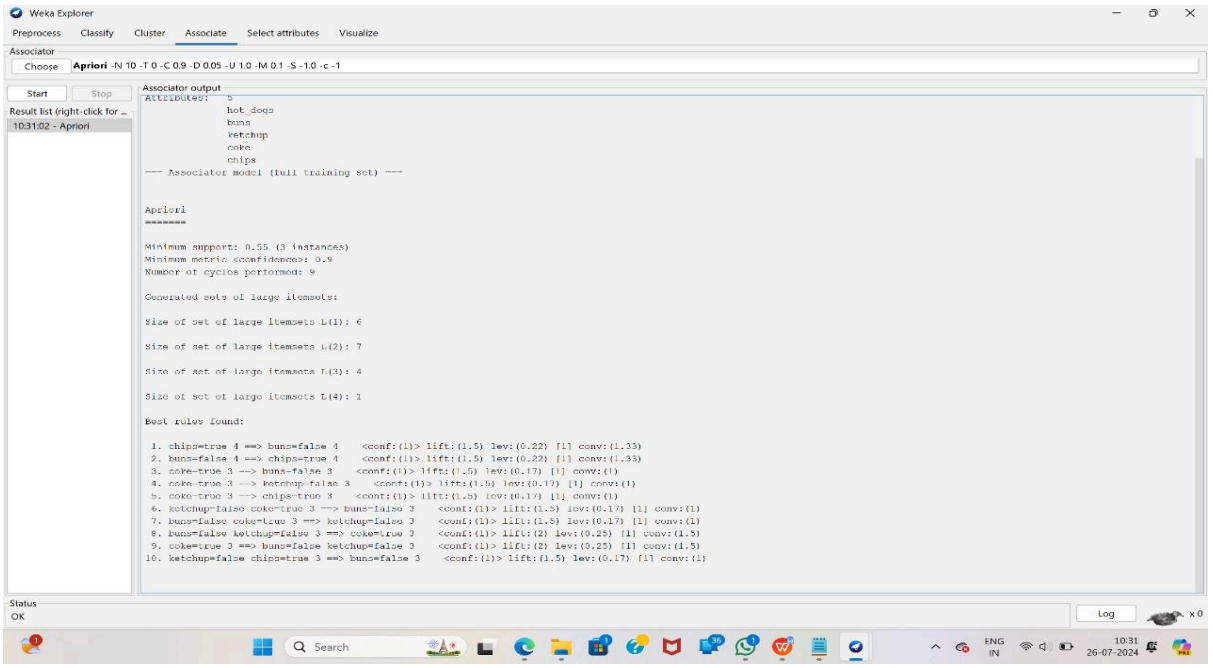
Logistic:



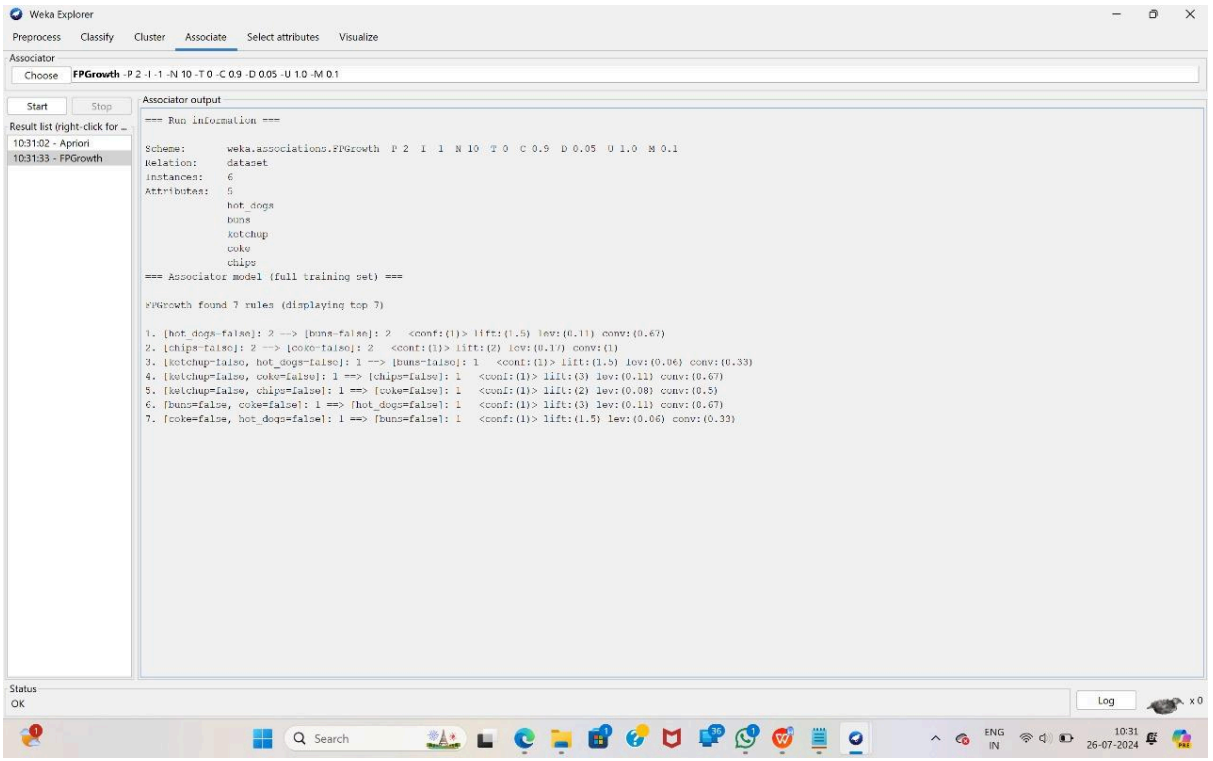
Q7:



Apriori Algorithm:

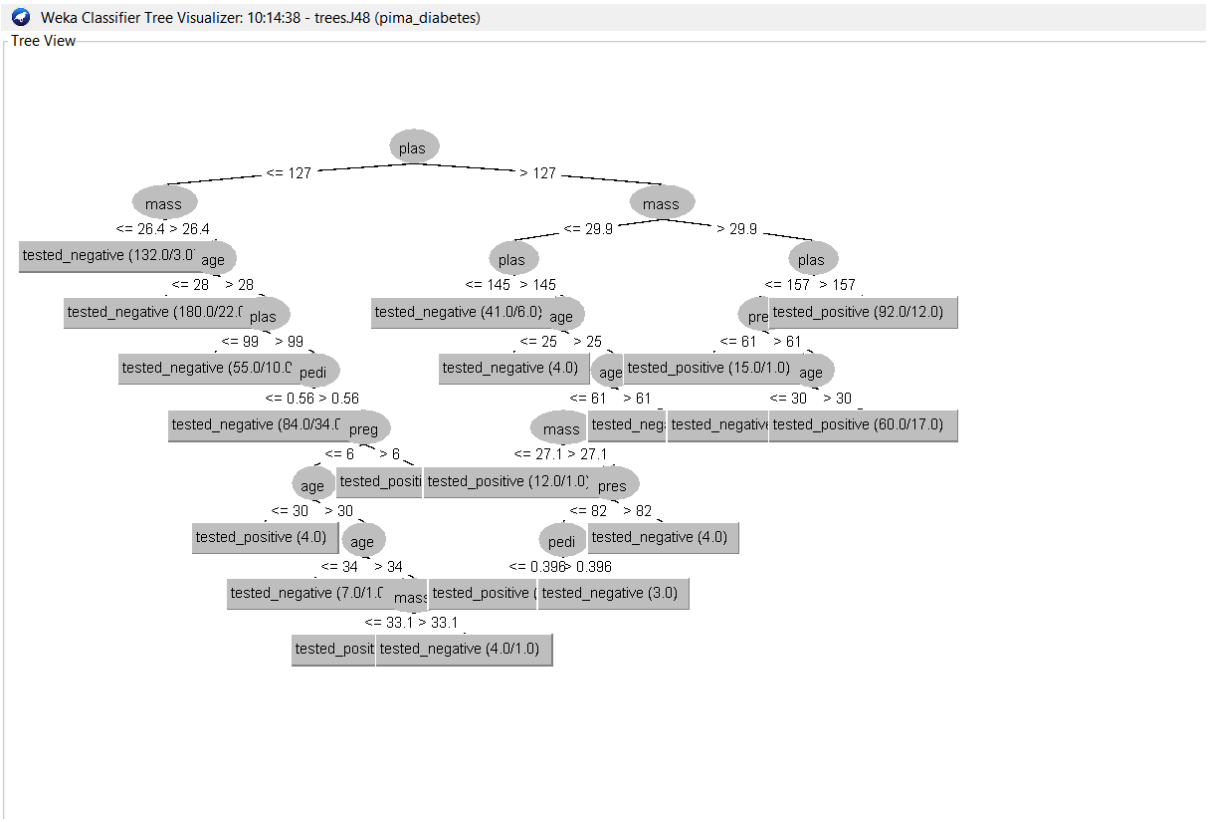


FP GROWTH:

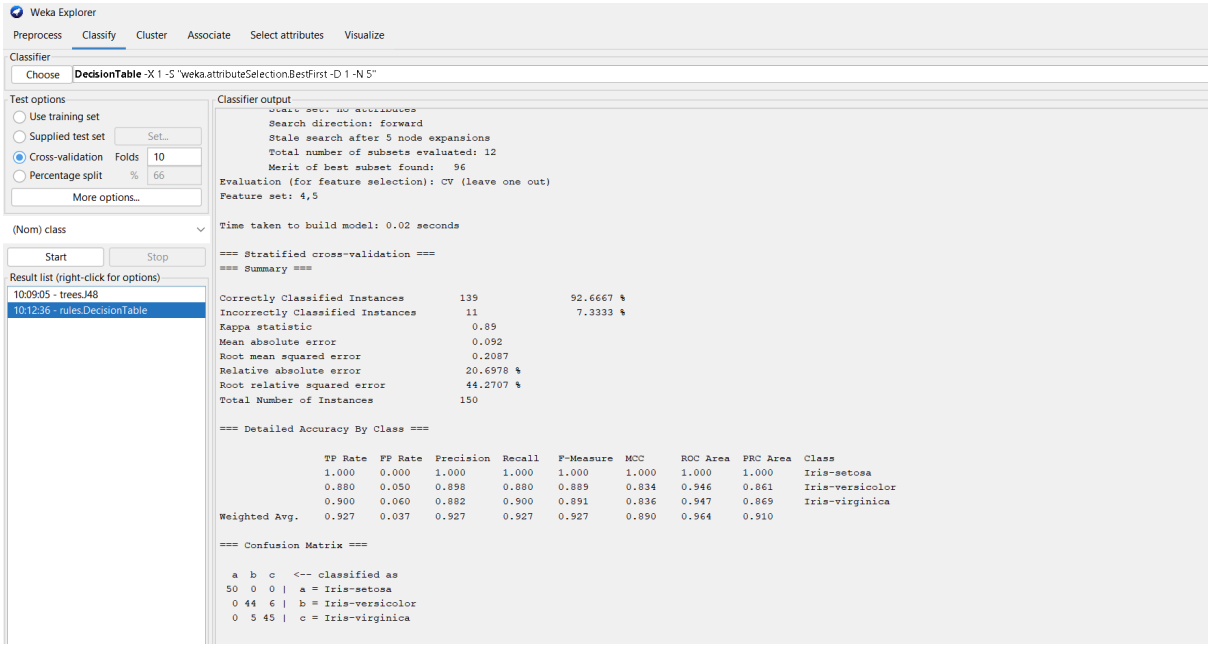


Q8:

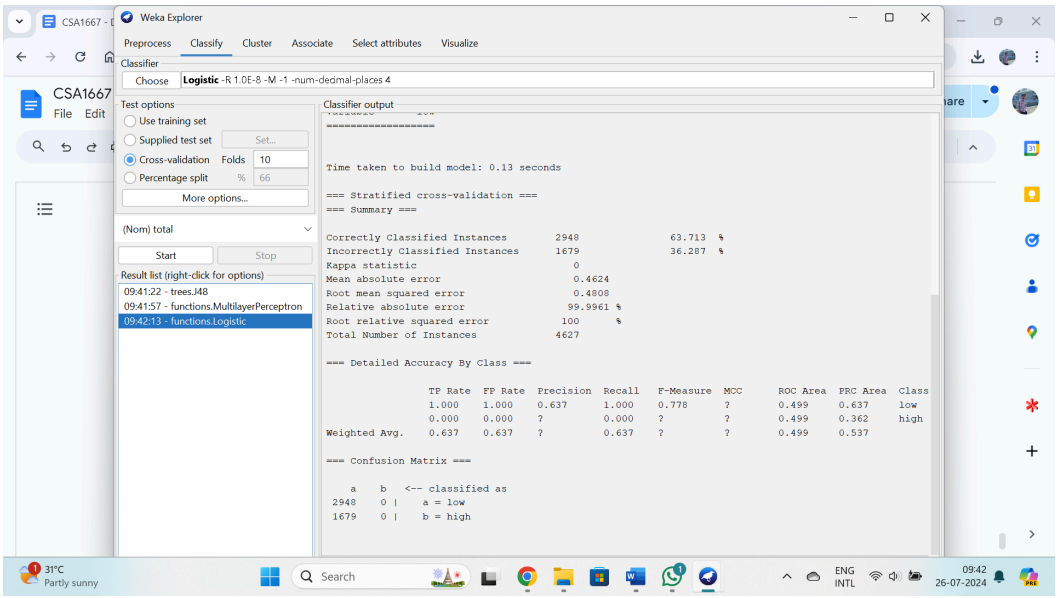
Tree:



Decision Tree:

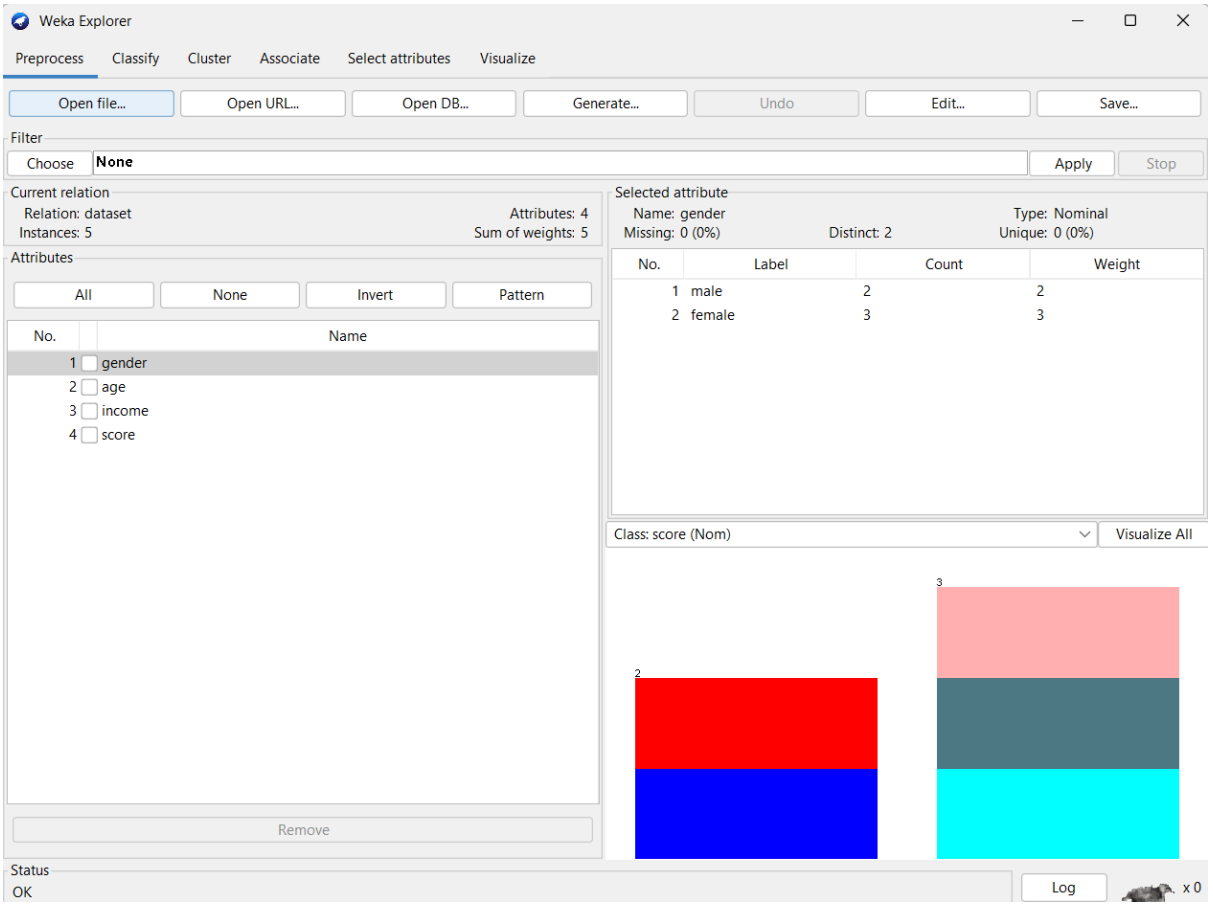


Logistic:

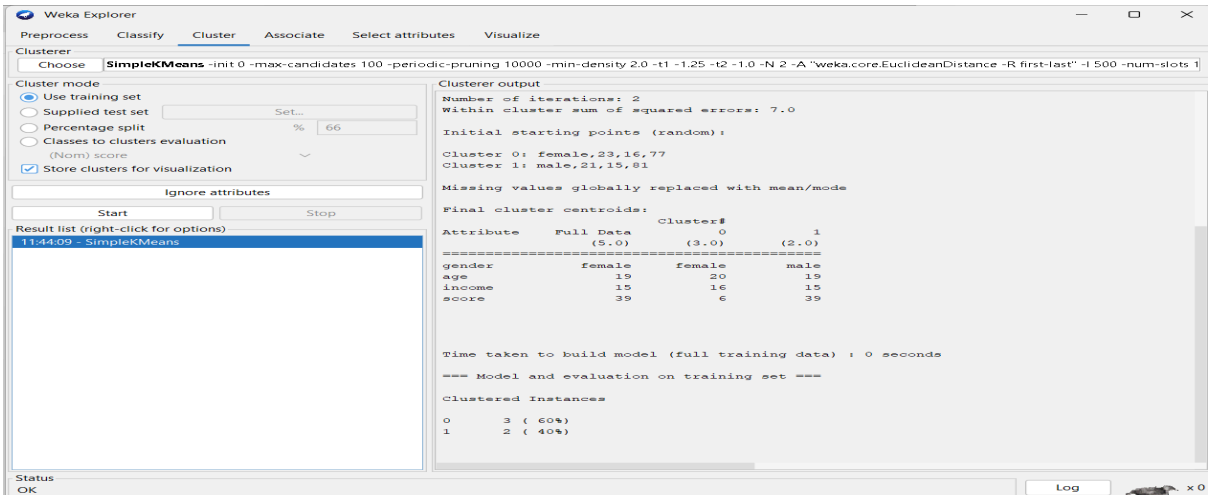


DAY-4

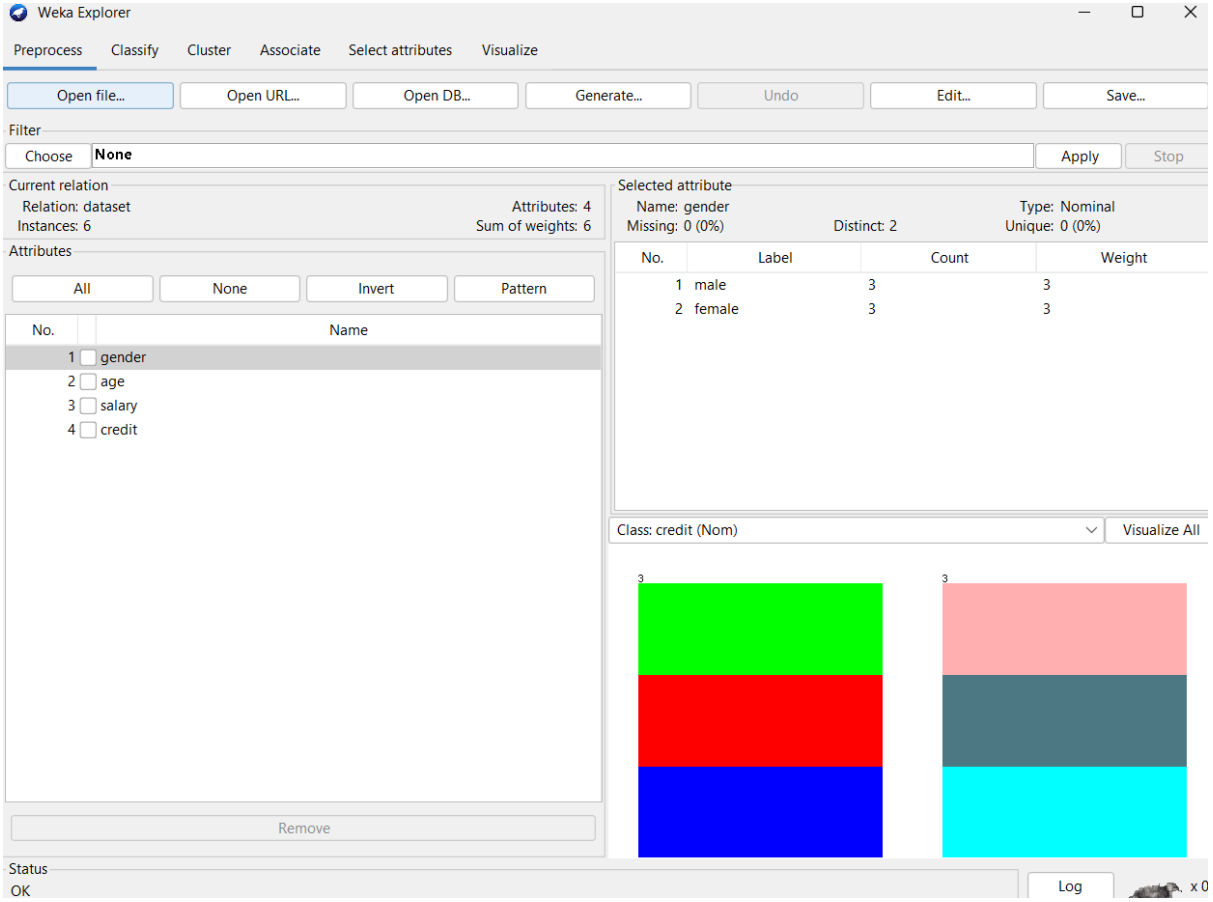
Q1:



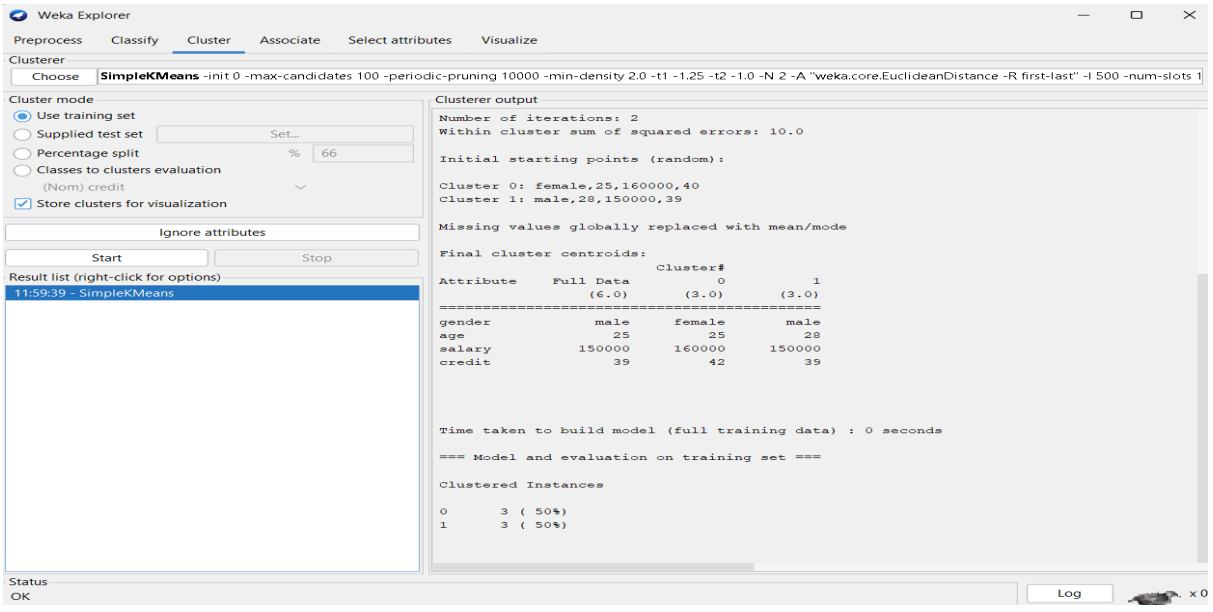
Clustering Analysis:



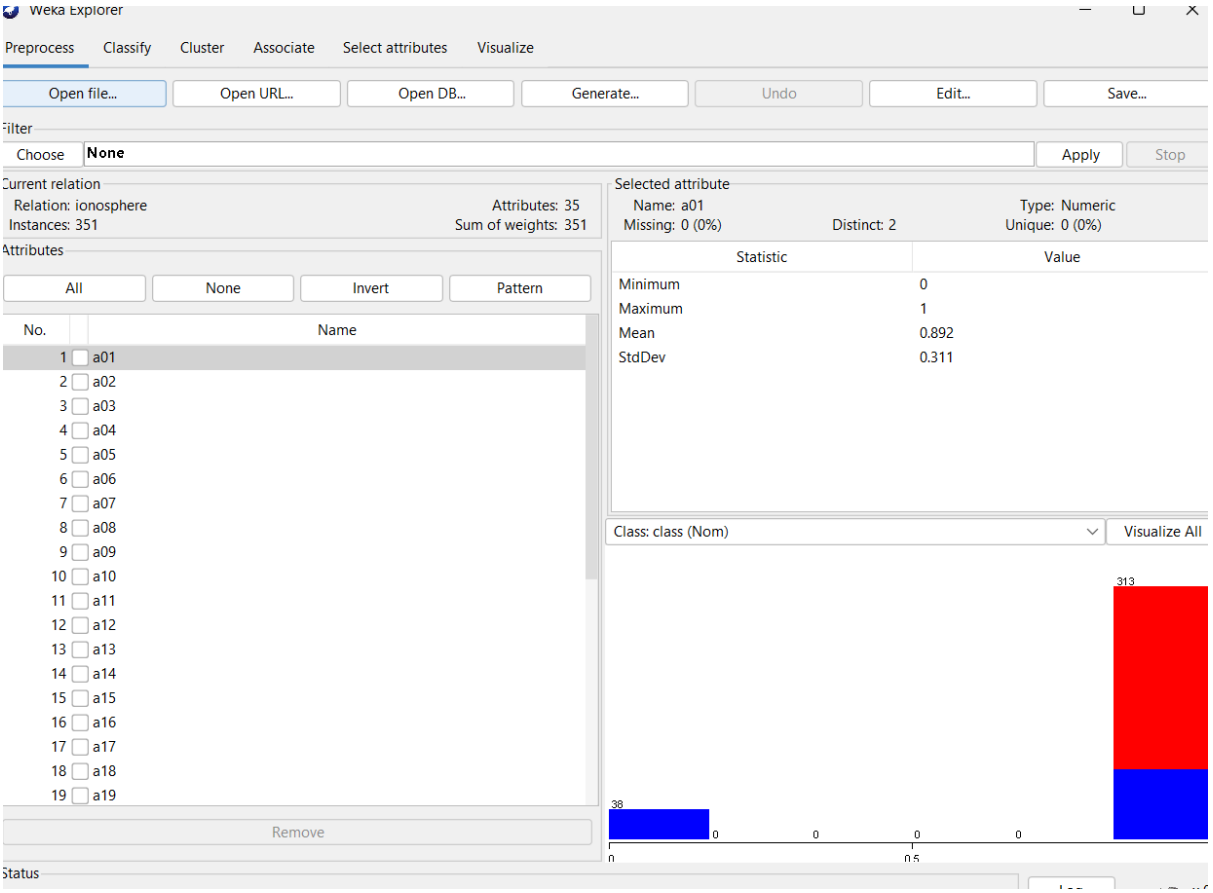
Q2:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Open file...
Open URL...
Open DB...
Generate...
Undo
Edit...
Save...
Filter
Choose
None
Apply
Stop
Current relation
Relation: dataset
Instances: 6
Attributes: 4
Sum of weights: 6
Attributes
All
None
Invert
Pattern
No.
Name
1 gender
2 age
3 salary
4 credit
Remove
Selected attribute
Name: gender
Missing: 0 (0%)
Distinct: 2
Type: Nominal
Unique: 0 (0%)
No.
Label
Count
Weight
1 male 3 3
2 female 3 3
Class: credit (Nom)
Visualize All
3
3
Status
OK
Log
x 0

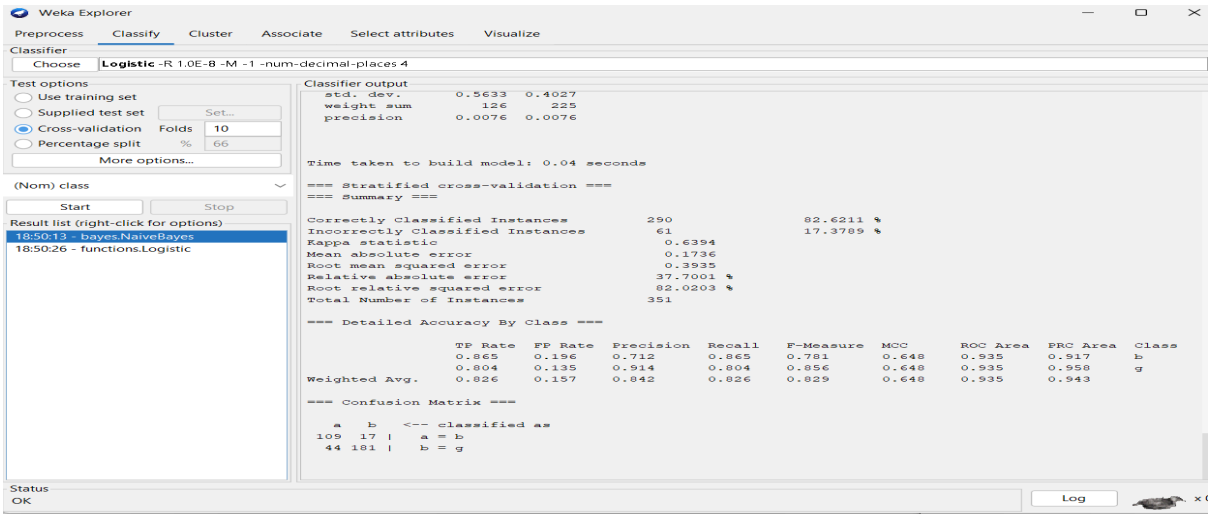
K- Means:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Clusterer
Choose
SimpleKMeans -init 0 -max-candidates 100 -periodic-pruning 10000 -min-density 2.0 -t1 -1.25 -t2 -1.0 -N 2 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1
Cluster mode
Use training set
Supplied test set
Set...
Percentage split
%
66
Classes to clusters evaluation
(Nom) credit
Store clusters for visualization
Ignore attributes
Start
Stop
Result list (right-click for options)
11:59:39 - SimpleKMeans
Clusterer output
Number of iterations: 2
Within cluster sum of squared errors: 10.0
Initial starting points (random):
Cluster 0: female,25,160000,40
Cluster 1: male,28,150000,39
Missing values globally replaced with mean/mode
Final cluster centroids:
Cluster#
Attribute Full Data 0 1
(6.0) (3.0) (3.0)
gender male female male
age 25 25 28
salary 150000 160000 150000
credit 39 42 39
Time taken to build model (full training data) : 0 seconds
=== Model and evaluation on training set ===
Clustered Instances
0 3 (50%)
1 3 (50%)
Status
OK
Log
x 0

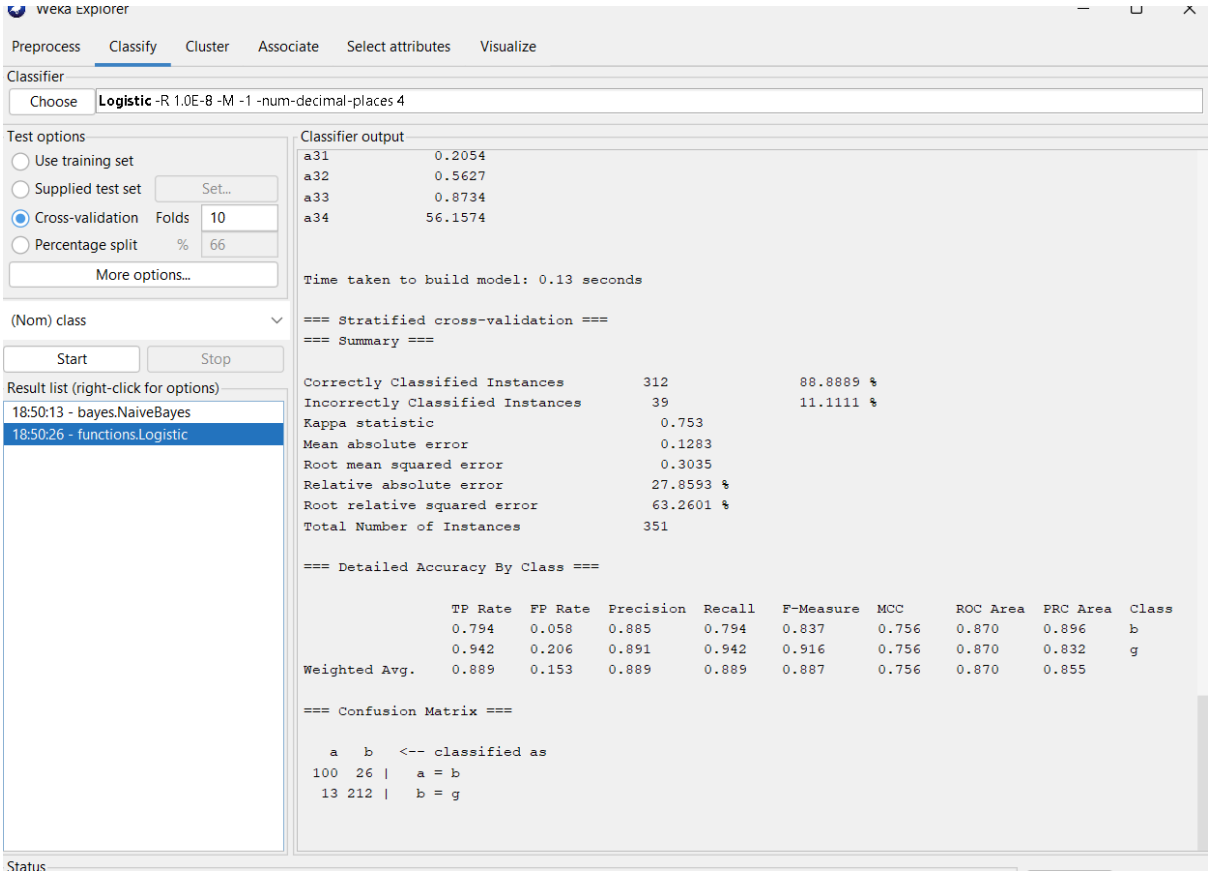
Q3:



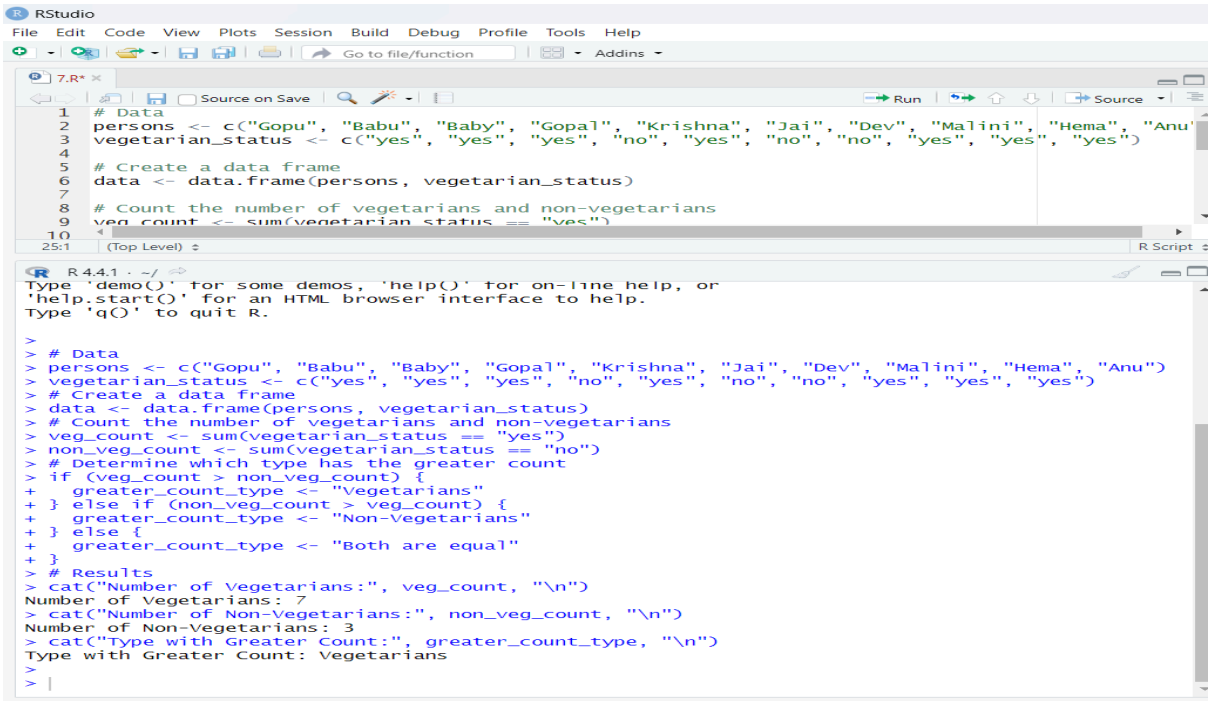
Naïve Bayes classification:



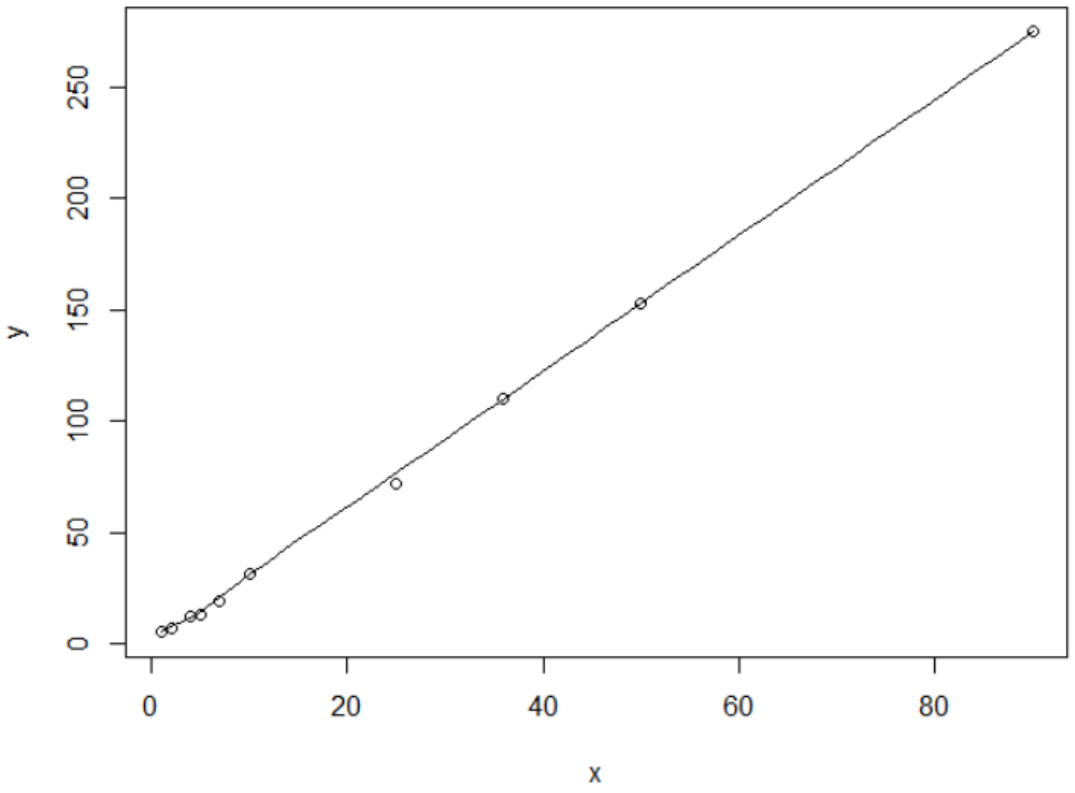
SVM:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Classifier
Choose
Logistic -R 1.0E-8 -M -1 -num-decimal-places 4
Test options
Use training set
Supplied test set
Set...
Cross-validation
Folds
10
Percentage split
%
66
More options...
(Nom) class
Start
Stop
Result list (right-click for options)
18:50:13 - bayes.NaiveBayes
18:50:26 - functions.Logistic
Classifier output
a31 0.2054
a32 0.5627
a33 0.8734
a34 56.1574
Time taken to build model: 0.13 seconds
=== Stratified cross-validation ===
=== Summary ===
Correctly Classified Instances 312 88.8889 %
Incorrectly Classified Instances 39 11.1111 %
Kappa statistic 0.753
Mean absolute error 0.1283
Root mean squared error 0.3035
Relative absolute error 27.8593 %
Root relative squared error 63.2601 %
Total Number of Instances 351
=== Detailed Accuracy By Class ===
TP Rate FP Rate Precision Recall F-Measure MCC ROC Area PRC Area Class
0.794 0.058 0.885 0.794 0.837 0.756 0.870 0.896 b
0.942 0.206 0.891 0.942 0.916 0.756 0.870 0.832 g
Weighted Avg. 0.889 0.153 0.889 0.889 0.887 0.756 0.870 0.855
=== Confusion Matrix ===
a b <-- classified as
100 26 | a = b
13 212 | b = g
Status

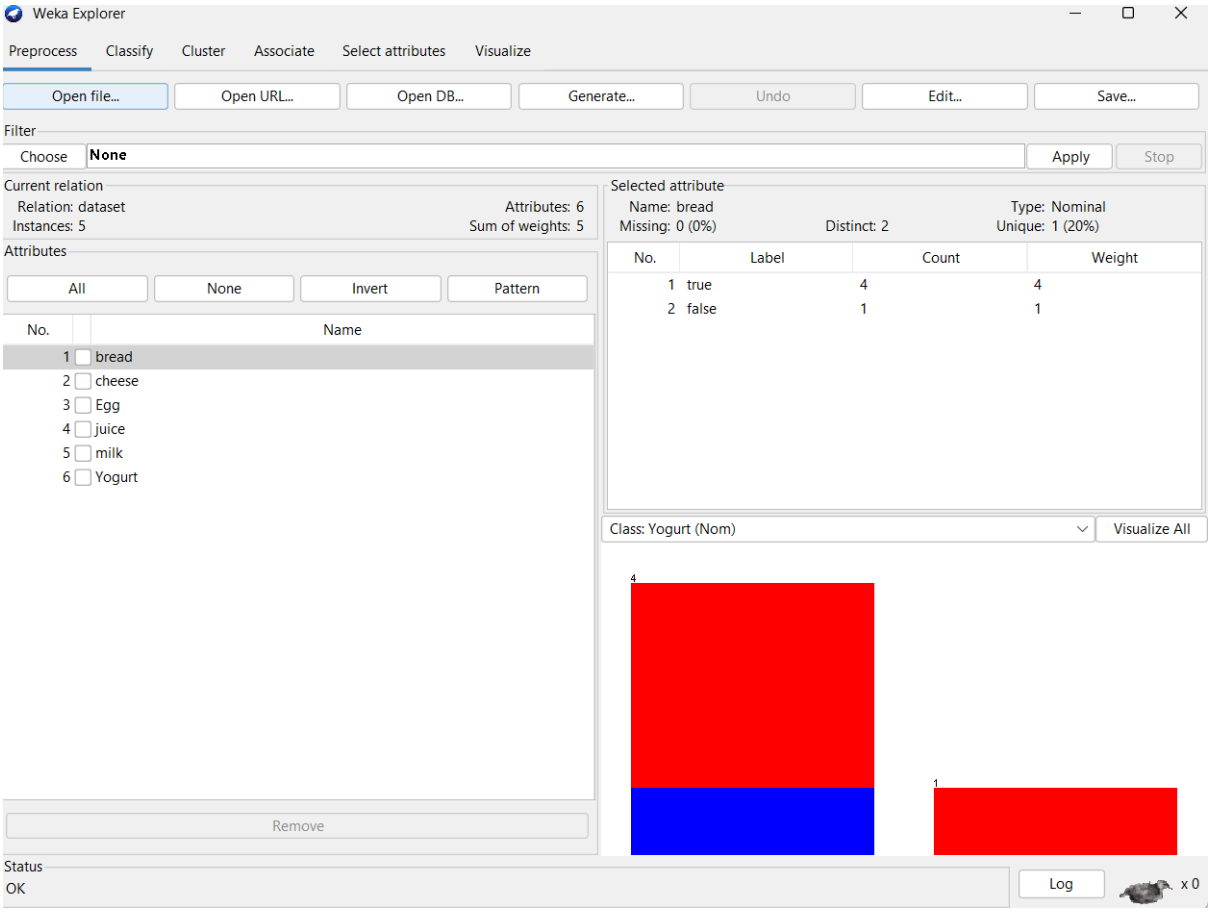
Q4:


RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
7.R*
Source on Save
Run
Source
# Data
persons <- c("Gopu", "Babu", "Baby", "Gopal", "Krishna", "Jai", "Dev", "Malini", "Hema", "Anu"
vegetarian_status <- c("yes", "yes", "yes", "no", "yes", "no", "no", "yes", "yes", "yes")
# Create a data frame
data <- data.frame(persons, vegetarian_status)
# Count the number of vegetarians and non-vegetarians
veg_count <- sum(vegetarian_status == "yes")
25:1 (Top Level)
R Script
R 4.4.1 · ~/
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> # Data
> persons <- c("Gopu", "Babu", "Baby", "Gopal", "Krishna", "Jai", "Dev", "Malini", "Hema", "Anu")
> vegetarian_status <- c("yes", "yes", "yes", "no", "yes", "no", "no", "yes", "yes", "yes")
> # Create a data frame
> data <- data.frame(persons, vegetarian_status)
> # Count the number of vegetarians and non-vegetarians
> veg_count <- sum(vegetarian_status == "yes")
> non_veg_count <- sum(vegetarian_status == "no")
> # Determine which type has the greater count
> if (veg_count > non_veg_count) {
+ greater_count_type <- "Vegetarians"
+ } else if (non_veg_count > veg_count) {
+ greater_count_type <- "Non-Vegetarians"
+ } else {
+ greater_count_type <- "Both are equal"
+ }
> # Results
> cat("Number of Vegetarians:", veg_count, "\n")
Number of Vegetarians: 7
> cat("Number of Non-Vegetarians:", non_veg_count, "\n")
Number of Non-Vegetarians: 3
> cat("Type with Greater Count:", greater_count_type, "\n")
Type with Greater Count: Vegetarians

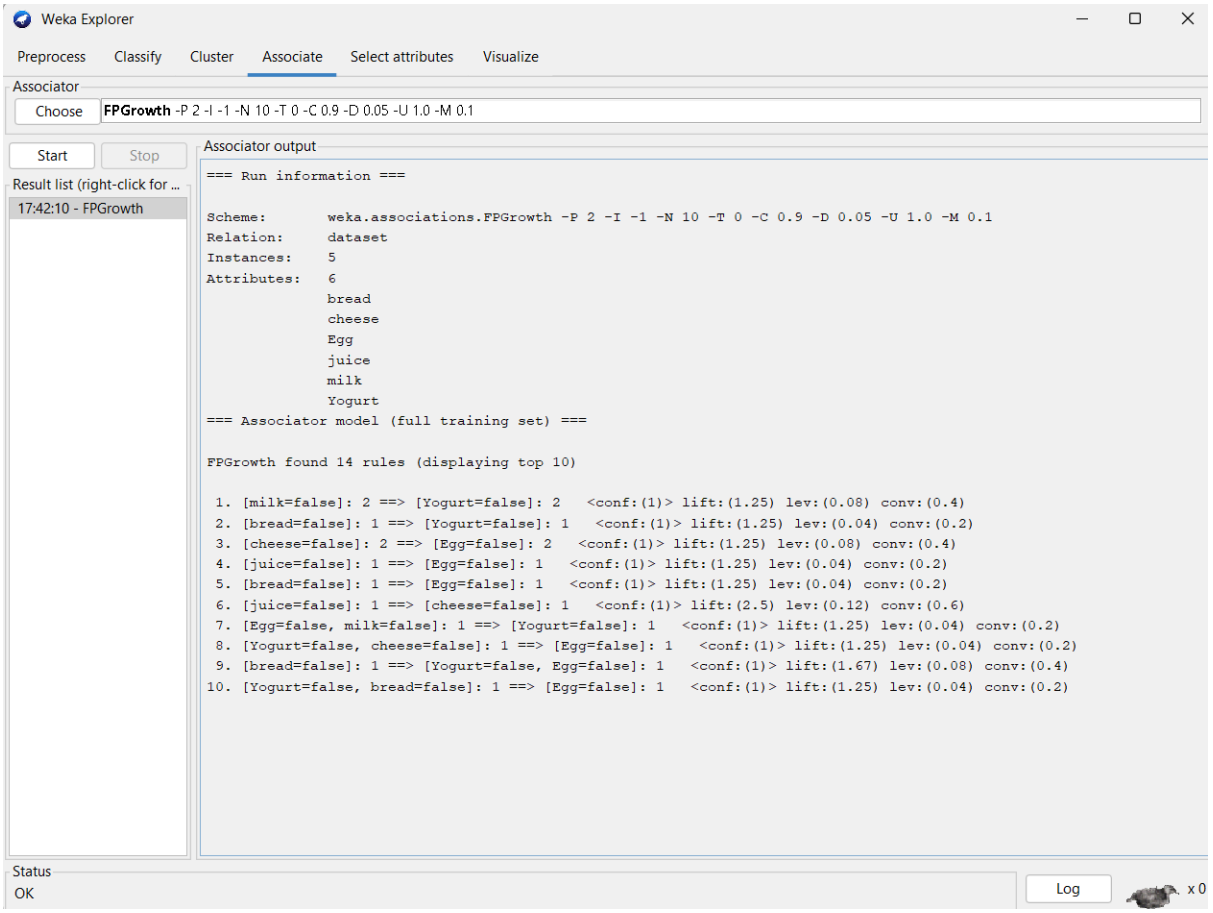
Q5:


y
0
50
100
150
200
250
0
20
40
60
80
x

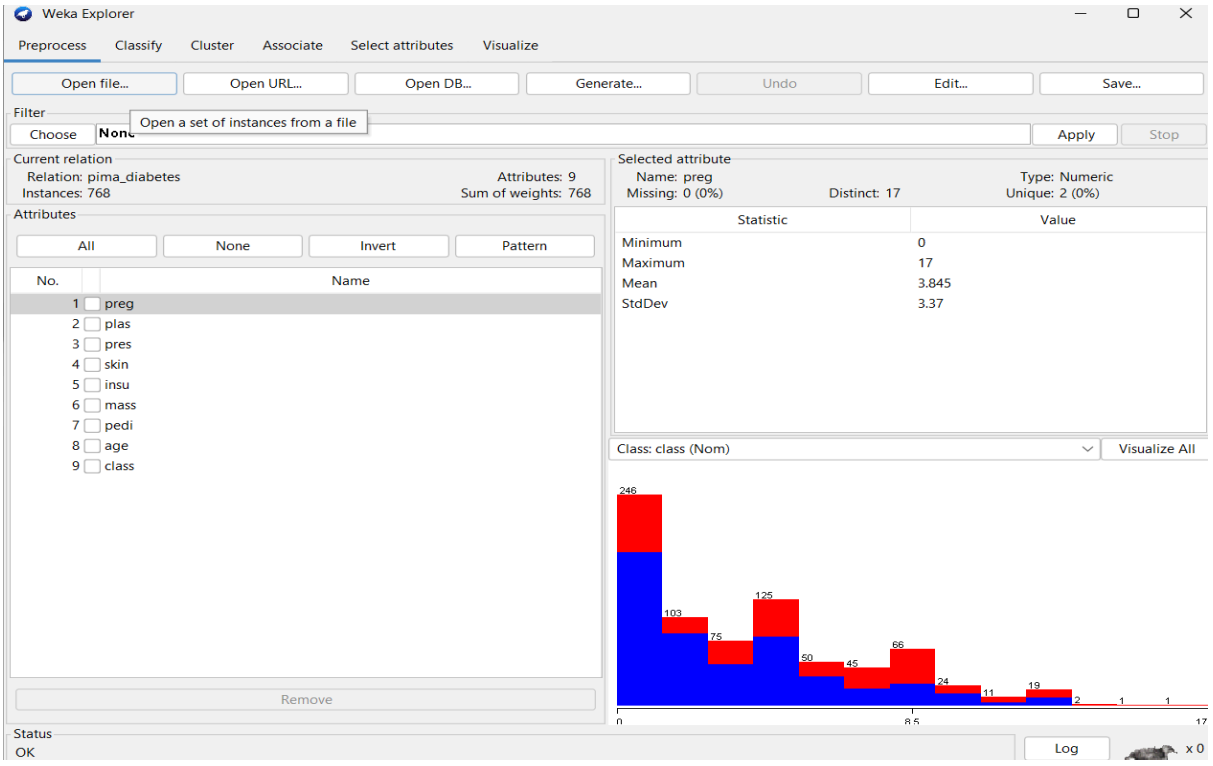
Q6:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Open file...
Open URL...
Open DB...
Generate...
Undo
Edit...
Save...
Filter
Choose
None
Apply
Stop
Current relation
Relation: dataset
Instances: 5
Attributes: 6
Sum of weights: 5
Attributes
All
None
Invert
Pattern
No.
Name
1 bread
2 cheese
3 Egg
4 juice
5 milk
6 Yogurt
Remove
Selected attribute
Name: bread
Missing: 0 (0%)
Distinct: 2
Type: Nominal
Unique: 1 (20%)
No.
Label
Count
Weight
1 true 4 4
2 false 1 1
Class: Yogurt (Nom)
Visualize All
4
1
Status
OK
Log
x 0

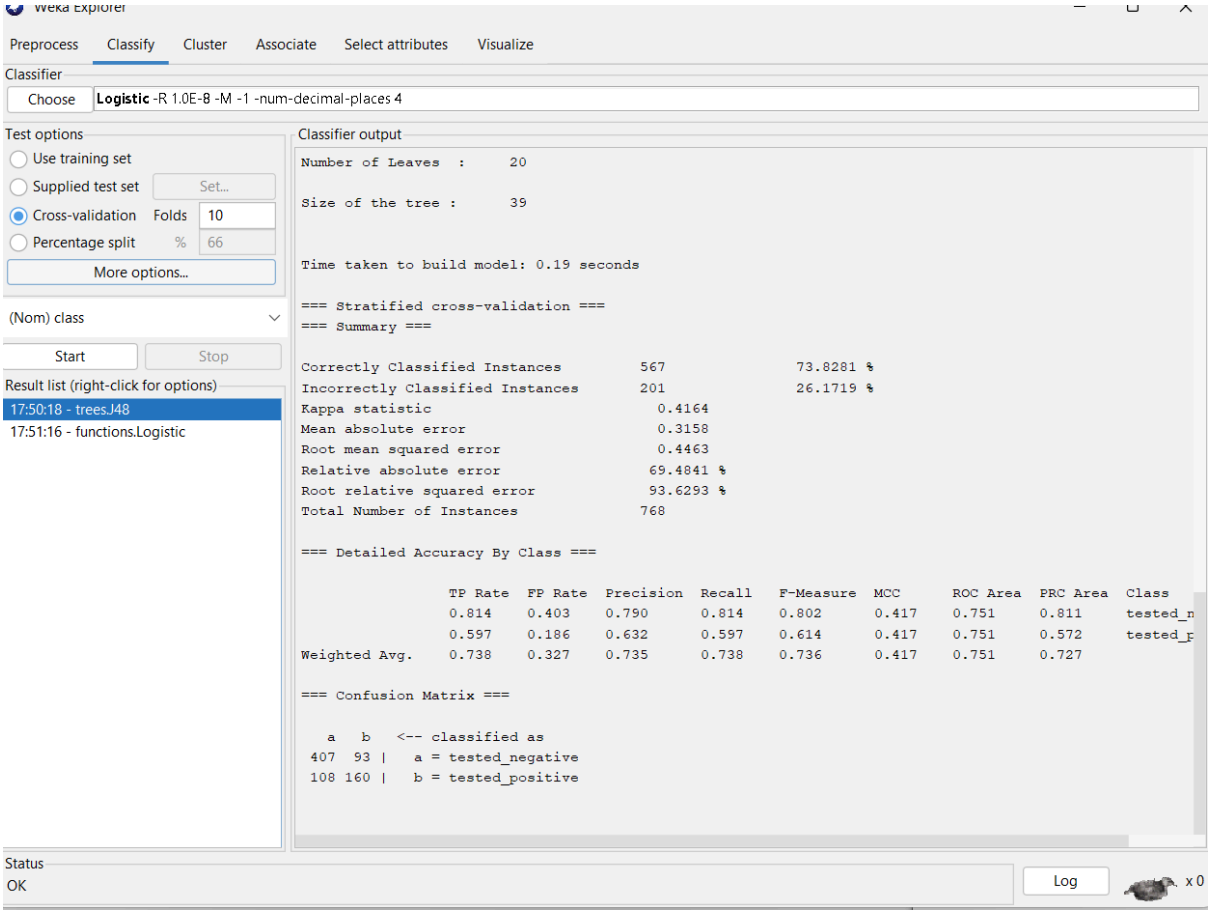
FP GROWTH:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Associator
Choose
FPGrowth -P 2 -I -1 -N 10 -T 0 -C 0.9 -D 0.05 -U 1.0 -M 0.1
Start
Stop
Result list (right-click for ...
17:42:10 - FPGrowth
Associator output
=== Run information ===
Scheme: weka.associations.FPGrowth -P 2 -I -1 -N 10 -T 0 -C 0.9 -D 0.05 -U 1.0 -M 0.1
Relation: dataset
Instances: 5
Attributes: 6
bread
cheese
Egg
juice
milk
Yogurt
=== Associator model (full training set) ===
FPGrowth found 14 rules (displaying top 10)
1. [milk=false]: 2 ==> [Yogurt=false]: 2 <conf:(1)> lift:(1.25) lev:(0.08) conv:(0.4)
2. [bread=false]: 1 ==> [Yogurt=false]: 1 <conf:(1)> lift:(1.25) lev:(0.04) conv:(0.2)
3. [cheese=false]: 2 ==> [Egg=false]: 2 <conf:(1)> lift:(1.25) lev:(0.08) conv:(0.4)
4. [juice=false]: 1 ==> [Egg=false]: 1 <conf:(1)> lift:(1.25) lev:(0.04) conv:(0.2)
5. [bread=false]: 1 ==> [Egg=false]: 1 <conf:(1)> lift:(1.25) lev:(0.04) conv:(0.2)
6. [juice=false]: 1 ==> [cheese=false]: 1 <conf:(1)> lift:(2.5) lev:(0.12) conv:(0.6)
7. [Egg=false, milk=false]: 1 ==> [Yogurt=false]: 1 <conf:(1)> lift:(1.25) lev:(0.04) conv:(0.2)
8. [Yogurt=false, cheese=false]: 1 ==> [Egg=false]: 1 <conf:(1)> lift:(1.25) lev:(0.04) conv:(0.2)
9. [bread=false]: 1 ==> [Yogurt=false, Egg=false]: 1 <conf:(1)> lift:(1.67) lev:(0.08) conv:(0.4)
10. [Yogurt=false, bread=false]: 1 ==> [Egg=false]: 1 <conf:(1)> lift:(1.25) lev:(0.04) conv:(0.2)
Status
OK
Log
x 0

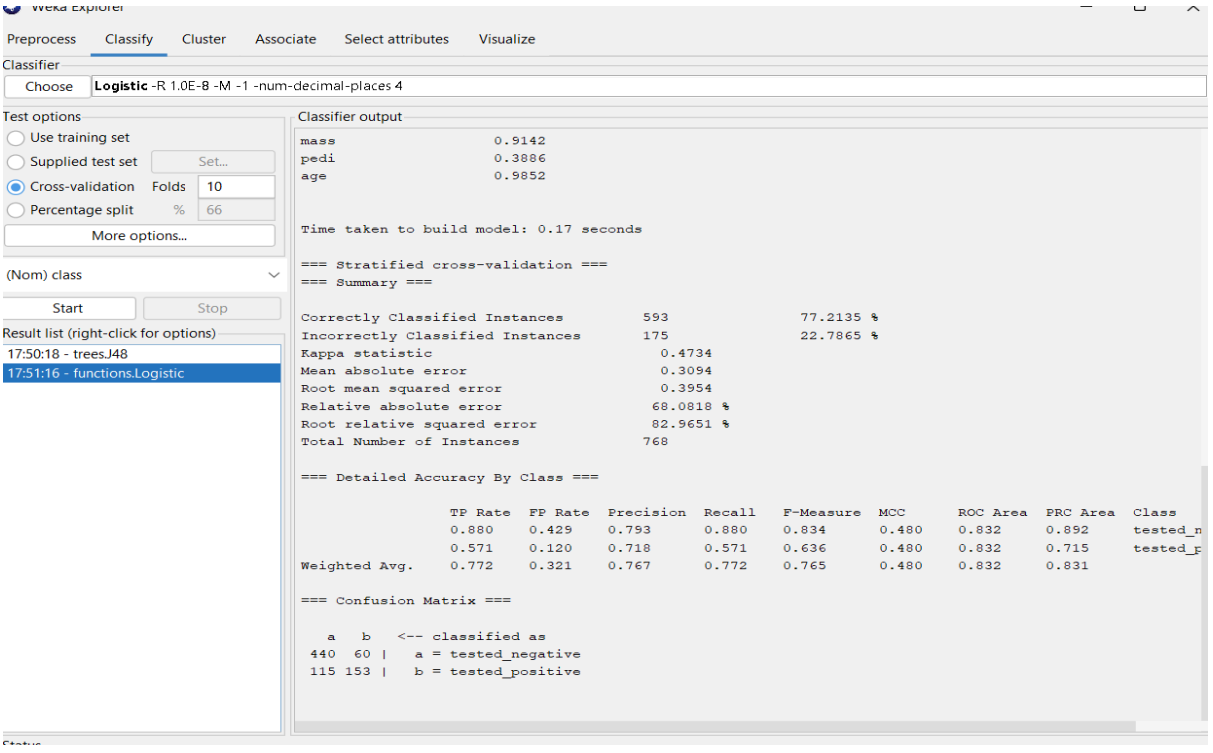
Q7:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Open file...
Open URL...
Open DB...
Generate...
Undo
Edit...
Save...
Filter
Choose
None
Open a set of instances from a file
Apply
Stop
Current relation
Relation: pima_diabetes
Instances: 768
Attributes: 9
Sum of weights: 768
Attributes
All
None
Invert
Pattern
No.
Name
1 preg
2 plas
3 pres
4 skin
5 insu
6 mass
7 pedi
8 age
9 class
Remove
Selected attribute
Name: preg
Missing: 0 (0%)
Distinct: 17
Type: Numeric
Unique: 2 (0%)
Statistic
Value
Minimum 0
Maximum 17
Mean 3.845
StdDev 3.37
Class: class (Nom)
Visualize All
246
103
75
125
50
45
66
24
11
19
2
1
1
0
8.5
17
Status
OK
Log
x 0

Decision Tree Classifier:



Support Vector Machine Classifier:



Q8:
INPUT:marks <- c(55, 60, 71, 63, 55, 65, 50, 55, 58, 59, 61, 63, 65, 67, 71, 72, 75)

bins_a <- cut(marks, breaks = 3, labels = c("Low", "Medium", "High"))

bins_b <- cut(marks, breaks = seq(min(marks), max(marks), length.out = 4), labels = c("Low", "Medium", "High"))

k <- 3

clusters <- kmeans(matrix(marks), centers = k)

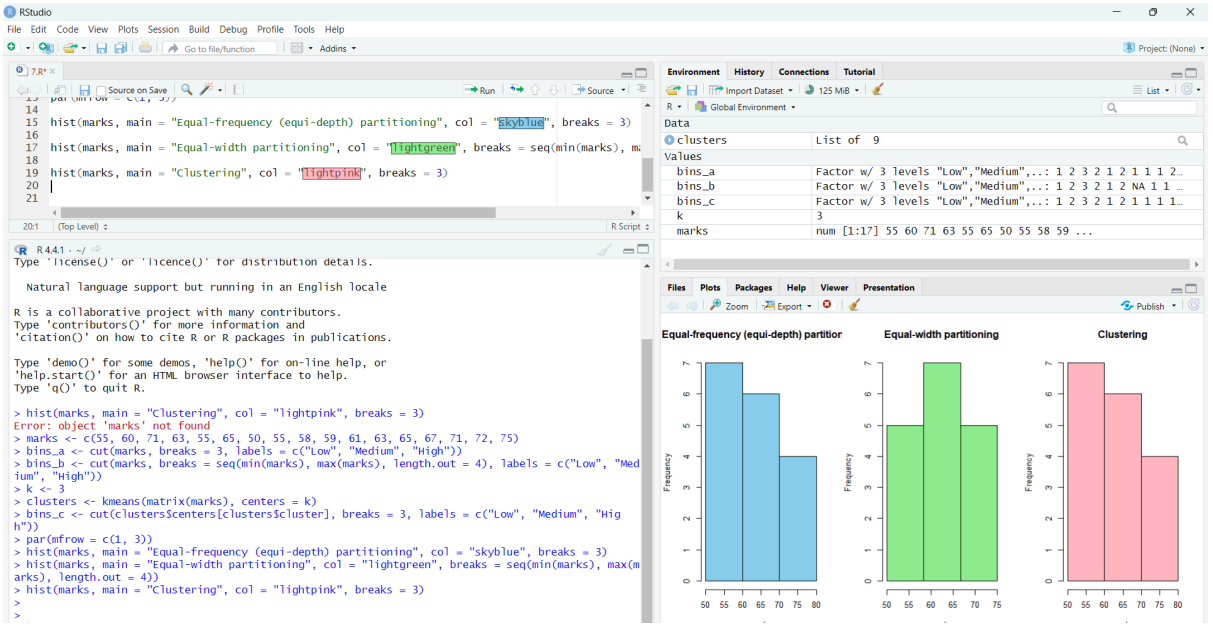
bins_c <- cut(clusters$centers[clusters$cluster], breaks = 3, labels = c("Low", "Medium", "High"))

par(mfrow = c(1, 3))

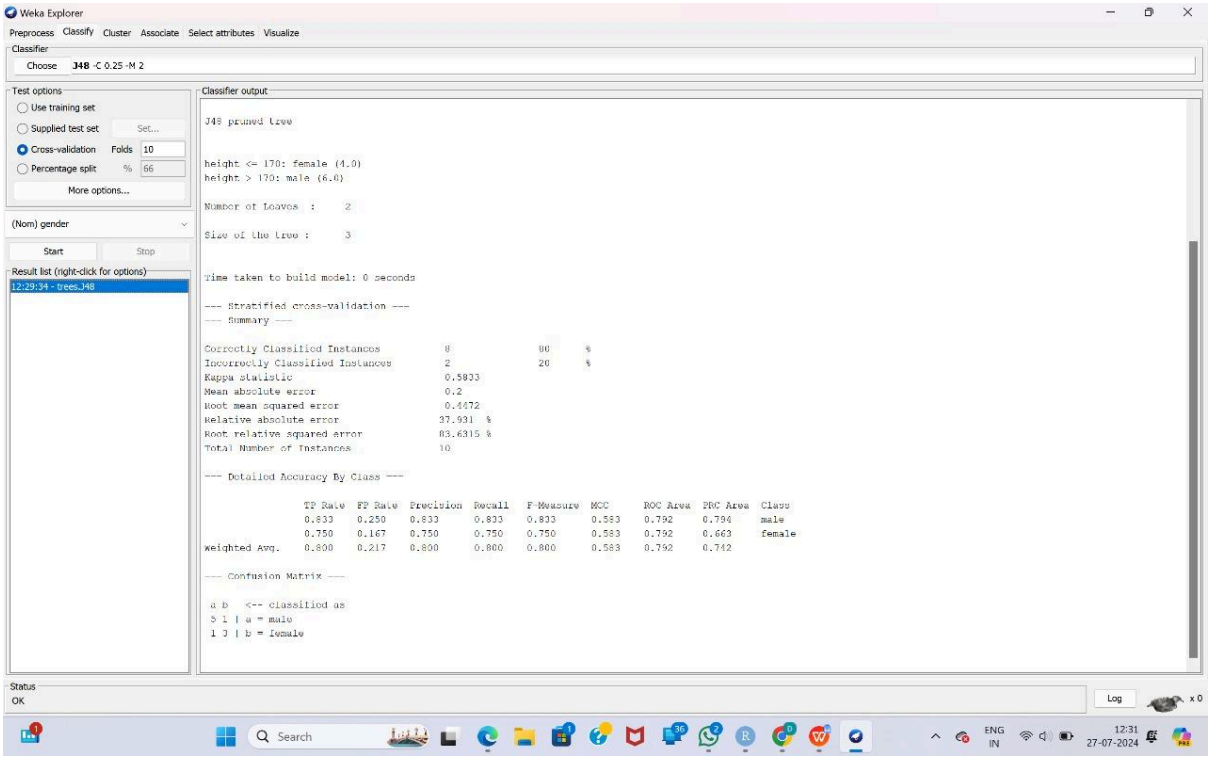
hist(marks, main = "Equal-frequency (equi-depth) partitioning", col = "skyblue", breaks = 3)

hist(marks, main = "Equal-width partitioning", col = "lightgreen", breaks = seq(min(marks), max(marks), length.out = 4))

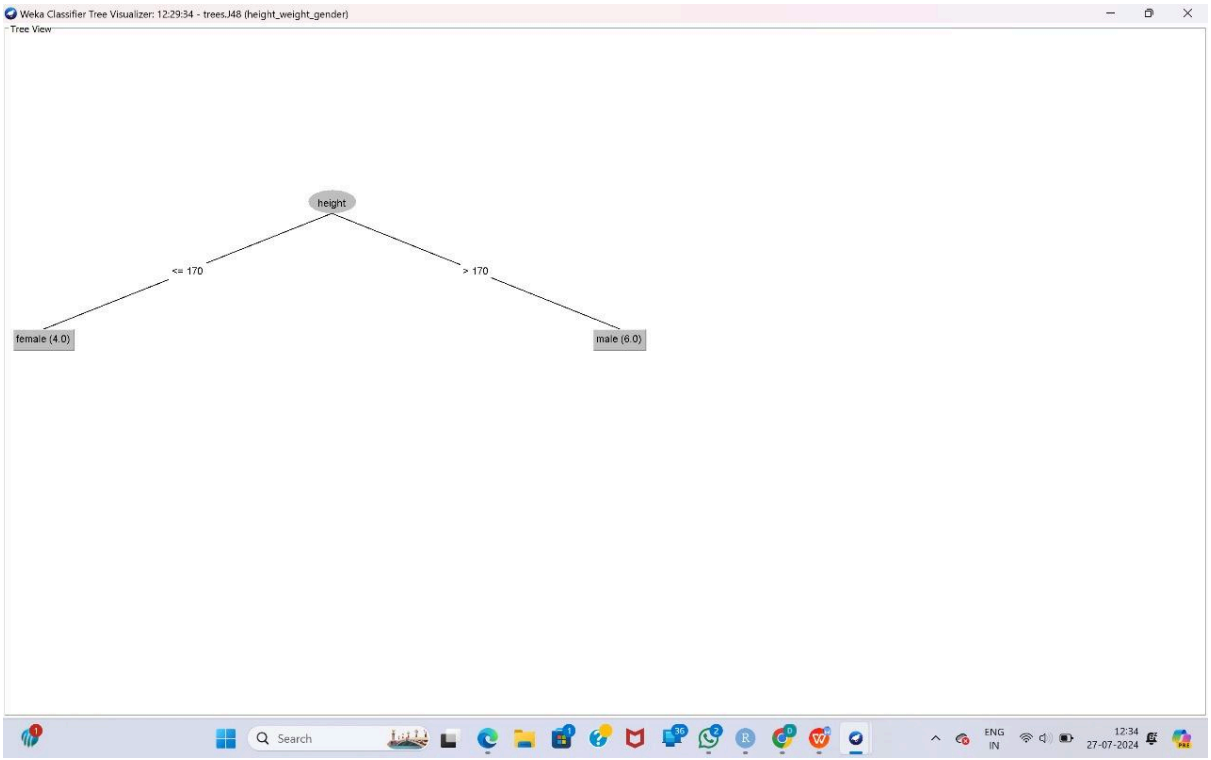
hist(marks, main = "Clustering", col = "lightpink", breaks = 3)



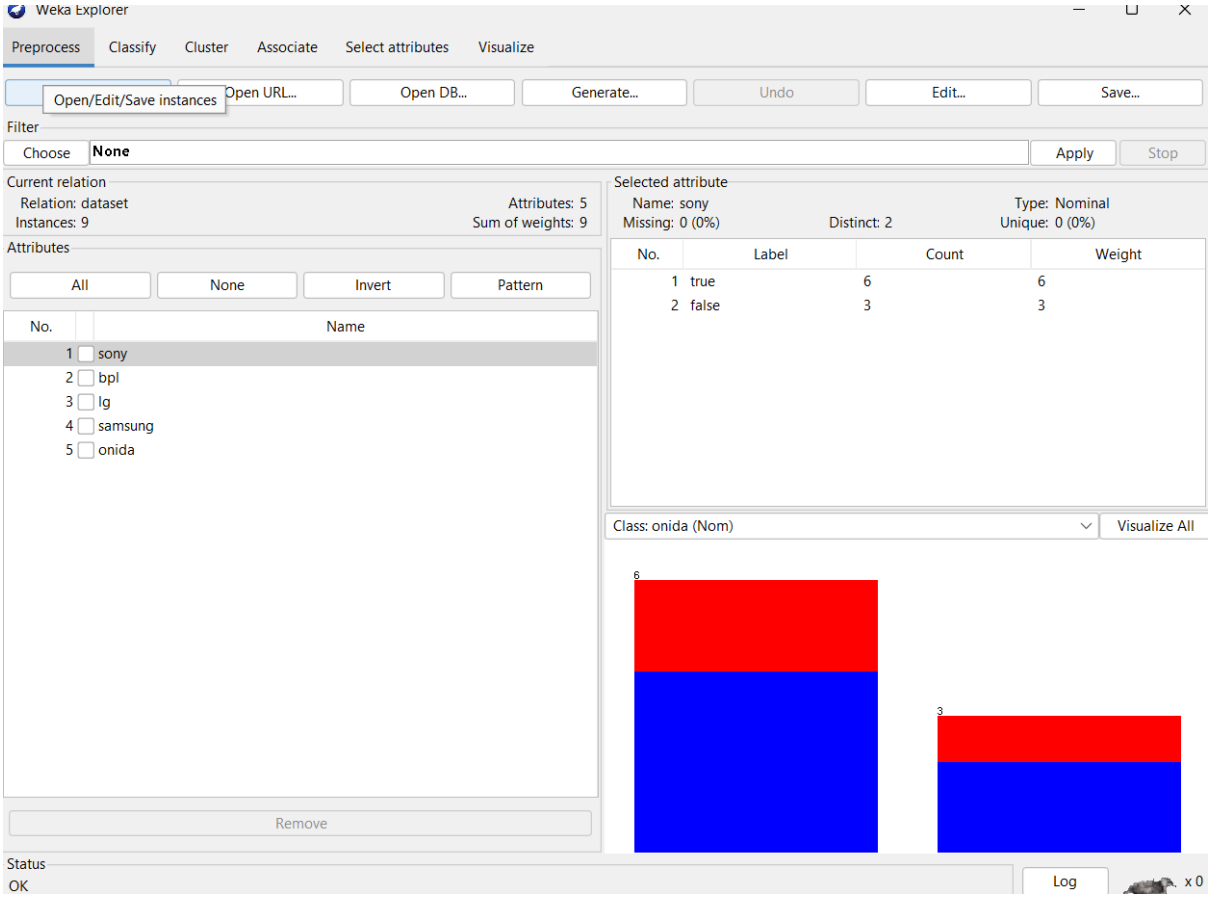
Q9:



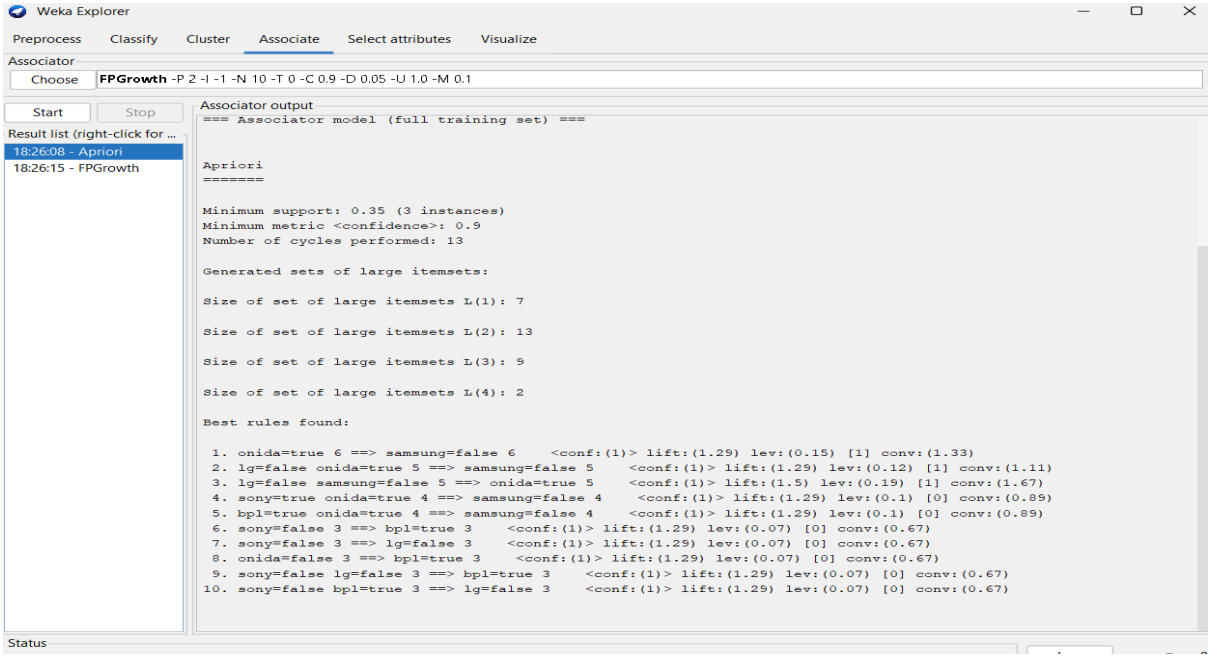
Decision Tree :



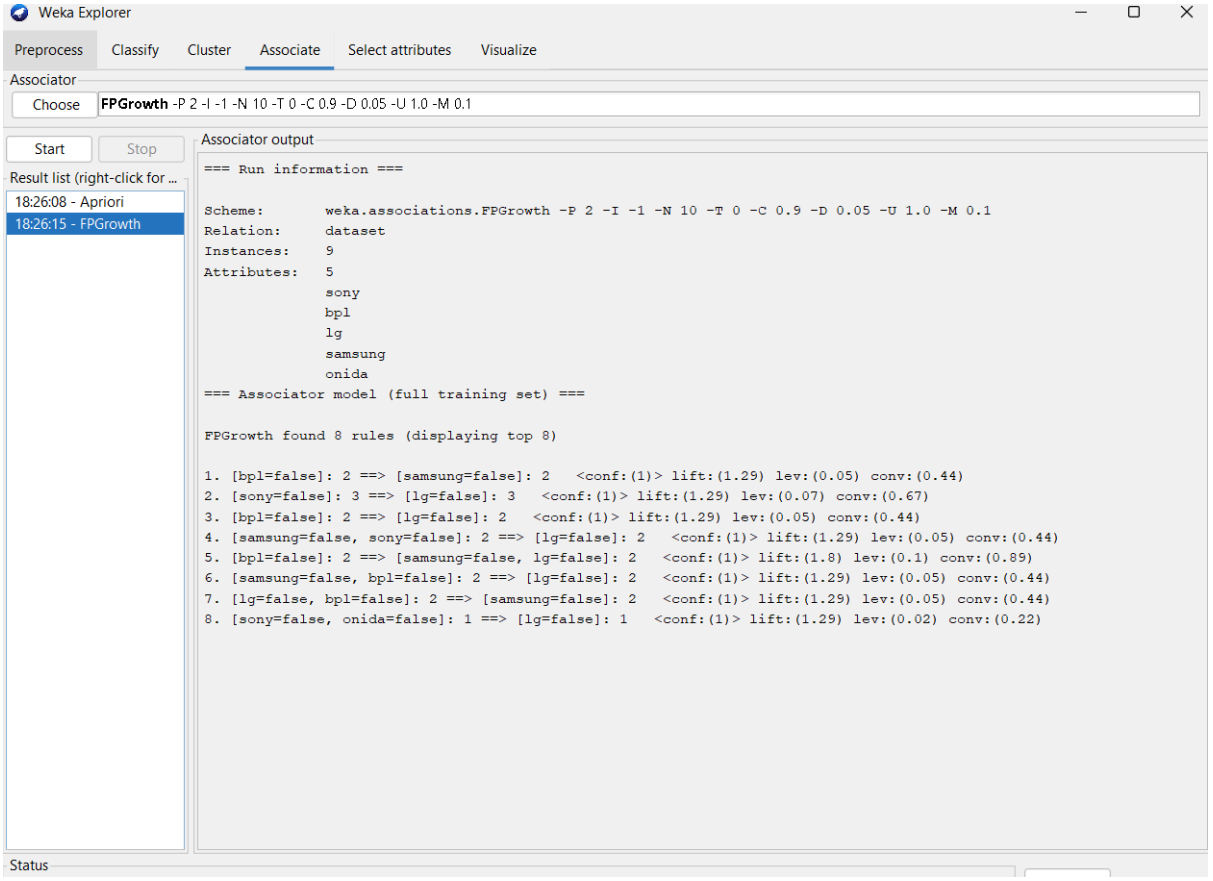
Q10:



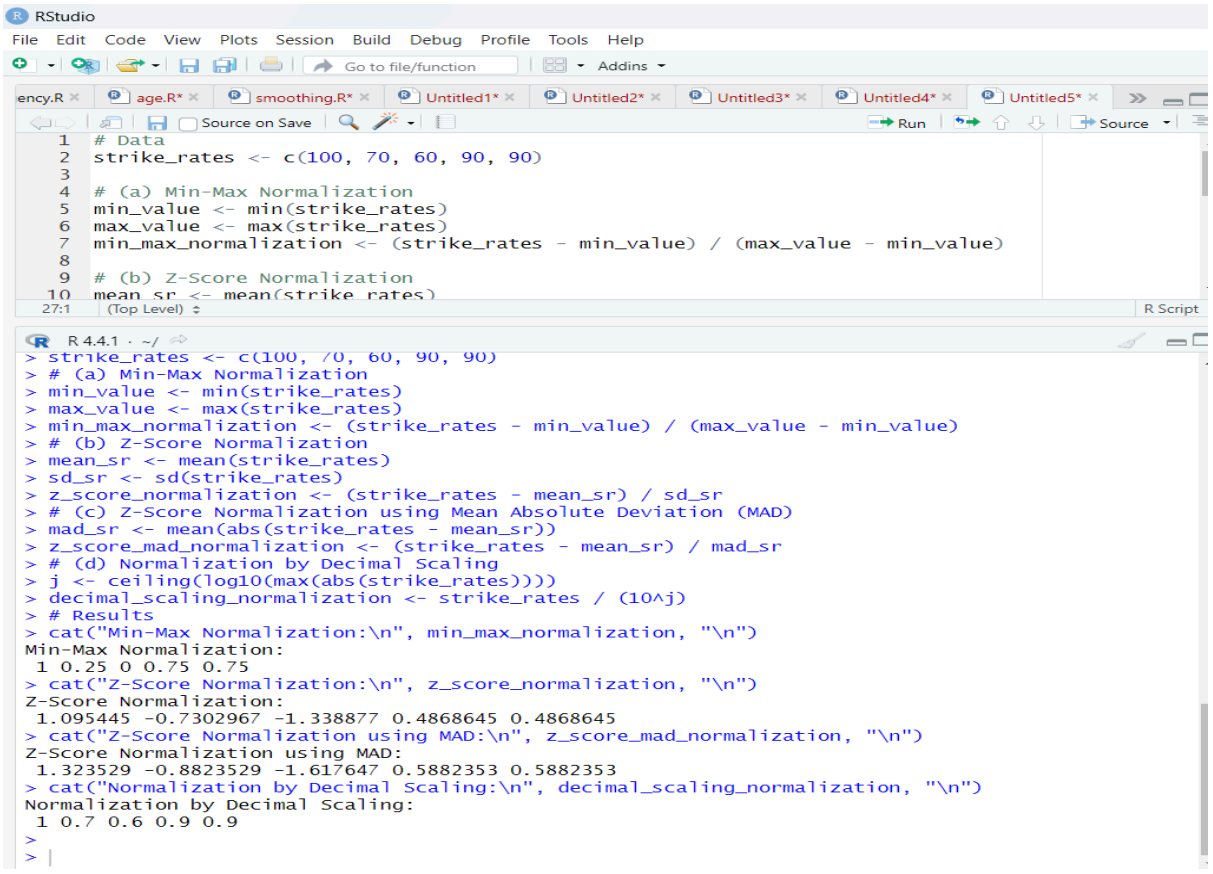
Apriori Algorithm:



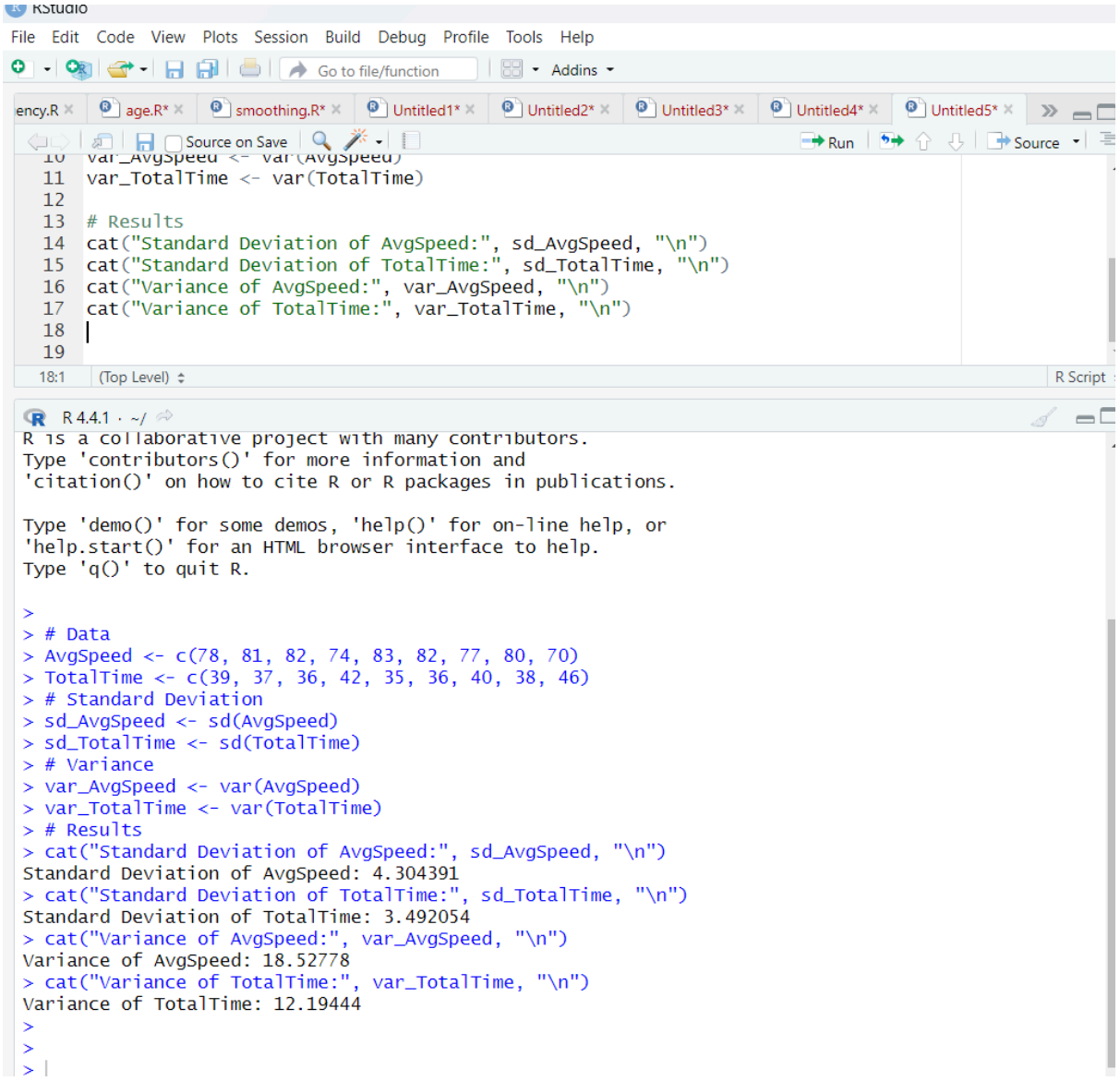
FP GROWTH:



Q11:



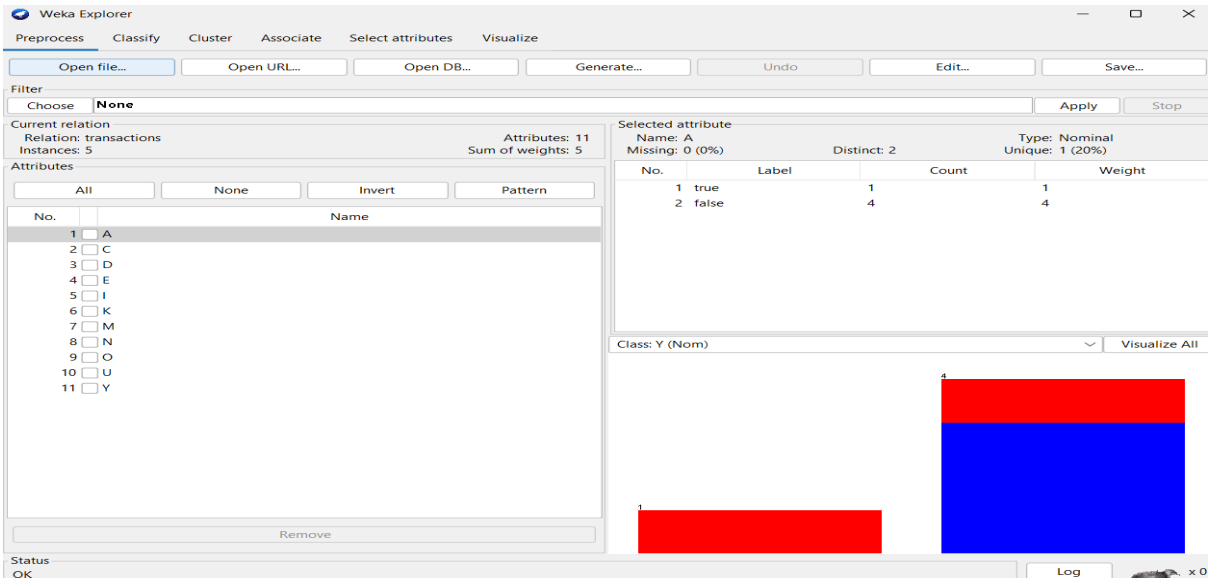
Q12:



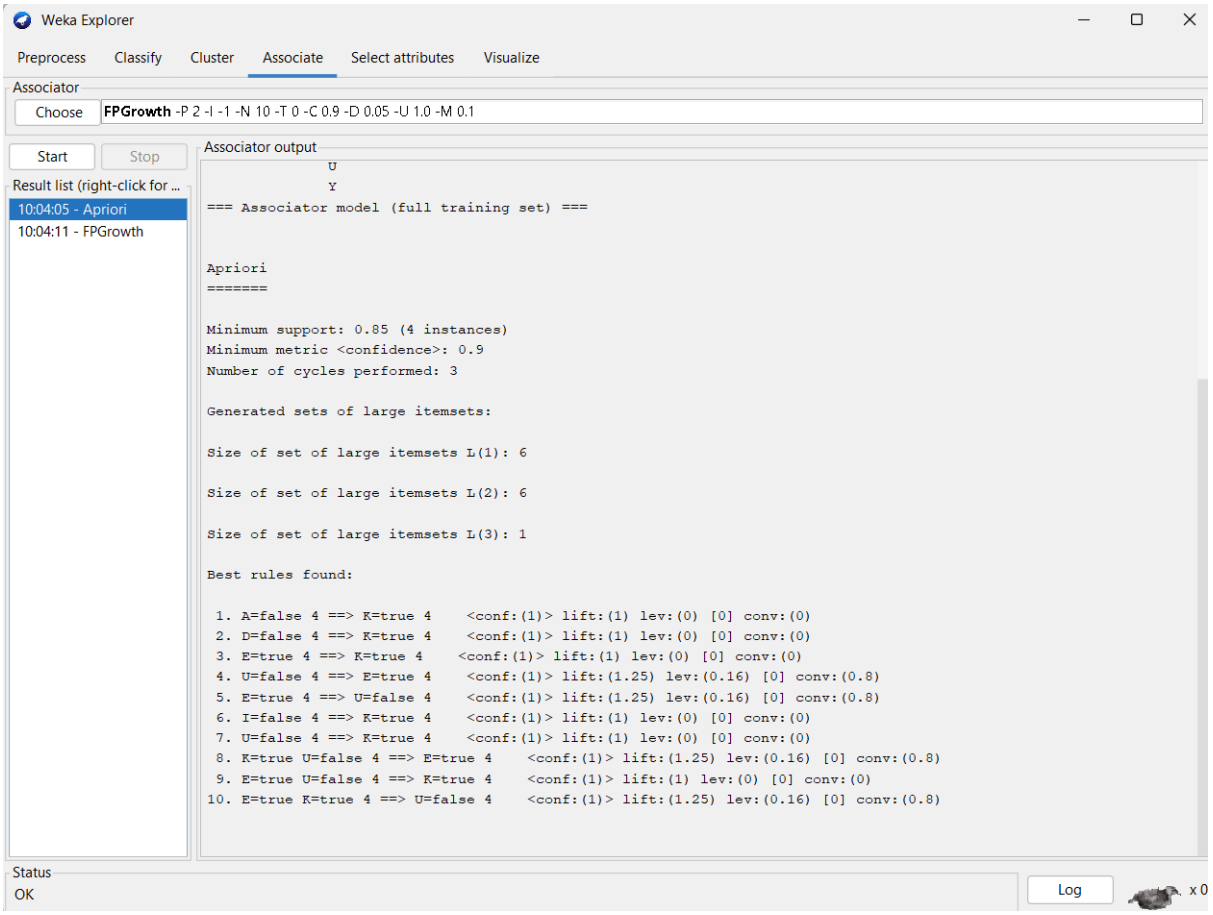
```
var_AvgSpeed <- var(AvgSpeed)
var_TotalTime <- var(TotalTime)

# Results
cat("Standard Deviation of AvgSpeed:", sd_AvgSpeed, "\n")
cat("Standard Deviation of TotalTime:", sd_TotalTime, "\n")
cat("Variance of AvgSpeed:", var_AvgSpeed, "\n")
cat("Variance of TotalTime:", var_TotalTime, "\n")
```

```
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> # Data
> AvgSpeed <- c(78, 81, 82, 74, 83, 82, 77, 80, 70)
> TotalTime <- c(39, 37, 36, 42, 35, 36, 40, 38, 46)
> # Standard Deviation
> sd_AvgSpeed <- sd(AvgSpeed)
> sd_TotalTime <- sd(TotalTime)
> # Variance
> var_AvgSpeed <- var(AvgSpeed)
> var_TotalTime <- var(TotalTime)
> # Results
> cat("Standard Deviation of AvgSpeed:", sd_AvgSpeed, "\n")
Standard Deviation of AvgSpeed: 4.304391
> cat("Standard Deviation of TotalTime:", sd_TotalTime, "\n")
Standard Deviation of TotalTime: 3.492054
> cat("Variance of AvgSpeed:", var_AvgSpeed, "\n")
Variance of AvgSpeed: 18.52778
> cat("Variance of TotalTime:", var_TotalTime, "\n")
Variance of TotalTime: 12.19444
>
>
>
```

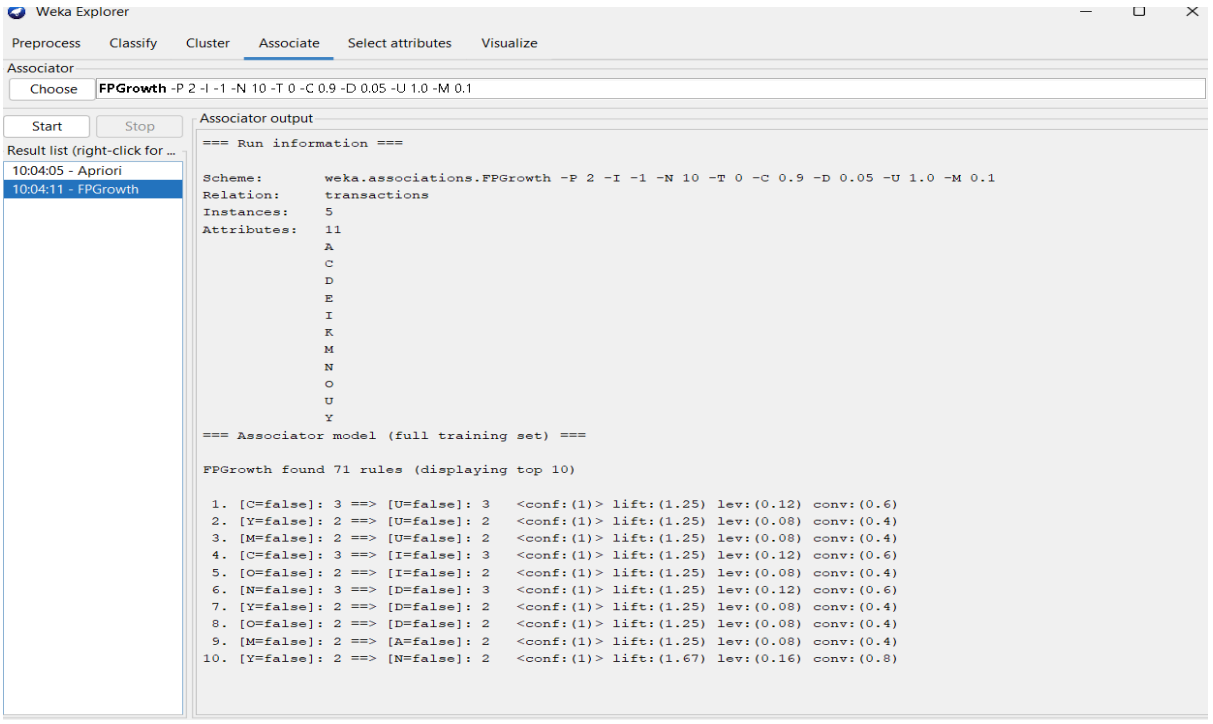
Q13:



Apriori Algorithm:



FP Growth:



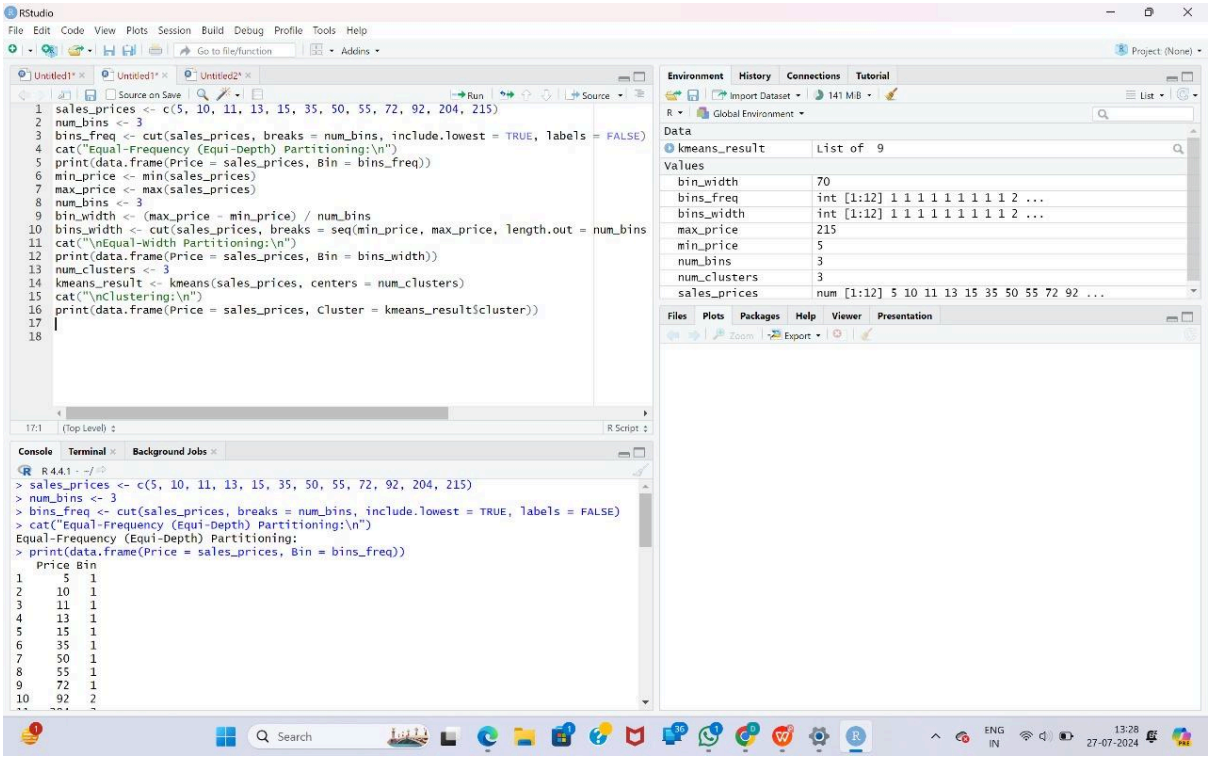
QUESTION BANK

Q1:

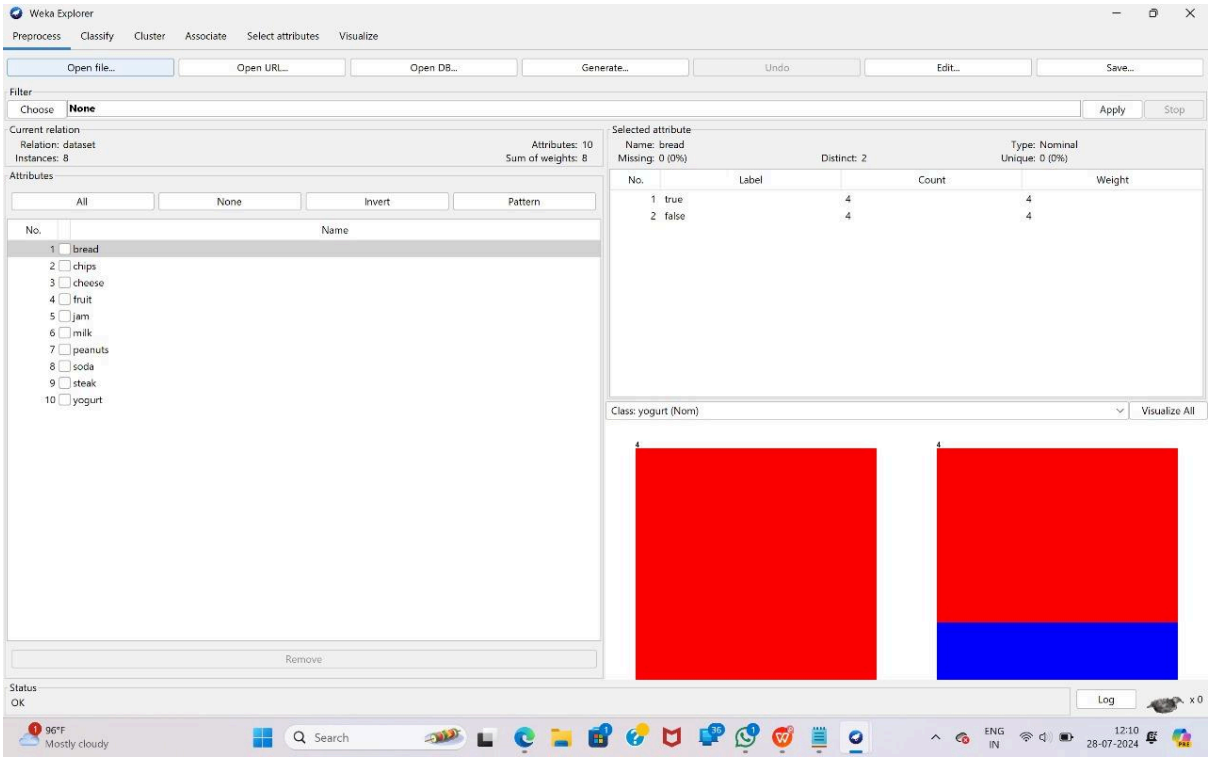
INPUT:

```
sales_prices <- c(5, 10, 11, 13, 15, 35, 50, 55, 72, 92, 204, 215)
num_bins <- 3
bins_freq <- cut(sales_prices, breaks = num_bins, include.lowest = TRUE, labels = FALSE)
cat("Equal-Frequency (Equi-Depth) Partitioning:\n")
print(data.frame(Price = sales_prices, Bin = bins_freq))
min_price <- min(sales_prices)
max_price <- max(sales_prices)
num_bins <- 3
bin_width <- (max_price - min_price) / num_bins
bins_width <- cut(sales_prices, breaks = seq(min_price, max_price, length.out = num_bins + 1), include.lowest = TRUE, labels = FALSE)
cat("\nEqual-Width Partitioning:\n")
print(data.frame(Price = sales_prices, Bin = bins_width))
num_clusters <- 3
kmeans_result <- kmeans(sales_prices, centers = num_clusters)
cat("\nClustering:\n")
print(data.frame(Price = sales_prices, Cluster = kmeans_result$cluster))
```

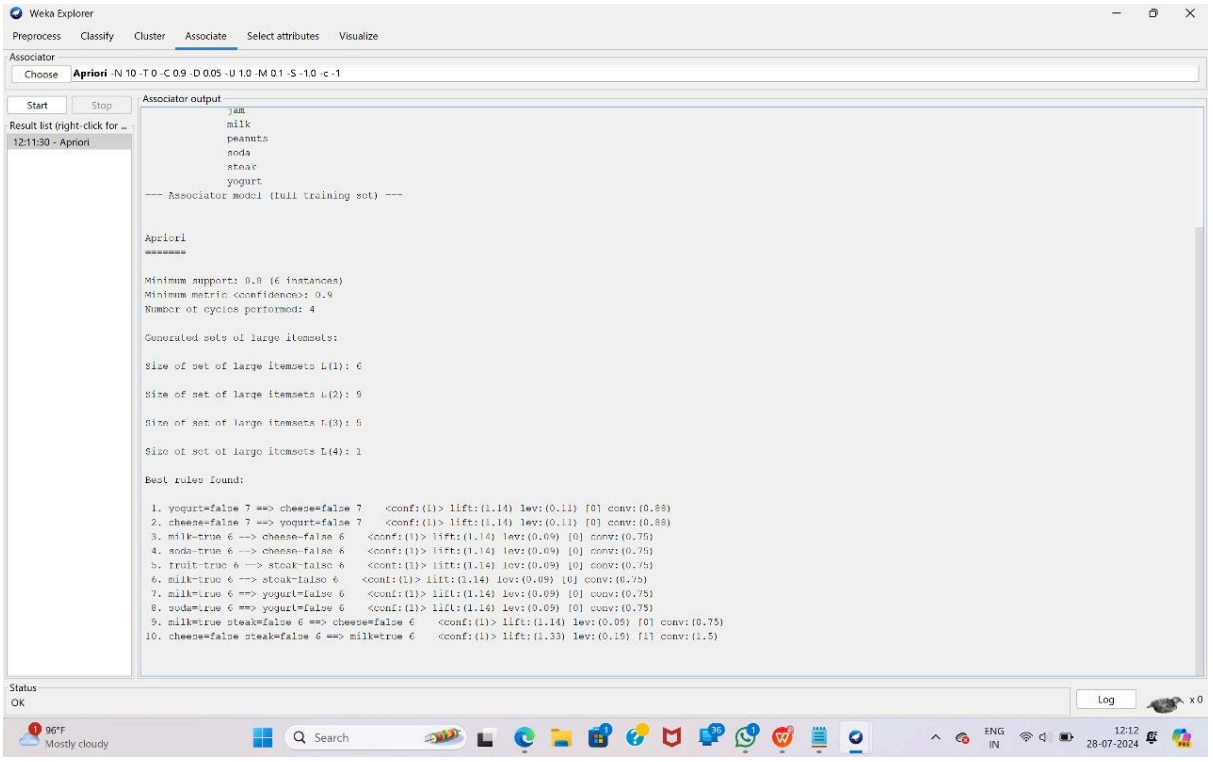
OUTPUT:



Q3:



Apriori Algorithm :

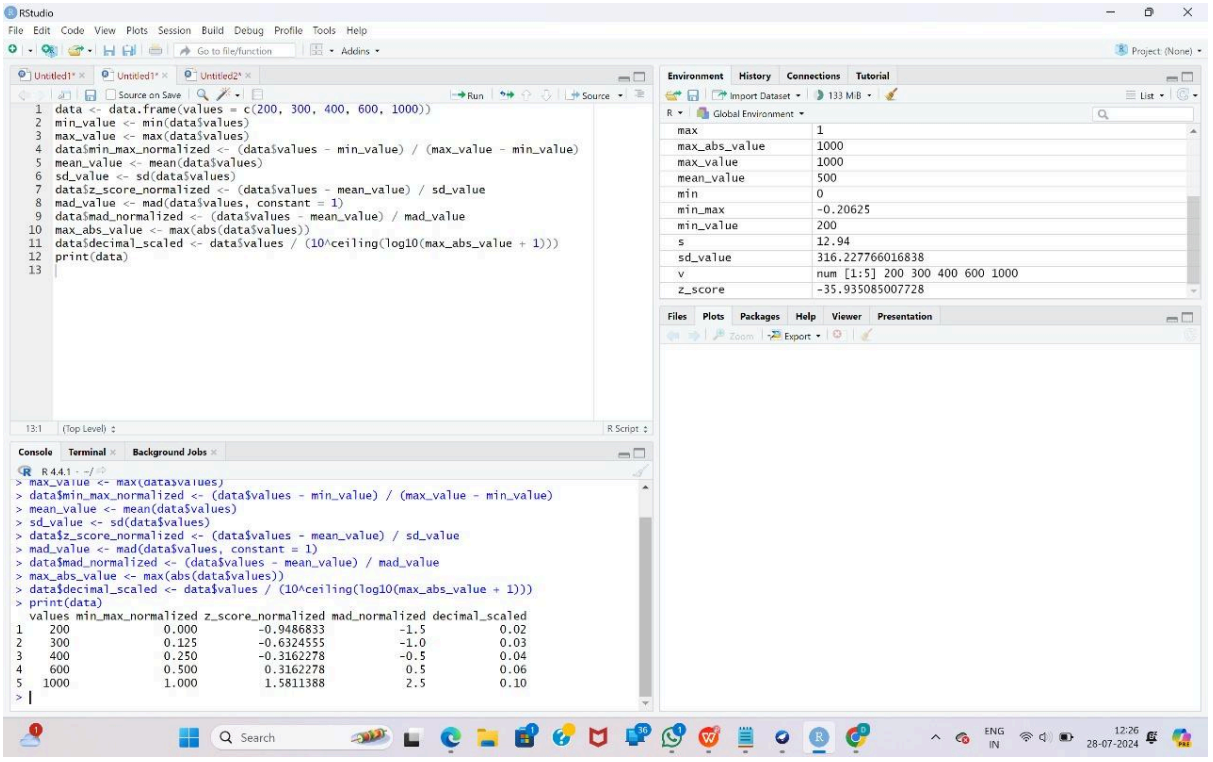


Q4:

INPUT:

```
data <- data.frame(values = c(200, 300, 400, 600, 1000))
min_value <- min(data$values)
max_value <- max(data$values)
data$min_max_normalized <- (data$values - min_value) / (max_value - min_value)
mean_value <- mean(data$values)
sd_value <- sd(data$values)
data$z_score_normalized <- (data$values - mean_value) / sd_value
mad_value <- mad(data$values, constant = 1)
data$mad_normalized <- (data$values - mean_value) / mad_value
max_abs_value <- max(abs(data$values))
data$decimal_scaled <- data$values / (10^ceiling(log10(max_abs_value + 1)))
print(data)
```

Output:

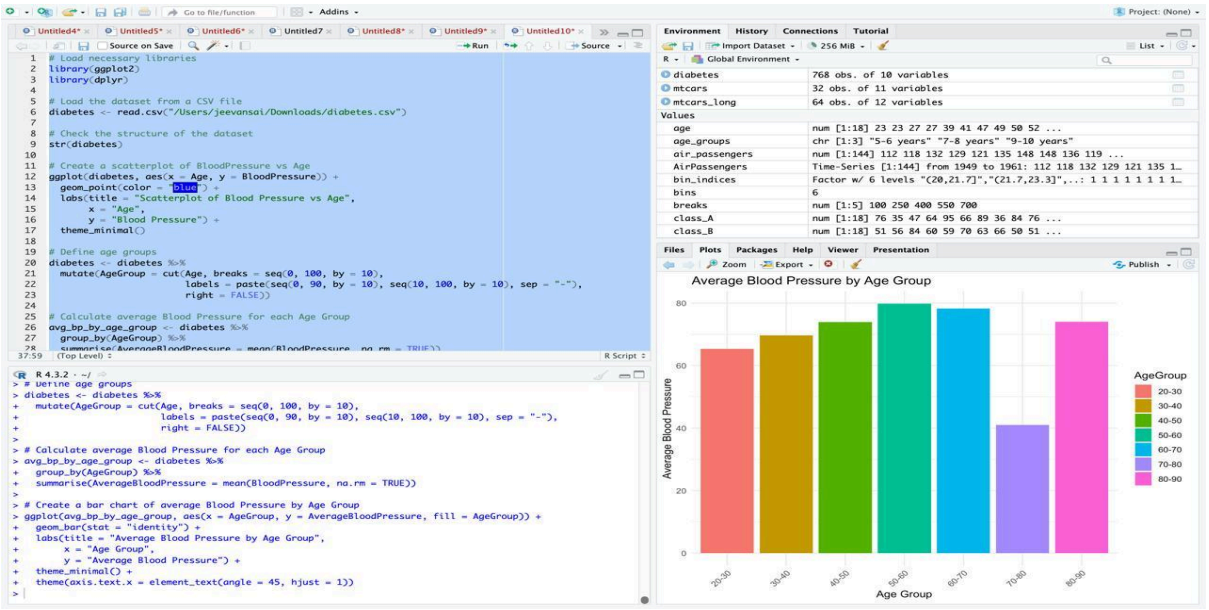


Q5:

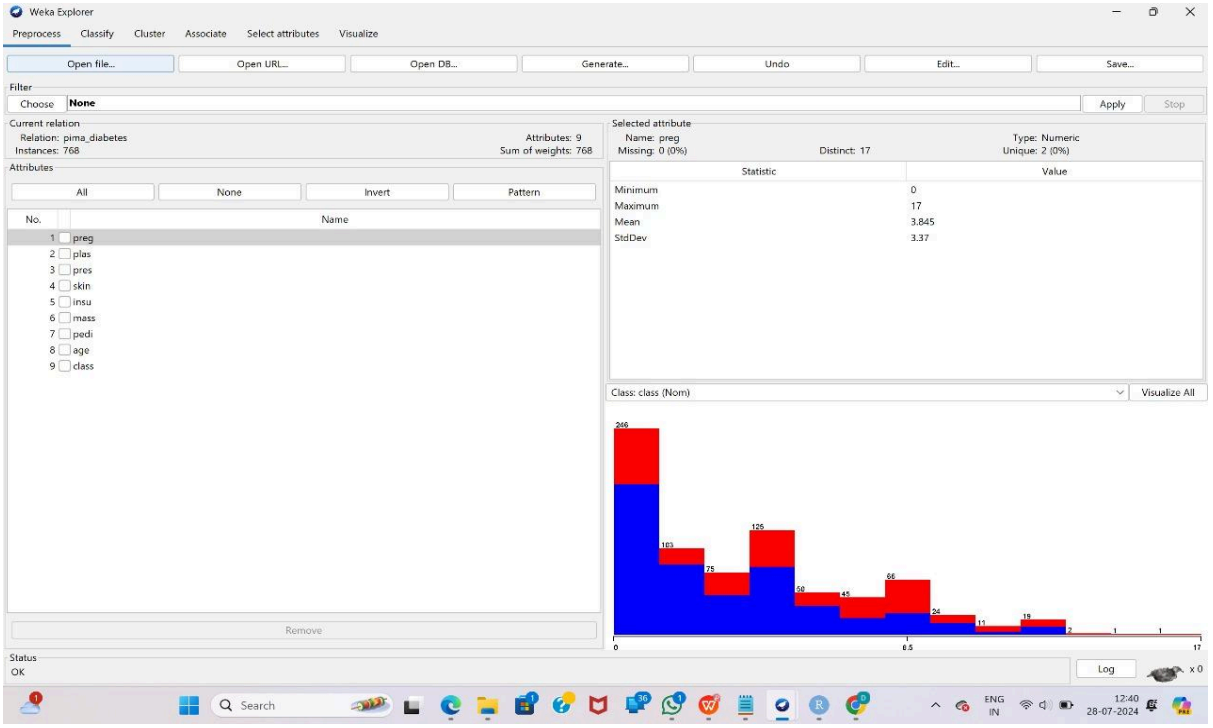
Input:

```
library(ggplot2)
library(dplyr)
diabetes <- read.csv("D:/DWDM/diabetes.csv")
str(diabetes)
ggplot(diabetes, aes(x = Age, y = BloodPressure)) +
  geom_point(color = "blue") +
  labs(title = "Scatterplot of Blood Pressure vs Age",
       x = "Age",
       y = "Blood Pressure") +
  theme_minimal()
diabetes <- diabetes %>%
  mutate(AgeGroup = cut(Age, breaks = seq(0, 100, by = 10),
                        labels = paste(seq(0, 90, by = 10), seq(10, 100, by = 10), sep = "-"),
                        right = FALSE))
avg_bp_by_age_group <- diabetes %>%
  group_by(AgeGroup) %>%
  summarise(AverageBloodPressure = mean(BloodPressure, na.rm = TRUE))
ggplot(avg_bp_by_age_group, aes(x = AgeGroup, y = AverageBloodPressure, fill =
AgeGroup)) +
  geom_bar(stat = "identity") +
  labs(title = "Average Blood Pressure by Age Group",
       x = "Age Group",
       y = "Average Blood Pressure") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

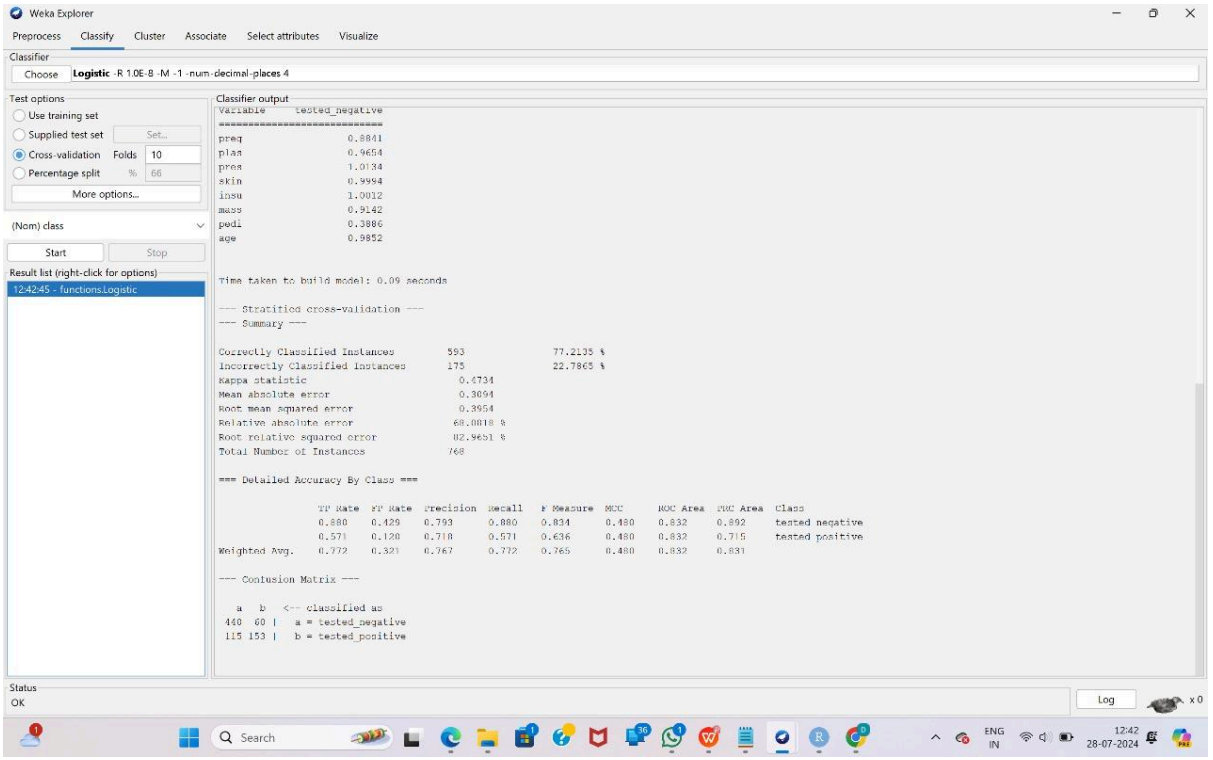
OUTPUT:



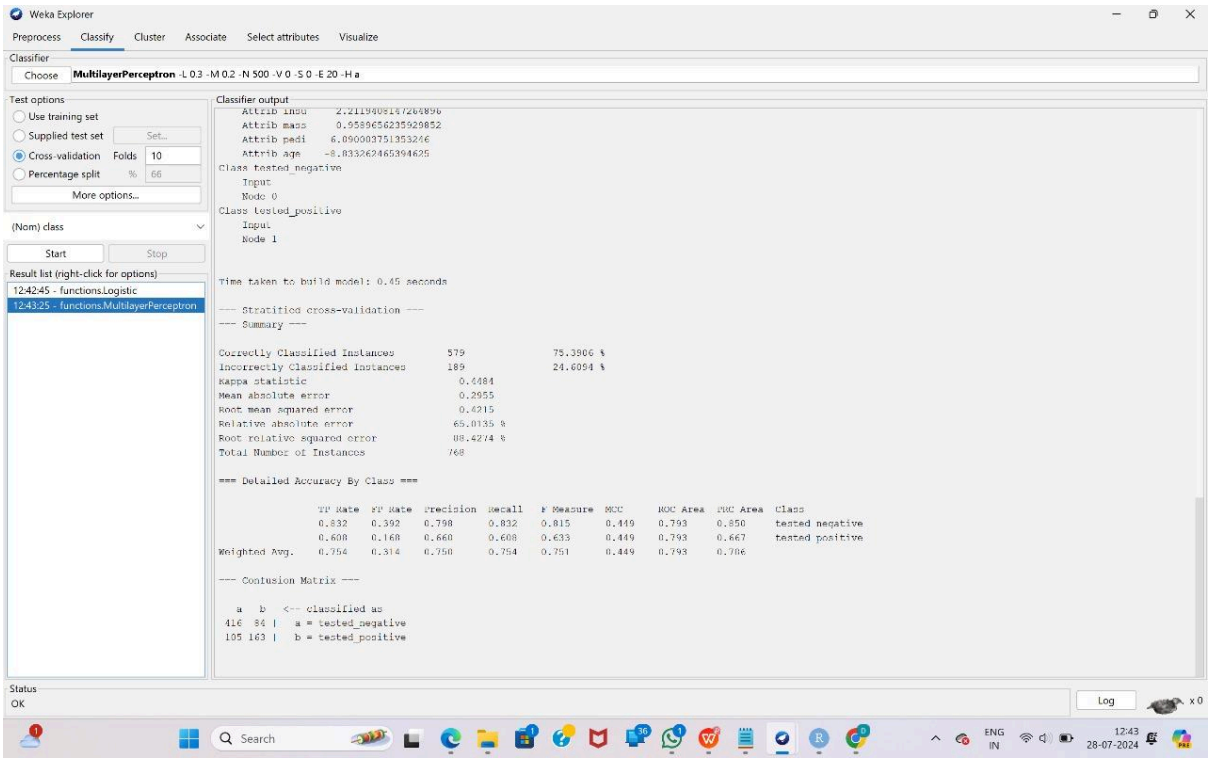
Q6:



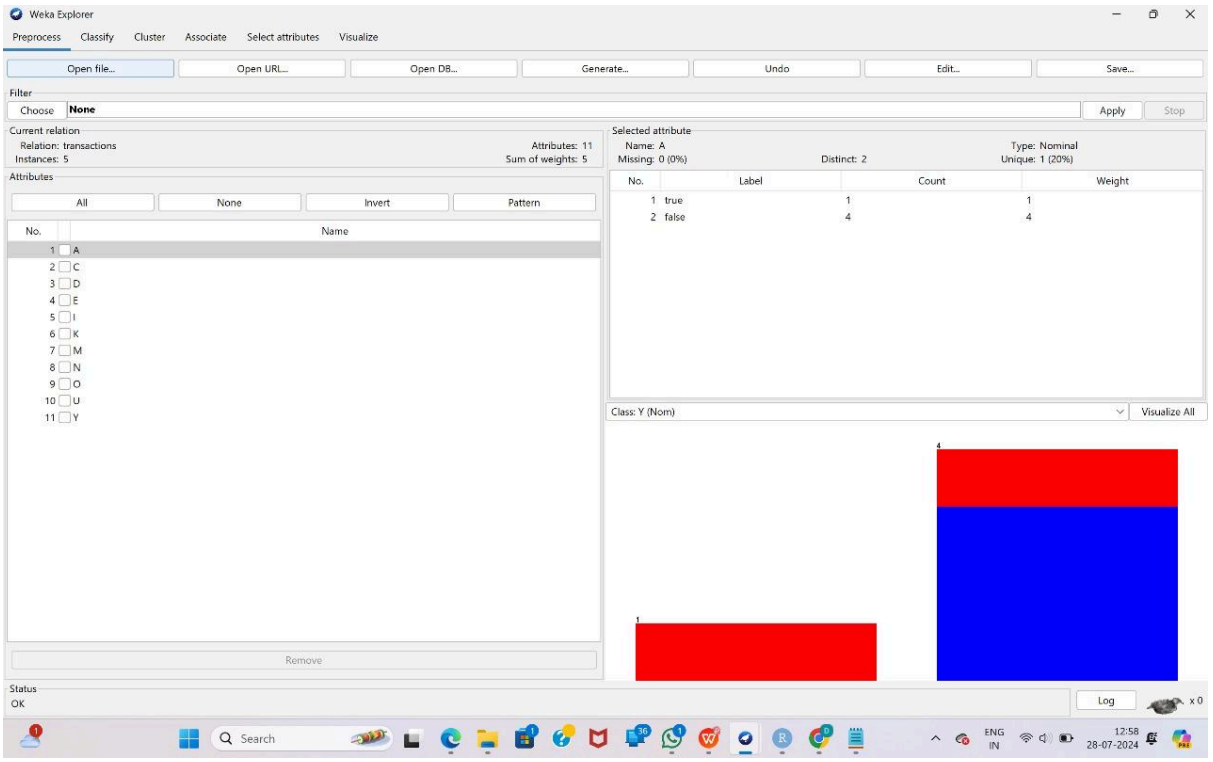
Linear regression:



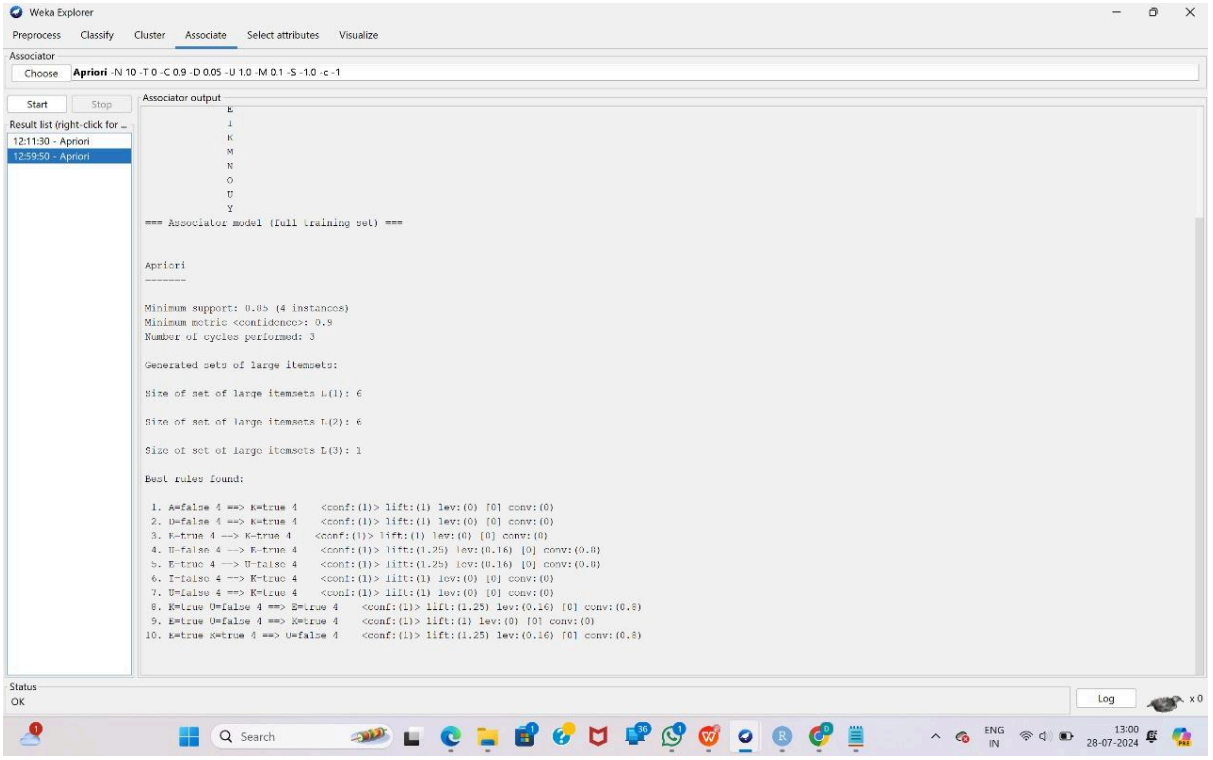
Multiple regression:



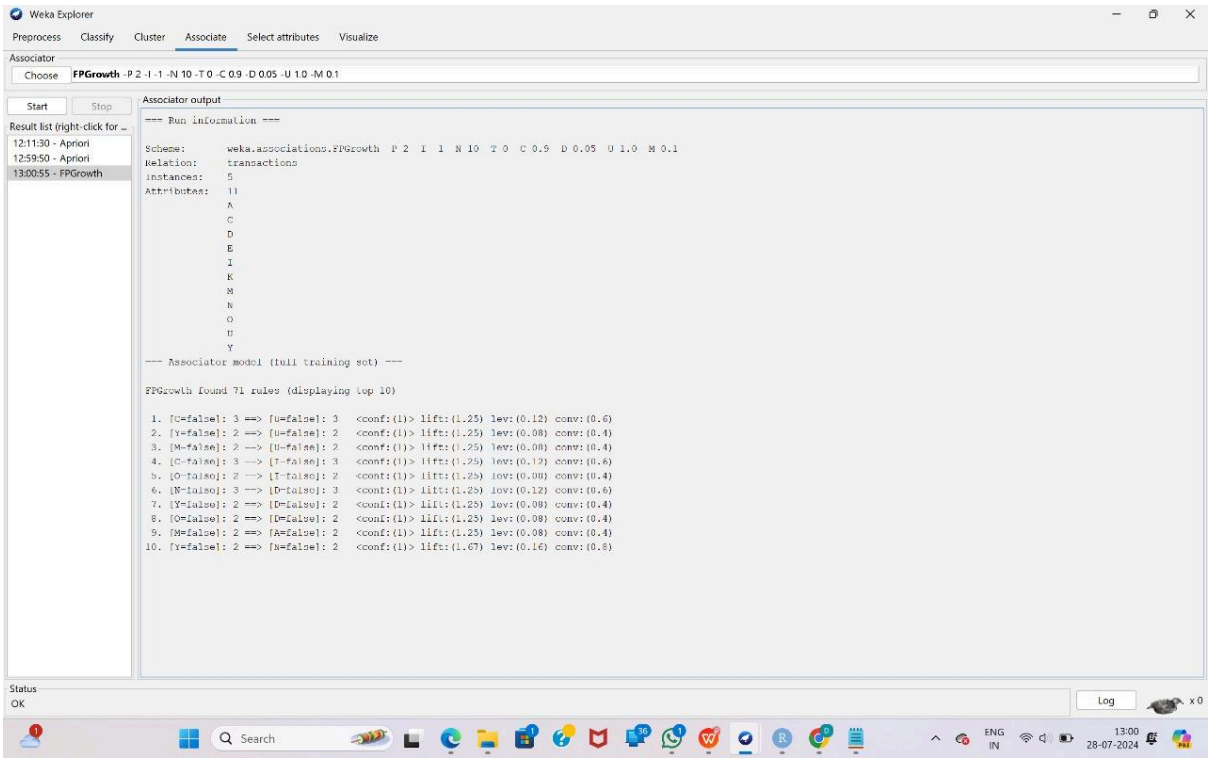
Q7:



Aprioralgorithm:

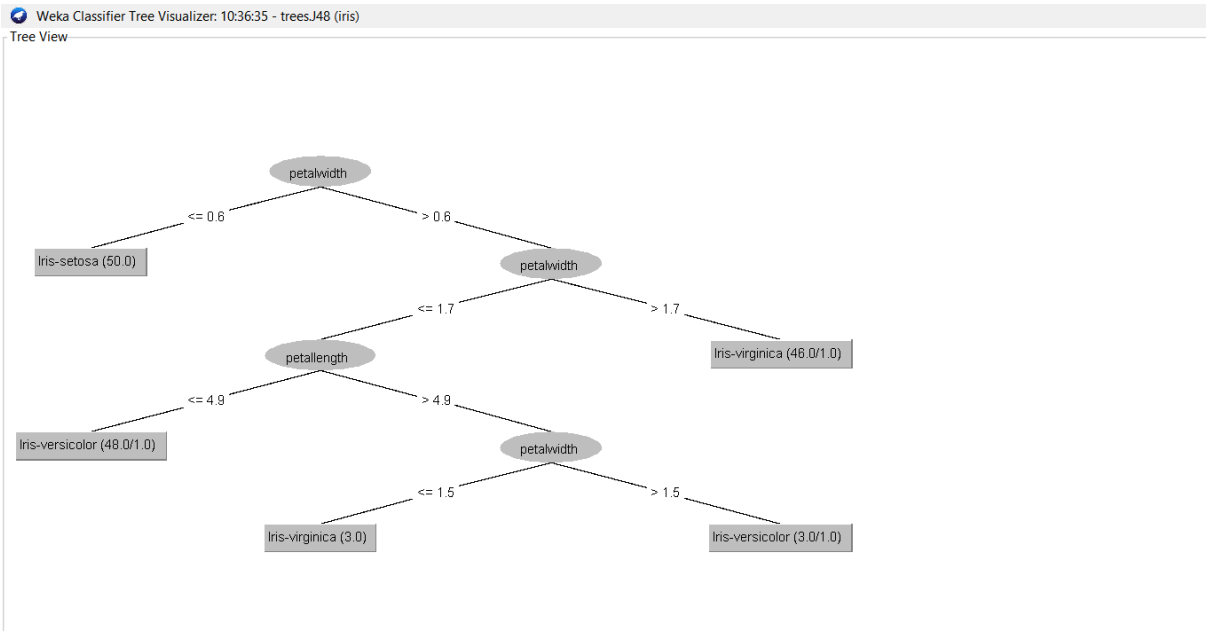


FP Growth:

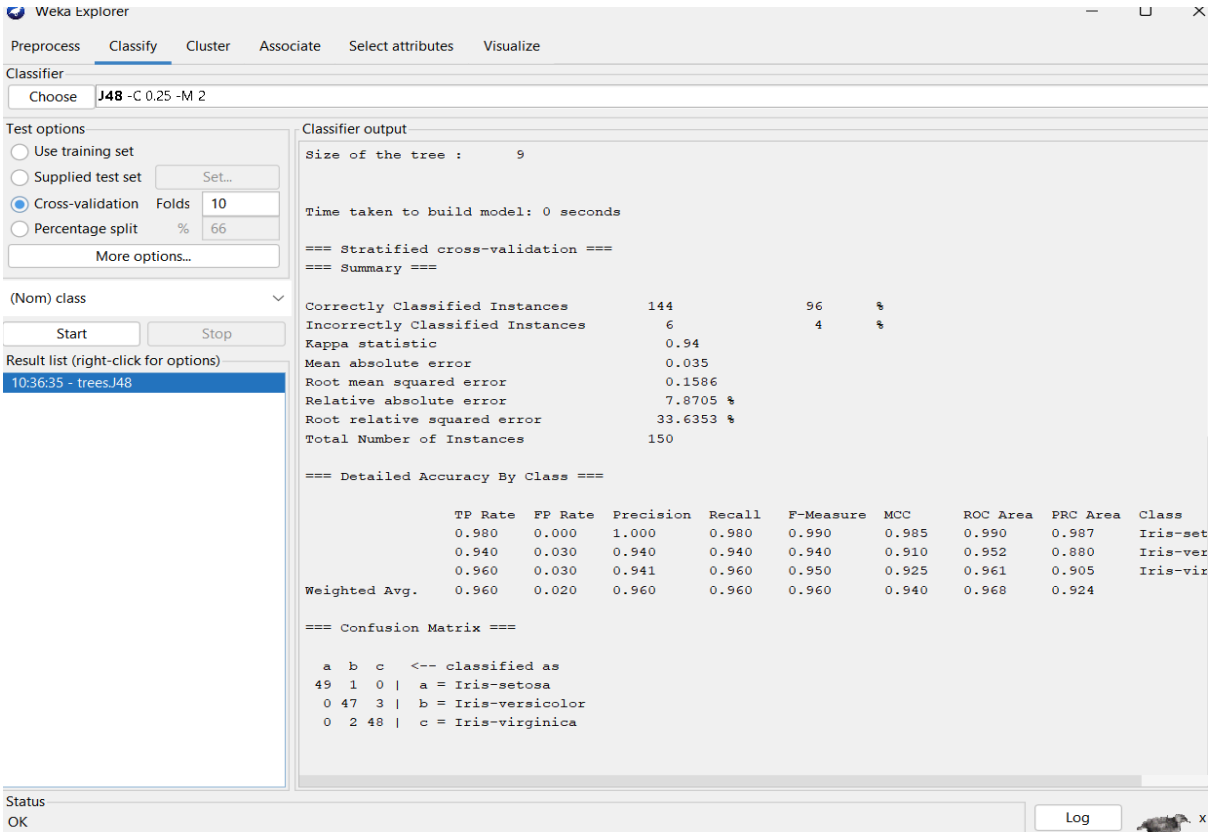


Q8:

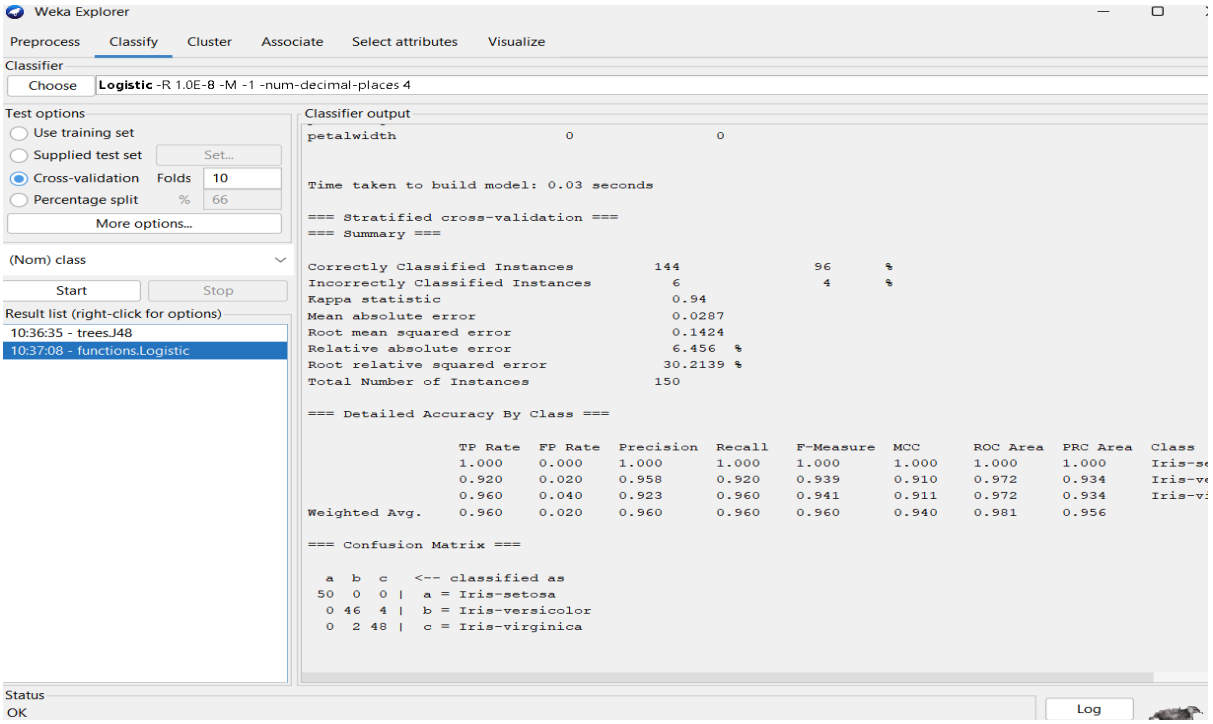
TREE:



PREPROCESS:



Logistic:



Q9:

INPUT:

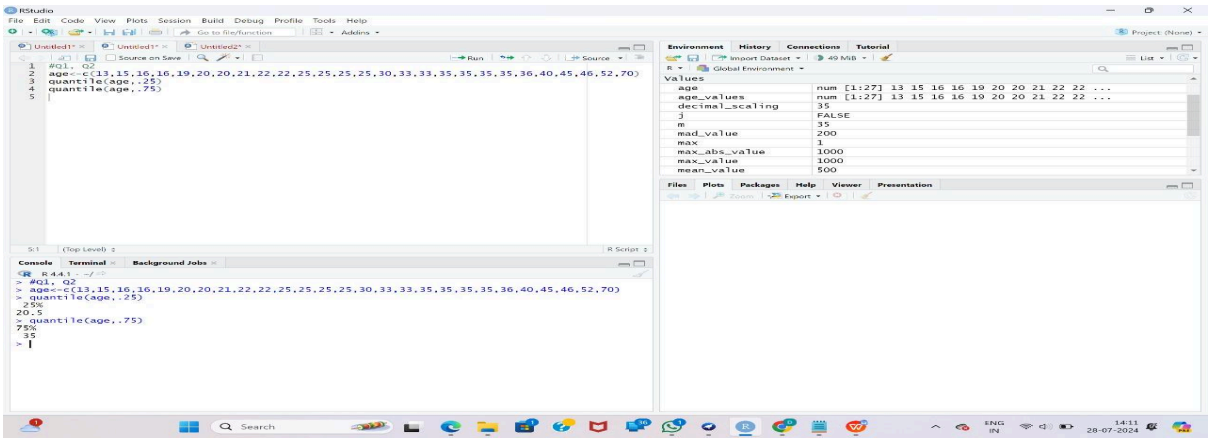
#Q1, Q2

age<-c(13,15,16,16,19,20,20,21,22,22,25,25,25,25,30,33,33,35,35,35,35,36,40,45,46,52,70)

quantile(age,.25)

quantile(age,.75)

Output:

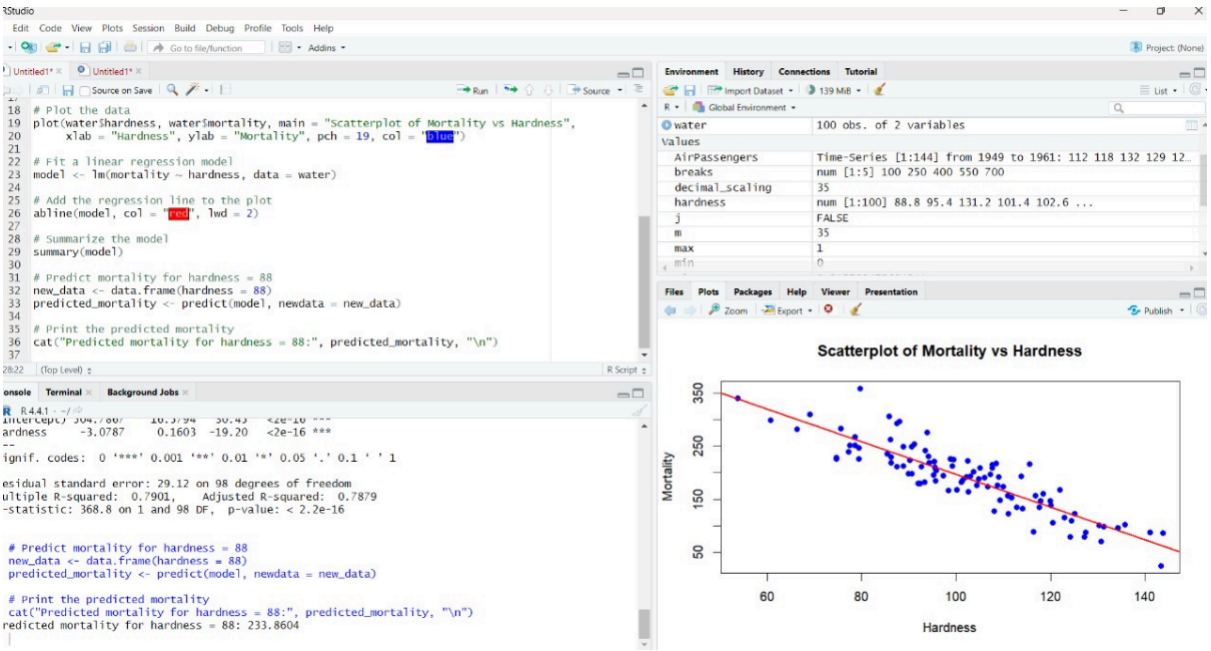


Q10:

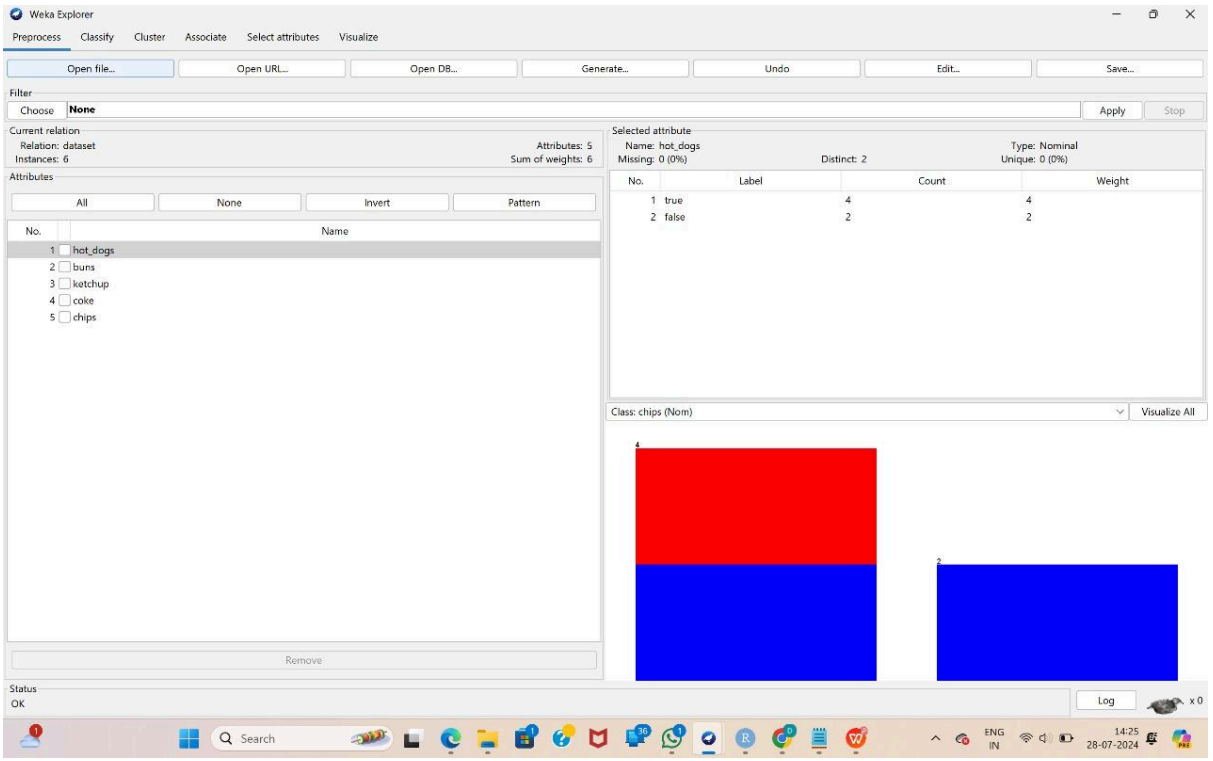
INPUT:

```
data(water, package="datasets")

plot(water$hardness, water$mortality, main="Scatterplot of Mortality vs Hardness",
xlab="Hardness", ylab="Mortality")

model <- lm(mortality ~ hardness, data=water)

abline(model, col="red")

predicted_mortality <- predict(model, newdata=data.frame(hardness=88))

predicted_mortality
```

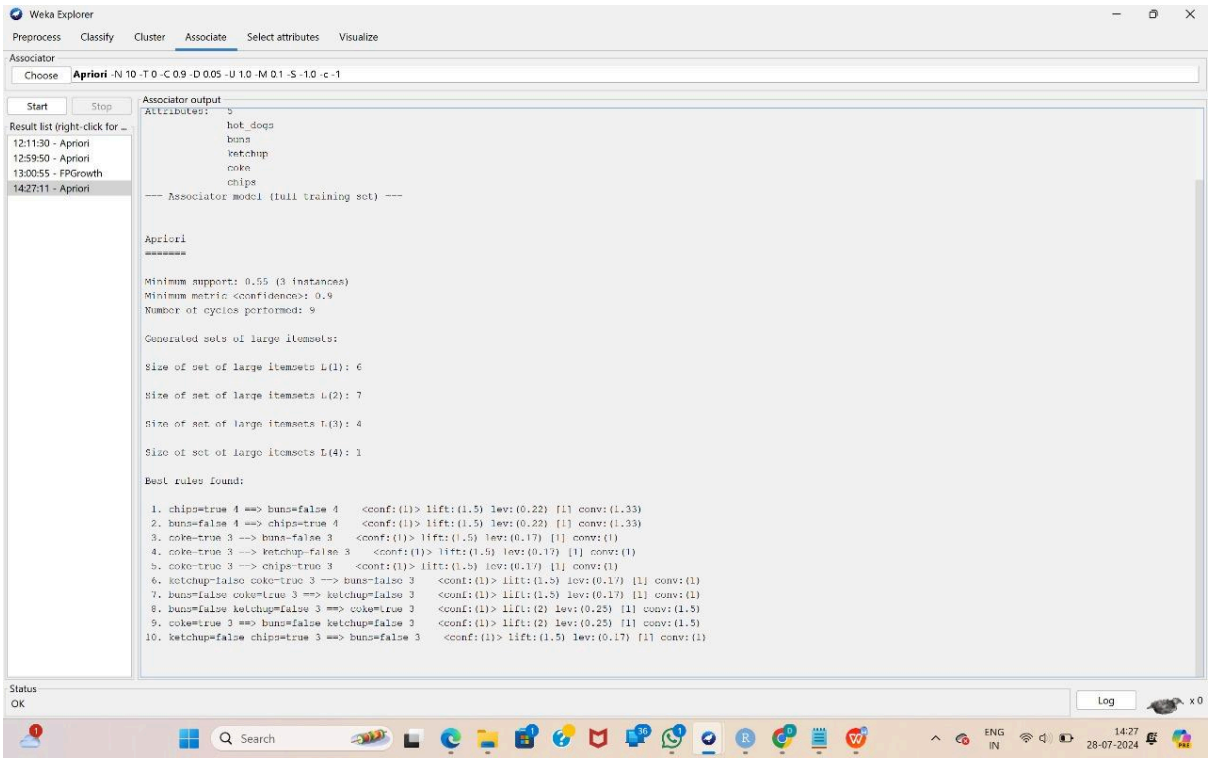
OUTPUT:



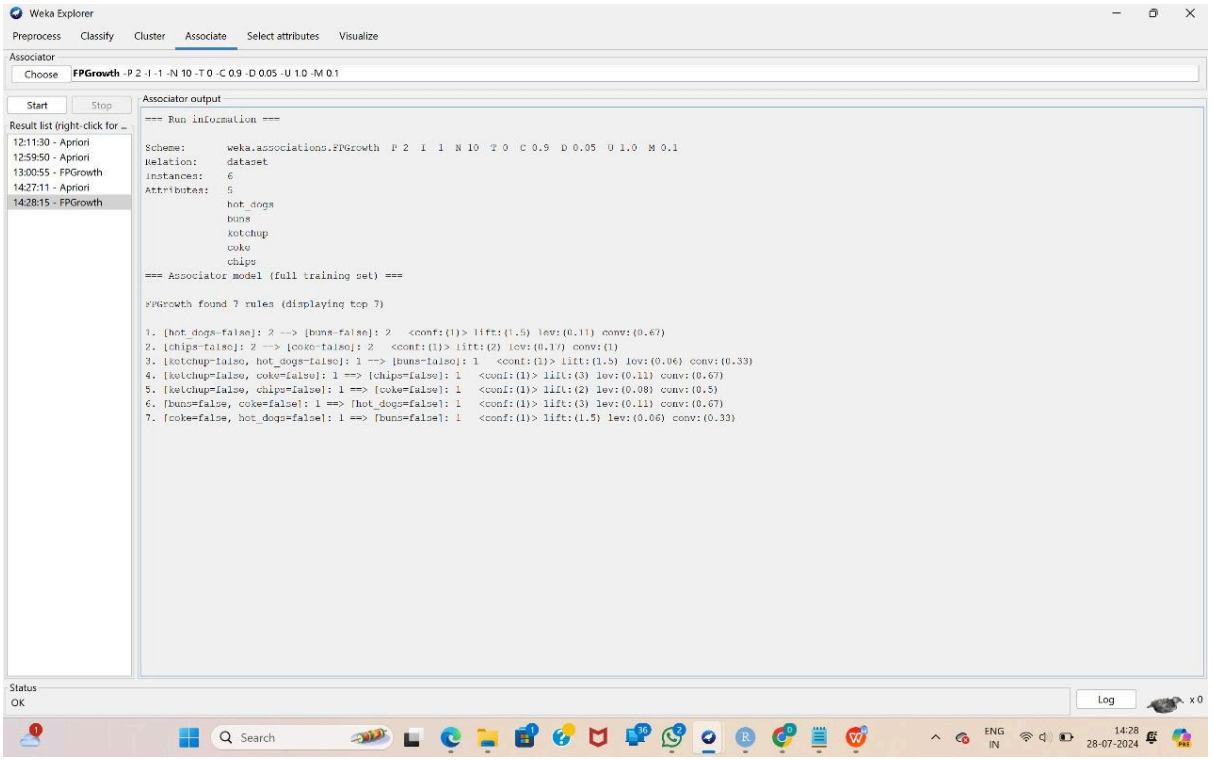
Q11:



Apriori Algorithm:

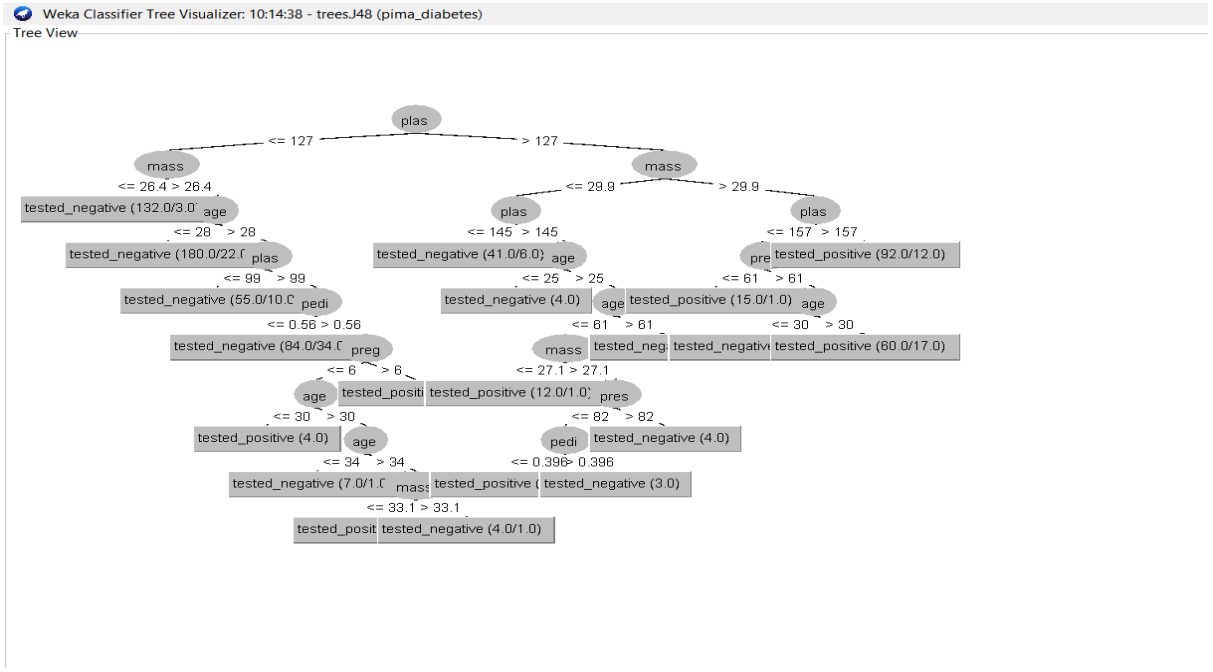


FP Growth:

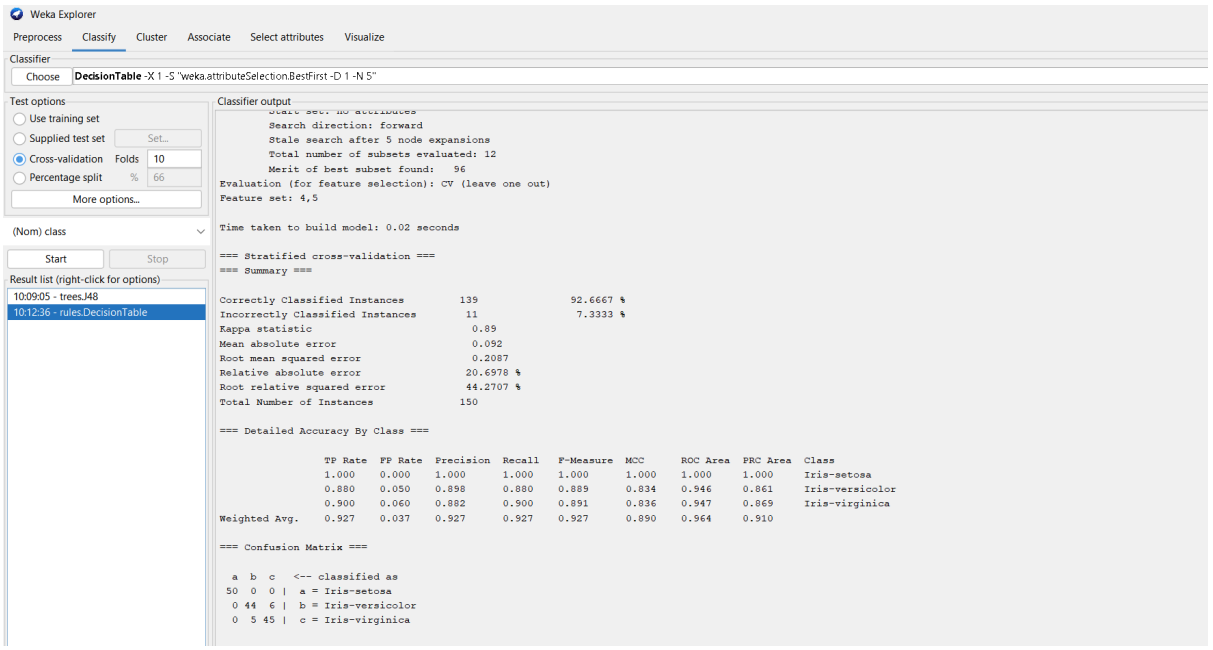


Q12:

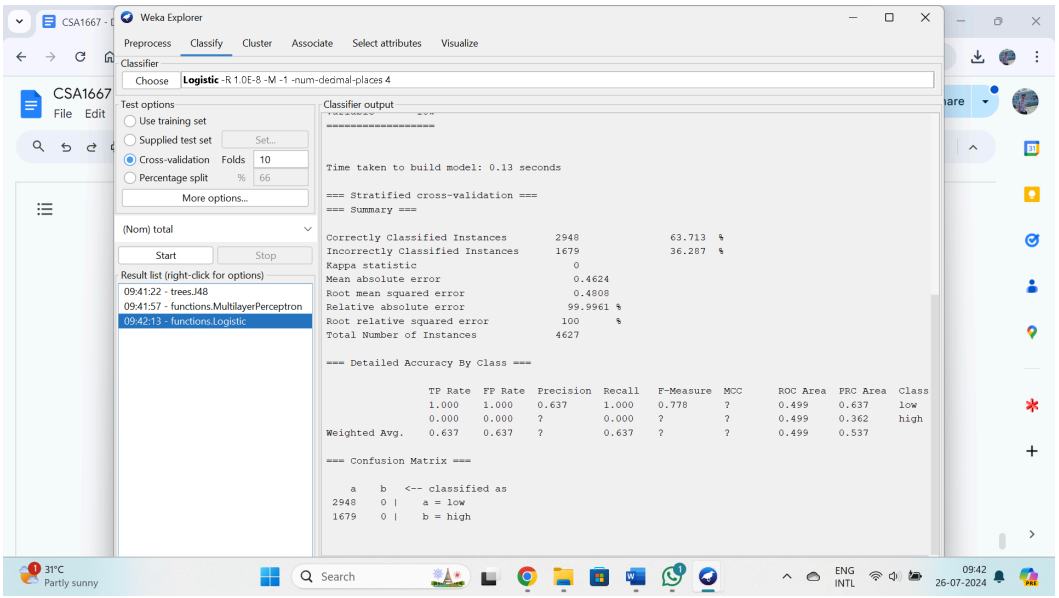
Tree:



Decision Tree:



Logistic:



Q13:

INPUT:

prices <- c(1, 1, 5, 5, 5, 5, 5, 8, 8, 10, 10, 10, 10, 12, 14, 14, 14, 15, 15, 15, 15, 15, 15, 18, 18, 18, 18, 18, 18, 18, 18, 20, 20, 20, 20, 20, 20, 20, 21, 21, 21, 21, 25, 25, 25, 25, 25, 28, 28, 30, 30, 30)

```
library(dplyr)

num_bins <- 3

bin_size <- length(prices) / num_bins

bins <- split(prices, ceiling(seq_along(prices) / bin_size))

print("Equal-frequency bins:")

print(bins)

bin_means <- lapply(bins, mean)

print("Smoothing by bin means:")

print(bin_means)

bin_boundaries <- lapply(bins, function(bin) {

  min_val <- min(bin)

  max_val <- max(bin)

  sapply(bin, function(x) {

    if (x - min_val < max_val - x) min_val else max_val

  })

})

print("Smoothing by bin boundaries:")

print(bin_boundaries)

bins_unlisted <- unlist(bins)
```

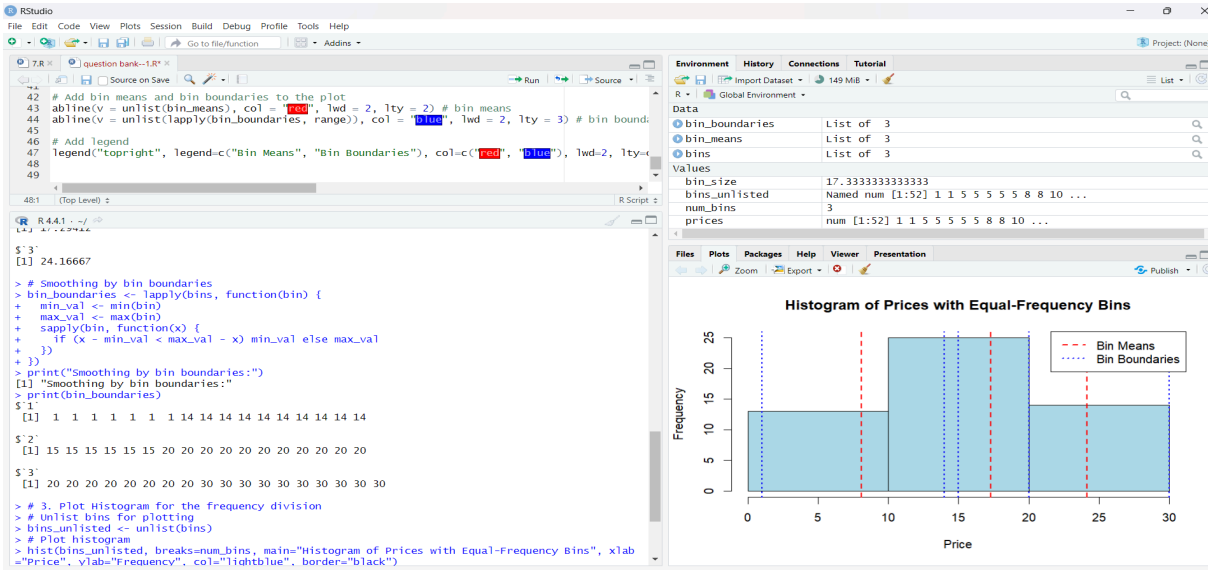
hist(bins_unlisted, breaks=num_bins, main="Histogram of Prices with Equal-Frequency Bins", xlab="Price", ylab="Frequency", col="lightblue", border="black")

abline(v = unlist(bin_means), col = "red", lwd = 2, lty = 2) # bin means

abline(v = unlist(lapply(bin_boundaries, range)), col = "blue", lwd = 2, lty = 3) # bin boundaries

legend("topright", legend=c("Bin Means", "Bin Boundaries"), col=c("red", "blue"), lwd=2, lty=c(2, 3))

OUTPUT:



Q14:

INPUT:

class_A <- c(76, 35, 47, 64, 95, 66, 89, 36, 84)

class_B <- c(51, 56, 84, 60, 59, 70, 63, 66, 50)

mean_A <- mean(class_A)

mean_B <- mean(class_B)

median_A <- median(class_A)

median_B <- median(class_B)

range_A <- range(class_A)

range_B <- range(class_B)

range_A_diff <- diff(range_A)

range_B_diff <- diff(range_B)

cat("Class A - Mean:", mean_A, " Median:", median_A, " Range:", range_A_diff, "\n")

cat("Class B - Mean:", mean_B, " Median:", median_B, " Range:", range_B_diff, "\n")

boxplot(class_A, class_B, names=c("Class A", "Class B"), main="Comparison of Class A and Class B Performance", ylab="Scores", col=c("lightblue", "lightgreen"))

abline(h=mean_A, col="blue", lty=2)

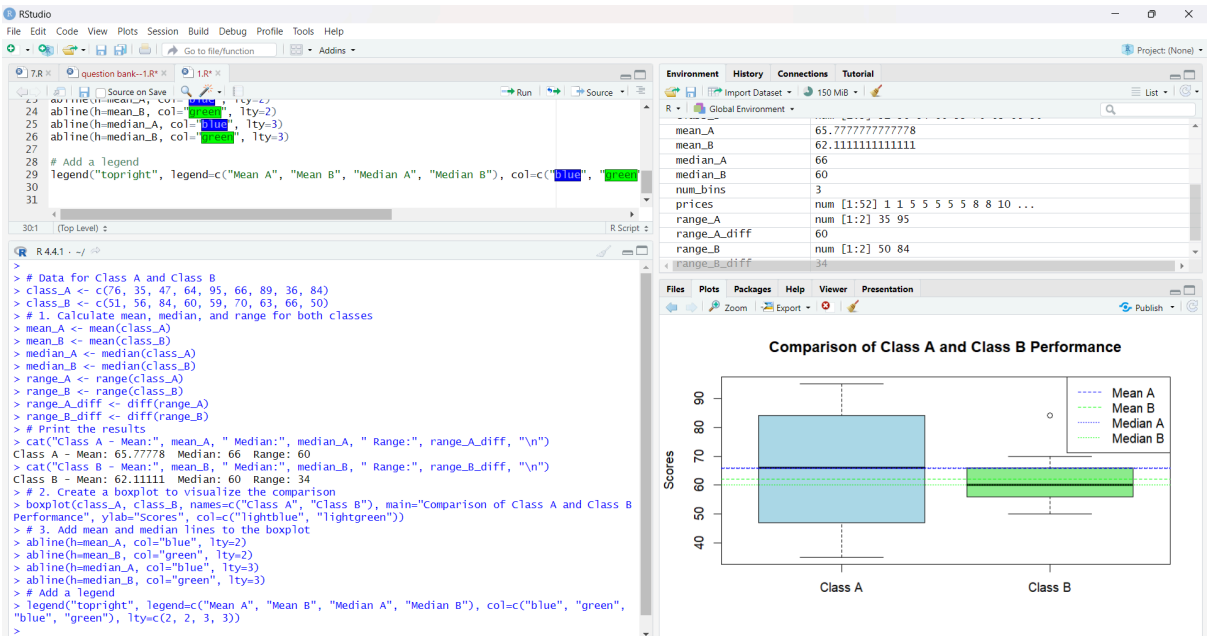
abline(h=mean_B, col="green", lty=2)

abline(h=median_A, col="blue", lty=3)

abline(h=median_B, col="green", lty=3)

legend("topright", legend=c("Mean A", "Mean B", "Median A", "Median B"), col=c("blue", "green", "blue", "green"), lty=c(2, 2, 3, 3))

OUTPUT:



Q16:

```
library(cluster)     # For clustering algorithms
library(factoextra)  # For clustering visualization
library(datasets)    # For sample datasets
set.seed(123)
customer_data <- data.frame(
  percentage_opened = runif(100, 0, 100),  # Percentage of emails opened
  clicks_per_email = runif(100, 0, 10),    # Number of clicks per email
  time_spent_viewing = runif(100, 0, 5)    # Time spent viewing email (in minutes)
)
customer_data_scaled <- scale(customer_data)
set.seed(123)
kmeans_result <- kmeans(customer_data_scaled, centers = 3, nstart = 25)
distances <- dist(customer_data_scaled)
hclust_result <- hclust(distances, method = "ward.D2")
cutree_result <- cutree(hclust_result, k = 3)
silhouette_kmeans <- silhouette(kmeans_result$cluster, distances)
silhouette_hclust <- silhouette(cutree_result, distances)
avg_silhouette_kmeans <- mean(silhouette_kmeans[, 3])
avg_silhouette_hclust <- mean(silhouette_hclust[, 3])
cat("Average Silhouette Score for k-means: ", avg_silhouette_kmeans, "\n")
cat("Average Silhouette Score for Hierarchical Clustering: ", avg_silhouette_hclust,
"\n")
fviz_cluster(kmeans_result, data = customer_data_scaled, geom = "point", stand =
FALSE, main = "K-means Clustering")
```

fviz_dend(hclust_result, k = 3, rect = TRUE, main = "Hierarchical Clustering Dendrogram")

if (avg_silhouette_kmeans > avg_silhouette_hclust) {

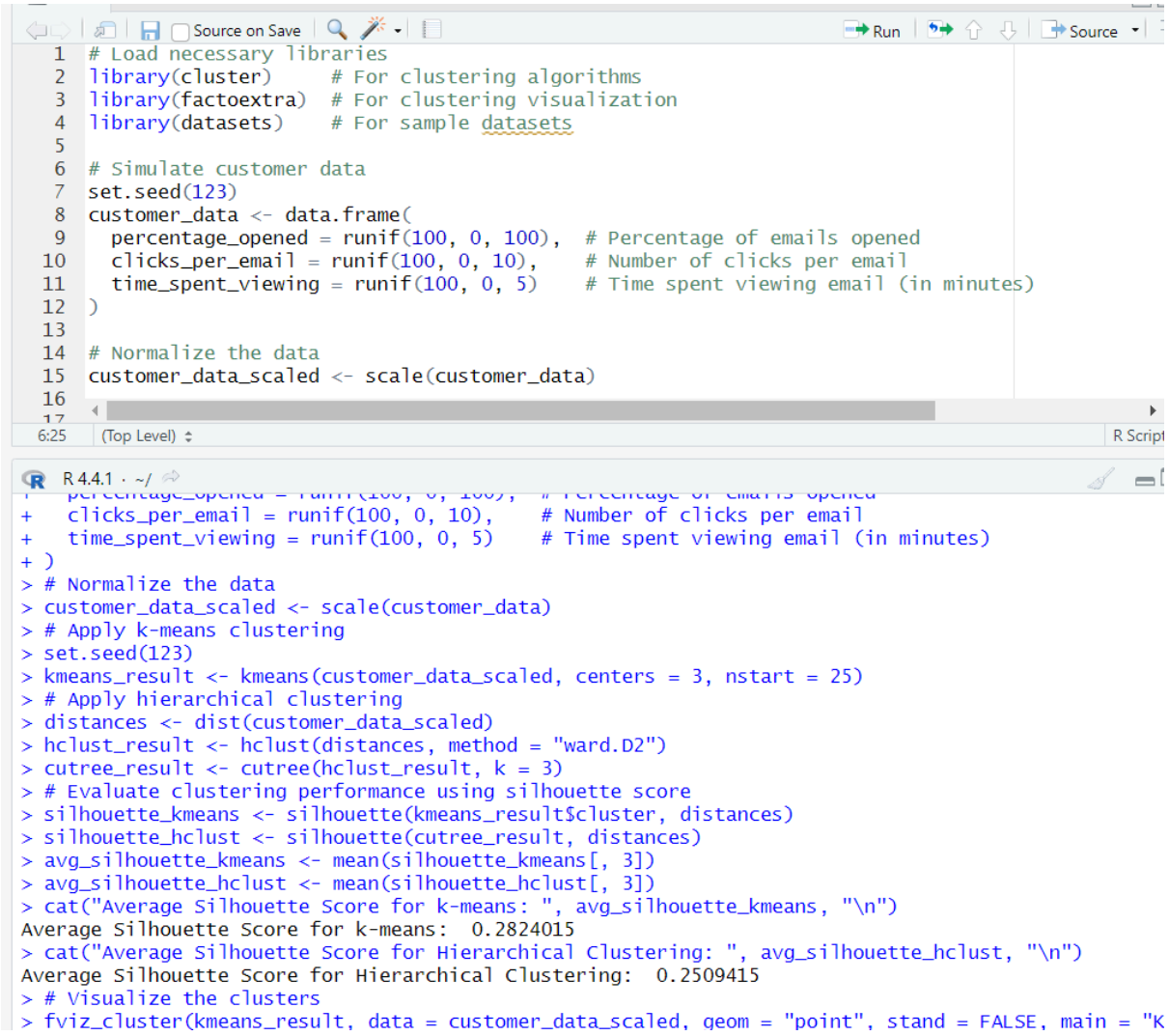
cat("K-means clustering performed better based on the silhouette score.\n")

} else {

cat("Hierarchical clustering performed better based on the silhouette score.\n")

}

OUTPUT:



```
# Load necessary libraries
library(cluster)     # For clustering algorithms
library(factoextra)  # For clustering visualization
library(datasets)    # For sample datasets

# Simulate customer data
set.seed(123)
customer_data <- data.frame(
  percentage_opened = runif(100, 0, 100),  # Percentage of emails opened
  clicks_per_email = runif(100, 0, 10),    # Number of clicks per email
  time_spent_viewing = runif(100, 0, 5)    # Time spent viewing email (in minutes)
)

# Normalize the data
customer_data_scaled <- scale(customer_data)
```

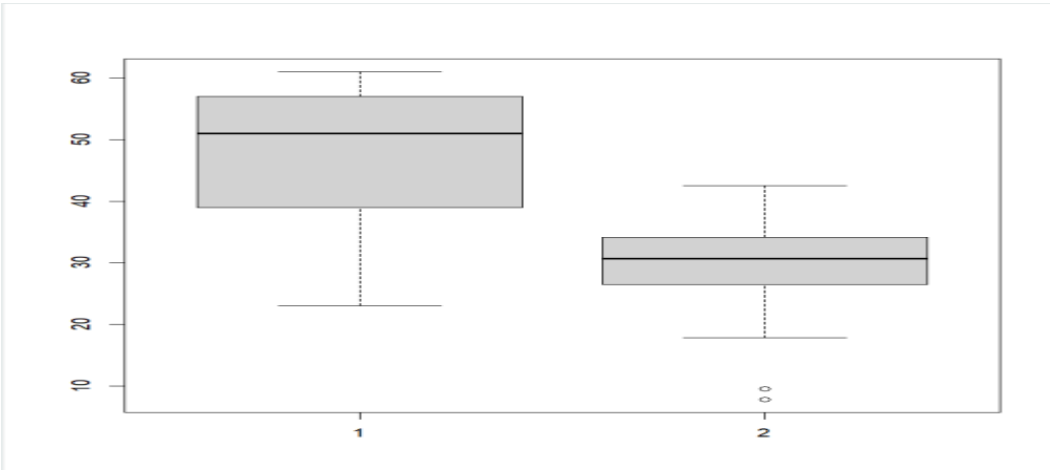
```
+   clicks_per_email = runif(100, 0, 10),    # Number of clicks per email
+   time_spent_viewing = runif(100, 0, 5)    # Time spent viewing email (in minutes)
+ )
> # Normalize the data
> customer_data_scaled <- scale(customer_data)
> # Apply k-means clustering
> set.seed(123)
> kmeans_result <- kmeans(customer_data_scaled, centers = 3, nstart = 25)
> # Apply hierarchical clustering
> distances <- dist(customer_data_scaled)
> hclust_result <- hclust(distances, method = "ward.D2")
> cutree_result <- cutree(hclust_result, k = 3)
> # Evaluate clustering performance using silhouette score
> silhouette_kmeans <- silhouette(kmeans_result$cluster, distances)
> silhouette_hclust <- silhouette(cutree_result, distances)
> avg_silhouette_kmeans <- mean(silhouette_kmeans[, 3])
> avg_silhouette_hclust <- mean(silhouette_hclust[, 3])
> cat("Average Silhouette Score for k-means: ", avg_silhouette_kmeans, "\n")
Average Silhouette Score for k-means:  0.2824015
> cat("Average Silhouette Score for Hierarchical Clustering: ", avg_silhouette_hclust, "\n")
Average Silhouette Score for Hierarchical Clustering:  0.2509415
> # Visualize the clusters
> fviz_cluster(kmeans_result, data = customer_data_scaled, geom = "point", stand = FALSE, main = "K
```

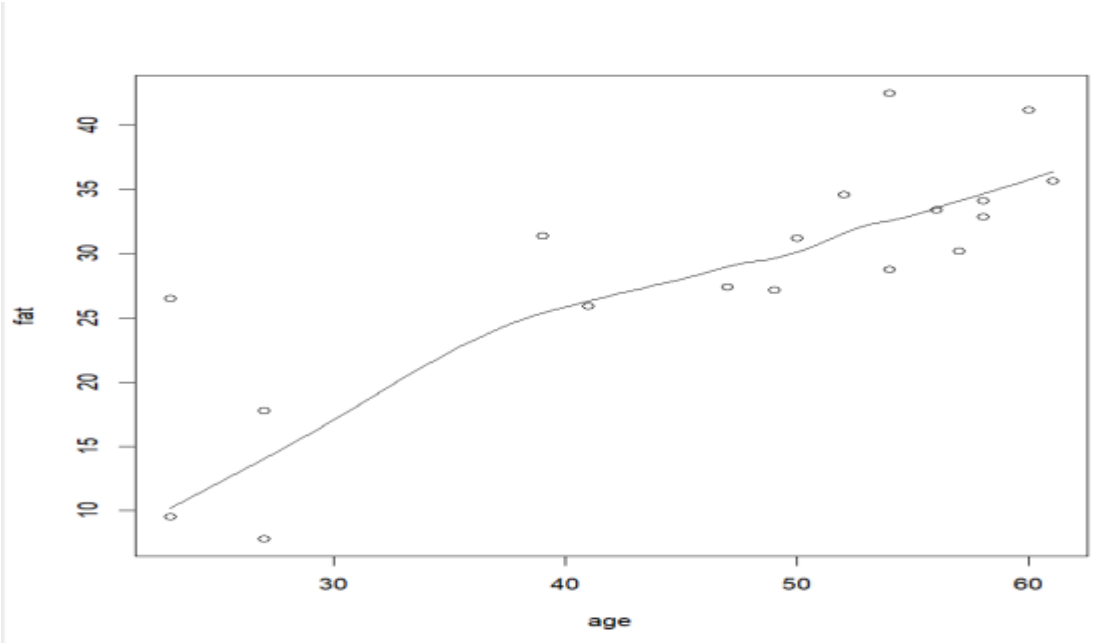
Q17:

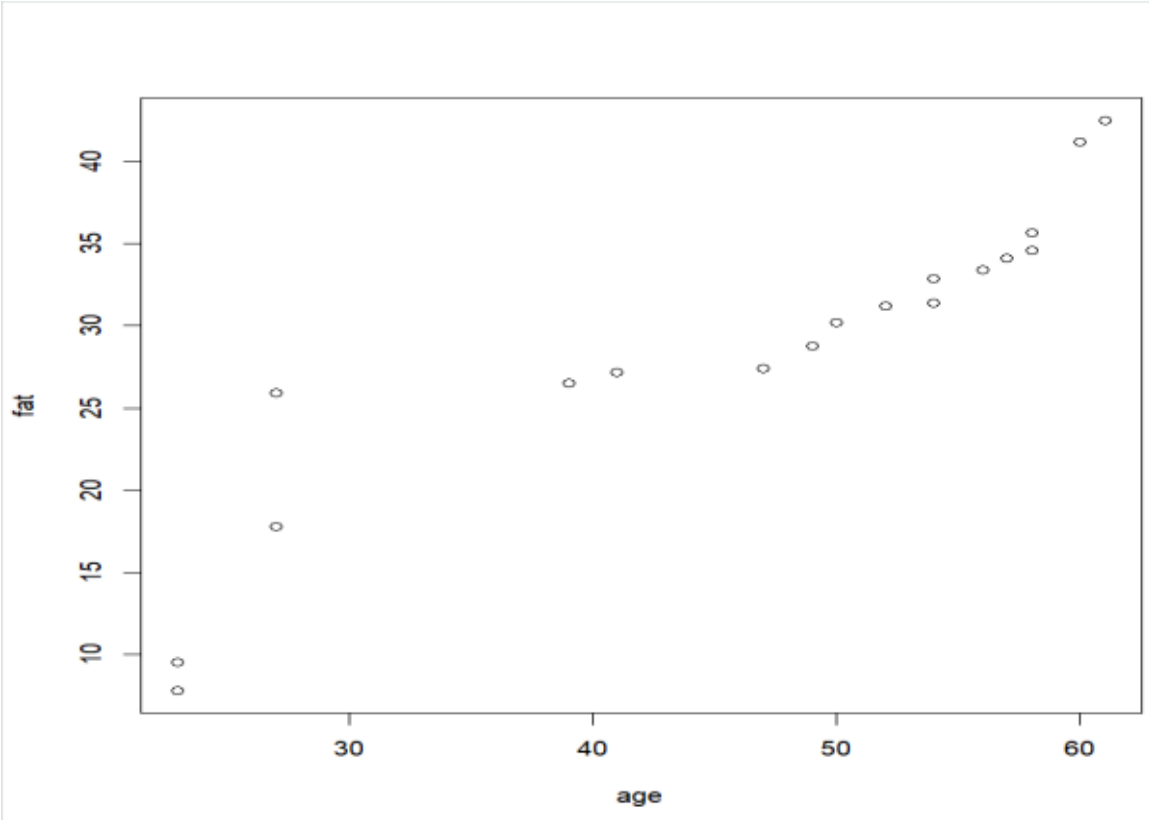
INPUT:

```
age<-c(23,23,27,27,39,41,47,49,50,52,54,54,56,57,58,58,60,61)

fat<-c(9.5,26.5,7.8,17.8,31.4,25.9,27.4,27.2,31.2,34.6,42.5,28.8,33.4,30.2,34.1,32.9,41.2,35.7)

mean(age)

median(age)

sd(age)

mean(fat)

median(fat)

sd(fat)

#boxplot

boxplot(age,fat)

#scatter plot

scatter.smooth(age,fat)

#qplot

qqplot(age,fat)
```

Output:




fat
10
15
20
25
30
35
40
30
40
50
60
age


fat
10
15
20
25
30
35
40
30
40
50
60
age

Q18:

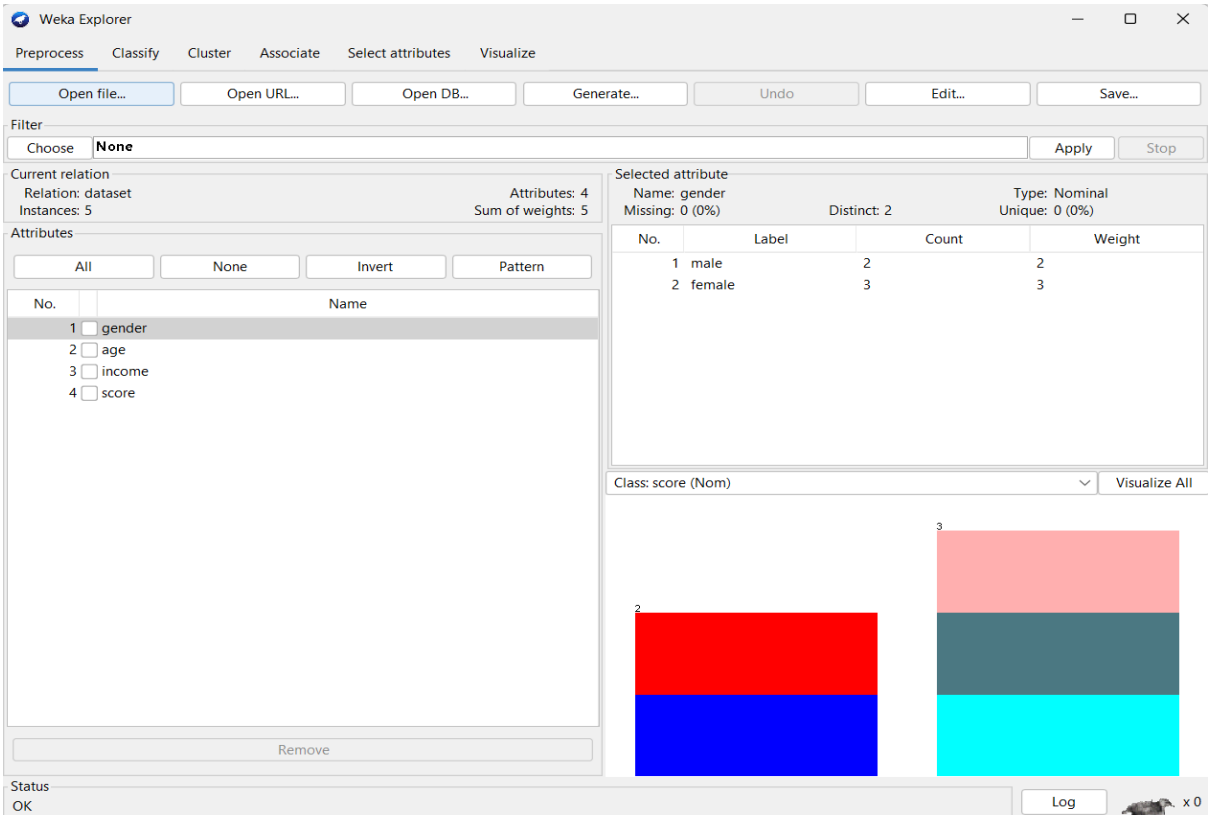
INPUT:

```
v<-c(23,23,27,27,39,41,47,49,50,52,54,54,56,57,58,58,60,61)

min<-0

max<-1

#min_max

min_max=((35-min(v))/(max(v)-min(v)))

print(min_max)

#z-score

m=mean(v)

s<-12.94

z_score=(35-m)/s

print(z_score)

#decimal scaling

m<-35

j=max(m)<1

decimal_scaling=m/10^j

print(decimal_scaling)
```

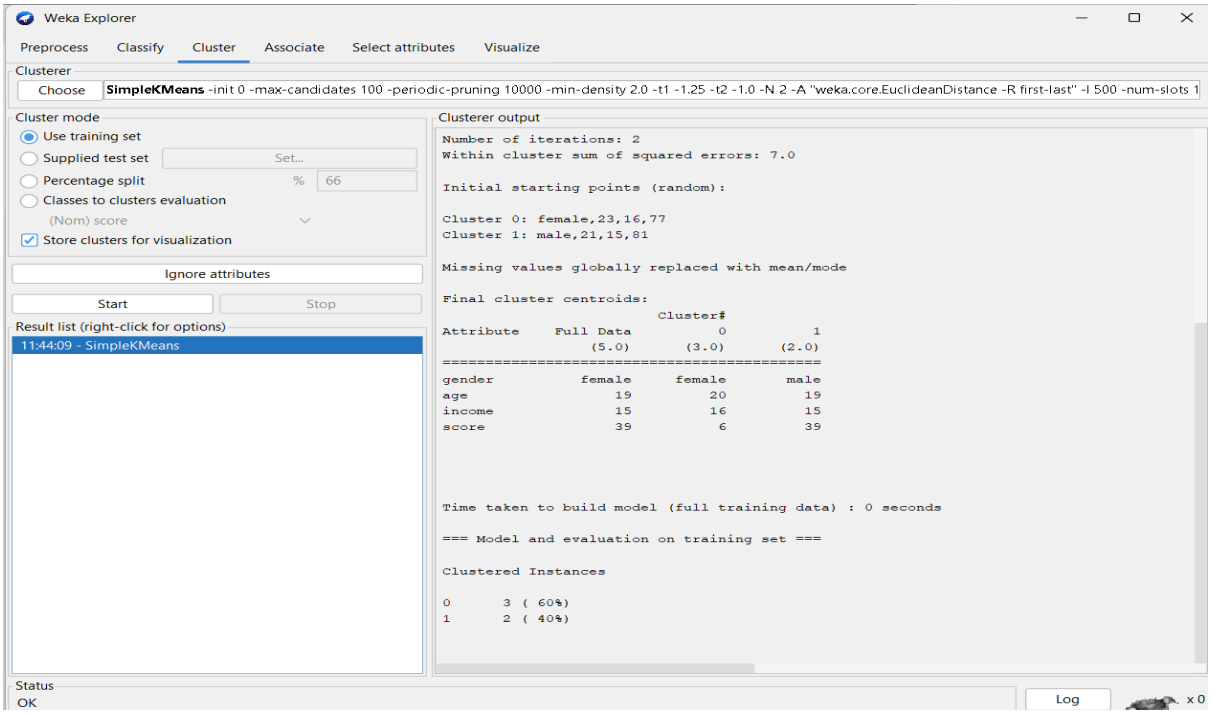
Output:

```
print(min_max)
] 0.3157895
#z-score
m=mean(v)
s<-12.94
z_score=(35-m)/s
print(z_score)
] -0.8844238
#decimal scaling
m<-35
j=max(m)<1
decimal_scaling=m/10^j
print(decimal_scaling)
] 35
```

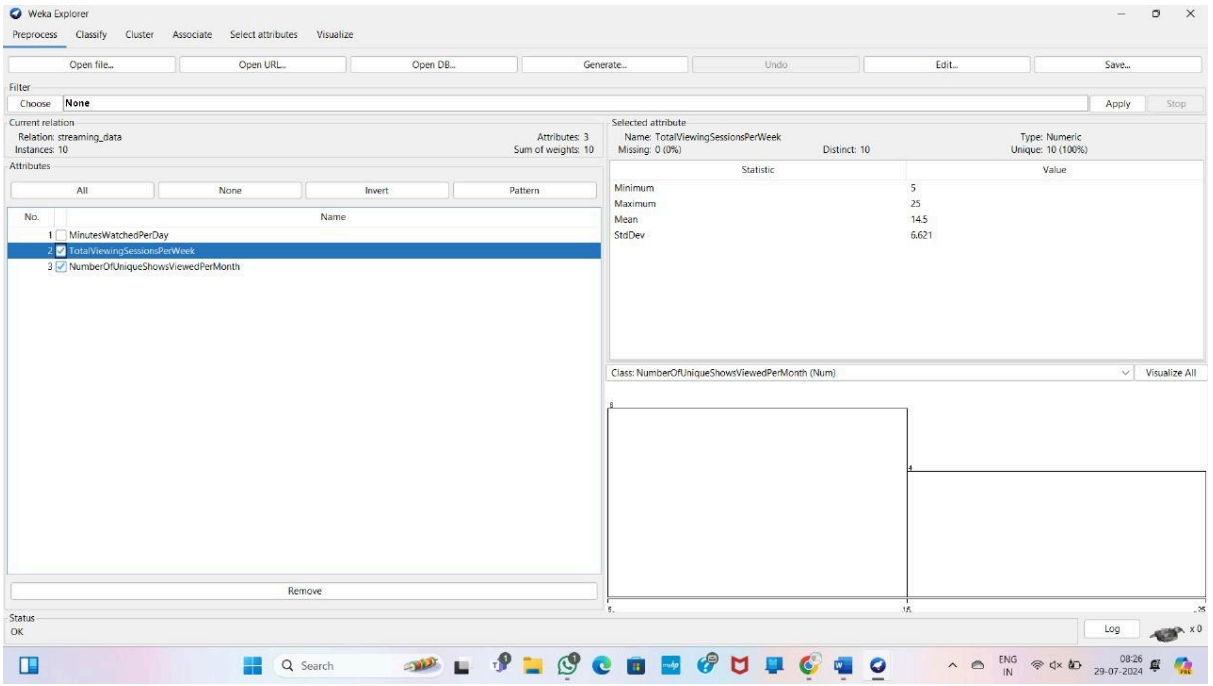
Q19:

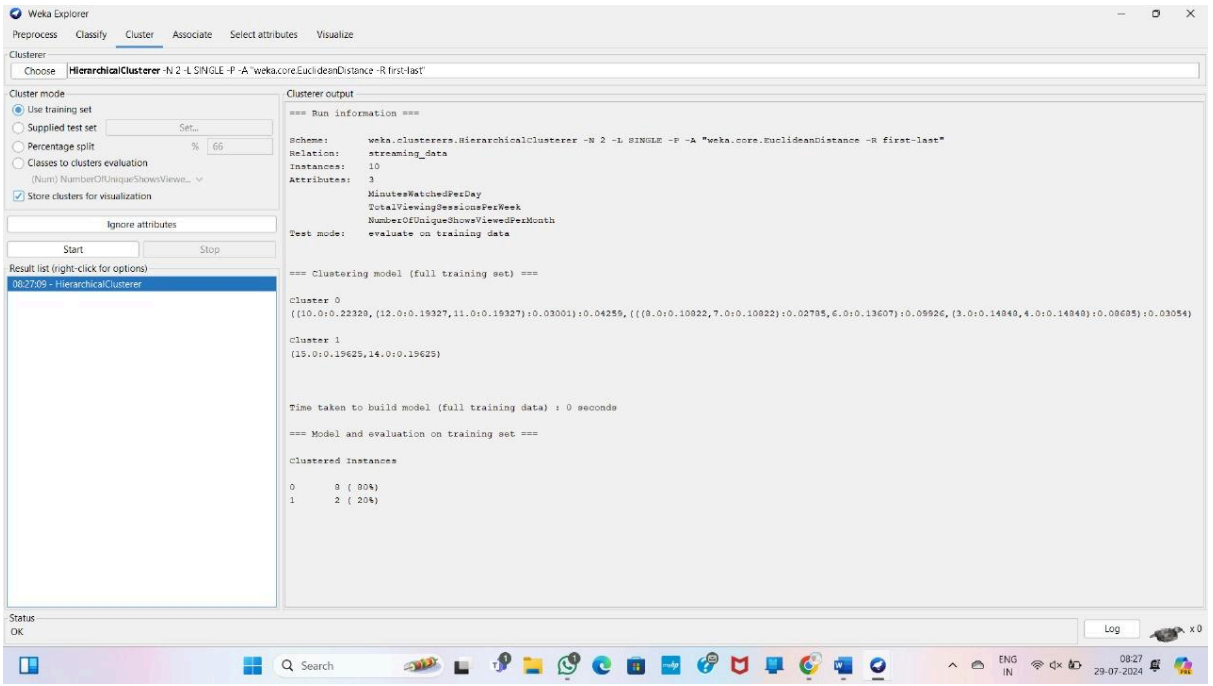


Clustering Analysis:



Q20:

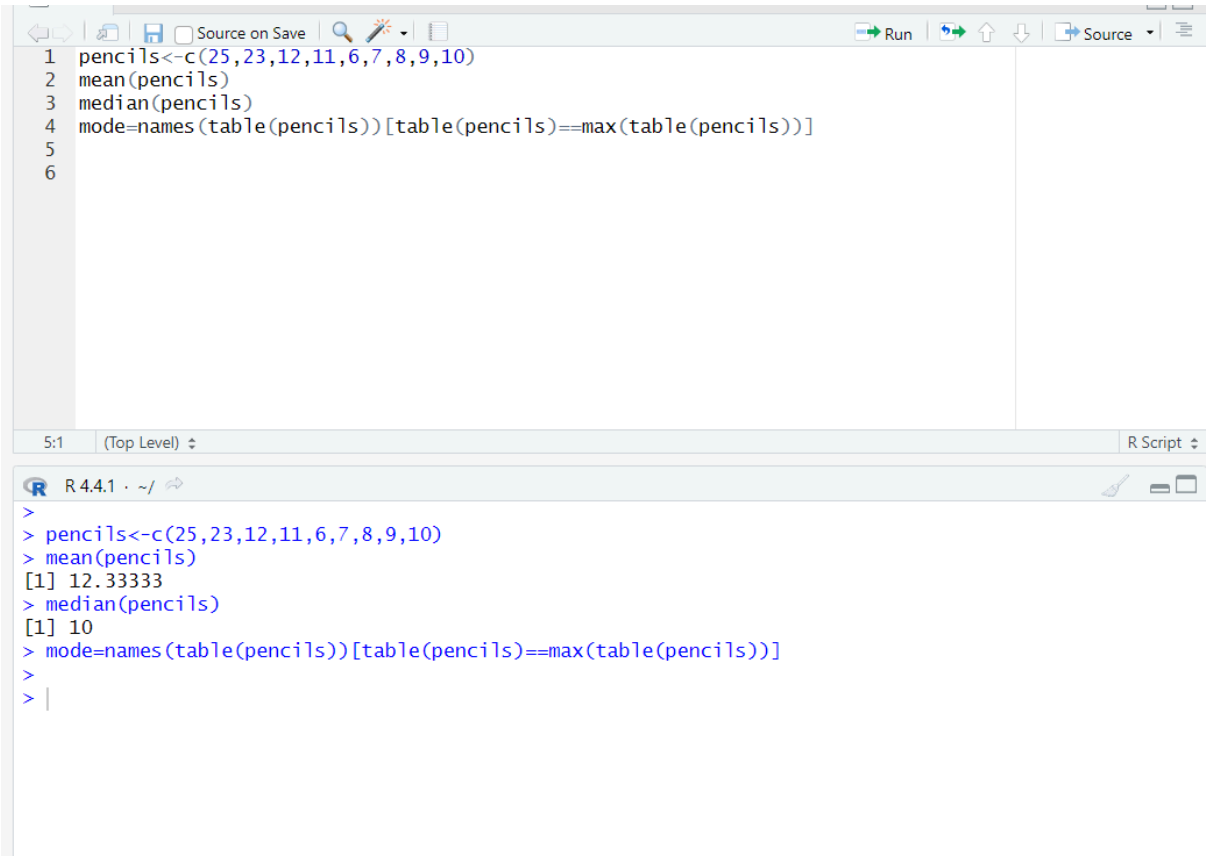

Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Open file...
Open URL...
Open DB...
Generate...
Undo
Edit...
Save...
Filter
Choose
None
Apply
Stop
Current relation
Relation: streaming_data
Instances: 10
Attributes: 3
Sum of weights: 10
Attributes
All
None
Invert
Pattern
No.
Name
1 MinutesWatchedPerDay
2 TotalViewingSessionsPerWeek
3 NumberOfUniqueShowsViewedPerMonth
Remove
Selected attribute
Name: TotalViewingSessionsPerWeek
Missing: 0 (0%)
Distinct: 10
Type: Numeric
Unique: 10 (100%)
Statistic
Value
Minimum 5
Maximum 25
Mean 14.5
StdDev 6.621
Class: NumberOfUniqueShowsViewedPerMonth (Num)
Visualize All
Status
OK
Log
x 0


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Clusterer
Choose
HierarchicalClusterer -N 2 -L SINGLE -P -A "weka.core.EuclideanDistance -R first-last"
Cluster mode
Use training set
Supplied test set
Set...
Percentage split
%
66
Classes to clusters evaluation
(Num) NumberOfUniqueShowsViewe...
Store clusters for visualization
Ignore attributes
Start
Stop
Result list (right-click for options)
08:27:09 - HierarchicalClusterer
Clusterer output
=== Run information ===
Scheme: weka.clusterers.HierarchicalClusterer -N 2 -L SINGLE -P -A "weka.core.EuclideanDistance -R first-last"
Relation: streaming_data
Instances: 10
Attributes: 3
MinutesWatchedPerDay
TotalViewingSessionsPerWeek
NumberOfUniqueShowsViewedPerMonth
Test mode: evaluate on training data
=== Clustering model (full training set) ===
Cluster 0
((10.0:0.22329,(12.0:0.19327,11.0:0.19327):0.03001):0.04255,(((8.0:0.10022,7.0:0.10022):0.02705,6.0:0.13607):0.09926,(3.0:0.14848,4.0:0.14848):0.08685):0.03054)
Cluster 1
(15.0:0.19625,14.0:0.19625)
Time taken to build model (full training data) : 0 seconds
=== Model and evaluation on training set ===
Clustered Instances
0 8 (80%)
1 2 (20%)
Status
OK
Log
x 0

Q21:
INPUT:

```
pencils<-c(25,23,12,11,6,7,8,9,10)
mean(pencils)
median(pencils)
mode=names(table(pencils))[table(pencils)==max(table(pencils))]
```

output:

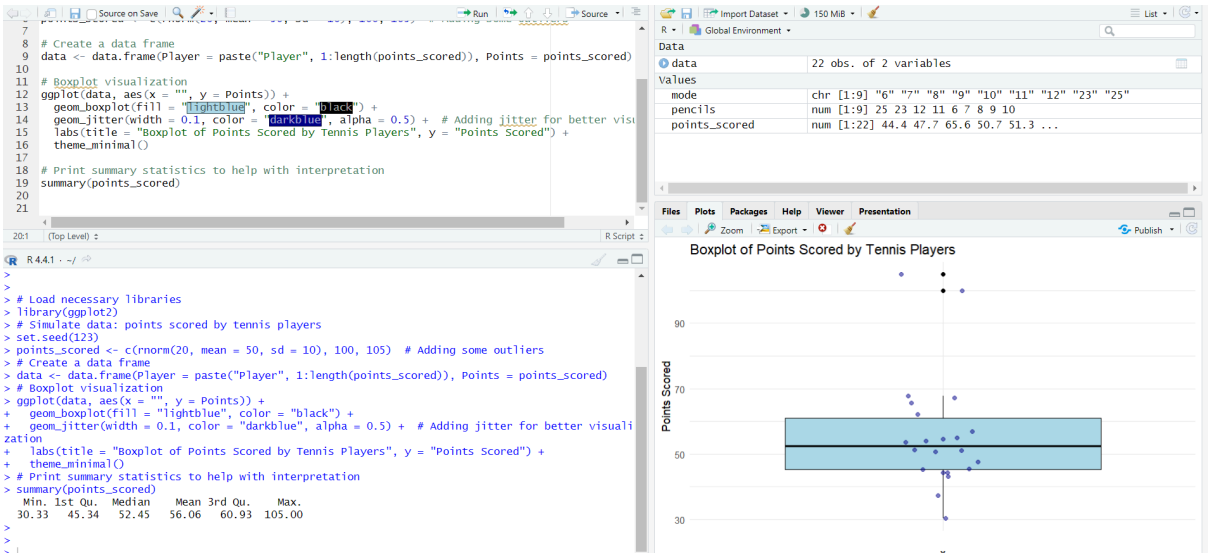


Q22:

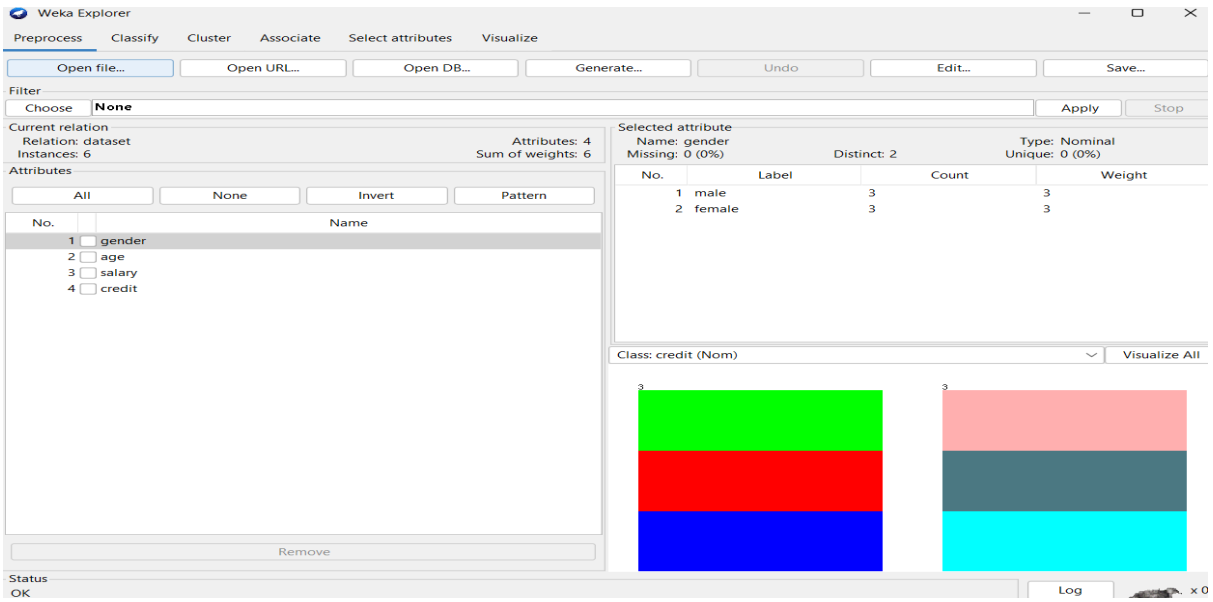
INPUT:

```
library(ggplot2)

set.seed(123)

points_scored <- c(rnorm(20, mean = 50, sd = 10), 100, 105)  # Adding some outliers

data <- data.frame(Player = paste("Player", 1:length(points_scored)), Points =
points_scored)
ggplot(data, aes(x = "", y = Points)) +
  geom_boxplot(fill = "lightblue", color = "black") +
  geom_jitter(width = 0.1, color = "darkblue", alpha = 0.5) +  # Adding jitter for better
visualization
  labs(title = "Boxplot of Points Scored by Tennis Players", y = "Points Scored") +
  theme_minimal()
summary(points_scored)
```

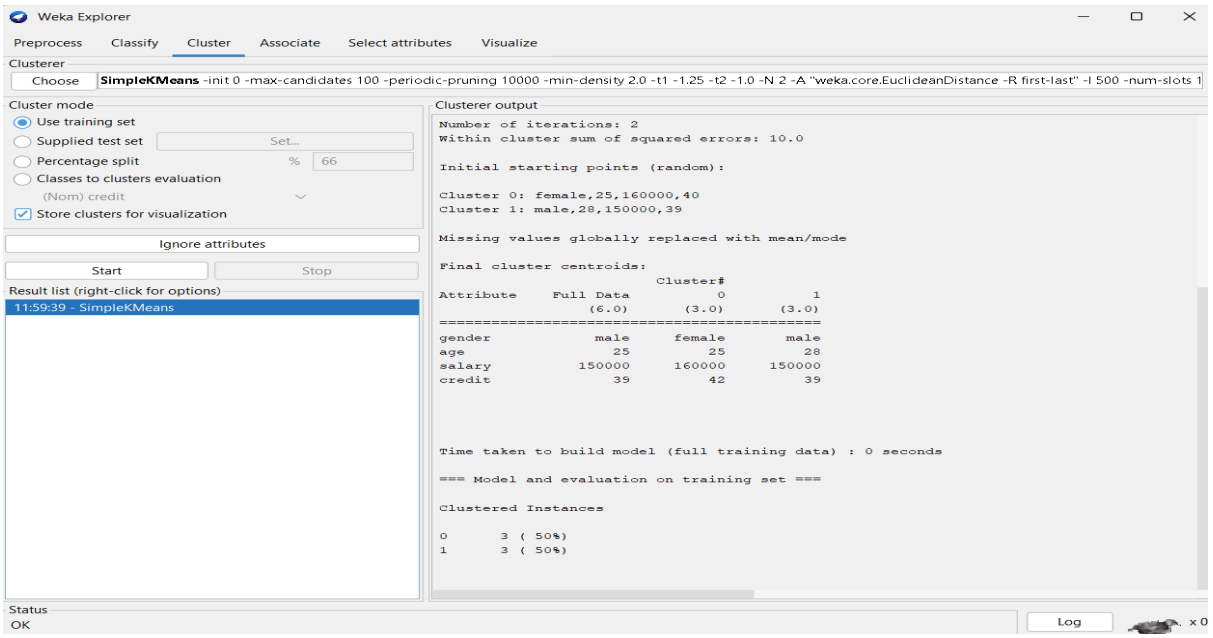
Output:


Boxplot of Points Scored by Tennis Players
Points Scored
90
70
50
30

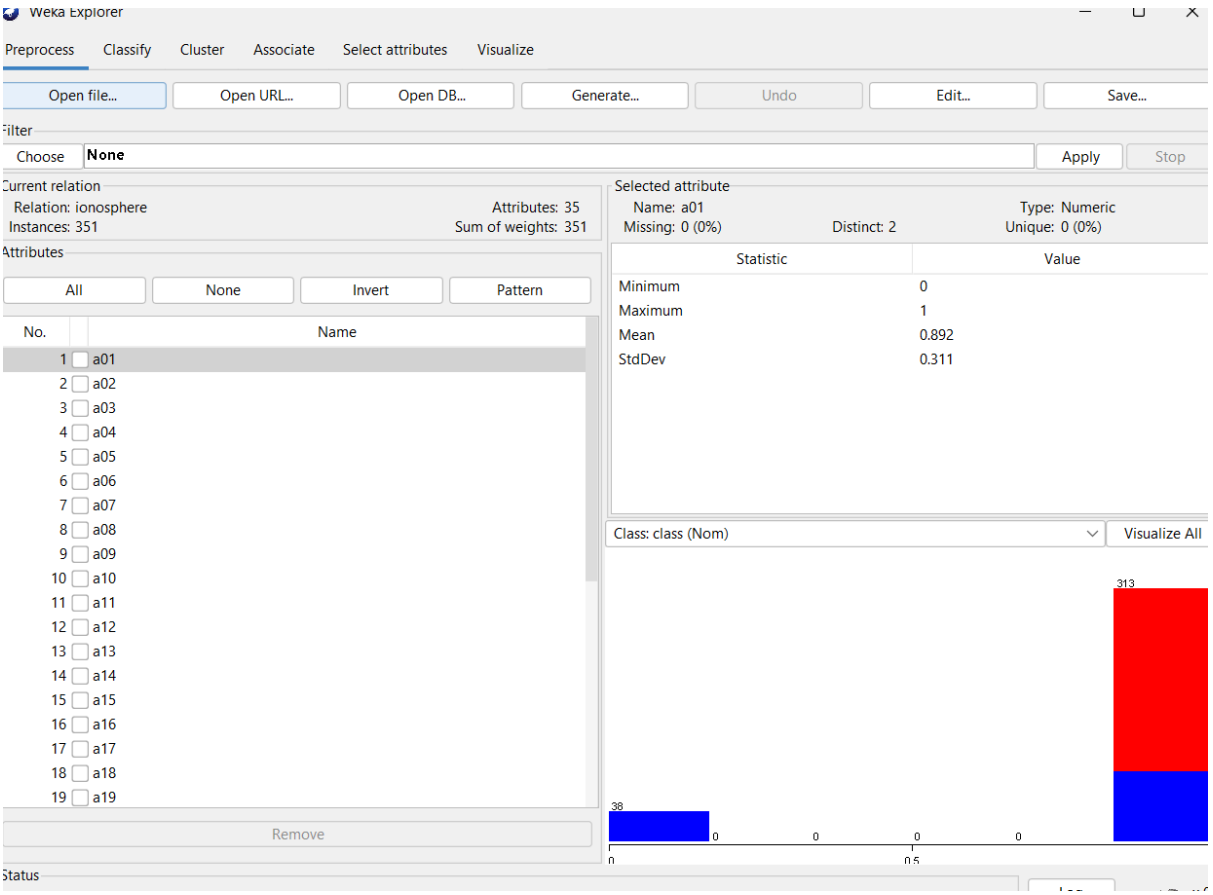
Q23:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Open file...
Open URL...
Open DB...
Generate...
Undo
Edit...
Save...
Filter
Choose
None
Apply
Stop
Current relation
Relation: dataset
Instances: 6
Attributes: 4
Sum of weights: 6
Attributes
All
None
Invert
Pattern
No.
Name
1 gender
2 age
3 salary
4 credit
Remove
Selected attribute
Name: gender
Missing: 0 (0%)
Distinct: 2
Type: Nominal
Unique: 0 (0%)
No.
Label
Count
Weight
1 male 3 3
2 female 3 3
Class: credit (Nom)
Visualize All
Status
OK
Log

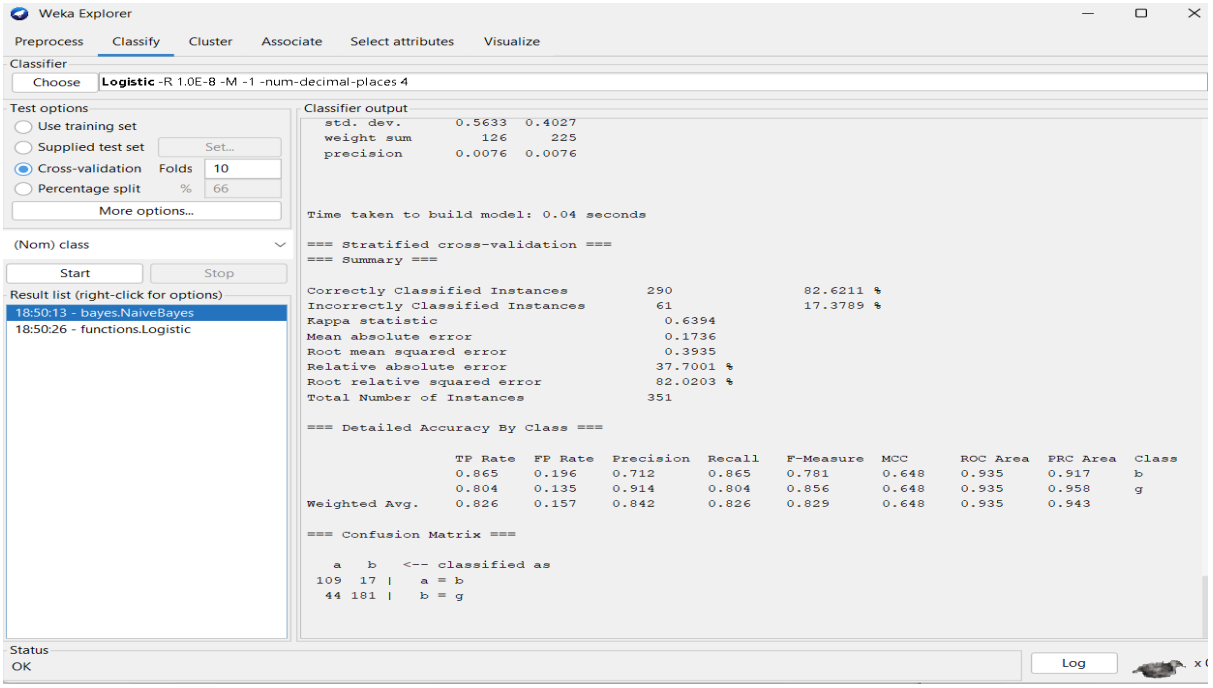
K Means:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Clusterer
Choose
SimpleKMeans -init 0 -max-candidates 100 -periodic-pruning 10000 -min-density 2.0 -t1 -1.25 -t2 -1.0 -N 2 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1
Cluster mode
Use training set
Supplied test set
Set...
Percentage split
%
66
Classes to clusters evaluation
(Nom) credit
Store clusters for visualization
Ignore attributes
Start
Stop
Result list (right-click for options)
11:59:39 - SimpleKMeans
Clusterer output
Number of iterations: 2
Within cluster sum of squared errors: 10.0
Initial starting points (random):
Cluster 0: female,25,160000,40
Cluster 1: male,28,150000,39
Missing values globally replaced with mean/mode
Final cluster centroids:
Cluster#
Attribute Full Data 0 1
(6.0) (3.0) (3.0)
gender male female male
age 25 25 28
salary 150000 160000 150000
credit 39 42 39
Time taken to build model (full training data) : 0 seconds
=== Model and evaluation on training set ===
Clustered Instances
0 3 (50%)
1 3 (50%)
Status
OK
Log

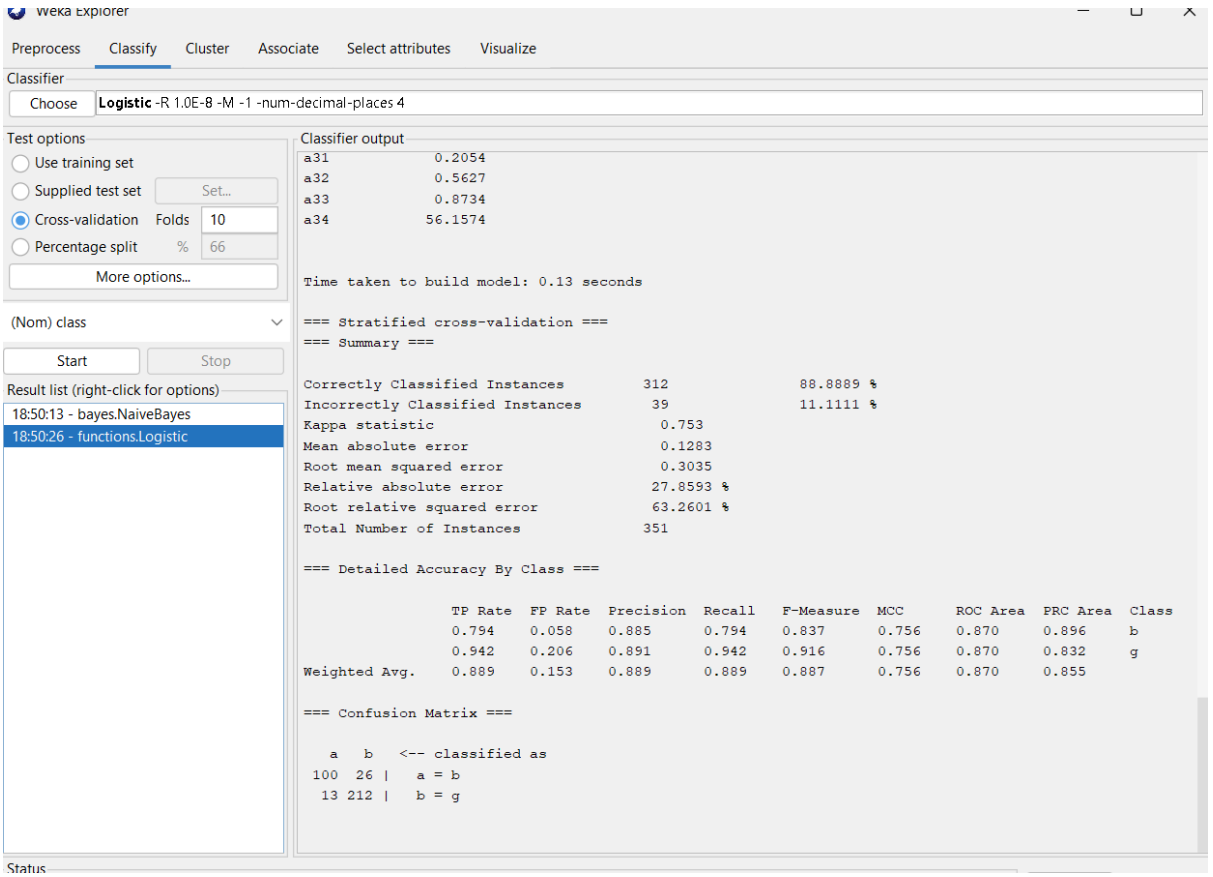
Q24:


Weka Explorer
Preprocess
Classify
Cluster
Associate
Select attributes
Visualize
Open file...
Open URL...
Open DB...
Generate...
Undo
Edit...
Save...
Filter
Choose
None
Apply
Stop
Current relation
Relation: ionosphere
Instances: 351
Attributes: 35
Sum of weights: 351
Attributes
All
None
Invert
Pattern
No.
Name
1 a01
2 a02
3 a03
4 a04
5 a05
6 a06
7 a07
8 a08
9 a09
10 a10
11 a11
12 a12
13 a13
14 a14
15 a15
16 a16
17 a17
18 a18
19 a19
Remove
Selected attribute
Name: a01
Missing: 0 (0%)
Distinct: 2
Type: Numeric
Unique: 0 (0%)
Statistic
Value
Minimum 0
Maximum 1
Mean 0.892
StdDev 0.311
Class: class (Nom)
Visualize All
313
38
0
0
0
0
0
0.5
Status

Naïve Bayes classification:



SVM:



Q25:

RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function | Addins

7.R*

Source on Save | Run | Source

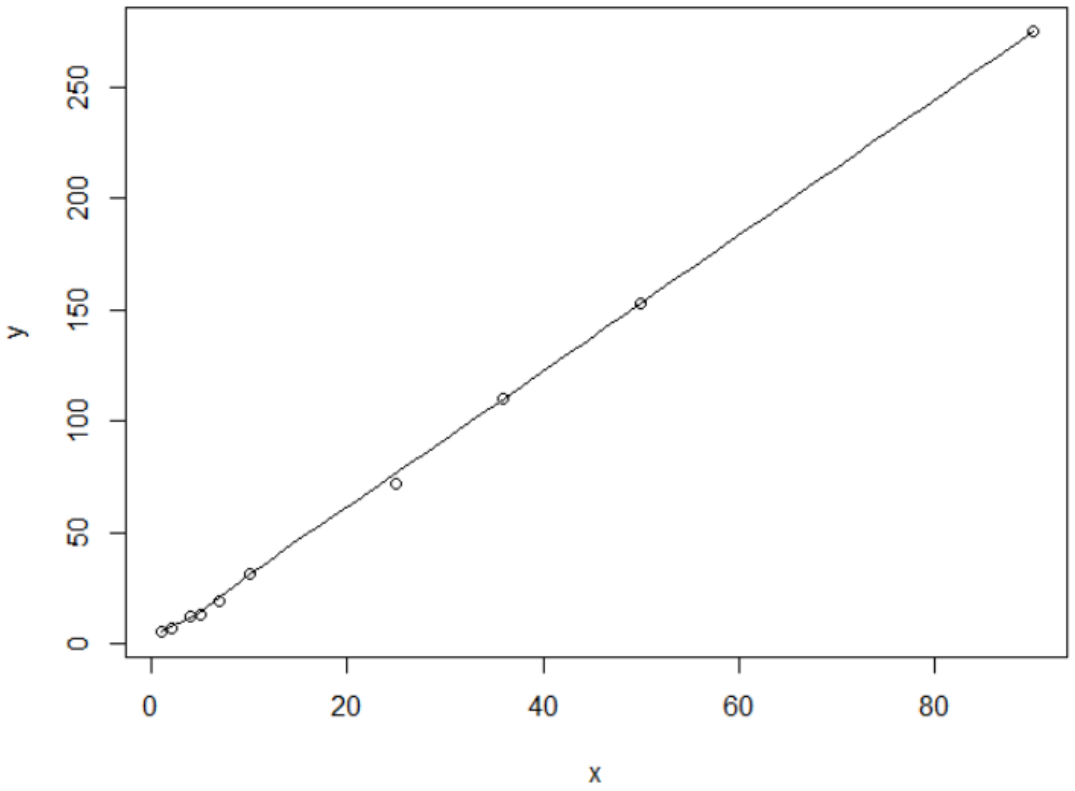
```
# Data
persons <- c("Gopu", "Babu", "Baby", "Gopal", "Krishna", "Jai", "Dev", "Malini", "Hema", "Anu"
vegetarian_status <- c("yes", "yes", "yes", "no", "yes", "no", "no", "yes", "yes", "yes")

# Create a data frame
data <- data.frame(persons, vegetarian_status)

# Count the number of vegetarians and non-vegetarians
veg_count <- sum(vegetarian_status == "yes")
```

25:1 (Top Level) R Script

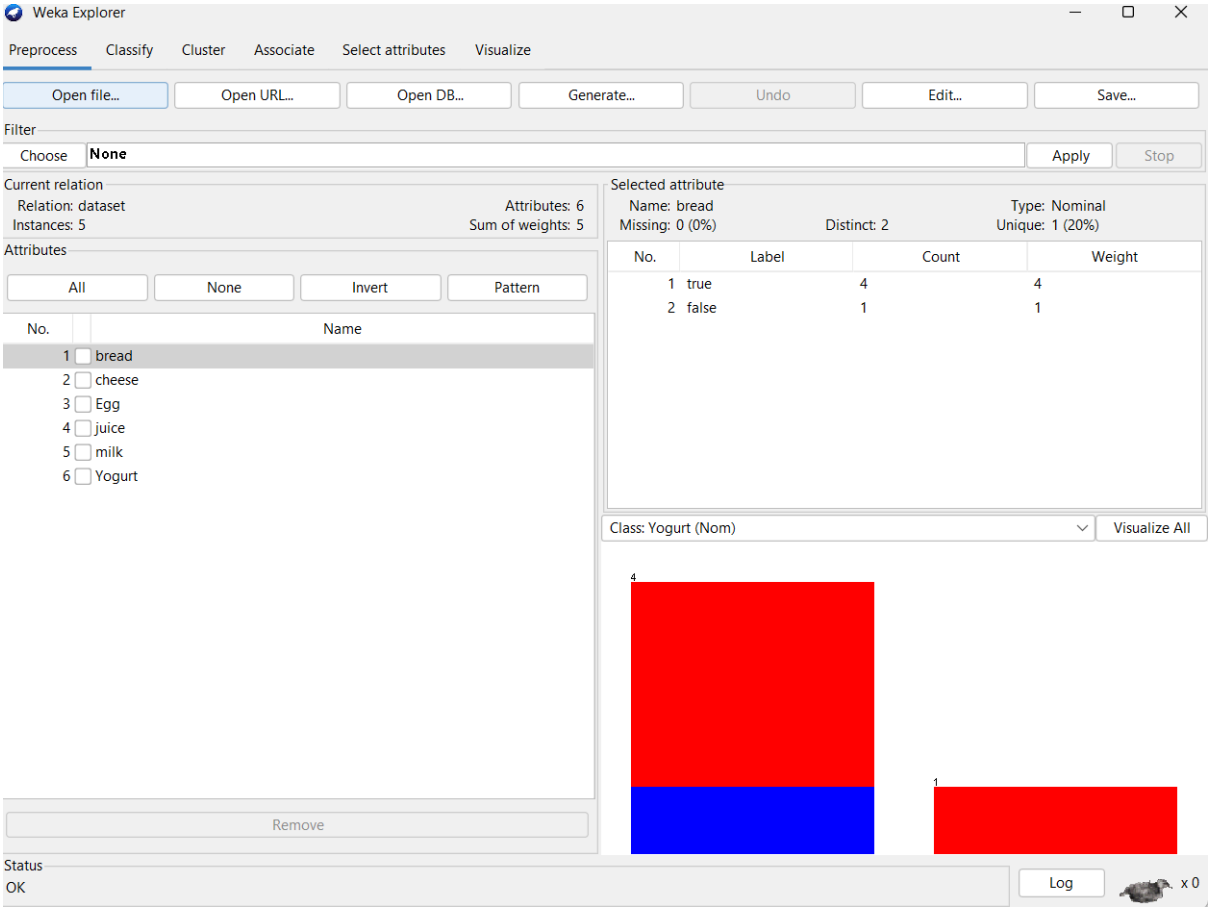
R 4.4.1 · ~/

```
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
> # Data
> persons <- c("Gopu", "Babu", "Baby", "Gopal", "Krishna", "Jai", "Dev", "Malini", "Hema", "Anu")
> vegetarian_status <- c("yes", "yes", "yes", "no", "yes", "no", "no", "yes", "yes", "yes")
> # Create a data frame
> data <- data.frame(persons, vegetarian_status)
> # Count the number of vegetarians and non-vegetarians
> veg_count <- sum(vegetarian_status == "yes")
> non_veg_count <- sum(vegetarian_status == "no")
> # Determine which type has the greater count
> if (veg_count > non_veg_count) {
+   greater_count_type <- "Vegetarians"
+ } else if (non_veg_count > veg_count) {
+   greater_count_type <- "Non-Vegetarians"
+ } else {
+   greater_count_type <- "Both are equal"
+ }
> # Results
> cat("Number of Vegetarians:", veg_count, "\n")
Number of Vegetarians: 7
> cat("Number of Non-Vegetarians:", non_veg_count, "\n")
Number of Non-Vegetarians: 3
> cat("Type with Greater Count:", greater_count_type, "\n")
Type with Greater Count: Vegetarians
>
>
```

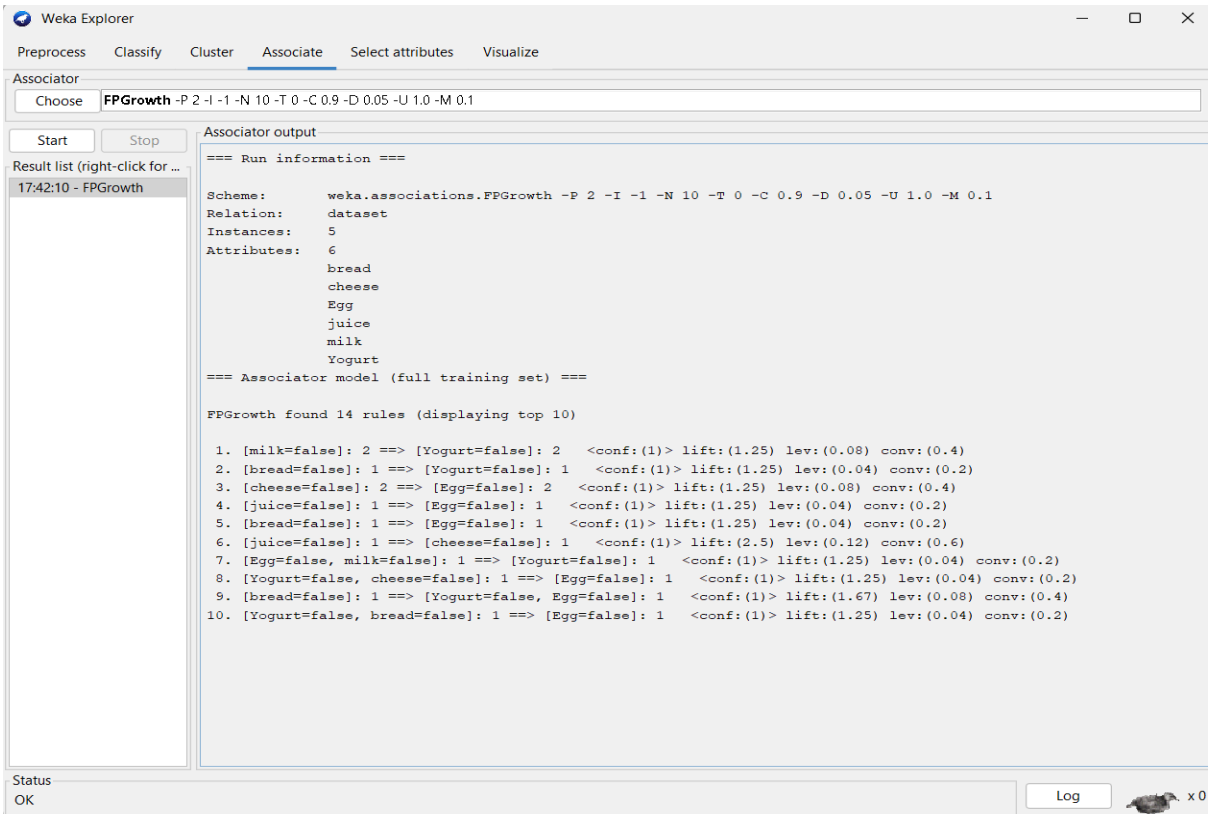
Q26:



Q27:



FP GROWTH:



Q28: