

Autism Spectrum Disorder Screening

R Markdown

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
library('dplyr')
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
## filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
## intersect, setdiff, setequal, union
```

```
library('tidyr')
```

```
library('ggplot2')
```

```
library('caret')
```

```
## Loading required package: lattice
```

```
library('e1071')
```

```
library('rpart')
```

```
library('neuralnet')
```

```
##
```

```
## Attaching package: 'neuralnet'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
## compute
```

```
library('caretEnsemble')
```

```
##
```

```
## Attaching package: 'caretEnsemble'
```

```
## The following object is masked from 'package:ggplot2':
##
## autoplot
```

```
# reading the autism dataset
```

```
aut_data <- read.csv("/Users/sanjanagorlla/Desktop/Autism project/autism_screening.csv")
```

```
# visualising first few rows of the dataset
```

```
head(aut_data)
```

```
##   A1_Score A2_Score A3_Score A4_Score A5_Score A6_Score A7_Score A8_Score
## 1         1         1         1         1         0         0         1         1
## 2         1         1         0         1         0         0         0         1
## 3         1         1         0         1         1         0         1         1
## 4         1         1         0         1         0         0         1         1
## 5         1         0         0         0         0         0         0         1
## 6         1         1         1         1         1         0         1         1
##   A9_Score A10_Score age gender ethnicity jundice austim contry_of_res
## 1         0         0  26     f White-European    no     no United States
## 2         0         1  24     m           Latino    no    yes      Brazil
## 3         1         1  27     m           Latino   yes    yes      Spain
## 4         0         1  35     f White-European    no    yes United States
## 5         0         0  40     f              ?    no    no      Egypt
## 6         1         1  36     m           Others   yes    no United States
##   used_app_before result age_desc relation Class.ASD
## 1                no    6 18 and more    Self      NO
## 2                no    5 18 and more    Self      NO
## 3                no    8 18 and more   Parent     YES
## 4                no    6 18 and more    Self      NO
## 5                no    2 18 and more     ?       NO
## 6                no    9 18 and more    Self     YES
```

```
# checking the dimension of the dataset
```

```
dim(aut_data)
```

```
## [1] 704  21
```

```
# the dataset has 704 rows and 21 columns
```

```
# checking the type of all variables in the dataset
```

```
str(aut_data)
```

```
## 'data.frame':    704 obs. of  21 variables:
##  $ A1_Score      : int  1 1 1 1 1 1 0 1 1 1 ...
##  $ A2_Score      : int  1 1 1 1 0 1 1 1 1 1 ...
##  $ A3_Score      : int  1 0 0 0 0 1 0 1 0 1 ...
##  $ A4_Score      : int  1 1 1 1 0 1 0 1 0 1 ...
##  $ A5_Score      : int  0 0 1 0 0 1 0 0 1 0 ...
##  $ A6_Score      : int  0 0 0 0 0 0 0 0 0 1 ...
##  $ A7_Score      : int  1 0 1 1 0 1 0 0 0 1 ...
##  $ A8_Score      : int  1 1 1 1 1 1 1 0 1 1 ...
##  $ A9_Score      : int  0 0 1 0 0 1 0 1 1 1 ...
```

```
## $ A10_Score      : int  0 1 1 1 0 1 0 0 1 0 ...
## $ age            : num  26 24 27 35 40 36 17 64 29 17 ...
## $ gender         : chr   "f" "m" "m" "f" ...
## $ ethnicity      : chr  "White-European" "Latino" "Latino" "White-European" ...
## $ jundice        : chr   "no" "no" "yes" "no" ...
## $ austim         : chr   "no" "yes" "yes" "yes" ...
## $ contry_of_res  : chr   "United States" "Brazil" "Spain" "United States" ...
## $ used_app_before: chr   "no" "no" "no" "no" ...
## $ result         : num   6 5 8 6 2 9 2 5 6 8 ...
## $ age_desc       : chr   "18 and more" "18 and more" "18 and more" "18 and more" ...
## $ relation       : chr   "Self" "Self" "Parent" "Self" ...
## $ Class.ASD      : chr   "NO" "NO" "YES" "NO" ...
```

```
# statistical summary of all the variables
summary(aut_data)
```

```
##      A1_Score      A2_Score      A3_Score      A4_Score
## Min.      :0.0000   Min.      :0.0000   Min.      :0.0000   Min.      :0.0000
## 1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
## Median :1.0000   Median :0.0000   Median :0.0000   Median :0.0000
## Mean    :0.7216   Mean    :0.4531   Mean    :0.4574   Mean    :0.4957
## 3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000
## Max.    :1.0000   Max.    :1.0000   Max.    :1.0000   Max.    :1.0000
##
##      A5_Score      A6_Score      A7_Score      A8_Score
## Min.      :0.0000   Min.      :0.0000   Min.      :0.0000   Min.      :0.0000
## 1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
## Median :0.0000   Median :0.0000   Median :0.0000   Median :1.0000
## Mean    :0.4986   Mean    :0.2841   Mean    :0.4176   Mean    :0.6491
## 3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000
## Max.    :1.0000   Max.    :1.0000   Max.    :1.0000   Max.    :1.0000
##
##      A9_Score      A10_Score      age      gender
## Min.      :0.0000   Min.      :0.0000   Min.      : 17.0   Length:704
## 1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.: 21.0   Class :character
## Median :0.0000   Median :1.0000   Median : 27.0   Mode  :character
## Mean    :0.3239   Mean    :0.5739   Mean    : 29.7
## 3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.: 35.0
## Max.    :1.0000   Max.    :1.0000   Max.    :383.0
##                      NA's      :2
##      ethnicity      jundice      austim      contry_of_res
## Length:704      Length:704      Length:704      Length:704
## Class :character  Class :character  Class :character  Class :character
## Mode  :character  Mode  :character  Mode  :character  Mode  :character
##
##
##
##      used_app_before      result      age_desc      relation
## Length:704      Min.      : 0.000   Length:704      Length:704
## Class :character  1st Qu.: 3.000   Class :character  Class :character
## Mode  :character  Median : 4.000   Mode  :character  Mode  :character
##                      Mean    : 4.875
##                      3rd Qu.: 7.000
```

```
##           Max.      :10.000
##
##   Class.ASD
## Length:704
##   Class :character
##   Mode  :character
##
##
##
##
```

```
# the max value of age is 383 which is invalid
# therefore removing the row with age = 383
rownames(aut_data[aut_data$age == 383,])
```

```
## [1] "53"    "NA"    "NA.1"
```

```
aut_data <- aut_data[-53,]
max(aut_data$age, na.rm = TRUE) # now the maximum value for age is 64
```

```
## [1] 64
```

```
# count of numerical columns
length(select_if(aut_data,is.numeric))
```

```
## [1] 12
```

```
# there are 12 numerical columns in the dataset
```

```
# count of categorical columns
length(select_if(aut_data,is.character))
```

```
## [1] 9
```

```
# there are 9 categorical columns in the dataset
```

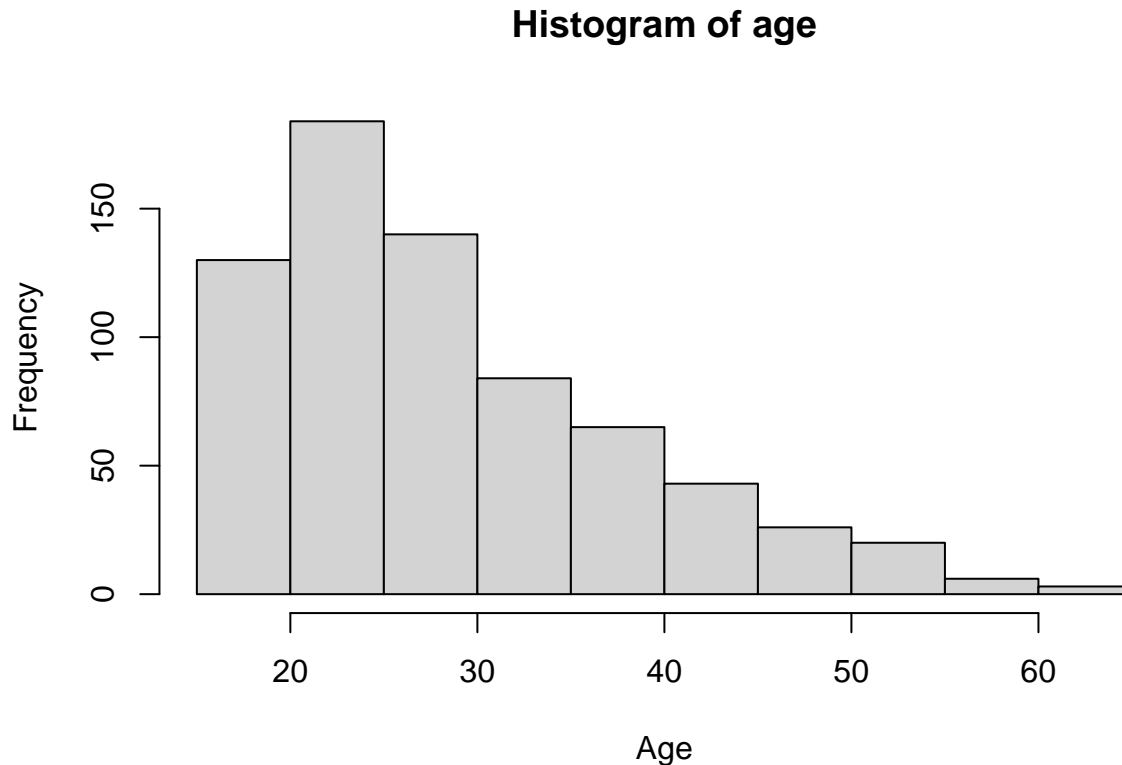
```
# checking for the distribution of all the variables
#library("psych")
#pairs.panels(aut_data)
```

```
# checking for missing values in the dataset
colSums(is.na(aut_data))
```

```
##      A1_Score      A2_Score      A3_Score      A4_Score      A5_Score
##           0           0           0           0           0
##      A6_Score      A7_Score      A8_Score      A9_Score     A10_Score
##           0           0           0           0           0
##           age      gender      ethnicity      jundice      austim
##           2           0           0           0           0
##  contry_of_res used_app_before      result      age_desc      relation
##           0           0           0           0           0
##      Class.ASD
##           0
```

```
# there are only 2 missing values for age in the entire dataset

# checking for the distribution of age column
hist(aut_data$age, main = 'Histogram of age', xlab = "Age")
```



```
# the distribution of age is positively skewed therefore we will impute the values
# using median
```

```
# imputing missing value with median age
aut_data$age[is.na(aut_data$age)] <- median(aut_data$age, na.rm = TRUE)
sum(is.na(aut_data$age))
```

```
## [1] 0
```

```
# selecting the continuous columns
num_aut_data <- select_if(aut_data, is.numeric)
```

```
# selecting the categorical columns
cat_aut_data <- select_if(aut_data, is.character)
```

```
# checking for count of unique values in categorical variables
cat_aut_data %>% summarise_all(n_distinct)
```

```
## gender ethnicity jundice austim contry_of_res used_app_before age_desc
```

```
## 1      2      12      2      2      67      2      1
##  relation Class.ASD
## 1      6      2
```

```
# Below are the column names with the count of unique values:
```

```
# gender - 2
# ethnicity - 12
# jundice - 2
# autism - 2
# country_of_res - 67
# used_app_before - 2
# age_desc - 1
# relation - 6
# Class.ASD - 2
```

```
# since age_desc has only one unique value it is of no use, so we can drop it
cat_aut_data <- cat_aut_data[,-7]
```

```
# further checking unique values in each column
unique(cat_aut_data$gender)
```

```
## [1] "f" "m"
```

```
unique(cat_aut_data$ethnicity)
```

```
## [1] "White-European" "Latino"      "?"           "Others"
## [5] "Black"          "Asian"       "Middle Eastern " "Pasifika"
## [9] "South Asian"    "Hispanic"    "Turkish"      "others"
```

```
# in ethnicity column there is a '?' that is an invalid value and 'Other' and 'others'
# are treated as different values, although they should be treated as same
```

```
# replacing '?' and 'others' with 'Others'
```

```
cat_aut_data$ethnicity[cat_aut_data$ethnicity == "?"] <- "Others"
cat_aut_data$ethnicity[cat_aut_data$ethnicity == "others"] <- "Others"
unique(cat_aut_data$ethnicity)
```

```
## [1] "White-European" "Latino"      "Others"      "Black"
## [5] "Asian"          "Middle Eastern " "Pasifika"    "South Asian"
## [9] "Hispanic"      "Turkish"
```

```
unique(cat_aut_data$jundice)
```

```
## [1] "no" "yes"
```

```
unique(cat_aut_data$austim)
```

```
## [1] "no" "yes"
```

```
unique(cat_aut_data$contry_of_res)
```

```
## [1] "United States"      "Brazil"              "Spain"
## [4] "Egypt"              "New Zealand"         "Bahamas"
## [7] "Burundi"           "Austria"             "Argentina"
## [10] "Jordan"             "Ireland"             "United Arab Emirates"
## [13] "Afghanistan"        "Lebanon"             "United Kingdom"
## [16] "South Africa"       "Italy"               "Pakistan"
## [19] "Bangladesh"         "Chile"               "France"
## [22] "China"              "Australia"           "Canada"
## [25] "Saudi Arabia"       "Netherlands"         "Romania"
## [28] "Sweden"             "Tonga"               "Oman"
## [31] "India"              "Philippines"         "Sri Lanka"
## [34] "Sierra Leone"      "Ethiopia"            "Viet Nam"
## [37] "Iran"               "Costa Rica"          "Germany"
## [40] "Mexico"             "Russia"              "Armenia"
## [43] "Iceland"            "Nicaragua"           "Hong Kong"
## [46] "Japan"              "Ukraine"             "Kazakhstan"
## [49] "AmericanSamoa"      "Uruguay"             "Serbia"
## [52] "Portugal"           "Malaysia"            "Ecuador"
## [55] "Niger"              "Belgium"             "Bolivia"
## [58] "Aruba"              "Finland"             "Turkey"
## [61] "Nepal"              "Indonesia"           "Angola"
## [64] "Azerbaijan"         "Iraq"                "Czech Republic"
## [67] "Cyprus"
```

```
unique(cat_aut_data$used_app_before)
```

```
## [1] "no" "yes"
```

```
unique(cat_aut_data$relation)
```

```
## [1] "Self"              "Parent"
## [3] "?"                 "Health care professional"
## [5] "Relative"          "Others"
```

```
# relation column also has an invalid value which is "?"
# replacing this "?" with "Others"
cat_aut_data$relation[cat_aut_data$relation == "?"] <- "Others"
unique(cat_aut_data$relation)
```

```
## [1] "Self"              "Parent"
## [3] "Others"            "Health care professional"
## [5] "Relative"
```

```
unique(cat_aut_data$Class.ASD)
```

```
## [1] "NO" "YES"
```

```
# checking the distribution of male and female in the data
table(cat_aut_data$gender)
```

```
##
##    f    m
## 336 367
```

```
# there are 336 females and 367 males
# plotting the same on the histogram
```

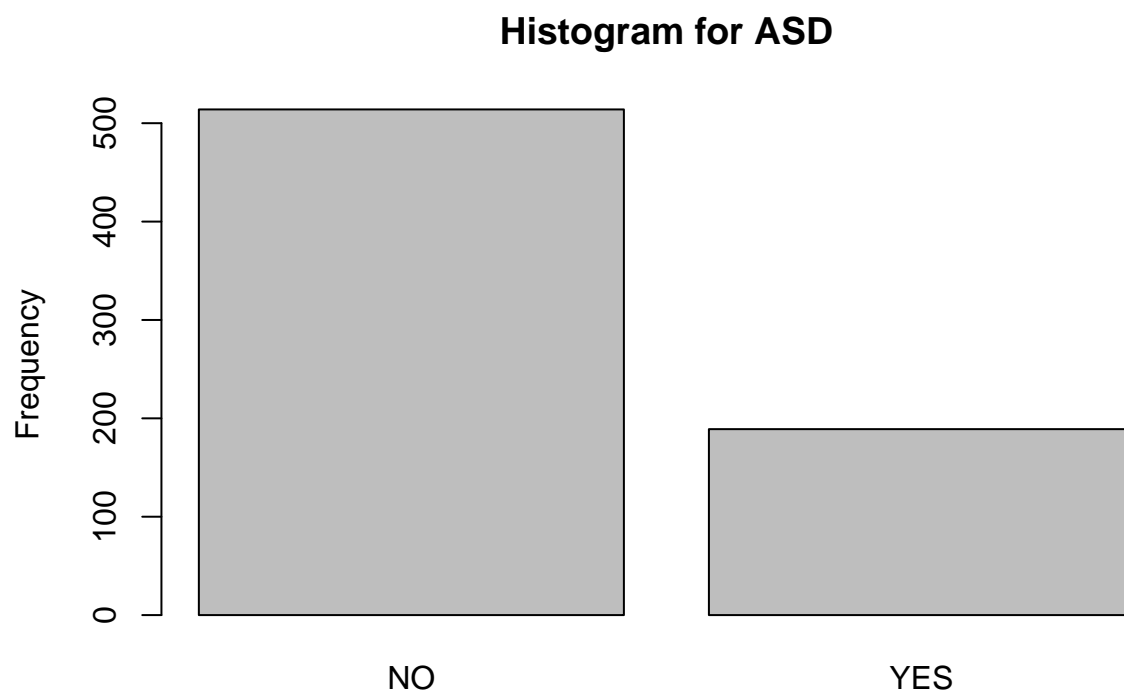
```
barplot(table(cat_aut_data$gender), main = "Histogram for Gender", ylab = "Frequency")
```



```
# checking for the count of Autism Spectrum Disorder (ASD)
table(cat_aut_data$Class.ASD)
```

```
##
## NO YES
## 514 189
```

```
barplot(table(cat_aut_data$Class.ASD), main = "Histogram for ASD", ylab = "Frequency")
```

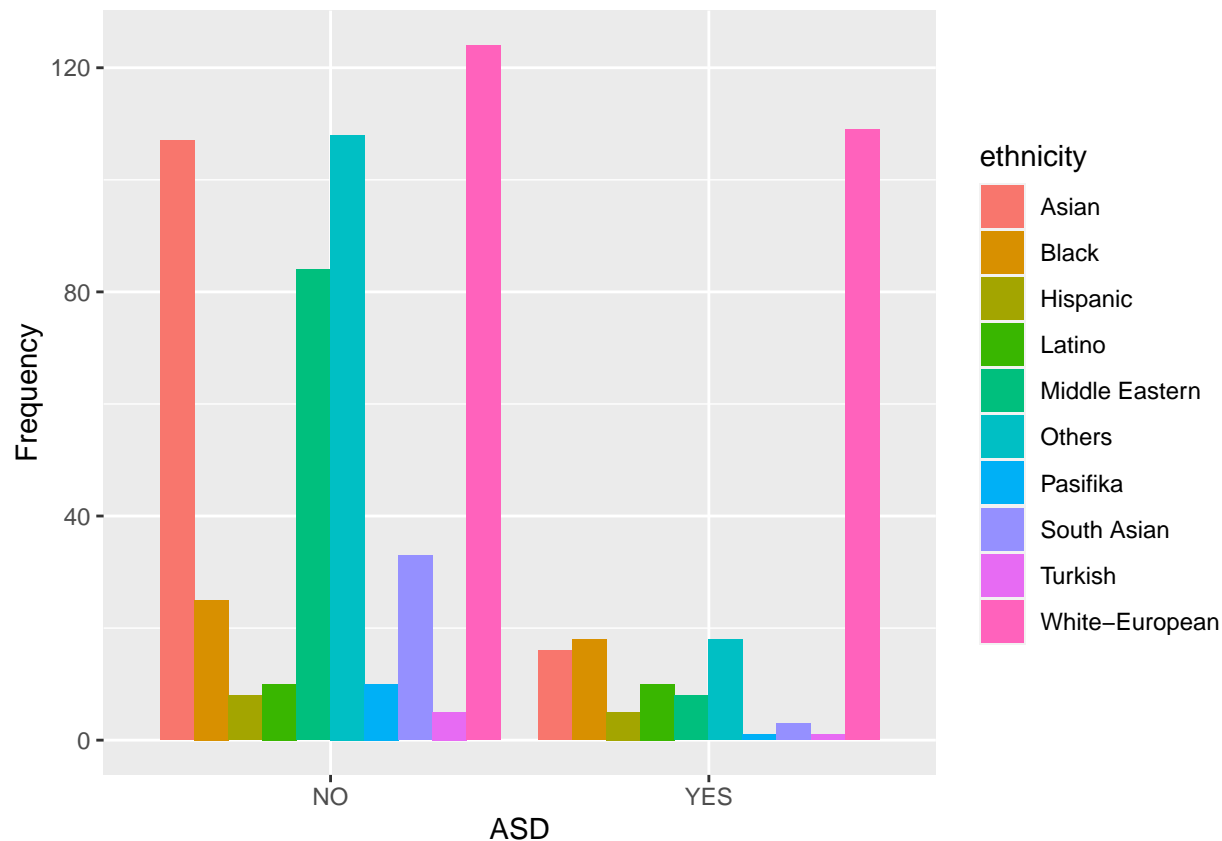



```
# there are 189 ASD patients and 514 normal patients
```

```
# plotting distribution of ASD with ethnicity
```

```
tbl <- with(cat_aut_data, table(ethnicity, Class.ASD))
```

```
ggplot(as.data.frame(tbl), aes(factor(Class.ASD), Freq, fill = ethnicity)) +  
  geom_col(position = 'dodge') + xlab("ASD") + ylab("Frequency")
```



*# from the plot we can see that Pacifica and Turkish have the least ASD patients
whereas White Europeans have maximum number of ASD patients
On the other hand Turkish have least number of normal people and White Europeans
have maximum number of normal people*

```
# label encoding the binary categorical variables gender, jundice, autism,  
# used_app_before, Class.ASD  
cat_aut_data$gender <- ifelse(cat_aut_data$gender == "m", 1, 0)  
cat_aut_data$jundice <- ifelse(cat_aut_data$jundice == "yes", 1, 0)  
cat_aut_data$austim <- ifelse(cat_aut_data$austim == "yes", 1, 0)  
cat_aut_data$used_app_before <- ifelse(cat_aut_data$used_app_before == "yes", 1, 0)  
cat_aut_data$Class.ASD <- ifelse(cat_aut_data$Class.ASD == "YES", 1, 0)
```

```
# One hot encoding for rest of the categorical variables  
dummy <- dummyVars(" ~ .", data = cat_aut_data, sep = "_")  
cat_aut_data <- data.frame(predict(dummy, newdata = cat_aut_data))  
head(cat_aut_data)
```

```
##   gender ethnicityAsian ethnicityBlack ethnicityHispanic ethnicityLatino  
## 1      0           0           0           0           0  
## 2      1           0           0           0           1  
## 3      1           0           0           0           1  
## 4      0           0           0           0           0  
## 5      0           0           0           0           0  
## 6      1           0           0           0           0  
##   ethnicityMiddle.Eastern. ethnicityOthers ethnicityPasifika
```

## 1	0	0	0		
## 2	0	0	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	1	0		
## 6	0	1	0		
##	ethnicitySouth.Asian	ethnicityTurkish	ethnicityWhite.European	jundice	austim
## 1	0	0	1	0	0
## 2	0	0	0	0	1
## 3	0	0	0	1	1
## 4	0	0	1	0	1
## 5	0	0	0	0	0
## 6	0	0	0	1	0
##	contry_of_resAfghanistan	contry_of_resAmericanSamoa	contry_of_resAngola		
## 1	0	0	0		
## 2	0	0	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	0	0		
## 6	0	0	0		
##	contry_of_resArgentina	contry_of_resArmenia	contry_of_resAruba		
## 1	0	0	0		
## 2	0	0	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	0	0		
## 6	0	0	0		
##	contry_of_resAustralia	contry_of_resAustria	contry_of_resAzerbaijan		
## 1	0	0	0		
## 2	0	0	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	0	0		
## 6	0	0	0		
##	contry_of_resBahamas	contry_of_resBangladesh	contry_of_resBelgium		
## 1	0	0	0		
## 2	0	0	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	0	0		
## 6	0	0	0		
##	contry_of_resBolivia	contry_of_resBrazil	contry_of_resBurundi		
## 1	0	0	0		
## 2	0	1	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	0	0		
## 6	0	0	0		
##	contry_of_resCanada	contry_of_resChile	contry_of_resChina		
## 1	0	0	0		
## 2	0	0	0		
## 3	0	0	0		
## 4	0	0	0		
## 5	0	0	0		

## 6	0	0	0
##	contry_of_resCosta.Rica	contry_of_resCyprus	contry_of_resCzech.Republic
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resEcuador	contry_of_resEgypt	contry_of_resEthiopia
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	1	0
## 6	0	0	0
##	contry_of_resFinland	contry_of_resFrance	contry_of_resGermany
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resHong.Kong	contry_of_resIceland	contry_of_resIndia
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resIndonesia	contry_of_resIran	contry_of_resIraq
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resIreland	contry_of_resItaly	contry_of_resJapan
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resJordan	contry_of_resKazakhstan	contry_of_resLebanon
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resMalaysia	contry_of_resMexico	contry_of_resNepal
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0

## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resNetherlands	contry_of_resNew.Zealand	contry_of_resNicaragua
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resNiger	contry_of_resOman	contry_of_resPakistan
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resPhilippines	contry_of_resPortugal	contry_of_resRomania
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resRussia	contry_of_resSaudi.Arabia	contry_of_resSerbia
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resSierra.Leone	contry_of_resSouth.Africa	contry_of_resSpain
## 1	0	0	0
## 2	0	0	0
## 3	0	0	1
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resSri.Lanka	contry_of_resSweden	contry_of_resTonga
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resTurkey	contry_of_resUkraine	contry_of_resUnited.Arab.Emirates
## 1	0	0	0
## 2	0	0	0
## 3	0	0	0
## 4	0	0	0
## 5	0	0	0
## 6	0	0	0
##	contry_of_resUnited.Kingdom	contry_of_resUnited.States	contry_of_resUruguay
## 1	0	1	0

```
## 2          0          0          0
## 3          0          0          0
## 4          0          1          0
## 5          0          0          0
## 6          0          1          0
##   contry_of_resViet.Nam used_app_before relationHealth.care.professional
## 1          0          0          0
## 2          0          0          0
## 3          0          0          0
## 4          0          0          0
## 5          0          0          0
## 6          0          0          0
##   relationOthers relationParent relationRelative relationSelf Class.ASD
## 1          0          0          0          1          0
## 2          0          0          0          1          0
## 3          0          1          0          0          1
## 4          0          0          0          1          0
## 5          1          0          0          0          0
## 6          0          0          0          1          1
```

```
# finding correaltion between variables
```

```
# using only numerical variables
```

```
num_cor_mat <- cor(cbind(num_aut_data, cat_aut_data$Class.ASD))
num_cor_mat
```

```
##           A1_Score  A2_Score  A3_Score  A4_Score
## A1_Score  1.00000000  0.01235387  0.07497267  0.128815732
## A2_Score  0.012353866  1.00000000  0.22299723  0.157917566
## A3_Score  0.074972671  0.22299723  1.00000000  0.411962183
## A4_Score  0.128815732  0.15791757  0.41196218  1.000000000
## A5_Score  0.170417460  0.15272770  0.26397007  0.305830076
## A6_Score  0.110817604  0.18520946  0.26826005  0.294552941
## A7_Score  0.218457514 -0.04291160  0.07719548  0.150223778
## A8_Score  0.149078792  0.03371085  0.01602520  0.006711761
## A9_Score  0.146153846  0.20471525  0.31450483  0.327036547
## A10_Score 0.119585715  0.06748434  0.16719877  0.209678422
## age      0.008118375  0.08257822  0.09855214  0.107580359
## result   0.399616880  0.39143303  0.55160565  0.585248791
## cat_aut_data$Class.ASD 0.298322602  0.31086167  0.44066179  0.469541685
##           A5_Score  A6_Score  A7_Score  A8_Score
## A1_Score  0.170417460  0.11081760  0.218457514  0.149078792
## A2_Score  0.152727704  0.18520946 -0.042911599  0.033710848
## A3_Score  0.263970068  0.26826005  0.077195477  0.016025203
## A4_Score  0.305830076  0.29455294  0.150223778  0.006711761
## A5_Score  1.000000000  0.39184869  0.237677618  0.100360028
## A6_Score  0.391848692  1.00000000  0.174868958  0.099062640
## A7_Score  0.237677618  0.17486896  1.000000000  0.083918040
## A8_Score  0.100360028  0.09906264  0.083918040  1.000000000
## A9_Score  0.396015052  0.47910011  0.188806572  0.100560301
## A10_Score 0.266358390  0.29375943  0.251077229  0.098761041
## age      0.009127665  0.09221083 -0.001250767 -0.064874480
## result   0.639051620  0.62987828  0.453988107  0.321994223
## cat_aut_data$Class.ASD 0.536664716  0.59186965  0.350969527  0.236361328
```

```
##          A9_Score A10_Score          age      result
## A1_Score      0.1461538 0.11958571  0.008118375 0.39961688
## A2_Score      0.2047153 0.06748434  0.082578217 0.39143303
## A3_Score      0.3145048 0.16719877  0.098552145 0.55160565
## A4_Score      0.3270365 0.20967842  0.107580359 0.58524879
## A5_Score      0.3960151 0.26635839  0.009127665 0.63905162
## A6_Score      0.4791001 0.29375943  0.092210833 0.62987828
## A7_Score      0.1888066 0.25107723 -0.001250767 0.45398811
## A8_Score      0.1005603 0.09876104 -0.064874480 0.32199422
## A9_Score      1.0000000 0.28256438  0.128297891 0.66103481
## A10_Score     0.2825644 1.00000000  0.046652646 0.53607543
## age          0.1282979 0.04665265  1.000000000 0.09825975
## result       0.6610348 0.53607543  0.098259748 1.00000000
## cat_aut_data$Class.ASD 0.6353617 0.38538689 0.132590609 0.82172939
##          cat_aut_data$Class.ASD
## A1_Score          0.2983226
## A2_Score          0.3108617
## A3_Score          0.4406618
## A4_Score          0.4695417
## A5_Score          0.5366647
## A6_Score          0.5918696
## A7_Score          0.3509695
## A8_Score          0.2363613
## A9_Score          0.6353617
## A10_Score         0.3853869
## age              0.1325906
## result           0.8217294
## cat_aut_data$Class.ASD          1.0000000
```

```
# variable result is showing high correlation of 0.8217294 with the target variable
# Class.ASD
# none of the other variables show high correlation among themselves

# using only encoded categorical variables
cat_cor_mat <- cor(cat_aut_data)
# relationOthers has high correlation with ethnicityOthers of 0.8183654
# therefore we will drop relationOthers
cat_aut_data <- cat_aut_data[, -83]

# None of the machine learning algorithms that we are using make the assumptions of
# normality or in another words they don't assume the distribution to be normal

# We will apply min max normalisation on the dataset mainly for bringing age and
# result column on the same scale and since other columns are binary they wont get
# affected by min max scaling
# function to implement min max scaling
min_max_scaler <- function(x) {
  (x - min(x)) / (max(x) - min(x))
}

# using min_max_scaler function to implement min max scaling
scaled_num_aut_data <- as.data.frame(lapply(num_aut_data, min_max_scaler))
```

```
# the total number of features in our dataset excluding the target variable are 97
# there is no need to apply feature engineering or derived features as there are
# no variables that can be combined to form a new feature or which can be split to
# create two new features, and another reason for not applying any kind of
# transformation on our features is that our algorithms does make assumption
# of normality and will not be affected even if the data does not have normal
# distribution
```

```
# using PCA for selecting feautres
# preparing data for performing PCA
pca_data <- cbind(num_aut_data, cat_aut_data)
# removing the target column before performing PCA
pca_data <- pca_data[,-98]
colnames(pca_data)
```

```
## [1] "A1_Score" "A2_Score"
## [3] "A3_Score" "A4_Score"
## [5] "A5_Score" "A6_Score"
## [7] "A7_Score" "A8_Score"
## [9] "A9_Score" "A10_Score"
## [11] "age" "result"
## [13] "gender" "ethnicityAsian"
## [15] "ethnicityBlack" "ethnicityHispanic"
## [17] "ethnicityLatino" "ethnicityMiddle.Eastern."
## [19] "ethnicityOthers" "ethnicityPasifika"
## [21] "ethnicitySouth.Asian" "ethnicityTurkish"
## [23] "ethnicityWhite.European" "jundice"
## [25] "austim" "contry_of_resAfghanistan"
## [27] "contry_of_resAmericanSamoa" "contry_of_resAngola"
## [29] "contry_of_resArgentina" "contry_of_resArmenia"
## [31] "contry_of_resAruba" "contry_of_resAustralia"
## [33] "contry_of_resAustria" "contry_of_resAzerbaijan"
## [35] "contry_of_resBahamas" "contry_of_resBangladesh"
## [37] "contry_of_resBelgium" "contry_of_resBolivia"
## [39] "contry_of_resBrazil" "contry_of_resBurundi"
## [41] "contry_of_resCanada" "contry_of_resChile"
## [43] "contry_of_resChina" "contry_of_resCosta.Rica"
## [45] "contry_of_resCyprus" "contry_of_resCzech.Republic"
## [47] "contry_of_resEcuador" "contry_of_resEgypt"
## [49] "contry_of_resEthiopia" "contry_of_resFinland"
## [51] "contry_of_resFrance" "contry_of_resGermany"
## [53] "contry_of_resHong.Kong" "contry_of_resIceland"
## [55] "contry_of_resIndia" "contry_of_resIndonesia"
## [57] "contry_of_resIran" "contry_of_resIraq"
## [59] "contry_of_resIreland" "contry_of_resItaly"
## [61] "contry_of_resJapan" "contry_of_resJordan"
## [63] "contry_of_resKazakhstan" "contry_of_resLebanon"
## [65] "contry_of_resMalaysia" "contry_of_resMexico"
## [67] "contry_of_resNepal" "contry_of_resNetherlands"
```



```
## [69] "contry_of_resNew.Zealand"      "contry_of_resNicaragua"
## [71] "contry_of_resNiger"           "contry_of_resOman"
## [73] "contry_of_resPakistan"        "contry_of_resPhilippines"
## [75] "contry_of_resPortugal"        "contry_of_resRomania"
## [77] "contry_of_resRussia"          "contry_of_resSaudi.Arabia"
## [79] "contry_of_resSerbia"          "contry_of_resSierra.Leone"
## [81] "contry_of_resSouth.Africa"    "contry_of_resSpain"
## [83] "contry_of_resSri.Lanka"       "contry_of_resSweden"
## [85] "contry_of_resTonga"          "contry_of_resTurkey"
## [87] "contry_of_resUkraine"         "contry_of_resUnited.Arab.Emirates"
## [89] "contry_of_resUnited.Kingdom"  "contry_of_resUnited.States"
## [91] "contry_of_resUruguay"         "contry_of_resViet.Nam"
## [93] "used_app_before"             "relationHealth.care.professional"
## [95] "relationParent"              "relationRelative"
## [97] "relationSelf"
```

```
# performing scaled PCA
```

```
pca_scaled <- prcomp(pca_data, scale. = TRUE, center = TRUE)
s_pca_scaled <- summary(pca_scaled)
s_pca_scaled$importance[2,]
```

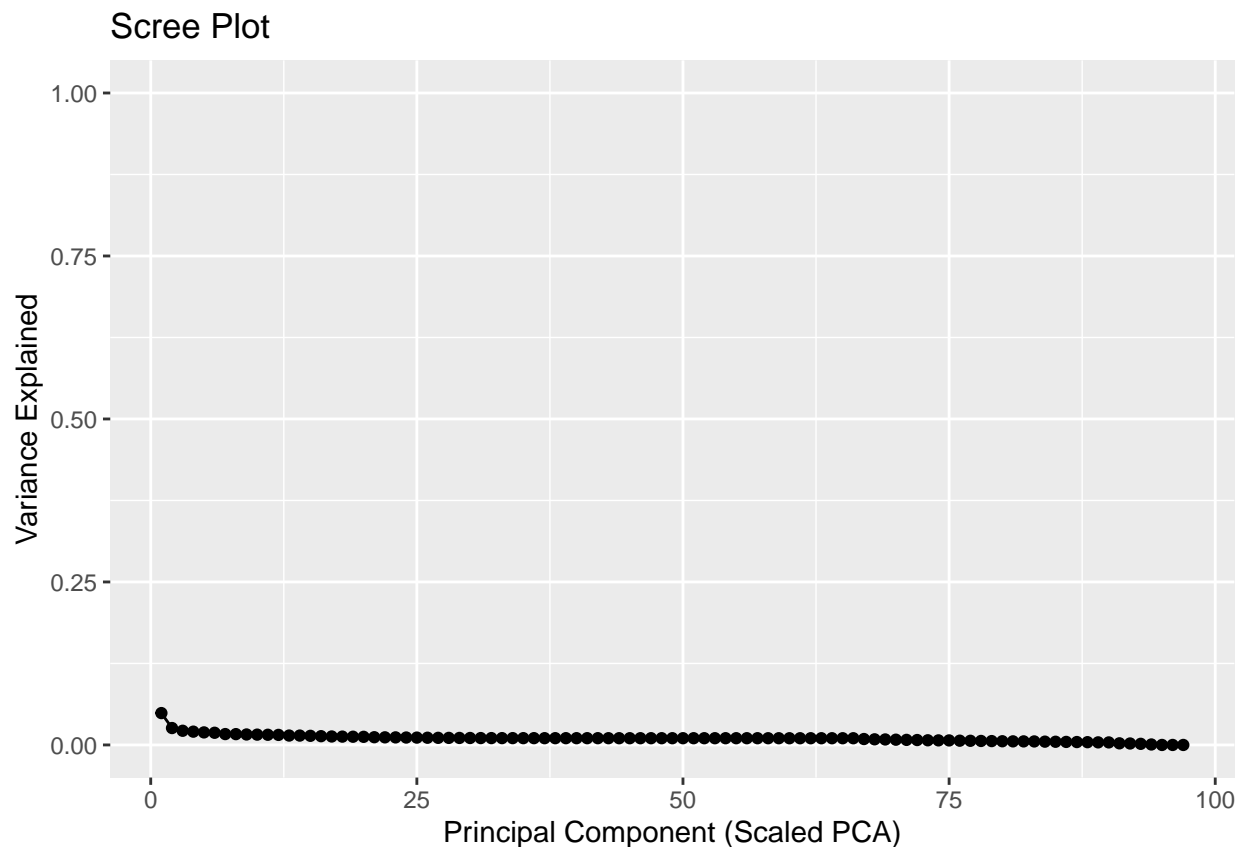
```
##      PC1      PC2      PC3      PC4      PC5      PC6      PC7      PC8      PC9      PC10
## 0.04889 0.02595 0.02177 0.02041 0.01926 0.01870 0.01667 0.01659 0.01609 0.01582
##      PC11     PC12     PC13     PC14     PC15     PC16     PC17     PC18     PC19     PC20
## 0.01564 0.01542 0.01445 0.01441 0.01401 0.01347 0.01299 0.01280 0.01264 0.01247
##      PC21     PC22     PC23     PC24     PC25     PC26     PC27     PC28     PC29     PC30
## 0.01188 0.01169 0.01161 0.01141 0.01128 0.01107 0.01092 0.01086 0.01074 0.01069
##      PC31     PC32     PC33     PC34     PC35     PC36     PC37     PC38     PC39     PC40
## 0.01055 0.01053 0.01047 0.01045 0.01043 0.01041 0.01040 0.01040 0.01038 0.01038
##      PC41     PC42     PC43     PC44     PC45     PC46     PC47     PC48     PC49     PC50
## 0.01038 0.01037 0.01037 0.01037 0.01036 0.01036 0.01035 0.01035 0.01035 0.01034
##      PC51     PC52     PC53     PC54     PC55     PC56     PC57     PC58     PC59     PC60
## 0.01034 0.01034 0.01034 0.01033 0.01033 0.01033 0.01033 0.01033 0.01033 0.01033
##      PC61     PC62     PC63     PC64     PC65     PC66     PC67     PC68     PC69     PC70
## 0.01032 0.01032 0.01032 0.01032 0.01032 0.01032 0.00909 0.00865 0.00844 0.00807
##      PC71     PC72     PC73     PC74     PC75     PC76     PC77     PC78     PC79     PC80
## 0.00779 0.00751 0.00716 0.00701 0.00697 0.00656 0.00640 0.00615 0.00592 0.00569
##      PC81     PC82     PC83     PC84     PC85     PC86     PC87     PC88     PC89     PC90
## 0.00551 0.00548 0.00541 0.00506 0.00491 0.00465 0.00446 0.00423 0.00396 0.00391
##      PC91     PC92     PC93     PC94     PC95     PC96     PC97
## 0.00249 0.00224 0.00171 0.00073 0.00000 0.00000 0.00000
```

```
var_explained_scaled <- pca_scaled$sdev^2 / sum(pca_scaled$sdev^2)
var_explained_scaled
```

```
## [1] 4.889256e-02 2.594803e-02 2.176510e-02 2.040904e-02 1.926158e-02
## [6] 1.869921e-02 1.666947e-02 1.658714e-02 1.608963e-02 1.581614e-02
## [11] 1.563715e-02 1.542423e-02 1.445229e-02 1.440710e-02 1.400860e-02
## [16] 1.347411e-02 1.298813e-02 1.279803e-02 1.263579e-02 1.247434e-02
## [21] 1.188109e-02 1.169255e-02 1.161020e-02 1.140667e-02 1.128418e-02
## [26] 1.106558e-02 1.091880e-02 1.085553e-02 1.073962e-02 1.068812e-02
## [31] 1.054898e-02 1.053097e-02 1.046834e-02 1.045115e-02 1.043235e-02
## [36] 1.041157e-02 1.040194e-02 1.039872e-02 1.038276e-02 1.037829e-02
```

```
## [41] 1.037630e-02 1.037073e-02 1.036893e-02 1.036726e-02 1.036068e-02
## [46] 1.035628e-02 1.035416e-02 1.035066e-02 1.034546e-02 1.034284e-02
## [51] 1.033965e-02 1.033812e-02 1.033652e-02 1.033415e-02 1.033211e-02
## [56] 1.033136e-02 1.032894e-02 1.032789e-02 1.032681e-02 1.032562e-02
## [61] 1.032492e-02 1.032468e-02 1.032440e-02 1.032399e-02 1.032396e-02
## [66] 1.032396e-02 9.092377e-03 8.649994e-03 8.440216e-03 8.066639e-03
## [71] 7.790055e-03 7.514609e-03 7.159540e-03 7.014764e-03 6.966526e-03
## [76] 6.560508e-03 6.399497e-03 6.151210e-03 5.923096e-03 5.688282e-03
## [81] 5.507526e-03 5.483477e-03 5.407426e-03 5.058265e-03 4.907720e-03
## [86] 4.649017e-03 4.458306e-03 4.233942e-03 3.961926e-03 3.905161e-03
## [91] 2.491824e-03 2.238729e-03 1.707774e-03 7.261360e-04 3.641344e-32
## [96] 1.865096e-32 1.001831e-32
```

```
# plotting scree plot for scaled PCA
qplot(c(1:97), var_explained_scaled) +
  geom_line() +
  xlab("Principal Component (Scaled PCA)") +
  ylab("Variance Explained") +
  ggtitle("Scree Plot") +
  ylim(0, 1)
```



```
# In scaled PCA, the first principal component explains 0.04889 or 4.9% of the
# variance and the second principal componenet explains 0.02595 or 2.6% of the
# variance
```

```
# performing unscaled PCA
pca_unscaled <- prcomp(pca_data)
s_pca_unscaled <- summary(pca_unscaled)
s_pca_unscaled
```

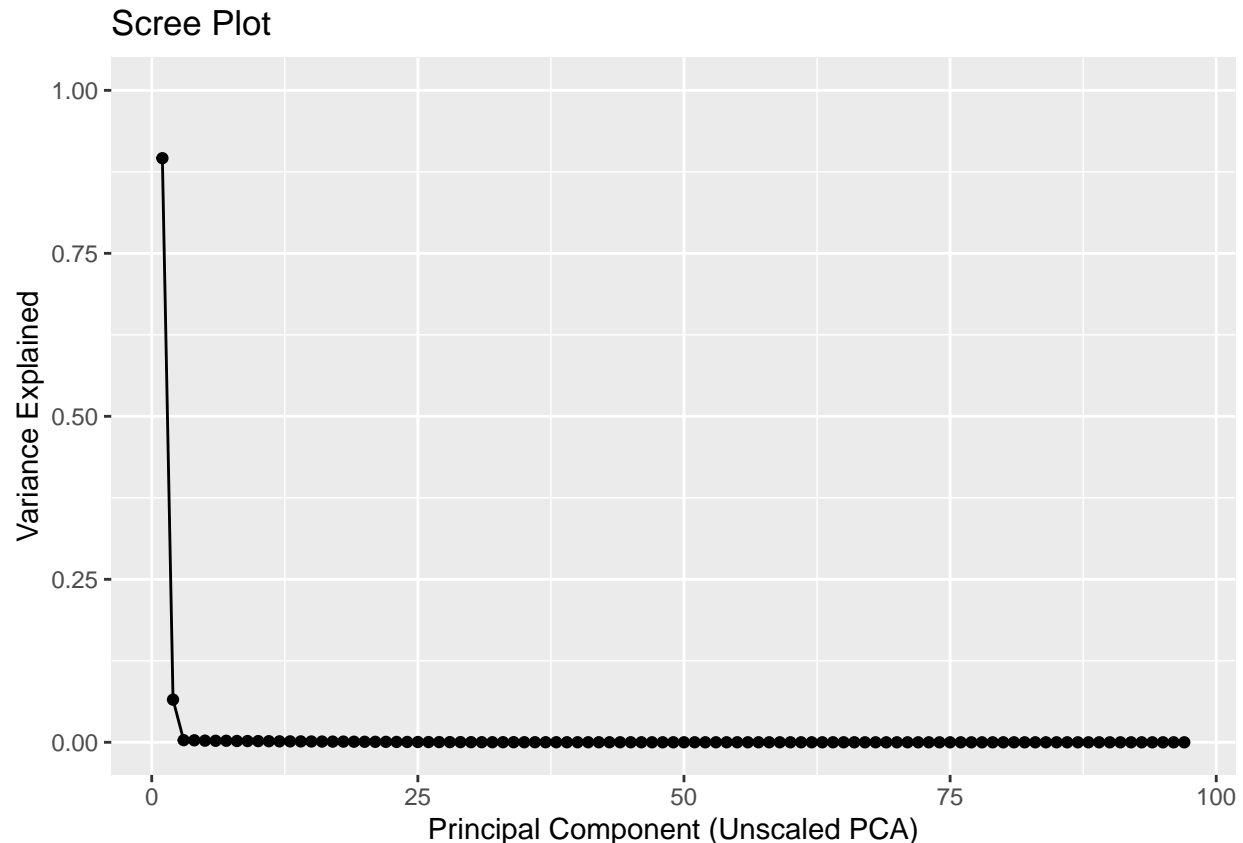
```
## Importance of components:
##          PC1      PC2      PC3      PC4      PC5      PC6      PC7
## Standard deviation  9.7048 2.62280 0.58556 0.56836 0.51553 0.49585 0.49331
## Proportion of Variance 0.8959 0.06543 0.00326 0.00307 0.00253 0.00234 0.00231
## Cumulative Proportion 0.8959 0.96130 0.96457 0.96764 0.97017 0.97250 0.97482
##          PC8      PC9      PC10     PC11     PC12     PC13     PC14
## Standard deviation  0.45747 0.44993 0.43774 0.41800 0.39434 0.38862 0.38472
## Proportion of Variance 0.00199 0.00193 0.00182 0.00166 0.00148 0.00144 0.00141
## Cumulative Proportion 0.97681 0.97874 0.98056 0.98222 0.98370 0.98514 0.98654
##          PC15     PC16     PC17     PC18     PC19     PC20     PC21
## Standard deviation  0.36234 0.34819 0.33639 0.33164 0.30533 0.29257 0.27853
## Proportion of Variance 0.00125 0.00115 0.00108 0.00105 0.00089 0.00081 0.00074
## Cumulative Proportion 0.98779 0.98895 0.99002 0.99107 0.99195 0.99277 0.99351
##          PC22     PC23     PC24     PC25     PC26     PC27     PC28
## Standard deviation  0.27380 0.24424 0.23817 0.21472 0.20061 0.18013 0.1776
## Proportion of Variance 0.00071 0.00057 0.00054 0.00044 0.00038 0.00031 0.0003
## Cumulative Proportion 0.99422 0.99479 0.99533 0.99577 0.99615 0.99646 0.9968
##          PC29     PC30     PC31     PC32     PC33     PC34     PC35
## Standard deviation  0.16740 0.14089 0.13616 0.13037 0.12906 0.12334 0.11707
## Proportion of Variance 0.00027 0.00019 0.00018 0.00016 0.00016 0.00014 0.00013
## Cumulative Proportion 0.99702 0.99721 0.99739 0.99755 0.99771 0.99785 0.99798
##          PC36     PC37     PC38     PC39     PC40     PC41     PC42
## Standard deviation  0.11102 0.10803 0.1043 0.09930 0.09768 0.09577 0.08868
## Proportion of Variance 0.00012 0.00011 0.0001 0.00009 0.00009 0.00009 0.00007
## Cumulative Proportion 0.99810 0.99821 0.9983 0.99841 0.99850 0.99859 0.99866
##          PC43     PC44     PC45     PC46     PC47     PC48     PC49
## Standard deviation  0.08394 0.08317 0.08144 0.07800 0.07566 0.07489 0.07388
## Proportion of Variance 0.00007 0.00007 0.00006 0.00006 0.00005 0.00005 0.00005
## Cumulative Proportion 0.99873 0.99880 0.99886 0.99892 0.99897 0.99902 0.99908
##          PC50     PC51     PC52     PC53     PC54     PC55     PC56
## Standard deviation  0.07209 0.06962 0.06763 0.06474 0.06382 0.06322 0.06238
## Proportion of Variance 0.00005 0.00005 0.00004 0.00004 0.00004 0.00004 0.00004
## Cumulative Proportion 0.99913 0.99917 0.99921 0.99925 0.99929 0.99933 0.99937
##          PC57     PC58     PC59     PC60     PC61     PC62     PC63
## Standard deviation  0.06084 0.05994 0.05613 0.05294 0.05232 0.05176 0.05111
## Proportion of Variance 0.00004 0.00003 0.00003 0.00003 0.00003 0.00003 0.00002
## Cumulative Proportion 0.99940 0.99944 0.99947 0.99949 0.99952 0.99955 0.99957
##          PC64     PC65     PC66     PC67     PC68     PC69     PC70
## Standard deviation  0.05052 0.05019 0.04805 0.04405 0.04074 0.03774 0.03774
## Proportion of Variance 0.00002 0.00002 0.00002 0.00002 0.00002 0.00001 0.00001
## Cumulative Proportion 0.99960 0.99962 0.99964 0.99966 0.99968 0.99969 0.99970
##          PC71     PC72     PC73     PC74     PC75     PC76     PC77
## Standard deviation  0.03774 0.03772 0.03770 0.03768 0.03761 0.03757 0.03750
## Proportion of Variance 0.00001 0.00001 0.00001 0.00001 0.00001 0.00001 0.00001
## Cumulative Proportion 0.99972 0.99973 0.99974 0.99976 0.99977 0.99978 0.99980
##          PC78     PC79     PC80     PC81     PC82     PC83     PC84
```

```
## Standard deviation      0.03742 0.03737 0.03733 0.03710 0.03686 0.03669 0.03659
## Proportion of Variance 0.00001 0.00001 0.00001 0.00001 0.00001 0.00001 0.00001
## Cumulative Proportion  0.99981 0.99982 0.99984 0.99985 0.99986 0.99988 0.99989
##          PC85      PC86      PC87      PC88      PC89      PC90      PC91
## Standard deviation      0.03640 0.03595 0.03584 0.03571 0.03521 0.03502 0.03341
## Proportion of Variance  0.00001 0.00001 0.00001 0.00001 0.00001 0.00001 0.00001
## Cumulative Proportion  0.99990 0.99991 0.99993 0.99994 0.99995 0.99996 0.99997
##          PC92      PC93      PC94      PC95      PC96      PC97
## Standard deviation      0.03329 0.03272 0.02874 4.343e-15 1.624e-15 2.24e-16
## Proportion of Variance  0.00001 0.00001 0.00001 0.000e+00 0.000e+00 0.00e+00
## Cumulative Proportion  0.99998 0.99999 1.00000 1.000e+00 1.000e+00 1.00e+00
```

```
var_explained_unscaled <- pca_unscaled$sdev^2 / sum(pca_unscaled$sdev^2)
var_explained_unscaled
```

```
## [1] 8.958702e-01 6.543343e-02 3.261449e-03 3.072710e-03 2.527994e-03
## [6] 2.338709e-03 2.314822e-03 1.990631e-03 1.925566e-03 1.822678e-03
## [11] 1.661943e-03 1.479140e-03 1.436535e-03 1.407821e-03 1.248821e-03
## [16] 1.153179e-03 1.076333e-03 1.046202e-03 8.867421e-04 8.141947e-04
## [21] 7.379317e-04 7.130993e-04 5.674283e-04 5.395552e-04 4.385650e-04
## [26] 3.828109e-04 3.086195e-04 2.999022e-04 2.665512e-04 1.888010e-04
## [31] 1.763498e-04 1.616571e-04 1.584417e-04 1.446959e-04 1.303671e-04
## [36] 1.172478e-04 1.110078e-04 1.035078e-04 9.380114e-05 9.076055e-05
## [41] 8.723607e-05 7.480831e-05 6.701534e-05 6.579001e-05 6.307995e-05
## [46] 5.786980e-05 5.444641e-05 5.334964e-05 5.192155e-05 4.943062e-05
## [51] 4.610092e-05 4.350214e-05 3.986910e-05 3.873665e-05 3.801895e-05
## [56] 3.700889e-05 3.521101e-05 3.417624e-05 2.997256e-05 2.665905e-05
## [61] 2.603710e-05 2.548463e-05 2.484677e-05 2.427758e-05 2.396233e-05
## [66] 2.195679e-05 1.845695e-05 1.578866e-05 1.354977e-05 1.354977e-05
## [71] 1.354848e-05 1.353519e-05 1.352157e-05 1.350200e-05 1.345758e-05
## [76] 1.342510e-05 1.337876e-05 1.331641e-05 1.328059e-05 1.325390e-05
## [81] 1.309374e-05 1.292344e-05 1.280331e-05 1.273584e-05 1.260238e-05
## [86] 1.229196e-05 1.222009e-05 1.213253e-05 1.179274e-05 1.166231e-05
## [91] 1.061660e-05 1.054368e-05 1.018294e-05 7.855719e-06 1.794417e-31
## [96] 2.508540e-32 4.772531e-34
```

```
# plotting scree plot for unscaled PCA
qplot(c(1:97), var_explained_unscaled) +
  geom_line() +
  xlab("Principal Component (Unscaled PCA)") +
  ylab("Variance Explained") +
  ggtitle("Scree Plot") +
  ylim(0, 1)
```



```
# In unscaled PCA, the first principal component explains 0.89587 or 89.6% of the
# variance and the second principal componenet explains 0.06543 or 6.5% of the
# variance, giving a cumulative explained variance of 0.96130 or 96.1%
# so we can use the first two principal components for visualizing our data in two
# dimensions in a scatter plot
# ans we can select first five principal components for using with Machine Learning
# algorithms
# First five principal components give us a cumulative proportion of 0.97017 or 97.02%

# After performing both scaled and unscaled PCA we can found out that unscaled PCA is
# performing better than scaled PCA in reducing the dimensions of the data

# choosing first five principal components as features for machine learning algorithms
# and adding the target column Class.ASD
Class.ASD <- cat_aut_data$Class.ASD
data <- cbind(as.data.frame(pca_unscaled$x[,1:5]), Class.ASD)

# splitting the data into training and testing set
# splitting is performed by random sampling of rown without replacement
# 20% of data is used as validation set and 80% as training set
# because training is the harder and the more complicated step of a machine learning
# algorithm and therefore training set should have a higher portion of data as
# compared to the testing or validation set
set.seed(10)
rows_test_set <- sample(rownames(data), 0.20 * nrow(data), replace = FALSE)
test_set <- data[rows_test_set,]
```

```

train_set <- data[!row.names(data) %in% rows_test_set,]

# All the implemented ML algorithms will be evaluated using
# confusion matrix, AUC, precision, recall and F1-score

# 1.) Implementing SVM
# SVM is compatible with the features in the dataset
SVM <- svm(formula = Class.ASD ~ .,
            data = train_set,
            type = "C-classification",
            kernel = "radial")

summary(SVM)

##
## Call:
## svm(formula = Class.ASD ~ ., data = train_set, type = "C-classification",
##      kernel = "radial")
##
##
## Parameters:
##      SVM-Type:  C-classification
##      SVM-Kernel: radial
##           cost:  1
##
## Number of Support Vectors:  115
##
##  ( 61 54 )
##
##
## Number of Classes:  2
##
## Levels:
##  0 1

# using our SVM to make predictions on the validation set
svmpred <- predict(SVM , test_set)

# creating SVM confusion matrix
SVM_confusion_matrix = table(svmpred, test_set$Class.ASD)
SVM_confusion_matrix

##
## svmpred    0    1
##           0 102    0
##           1   0  38

# SVM is able to correctly classify all 38 ASD patients and all 102 normal people

# Calculating SVM misclassification rate
SVM_miss_class_rate <- mean(svmpred != test_set$Class.ASD) * 100
SVM_miss_class_rate

```

```
## [1] 0
```

```
# SVM has a misclassification rate of 0%
```

```
# Calculating SVM accuracy
```

```
SVM_acc <- sum(diag(SVM_confusion_matrix)) / sum(SVM_confusion_matrix) * 100  
SVM_acc
```

```
## [1] 100
```

```
# the accuracy of SVM is 100%
```

```
# finding true positive, true negative, false positive and false negative from  
# SVM confusion matrix
```

```
true_pos_svm <- SVM_confusion_matrix[2,2]  
true_neg_svm <- SVM_confusion_matrix[1,1]  
false_pos_svm <- SVM_confusion_matrix[2,1]  
false_neg_svm <- SVM_confusion_matrix[1,2]
```

```
# Calculating SVM precision
```

```
SVM_prec <- true_pos_svm/(true_pos_svm + false_pos_svm)  
SVM_prec
```

```
## [1] 1
```

```
# the precision of SVM is 1
```

```
# Calculating SVM recall
```

```
SVM_rec <- true_pos_svm/(true_pos_svm + false_neg_svm)  
SVM_rec
```

```
## [1] 1
```

```
# the recall of SVM is 1
```

```
# Calculating F1 score for SVM
```

```
SVM_F1 <- 2 * ((SVM_prec * SVM_rec)/(SVM_prec + SVM_rec))  
SVM_F1
```

```
## [1] 1
```

```
# the F1 score for decision tree is 1
```

```
# We can use k-fold cross validation for SVM but we should not use it because the  
# algorithm is already performing well and there is no point in splitting the dataset  
# repeatedly and training/tesing the model on different portions of the dataset.
```

```
# 2.) Implementing Decision Tree
```

```
# Decision Tree is compatible with the features in the dataset
```

```
decision_tree <- rpart(Class.ASD ~., data = train_set, method = 'class')  
summary(decision_tree)
```

```
## Call:
## rpart(formula = Class.ASD ~ ., data = train_set, method = "class")
##   n= 563
##
##           CP nsplit  rel error      xerror      xstd
## 1 0.986755      0 1.00000000 1.00000000 0.069615498
## 2 0.010000      1 0.01324503 0.01324503 0.009349003
##
## Variable importance
## PC2 PC1
## 98  2
##
## Node number 1: 563 observations,      complexity param=0.986755
##   predicted class=0   expected loss=0.268206   P(node) =1
##   class counts:    412    151
##   probabilities: 0.732 0.268
##   left son=2 (410 obs) right son=3 (153 obs)
##   Primary splits:
##     PC2 < -1.524075 to the right, improve=217.054100, (0 missing)
##     PC1 < -0.8545333 to the right, improve= 8.850475, (0 missing)
##     PC3 < -0.5720943 to the left, improve= 7.738034, (0 missing)
##     PC4 < 0.7781198 to the right, improve= 4.446326, (0 missing)
##     PC5 < 0.7869657 to the right, improve= 3.325045, (0 missing)
##   Surrogate splits:
##     PC1 < -25.85237 to the right, agree=0.734, adj=0.02, (0 split)
##
## Node number 2: 410 observations
##   predicted class=0   expected loss=0   P(node) =0.7282416
##   class counts:    410      0
##   probabilities: 1.000 0.000
##
## Node number 3: 153 observations
##   predicted class=1   expected loss=0.0130719   P(node) =0.2717584
##   class counts:      2    151
##   probabilities: 0.013 0.987
```

```
# using our decision tree to make predictions on the validation set
pred_dec_tree <- predict(decision_tree, test_set, type="class")
```

```
# creating decision tree confusion matrix
dec_tree_confusion_matrix = table(pred_dec_tree, test_set$Class.ASD)
dec_tree_confusion_matrix
```

```
##
## pred_dec_tree    0    1
##               0 101    1
##               1   1   37
```

```
# Decision Tree is able to correctly classify 37 ASD patients and 101 normal people
# but it misclassifies 1 normal person as ASD patient (false positive) and
# misclassifies 1 ASD patient as normal person (false negative)
```

```
# Calculating decision tree misclassification rate
```



```
dec_tree_miss_class_rate <- mean(pred_dec_tree != test_set$Class.ASD) * 100
dec_tree_miss_class_rate
```

```
## [1] 1.428571
```

```
# Decision tree has a misclassification rate of 1.428571%
```

```
# Calculating decision tree accuracy
```

```
dec_tree_acc <- sum(diag(dec_tree_confusion_matrix)) / sum(dec_tree_confusion_matrix) * 100
dec_tree_acc
```

```
## [1] 98.57143
```

```
# the accuracy of decision tree is 98.57143%
```

```
# finding true positive, true negative, false positive and false negative from
```

```
# decision tree confusion matrix
```

```
true_pos_dec_tree <- dec_tree_confusion_matrix[2,2]
true_neg_dec_tree <- dec_tree_confusion_matrix[1,1]
false_pos_dec_tree <- dec_tree_confusion_matrix[2,1]
false_neg_dec_tree <- dec_tree_confusion_matrix[1,2]
```

```
# Calculating dec_tree precision
```

```
dec_tree_prec <- true_pos_dec_tree/(true_pos_dec_tree + false_pos_dec_tree)
dec_tree_prec
```

```
## [1] 0.9736842
```

```
# the precision of dec_tree is 0.9736842
```

```
# Calculating dec_tree recall
```

```
dec_tree_rec <- true_pos_dec_tree/(true_pos_dec_tree + false_neg_dec_tree)
dec_tree_rec
```

```
## [1] 0.9736842
```

```
# the recall of dec_tree is 0.9736842
```

```
# Calculating F1 score for dec_tree
```

```
dec_tree_F1 <- 2 * ((dec_tree_prec * dec_tree_rec)/(dec_tree_prec + dec_tree_rec))
dec_tree_F1
```

```
## [1] 0.9736842
```

```
# the F1 score for decision tree is 0.9736842
```

```
# implementing k fold cross validation for decision tree
```

```
# setting seed so that the results are reproducible
```

```
set.seed(10)
```

```
# function trainControl generates parameters that control how models will be created
# here we are applying 10 fold cross validation
train_control <- trainControl(method = "cv", number = 10, savePredictions=TRUE)
```

```
# building the decision tree model with 10 fold cross validation
# we pass entire data inside train function because train and test splitting will
# be done by k fold cross validation
model <- train(factor(Class.ASD) ~., data = data,
               trControl = train_control,
               method = "rpart")
```

```
model
```

```
## CART
##
## 703 samples
## 5 predictor
## 2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 633, 633, 632, 632, 633, 633, ...
## Resampling results across tuning parameters:
##
##   cp          Accuracy   Kappa
## 0.000000  0.9914487  0.9780722
## 0.489418  0.9914487  0.9780722
## 0.978836  0.8036419  0.2780722
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.489418.
```

```
# we are getting an accuracy of 0.9914475 at cp = 0.489418 using k-fold cross validation
```

```
# 3.) Implementing Logistic Regression
# Logistic Regression is compatible with the features in the dataset
log_reg_model <- glm(Class.ASD ~.,
                    data = train_set,
                    family = "binomial")
```

```
## Warning: glm.fit: algorithm did not converge
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
summary(log_reg_model)
```

```
##
## Call:
## glm(formula = Class.ASD ~ ., family = "binomial", data = train_set)
```

```
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -5.138e-05 -2.100e-08 -2.100e-08  2.100e-08  6.283e-05
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -74.329   13368.736  -0.006    0.996
## PC1           -1.272     603.456  -0.002    0.998
## PC2          -43.353    7629.752  -0.006    0.995
## PC3           -2.106    6985.649   0.000    1.000
## PC4           -2.228    8204.870   0.000    1.000
## PC5            0.320     8733.300   0.000    1.000
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 6.5473e+02  on 562  degrees of freedom
## Residual deviance: 5.2698e-08  on 557  degrees of freedom
## AIC: 12
##
## Number of Fisher Scoring iterations: 25

# using our Logistic Regression model to make predictions on the validation set
pred_log_reg <- predict(log_reg_model, test_set, type="response")
pred_log_reg <- ifelse(pred_log_reg > 0.5, 1, 0)

# creating logistic regression confusion matrix
log_reg_confusion_matrix = table(pred_log_reg, test_set$Class.ASD)
log_reg_confusion_matrix

##
## pred_log_reg    0    1
##           0 102    0
##           1    0   38

# Logistic Regression is able to correctly classify all ASD patients and all normal
# people

# Calculating logistic regression misclassification rate
log_reg_miss_class_rate <- mean(pred_log_reg != test_set$Class.ASD) * 100
log_reg_miss_class_rate

## [1] 0

# Decision tree has a misclassification rate of 0%

# Calculating logistic regression accuracy
log_reg_acc <- sum(diag(log_reg_confusion_matrix)) / sum(log_reg_confusion_matrix) * 100
log_reg_acc

## [1] 100
```

```

# the accuracy of decision tree is 100%

# finding true positive, true negative, false positive and false negative from
# logistic regression confusion matrix
true_pos_log_reg <- log_reg_confusion_matrix[2,2]
true_neg_log_reg <- log_reg_confusion_matrix[1,1]
false_pos_log_reg <- log_reg_confusion_matrix[2,1]
false_neg_log_reg <- log_reg_confusion_matrix[1,2]

# Calculating log_reg precision
log_reg_prec <- true_pos_log_reg/(true_pos_log_reg + false_pos_log_reg)
log_reg_prec

```

```
## [1] 1
```

```

# the precision of log_reg is 1

# Calculating log_reg recall
log_reg_rec <- true_pos_log_reg/(true_pos_log_reg + false_neg_log_reg)
log_reg_rec

```

```
## [1] 1
```

```

# the recall of log_reg is 1

# Calculating F1 score for log_reg
log_reg_F1 <- 2 * ((log_reg_prec * log_reg_rec)/(log_reg_prec + log_reg_rec))
log_reg_F1

```

```
## [1] 1
```

```

# the F1 score for logistic regression is 1

# We can use k-fold cross validation for logistic regression but we should not use it
# because the algorithm is already performing well and there is no point in splitting
# the dataset repeatedly and training/testing the model on different portions of the
# dataset.

```

```

# 3.) Implementing Artificial Neural Network
# Logistic Regression is compatible with the features in the dataset

# fitting the neural network
set.seed(10)
ANN <- neuralnet(Class.ASD ~ .,
                  data = train_set,
                  hidden = c(4))

# number of neurons in the hidden layer taken as 1 less than the number of features

```

```

# making predictions using ANN
ANN_result <- compute(ANN, rep = 1, test_set[, -6])
ANN_predictions <- ANN_result$net.result
ANN_predictions <- ifelse(ANN_predictions > 0.5, 1, 0)

# creating ANN confusion matrix
ANN_confusion_matrix <- table(ANN_predictions, test_set$Class.ASD)
ANN_confusion_matrix

##
## ANN_predictions    0    1
##                0 102    0
##                1   0   38

# ANN is able to correctly classify all ASD patients and all normal people

# calculating ANN misclassification rate
ANN_misclass_rate <- mean(ANN_predictions != test_set$Class.ASD) * 100
ANN_misclass_rate

## [1] 0

# ANN misclassification rate is 0%

# calculating ANN accuracy
ANN_acc <- sum(diag(ANN_confusion_matrix)) / sum(ANN_confusion_matrix) * 100
ANN_acc

## [1] 100

# the accuracy from neural network is 100%

# calculating true positive, true negative, false positive and false negative
# from the ANN confusion matrix
true_pos_ANN <- ANN_confusion_matrix[2,2]
true_neg_ANN <- ANN_confusion_matrix[1,1]
false_pos_ANN <- ANN_confusion_matrix[2,1]
false_neg_ANN <- ANN_confusion_matrix[1,2]

# calculating ANN precision
ANN_prec <- true_pos_ANN/(true_pos_ANN + false_pos_ANN)
ANN_prec

## [1] 1

# ANN precision is 1

# calculating ANN recall
ANN_recall <- true_pos_ANN/(true_pos_ANN + false_neg_ANN)
ANN_recall

```

```
## [1] 1
```

```
# ANN recall is 1
```

```
# Calculating F1 score for log_reg
```

```
ANN_F1 <- 2 * ((ANN_prec * ANN_recall)/(ANN_prec + ANN_recall))
```

```
ANN_F1
```

```
## [1] 1
```

```
# the F1 score for ANN is 1
```

```
# We can use k-fold cross validation for logistic regression but we should not use it  
# because the algorithm is already performing well and there is no point in splitting  
# the dataset repeatedly and training/testing the model on different portions of the  
# dataset.
```

```
# Applying two ensemble techniques bagging and boosting
```

```
# Applying two Bagging algorithms:
```

```
# 1.) Treebag
```

```
control <- trainControl(method="repeatedcv", number=10, repeats=3)
```

```
seed <- 7
```

```
metric <- "Accuracy"
```

```
# Bagged CART
```

```
set.seed(seed)
```

```
fit.treebag <- train(factor(Class.ASD)~., data=data, method="treebag", metric=metric, trControl=control)
```

```
# 2.) Random Forest
```

```
set.seed(seed)
```

```
fit.rf <- train(factor(Class.ASD)~., data=data, method="rf", metric=metric, trControl=control)
```

```
# summarize results for both bagging algorithms
```

```
bagging_results <- resamples(list(treebag=fit.treebag, rf=fit.rf))
```

```
summary(bagging_results)
```

```
##
```

```
## Call:
```

```
## summary.resamples(object = bagging_results)
```

```
##
```

```
## Models: treebag, rf
```

```
## Number of resamples: 30
```

```
##
```

```
## Accuracy
```

```
##           Min.    1st Qu.    Median      Mean 3rd Qu.  Max. NA's
```

```
## treebag 0.9571429 0.9857143 0.9859155 0.9905229      1      1      0
```

```
## rf      0.9714286 1.0000000 1.0000000 0.9966732      1      1      0
```

```
##
```

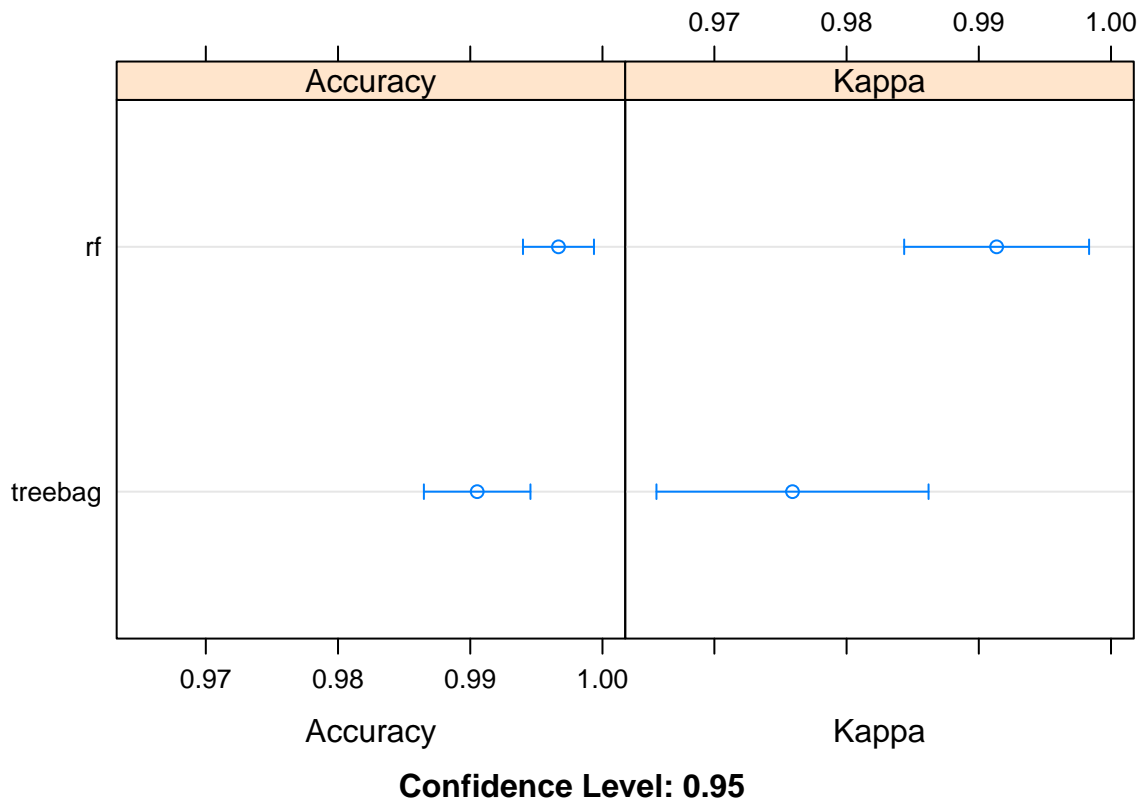
```
## Kappa
```

```
##           Min.    1st Qu.    Median      Mean 3rd Qu.  Max. NA's
```

```
## treebag 0.8898216 0.9637107 0.964659 0.9759094      1      1      0
```

```
## rf      0.9252935 1.0000000 1.000000 0.9913496      1      1      0
```

```
dotplot(bagging_results)
```



```
# treebag is giving a mean accuracy of 0.9856107 whereas random forest is giving
# a mean accuracy of 0.9926671

# Applying two boosting algorithms:
# C5.0
set.seed(seed)
fit.c50 <- train(factor(Class.ASD)~., data=data, method="C5.0", metric=metric, trControl=control)

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 9 for this object. Predictions generated using 9
## trials

## Warning: 'trials' should be <= 9 for this object. Predictions generated using 9
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials
```

```
## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials
```



```
## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials
```

```
## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials
```

```
## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials
```

```
## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 4 for this object. Predictions generated using 4
## trials

## Warning: 'trials' should be <= 4 for this object. Predictions generated using 4
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 8 for this object. Predictions generated using 8
## trials

## Warning: 'trials' should be <= 7 for this object. Predictions generated using 7
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials

## Warning: 'trials' should be <= 1 for this object. Predictions generated using 1
## trials

## Warning: 'trials' should be <= 3 for this object. Predictions generated using 3
## trials
```

```
## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials
```

```
## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials
```

```
## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials
```

```
## Warning: 'trials' should be <= 6 for this object. Predictions generated using 6
## trials
```

```
# Stochastic Gradient Boosting
```

```
set.seed(seed)
```

```
fit.gbm <- train(factor(Class.ASD)~., data=data, method="gbm", metric=metric, trControl=control, verbose=0)
```

```
# summarize results
```

```
boosting_results <- resamples(list(c5.0=fit.c50, gbm=fit.gbm))
```

```
summary(boosting_results)
```

```
##
```

```
## Call:
```

```
## summary.resamples(object = boosting_results)
```

```
##
```

```
## Models: c5.0, gbm
```

```
## Number of resamples: 30
```

```
##
```

```
## Accuracy
```

```
##           Min.    1st Qu. Median      Mean 3rd Qu. Max. NA's
```

```
## c5.0 0.9571429 1.0000000      1 0.9957277      1    1    0
```

```
## gbm  0.9855072 0.9894366      1 0.9962037      1    1    0
```

```
##
```

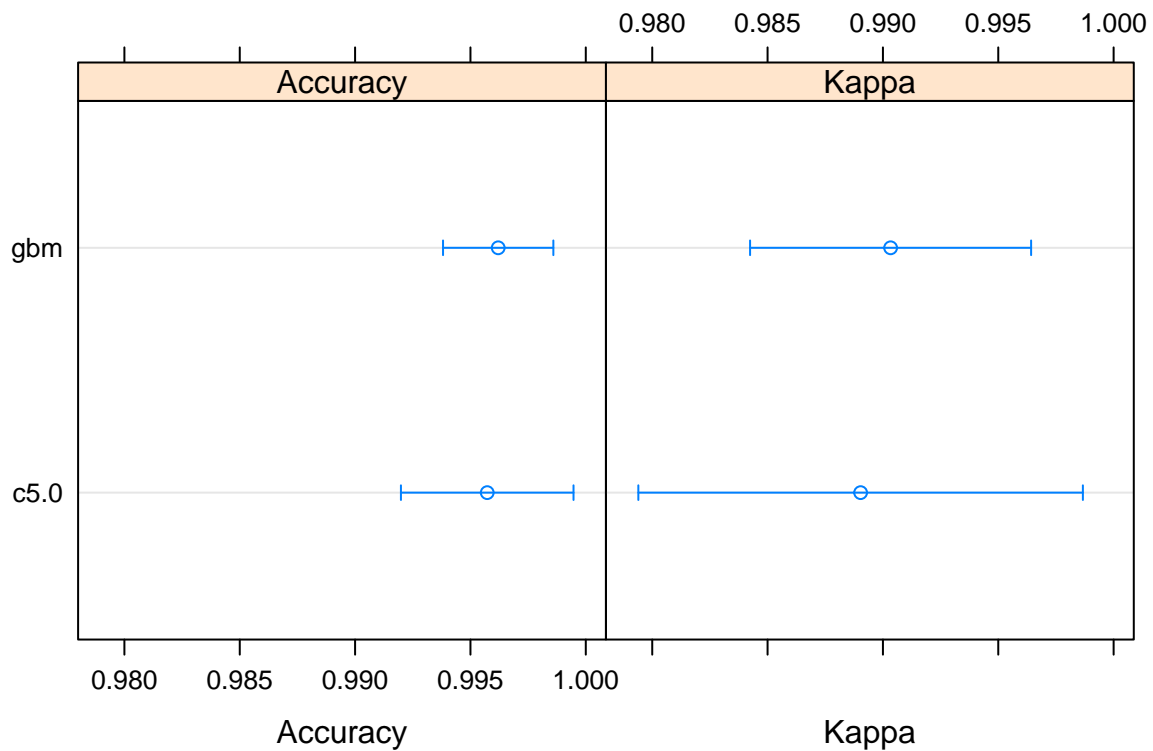
```
## Kappa
```

```
##           Min.    1st Qu. Median      Mean 3rd Qu. Max. NA's
```

```
## c5.0 0.8898216 1.0000000      1 0.9890325      1    1    0
```

```
## gbm  0.9617304 0.9734943      1 0.9903330      1    1    0
```

```
dotplot(boosting_results)
```



Confidence Level: 0.95

```
# Mean accuracy of C5.0 is 0.9971429
# Mean accuracy of gbm is also 0.9971429
# both the boosting algorithms are giving same accuracy

# Performing hyperparameter tuning for stochastic gradient boosting
hyperparameter_grid <- expand.grid(
  .n.trees = c(250, 500),
  .interaction.depth=c(2,3),
  .shrinkage=0.5,
  .n.minobsinnode=10
)

data_2 <- data[,-6]
target_class <- factor(ifelse(data$Class.ASD == 0, "No", "Yes"))
data_2 <- cbind(data_2, target_class)
fit_tuned <- train(target_class ~ . , data = data_2,
  method = "gbm",
  trControl = trainControl(method="cv", number = 5, verboseIter = TRUE, classProbs = TRUE),
  tuneGrid = hyperparameter_grid)

## + Fold1: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## Iter  TrainDeviance  ValidDeviance  StepSize  Improve
##      1           0.4599           nan      0.5000   0.3435
##      2           0.2674           nan      0.5000   0.0939
##      3           0.1683           nan      0.5000   0.0467
##      4           0.1118           nan      0.5000   0.0244
```

##	5	0.0811	nan	0.5000	0.0118
##	6	0.0524	nan	0.5000	0.0102
##	7	0.0416	nan	0.5000	-0.0002
##	8	0.0257	nan	0.5000	0.0046
##	9	0.0226	nan	0.5000	-0.0001
##	10	0.0220	nan	0.5000	-0.0009
##	20	0.0132	nan	0.5000	-0.0039
##	40	0.0054	nan	0.5000	-0.0008
##	60	0.0033	nan	0.5000	-0.0008
##	80	0.0004	nan	0.5000	-0.0001
##	100	0.0003	nan	0.5000	-0.0001
##	120	0.0003	nan	0.5000	-0.0001
##	140	0.0002	nan	0.5000	-0.0000
##	160	0.0000	nan	0.5000	-0.0000
##	180	0.0000	nan	0.5000	-0.0000
##	200	0.0000	nan	0.5000	-0.0000
##	220	0.0000	nan	0.5000	-0.0000
##	240	0.0000	nan	0.5000	0.0000
##	260	0.0001	nan	0.5000	-0.0001
##	280	0.0000	nan	0.5000	-0.0000
##	300	0.0000	nan	0.5000	-0.0000
##	320	0.0000	nan	0.5000	-0.0000
##	340	0.0002	nan	0.5000	-0.0001
##	360	0.0000	nan	0.5000	-0.0000
##	380	0.0000	nan	0.5000	-0.0000
##	400	0.0000	nan	0.5000	-0.0000
##	420	0.0000	nan	0.5000	-0.0000
##	440	0.0000	nan	0.5000	-0.0000
##	460	0.0001	nan	0.5000	-0.0000
##	480	0.0001	nan	0.5000	-0.0000
##	500	0.0000	nan	0.5000	-0.0000

##

- Fold1: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500

+ Fold1: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500

##	Iter	TrainDeviance	ValidDeviance	StepSize	Improve
##	1	0.4595	nan	0.5000	0.3808
##	2	0.2714	nan	0.5000	0.0879
##	3	0.1679	nan	0.5000	0.0498
##	4	0.1078	nan	0.5000	0.0278
##	5	0.0616	nan	0.5000	0.0248
##	6	0.0382	nan	0.5000	0.0079
##	7	0.0265	nan	0.5000	0.0040
##	8	0.0205	nan	0.5000	0.0019
##	9	0.0164	nan	0.5000	0.0001
##	10	0.0134	nan	0.5000	0.0012
##	20	0.0065	nan	0.5000	-0.0007
##	40	0.0012	nan	0.5000	-0.0002
##	60	0.0012	nan	0.5000	-0.0003
##	80	0.0011	nan	0.5000	-0.0000
##	100	0.0009	nan	0.5000	-0.0000
##	120	0.0006	nan	0.5000	-0.0001
##	140	0.0008	nan	0.5000	-0.0002
##	160	0.0016	nan	0.5000	-0.0005
##	180	0.0005	nan	0.5000	-0.0001

```

##      200      0.0004      nan      0.5000      0.0000
##      220      0.0004      nan      0.5000     -0.0001
##      240      0.0004      nan      0.5000     -0.0001
##      260      0.0006      nan      0.5000     -0.0002
##      280      0.0003      nan      0.5000     -0.0000
##      300      0.0001      nan      0.5000     -0.0000
##      320      0.0006      nan      0.5000     -0.0002
##      340      0.0002      nan      0.5000     -0.0000
##      360      0.0000      nan      0.5000     -0.0000
##      380      0.0005      nan      0.5000     -0.0002
##      400      0.0001      nan      0.5000     -0.0000
##      420      0.0000      nan      0.5000     -0.0000
##      440      0.0000      nan      0.5000     -0.0000
##      460      0.0003      nan      0.5000     -0.0001
##      480      0.0001      nan      0.5000     -0.0000
##      500      0.0000      nan      0.5000     -0.0000
##
## - Fold1: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## + Fold2: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4597      nan      0.5000      0.3460
##      2      0.2610      nan      0.5000      0.0956
##      3      0.1649      nan      0.5000      0.0466
##      4      0.1108      nan      0.5000      0.0229
##      5      0.0660      nan      0.5000      0.0160
##      6      0.0455      nan      0.5000      0.0089
##      7      0.0351      nan      0.5000      0.0039
##      8      0.0270      nan      0.5000      0.0014
##      9      0.0241      nan      0.5000      0.0007
##     10      0.0208      nan      0.5000     -0.0006
##     20      0.0027      nan      0.5000      0.0004
##     40      0.0007      nan      0.5000     -0.0001
##     60      0.0003      nan      0.5000      0.0000
##     80      0.0005      nan      0.5000      0.0001
##    100      0.0001      nan      0.5000      0.0000
##    120      0.0001      nan      0.5000     -0.0000
##    140      0.0002      nan      0.5000     -0.0001
##    160      0.0000      nan      0.5000     -0.0000
##    180      0.0000      nan      0.5000     -0.0000
##    200      0.0000      nan      0.5000     -0.0000
##    220      0.0000      nan      0.5000     -0.0000
##    240      0.0000      nan      0.5000     -0.0000
##    260      0.0000      nan      0.5000     -0.0000
##    280      0.0000      nan      0.5000     -0.0000
##    300      0.0000      nan      0.5000     -0.0000
##    320      0.0000      nan      0.5000     -0.0000
##    340      0.0000      nan      0.5000     -0.0000
##    360      0.0000      nan      0.5000     -0.0000
##    380      0.0000      nan      0.5000     -0.0000
##    400      0.0000      nan      0.5000     -0.0000
##    420      0.0000      nan      0.5000     -0.0000
##    440      0.0000      nan      0.5000     -0.0000
##    460      0.0000      nan      0.5000     -0.0000
##    480      0.0000      nan      0.5000     -0.0000

```



```

##      500      0.0000      nan      0.5000     -0.0000
##
## - Fold2: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## + Fold2: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4612      nan      0.5000     0.3445
##      2      0.2650      nan      0.5000     0.0968
##      3      0.1638      nan      0.5000     0.0510
##      4      0.1075      nan      0.5000     0.0256
##      5      0.0747      nan      0.5000     0.0120
##      6      0.0478      nan      0.5000     0.0118
##      7      0.0331      nan      0.5000     0.0051
##      8      0.0214      nan      0.5000     0.0030
##      9      0.0148      nan      0.5000     0.0031
##     10      0.0133      nan      0.5000    -0.0006
##     20      0.0049      nan      0.5000    -0.0002
##     40      0.0046      nan      0.5000    -0.0003
##     60      0.0003      nan      0.5000    -0.0001
##     80      0.0002      nan      0.5000    -0.0000
##    100      0.0000      nan      0.5000    -0.0000
##    120      0.0001      nan      0.5000    -0.0000
##    140      0.0000      nan      0.5000    -0.0000
##    160      0.0000      nan      0.5000    -0.0000
##    180      0.0000      nan      0.5000    -0.0000
##    200      0.0000      nan      0.5000     0.0000
##    220      0.0000      nan      0.5000    -0.0000
##    240      0.0000      nan      0.5000    -0.0000
##    260      0.0000      nan      0.5000    -0.0000
##    280      0.0000      nan      0.5000    -0.0000
##    300      0.0000      nan      0.5000    -0.0000
##    320      0.0000      nan      0.5000    -0.0000
##    340      0.0000      nan      0.5000    -0.0000
##    360      0.0000      nan      0.5000     0.0000
##    380      0.0000      nan      0.5000    -0.0000
##    400      0.0000      nan      0.5000    -0.0000
##    420      0.0000      nan      0.5000    -0.0000
##    440      0.0000      nan      0.5000    -0.0000
##    460      0.0000      nan      0.5000    -0.0000
##    480      0.0000      nan      0.5000    -0.0000
##    500      0.0000      nan      0.5000    -0.0000
##
## - Fold2: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## + Fold3: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4643      nan      0.5000     0.3402
##      2      0.2622      nan      0.5000     0.1039
##      3      0.1598      nan      0.5000     0.0501
##      4      0.1020      nan      0.5000     0.0281
##      5      0.0680      nan      0.5000     0.0150
##      6      0.0483      nan      0.5000     0.0077
##      7      0.0311      nan      0.5000     0.0057
##      8      0.0217      nan      0.5000     0.0027
##      9      0.0184      nan      0.5000     0.0005
##     10      0.0126      nan      0.5000     0.0013

```

```

##      20      0.0018      nan      0.5000      0.0001
##      40      0.0032      nan      0.5000     -0.0007
##      60      0.0015      nan      0.5000     -0.0004
##      80      0.0007      nan      0.5000     -0.0001
##     100      0.0005      nan      0.5000     -0.0001
##     120      0.0002      nan      0.5000     -0.0000
##     140      0.0001      nan      0.5000     -0.0000
##     160      0.0001      nan      0.5000     -0.0000
##     180      0.0001      nan      0.5000     -0.0000
##     200      0.0000      nan      0.5000     -0.0000
##     220      0.0000      nan      0.5000     -0.0000
##     240      0.0000      nan      0.5000      0.0000
##     260      0.0000      nan      0.5000      0.0000
##     280      0.0000      nan      0.5000      0.0000
##     300      0.0000      nan      0.5000     -0.0000
##     320      0.0000      nan      0.5000     -0.0000
##     340      0.0000      nan      0.5000     -0.0000
##     360      0.0000      nan      0.5000      0.0000
##     380      0.0000      nan      0.5000     -0.0000
##     400      0.0000      nan      0.5000      0.0000
##     420      0.0000      nan      0.5000     -0.0000
##     440      0.0000      nan      0.5000     -0.0000
##     460      0.0000      nan      0.5000     -0.0000
##     480      0.0000      nan      0.5000     -0.0000
##     500      0.0000      nan      0.5000     -0.0000
##
## - Fold3: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## + Fold3: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1         0.4548         nan      0.5000    0.3306
##      2         0.2636         nan      0.5000    0.0929
##      3         0.1634         nan      0.5000    0.0474
##      4         0.1085         nan      0.5000    0.0257
##      5         0.0762         nan      0.5000    0.0139
##      6         0.0536         nan      0.5000    0.0083
##      7         0.0316         nan      0.5000    0.0110
##      8         0.0264         nan      0.5000    0.0011
##      9         0.0172         nan      0.5000    0.0003
##     10         0.0144         nan      0.5000   -0.0012
##     20         0.0059         nan      0.5000   -0.0007
##     40         0.0032         nan      0.5000   -0.0007
##     60         0.0010         nan      0.5000   -0.0001
##     80         0.0035         nan      0.5000   -0.0008
##    100         0.0007         nan      0.5000   -0.0000
##    120         0.0004         nan      0.5000   -0.0000
##    140         0.0011         nan      0.5000    0.0006
##    160         0.0004         nan      0.5000   -0.0000
##    180         0.0003         nan      0.5000   -0.0000
##    200         0.0008         nan      0.5000   -0.0003
##    220         0.0001         nan      0.5000   -0.0000
##    240         0.0006         nan      0.5000   -0.0002
##    260         0.0001         nan      0.5000   -0.0000
##    280         0.0001         nan      0.5000   -0.0000
##    300         0.0001         nan      0.5000   -0.0000

```

```

##      320      0.0001      nan      0.5000     -0.0000
##      340      0.0001      nan      0.5000     -0.0000
##      360      0.0001      nan      0.5000     -0.0000
##      380      0.0001      nan      0.5000     -0.0000
##      400      0.0002      nan      0.5000     -0.0001
##      420      0.0003      nan      0.5000     -0.0001
##      440      0.0001      nan      0.5000     -0.0000
##      460      0.0002      nan      0.5000      0.0001
##      480      0.0001      nan      0.5000     -0.0000
##      500      0.0000      nan      0.5000     -0.0000
##
## - Fold3: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## + Fold4: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4479      nan      0.5000    0.3721
##      2      0.2580      nan      0.5000    0.0902
##      3      0.1564      nan      0.5000    0.0500
##      4      0.0967      nan      0.5000    0.0274
##      5      0.0634      nan      0.5000    0.0164
##      6      0.0416      nan      0.5000    0.0099
##      7      0.0297      nan      0.5000    0.0049
##      8      0.0213      nan      0.5000    0.0027
##      9      0.0116      nan      0.5000    0.0019
##     10      0.0102      nan      0.5000   -0.0002
##     20      0.0029      nan      0.5000   -0.0005
##     40      0.0006      nan      0.5000   -0.0001
##     60      0.0003      nan      0.5000   -0.0001
##     80      0.0002      nan      0.5000   -0.0000
##    100      0.0002      nan      0.5000   -0.0000
##    120      0.0000      nan      0.5000    0.0000
##    140      0.0000      nan      0.5000   -0.0000
##    160      0.0000      nan      0.5000    0.0000
##    180      0.0001      nan      0.5000   -0.0000
##    200      0.0001      nan      0.5000    0.0000
##    220      0.0000      nan      0.5000    0.0000
##    240      0.0000      nan      0.5000   -0.0000
##    260      0.0000      nan      0.5000   -0.0000
##    280      0.0000      nan      0.5000    0.0000
##    300      0.0000      nan      0.5000    0.0000
##    320      0.0000      nan      0.5000   -0.0000
##    340      0.0000      nan      0.5000    0.0000
##    360      0.0000      nan      0.5000   -0.0000
##    380      0.0000      nan      0.5000   -0.0000
##    400      0.0000      nan      0.5000    0.0000
##    420      0.0000      nan      0.5000   -0.0000
##    440      0.0000      nan      0.5000   -0.0000
##    460      0.0000      nan      0.5000   -0.0000
##    480      0.0000      nan      0.5000    0.0000
##    500      0.0000      nan      0.5000    0.0000
##
## - Fold4: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## + Fold4: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4558      nan      0.5000    0.3571

```

##	2	0.2585	nan	0.5000	0.0960
##	3	0.1557	nan	0.5000	0.0504
##	4	0.0968	nan	0.5000	0.0287
##	5	0.0603	nan	0.5000	0.0174
##	6	0.0412	nan	0.5000	0.0078
##	7	0.0312	nan	0.5000	0.0034
##	8	0.0224	nan	0.5000	0.0023
##	9	0.0136	nan	0.5000	0.0012
##	10	0.0101	nan	0.5000	0.0010
##	20	0.0032	nan	0.5000	-0.0006
##	40	0.0009	nan	0.5000	-0.0001
##	60	0.0008	nan	0.5000	0.0000
##	80	0.0002	nan	0.5000	-0.0000
##	100	0.0001	nan	0.5000	-0.0000
##	120	0.0000	nan	0.5000	0.0000
##	140	0.0001	nan	0.5000	-0.0000
##	160	0.0000	nan	0.5000	-0.0000
##	180	0.0000	nan	0.5000	-0.0000
##	200	0.0000	nan	0.5000	-0.0000
##	220	0.0000	nan	0.5000	0.0000
##	240	0.0000	nan	0.5000	0.0000
##	260	0.0000	nan	0.5000	-0.0000
##	280	0.0000	nan	0.5000	-0.0000
##	300	0.0000	nan	0.5000	-0.0000
##	320	0.0000	nan	0.5000	-0.0000
##	340	0.0000	nan	0.5000	-0.0000
##	360	0.0000	nan	0.5000	0.0000
##	380	0.0000	nan	0.5000	-0.0000
##	400	0.0000	nan	0.5000	-0.0000
##	420	0.0000	nan	0.5000	-0.0000
##	440	0.0000	nan	0.5000	-0.0000
##	460	0.0000	nan	0.5000	-0.0000
##	480	0.0000	nan	0.5000	-0.0000
##	500	0.0000	nan	0.5000	-0.0000

##

- Fold4: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500

+ Fold5: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500

##	Iter	TrainDeviance	ValidDeviance	StepSize	Improve
##	1	0.4513	nan	0.5000	0.3659
##	2	0.2601	nan	0.5000	0.0941
##	3	0.1607	nan	0.5000	0.0458
##	4	0.1010	nan	0.5000	0.0279
##	5	0.0672	nan	0.5000	0.0143
##	6	0.0426	nan	0.5000	0.0101
##	7	0.0306	nan	0.5000	0.0053
##	8	0.0219	nan	0.5000	0.0012
##	9	0.0201	nan	0.5000	-0.0000
##	10	0.0163	nan	0.5000	0.0011
##	20	0.0044	nan	0.5000	-0.0003
##	40	0.0014	nan	0.5000	-0.0001
##	60	0.0017	nan	0.5000	-0.0002
##	80	0.0022	nan	0.5000	-0.0006
##	100	0.0009	nan	0.5000	-0.0000
##	120	0.0007	nan	0.5000	-0.0001

```

##      140      0.0008      nan      0.5000     -0.0001
##      160      0.0002      nan      0.5000      0.0000
##      180      0.0001      nan      0.5000     -0.0000
##      200      0.0001      nan      0.5000     -0.0000
##      220      0.0001      nan      0.5000     -0.0000
##      240      0.0000      nan      0.5000     -0.0000
##      260      0.0000      nan      0.5000     -0.0000
##      280      0.0000      nan      0.5000     -0.0000
##      300      0.0001      nan      0.5000     -0.0000
##      320      0.0000      nan      0.5000     -0.0000
##      340      0.0000      nan      0.5000     -0.0000
##      360      0.0000      nan      0.5000     -0.0000
##      380      0.0000      nan      0.5000     -0.0000
##      400      0.0000      nan      0.5000     -0.0000
##      420      0.0001      nan      0.5000     -0.0000
##      440      0.0000      nan      0.5000     -0.0000
##      460      0.0001      nan      0.5000      0.0000
##      480      0.0000      nan      0.5000     -0.0000
##      500      0.0001      nan      0.5000     -0.0000
##
## - Fold5: shrinkage=0.5, interaction.depth=2, n.minobsinnode=10, n.trees=500
## + Fold5: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4505      nan      0.5000    0.3436
##      2      0.2590      nan      0.5000    0.0943
##      3      0.1580      nan      0.5000    0.0482
##      4      0.1004      nan      0.5000    0.0262
##      5      0.0690      nan      0.5000    0.0137
##      6      0.0384      nan      0.5000    0.0128
##      7      0.0273      nan      0.5000    0.0047
##      8      0.0185      nan      0.5000    0.0010
##      9      0.0130      nan      0.5000    0.0019
##     10      0.0090      nan      0.5000    0.0023
##     20      0.0031      nan      0.5000   -0.0003
##     40      0.0034      nan      0.5000   -0.0007
##     60      0.0029      nan      0.5000   -0.0006
##     80      0.0105      nan      0.5000    0.0017
##    100      0.0016      nan      0.5000   -0.0005
##    120      0.0003      nan      0.5000   -0.0000
##    140      0.0002      nan      0.5000   -0.0000
##    160      0.0001      nan      0.5000   -0.0000
##    180      0.0004      nan      0.5000    0.0002
##    200      0.0002      nan      0.5000   -0.0001
##    220      0.0004      nan      0.5000   -0.0001
##    240      0.0001      nan      0.5000   -0.0000
##    260      0.0001      nan      0.5000   -0.0000
##    280      0.0000      nan      0.5000    0.0000
##    300      0.0000      nan      0.5000   -0.0000
##    320      0.0001      nan      0.5000   -0.0000
##    340      0.0000      nan      0.5000   -0.0000
##    360      0.0001      nan      0.5000   -0.0000
##    380      0.0002      nan      0.5000   -0.0001
##    400      0.0001      nan      0.5000   -0.0000
##    420      0.0000      nan      0.5000   -0.0000

```

```

##      440      0.0000      nan    0.5000   -0.0000
##      460      0.0002      nan    0.5000   -0.0000
##      480      0.0000      nan    0.5000   -0.0000
##      500      0.0000      nan    0.5000   -0.0000
##
## - Fold5: shrinkage=0.5, interaction.depth=3, n.minobsinnode=10, n.trees=500
## Aggregating results
## Selecting tuning parameters
## Fitting n.trees = 500, interaction.depth = 3, shrinkage = 0.5, n.minobsinnode = 10 on full training s
## Iter   TrainDeviance   ValidDeviance   StepSize   Improve
##      1      0.4581      nan    0.5000    0.3488
##      2      0.2632      nan    0.5000    0.0920
##      3      0.1602      nan    0.5000    0.0515
##      4      0.1030      nan    0.5000    0.0275
##      5      0.0685      nan    0.5000    0.0151
##      6      0.0479      nan    0.5000    0.0089
##      7      0.0368      nan    0.5000    0.0040
##      8      0.0281      nan    0.5000    0.0030
##      9      0.0202      nan    0.5000    0.0015
##     10      0.0172      nan    0.5000    0.0003
##     20      0.0104      nan    0.5000   -0.0007
##     40      0.0103      nan    0.5000   -0.0011
##     60      0.0030      nan    0.5000   -0.0007
##     80      0.0016      nan    0.5000   -0.0003
##    100      0.0019      nan    0.5000   -0.0005
##    120      0.0003      nan    0.5000    0.0000
##    140      0.0005      nan    0.5000   -0.0002
##    160      0.0005      nan    0.5000   -0.0002
##    180      0.0003      nan    0.5000   -0.0000
##    200      0.0003      nan    0.5000   -0.0000
##    220      0.0004      nan    0.5000   -0.0001
##    240      0.0003      nan    0.5000   -0.0000
##    260      0.0002      nan    0.5000   -0.0001
##    280      0.0002      nan    0.5000   -0.0000
##    300      0.0003      nan    0.5000   -0.0001
##    320      0.0007      nan    0.5000   -0.0002
##    340      0.0002      nan    0.5000   -0.0000
##    360      0.0001      nan    0.5000   -0.0000
##    380      0.0015      nan    0.5000    0.0007
##    400      0.0004      nan    0.5000   -0.0000
##    420      0.0001      nan    0.5000   -0.0000
##    440      0.0003      nan    0.5000   -0.0000
##    460      0.0003      nan    0.5000   -0.0000
##    480      0.0005      nan    0.5000   -0.0002
##    500      0.0004      nan    0.5000   -0.0001

```

```
print(fit_tuned)
```

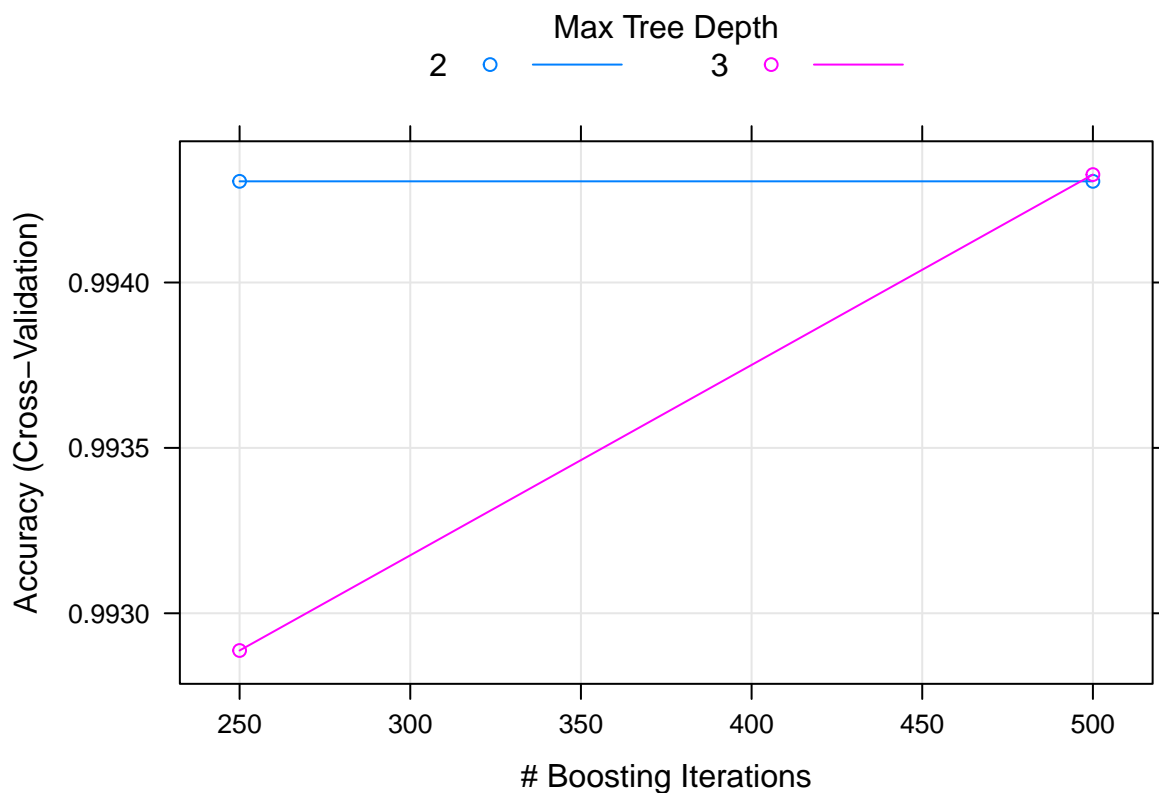
```

## Stochastic Gradient Boosting
##
## 703 samples
## 5 predictor
## 2 classes: 'No', 'Yes'
##

```

```
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 564, 562, 562, 562, 562
## Resampling results across tuning parameters:
##
##   interaction.depth  n.trees  Accuracy   Kappa
##   2                  250      0.9943058  0.9855108
##   2                  500      0.9943058  0.9855108
##   3                  250      0.9928874  0.9818179
##   3                  500      0.9943262  0.9854695
##
## Tuning parameter 'shrinkage' was held constant at a value of 0.5
##
## Tuning parameter 'n.minobsinnode' was held constant at a value of 10
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were n.trees = 500, interaction.depth =
##   3, shrinkage = 0.5 and n.minobsinnode = 10.
```

```
plot(fit_tuned)
```



```
# The following accuracies were obtained corresponding to the hyperparameters
# interaction.depth  n.trees  Accuracy   Kappa
# 2                  250      0.9971631  0.9927946
# 2                  500      0.9957447  0.9892223
# 3                  250      0.9971631  0.9926734
```

```
# 3          500      0.9957345  0.9891526

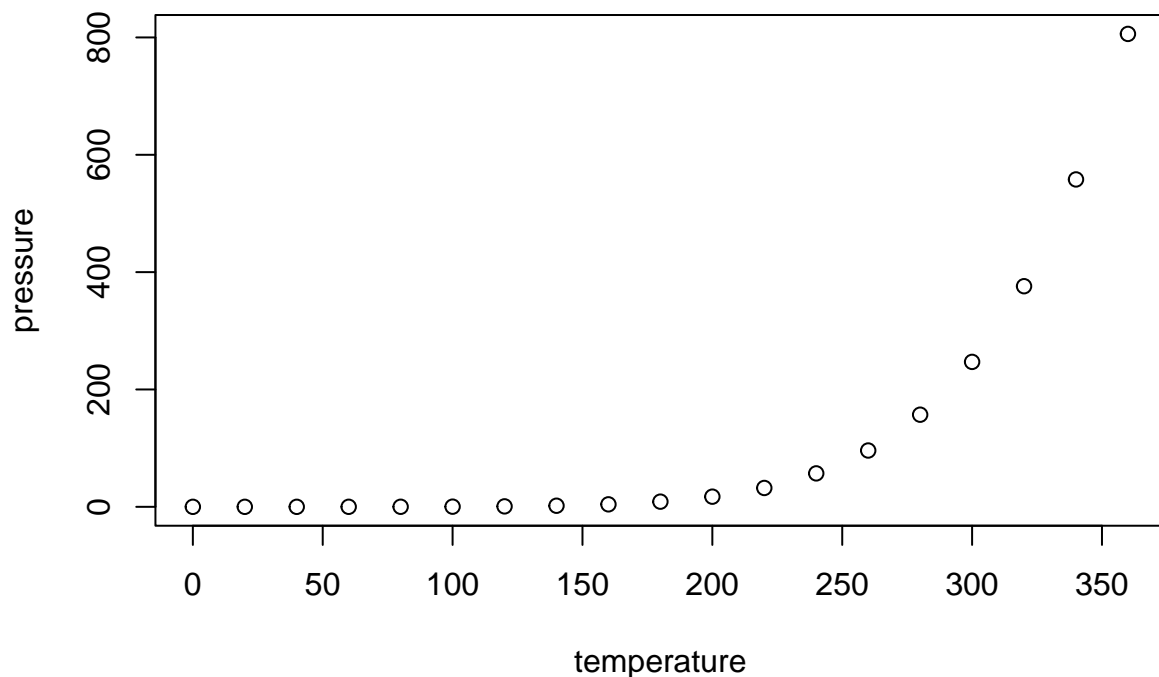
# We can see that the after hyperparameter tuning the accuracy of gbm slightly
# increased from 0.9971429 to 0.9971631 at interaction depth 2 and number of trees
# equal to 250

# To conclude, all the implemented algorithms performed well on our dataset
# in classifying the people into ASD patients and normal based on the 20 independent
# features. PCA was performed on these 20 features and first five principal components
# were selected as they covered more than 95% variation in the dataset and all the
# machine learning algorithms and ANN was implemented using these 5 principal
# components as independent features.
```

Including Plots

You can also embed plots, for example:

```
plot(pressure)
```



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.