A Case Study Of Analyzing 2013 Chicago Youth Health Risk Behavior Data By Machine Learning With CRISP-DM Methodology

Submitted as final project fulfillment of Course: ISTE790 Data Analytics for Emerging Technologies

Group: 5

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Abstract

The objective of this paper is to use data mining techniques to analyze the 2013 Chicago youth risk behavior surveillance survey data,Collected by the centers for Disease Control and Prevention in USA, to investigate interesting relations and patterns in collected data, and provide a recommendation based on findings that been discovered by applying machine learning algorithms such apriori decision tree. . . etc. following CRISP-DM steps methodology, staring by business understanding, data understanding, data preparation, modeling, and evaluation. R open-source software will be used among all the process steps.

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Figure 1: test

1 Executive Summary.

- The main objective of this project is to examine the associations between victimization, substance use, and suicide attempt among youth using the Youth Health Risk Behavior Survey data for the year 2013.
- The data used consists of information from 1581 respondents, consist of Record Id & 28 variables that are categorized into 4 categories:
  1. Demographic
  2. Victimization
  3. Suicide Attempt
  4. Substance Use
- Each respondent is identified by a record ID and are mostly between the ages of 15-19 studying in grades 9-12.
- Most of the data consists of “Yes” / “No” answers to questions from the survey.
  - Among the victimization variables, most common “Yes” answer was to the question ‘Fought school 1+ times 12 months – around 15% of records
  - Among the substance use variables, most common “Yes” answer was to the question ‘Tried marijuana 1+ times in life’ – around 50% of records
  - Among the suicide attempts variables, most common “Yes” answer was to the question ‘Considered suicide 12 months – around 16% of records
  - There are many NA/missing values in the dataset and after omitting these, we got 934 records that could be used for analysis.
  - In the data preparation stage, the following transformations and modifications are done.
  - Combining variables from each category into one variable each for victimization, substance use and suicide attempt
  - Generating data in transaction format to do association analysis

- In the first part of modeling, we used apriori algorithm to identify most common associations between victimization, suicide attempt and substance use. The major findings are:
    - There is association between suicide attempt and substance use at support of 17% and confidence of around 70%, but the association between suicide attempt and victimization is weaker at support of around 12% and confidence of around 49%.
    - The strongest association between individual variables is between qn27 (Considered suicide in last 12 months) and qn47 (Tried marijuana 1+ times in life) at support of around 11% and confidence of around 62%.
- In the second part of modeling, we used decision tree machine learning techniques to automatically segment the class gradeand determine how well these derived groupings correspond to victimization and suicide attempt and predict 'suicide attempt' using the aggregated variables variables 'victimization' and 'substance use' for class 'grade'.

2 Introduction.

2.1 Background.

Health behaviors and experiences related to sexual behavior, high-risk substance use, violence victimization, mental health and suicide contribute to substantial morbidity for adolescents, including risk for HIV, STDs, and teen pregnancy.The Centers for Disease Control and Prevention in the United States monitors rotinely youth health behaviours and experiances by conducting a yearly servuey across the country in clloaboration with schools to help in prevent futture prevention of spread of HIV, drug uses, sexually transmitted diseases, and unintend teen pregnancy in goal to raise awareness and understanding. Collected under the flag of YRBSS system which is developed in 1990 to monitor those risks.From 1991 untill 2013, A total 2.6 million high school student data was collected in more than 1,100 separate surveys. In this paper the anlysis will be performed on 2013 YRBSS Chicago dataset, downloaded from the Centers for Disease Control and Prevention, CRISP-DM methodolgy steps will be followed. R open-source software for report generating, analysis, and to communcate findings.

2.1.1 Overview of CRISP-DM:

CRISP-DM was conceived in 1996 and immature data mining market as a standrized process for data mining projects, The methodolgy provides an overview of the life cycle of a data mining project, In six major steps; Bussniess understanding, Data understanding, Data preparation, Modeling, And Evaluation. According to latest poll (2014) results by https://www.kdnuggets.com/, crisp-dm methodology is still the most popular data mining with 43%, placed by SEMMA by SAS institute, and followed by KDD process.

Why is data mining important?

Data mining is an innovative and potentially powerful business strategy. A great deal of work involves the analysis of large amounts of information in an attempt to discover underlying patterns in a large amount of data. The process is called data mining because data mining is a process that "mining" data to search for patterns. Such techniques can not only find hidden patterns but identify patterns that would be hard to find through traditional data mining methods

Note:

- As per the course requirment deployment step is not included in process.

2.2 Business Challenges.

This case study examines the associations between victimization, substance use, and suicide attempt among youth in Chicago at 2013, challenges are:

- Are there relations between victimization (fighting, bullying, sexual abuse) and substanceuse (Tabaco, alcohol and other drug use)?

- Are there relations between victimization (fighting, bullying, sexual abuse) and suicide attempts?
- Are there relations between substance use (Tabaco, alcohol and other substance use) and suicide attempt?

3 Business Understanding:

3.1 Objective:

The main objective of this project is to examine the associations between victimization, substance use, and suicide attempt among youth using the Youth Health Risk Behavior Survey data for the year 2013. We will be using Apriori (an algorithm for frequent item set mining and association rule learning) and Decision Tree. This study has several addressing association of youth mental health with substance use, suicide attempt, and victimization. Data sample includes only youth, and thus focuses on health related outcomes not limited to substance use, suicide, or victimization. Most importantly, by using a representative sample of youth who were not age-cohorted, The data set will allow for identification of a number of potentially valuable insights.

Using the above mentioned algorithms we are going to answer the following questions:

1. Are there relations between victimization (fighting, bullying, sexual abuse) and suicide attempt?

2. Are there relations between substance use (Tabaco, alcohol and other substance use) and suicide attempt?

3. Apply machine learning techniques to automatically segment the class grade into clusters and determine how well these derived groupings correspond to victimization and suicide attempt.

3.2 Motivation:

Youth suicide is a substantial concern for health professionals, educators, lawmakers and society in general. Researchers have estimated that around 11% of all deaths among 12-19 year olds is due to suicide. It is assumed that there is high association between victimization, substance use and suicide attempt. Studying these associations will help in understanding youth behaviors and reducing adverse events. This type of analysis will also help doctors make decisions after taking into account the risk of suicide among their youth patients with history of victimization and/or substance use.

It is also critical to identify high risk groups who may be more associated with suicide attempt so that targeted preventive measures can be taken. For example, the CDC states that historical suicide rates for teens aged 15-19 years in the US differ significantly between genders.

3.3 Data Description:

The Youth Health Risk Behavior Survey is a biannual study undertaken by UNITED STATE CDC that monitors several categories of health-related behaviors among youth. The survey includes adolescents from grades 9-12 in the age group of 14-19 years. In our analysis, we consider behaviors related to victimization (fighting, bullying, sexual abuse, etc.), substance use (tobacco, alcohol, marijuana, etc.) and suicide attempt (considered suicide, attempted suicide, etc.). The responses of the survey questions are initially processed by the CDC to identify logical inconsistencies, convert responses to usable form, create derived variables from responses, etc. We use a subset of the full data and analyze only demographic, victimization, substance use and suicide attempt information.

3.3.1 About the dataset:

This case study is from the Youth Risk Behavior Survey (YRBS) data which are free for use. (Seen from http://www.cdc.gov/healthyyouth/data/yrbs/data.htm).

4 Data Understanding.

The dataset used in this project consists of Record ID that serves as a unique identifier, 4 demographic variables, 7 victimization variables, 4 suicide attempt variables and 13 substance use variables. The data is provided in csv format.

4.1 Metadata Description.

Here shows a full description of all dataset variables, with detailsfor all variables.

```r
variableDescription <- read.csv('DataDescription.csv', header=TRUE)
pander(head(variableDescription, n=nrow(variableDescription)))
```

Variable	Description	Short.Description
record	Record ID of participant	Record
age	Age of participant	Age
sex	Sex of participant	Sex
grade	Grade in which participant was studying	Grade
race4	Race/ethnicity of participant	Race
qn16	Unsafe at school 1 or more times in the past 30 days	Unsafe
qn17	Threatened at school 1 or more times in the past 12 months	Threatened
qn19	Injured at school 1 or more times in the past 12 months	Injured
qn20	Fought at school 1 or more times in the past 12 months	Fought
qn21	Forced to have sex	ForcedSex
qn24	Bullied 1 or more times in the past 12 months	Builled
qn25	Electronically bullied 1 or more times in the past 12 months	Ebuilled
qn27	Considered suicide in the past 12 months	ConsideredSuicide
qn28	Made suicide plan in the past 12 months	MadeSuicidePlan
qn29	Attempted suicide in the past 12 months	AttemptSuicide
qn30	Suicide attempt with or without injury in the past 12 months	SuicideWithOrWithoutInjury
qn33	Smoked 1 or more times in the past 30 days	SmokedMonth
qn37	Smoked daily for 30 days	SmokedDaily
qn43	Had drinks 1 or more times in the past 30 days	Drinks1+
qn45	Had drinks 10 or more times in the past 30 days	Drinks10+
qn47	Tried marijuana 1 or more times in life	Marijuana1+
qn50	Used cocaine 1 or more times in life	Cocaine1+
qn51	Sniffed glue 1 or more times in life	SniffedGlue1+
qn52	Used heroin 1 or more times in life	Heroin1+
qn53	Used meth 1 or more times in life	Meth1+
qn54	Used ecstasy 1 or more times in life	Ecstasy1+
qn55	Took steroids 1 or more times in life	Steroids1+
qn56	Taken prescription drug without prescription 1 or more times in life	PrescriptionDrug
qn57	Injected drugs 1 or more times in life	InjectedDrugs

4.2 Loading, Retrieving, Viewing Data.

Loading the data from the main source and veiw the 5 occurances from each variable.

```
data <- read.csv("CaseStudy10_YouthHealthRiskBehavior_Data.csv",header = TRUE)
panderOptions('table.split.table', 100)
pander(head(data),caption = "First 5 rows of dataset")
```

Table 2: First 5 rows of dataset (continued below)

record	age	sex	grade	race4	qn16	qn17	qn19	qn20	qn21	qn24	qn25	qn27	qn28	qn29	qn30	qn33	qn37	qn43	qn45	qn47	qn50	qn51	qn52	qn53	qn54	qn55	qn56	qn57
1115896	NA	NA	NA	2	1	1	2	1	NA	NA	2	1	NA	NA	NA	NA	NA	NA	NA	1	NA	1	2	2	2	1	2	2
1115897	NA	NA	4	3	1	2	2	2	2	1	2	1	1	2	2	2	2	1	2	2	2	2	2	2	2	2	1	2
1115898	1	NA	NA	4	1	2	1	1	2	2	2	1	1	NA	NA	NA	1	NA	NA	1	1	1	1	2	1	1	1	2
1115899	2	NA	2	3	NA	1	1	NA	2	NA	2	2	NA	1	2	NA	2	1	2	NA	1	1	1	1	1	1	1	1
1115900	3	NA	3	NA	1	1	1	1	NA	2	2	2	2	2	2	NA	2	2	2	1	2	2	2	2	2	2	2	2
1115901	4	NA	1	3	NA	NA	NA	NA	1	2	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

4.3 Exploratory data analysis.

This section introduce an an exploration to dataset by insvistigating all the variables, and observations, missing and completed rows.

```
# Overview on data structure (Number of observations and cols, type of variables and their values.)
# str(data)
pander(introduce(data), caption = "Describe basic informations of dataset")
```

Table 4: Describe basic informations of dataset (continued below)

rows	columns	discrete_columns	continuous_columns	all_missing_columns	total_missing_values	complete_rows	total_observations	memory_usage
1581	29	0	29	0	1841	934	45849	189816

```
# library(skimr)
# library(kableExtra)
# skim(data) %>% skimr::kable(format = "latex", booktabs = T, caption = "Sample of observations with Em
```

```
#Data Overview With Selected Cols
displayTable <-head(data[2:15], n=2)
```

```
pander(displayTable, caption = "Sample of observations with Empty values")
```

Table 6: Sample of observations with Empty values

age	sex	grade	race4	qn16	qn17	qn19	qn20	qn21	qn24	qn25	qn27	qn28	qn29
NA	NA	NA	2	1	1	2	1	NA	NA	2	1	NA	NA
NA	NA	4	3	1	2	2	2	2	1	2	1	1	2

- Summary:

It is clear that, there are many NA values in the data. that will addresed and preprocessed in the following steps.

4.4 Demographic Variables Description

Description of the factor levels of demographic variables:

In dataset there are 4 demographic variables, grouped as a levels as the below:

- Age: (1= <=12 years old, 2=13 years old, 3=14 years old, 4=15 years old, 5=16 years old, 6=17 years old, 7=18+ years old).
- Sex: (1=Female, 2=Male).
- Race: (1=White, 2=Black/African American, 3=Hispanic/Latino, 4=All other races).
- Grade (1=9th, 2=10th, 3=11th, 4=12th).

Data from the questions are all dichotomous (ordinal) as numerical values with levels “1”, “2”…etc or NA for missing value.

Note:

- Considering “1” corresponds to “Yes” and “2” corresponds to a “No”.

5 Data Preprocessing (Demographics)

This section will implement data cleaning process for all non needed varibles.

5.1 Creating A Custom R Function To Handle Missing Data For Specific/All Observations

This function takes the dataset and the cols to omit the na values

Note:

- This function will used to clean data in two phases, phase (1) will handle the demographic variables, and phase (2) handles the other victimization variables, suicide attempt variables and 13 substance use variables.

```
#This function takes the dataset and the cols to omit the na values
omitNaForSpecificCols <- function(d, desiredCols) {
    completeVec <- complete.cases(d[, desiredCols])
    return(d[completeVec, ])
}
```

5.2 Data Distribution Overview (Demographics).

Here and overview of the dataset cleaned data from any Na observation

- Summary:

New dataset has a 1514 obs. out of 5 demographic variables (age,sex,grade,race), and non empty observations, and levels have been changed into categorical (texts) for analysis in the next steps.

```r
#Takes cols related to Demographic variables
#This will take the range of cols from 2 to 5 i.e(2(age),3(sex),4(grade),5(race))
dataOverview<-data[, 2:5]
dataOverview$sex <- factor(dataOverview$sex, labels = c('Female','Male'), ordered = TRUE)
dataOverview$age <- factor(dataOverview$age, labels = c('<=12','13','14','15','16','17',
                                                        '18+'),ordered = TRUE)
dataOverview$race <- factor(dataOverview$race4, labels = c('White','Black/African American',
                                                           'Hispanic/Latino','All other races')
                            , ordered = TRUE)
dataOverview$grade <- factor(dataOverview$grade, labels = c('9th','10th','11th','12th'),
                             ordered = TRUE)
#Cleaning the data using omitNaForSpecificCols() created above.
dataOverview<- omitNaForSpecificCols(dataOverview,c("sex","age","race","grade"))
#Structure For Manipulated Data
str(dataOverview)
```

```
## 'data.frame':    1514 obs. of  5 variables:
##  $ age  : Ord.factor w/ 7 levels "<=12"<"13"<"14"<..: 1 1 1 3 3 3 3 3 3 3 ...
##  $ sex  : Ord.factor w/ 2 levels "Female"<"Male": 2 2 2 2 2 2 2 2 2 2 ...
##  $ grade: Ord.factor w/ 4 levels "9th"<"10th"<"11th"<..: 2 4 3 1 1 1 1 1 1 1 ...
##  $ race4: int  3 3 4 2 3 2 3 3 2 3 ...
##  $ race : Ord.factor w/ 4 levels "White"<"Black/African American"<..: 3 3 4 2 3 2 3 3 2 3 ...
```

5.3 Data Distribution Overview (Demographics).

Summary of all Demographic variables that shows the level of each variable in dataset

- Note:

NA in this output shows only an empty level eg: "sex variable according to dataset description has only two levels"

```r
#Data Summary
pander(summary(dataOverview), caption = "Data summary table")
```

Table 7: Data summary table

age	sex	grade	race4	race
<=12: 4	Female:866	9th :259	Min. :1.000	White :132
13 : 0	Male :648	10th:374	1st Qu.:2.000	Black/African American:549
14 :106	NA	11th:434	Median :3.000	Hispanic/Latino :705
15 :279	NA	12th:447	Mean :2.548	All other races :128
16 :397	NA	NA	3rd Qu.:3.000	NA
17 :427	NA	NA	Max. :4.000	NA
18+ :301	NA	NA	NA	NA

6 Data Overview (Demographics).

Here shows a sample of dataset after cleaning, and transforming the variables.

```
#Overview On Our Current Dataframe With Demographic Variables Only(As Is)
displayTable<-head(dataOverview[1:4], n=5)
knitr::kable(displayTable, caption = "New demographic variables")
```

Table 8: New demographic variables

	age	sex	grade	race4
15	<=12	Male	10th	3
17	<=12	Male	12th	3
18	<=12	Male	11th	4
19	14	Male	9th	2
20	14	Male	9th	3

7 Statistical Summary Of Grouped Data (Demographics).

Here shows a statistical summary of all grouped demographic variables, this give a meaning how well are our data variables are distributed, and if data set is biased toward a certain varible. A biased dataset in many cases can effect all the anlaysis results and give a non relastic insights.

- Summary:

Sex groups variables are normaly distributed.

Race groups variables are normaly distributed.

Age groups variables are normaly distributed.

Grade groups are skwedtowards 12th, and 11th observations.

Table 9: Sex Groups statistics

sex	count
Male	648
Female	866

Table 10: Race groups statistics

race	count
All other races	128
Hispanic/Latino	705
Black/African American	549
White	132

Table 11: Age groups statistics

age	count
18+	301
17	427

age	count
16	397
15	279
14	106
<=12	4

Table 12: Grade groups statistics

grade	count
12th	447
11th	434
10th	374
9th	259

Table 13: Race/Sex groups statistics

race	sex	count
White	Female	78
White	Male	54
Black/African American	Female	323
Black/African American	Male	226
Hispanic/Latino	Female	398
Hispanic/Latino	Male	307
All other races	Female	67
All other races	Male	61

7.1 Density Distribution (Demographics).

```
cleanedData<-omitNaForSpecificCols(dataOverview, c("sex","race","grade","age"))
par(mfrow=c(2,2))
plot(density(unclass(cleanedData$age)), xlab = "Age",main = "ssksss")
plot(density(unclass(cleanedData$race)), xlab = "Race",main = "")
plot(density(unclass(cleanedData$sex)), xlab = "Sex",main = "")
plot(density(unclass(cleanedData$grade)), xlab = "Grade",main = "")
```

```
#
# DataExplorer::plot_str(cleanedData)
#
# DataExplorer::plot_missing(cleanedData)
#
# DataExplorer::plot_density(cleanedData)
#
# DataExplorer::plot_bar(cleanedData)

library(SmartEDA)
pander(ExpCTable(cleanedData))
```

Variable	Valid	Frequency	Percent	CumPercent
age	<=12	4	0.26	0.26

Variable	Valid	Frequency	Percent	CumPercent
age	14	106	7	7.26
age	15	279	18.43	25.69
age	16	397	26.22	51.91
age	17	427	28.2	80.11
age	18+	301	19.88	99.99
age	TOTAL	1514	NA	NA
sex	Female	866	57.2	57.2
sex	Male	648	42.8	100
sex	TOTAL	1514	NA	NA
grade	10th	374	24.7	24.7
grade	11th	434	28.67	53.37
grade	12th	447	29.52	82.89
grade	9th	259	17.11	100
grade	TOTAL	1514	NA	NA
race	All other races	128	8.45	8.45
race	Black/African American	549	36.26	44.71
race	Hispanic/Latino	705	46.57	91.28
race	White	132	8.72	100
race	TOTAL	1514	NA	NA

```
pander(ExpData(data, type = 2))
```

S.no	Variable Name	Variable Type	% of Missing	No. of Unique values
1	record	integer	0	1581
2	age	integer	0	8
3	sex	integer	0.01	3
4	grade	integer	0.01	5
5	race4	integer	0.03	5
6	qn16	integer	0.02	3
7	qn17	integer	0	3
8	qn19	integer	0.01	3
9	qn20	integer	0.01	3
10	qn21	integer	0.01	3
11	qn24	integer	0.01	3
12	qn25	integer	0.01	3
13	qn27	integer	0.02	3
14	qn28	integer	0.02	3
15	qn29	integer	0.17	3
16	qn30	integer	0.17	3
17	qn33	integer	0.08	3
18	qn37	integer	0.06	3
19	qn43	integer	0.15	3
20	qn45	integer	0.12	3
21	qn47	integer	0.06	3
22	qn50	integer	0.02	3
23	qn51	integer	0.02	3
24	qn52	integer	0.03	3
25	qn53	integer	0.02	3
26	qn54	integer	0.02	3
27	qn55	integer	0.02	3
28	qn56	integer	0.02	3

S.no	Variable Name	Variable Type	% of Missing	No. of Unique values
29	qn57	integer	0.03	3

```r
DataExplorer::plot_density(data[,c("sex","grade","age","race4")], ncol = 2L)
```

```r
# skim(data)
```

7.2 Demographic Details(Age,Race,Sex & Grade) of Respondents

```r
cleanedData<-omitNaForSpecificCols(dataOverview, c("sex","race","grade","age"))
#RESPONDENTS BY GENDER
plot1<-ggplot(data = cleanedData, aes(x = sex,fill =sex)) +
        ggtitle("RESPONDENTS BY GENDER") +
        labs(x = "GENDER", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)

#RESPONDENTS BY AGE
cleanedData<-omitNaForSpecificCols(dataOverview, c("age"))
plot2<-ggplot(data =cleanedData, aes(x = age, fill =age)) +
        ggtitle("RESPONDENTS BY AGE") +
        labs(x = "Age(Years)", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)

#Respondents by Grade
cleanedData<-omitNaForSpecificCols(dataOverview, c("grade"))
plot3<- ggplot(data = cleanedData,
           aes(x = grade, fill = grade)) +
        ggtitle("Respondents by Grade") +
        geom_bar(alpha = 0.7
                     , col = 'black')

#RESPONDENTS BY RACE
cleanedData<-omitNaForSpecificCols(dataOverview, c("race"))
plot4<-ggplot(data = cleanedData, aes(x = race,fill =race)) +
        ggtitle("RESPONDENTS BY RACE") +
        labs(x = "RACE", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)  +
          theme(axis.title.x=element_blank(),
                axis.text.x=element_blank())


#RESPONDENTS BY AGE  & GENDER
cleanedData<-omitNaForSpecificCols(dataOverview, c("age","sex"))
plot5<-ggplot(data = cleanedData, aes(x = age,fill =sex)) +
        ggtitle("RESPONDENTS BY AGE  & GENDER") +
        labs(x = "Age(Years)", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)

#RESPONDENTS BY GRADE & RACE
cleanedData<-omitNaForSpecificCols(dataOverview, c("race","grade"))
plot6<-ggplot(cleanedData, aes(x = grade,fill =race)) +
        ggtitle("RESPONDENTS BY GRADE & RACE") +
```

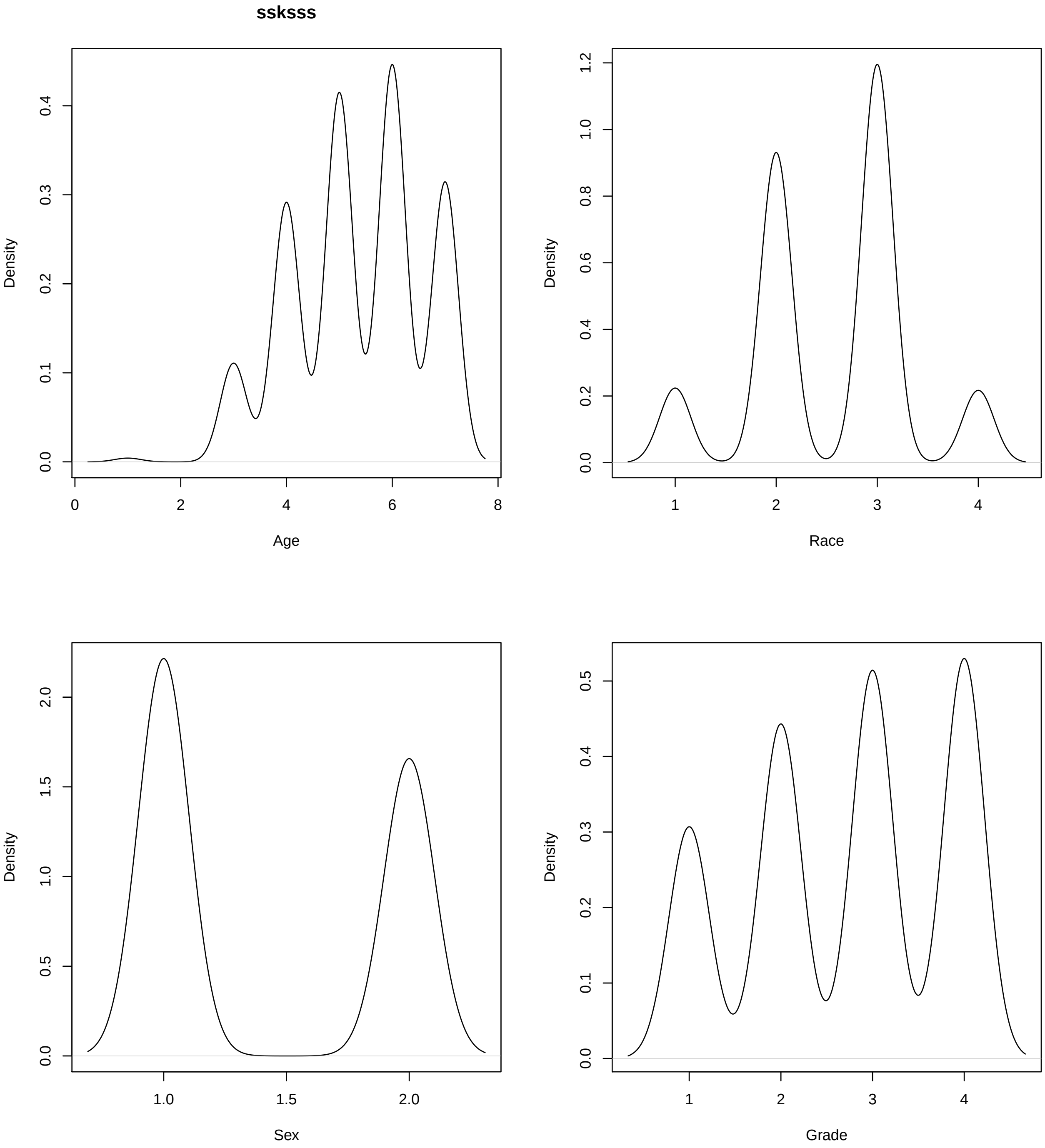


Figure 2: Density plot

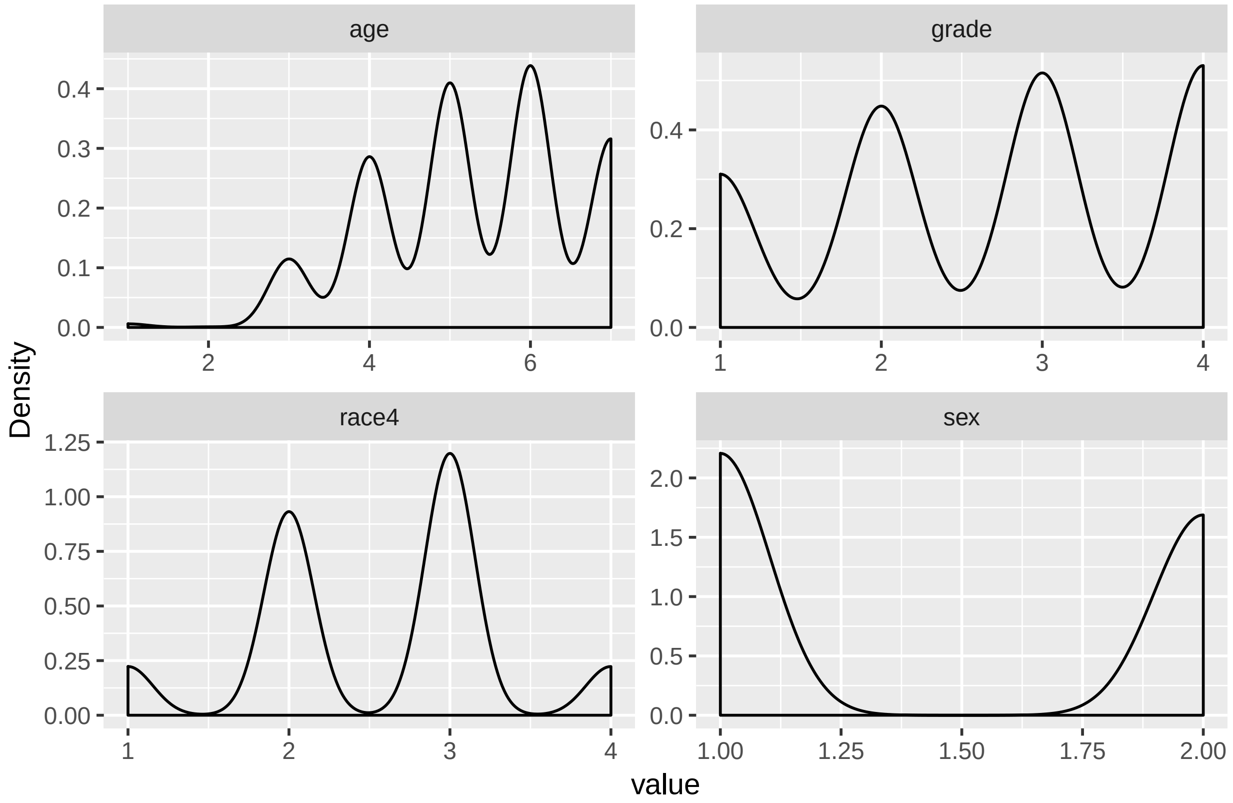
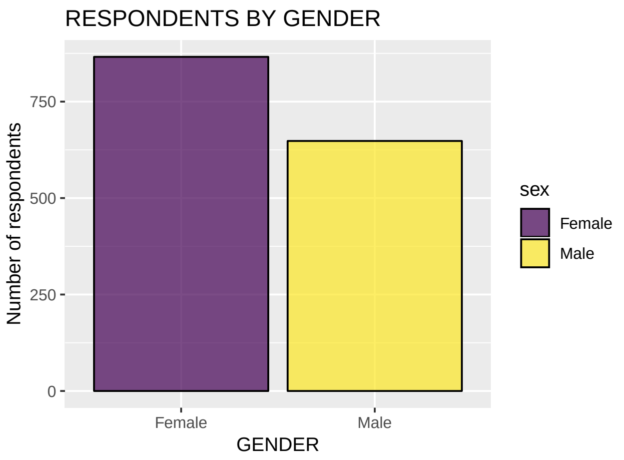
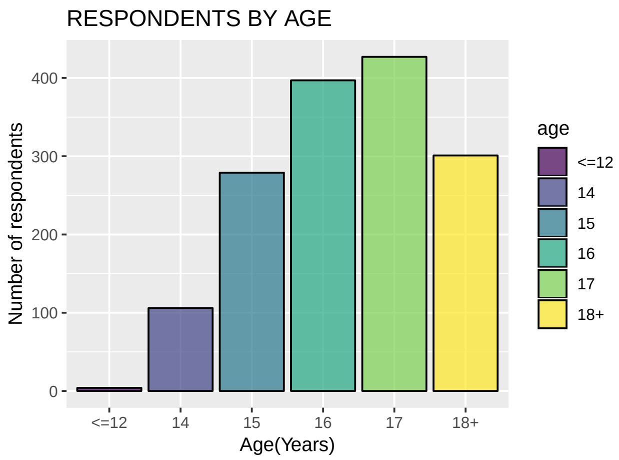
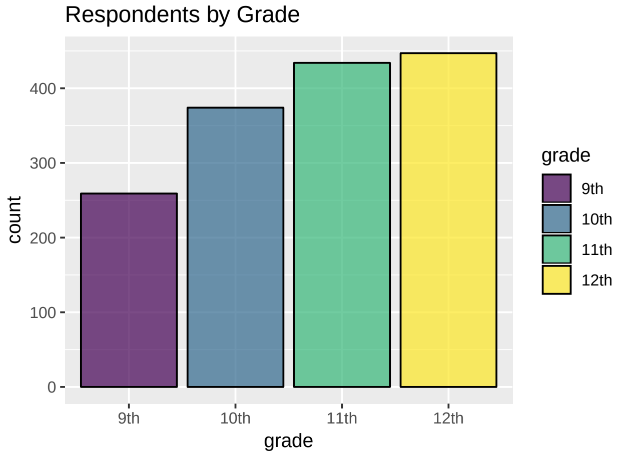


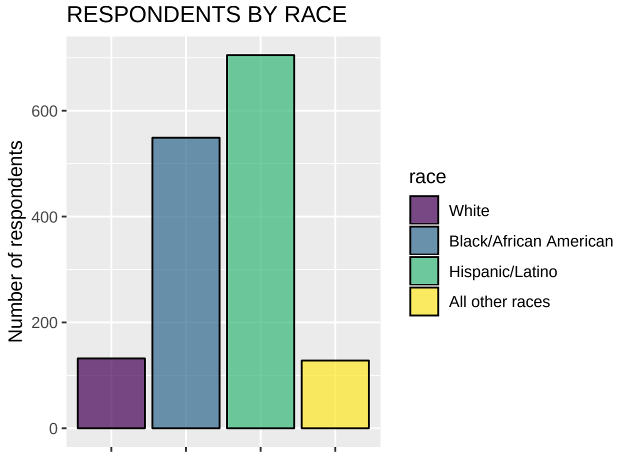
Figure 3: Density plot

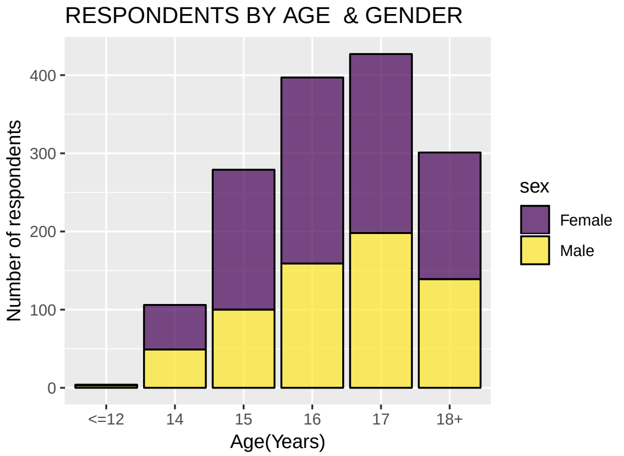
```
        labs(x = "RACE", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)



#RESPONDENTS BY RACE & GENDER
cleanedData<-omitNaForSpecificCols(dataOverview, c("sex","race"))
plot7<-ggplot(data = cleanedData, aes(x = age,fill =sex)) +
        ggtitle("RESPONDENTS BY RACE  & GENDER") +
        labs(x = "Age(Years)", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)

#RESPONDENTS BY GENDER & GRADE
cleanedData<-omitNaForSpecificCols(dataOverview, c("sex","grade"))
plot8<-ggplot(data = cleanedData, aes(x = age,fill =sex)) +
        ggtitle("RESPONDENTS BY GENDER  & GRADE") +
        labs(x = "Age(Years)", y = "Number of respondents") +
        geom_bar(alpha = 0.7, col = 'black',show.legend = TRUE)

grid.arrange(plot1,plot2,plot3,plot4,plot5,plot6, ncol=2)
```

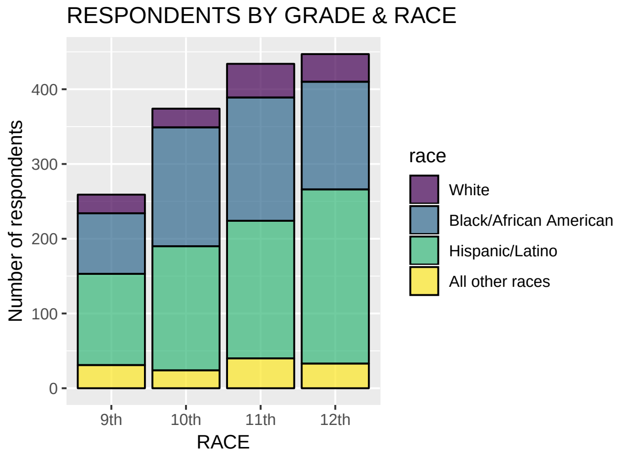

RESPONDENTS BY GENDER


RESPONDENTS BY AGE


Respondents by Grade


RESPONDENTS BY RACE

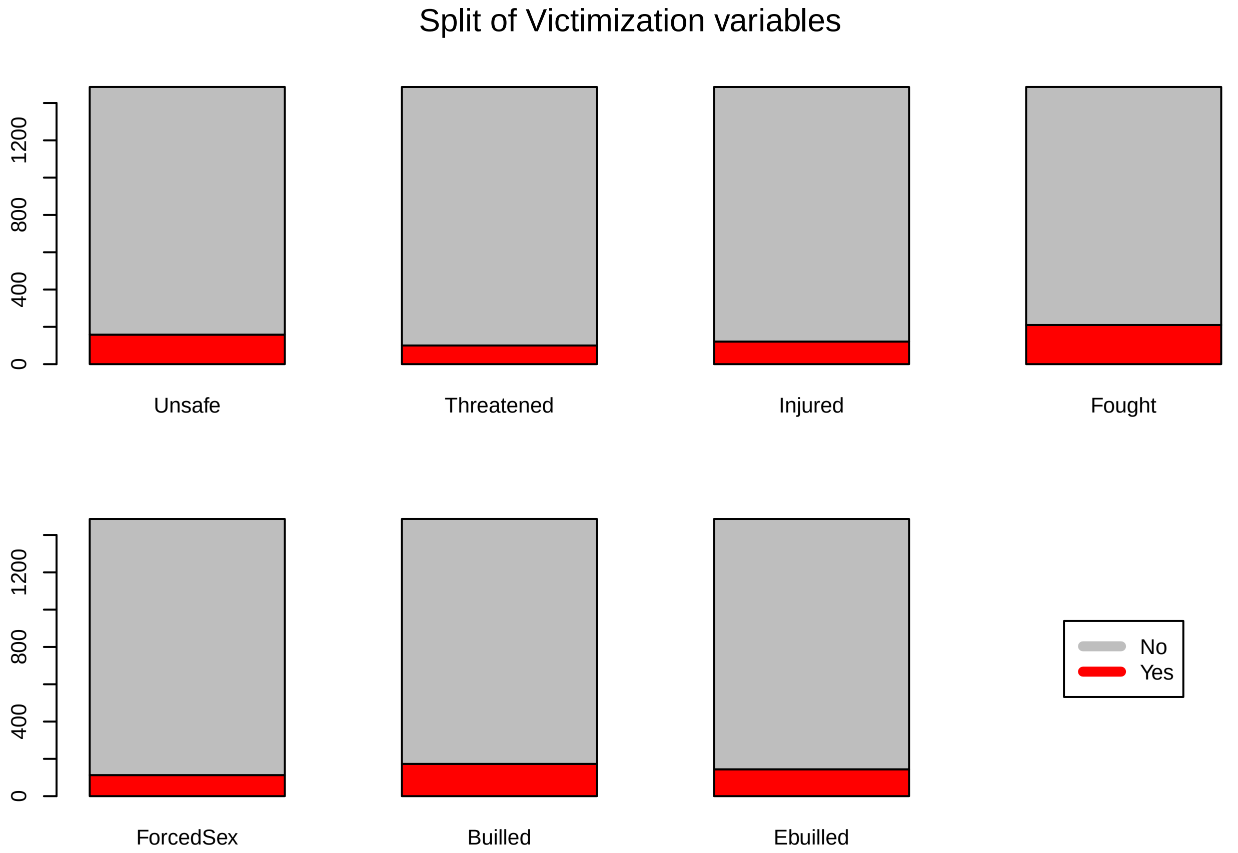

RESPONDENTS BY AGE & GENDER


RESPONDENTS BY GRADE & RACE

7.3 Victimization Proportion For The Given Data

```r
cleanedData<-omitNaForSpecificCols(data, c("qn16","qn17","qn19","qn20","qn21","qn24","qn25"))
par(mfrow=c(2,4), mgp=c(1,2,1), mar=c(2,3,4,1))
barplot(as.matrix(table(cleanedData$qn16)), xlab = 'Unsafe', col = c("red", "grey"))
barplot(as.matrix(table(cleanedData$qn17)), xlab = 'Threatened', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn19)), xlab = 'Injured', col = c("red", "grey"),
        axes=FALSE)
```

```
barplot(as.matrix(table(cleanedData$qn20)), xlab = 'Fought', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn21)), xlab = 'ForcedSex', col = c("red", "grey"))
barplot(as.matrix(table(cleanedData$qn24)), xlab = 'Builled', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn25)), xlab = 'Ebuilled', col = c("red", "grey"),
        axes=FALSE)
plot(1, type = "n", axes=FALSE, xlab="", ylab="")
legend(x="center", inset=1, legend=c("No", "Yes"), col=c("grey", "red"), lwd=5, cex=1)
mtext("Split of Victimization variables", side = 3, outer = TRUE, line=-2)
```



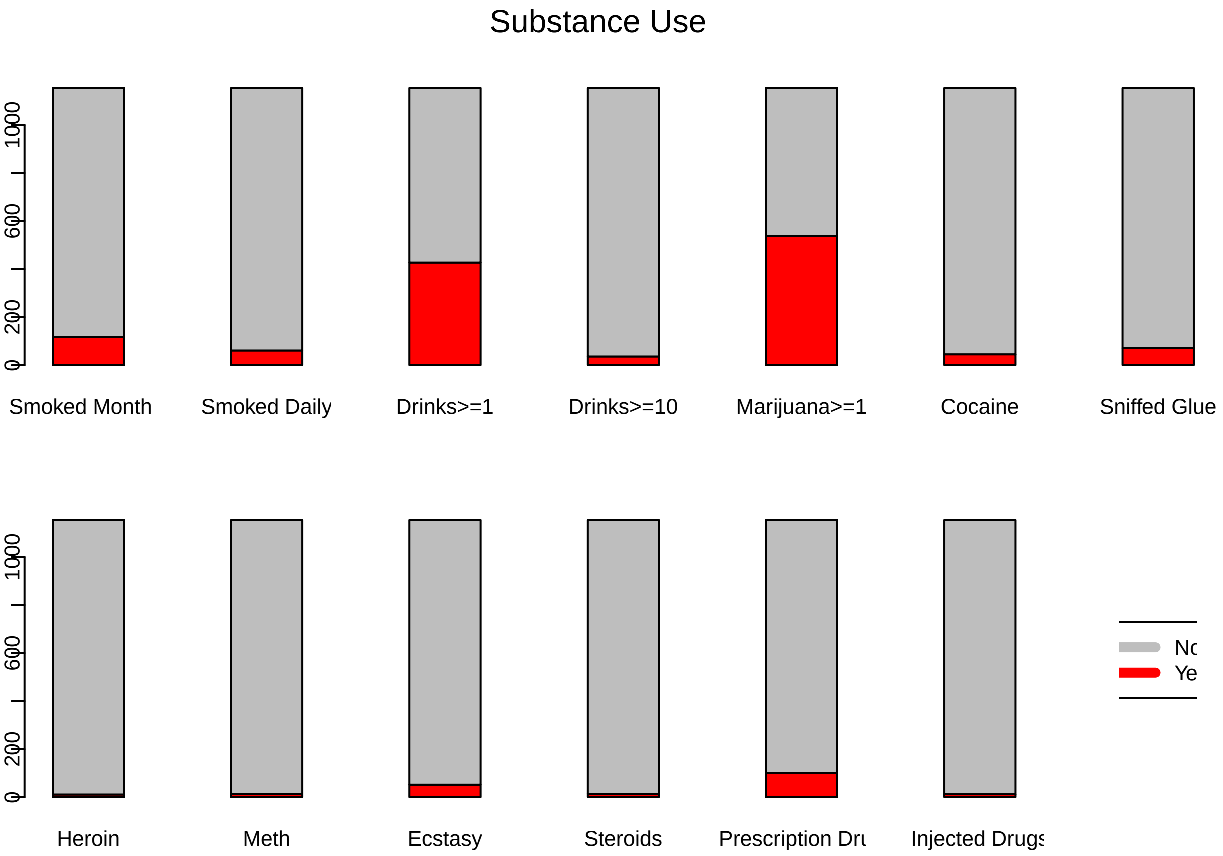
Victimization's highest percentage are:

1. Fought school 1+ times 12 months : around 15%
2. Missed school b/c unsafe 1+ 30 days : around 12%
3. Bullied at school 12 months : around 12%

7.4 Substance Use Proportion For The Given Data

```
cleanedData<-omitNaForSpecificCols(data, c("qn33","qn37","qn43","qn45","qn47","qn50","qn51",
                                          "qn52","qn53","qn54","qn55","qn56","qn57"))
par(mfrow=c(2,7), mgp=c(1,1,1), mar=c(2,3,4,1))
barplot(as.matrix(table(cleanedData$qn33)), xlab = 'Smoked Monthly', col = c("red", "grey"))
barplot(as.matrix(table(cleanedData$qn37)), xlab = 'Smoked Daily', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn43)), xlab = 'Drinks>=1', col = c("red", "grey"),
        axes=FALSE)
```

```
barplot(as.matrix(table(cleanedData$qn45)), xlab = 'Drinks>=10', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn47)), xlab = 'Marijuana>=1', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn50)), xlab = 'Cocaine', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn51)), xlab = 'Sniffed Glue', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn52)), xlab = 'Heroin', col = c("red", "grey"))
barplot(as.matrix(table(cleanedData$qn53)), xlab = 'Meth', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn54)), xlab = 'Ecstasy', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn55)), xlab = 'Steroids', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn56)), xlab = 'Prescription Drug', col = c("red", "grey"),
        axes=FALSE)
barplot(as.matrix(table(cleanedData$qn57)), xlab = 'Injected Drugs', col = c("red", "grey"),
        axes=FALSE)

plot(1, type = "n", axes=FALSE, xlab="", ylab="")
legend(x="center", inset=1, legend=c("No", "Yes"), col=c("grey", "red"), lwd=5, cex=1)
mtext("Substance Use", side = 3, outer = TRUE, line=-2)
```



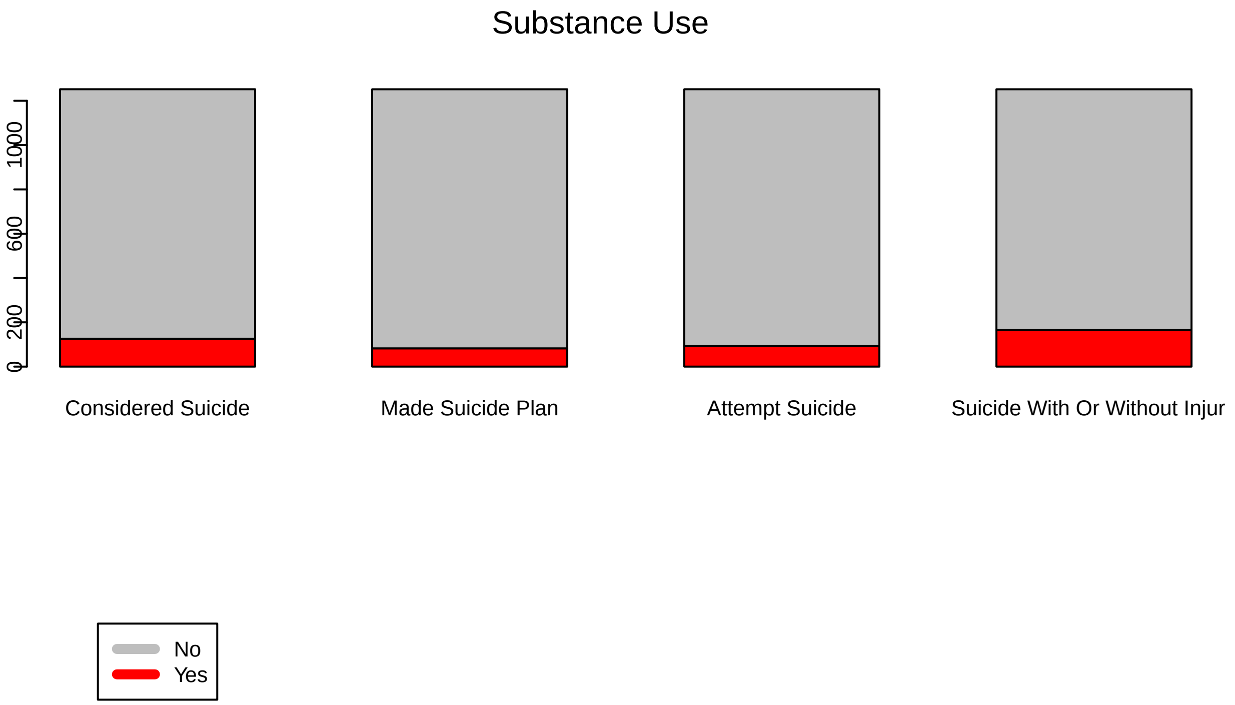
Substance use highest percentage are:

1. Tried marijuana 1+ times in life : around 50%

2. Had 1+ drinks past 30 days : around 39%

7.5 Suicide Attempts Proportion For The Given Data

```
cleanedData<-omitNaForSpecificCols(data, c("qn27","qn28","qn29","qn30"))
par(mfrow=c(2,4), mgp=c(1,1,1), mar=c(2,3,4,1))
barplot(as.matrix(table(cleanedData$qn16)), xlab = 'Considered Suicide',
        col = c("red", "grey"))
barplot(as.matrix(table(cleanedData$qn17)), xlab = 'Made Suicide Plan',
        col = c("red", "grey"), axes=FALSE)
barplot(as.matrix(table(cleanedData$qn19)), xlab = 'Attempt Suicide',
        col = c("red", "grey"), axes=FALSE)
barplot(as.matrix(table(cleanedData$qn20)), xlab = 'Suicide With Or Without Injury',
        col = c("red", "grey"),
        axes=FALSE)
plot(1, type = "n", axes=FALSE, xlab="", ylab="")
legend(x="center", inset=1, legend=c("No", "Yes"), col=c("grey", "red"), lwd=5, cex=1)
mtext("Substance Use", side = 3, outer = TRUE, line=-2)
```



Suicide attempts highest percentage are:

1. Considered suicide 12 month : around 16%
2. Made suicide plan 12 moonth : around 14%

8 Data Preparation

In the above section, we noticed that there are many NA values in the data. We check the number of missing values in each field using the following:

```
    sapply(data, function(x) sum(is.na(x)))
```

```
## record    age    sex  grade  race4   qn16   qn17   qn19   qn20   qn21
##      0      4     12     23     44     38      6     11     12     23
##   qn24   qn25   qn27   qn28   qn29   qn30   qn33   qn37   qn43   qn45
##     23     14     24     36    270    271    130     96    239    191
##   qn47   qn50   qn51   qn52   qn53   qn54   qn55   qn56   qn57
##     90     33     36     40     36     39     31     28     41
```

Question 29, question 30 and question 43 have the most NA values. These are 'Attempted suicide 1+ times 12 months, 'Suicide attempt with injury 12 months and 'Had 1+ drinks past 30 days'.

8.1 Creating A Custom R Function To Handle Missing Data For Specific/All Observations

This function takes the dataset and the cols to omit the na values

```
omitNaForSpecificCols <- function(d, desiredCols) {
    completeVec <- complete.cases(d[, desiredCols])
    return(d[completeVec, ])
}
```

8.2 Cleaning The Data Using "omitNaForSpecificCols" Custom Function

```
#Clean the overall data since we are going to use all variables except demographic
dataCleaned<-omitNaForSpecificCols(data[0:29])

#Confirm that, there is no missing values
sapply(dataCleaned, function(x) sum(is.na(x)))
```

```
## record    age    sex  grade  race4   qn16   qn17   qn19   qn20   qn21
##      0      0      0      0      0      0      0      0      0      0
##   qn24   qn25   qn27   qn28   qn29   qn30   qn33   qn37   qn43   qn45
##      0      0      0      0      0      0      0      0      0      0
##   qn47   qn50   qn51   qn52   qn53   qn54   qn55   qn56   qn57
##      0      0      0      0      0      0      0      0      0
```

```
#View brief details of the cleaned data

displayTable<- head(dataCleaned[1:3,2:10])
knitr::kable(displayTable)
```

	age	sex	grade	race4	qn16	qn17	qn19	qn20	qn21
15	1	2	2	3	2	2	2	2	2
20	3	2	1	3	1	2	1	2	2
22	3	2	1	3	2	2	2	2	2

8.3 Data Aggregation

In this section, we also do some data transformations that will help in analysis and modeling. Specifically, we do the following:

1. Combine variables for victimization, suicide and substance use into one variable each.
2. Convert the clean data into transaction format to do association analysis The above steps are performed below.

```
# Initializing three aggregated columns for victimization,substance use and suicide attempt
dataCleaned$victimization <- ""
dataCleaned$substanceUse <- ""
dataCleaned$suicideAttempt <- ""

#Initializing descriptive headings for our dataset

headings<-c("Record","Age","Sex","Grade","Race","Unsafe","Threatened","Injured",
            "Fought","ForcedSex","Builled","Ebuilled","ConsideredSuicide",
            "MadeSuicidePlan","AttemptSuicide","SuicideWithOrWithoutInjury",
            "SmokedMonth","SmokedDaily","Drinks1+","Drinks10+","Marijuana1+",
            "Cocaine1+","SniffedGlue1+","Heroin1+","Meth1+","Ecstasy1+","Steroids1+",
            "PrescriptionDrug","InjectedDrugs","victimization","substanceUse"
            ,"suicideAttempt")


#Adding a descriptive headings for our data
colnames(dataCleaned)=headings

#Combining variables into one for victimization, substance use and suicide attempt:

#Get Victimization related variables from the dataset
victimizationVariables<-colnames(dataCleaned[6:12])
#View the headings
head(victimizationVariables)
```

```
## [1] "Unsafe"     "Threatened" "Injured"    "Fought"     "ForcedSex"
## [6] "Builled"
```

```
#Convert 1 and 2 row values to 0 and 1, in order to represent Yes or No
dataCleaned$victimization <- apply(dataCleaned[,c(victimizationVariables)], 1,
                                   function(r) ifelse(any(r %in% c("1")),1,0))


#Get Substance use related variables from the dataset
substanceVariables<-colnames(dataCleaned[17:29])
#View the headings
head(substanceVariables)
```

```
## [1] "SmokedMonth" "SmokedDaily" "Drinks1+"    "Drinks10+"   "Marijuana1+"
## [6] "Cocaine1+"
```

```
#Convert 1 and 2 row values to 0 and 1, in order to represent Yes or No
dataCleaned$substanceUse <- apply(dataCleaned[,c(substanceVariables)], 1,
                                  function(r) ifelse(any(r %in% c("1")),1,0))


#Get Suicide related variables from the dataset
```

```
suicideVariables<-colnames(dataCleaned[13:16])
#View the headings
head(suicideVariables)
```

```
## [1] "ConsideredSuicide"          "MadeSuicidePlan"
## [3] "AttemptSuicide"             "SuicideWithOrWithoutInjury"
```

```
#Convert 1 and 2 row values to 0 and 1, in order to represent Yes or No
dataCleaned$suicideAttempt <- apply(dataCleaned[,c(suicideVariables)], 1,
                                    function(r) ifelse(any(r %in% c("1")),1,0))

#View brief details of aggregated data
displayTable<-head(dataCleaned[30:32], n=5)
knitr::kable(displayTable)
```

	victimization	substanceUse	suicideAttempt
15	0	1	0
20	1	0	1
22	0	1	0
23	0	1	0
25	0	0	0

```
#Generating data in transaction format to do association rules analysis
dataCleanedAggregatedTransactions <- data.frame(record=character(), qn=character(),
                                                stringsAsFactors=FALSE)
for (i in 1:nrow(dataCleaned)){
    #Here we use data from index 30:32 which is our aggregated cols
    for (j in (ncol(dataCleaned)-2):ncol(dataCleaned)){
        if (dataCleaned[i,j]==1){
            temp <- data.frame(record=as.character(dataCleaned[i,1]),
                               qn=as.character(colnames(dataCleaned)[j]),
                               stringsAsFactors = FALSE)
            dataCleanedAggregatedTransactions <- rbind(dataCleanedAggregatedTransactions, temp)
        }
    }
}

dataCleanedAggregatedTransactions <-
    as(split(dataCleanedAggregatedTransactions[,"qn"],
             dataCleanedAggregatedTransactions[,"record"]), "transactions")
# Viewing summary of the generated data
summary(dataCleanedAggregatedTransactions)
```

```
## transactions as itemMatrix in sparse format with
##  672 rows (elements/itemsets/transactions) and
##  3 columns (items) and a density of 0.5128968
##
## most frequent items:
##   substanceUse  victimization suicideAttempt        (Other)
##            558            312            164              0
##
## element (itemset/transaction) length distribution:
## sizes
##   1   2   3
## 369 244  59
##
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   1.539   2.000   3.000
##
## includes extended item information - examples:
##           labels
## 1   substanceUse
## 2 suicideAttempt
## 3  victimization
##
## includes extended transaction information - examples:
##   transactionID
## 1       1115910
## 2       1115915
## 3       1115917
```

```r
crossTable(dataCleanedAggregatedTransactions)
```

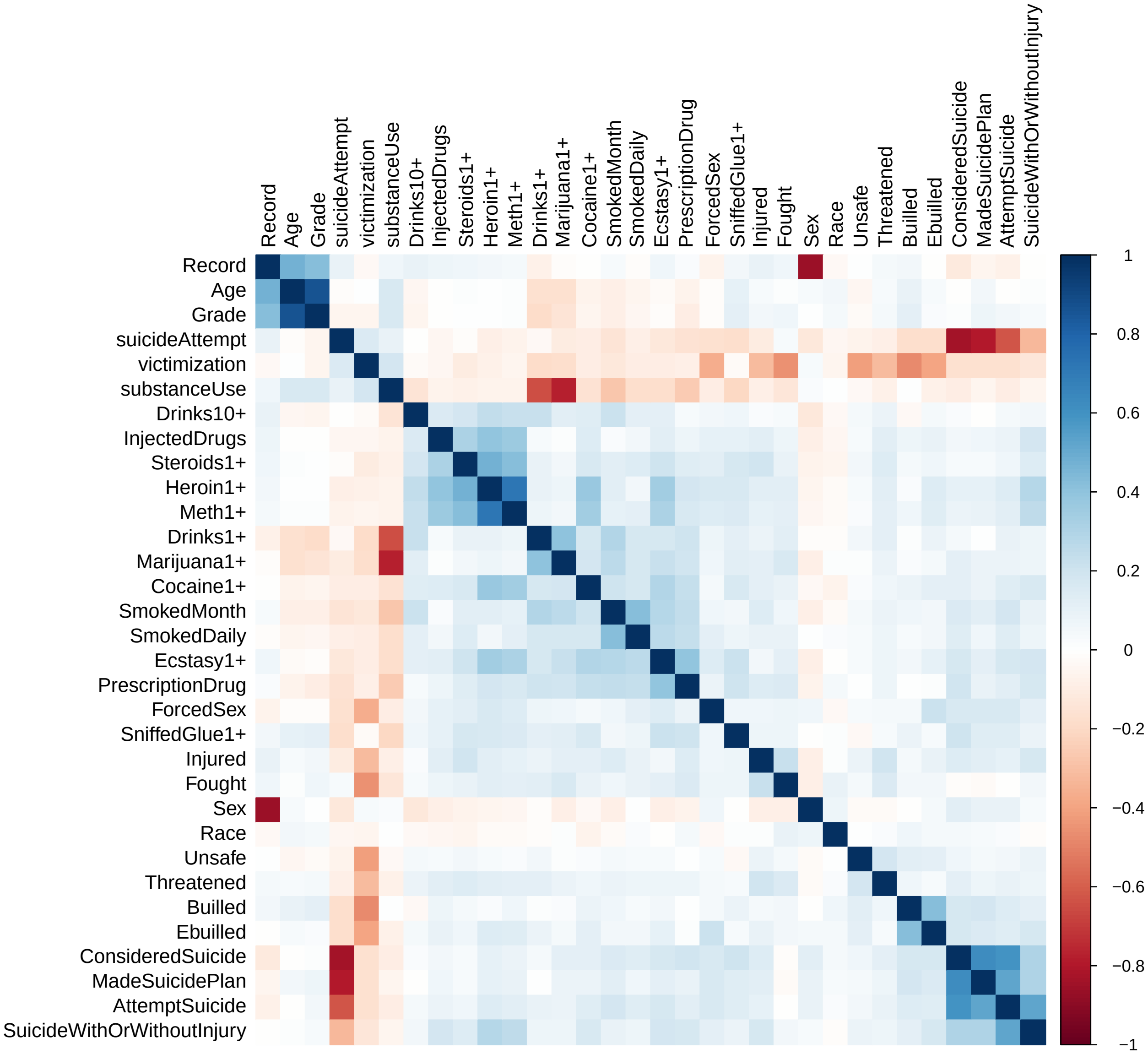
```
##                 substanceUse suicideAttempt victimization
## substanceUse             558            114           226
## suicideAttempt           114            164            81
## victimization            226             81           312
```

```r
#Generating data in transaction format to do association rules analysis for all items
dataCleanedTransactions <- data.frame(record=character(), qn=character(),
                                      stringsAsFactors=FALSE)
for (i in 1:nrow(dataCleaned)){
    #Here we start from index 6, excluding our demographic data
    for (j in 6:(ncol(dataCleaned)-3)){
        if (dataCleaned[i,j]=='1'){
            temp <- data.frame(record=as.character(dataCleaned[i,1]),
                               qn=as.character(colnames(dataCleaned)[j]),
                               stringsAsFactors = FALSE)
            dataCleanedTransactions <- rbind(dataCleanedTransactions, temp)
        }
    }
}

dataCleanedTransactions <- as(split(dataCleanedTransactions[,"qn"],
                                    dataCleanedTransactions[,"record"]), "transactions")
summary(dataCleanedTransactions)
```

```
## transactions as itemMatrix in sparse format with
##  672 rows (elements/itemsets/transactions) and
##  24 columns (items) and a density of 0.1229539
##
## most frequent items:
##       Marijuana1+          Drinks1+ ConsideredSuicide   MadeSuicidePlan
##               438               354               120               110
##           Builled           (Other)
##                94               867
##
## element (itemset/transaction) length distribution:
```

```
## sizes
##   1   2   3   4   5   6   7   8   9  10  12  13  20  24 
## 200 165 119  71  31  34  21  15   9   1   1   3   1   1 
## 
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   1.000   1.000   2.000   2.951   4.000  24.000 
## 
## includes extended item information - examples:
##           labels
## 1 AttemptSuicide
## 2        Builled
## 3      Cocaine1+
## 
## includes extended transaction information - examples:
##   transactionID
## 1       1115910
## 2       1115915
## 3       1115917
```

```
# corr <- cor(dataCleaned, method = "spearman")

#corplot <- colorRampPalette(c("#BB4444", "#EE9988", "#FFFFFF", "#77AADD", "#4477AA"))
corrplot(cor(dataCleaned, method = "spearman")
         ,method="color", order="hclust",
         tl.col="black", tl.srt=90)
```



```
# source of using spearman correlation
# https://www.statisticssolutions.com/wp-content/uploads/wp-post-to-pdf-enhanced-cache/1/correlation-pe
```

9 Modeling

9.1 Association Rules Algorithms(Apriori & Eclat)

9.1.1 Generate Association Rules For All Itemsets Without Aggregation(Victimization,Substance & Suicide)

```r
#Getting frequent k-itemsets using eclat
eclatRules <- eclat(dataCleanedTransactions, parameter = list(supp = 0.1,minlen=2))
```

```
## Eclat
##
## parameter specification:
##  tidLists support minlen maxlen            target   ext
##     FALSE     0.1      2     10 frequent itemsets FALSE
##
## algorithmic control:
##  sparse sort verbose
##       7   -2    TRUE
##
## Absolute minimum support count: 67
##
## create itemset ...
## set transactions ...[24 item(s), 672 transaction(s)] done [0.00s].
## sorting and recoding items ... [11 item(s)] done [0.00s].
## creating bit matrix ... [11 row(s), 672 column(s)] done [0.00s].
## writing  ... [5 set(s)] done [0.00s].
## Creating S4 object  ... done [0.00s].
```

```r
#inding strong association rules apriori
aprioriRules <- apriori(dataCleanedTransactions, parameter = list(supp=0.1,
                                                                  minlen=2,confidence = 0.2))
```

```
## Apriori
##
## Parameter specification:
##  confidence minval smax arem  aval originalSupport maxtime support minlen
##         0.2    0.1    1 none FALSE            TRUE       5     0.1      2
##  maxlen target   ext
##      10  rules FALSE
##
## Algorithmic control:
##  filter tree heap memopt load sort verbose
##     0.1 TRUE TRUE  FALSE TRUE    2    TRUE
##
## Absolute minimum support count: 67
##
## set item appearances ...[0 item(s)] done [0.00s].
## set transactions ...[24 item(s), 672 transaction(s)] done [0.00s].
## sorting and recoding items ... [11 item(s)] done [0.00s].
## creating transaction tree ... done [0.00s].
## checking subsets of size 1 2 3 done [0.00s].
## writing ... [8 rule(s)] done [0.00s].
## creating S4 object  ... done [0.00s].
```

```
#Remove deplicate itemsets if you are using apriori(lhs,rhs)
aprioriRules<-aprioriRules[-(which(duplicated(
    generatingItemsets(aprioriRules))))]


#Inspect the association rules generated apriori
inspect(aprioriRules)
```

```
##     lhs                    rhs                support   confidence
## [1] {SmokedMonth}       => {Drinks1+}          0.1116071 0.8064516
## [2] {SmokedMonth}       => {Marijuana1+}       0.1205357 0.8709677
## [3] {MadeSuicidePlan}   => {ConsideredSuicide} 0.1145833 0.7000000
## [4] {ConsideredSuicide} => {Marijuana1+}       0.1101190 0.6166667
## [5] {Drinks1+}          => {Marijuana1+}       0.3839286 0.7288136
##     lift      count
## [1] 1.5308912  75
## [2] 1.3362793  81
## [3] 3.9200000  77
## [4] 0.9461187  74
## [5] 1.1181797 258
```

```
#Inspect the association rules generated eclat
inspect(eclatRules)
```

```
##     items                               support   count
## [1] {Marijuana1+,SmokedMonth}           0.1205357  81
## [2] {Drinks1+,SmokedMonth}              0.1116071  75
## [3] {ConsideredSuicide,MadeSuicidePlan} 0.1145833  77
## [4] {ConsideredSuicide,Marijuana1+}     0.1101190  74
## [5] {Drinks1+,Marijuana1+}              0.3839286 258
```

9.1.2 Generate For All Itemsets With Aggregation(Victimization,Substance & Suicide)

```
# Getting frequent k-itemsets
eclatRules <- eclat(dataCleanedAggregatedTransactions, parameter = list(supp = 0.1,minlen=2))
```

```
## Eclat
##
## parameter specification:
##  tidLists support minlen maxlen            target   ext
##     FALSE     0.1      2     10 frequent itemsets FALSE
##
## algorithmic control:
##  sparse sort verbose
##       7   -2    TRUE
##
## Absolute minimum support count: 67
##
## create itemset ...
## set transactions ...[3 item(s), 672 transaction(s)] done [0.00s].
## sorting and recoding items ... [3 item(s)] done [0.00s].
## creating bit matrix ... [3 row(s), 672 column(s)] done [0.00s].
## writing  ... [3 set(s)] done [0.00s].
## Creating S4 object  ... done [0.00s].
```

```
# Finding strong association rules
aprioriAggregatedRules <- apriori(dataCleanedAggregatedTransactions, parameter =
                                    list(supp=0.1, minlen=2,  conf=0.2))
```

```
## Apriori
##
## Parameter specification:
##  confidence minval smax arem  aval originalSupport maxtime support minlen
##         0.2    0.1    1 none FALSE            TRUE       5     0.1      2
##  maxlen target   ext
##      10  rules FALSE
##
## Algorithmic control:
##  filter tree heap memopt load sort verbose
##     0.1 TRUE TRUE  FALSE TRUE    2    TRUE
##
## Absolute minimum support count: 67
##
## set item appearances ...[0 item(s)] done [0.00s].
## set transactions ...[3 item(s), 672 transaction(s)] done [0.00s].
## sorting and recoding items ... [3 item(s)] done [0.00s].
## creating transaction tree ... done [0.00s].
## checking subsets of size 1 2 3 done [0.00s].
## writing ... [6 rule(s)] done [0.00s].
## creating S4 object  ... done [0.00s].
```

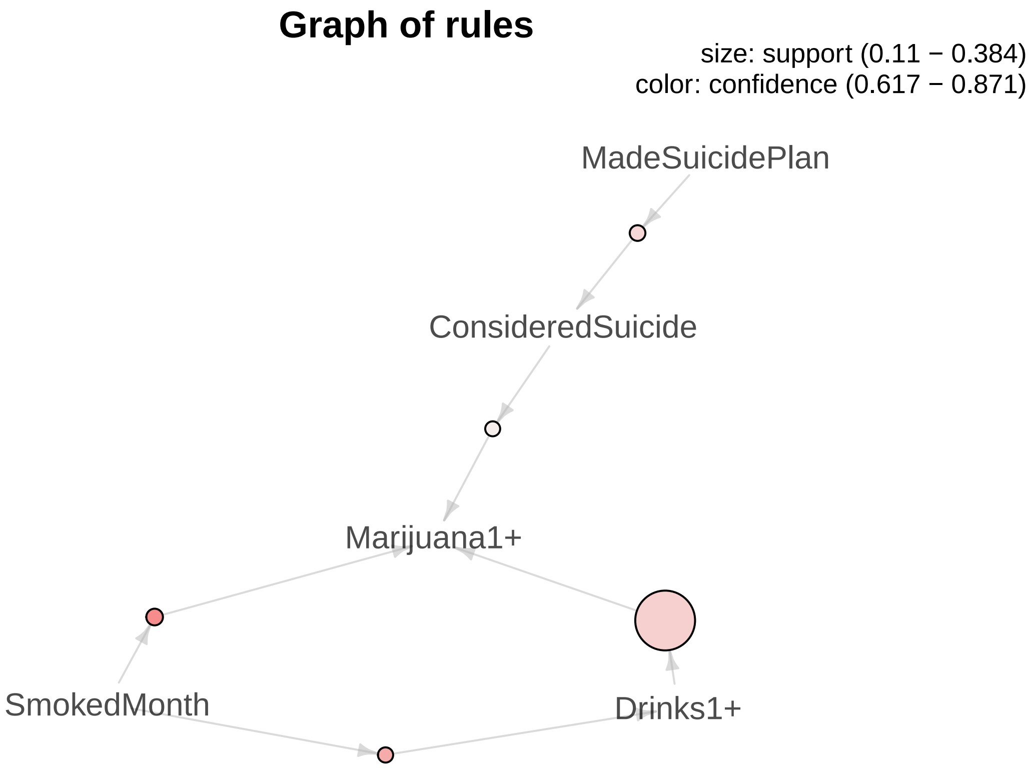
```
#Remove deplicate itemsets if you are using apriori(lhs,rhs)
aprioriAggregatedRules<-aprioriAggregatedRules[-(which(duplicated(
    generatingItemsets(aprioriRules))))]

#Inspect the association rules generated apriori
inspect(aprioriAggregatedRules)
```

```
#Inspect the association rules generated eclat
inspect(eclatRules)
```

```
##     items                           support   count
## [1] {substanceUse,suicideAttempt}   0.1696429 114
## [2] {suicideAttempt,victimization} 0.1205357  81
## [3] {substanceUse,victimization}   0.3363095 226
```

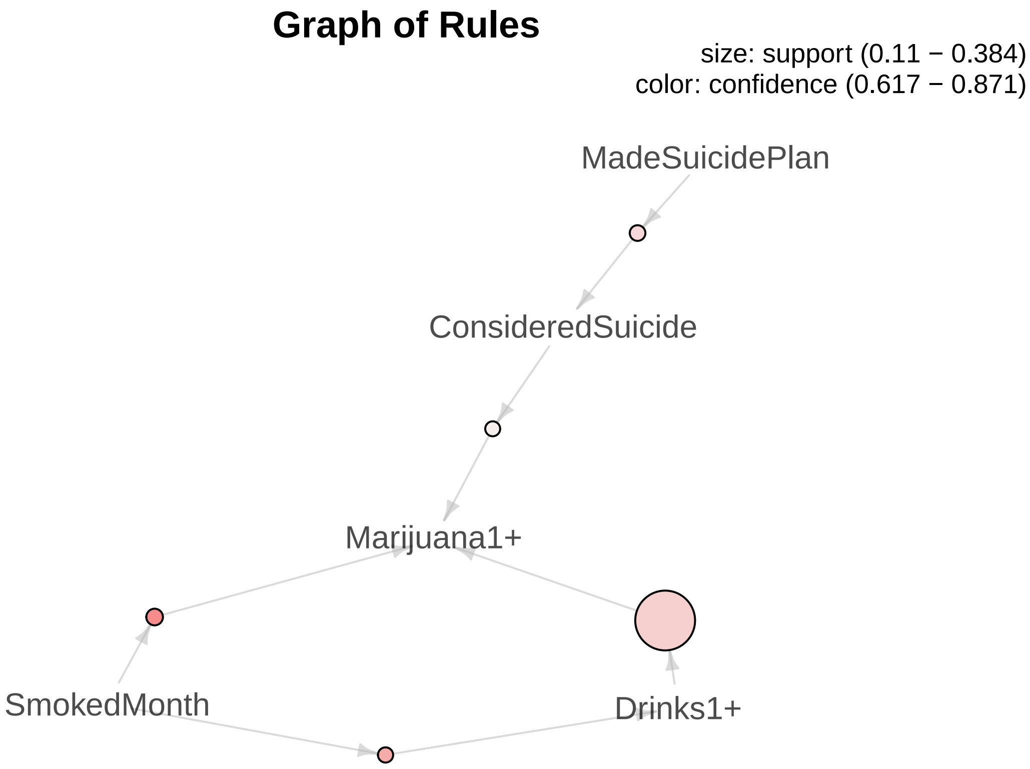
9.1.3 Graphing The Strong Association Rules Without Aggregation(Victimization,Substance & Suicide)

```
#Graph of association rules for all items for minimum support of 0.1
#and minimum confidence of 0.2
set.seed(1234)
plot(aprioriRules, method='graph', shading='confidence',
     control=list(main="Graph of rules"))
```



9.1.4 Graphing The Strong Association Rules With Aggregation(Victimization,Substance & Suicide)

```
#Graph of association rules Aggregating(Victimization,Substance & Suicide)
#for minimum support of 0.1 and minimum confidence of 0.2
set.seed(1234)
plot(aprioriRules, method='graph', shading='confidence',
     control=list(main="Graph of Rules"))
```



```
# The association between suicide attempt and substance use is stronger
#than the association between suicide attempt and victimization
```

9.2 Decision Tree

Apply machine learning techniques to automatically segment the class grade and determine how well these derived groupings correspond to victimization and suicide attempt

9.2.1 Viewing the structure of the observations for class grade and it's relation with victimization and suicide attempts

```
# Decision Tree to predict suicide attempt
dtData <- dataCleaned[,c("Grade", "substanceUse", "victimization", "suicideAttempt")]
dtData$substanceUse <- as.factor(dtData$substanceUse)
dtData$victimization <- as.factor(dtData$victimization)
dtData$suicideAttempt <- as.factor(dtData$suicideAttempt)
str(dtData)
```

```
## 'data.frame':    934 obs. of  4 variables:
##  $ Grade         : int  2 1 1 1 1 1 1 1 1 1 ...
##  $ substanceUse  : Factor w/ 2 levels "0","1": 2 1 2 2 1 1 1 1 2 2 ...
##  $ victimization : Factor w/ 2 levels "0","1": 1 2 1 1 1 1 1 1 1 1 ...
##  $ suicideAttempt: Factor w/ 2 levels "0","1": 1 2 1 1 1 1 1 1 1 1 ...
```

```
#View brief details of aggregated data

displayTable<-head(dtData[,c("Grade","substanceUse", "victimization", "suicideAttempt")],
                   n=10)
knitr::kable(displayTable)
```

	Grade	substanceUse	victimization	suicideAttempt
15	2	1	0	0
20	1	0	1	1
22	1	1	0	0
23	1	1	0	0
25	1	0	0	0
26	1	0	0	0
27	1	0	0	0
28	1	0	0	0
29	1	1	0	0
30	1	1	0	0

9.2.2 Create Train and Test Samples

```
# Create train and test datasets
set.seed(1234)
#Here we are creating two samples(Training(80%) & Test(20%))
sdata<- sample(2, nrow(dtData), replace=TRUE, prob = c(0.8,0.2))
trainData <- dtData[sdata==1,]
#View dimension for our train data
dim(trainData)
```

```
## [1] 740   4
```

```
testData <- dtData[sdata==2,]
#View dimension for our test data
dim(testData)
```

```
## [1] 194   4
```

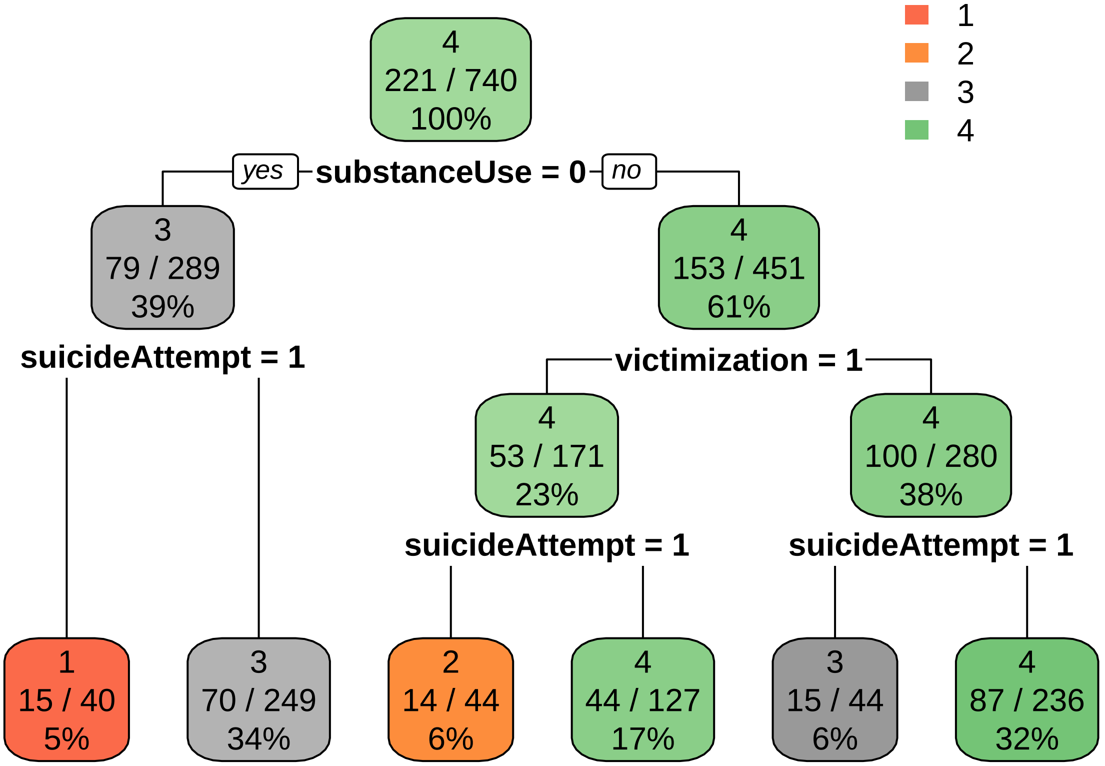
9.2.3 Create Model For Recursive Partitioning and Regression Tree

```
#Create A Model
dtModel<-rpart(Grade~substanceUse+victimization+suicideAttempt,trainData,method = "class",
           control=rpart.control(minsplit=20, minbucket=1, cp = 0.001))

#View the tree
dtModel
```

```
## n= 740
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
##  1) root 740 519 4 (0.17432432 0.23648649 0.29054054 0.29864865)
##    2) substanceUse=0 289 210 3 (0.25605536 0.23529412 0.27335640 0.23529412)
##      4) suicideAttempt=1 40  25 1 (0.37500000 0.17500000 0.22500000 0.22500000) *
##      5) suicideAttempt=0 249 179 3 (0.23694779 0.24497992 0.28112450 0.23694779) *
##    3) substanceUse=1 451 298 4 (0.12195122 0.23725055 0.30155211 0.33924612)
##      6) victimization=1 171 118 4 (0.18128655 0.23976608 0.26900585 0.30994152)
##       12) suicideAttempt=1 44  30 2 (0.15909091 0.31818182 0.31818182 0.20454545) *
##       13) suicideAttempt=0 127  83 4 (0.18897638 0.21259843 0.25196850 0.34645669) *
##      7) victimization=0 280 180 4 (0.08571429 0.23571429 0.32142857 0.35714286)
##       14) suicideAttempt=1 44  29 3 (0.11363636 0.25000000 0.34090909 0.29545455) *
##        15) suicideAttempt=0 236 149 4 (0.08050847 0.23305085 0.31779661 0.36864407) *
```

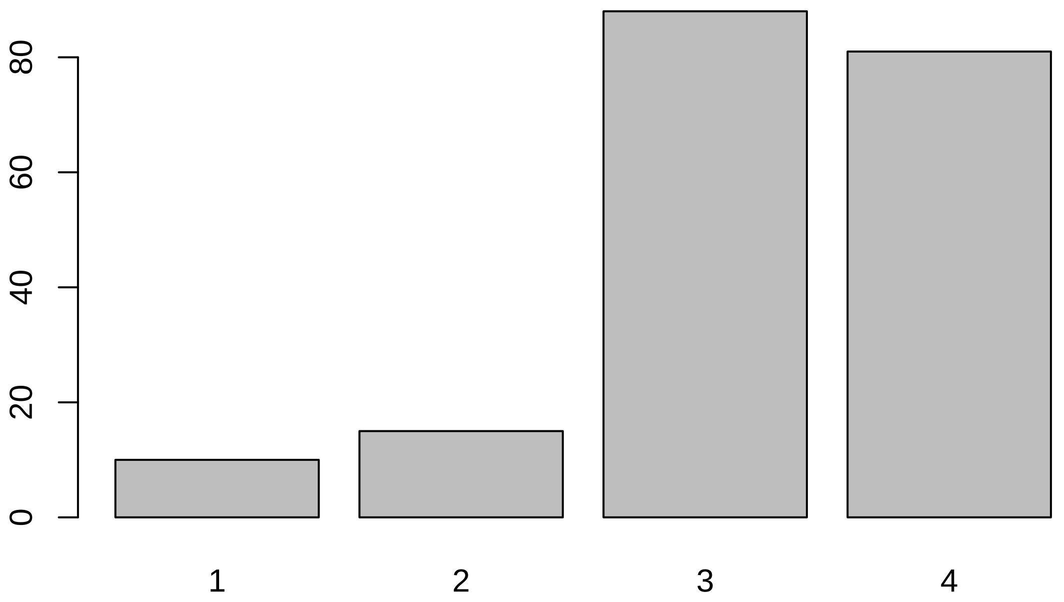
9.2.4 Visualization Model Decision Tree Based On Training Data

```
#Visualization of decision tree
rpart.plot(dtModel,type =2, extra=102)
```



9.2.5 Creating Prediction Model

```
#Creating prediction model
pModel<-rpart.predict(dtModel, testData, type = "class")

plot(pModel)
```



```r
#View the prediction model
```

```r
#Show the table of the results
table(testData[,4], pModel)
```

```
##    pModel
##      1  2  3  4
##   0  0  0 77 81
##   1 10 15 11  0
```

9.2.6 Create additional model based o

```r
# #Create A Model
# dtModel<-rpart(Grade~substanceUse+victimization+suicideAttempt,trainData,method = "class",
#             control=rpart.control(minsplit=20, minbucket=1, cp = 0.001))
# #View the tree
# library(OneR)
# oner_Model<-rpart(Grade~substanceUse+victimization+suicideAttempt,trainData,method = "class",
#             control=rpart.control(minsplit=20, minbucket=1, cp = 0.001))
# summary(oner_Model)
# prediction_r <- predict(model, data)
# eval_model(prediction_r, data)
```

10 Conclusion

In this project, we studied the Youth Health Risk Behavior using the Observational Data to examine the relations between victimization, substance use and suicide attempt. We used the apriori algorithm to understand strong associations and built a decision tree to understand what influences suicide attempt. The results of this project tells us that adolescents who consider or attempt suicide tend to use substances. By assessing whether an adolescent was victimized and by looking at their sex, it is possible to predict if they are more likely to consider or attempt suicide. This type of analysis is very important from a medical point of view. It provides a data supported backing of what doctors seem to already believe through experience. This also shows the importance of using machine learning techniques to answer key questions and find solutions in society. Overall, we were successful in identifying associations between victimization, substance use and suicide attempt. We can further improve this project by experimenting with other algorithms like logistic regression and random forest and by considering other types of groupings like race.

11 References

- [AS94] R. Agrawal and R. Srikant, Fast Algorithms for Mining Association Rules (1994) Proc. 20th Int. Conf. Very Large Data Bases, VLDB-94. http://www.vldb.org/conf/1994/P487.PDF

12 Appendices

12.1 Load Required Libraries

```
#install.packages("dplyr")
#install.packages("dplyr")
#install.packages("arules")
#install.packages("arulesViz")
#library(knitr)
#library(arulesViz)
#library(arules)
#library(arules)
#library(arulesViz)
#library(data.table)
#library(ggplot2)
#library(ggrepel)
#library(plotly)
#library(dplyr)
#require(graphics)
#require(gridExtra)
#library(arules)
#library(arulesViz)
#library(party)
#library(rpart)
#library(rpart.plot)
#library(viridisLite)
```

12.1.1 Session Information.

Listing Machine been used for the project, operating system, R version, And used libraries with their versions for future repreducbility of the project.

```
#leaded machine and R session informatiion
#session_info
#utils:::print.sessionInfo(sessionInfo()[-7]) # thanks @r2evans
#session_info_compact
pander(sessionInfo(), compact = TRUE)
```

R version 3.6.0 (2019-04-26)

Platform: x86_64-apple-darwin15.6.0 (64-bit)

locale: en_US.UTF-8||en_US.UTF-8||en_US.UTF-8||C||en_US.UTF-8||en_US.UTF-8

attached base packages: *stats4*, *grid*, *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *SmartEDA(v.0.3.2)*, *DataExplorer(v.0.8.0)*, *pander(v.0.6.3)*, *corrplot(v.0.84)*, *knitr(v.1.23)*, *viridisLite(v.0.3.0)*, *rpart.plot(v.3.0.7)*, *rpart(v.4.1-15)*, *party(v.1.3-3)*, *strucchange(v.1.5-1)*, *sandwich(v.2.5-1)*, *zoo(v.1.8-6)*, *modeltools(v.0.2-22)*, *mvtnorm(v.1.0-11)*, *gridExtra(v.2.3)*, *ggrepel(v.0.8.1)*, *data.table(v.1.12.2)*, *arulesViz(v.1.3-3)*, *arules(v.1.6-3)*, *Matrix(v.1.2-17)*, *forcats(v.0.4.0)*, *stringr(v.1.4.0)*, *dplyr(v.0.8.1)*, *purrr(v.0.3.2)*, *readr(v.1.3.1)*, *tidyr(v.0.8.3)*, *tibble(v.2.1.3)*, *ggplot2(v.3.1.1)* and *tidyverse(v.1.2.1)*

loaded via a namespace (and not attached): *nlme(v.3.1-139)*, *bitops(v.1.0-6)*, *matrixStats(v.0.54.0)*, *lubridate(v.1.7.4)*, *RColorBrewer(v.1.1-2)*, *httr(v.1.4.0)*, *tools(v.3.6.0)*, *backports(v.1.1.4)*, *R6(v.2.4.0)*, *DT(v.0.6)*, *KernSmooth(v.2.23-15)*, *lazyeval(v.0.2.2)*, *colorspace(v.1.4-1)*, *withr(v.2.1.2)*, *GGally(v.1.4.0)*, *tidyselect(v.0.2.5)*, *compiler(v.3.6.0)*, *cli(v.1.1.0)*, *rvest(v.0.3.4)*, *TSP(v.1.1-7)*, *xml2(v.1.2.0)*, *plotly(v.4.9.0)*, *labeling(v.0.3)*, *caTools(v.1.17.1.2)*, *scales(v.1.0.0)*, *lmtest(v.0.9-37)*, *digest(v.0.6.19)*, *rmarkdown(v.1.13)*, *pkgconfig(v.2.0.2)*, *htmltools(v.0.3.6)*, *highr(v.0.8)*, *htmlwidgets(v.1.3)*, *rlang(v.0.4.0)*, *readxl(v.1.3.1)*, *rstudioapi(v.0.10)*, *visNetwork(v.2.0.7)*, *generics(v.0.0.2)*, *jsonlite(v.1.6)*, *gtools(v.3.8.1)*, *dendextend(v.1.12.0)*, *magrittr(v.1.5)*, *Rcpp(v.1.0.1)*, *munsell(v.0.5.0)*, *viridis(v.0.5.1)*, *multcomp(v.1.4-10)*, *scatterplot3d(v.0.3-41)*, *stringi(v.1.4.3)*, *yaml(v.2.2.0)*, *MASS(v.7.3-51.4)*, *gplots(v.3.0.1.1)*, *plyr(v.1.8.4)*, *parallel(v.3.6.0)*, *gdata(v.2.18.0)*, *crayon(v.1.3.4)*, *lattice(v.0.20-38)*, *haven(v.2.1.0)*, *splines(v.3.6.0)*, *hms(v.0.4.2)*, *pillar(v.1.4.1)*, *igraph(v.1.2.4.1)*, *lpSolve(v.5.6.13.3)*, *codetools(v.0.2-16)*, *glue(v.1.3.1)*, *gclus(v.1.3.2)*, *evaluate(v.0.14)*, *modelr(v.0.1.4)*, *vcd(v.1.4-4)*, *foreach(v.1.4.4)*, *networkD3(v.0.4)*, *cellranger(v.1.1.0)*, *gtable(v.0.3.0)*, *reshape(v.0.8.8)*, *assertthat(v.0.2.1)*, *xfun(v.0.7)*, *coin(v.1.3-0)*, *libcoin(v.1.0-4)*, *broom(v.0.5.2)*, *survival(v.2.44-1.1)*, *seriation(v.1.2-6)*, *iterators(v.1.0.10)*, *registry(v.0.5-1)*, *cluster(v.2.0.8)*, *TH.data(v.1.0-10)* and *sampling(v.2.8)*