Project

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R Markdown

```
library(dplyr)
library(tidyr)
library(tibble)
library(readr)
library(tidyverse)
library(ggplot2)
library(GGally)
library(corrplot)
library(plotmo)
library(caret)
library(kernlab)
library(earth)
library(skimr)
library(psych)
library(reshape2)
library(gt)
library(ROSE)


rseed <- 123
```

```
dir_prefix <- getwd()
print(dir_prefix)
```

```
## [1] "C:/Users/Jeremiah/Desktop/MSADS/ADS-503/ADS503-Group6"
```

```
### Connection info for GitHub File
url <- paste(dir_prefix, 'healthcare-dataset-stroke-data.csv', sep ='/')
df_orig <- read_csv(url)
print(url)
```

```
## [1] "C:/Users/Jeremiah/Desktop/MSADS/ADS-503/ADS503-Group6/healthcare-dataset-stroke-data.csv"
```

```
describe(df_orig)
```

```
##                   vars    n     mean       sd   median  trimmed      mad   min
## id                   1 5110 36517.83 21161.72 36932.00 36542.26 27413.27 67.00
## gender*              2 5110     1.41     0.49     1.00     1.39     0.00  1.00
## age                  3 5110    43.23    22.61    45.00    43.61    26.69  0.08
## hypertension         4 5110     0.10     0.30     0.00     0.00     0.00  0.00
## heart_disease        5 5110     0.05     0.23     0.00     0.00     0.00  0.00
## ever_married*        6 5110     1.66     0.48     2.00     1.70     0.00  1.00
```

```
## work_type*           7 5110     3.50     1.28     4.00     3.62     0.00  1.00
## Residence_type*      8 5110     1.51     0.50     2.00     1.51     0.00  1.00
## avg_glucose_level    9 5110   106.15    45.28    91.88    97.85    26.06 55.12
## bmi*                10 5110   172.19    88.96   158.00   163.08    74.13  1.00
## smoking_status*     11 5110     2.59     1.09     2.00     2.61     1.48  1.00
## stroke              12 5110     0.05     0.22     0.00     0.00     0.00  0.00
##                        max    range  skew kurtosis     se
## id                 72940.00 72873.00 -0.02    -1.21 296.03
## gender*                3.00     2.00  0.35    -1.86   0.01
## age                   82.00    81.92 -0.14    -0.99   0.32
## hypertension           1.00     1.00  2.71     5.37   0.00
## heart_disease          1.00     1.00  3.94    13.57   0.00
## ever_married*          2.00     1.00 -0.66    -1.57   0.01
## work_type*             5.00     4.00 -0.91    -0.49   0.02
## Residence_type*        2.00     1.00 -0.03    -2.00   0.01
## avg_glucose_level    271.74   216.62  1.57     1.68   0.63
## bmi*                 419.00   418.00  0.97     0.87   1.24
## smoking_status*        4.00     3.00  0.08    -1.35   0.02
## stroke                 1.00     1.00  4.19    15.57   0.00
```

Exploratory Data Analysis (EDA)

```
###graphical and non-graphical representations of relationships between the response variable and predi

df_eda <- df_orig

rownames(df_eda) <- df_eda$id
```

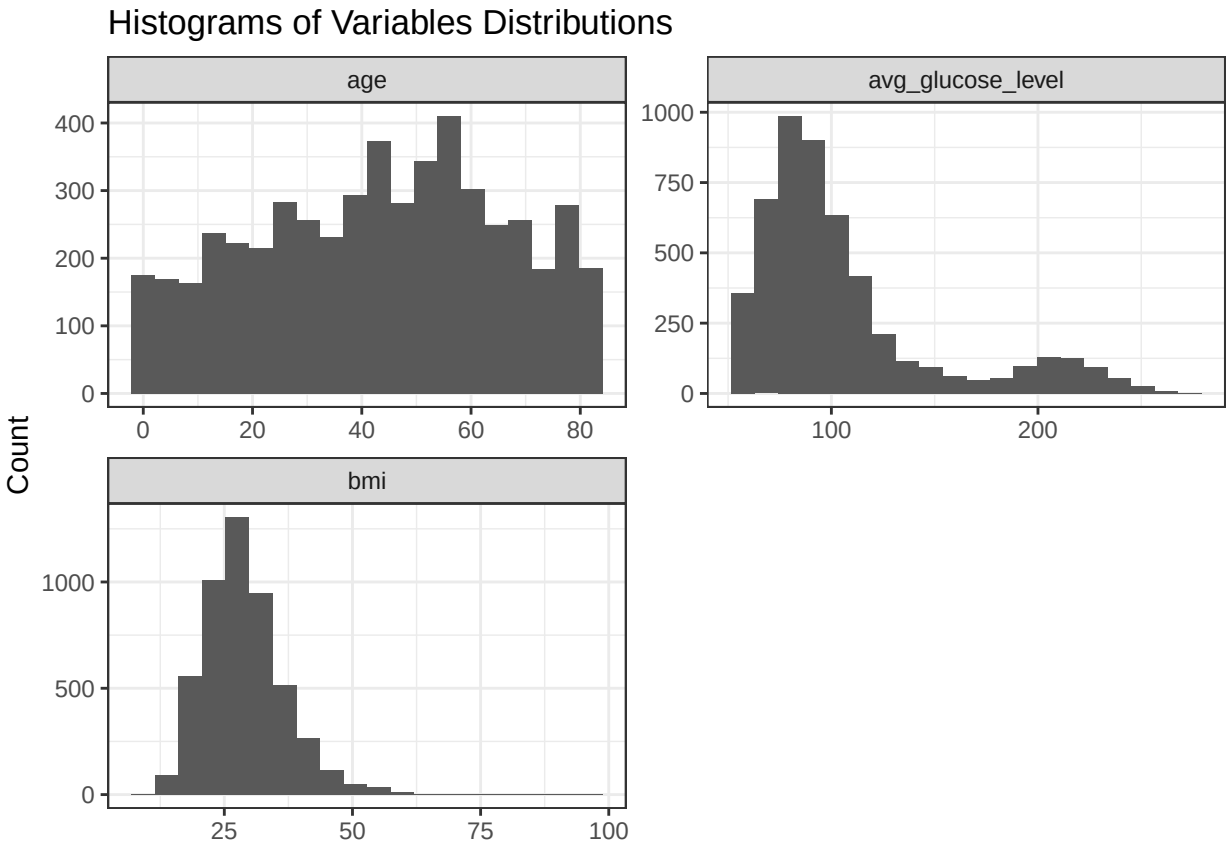
```
## Warning: Setting row names on a tibble is deprecated.
```

```
df_eda <- dplyr::select(df_eda, -id)

print(df_eda)
```

```
## # A tibble: 5,110 x 11
##    gender   age hypertension heart_disease ever_married work_type Residence_type
##    <chr>  <dbl>        <dbl>         <dbl> <chr>        <chr>     <chr>
##  1 Male      67            0             1 Yes          Private   Urban
##  2 Female    61            0             0 Yes          Self-emp~ Rural
##  3 Male      80            0             1 Yes          Private   Rural
##  4 Female    49            0             0 Yes          Private   Urban
##  5 Female    79            1             0 Yes          Self-emp~ Rural
##  6 Male      81            0             0 Yes          Private   Urban
##  7 Male      74            1             1 Yes          Private   Rural
##  8 Female    69            0             0 No           Private   Urban
##  9 Female    59            0             0 Yes          Private   Rural
## 10 Female    78            0             0 Yes          Private   Urban
## # i 5,100 more rows
## # i 4 more variables: avg_glucose_level <dbl>, bmi <chr>, smoking_status <chr>,
## #   stroke <dbl>
```

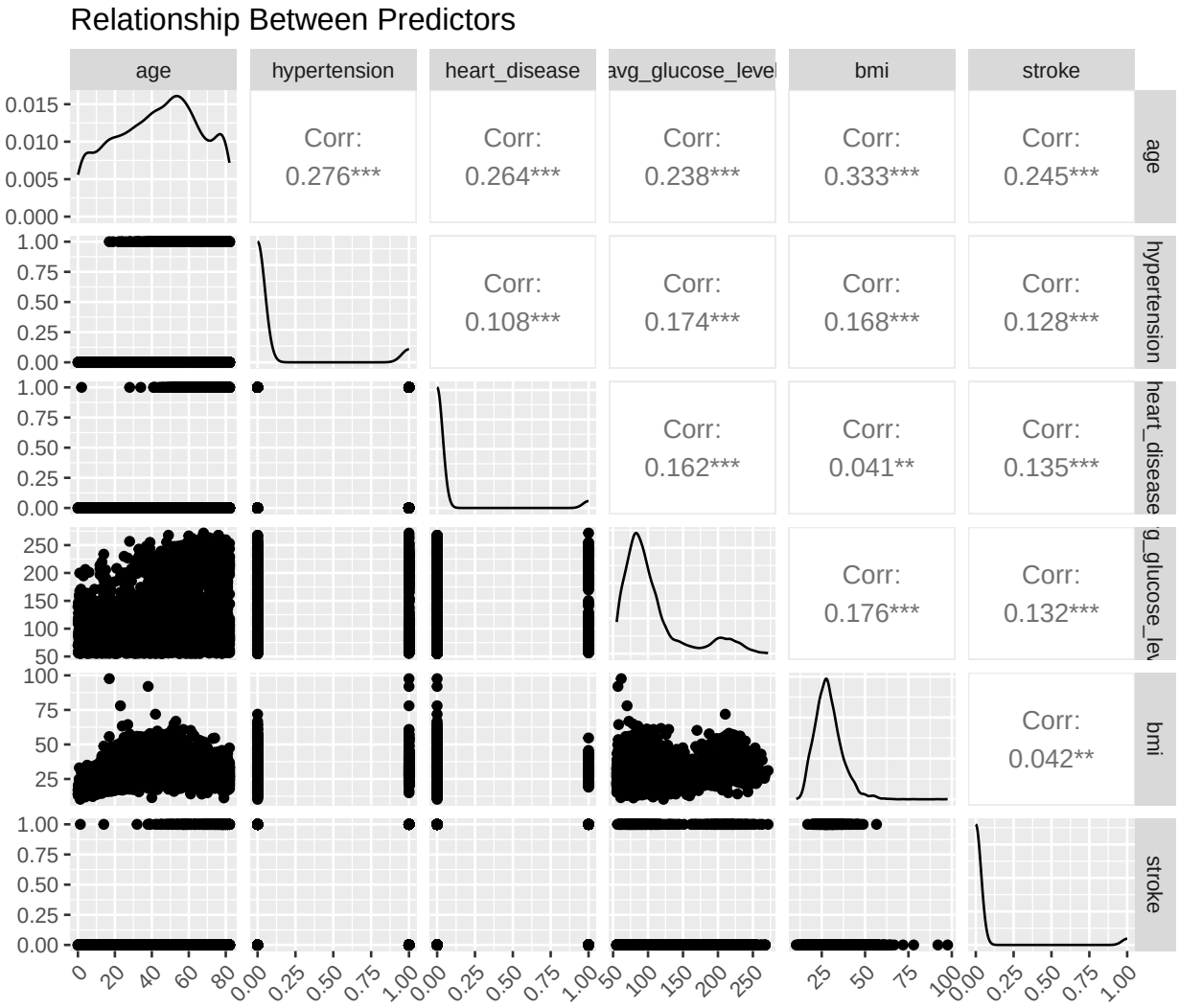
Histograms

```r
# Filter out N/A values for bmi and convert to numeric
df_eda <- df_eda %>%
  filter(!is.na(bmi)) %>%
  mutate(bmi = as.numeric(bmi))

# Pivot longer and convert value column to numeric if possible
df_long <- df_eda %>%
  pivot_longer(-c(stroke, ever_married, gender, hypertension, heart_disease, Residence_type, work_type,
  mutate(value = as.numeric(value))

# Plot histograms
ggplot(df_long, aes(x = value)) +
  geom_histogram(bins = 20) +
  facet_wrap(~Variable, scales = "free", ncol = 2) +
  theme_bw() +
  labs(title = 'Histograms of Variables Distributions', x = NULL, y = "Count")
```



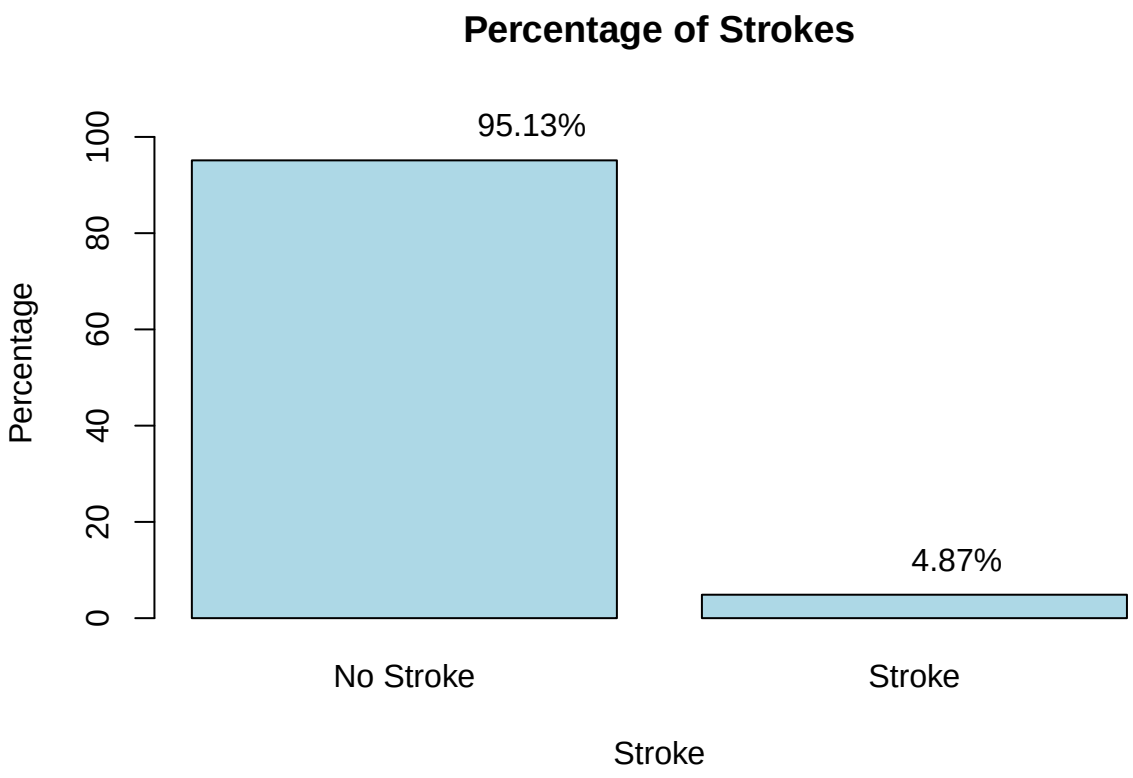
Corrplot

```r
numeric_df <- df_eda[sapply(df_eda, is.numeric)]

numeric_df |>
  ggpairs(title = "Relationship Between Predictors", progress = FALSE)+
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



Class Balance

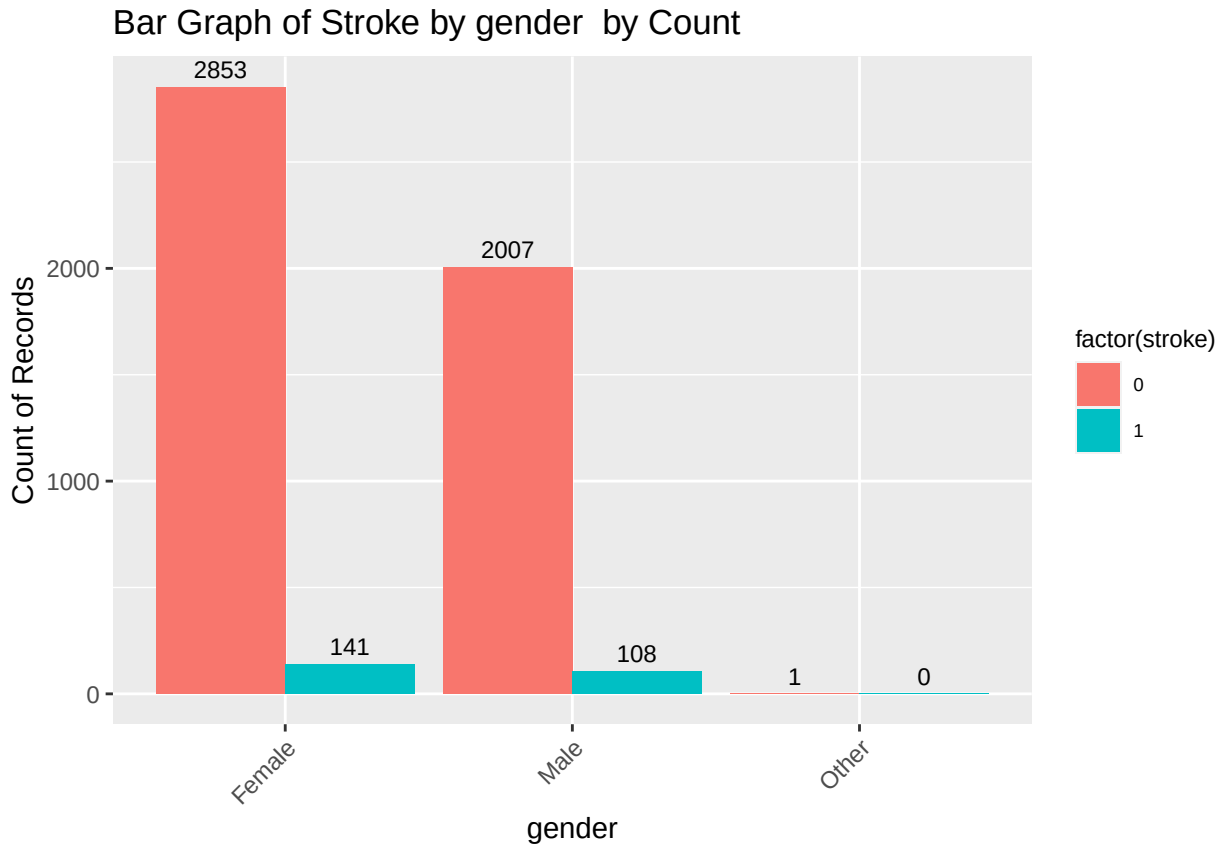
```
stroke_percent <- prop.table(table(df_eda$stroke)) * 100

barplot(stroke_percent,
        main = "Percentage of Strokes",
        xlab = "Stroke",
        ylab = "Percentage",
        col = "lightblue",
        ylim = c(0, max(stroke_percent) + 11),
        names.arg = c("No Stroke", "Stroke"))

label_pos <- stroke_percent + 1

### Add labels
text(x = 1:length(stroke_percent),
     y = label_pos,
     labels = paste0(round(stroke_percent, 2), "%"),
     pos = 3)
```

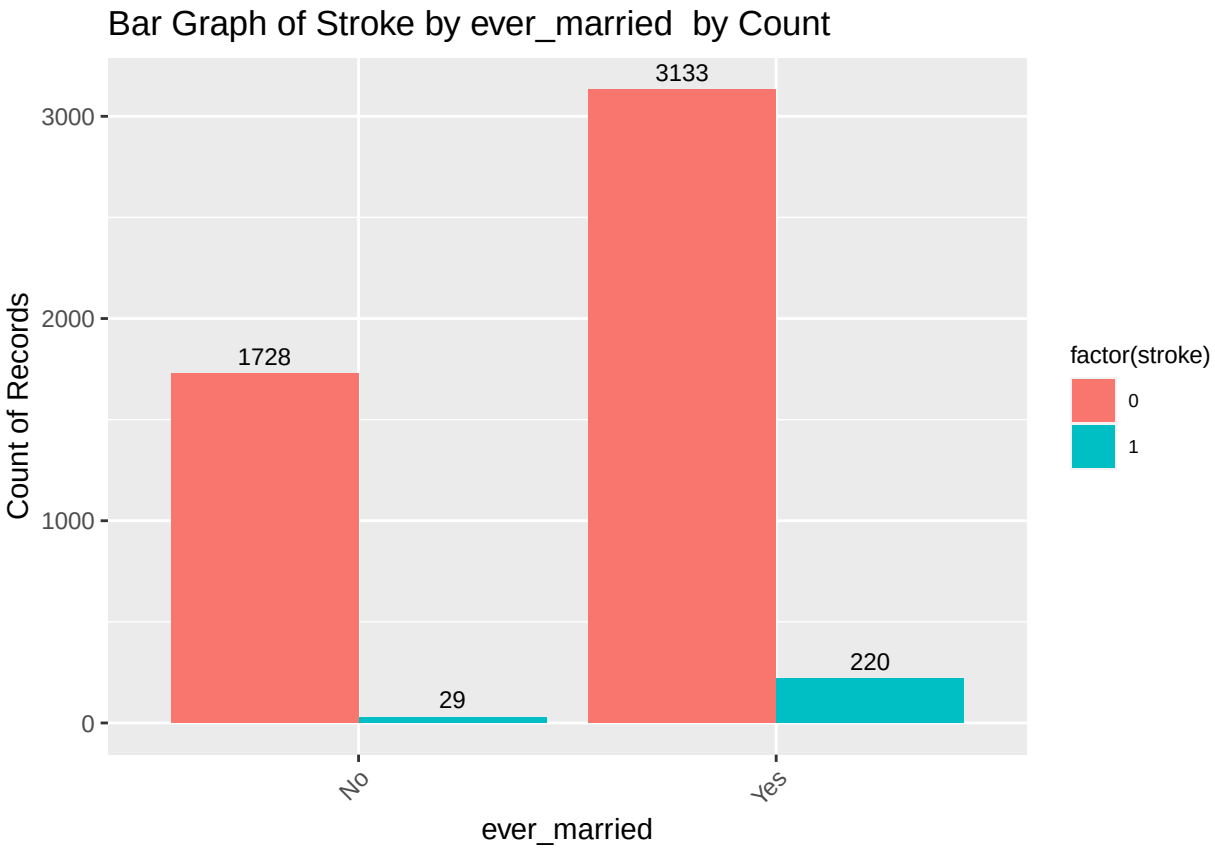


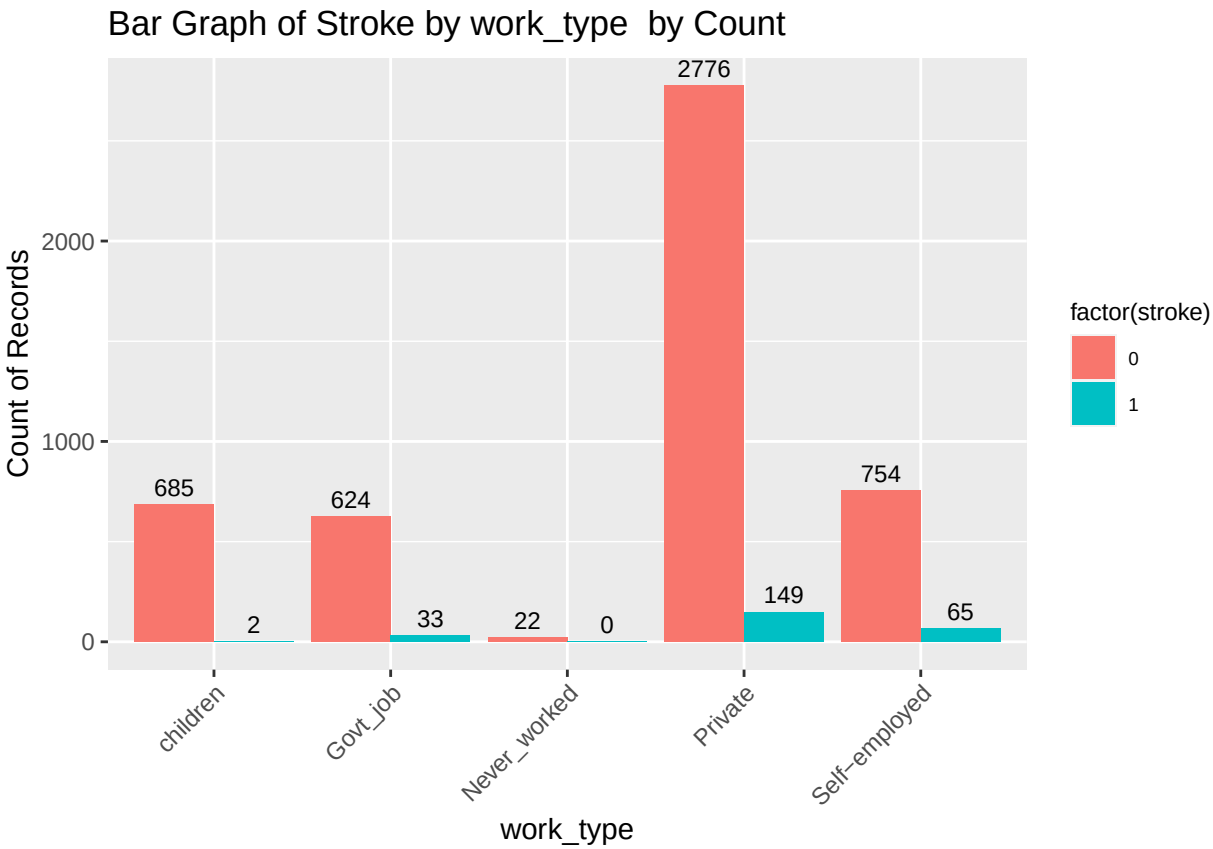
Distributions of Values (Counts)

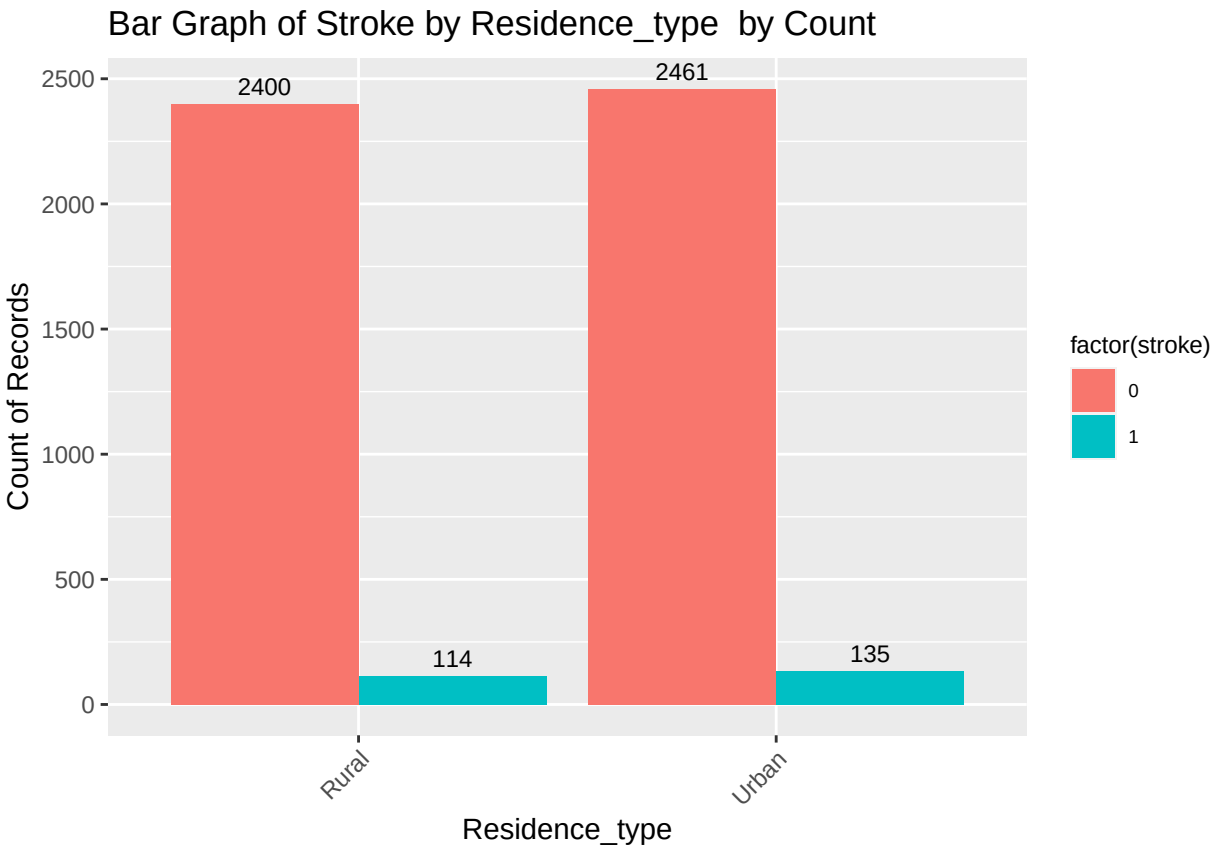
```
wrap_text <- function(x, width) {
  sapply(strwrap(x, width = width, simplify = FALSE), paste, collapse = "\n")
}

# Select non-numeric columns
non_numeric_columns <- names(df_eda)[sapply(df_eda, is.factor) | sapply(df_eda, is.character)]

# Function to create plots
create_plots <- function(col) {
  counts <- table(df_eda[[col]], df_eda$stroke)
  counts_df <- as.data.frame(counts)
  names(counts_df) <- c(col, "stroke", "count")

  ggplot(counts_df, aes(x = !!sym(col), y = count, fill = factor(stroke))) +
    geom_bar(stat = "identity", position = "dodge") +
    geom_text(aes(label = paste0(count)),
              vjust = -0.5, size = 3, position = position_dodge(width = 0.9)) +  # Add count / percent
    labs(x = col, y = "Count of Records",
         title = paste("Bar Graph of Stroke by", col, " by Count")) +
    theme(axis.text.x = element_text(angle = 45, hjust = 1),
          panel.spacing = unit(3, "lines"),
          legend.text = element_text(size = 7),  # Adjust legend text size
          legend.title = element_text(size = 9))  # Adjust legend title size
```

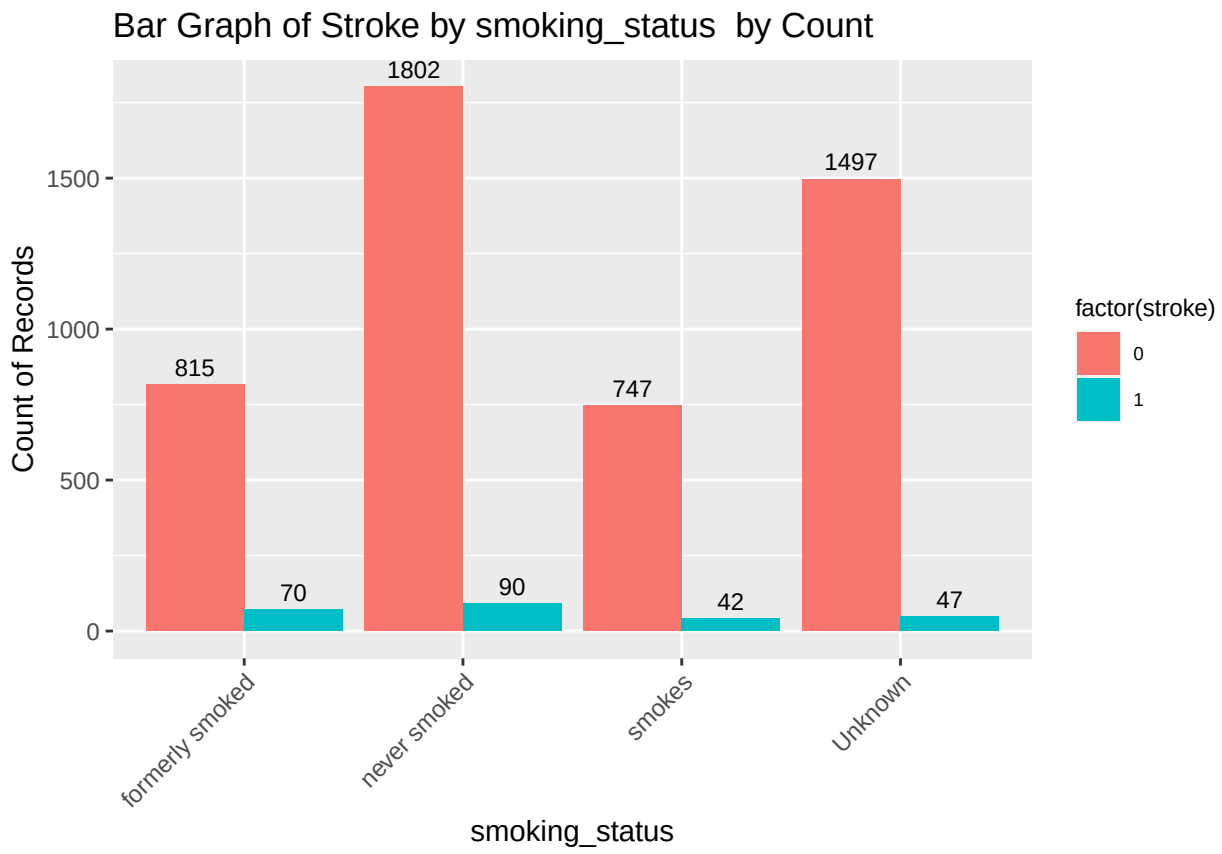
```
}

# Create plots for each non-numeric column
plots_list <- map(non_numeric_columns, ~ create_plots(.x))

# Print plots
walk(plots_list, print)
```




Bar Graph of Stroke by ever_married by Count
Count of Records
3000
2000
1000
0
1728
29
3133
220
No
Yes
ever_married
factor(stroke)
0
1


Bar Graph of Stroke by work_type by Count
Count of Records
2000
1000
0
685
2
624
33
22
0
2776
149
754
65
children
Govt_job
Never_worked
Private
Self-employed
work_type
factor(stroke)
0
1

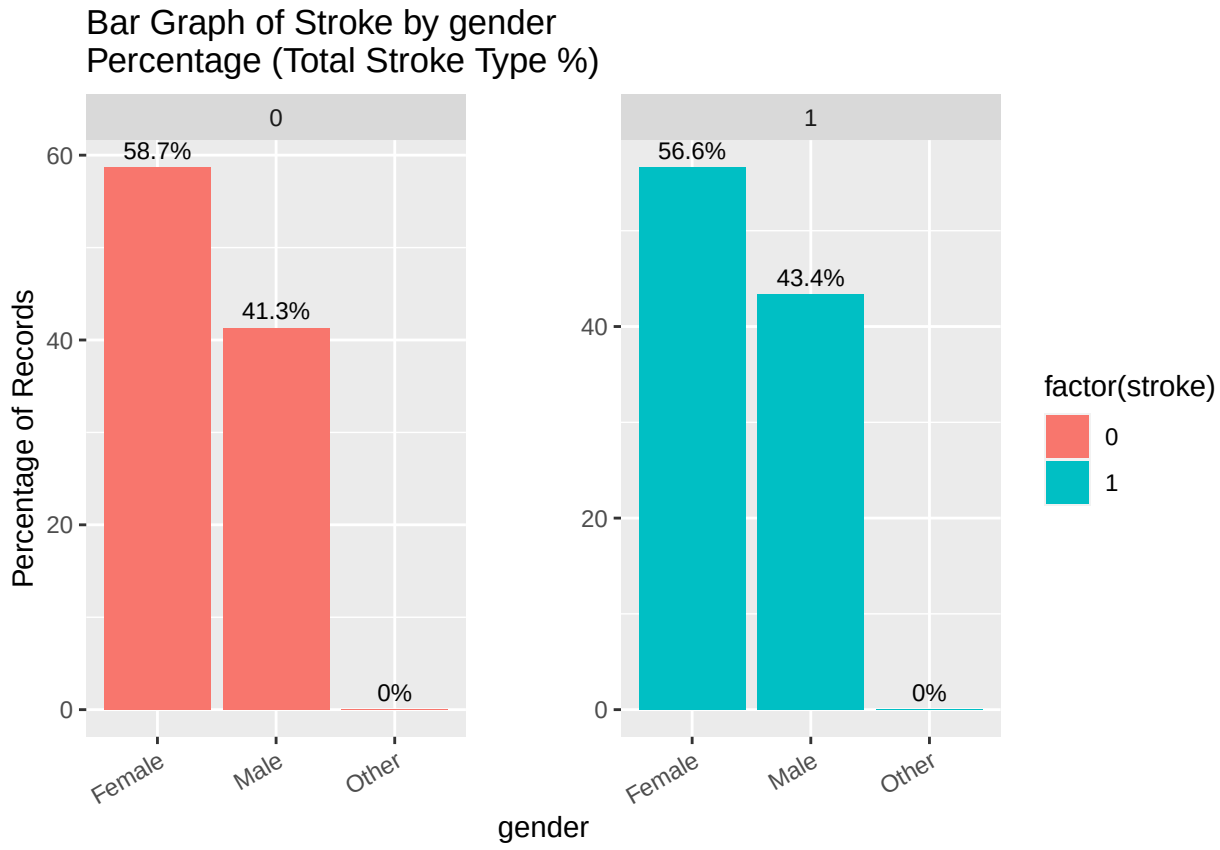

Bar Graph of Stroke by Residence_type by Count
Count of Records
2500
2000
1500
1000
500
0
2400
114
2461
135
Rural
Urban
Residence_type
factor(stroke)
0
1

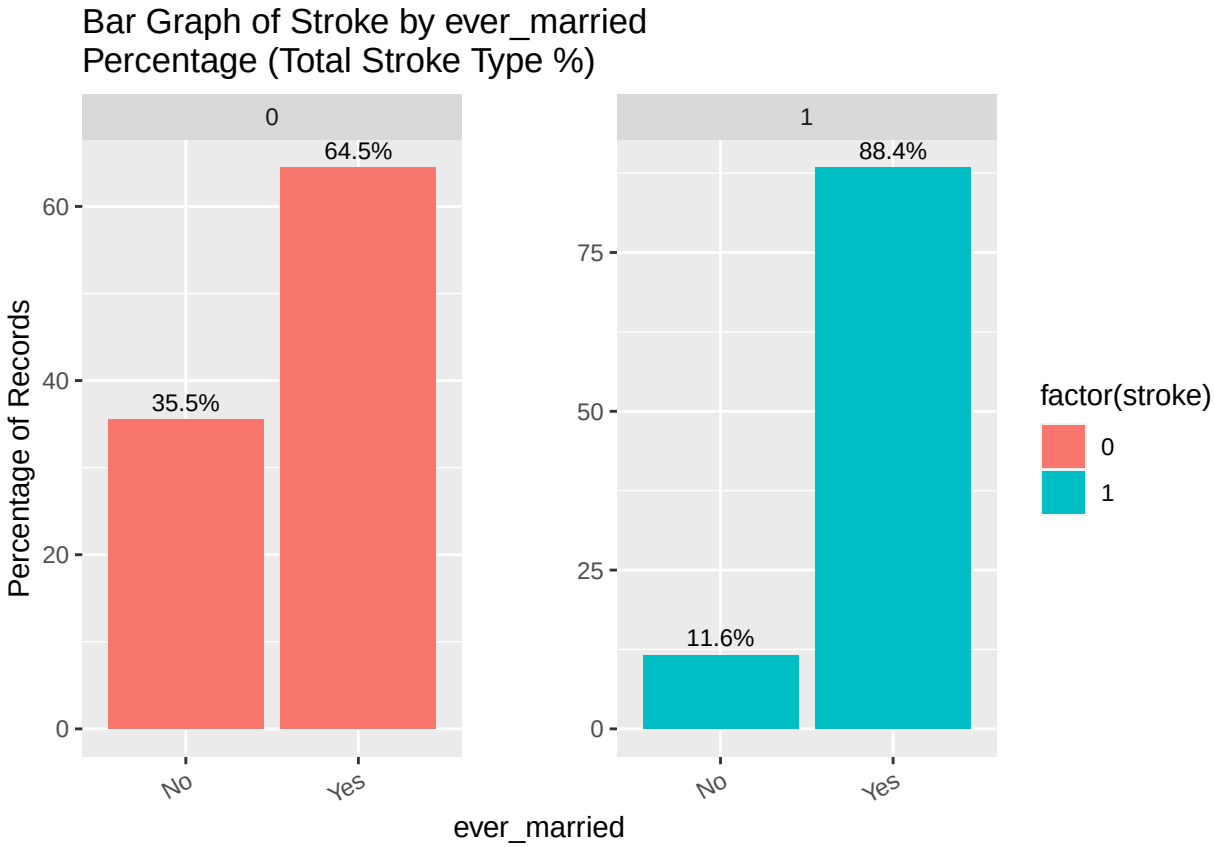


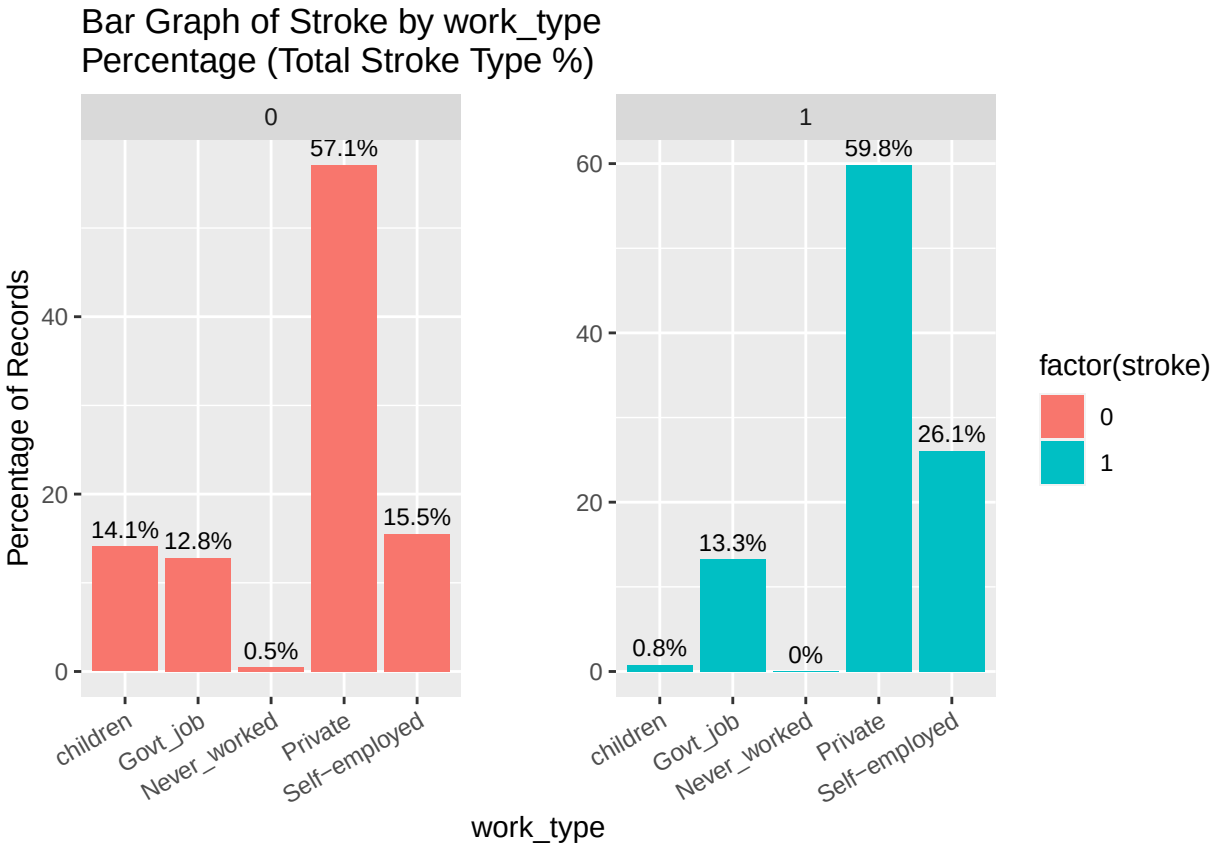
Distributions of Values (Percentages)

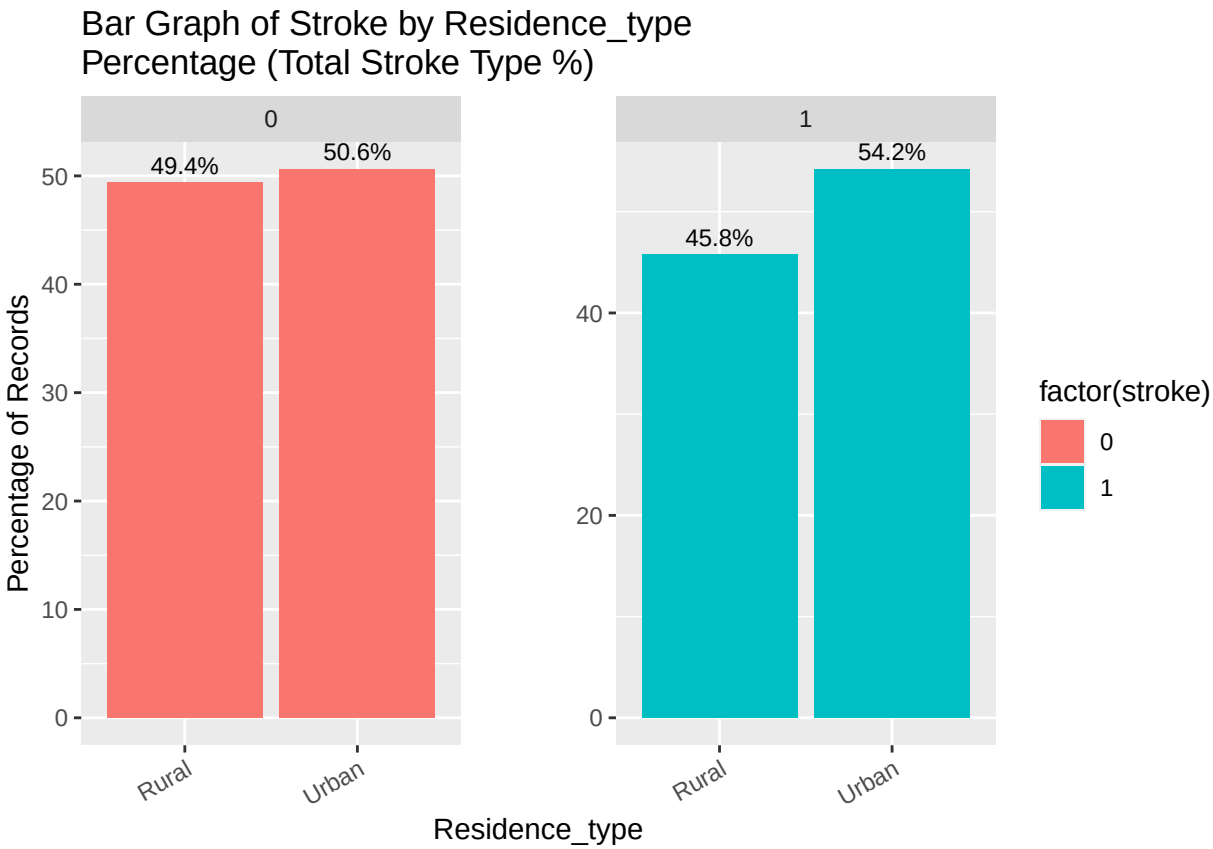
```
# Function to create plots
create_plots <- function(col) {
  counts <- table(df_eda[[col]], df_eda$stroke)
  counts_df <- as.data.frame(counts)
  names(counts_df) <- c(col, "stroke", "count")

  # Calculate percentages within each category
  counts_df <- counts_df %>%
    group_by(stroke) %>%
    mutate(percent = count / sum(count) * 100) %>%
    ungroup()

  ggplot(counts_df, aes(x = !!sym(col), y = percent, fill = factor(stroke))) +
    geom_bar(stat = "identity") +
    geom_text(aes(label = paste0(round(percent, 1), "%")),
              vjust = -0.5, size = 3) +  # Add percent labels
    labs(x = col, y = "Percentage of Records",
         title = paste("Bar Graph of Stroke by", col, "\nPercentage (Total Stroke Type %)")) +
    facet_wrap(~stroke, scales = "free") +  # Facet by stroke
    theme(axis.text.x = element_text(angle = 30, hjust = 1),
          panel.spacing = unit(3, "lines")
)}
```

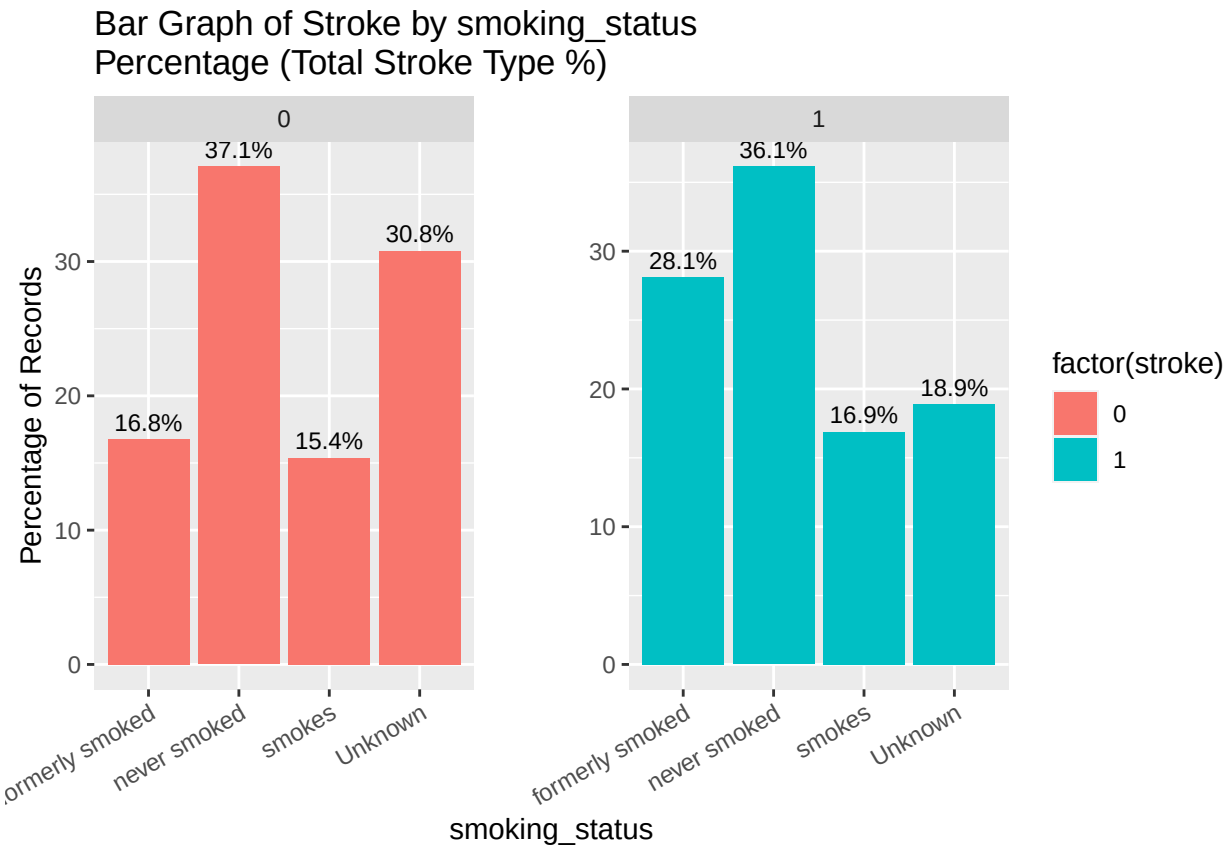
```r
# Create plots for each non-numeric column
plots_list <- map(non_numeric_columns, ~ create_plots(.x))

# Print plots
walk(plots_list, print)
```




Bar Graph of Stroke by ever_married
Percentage (Total Stroke Type %)
0
1
64.5%
88.4%
35.5%
11.6%
Percentage of Records
60
40
20
0
75
50
25
0
No
Yes
ever_married
factor(stroke)
0
1

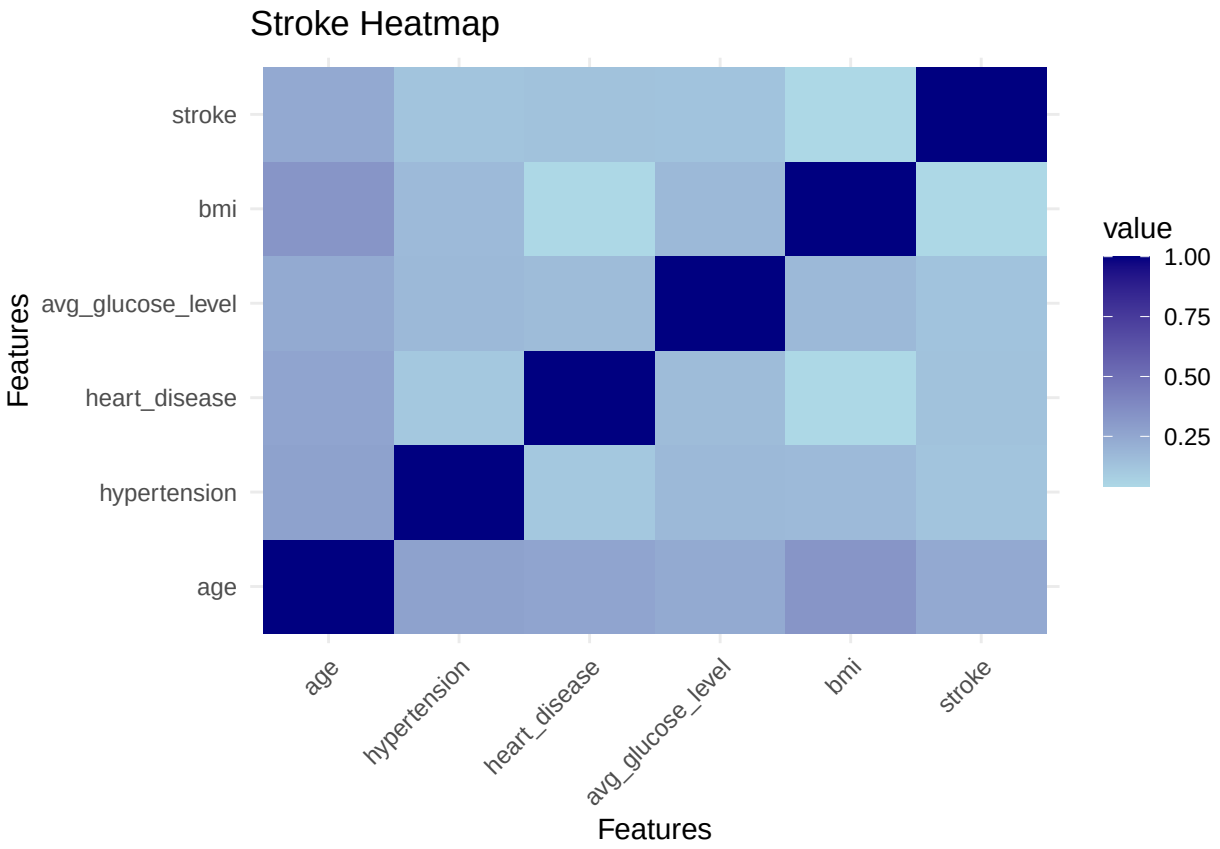

Bar Graph of Stroke by work_type
Percentage (Total Stroke Type %)
0
1
Percentage of Records
0
20
40
60
57.1%
14.1%
12.8%
0.5%
15.5%
59.8%
0.8%
13.3%
0%
26.1%
children
Govt_job
Never_worked
Private
Self−employed
work_type
factor(stroke)
0
1


Bar Graph of Stroke by Residence_type
Percentage (Total Stroke Type %)
0
1
49.4%
50.6%
45.8%
54.2%
Percentage of Records
50
40
30
20
10
0
Rural
Urban
Residence_type
factor(stroke)
0
1



Heatmap

```
##### HEAT MAP #### For Feature Selection ###################################
# Numeric Columns for EDA
heatmap_data <- df_eda %>%
  select(age, hypertension, heart_disease, avg_glucose_level, bmi, stroke)

# Correlation Matrix
correlation_matrix <- cor(heatmap_data, use = "pairwise.complete.obs")

# Heatmap Plot
ggplot(data = melt(correlation_matrix), aes(x = Var1, y = Var2, fill = value)) +
  geom_tile() +
  scale_fill_gradient(low = "Light Blue", high = "Navy Blue") +
  labs(x = "Features", y = "Features", title = "Stroke Heatmap") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



Data Splitting - Training & Test

```
###training, validation, and test sets
###Split
trainIndex <- createDataPartition(df_eda$stroke, p = 0.8, ### saving 20% for test
                                  list = FALSE,
                                  times = 1)

# Subset data into training and testing sets
trainData <- df_eda[trainIndex, ]
testData <- df_eda[-trainIndex, ]
```

Data Wrangling and Pre-Processing

Missing Values

```
table(trainData$gender)
```

```
##
## Female   Male  Other
##   2385   1702      1
```

```
trainData$gender[trainData$gender == "Other"] <- {
  ux <- unique(trainData$gender)
  mode_gender <- ux[which.max(tabulate(match(trainData$gender, ux)))]
  mode_gender
```

```
}

testData$gender[testData$gender == "Other"] <- {
  ux <- unique(testData$gender)
  mode_gender <- ux[which.max(tabulate(match(testData$gender, ux)))]
  mode_gender
}
table(trainData$gender)
```

```
##
## Female   Male
##   2386   1702
```

```
# Check for missing data
colSums(is.na(trainData))
```

```
##            gender               age      hypertension     heart_disease
##                 0                 0                 0                 0
##      ever_married         work_type    Residence_type avg_glucose_level
##                 0                 0                 0                 0
##               bmi    smoking_status            stroke
##               164                 0                 0
```

```
### bagImpute used because missing data is random
bag_missing <- preProcess(trainData, method = "bagImpute")  ##### CHANGE? knn ??
trainData <- predict(bag_missing, newdata = trainData)

# bagImpute for Test Data
testData <- predict(bag_missing, newdata = testData)

colSums(is.na(trainData))
```

```
##            gender               age      hypertension     heart_disease
##                 0                 0                 0                 0
##      ever_married         work_type    Residence_type avg_glucose_level
##                 0                 0                 0                 0
##               bmi    smoking_status            stroke
##                 0                 0                 0
```

Setting up Factors

```
### Factor Train
non_numeric_cols <- sapply(trainData, function(x) !is.numeric(x))
# Convert non-numeric columns to factors
trainData <- trainData %>%
  mutate_if(non_numeric_cols, as.factor)

### Factor Test
non_numeric_cols <- sapply(testData, function(x) !is.numeric(x))
# Convert non-numeric columns to factors Test
testData <- testData %>%
  mutate_if(non_numeric_cols, as.factor)

#str(trainData)
#str(testData)
```

Dummy Variables

```
### dummy variables for Trfactors
dummy_model1 <- dummyVars(stroke ~ gender + ever_married + work_type + Residence_type + smoking_status,

trainData_dummy <- as.data.frame(predict(dummy_model1, newdata = trainData))
trainData_dummy <- as.data.frame(lapply(trainData_dummy, as.factor))

### dummy variables for test factors
dummy_model2 <- dummyVars(stroke ~ gender + ever_married + work_type + Residence_type + smoking_status,

testData_dummy <- as.data.frame(predict(dummy_model2, newdata = testData))
testData_dummy <- as.data.frame(lapply(testData_dummy, as.factor))

#head(trainData_dummy)
#head(testData_dummy)
```

```
### Dropping columns that can be inferred from the others to avoid multicollinearity
trainData_dummy <-select(trainData_dummy, -gender.Female, -ever_married.No, -work_type.children, -Reside

#head(trainData_dummy)
trainData_selected <- select(trainData, age, hypertension, heart_disease, avg_glucose_level, bmi, stroke
#str(trainData_selected)

### Test Dropping columns that can be inferred from the others to avoid multicollinearity
testData_dummy <-select(testData_dummy, -gender.Female, -ever_married.No, -work_type.children, -Residen
testData_selected <- select(testData, age, hypertension, heart_disease, avg_glucose_level, bmi, stroke)
#str(testData_dummy)
```

```
# Train
trainData_ready <- cbind(trainData_dummy, trainData_selected)
trainData_ready <- trainData_ready %>%
  mutate(across(all_of(c("hypertension", "heart_disease", "stroke")), as.factor))
names(trainData_ready) <- gsub("\\.", "_", names(trainData_ready))
names(trainData_ready) <- gsub("_Yes", "", names(trainData_ready))
trainData_ready$stroke <- as.factor(make.names(as.character(trainData_ready$stroke)))
head(trainData_ready)
```

```
##   gender_Male ever_married work_type_Govt_job work_type_Never_worked
## 1           1            1                  0                      0
## 2           0            1                  0                      0
## 3           1            1                  0                      0
## 4           0            1                  0                      0
## 5           1            1                  0                      0
## 6           1            1                  0                      0
##   work_type_Private work_type_Self_employed Residence_type_Urban
## 1                 1                       0                    1
## 2                 0                       1                    0
## 3                 1                       0                    0
## 4                 1                       0                    1
## 5                 1                       0                    1
## 6                 1                       0                    0
##   smoking_status_formerly_smoked smoking_status_never_smoked
## 1                              1                           0
## 2                              0                           1
```

```
## 3                             0                         1
## 4                             0                         0
## 5                             1                         0
## 6                             0                         1
##   smoking_status_smokes age hypertension heart_disease avg_glucose_level
## 1                     0  67            0             1            228.69
## 2                     0  61            0             0            202.21
## 3                     0  80            0             1            105.92
## 4                     1  49            0             0            171.23
## 5                     0  81            0             0            186.21
## 6                     0  74            1             1             70.09
##        bmi stroke
## 1 36.60000     X1
## 2 34.02395     X1
## 3 32.50000     X1
## 4 34.40000     X1
## 5 29.00000     X1
## 6 27.40000     X1
```

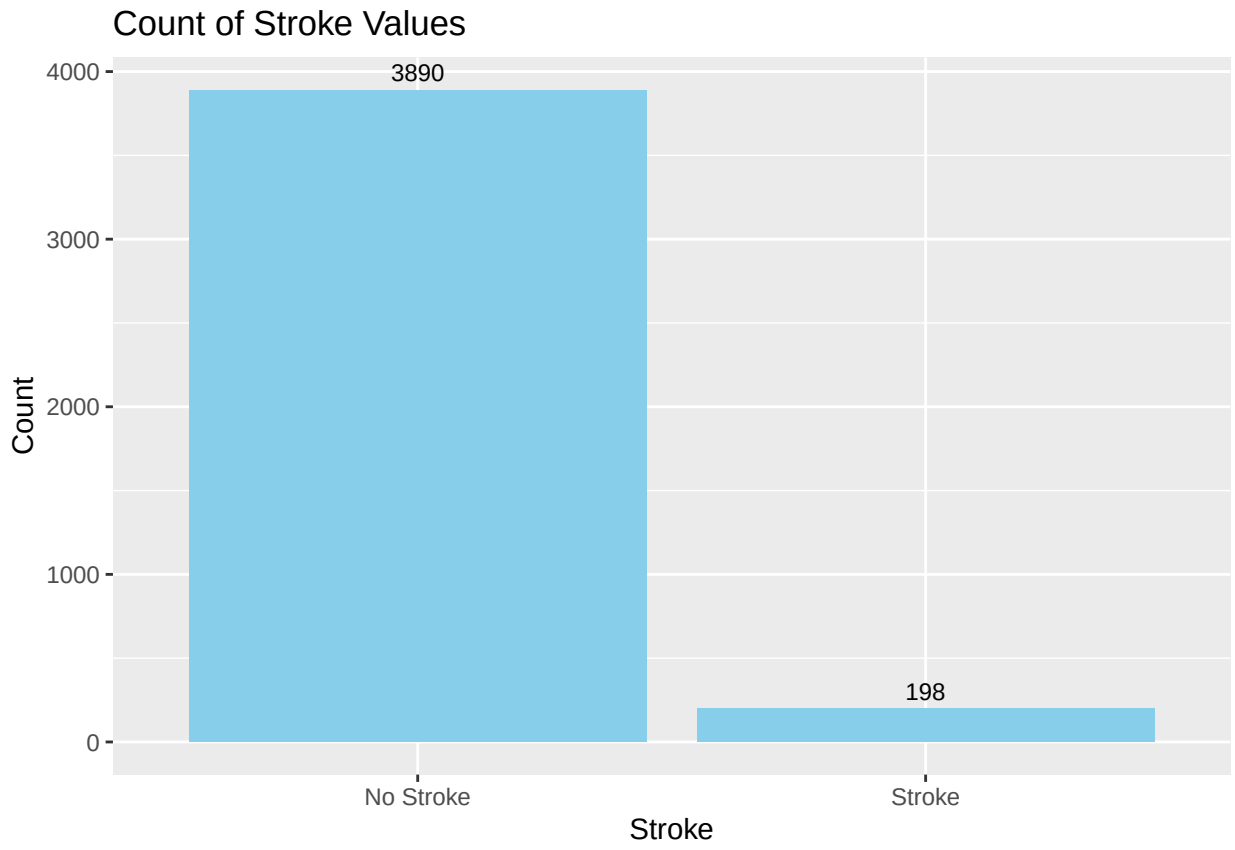
```r
# Test
testData_ready <- cbind(testData_dummy, testData_selected)
testData_ready <- testData_ready %>%
  mutate(across(all_of(c("hypertension", "heart_disease", "stroke")), as.factor))
names(testData_ready) <- gsub("\\.", "_", names(testData_ready))
names(testData_ready) <- gsub("_Yes", "", names(testData_ready))
testData_ready$stroke <- as.factor(make.names(as.character(testData_ready$stroke)))
str(testData_ready)
```

```
## 'data.frame':    1022 obs. of  16 variables:
##  $ gender_Male                   : Factor w/ 2 levels "0","1": 1 1 2 2 2 1 1 2 2 2 ...
##  $ ever_married                  : Factor w/ 2 levels "0","1": 2 2 2 2 2 1 2 2 2 2 ...
##  $ work_type_Govt_job            : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ work_type_Never_worked        : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ work_type_Private             : Factor w/ 2 levels "0","1": 1 2 2 2 2 2 1 2 1 2 ...
##  $ work_type_Self_employed       : Factor w/ 2 levels "0","1": 2 1 1 1 1 1 2 1 2 1 ...
##  $ Residence_type_Urban          : Factor w/ 2 levels "0","1": 1 2 2 2 2 2 2 2 2 2 ...
##  $ smoking_status_formerly_smoked: Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 2 1 1 ...
##  $ smoking_status_never_smoked   : Factor w/ 2 levels "0","1": 2 1 1 1 1 2 2 1 1 1 ...
##  $ smoking_status_smokes         : Factor w/ 2 levels "0","1": 1 1 1 2 2 1 1 1 2 2 ...
##  $ age                           : num  79 78 78 64 75 60 52 71 69 57 ...
##  $ hypertension                  : Factor w/ 2 levels "0","1": 2 1 1 1 2 1 2 1 1 2 ...
##  $ heart_disease                 : Factor w/ 2 levels "0","1": 1 1 2 2 1 1 1 1 2 1 ...
##  $ avg_glucose_level             : num  174.1 58.6 219.8 191.6 221.3 ...
##  $ bmi                           : num  24 24.2 32.5 37.5 25.8 ...
##  $ stroke                        : Factor w/ 2 levels "X0","X1": 2 2 2 2 2 2 2 2 2 2 ...
```

Class Imbalance (ROSE Method)

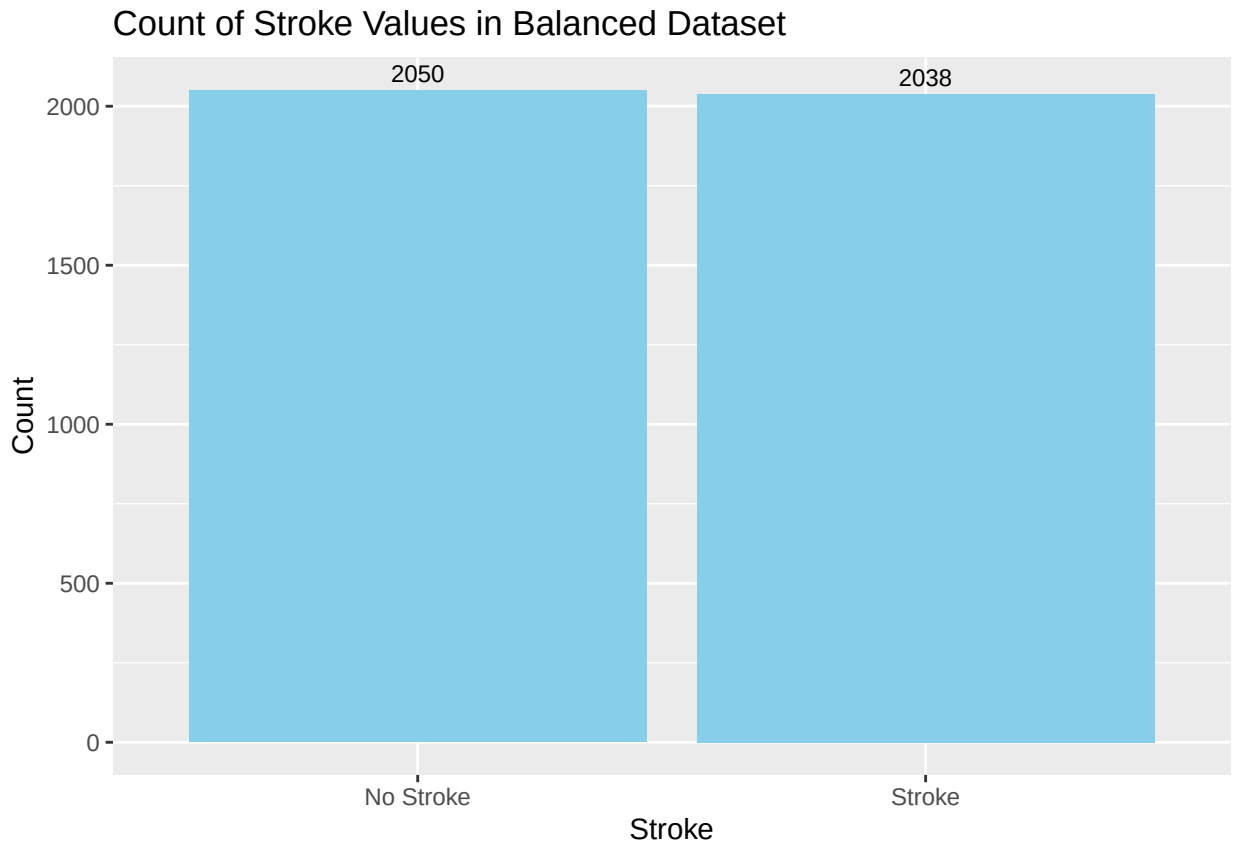
```r
# Calculate counts and convert to data frame
stroke_counts <- as.data.frame(table(trainData_ready$stroke))
colnames(stroke_counts) <- c("Stroke", "Count")
stroke_counts$Stroke <- factor(stroke_counts$Stroke, levels = c('X0', 'X1'), labels = c("No Stroke", "S

### Bar Chart
ggplot(stroke_counts, aes(x = Stroke, y = Count)) +
```

```
  geom_bar(stat = "identity", fill = "skyblue") +
  labs(title = "Count of Stroke Values",
       x = "Stroke",
       y = "Count") +
  geom_text(aes(label = Count),
            vjust = -0.5,  # Position above the bars
            size = 3,  # Size of the text
            color = "black")  # Color of the text
```




```
set.seed(rseed)

# Apply ROSE to balance the dataset
rose_train <- ROSE(stroke ~ ., data = trainData_ready)$data

# Separate predictors (features) and target variable (stroke)
train_X <- rose_train[, !(names(rose_train) %in% "stroke")]
train_y <- rose_train$stroke

train_y_df <- data.frame(stroke = train_y)

stroke_counts <- as.data.frame(table(train_y_df$stroke))
colnames(stroke_counts) <- c("Stroke", "Count")
stroke_counts$Stroke <- factor(stroke_counts$Stroke,
                               levels = c('X0', 'X1'), labels = c("No Stroke", "Stroke"))
### Bar chart
ggplot(stroke_counts, aes(x = Stroke, y = Count)) +
```

```
  geom_bar(stat = "identity", fill = "skyblue") +
  labs(title = "Count of Stroke Values in Balanced Dataset",
       x = "Stroke",
       y = "Count") +
  geom_text(aes(label = Count),
            vjust = -0.5,
            size = 3,
            color = "black")
```




```
trainData_ready <- data.frame(rose_train)
```

Baseline Model to Beat

```
set.seed(123)
### Parameters for Tuning
ctrl <- trainControl(method = "repeatedcv",
                     number = 5,
                     repeats = 3,
                     verboseIter = FALSE,
                     classProbs = TRUE,
                     summaryFunction = twoClassSummary)
```

```
### Base Model Logistic Regression Model

# Fit logistic regression model
lrm_base_model <- train(stroke ~ .,
```

```
                        data = trainData_ready,
                        method = "glm",
                        family = "binomial",
                        trControl = ctrl)
```

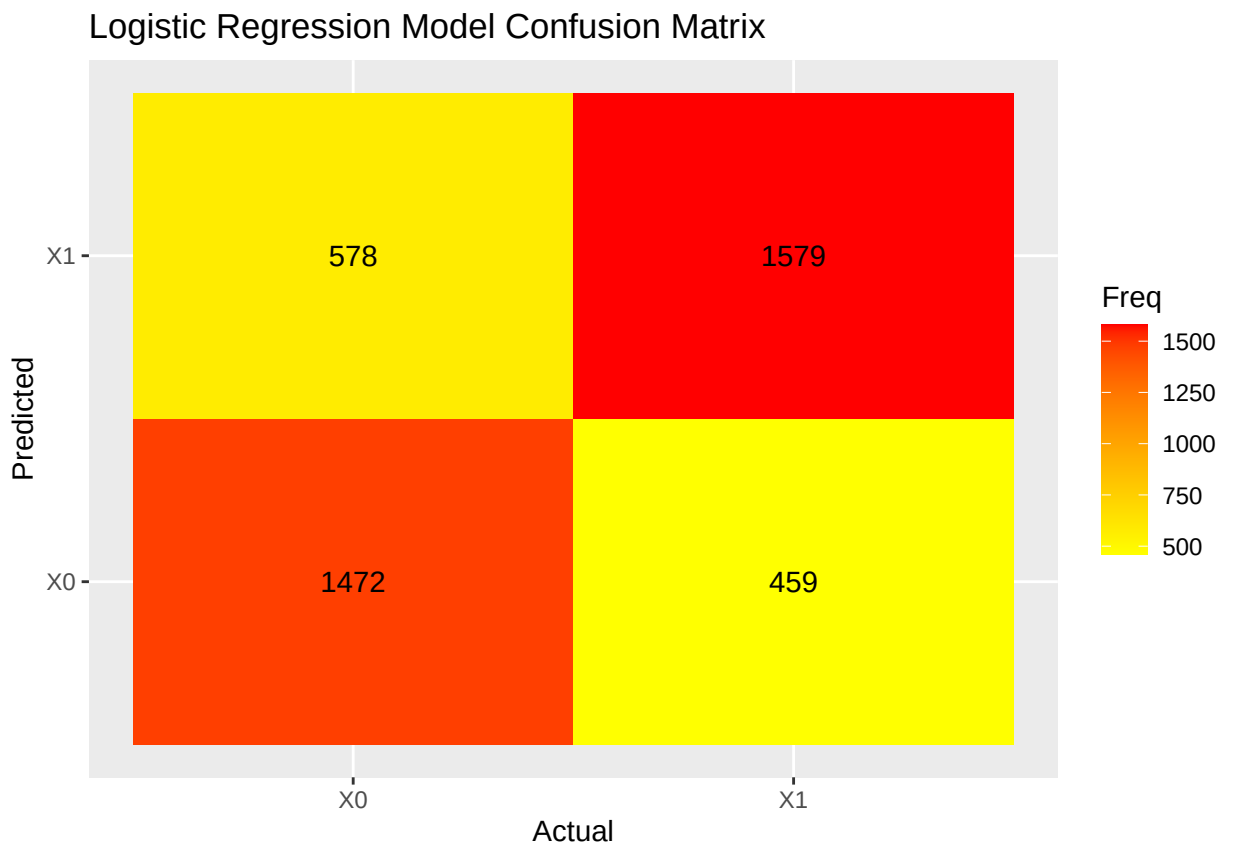
```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
## in the result set. ROC will be used instead.
```

```
# View model summary
summary(lrm_base_model)
```

```
##
## Call:
## NULL
##
## Coefficients:
##                                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     -3.934e+00  2.820e-01 -13.950  < 2e-16 ***
## gender_Male1                    -3.480e-01  7.911e-02  -4.399 1.09e-05 ***
## ever_married1                    1.313e-02  1.194e-01   0.110  0.91238
## work_type_Govt_job1             -8.157e-01  3.128e-01  -2.608  0.00911 **
## work_type_Never_worked1         -1.166e+01  2.102e+02  -0.055  0.95576
## work_type_Private1              -6.165e-01  3.032e-01  -2.033  0.04202 *
## work_type_Self_employed1        -7.821e-01  3.205e-01  -2.440  0.01468 *
## Residence_type_Urban1            1.256e-01  7.674e-02   1.636  0.10174
## smoking_status_formerly_smoked1  1.886e-01  1.178e-01   1.601  0.10929
## smoking_status_never_smoked1     3.447e-02  1.071e-01   0.322  0.74756
## smoking_status_smokes1           2.932e-01  1.269e-01   2.310  0.02089 *
## age                              6.415e-02  2.750e-03  23.329  < 2e-16 ***
## hypertension1                    4.267e-01  1.073e-01   3.975 7.03e-05 ***
## heart_disease1                   6.467e-01  1.319e-01   4.901 9.51e-07 ***
## avg_glucose_level                2.318e-03  6.935e-04   3.343  0.00083 ***
## bmi                              1.829e-02  5.631e-03   3.247  0.00117 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 5667.1  on 4087  degrees of freedom
## Residual deviance: 4172.5  on 4072  degrees of freedom
## AIC: 4204.5
##
## Number of Fisher Scoring iterations: 12
```

```
# LogReg Predictions
predictions <- predict(lrm_base_model, newdata = trainData_ready)

# LogReg Confusion Matrix
logregCM <- confusionMatrix(predictions, trainData_ready$stroke)

# Confusion Matrix Plot
conf_matrix <- as.data.frame(logregCM$table)
ggplot(data = conf_matrix, aes(x = Reference, y = Prediction)) +
geom_tile(aes(fill = Freq)) +
geom_text(aes(label = Freq)) +
```

```
scale_fill_gradient(low = 'yellow', high = 'red') +
labs(title = 'Logistic Regression Model Confusion Matrix', x = 'Actual', y = 'Predicted')
```



Data Prep

```
# Exclude stroke and Identify and remove variables with zero variance
Zero_Var_vars <- nearZeroVar(trainData_ready[, -which(names(trainData_ready) == "stroke"), drop = FALSE]
trainData_ready <- trainData_ready[, -Zero_Var_vars, drop = FALSE]
print(names(Zero_Var_vars))
```

```
## NULL
```

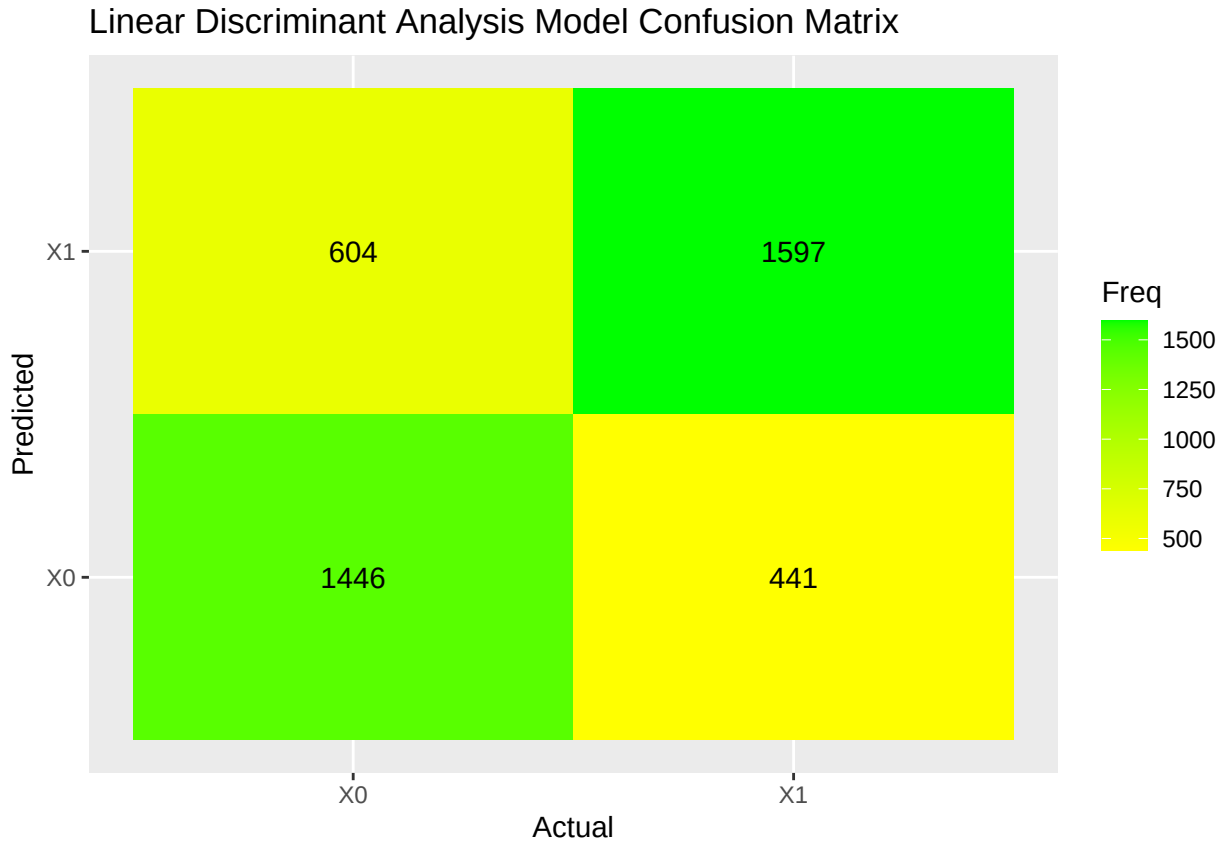
Models

Model #1 - Linear Discriminant Analysis (LDR)

```
rseed <- 123
set.seed(rseed)
# Linear Discriminant Analysis
ldaFit_stroke <- train(stroke ~ .,
                       data = trainData_ready,
                       method = 'lda',
                       preProc = c("center","scale"),
                       metric = 'ROC',
                       trControl = ctrl)
ldaFit_stroke
```

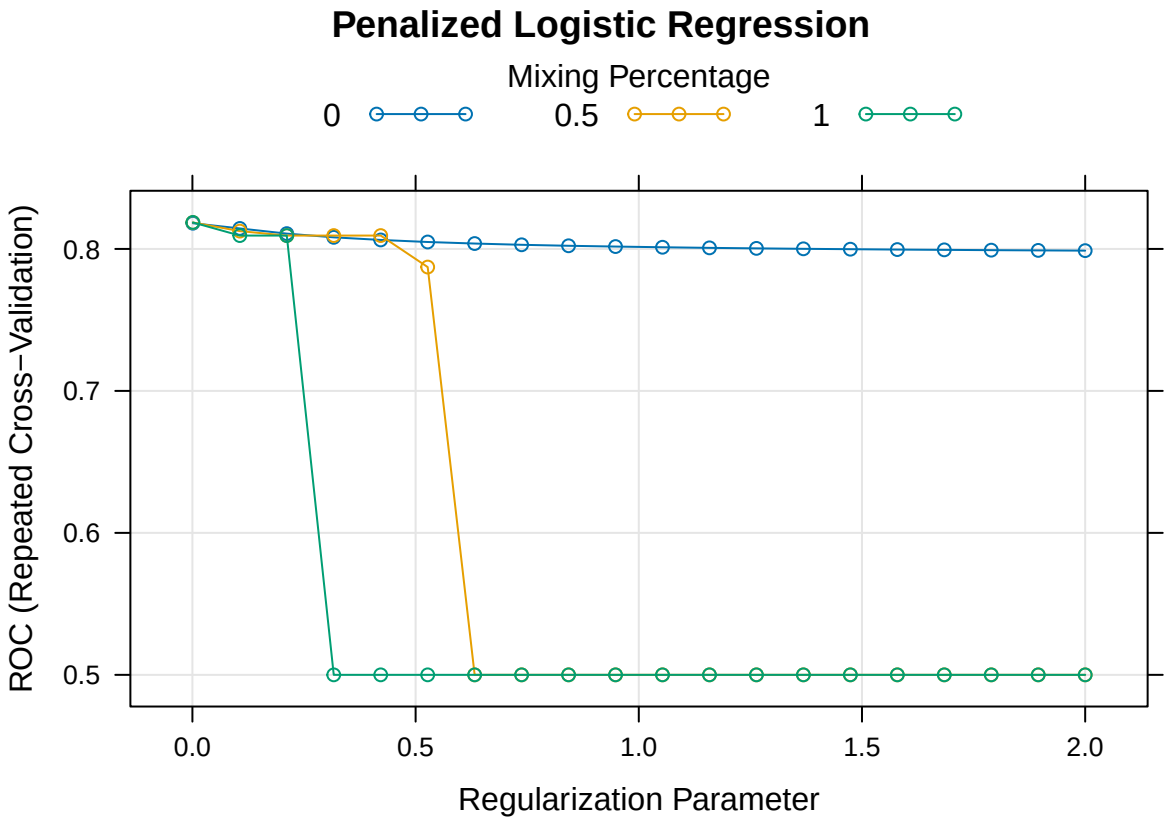
```
## Linear Discriminant Analysis
##
## 4088 samples
##   14 predictor
##    2 classes: 'X0', 'X1'
##
## Pre-processing: centered (14), scaled (14)
## Resampling: Cross-Validated (5 fold, repeated 3 times)
## Summary of sample sizes: 3270, 3270, 3270, 3271, 3271, 3271, ...
## Resampling results:
##
##   ROC        Sens       Spec
##   0.8191246  0.7065041  0.779191
```

```
# LDA Predictions
predictions <- predict(ldaFit_stroke, newdata = trainData_ready)

# LDA Confusion Matrix
ldaCM_stroke <- confusionMatrix(predictions, trainData_ready$stroke)

# Confusion Matrix Plot
conf_matrix <- as.data.frame(ldaCM_stroke$table)
ggplot(data = conf_matrix, aes(x = Reference, y = Prediction)) +
geom_tile(aes(fill = Freq)) +
geom_text(aes(label = Freq)) +
scale_fill_gradient(low = 'yellow', high = 'green') +
labs(title = 'Linear Discriminant Analysis Model Confusion Matrix', x = 'Actual', y = 'Predicted')
```



Model #2 - Penalized Logistic Regression (PLR)

```
set.seed(rseed)

glmnGrid <- expand.grid(alpha = c( 0, .5, 1),
lambda = seq(.001, 2, length = 20))

# Penalized Logistic Regression
plrFit_stroke <- train(stroke ~ .,
                    data = trainData_ready,
                    method = 'glmnet',
                    tuneGrid = glmnGrid,
                    preProc = c('center', 'scale'),
                    metric = 'ROC',
                    trControl = ctrl)

plot(plrFit_stroke, main = 'Penalized Logistic Regression')
```




```
# Best tuning parameters
optimal_plr_tune <- plrFit_stroke$bestTune
print(paste('Best Alpha and Lambda tuning parameters for Penalized Logistic Regression:', paste(optimal
```

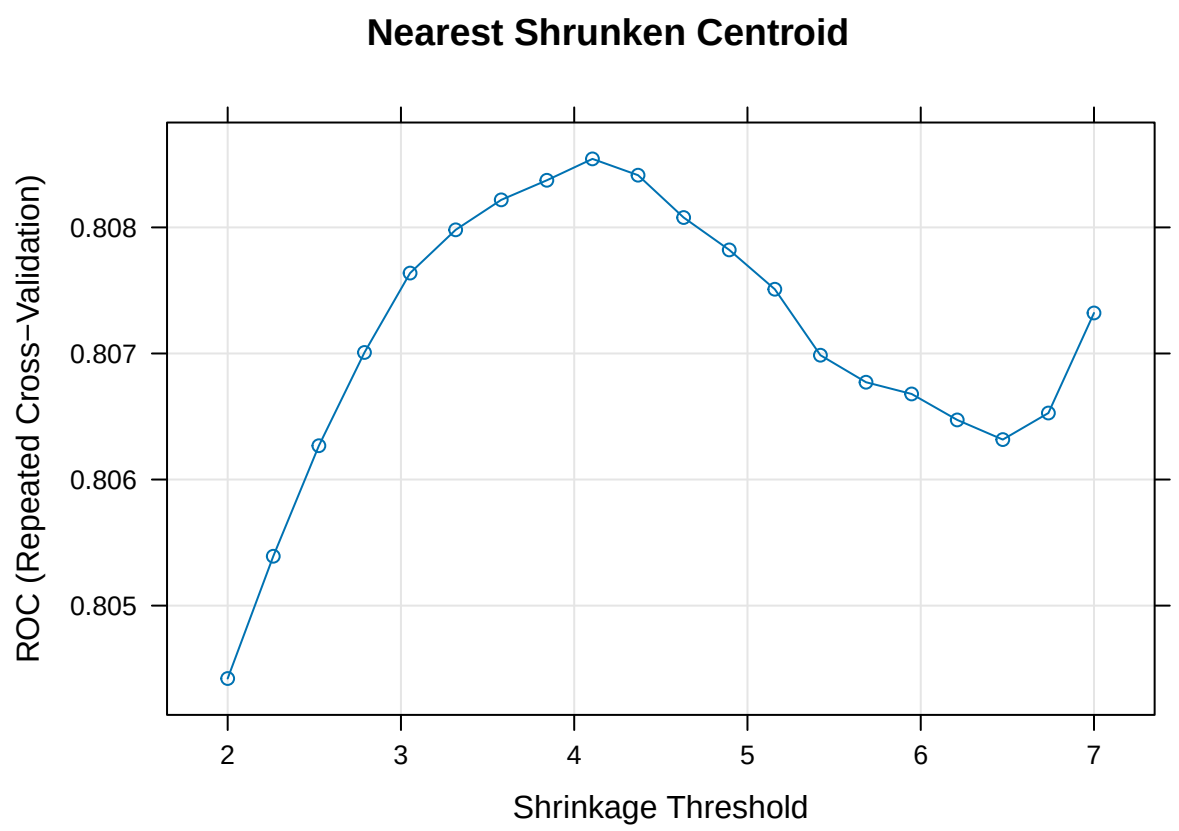
```
## [1] "Best Alpha and Lambda tuning parameters for Penalized Logistic Regression: 1,0.001"
```

Model #3 - Nearest Shrunken Centroids

```
set.seed(rseed)
nscGrid <- data.frame(threshold = seq(2, 7, length = 20))


# Nearest Shrunken Centroids
nscFit_stroke <- train(stroke ~ .,
                       data = trainData_ready,
                       method = 'pam',
                       preProc = c('center', 'scale'),
                       tuneGrid = nscGrid,
                       metric = 'ROC',
                       trControl = ctrl)
```

```
## 1111111111111111
```

```r
plot(nscFit_stroke, main = 'Nearest Shrunken Centroid')
```

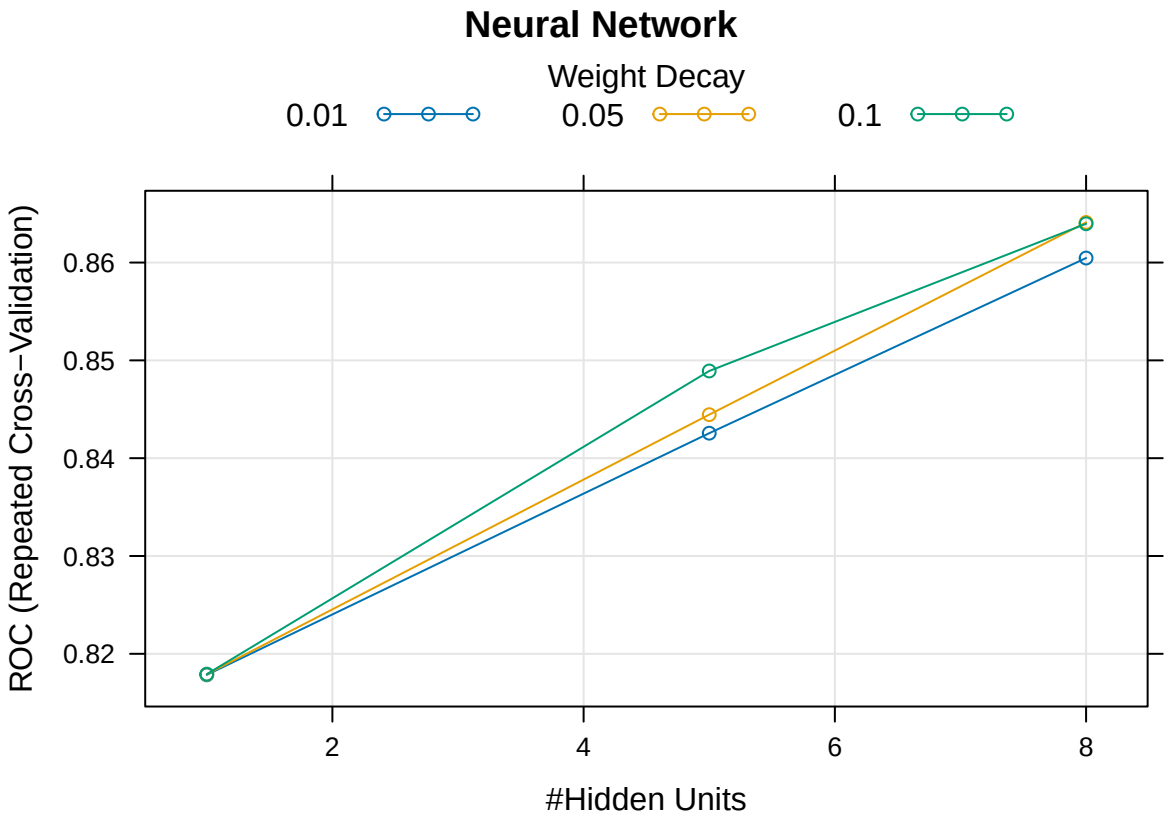



```r
# Best tuning parameters
optimal_nsc_tune <- nscFit_stroke$bestTune
print(paste('Best threshold tuning parameter for Nearest Shrunken Centroids:', paste(optimal_nsc_tune,
```

```
## [1] "Best threshold tuning parameter for Nearest Shrunken Centroids: 4.10526315789474"
```

Model #4 - Neural Network

```r
set.seed(rseed)

grid <- expand.grid(size = c(1, 5, 8),      # Number of hidden units
                    decay = c( 0.01, 0.05, .1))  # Weight decay
# Neural Networks
nnFit_stroke <- train(stroke ~ .,
                      data = trainData_ready,
                      method = 'nnet',
                      maxit = 500,
                      preProcess = c('center', 'scale'),
                      metric = 'ROC',
                      trControl = ctrl,
                      tuneGrid = grid,
                      trace = FALSE)
plot(nnFit_stroke, main = 'Neural Network')
```




```
# Best tuning parameters
optimal_nn_tune <- nnFit_stroke$bestTune
print(paste('Best Size and Decay tuning parameters for Neural Network:', paste(optimal_nn_tune, collaps
```

```
## [1] "Best Size and Decay tuning parameters for Neural Network: 8,0.05"
```

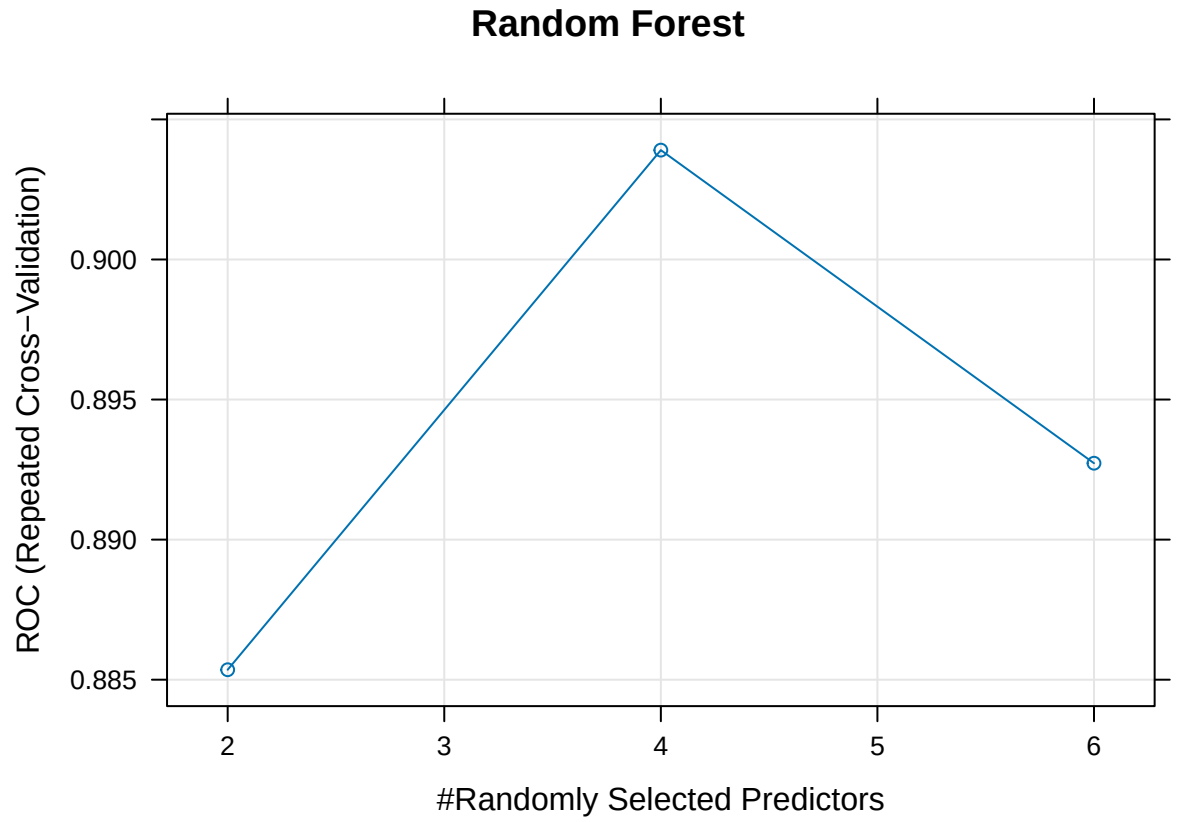
Model #5 - Random Forest

```
# Set seed for reproducibility
set.seed(rseed)

# Random Forest
rf_grid <- expand.grid(
  mtry = c(2, 4, 6)
)

rfFit_stroke <- train(
  stroke ~ .,
  data = trainData_ready,
  method = "rf",
  trControl = ctrl,
  tuneGrid = rf_grid,
  ntree = 100,
  trace = FALSE
)
```

```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
```

```
## in the result set. ROC will be used instead.
```

```
# Print the best parameters and performance metrics
plot(rfFit_stroke, main = 'Random Forest')
```




```
# Best tuning parameters
optimal_rf_tune <- rfFit_stroke$bestTune
print(paste('Best Size and Decay tuning parameters for Random Forest:', paste(optimal_rf_tune, collapse
```

```
## [1] "Best Size and Decay tuning parameters for Random Forest: 4"
```

Results - Summary Table

```
# 1.Make predictions for Linear Discriminant Analysis
lda_pred <- predict(ldaFit_stroke, newdata = testData_ready)
lda_cm <- confusionMatrix(lda_pred, testData_ready$stroke)

# 2.Make predictions for Penalized Logistic Regression
plr_pred <- predict(plrFit_stroke, newdata = testData_ready)
plr_cm <- confusionMatrix(plr_pred, testData_ready$stroke)

# 3.Make predictions for Nearest Shrunken Centroids
nsc_pred <- predict(nscFit_stroke, newdata = testData_ready)
nsc_cm <- confusionMatrix(nsc_pred, testData_ready$stroke)

# 4.Make predictions for Neural Network
nn_pred <- predict(nnFit_stroke, newdata = testData_ready)
```

```r
nn_cm <- confusionMatrix(nn_pred, testData_ready$stroke)

# 5.Make predictions for Random Forest
rf_pred <- predict(rfFit_stroke, newdata = testData_ready)
rf_cm <- confusionMatrix(rf_pred, testData_ready$stroke)

extract_accuracy <- function(model, cm) {
  tibble(
    model = model,
    Accuracy = cm$overall['Accuracy'],
    `CI Lower` = cm$overall['AccuracyLower'],
    `CI Upper` = cm$overall['AccuracyUpper']
  )
}

# Combine accuracies into a table
accuracies <- bind_rows(
  extract_accuracy('Linear Discriminant Analysis', lda_cm),
  extract_accuracy('Penalized Logistic Regression', plr_cm),
  extract_accuracy('Nearest Shrunken Centroids', nsc_cm),
  extract_accuracy('Neural Network', nn_cm),
  extract_accuracy('Random Forest', rf_cm)
)

# Display the table using gt package
accuracies %>%
  arrange(-Accuracy) %>%
  gt() %>%
  fmt_number(columns = c(Accuracy, `CI Lower`, `CI Upper`), decimals = 3)
```

model	Accuracy	CI Lower	CI Upper
Random Forest	0.780	0.753	0.805
Penalized Logistic Regression	0.730	0.702	0.757
Linear Discriminant Analysis	0.724	0.696	0.751
Neural Network	0.724	0.696	0.751
Nearest Shrunken Centroids	0.679	0.649	0.708

Tuned Models

```r
set.seed(rseed)
# Penalized Logistic Regression with optimal parameters
plrFit_final <- train(stroke ~ .,
                      data = trainData_ready,
                      method = 'glmnet',
                      preProc = c('center', 'scale'),
                      metric = 'ROC',
                      trControl = ctrl,
                      tuneGrid = expand.grid(
                        alpha = optimal_plr_tune$alpha,
                        lambda = optimal_plr_tune$lambda
                      ))
set.seed(rseed)
```

```
# Retrain NSC with optimal parameters
nscFit_final <- train(stroke ~ .,
                      data = trainData_ready,
                      method = 'pam',
                      preProc = c('center', 'scale'),
                      metric = 'ROC',
                      trControl = ctrl,
                      tuneGrid = expand.grid(
                        threshold = optimal_nsc_tune$threshold
                      ))
```

```
## 1111111111111111
```

```
set.seed(rseed)
# Retrain NN with optimal parameters
nnFit_final <- train(stroke ~ .,
                     data = trainData_ready,
                     method = 'nnet',
                     maxit = 500,
                     preProcess = c('center', 'scale'),
                     metric = 'ROC',
                     trControl = ctrl,
                     tuneGrid = expand.grid(
                       size = optimal_nn_tune$size,
                       decay = optimal_nn_tune$decay
                       ),
                     trace = FALSE)
set.seed(rseed)
# Retrain RF with optimal parameters
rfFit_final <- train(stroke ~ .,
                    data = trainData_ready,
                    method = "rf",
                    ntree = 100,
                    trControl = ctrl,
                    tuneGrid = expand.grid(
                       mtry = optimal_rf_tune$mtry
                       ))
```

```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
## in the result set. ROC will be used instead.
```

Summary for Tuned Models

```
set.seed(rseed)
# Make predictions for Linear Discriminant Analysis
lda_pred <- predict(ldaFit_stroke, newdata = testData_ready)
lda_cm2 <- confusionMatrix(lda_pred, testData_ready$stroke)

# Make predictions for Penalized Logistic Regression
plr_pred2 <- predict(plrFit_final, newdata = testData_ready)
plr_cm2 <- confusionMatrix(plr_pred2, testData_ready$stroke)

# Make predictions for Nearest Shrunken Centroids
nsc_pred2 <- predict(nscFit_final, newdata = testData_ready)
```

```r
nsc_cm2 <- confusionMatrix(nsc_pred2, testData_ready$stroke)

# Make predictions for Neural Network
nn_pred2 <- predict(nnFit_final, newdata = testData_ready)
nn_cm2 <- confusionMatrix(nn_pred2, testData_ready$stroke)

# Make predictions for Random Forest
rf_pred2 <- predict(rfFit_final, newdata = testData_ready)
rf_cm2 <- confusionMatrix(rf_pred2, testData_ready$stroke)


extract_accuracy <- function(model, cm) {
  tibble(
    model = model,
    Accuracy = cm$overall['Accuracy'],
    `CI Lower` = cm$overall['AccuracyLower'],
    `CI Upper` = cm$overall['AccuracyUpper']
  )
}

# Combine accuracies into a table
accuracies <- bind_rows(
  extract_accuracy('Linear Discriminant Analysis', lda_cm2),
  extract_accuracy('Penalized Logistic Regression', plr_cm2),
  extract_accuracy('Nearest Shrunken Centroids', nsc_cm2),
  extract_accuracy('Neural Network', nn_cm2),
  extract_accuracy('Random Forest', rf_cm2),
)

# Display the table using gt package
accuracies %>%
  arrange(-Accuracy) %>%
  gt() %>%
  fmt_number(columns = c(Accuracy, `CI Lower`, `CI Upper`), decimals = 3)
```

model	Accuracy	CI Lower	CI Upper
Random Forest	0.771	0.744	0.796
Neural Network	0.731	0.703	0.758
Penalized Logistic Regression	0.730	0.702	0.757
Linear Discriminant Analysis	0.724	0.696	0.751
Nearest Shrunken Centroids	0.679	0.649	0.708

Final Model

```r
rfFit_final$finalModel
```

```
##
## Call:
##  randomForest(x = x, y = y, ntree = 100, mtry = param$mtry)
##                Type of random forest: classification
##                      Number of trees: 100
## No. of variables tried at each split: 4
```

```
##
##         OOB estimate of  error rate: 18.1%
## Confusion matrix:
##      X0   X1 class.error
## X0 1569  481   0.2346341
## X1  259 1779   0.1270854
```