

# Exploratory Data Analysis for ASD-Toddler dataset

## Dataset

Autism Spectrum Disorder for Toddlers

## Description

Use for Autism Screening contributed by Dr. Fadi Fayez.

UCI: [https://archive.ics.uci.edu/ml/datasets/Autistic+Spectrum+Disorder+Screening+Data+for+Children+](https://archive.ics.uci.edu/ml/datasets/Autistic+Spectrum+Disorder+Screening+Data+for+Children)  
+

(this is not the exact dataset rather related with same variable descriptors but differentiates with the dimensionality)

Use funModeling package developed by Pablo Casas

## Problem:

Use Supervised Learning Techniques such as rule-based classifiers to predict the outcome of a categorical variable “Class” on whether a toddler is positively labelled with Autism traits or not.

## Start of EDA

```
# Install Required Packages  
#install.packages("tidyverse", repos = "http://cran.us.r-project.org")  
#install.packages("funModeling", repos = "http://cran.us.r-project.org") # EDA tool  
#install.packages("Hmisc", repos = "http://cran.us.r-project.org") # gives an overview of all the  
#variables in tabular format  
#install.packages("FREQ", repos = "http://cran.us.r-project.org")
```

```
library(knitr)  
library(funModeling)
```

```
## Loading required package: Hmisc  
## Loading required package: lattice  
## Loading required package: survival  
## Loading required package: Formula  
## Loading required package: ggplot2  
##  
## Attaching package: 'Hmisc'  
## The following objects are masked from 'package:base':  
##  
##      format.pval, units
```

```
## funModeling v.1.6.8 :)
## Examples and tutorials at livebook.datascienceheroes.com

library(Hmisc)
library(FREQ)

##
## Attaching package: 'FREQ'

## The following object is masked from 'package:funModeling':
##
##      freq

library(tibble)

# load asd toddler dataset
asd <- read.csv("/Users/rmph/Desktop/Projects - current/Project ADA.A/dataset/toddler.csv")

# Start Profiling Categorical Variables
# Report missing values, descriptive statistics
describe(asd) # numerical and categorical profiling (quantitative)
```

```
## asd
##
## 18 Variables      1054 Observations
## -----
## A1
##      n missing distinct    Info    Sum    Mean    Gmd
##    1054      0         2    0.738    594    0.5636    0.4924
##
## -----
## A2
##      n missing distinct    Info    Sum    Mean    Gmd
##    1054      0         2    0.742    473    0.4488    0.4952
##
## -----
## A3
##      n missing distinct    Info    Sum    Mean    Gmd
##    1054      0         2    0.721    423    0.4013    0.481
##
## -----
## A4
##      n missing distinct    Info    Sum    Mean    Gmd
##    1054      0         2    0.75     540    0.5123    0.5002
##
## -----
## A5
##      n missing distinct    Info    Sum    Mean    Gmd
##    1054      0         2    0.748    553    0.5247    0.4993
##
## -----
## A6
##      n missing distinct    Info    Sum    Mean    Gmd
##    1054      0         2    0.732    608    0.5769    0.4887
##
## -----
```

```

## A7
##      n missing distinct      Info      Sum      Mean      Gmd
##    1054         0         2    0.683      685    0.6499    0.4555
##
## -----
## A8
##      n missing distinct      Info      Sum      Mean      Gmd
##    1054         0         2    0.745      484    0.4592    0.4971
##
## -----
## A9
##      n missing distinct      Info      Sum      Mean      Gmd
##    1054         0         2    0.75       516    0.4896    0.5003
##
## -----
## A10
##      n missing distinct      Info      Sum      Mean      Gmd
##    1054         0         2    0.728      618    0.5863    0.4856
##
## -----
## Age_Mons
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    1054         0         25    0.971     27.87    8.859      12      15
##      .25      .50      .75      .90      .95
##      23       30       36       36       36
##
## lowest : 12 13 14 15 16, highest: 32 33 34 35 36
## -----
## Score
##      n missing distinct      Info      Mean      Gmd      .05      .10
##    1054         0         11    0.991     5.213    3.338        0        1
##      .25      .50      .75      .90      .95
##      3        5        8        9       10
##
## Value      0      1      2      3      4      5      6      7      8      9
## Frequency   54     88     88     96    110    120     96    135     97     95
## Proportion 0.051 0.083 0.083 0.091 0.104 0.114 0.091 0.128 0.092 0.090
##
## Value      10
## Frequency   75
## Proportion 0.071
## -----
## Sex
##      n missing distinct
##    1054         0         2
##
## Value      f      m
## Frequency   319    735
## Proportion 0.303 0.697
## -----
## Ethnicity
##      n missing distinct
##    1054         0         11
##

```

```

## asian (299, 0.284), black (53, 0.050), Hispanic (40, 0.038), Latino (26,
## 0.025), middle eastern (188, 0.178), mixed (8, 0.008), Native Indian (3,
## 0.003), Others (35, 0.033), Pacifica (8, 0.008), south asian (60, 0.057),
## White European (334, 0.317)
## -----
## Jauundice
##      n missing distinct
## 1054      0          2
##
## Value      no  yes
## Frequency  766  288
## Proportion 0.727 0.273
## -----
## Family_ASD
##      n missing distinct
## 1054      0          2
##
## Value      no  yes
## Frequency  884  170
## Proportion 0.839 0.161
## -----
## Who.completed.the.test
##      n missing distinct
## 1054      0          5
##
## family member (1018, 0.966), Health care professional (5, 0.005), Health
## Care Professional (24, 0.023), Others (3, 0.003), Self (4, 0.004)
## -----
## Class
##      n missing distinct
## 1054      0          2
##
## Value      No  Yes
## Frequency  326  728
## Proportion 0.309 0.691
## -----

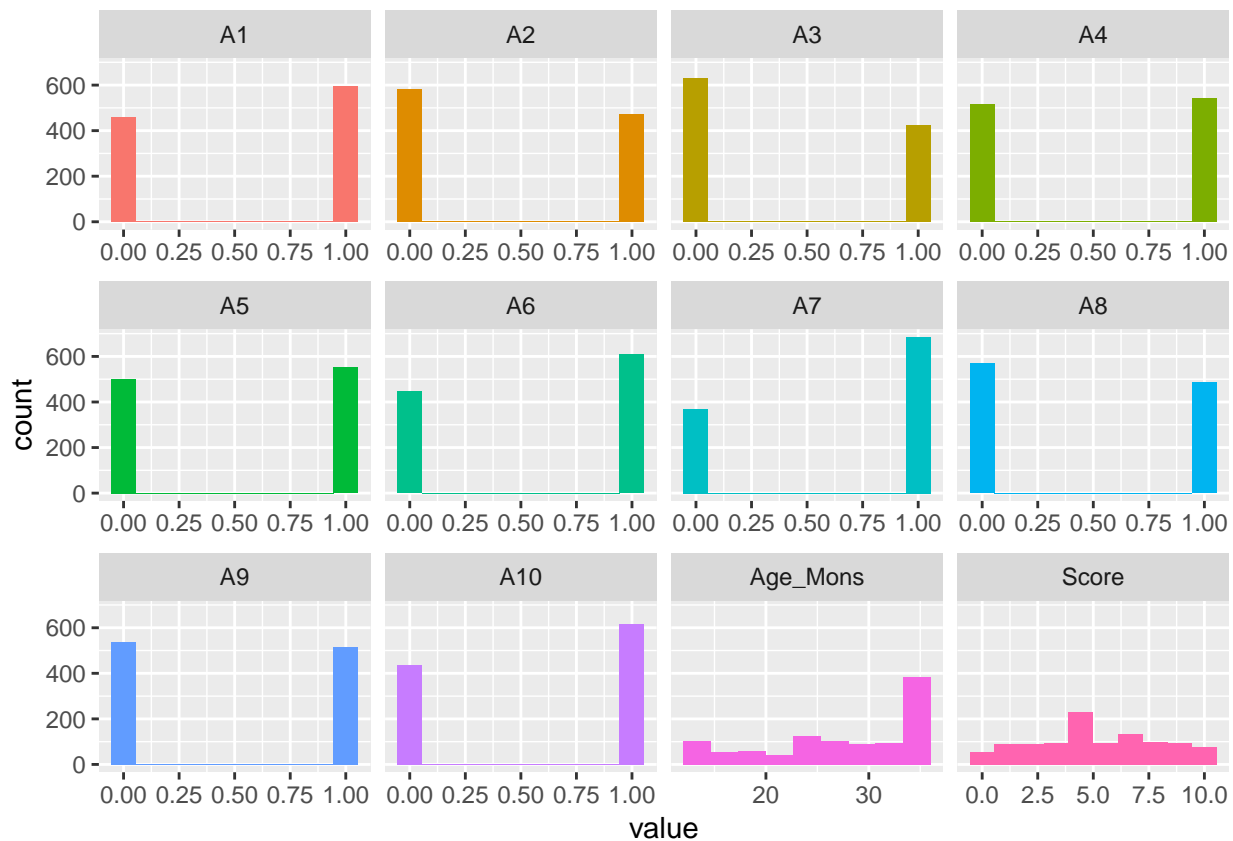
```

## Visualisation for Toddler-Dataset

```

#freq(asd) # categorical variable profiling (quantitative and plot), path_out = "." (export plots)
plot_num(asd) # report distribution of numeric variables

```



```
# Linear correlation: For all numerical variables only
# Pearson coefficient (standard correlation measure)
# Score variable is the most important numerical variable, higher the value the higher the possibility
# Age_mons the lower the value and is less significant to the target class
correlation_table(asd, "Class")
```

```
## Variable Class
## 1 Class 1.00
## 2 Score 0.81
## 3 Age_Mons 0.07
```

```
# Calculates correlation of variables based on information theory metrics
# between the target class and the input variables
var_rank_info(asd, "Class")
```

```
##          var    en    mi    ig    gr
## 1          A9 1.614 0.278 0.277909239 0.277996613
## 2        Score 3.425 0.892 0.892361356 0.260515585
## 3          A5 1.639 0.252 0.251609995 0.252052724
## 4          A6 1.629 0.246 0.246159748 0.250444521
## 5          A7 1.597 0.229 0.229182242 0.245337007
## 6          A4 1.693 0.199 0.199315809 0.199403345
## 7          A1 1.690 0.191 0.190788892 0.193045776
## 8          A2 1.711 0.174 0.173790565 0.175119204
## 9          A8 1.744 0.144 0.143630174 0.144324050
## 10         A3 1.727 0.137 0.137305737 0.141301418
## 11         A10 1.848 0.023 0.023145729 0.023657112
## 12 Who.completed.the.test 1.153 0.003 0.003077339 0.011661620
```

```
## 13      Ethnicity 3.405 0.030 0.029537696 0.011620373
## 14      Sex 1.767 0.010 0.009769513 0.011045063
## 15      Age_Mons 4.810 0.039 0.038566543 0.009749532
## 16      Jauundice 1.734 0.004 0.004052141 0.004789299
## 17      Family_ASD 1.530 0.000 0.000130644 0.000204968
```

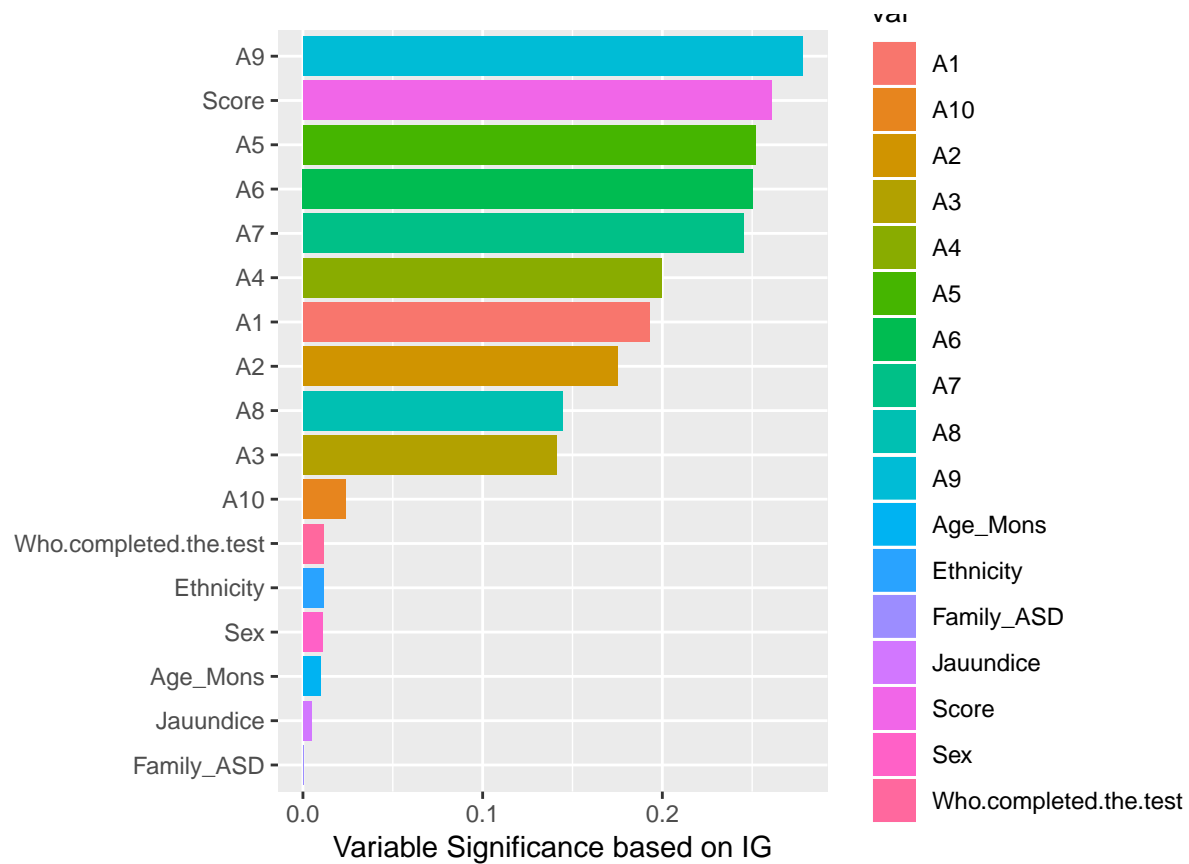
```
sigvar <- var_rank_info(asd, target ="Class")
sigvar
```

```
##      var      en      mi      ig      gr
## 1      A9 1.614 0.278 0.277909239 0.277996613
## 2      Score 3.425 0.892 0.892361356 0.260515585
## 3      A5 1.639 0.252 0.251609995 0.252052724
## 4      A6 1.629 0.246 0.246159748 0.250444521
## 5      A7 1.597 0.229 0.229182242 0.245337007
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## 16      Jauundice 1.734 0.004 0.004052141 0.004789299
## 17      Family_ASD 1.530 0.000 0.000130644 0.000204968
```

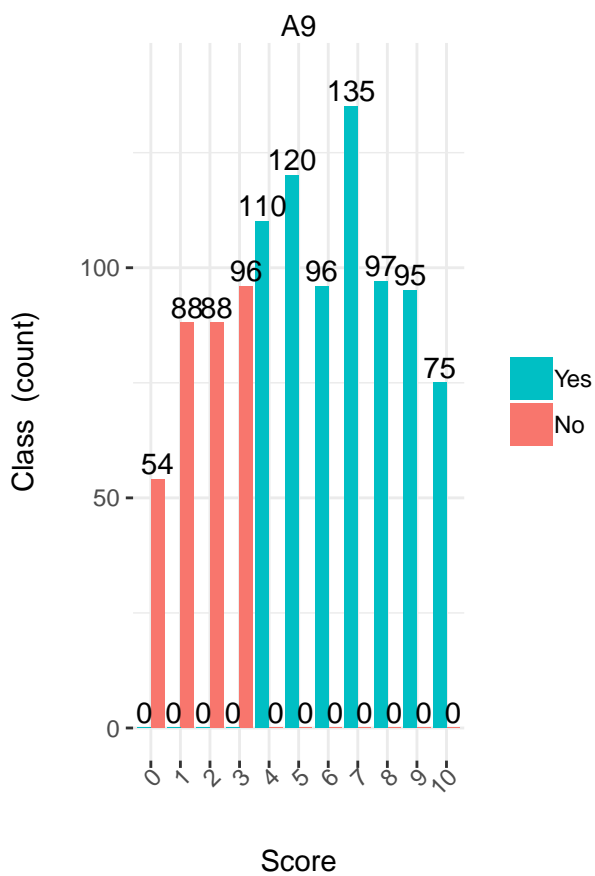
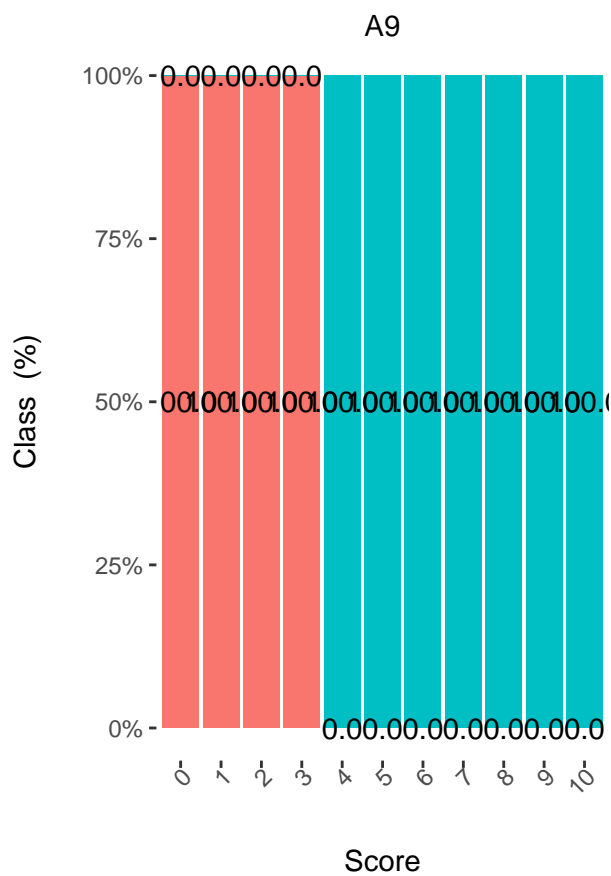
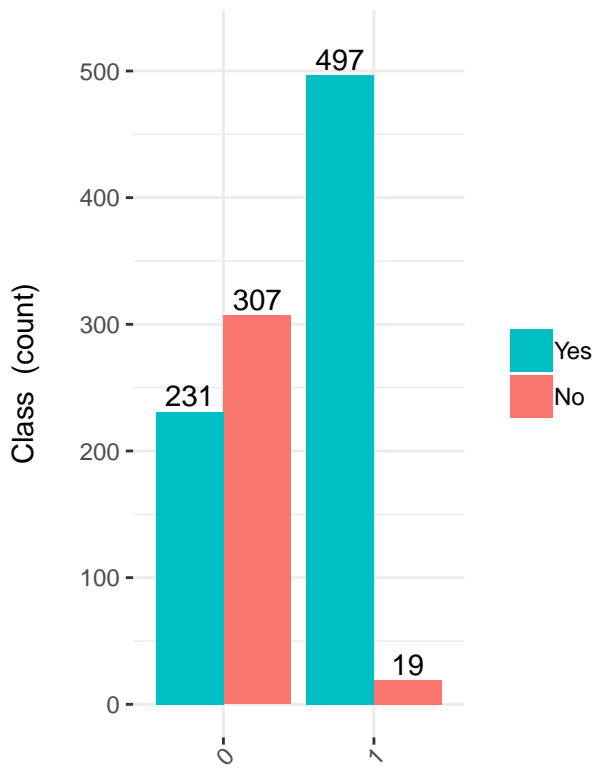
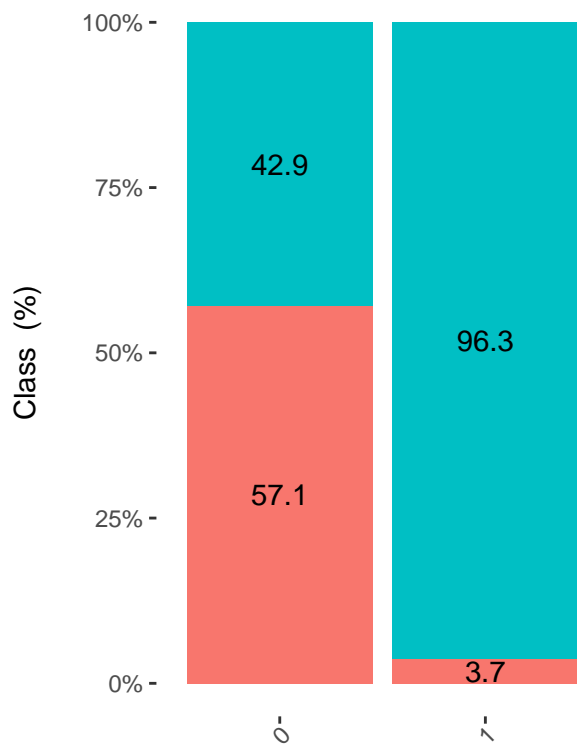
```
#plotting variable significance
```

```
# the highest gr (gain ratio) is for variable A9 which maps to the QChat question and most relevant to
# The rest of the categorical variables are the ranked lowest by IG
```

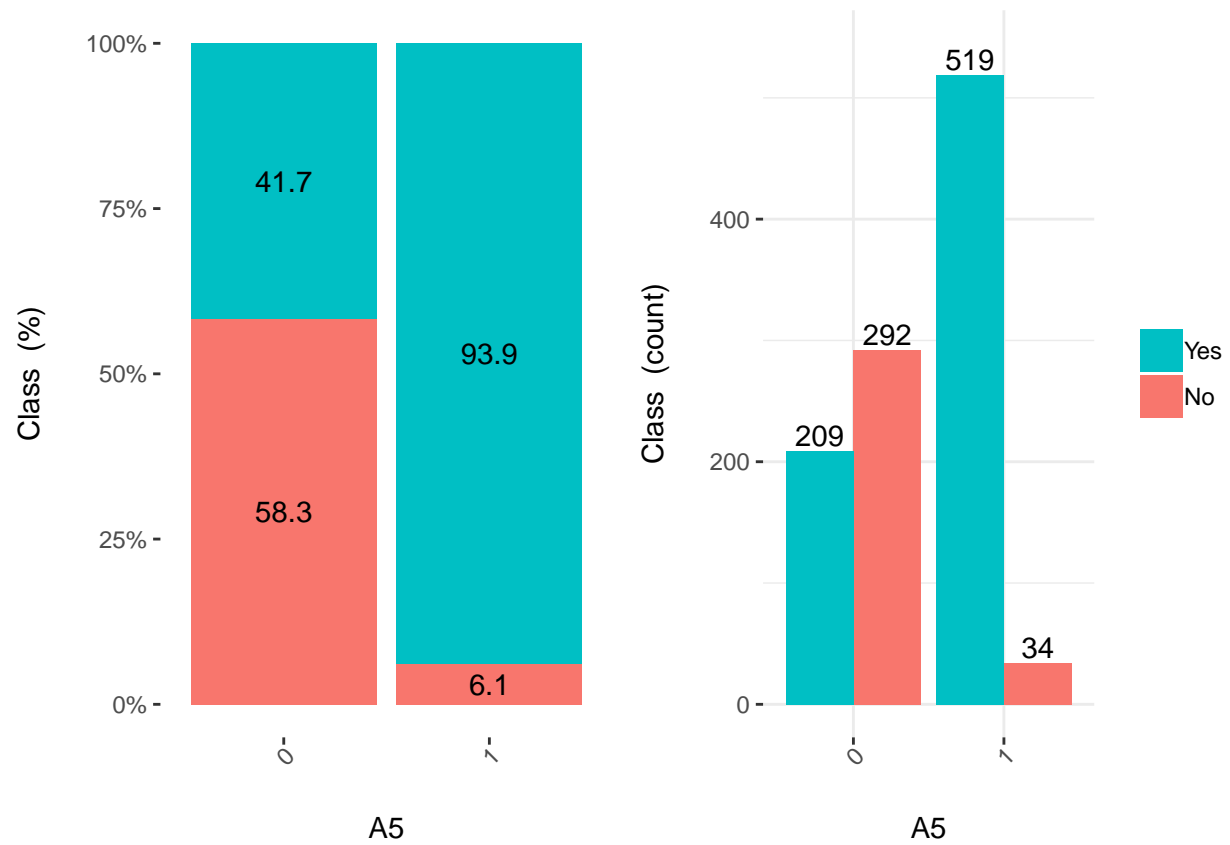
```
r <- ggplot(data=sigvar, aes(x=reorder(var,gr), y=gr, fill=var))
r + geom_bar(stat = "identity") +
  coord_flip() +
  theme_get() +
  xlab("") +
  ylab("Variable Significance based on IG")
```



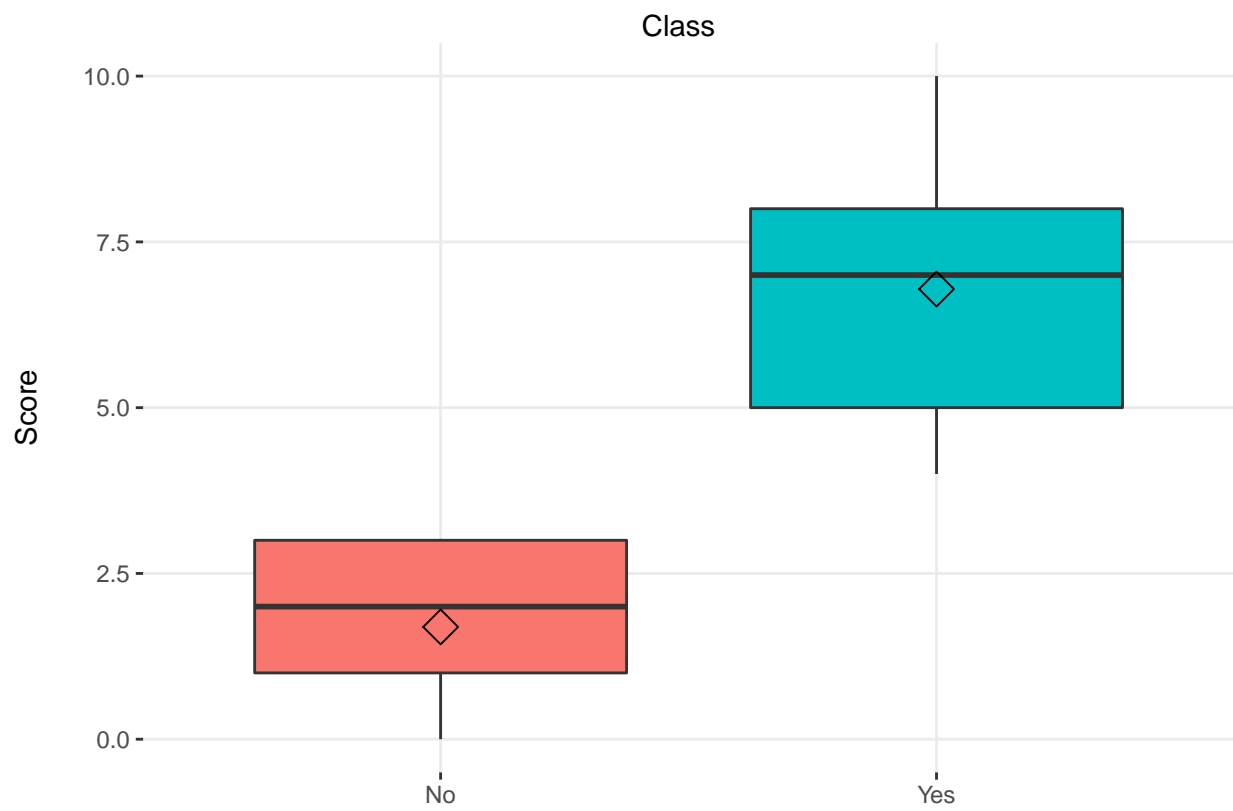
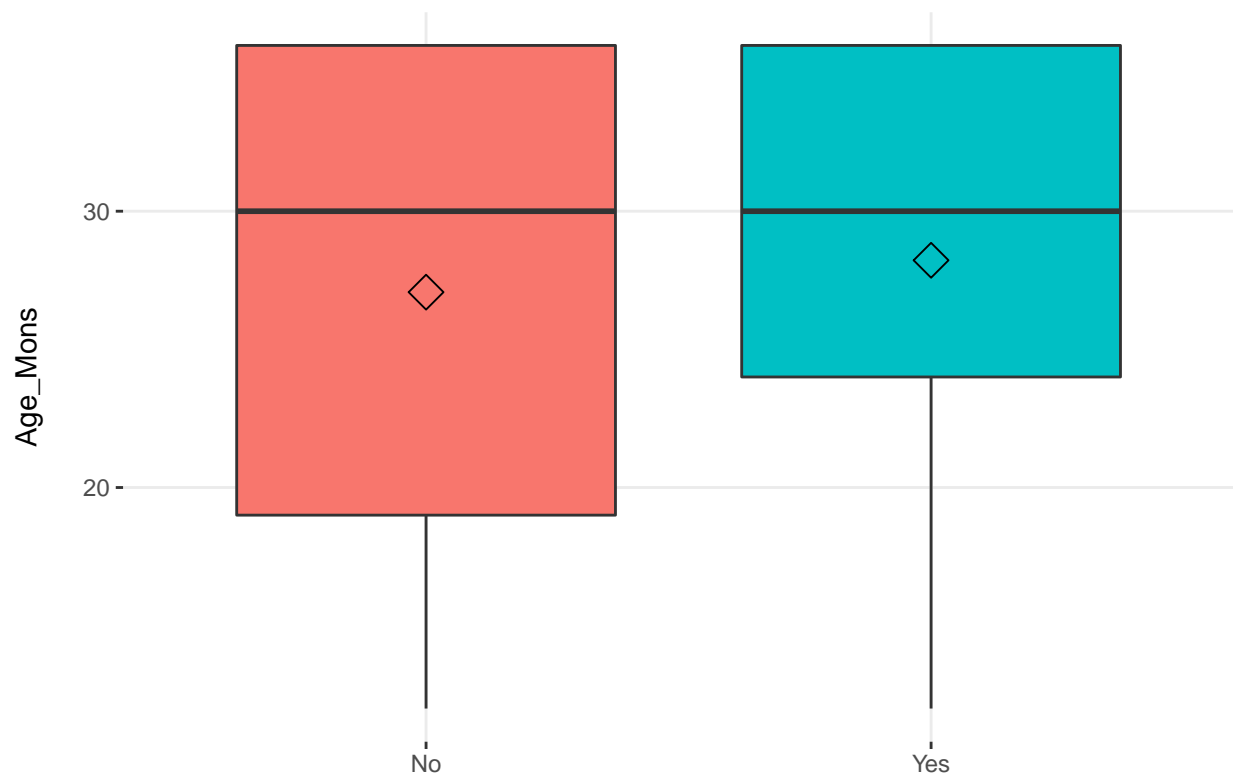
```
# Plot distribution between input and output variables.
# Reports if a variable is significant or not
# variables to analyse
f1 <- c("A9", "Score", "A5")
cross_plot(asd, input=f1, target = "Class")
```



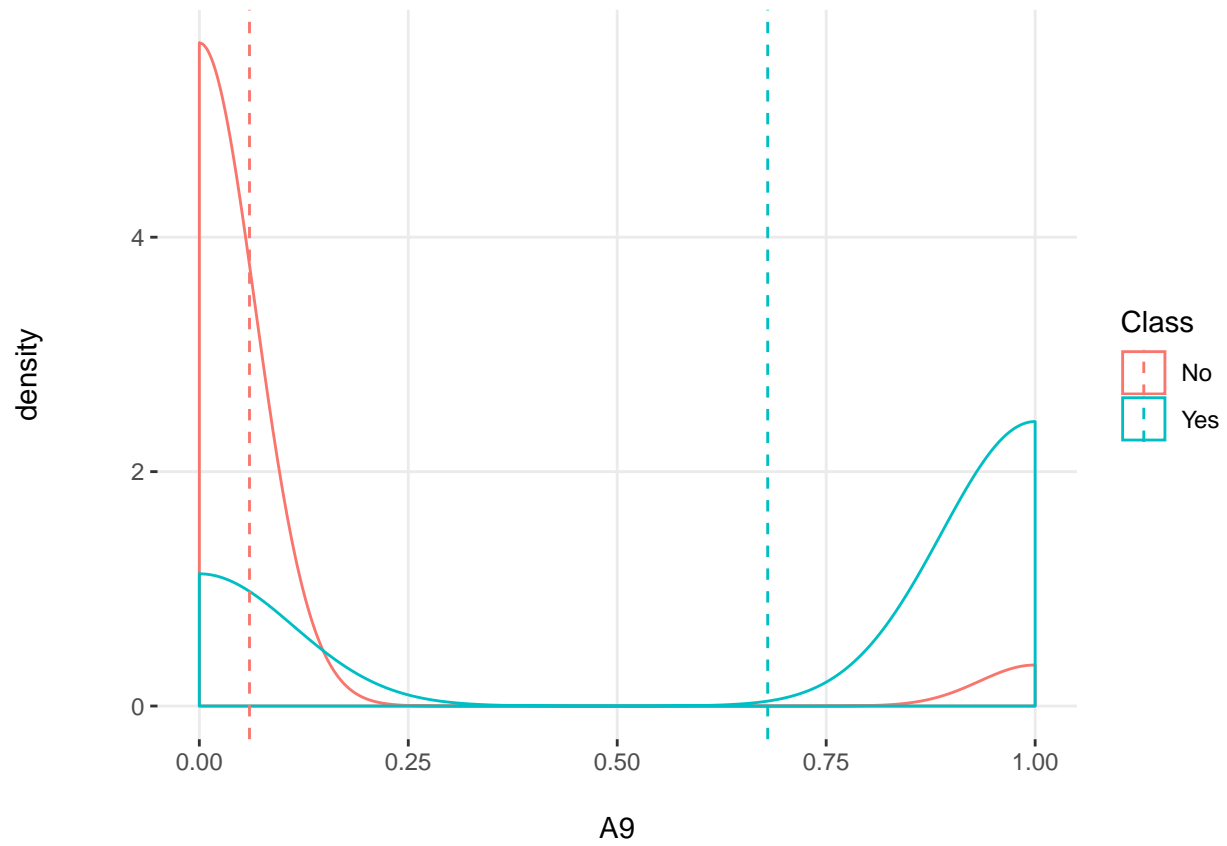


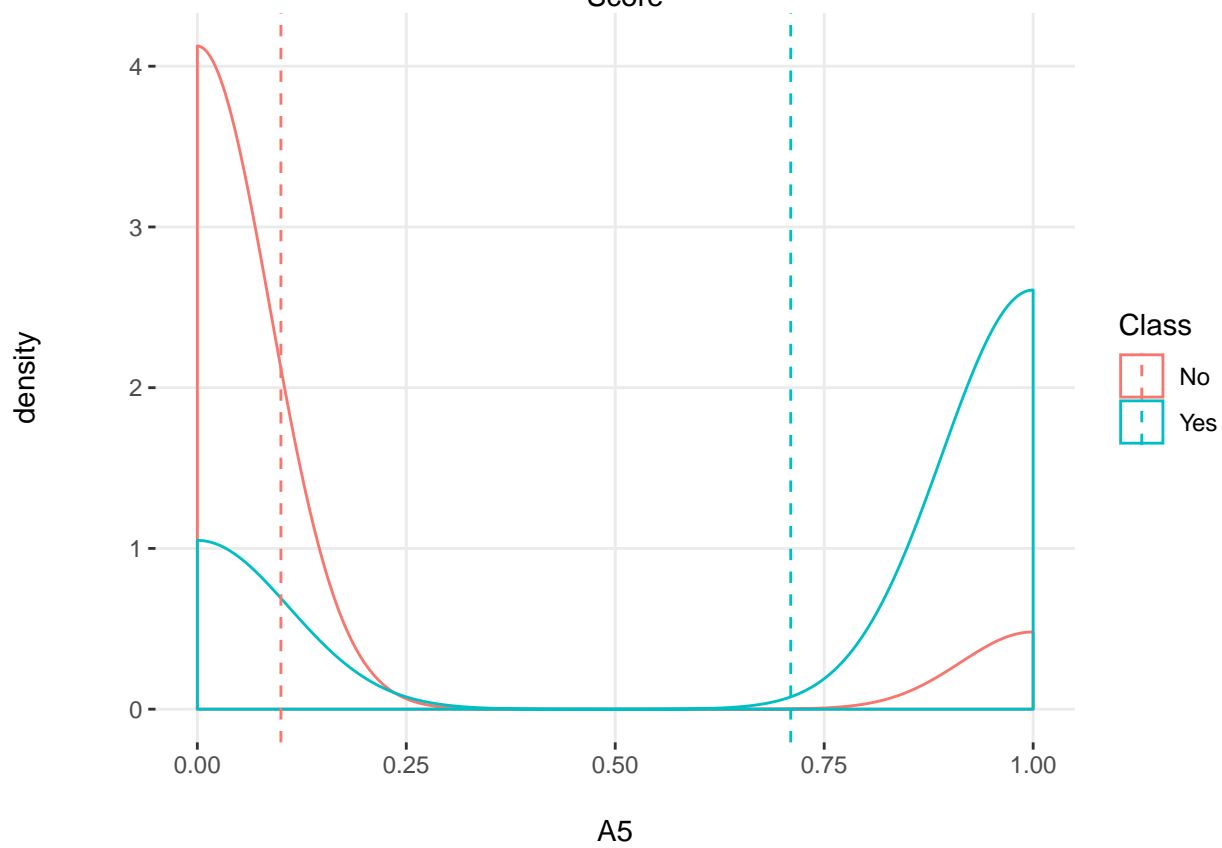
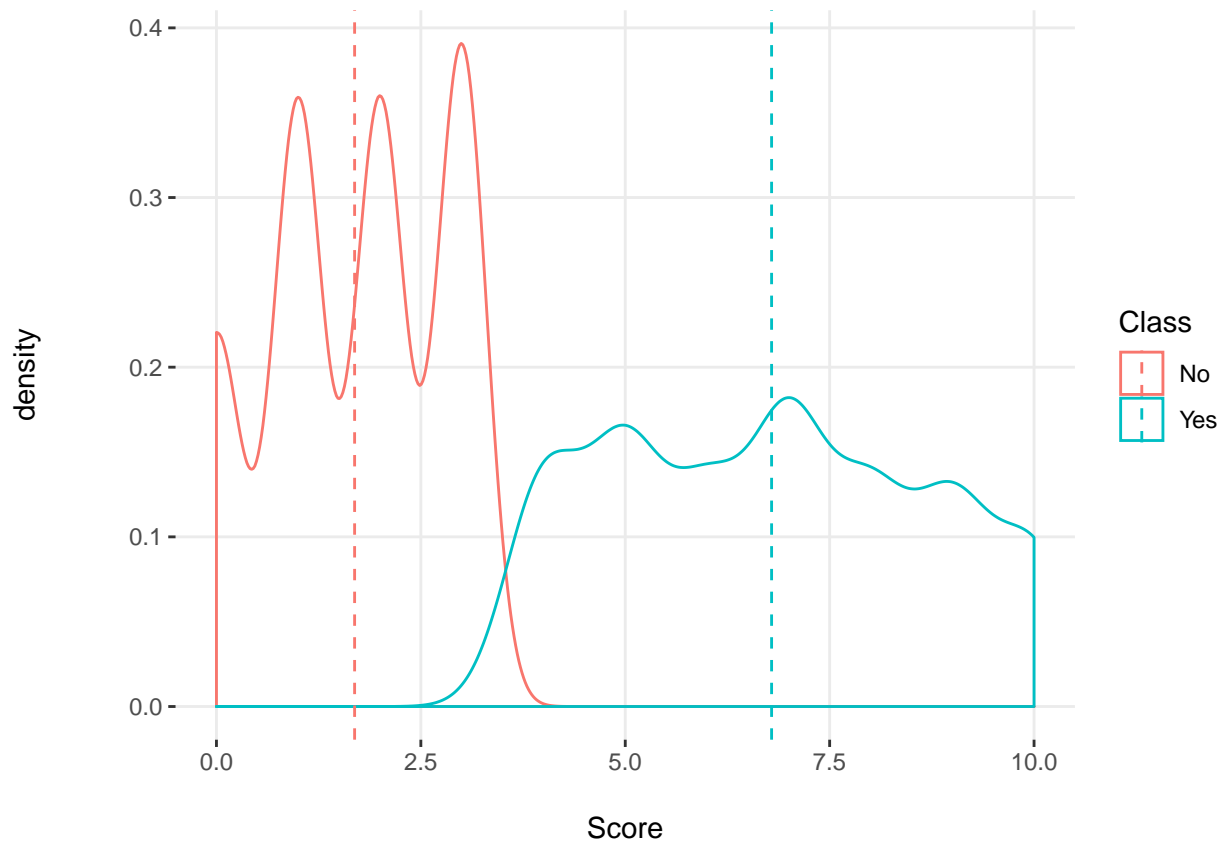


*# Report variable significance without Predictive Modelling based on Information Theory*  
`plotar(asd, target = "Class", plot_type="boxplot")`



```
plotar(asd, input=f1, target ="Class", plot_type="histdens")
```





## **Conclusion:**

Findings in EDA are not final rather than suggestive in nature to investigate the correlations of the dependent variables and independent variables and might lead to answer the Problem. This process is part of Data Understanding for CRISP-DM framework that will assist us in the next stage which is Data Preprocessing.

## **Variables showing high correlation to the target Class based on Information Gain (IG)**

Significant variables: A9, Score, A5, A6, A7, Score

## **Least significant variables:**

Age\_Mons, Sex, Ethnicity

## **Features to include**

Important to include Jaundice feature to to build predictive model even if it has low information gain merit as this was identified a contributing factor to asd by medical practitioners.

Note: profiling for categorical variables were excluded as it's throwing errors during PDF compilation, will include in another file.