# Project

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## R Markdown

```r
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
```

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

```
## [1] "C:/Users/ToriT/ADS503-Group6"
```

```r
### 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/ToriT/ADS503-Group6/healthcare-dataset-stroke-data.csv"
```

```r
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
```

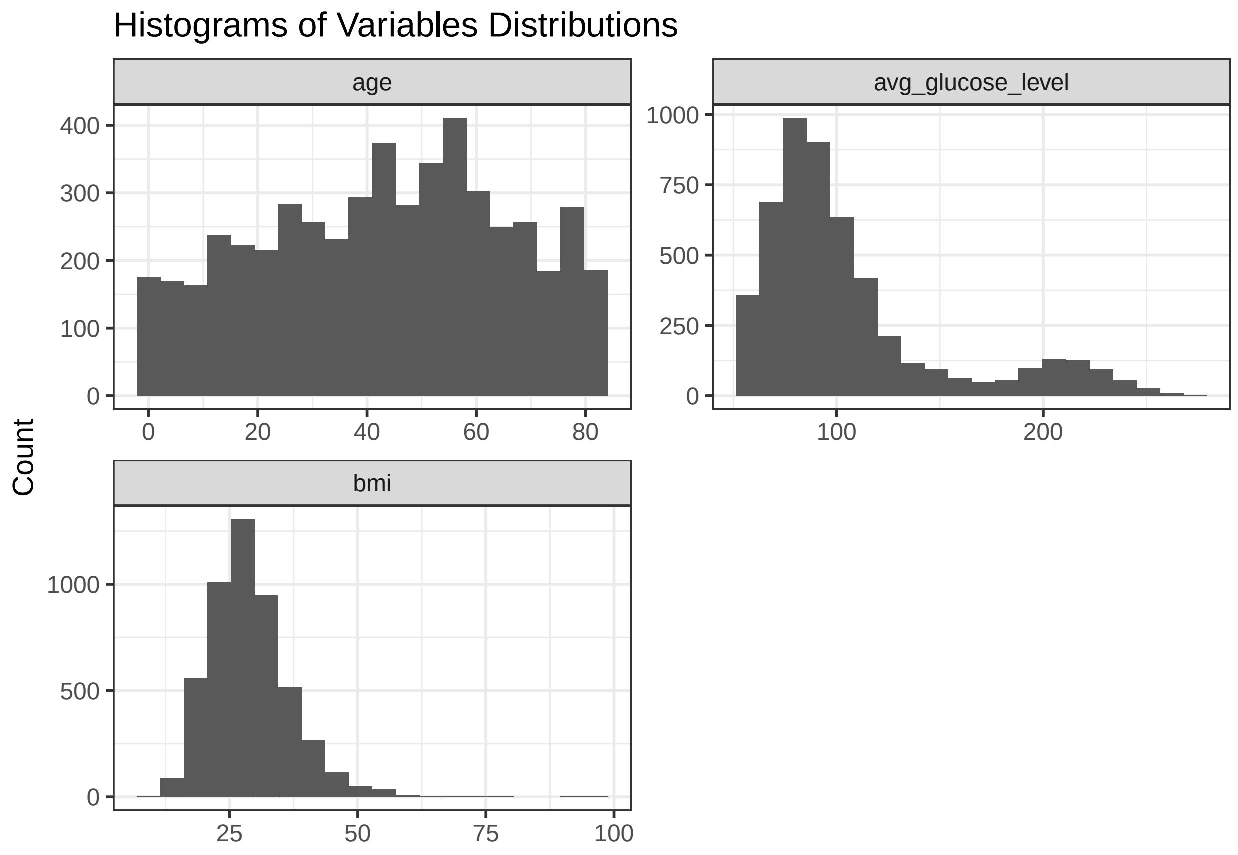
```
## Warning: Setting row names on a tibble is deprecated.
```

```
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>
```

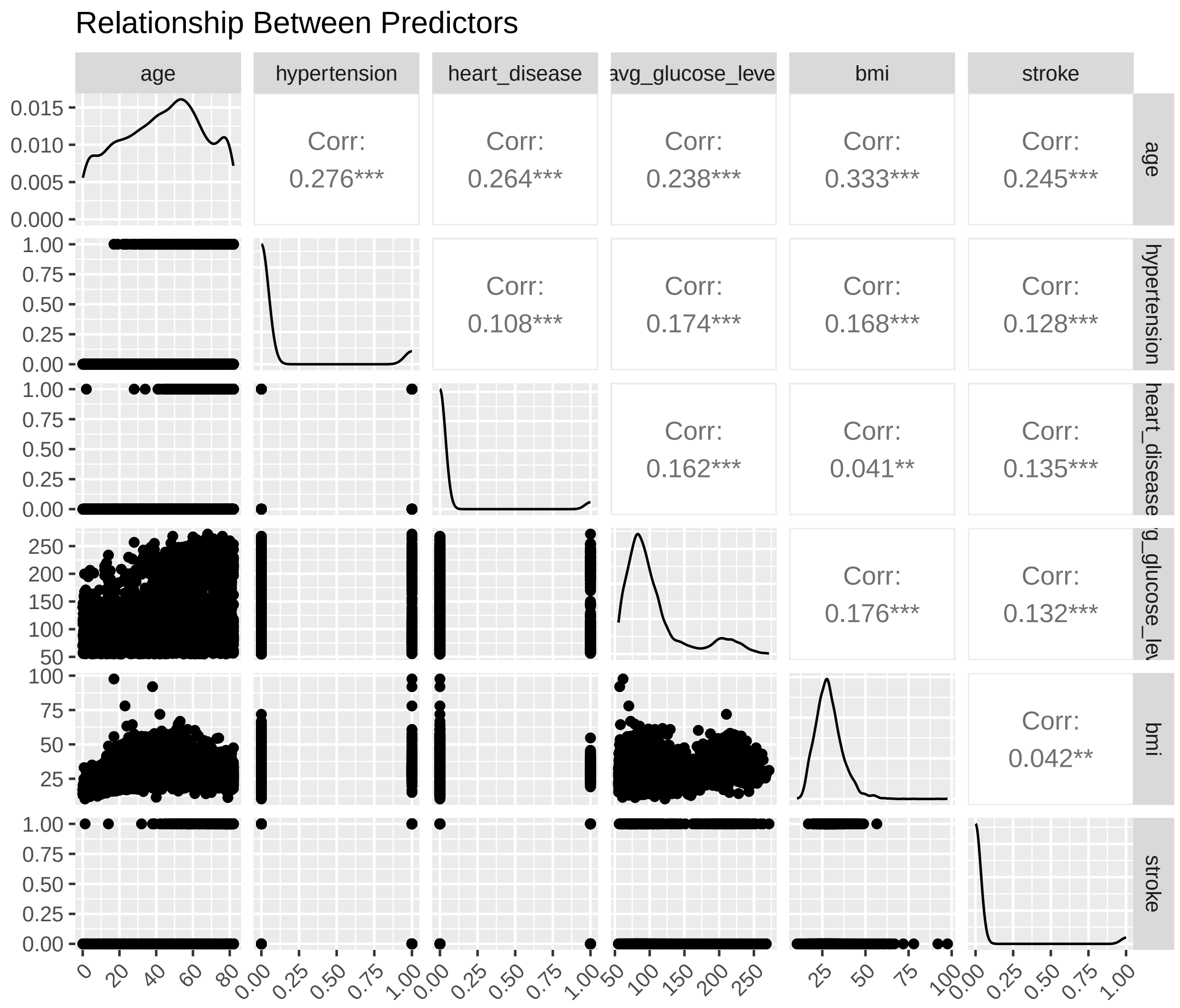
### Histograms

```
# 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")
```



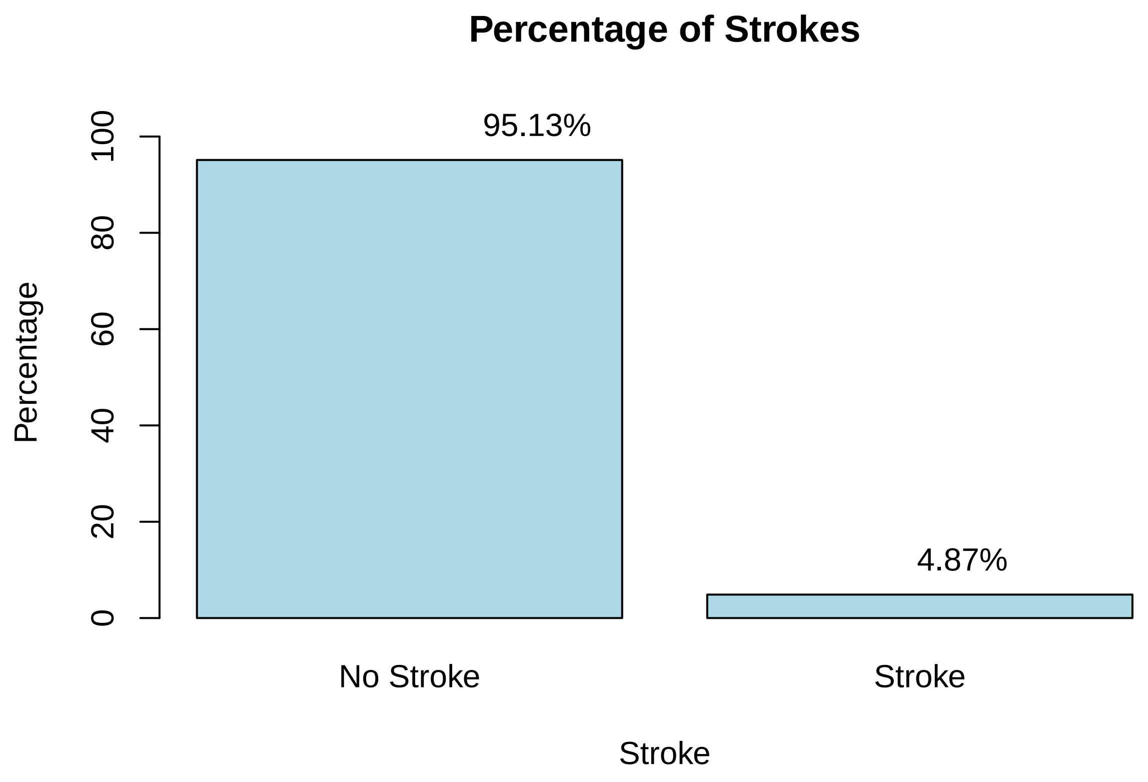
**Corrplot**

```
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

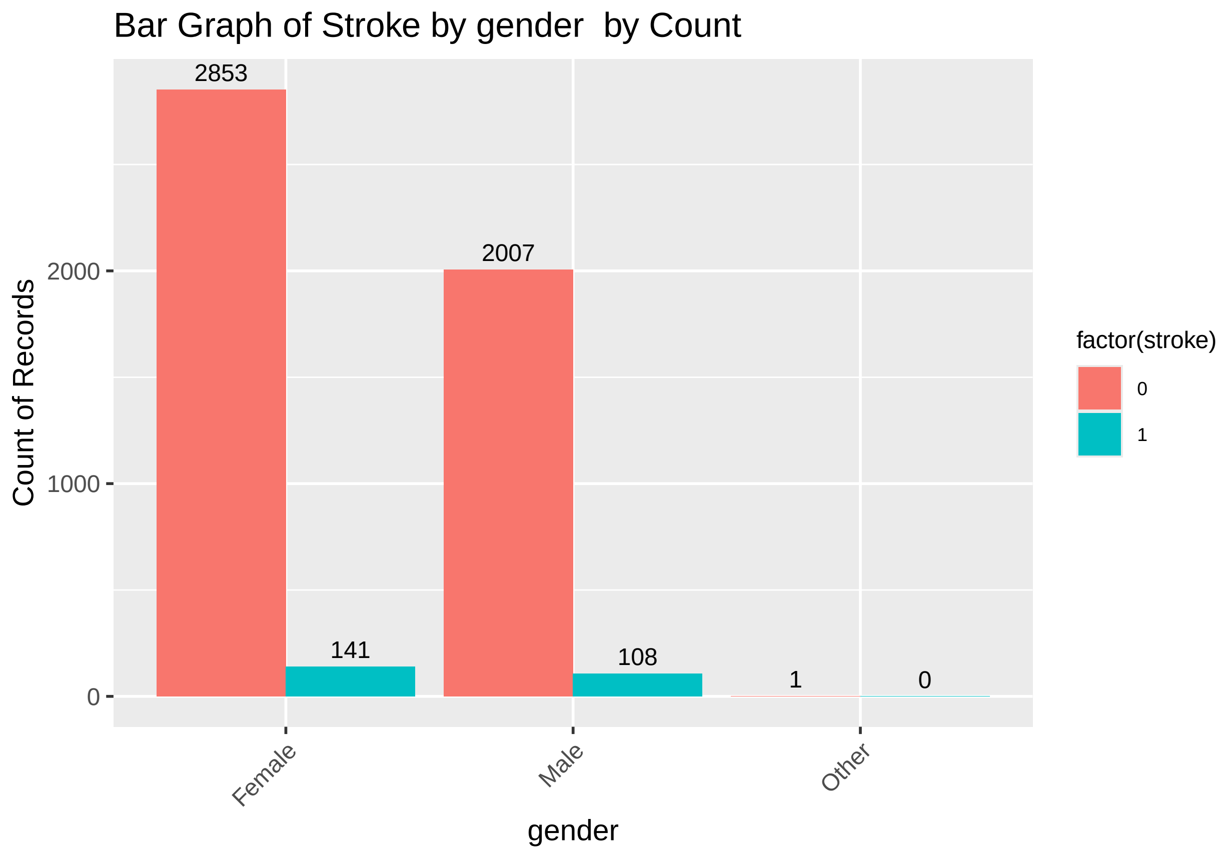
```
stroke_percent <- prop.table(table(df_eda$stroke)) * 100

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)
```

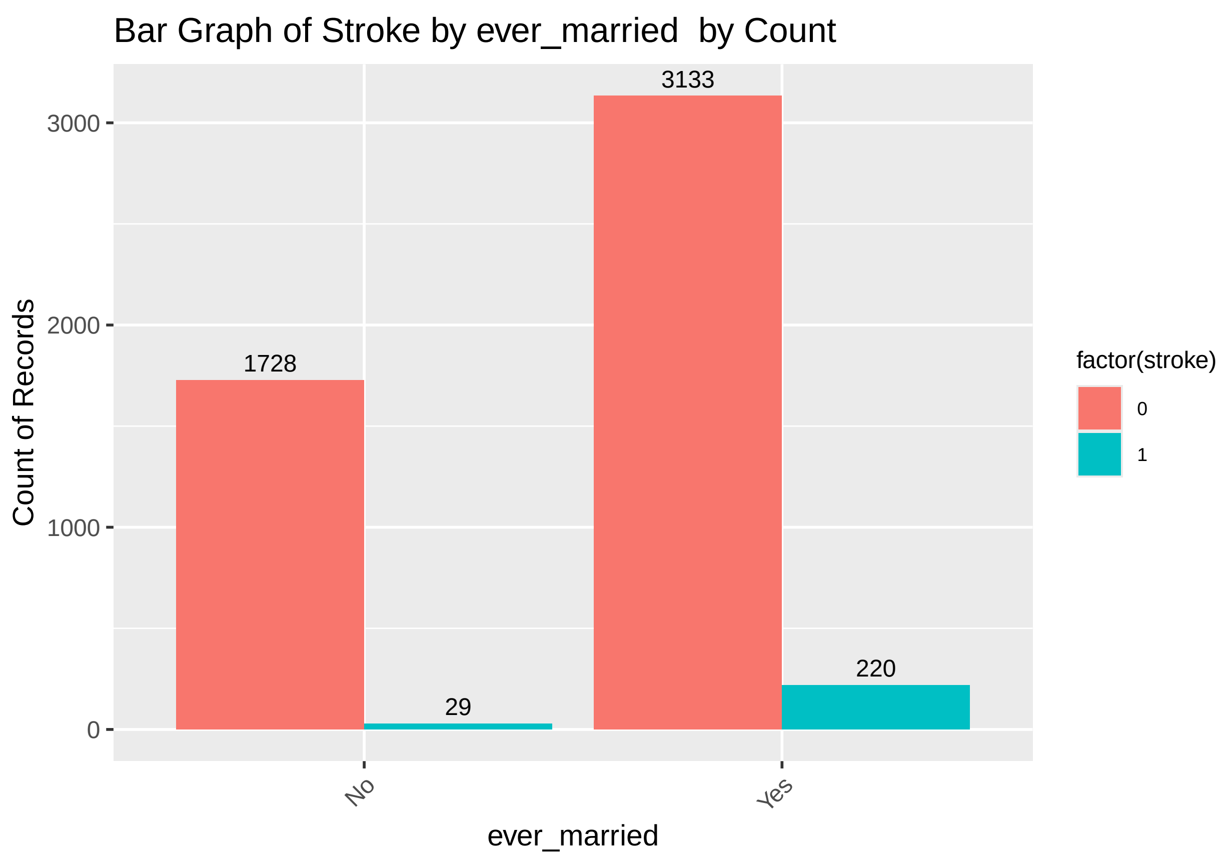


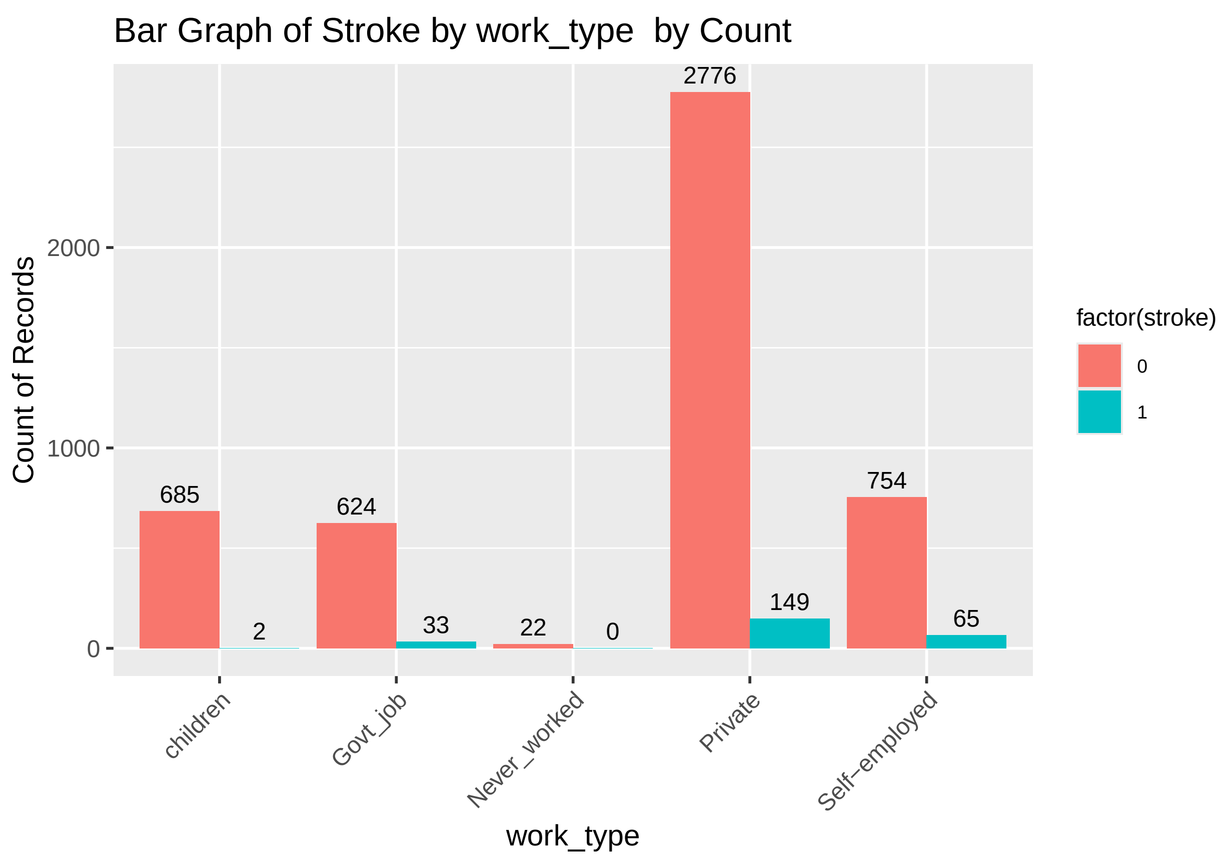
**Distributions of Values (Counts)**

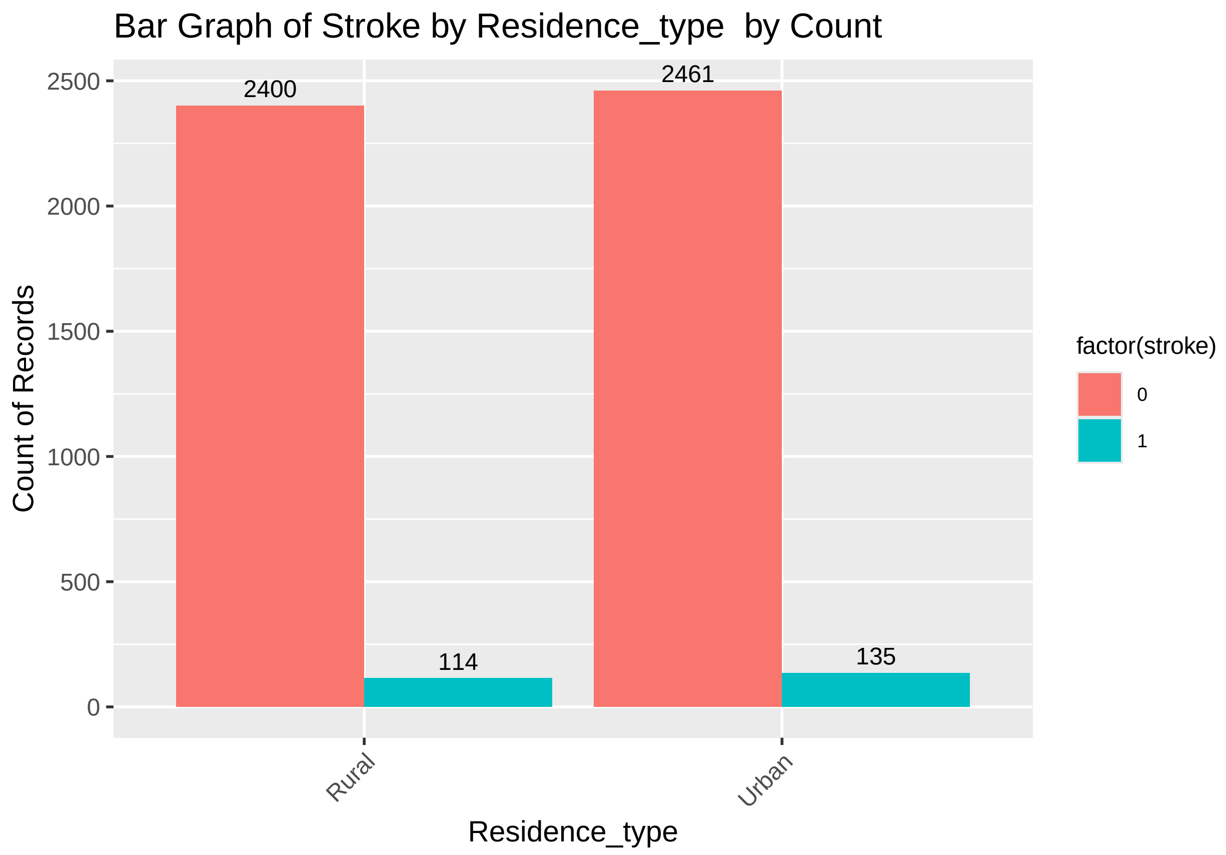
```
wrap_text <- function(x, width) {
  sapply(strwrap(x, width = width, simplify = FALSE), paste, collapse = "\n")
}

# 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
```

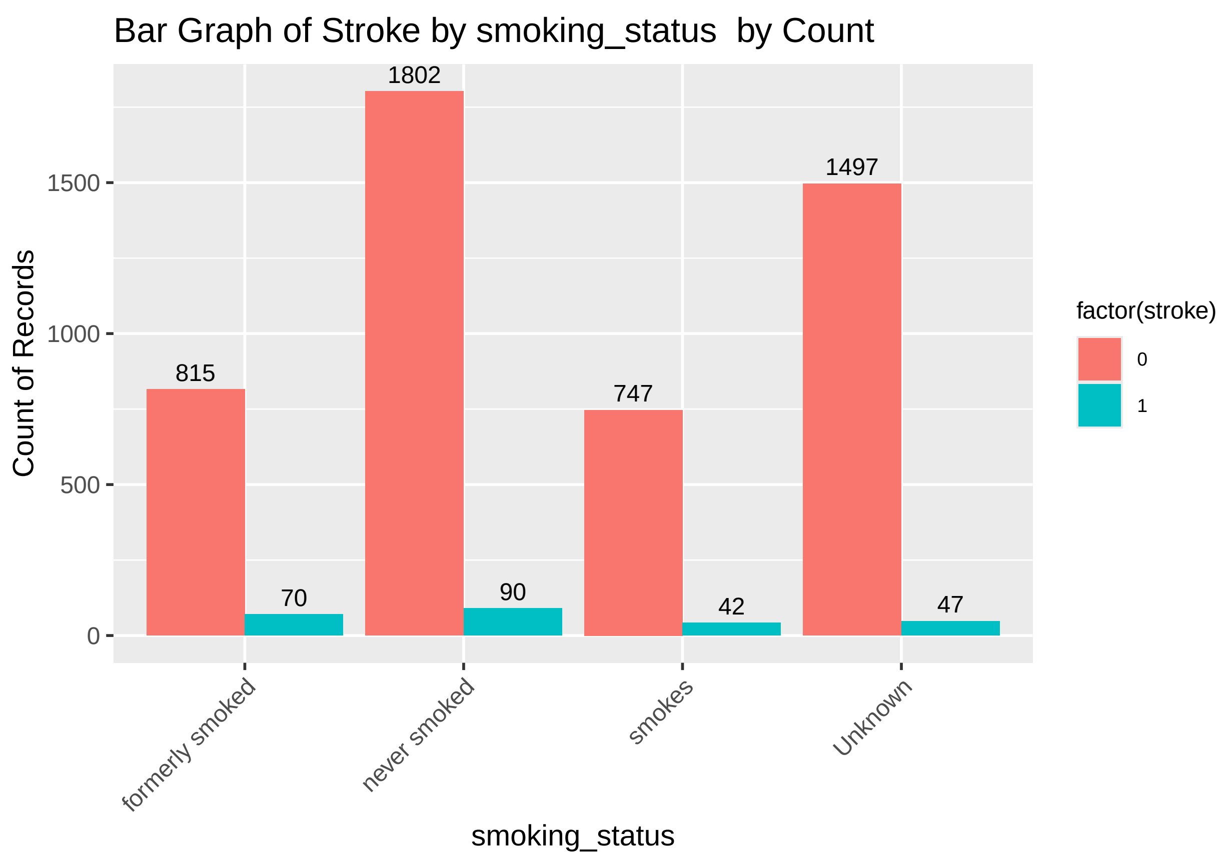
```r
}

# 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 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

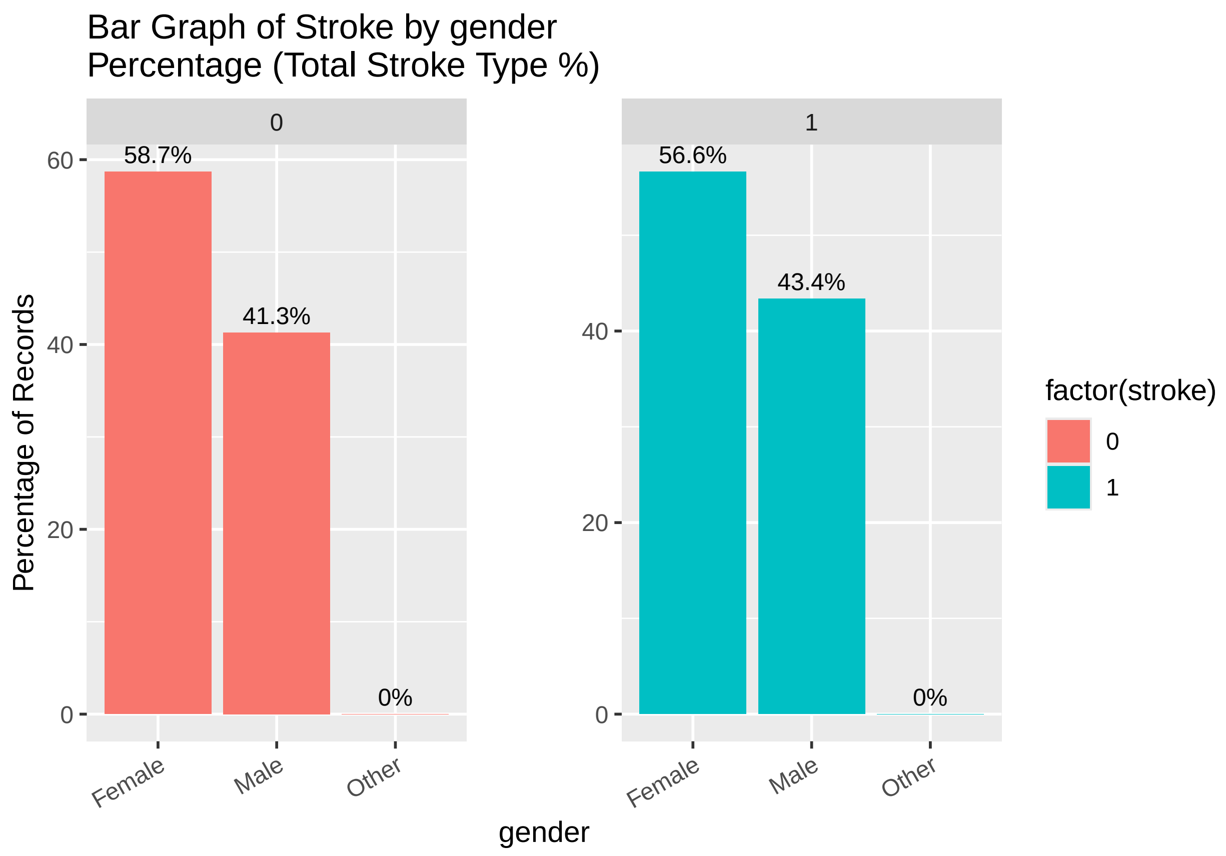

Bar Graph of Stroke by Residence_type by Count
Count of Records
2500
2000
1500
1000
500
0
2400
114
2461
135
Rural
Urban
Residence_type
factor(stroke)
0
1

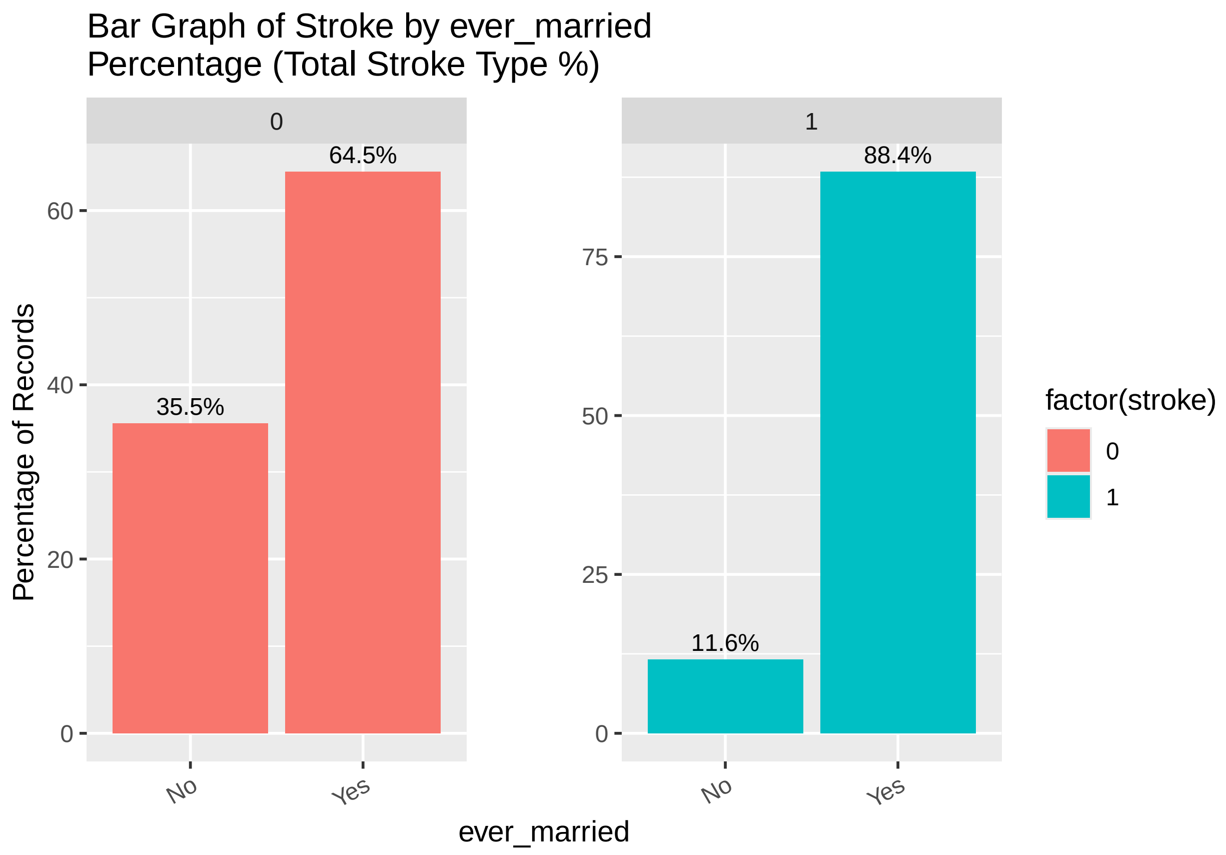


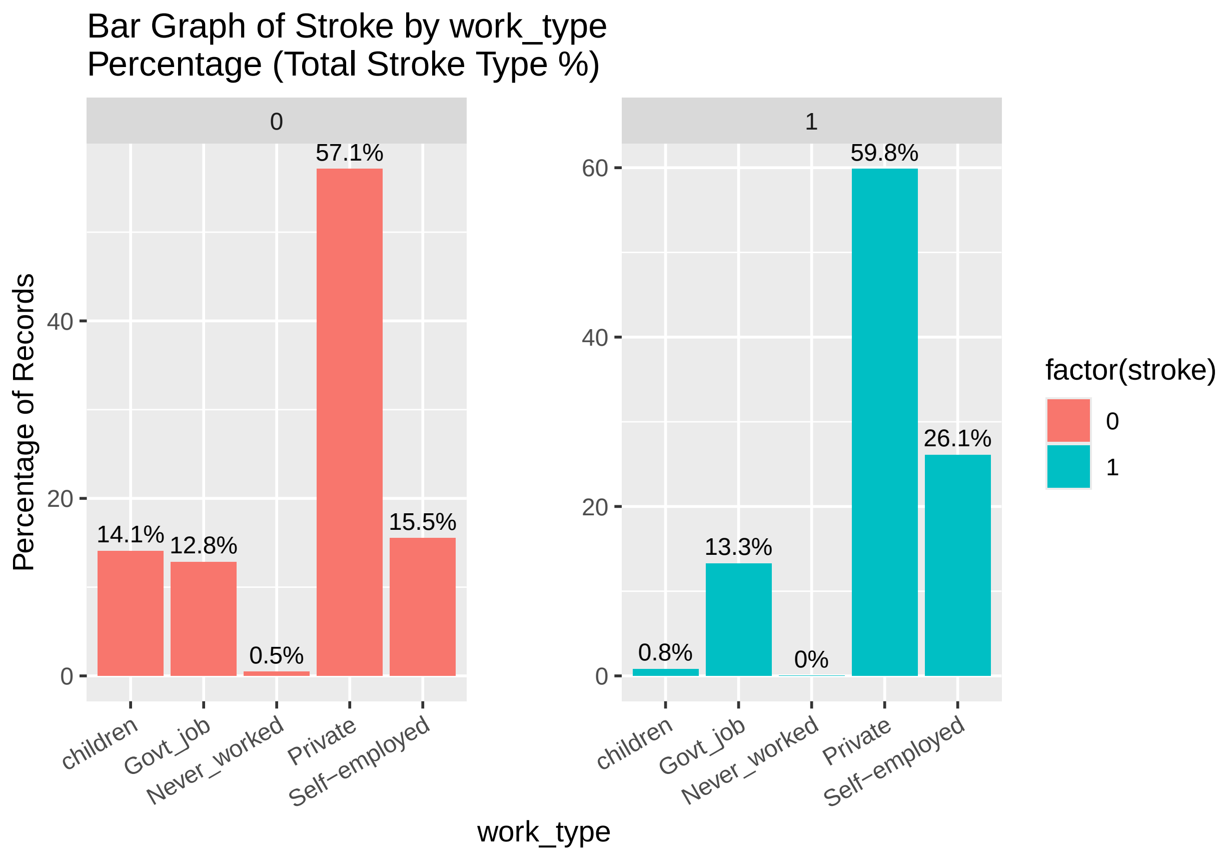
### Distributions of Values (Percentages)

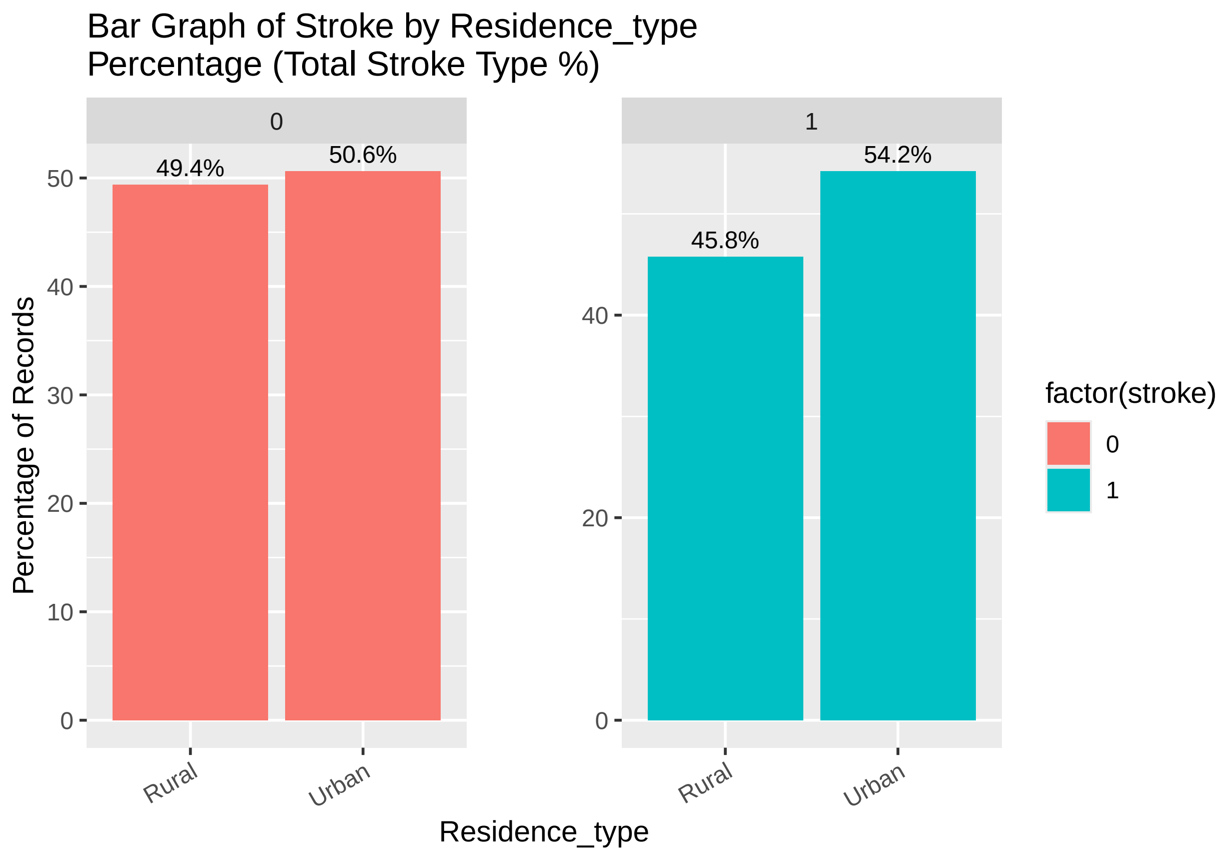
```
# Function to create plots
create_plots <- function(col) {
  counts <- table(df_eda[[col]], df_eda$stroke)
  counts_df <- as.data.frame(counts)
  names(counts_df) <- c(col, "stroke", "count")

  # 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")
)}
```

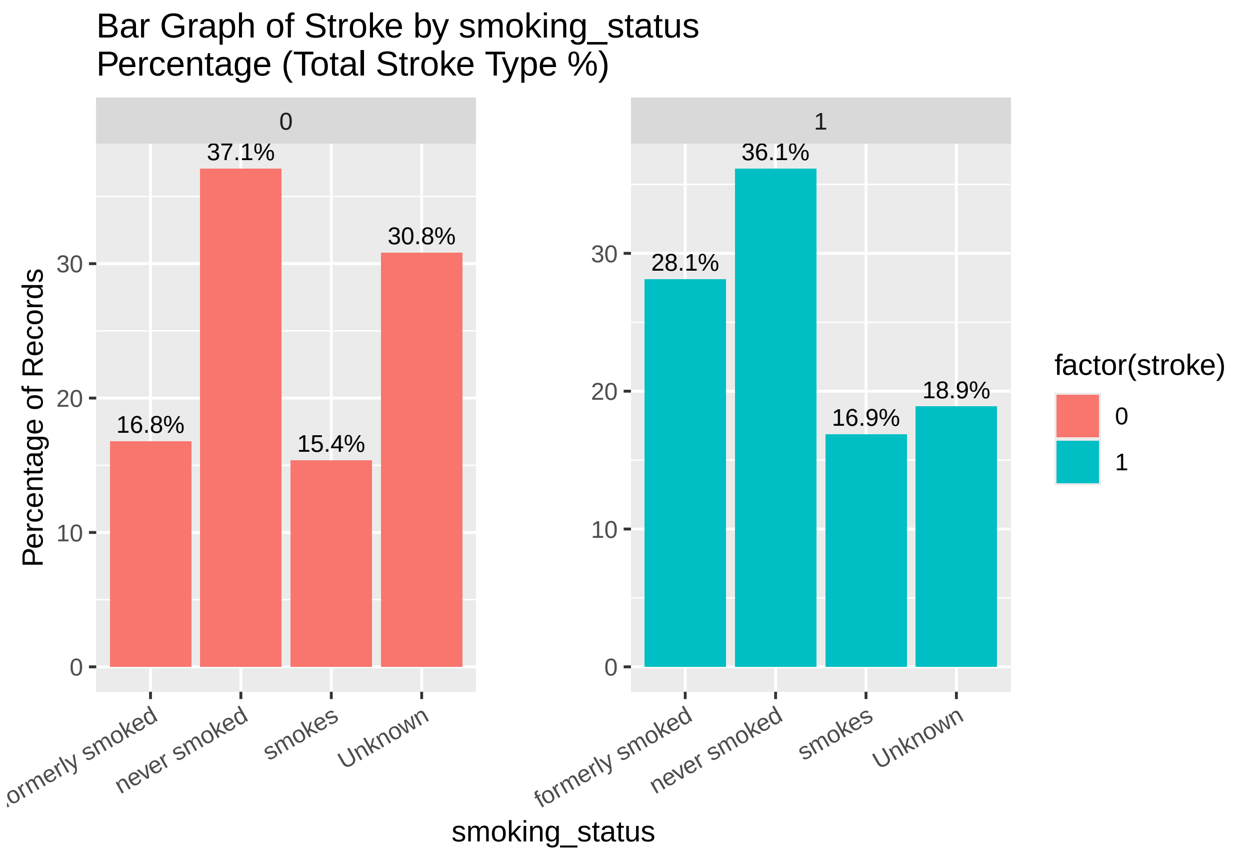
```r
# Create plots for each non-numeric column
plots_list <- map(non_numeric_columns, ~ create_plots(.x))

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




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

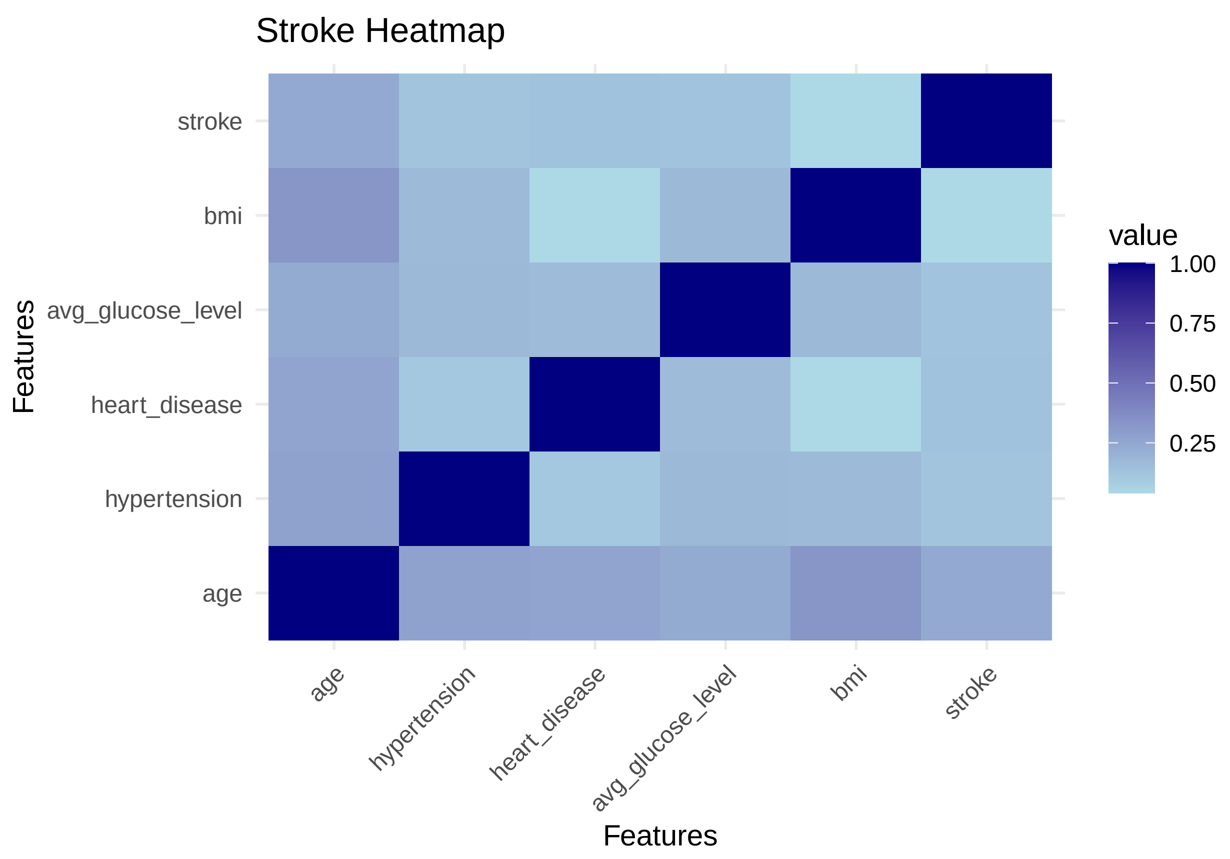

Bar Graph of Stroke by work_type
Percentage (Total Stroke Type %)
0
1
Percentage of Records
0
20
40
60
14.1%
12.8%
0.5%
57.1%
15.5%
0.8%
13.3%
0%
59.8%
26.1%
children
Govt_job
Never_worked
Private
Self−employed
work_type
factor(stroke)
0
1


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**

```r
##### 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
##   2395   1692      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
##   2396   1692
```

```
# 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
##               159                 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, -Residenc
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           0            1                  0                      0
## 4           1            1                  0                      0
## 5           1            1                  0                      0
## 6           0            0                  0                      0
##   work_type_Private work_type_Self_employed Residence_type_Urban
## 1                 1                       0                    1
## 2                 0                       1                    0
## 3                 1                       0                    1
## 4                 1                       0                    1
## 5                 1                       0                    0
## 6                 1                       0                    1
##   smoking_status_formerly_smoked smoking_status_never_smoked
## 1                              1                           0
## 2                              0                           1
## 3                              0                            0
## 4                              1                            0
## 5                              0                            1
## 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                     1  49            0             0            171.23
## 4                     0  81            0             0            186.21
## 5                     0  74            1             1             70.09
## 6                     0  69            0             0             94.39
##        bmi stroke
## 1 36.60000     X1
## 2 33.74876     X1
## 3 34.40000     X1
## 4 29.00000     X1
## 5 27.40000     X1
## 6 22.80000     X1
```

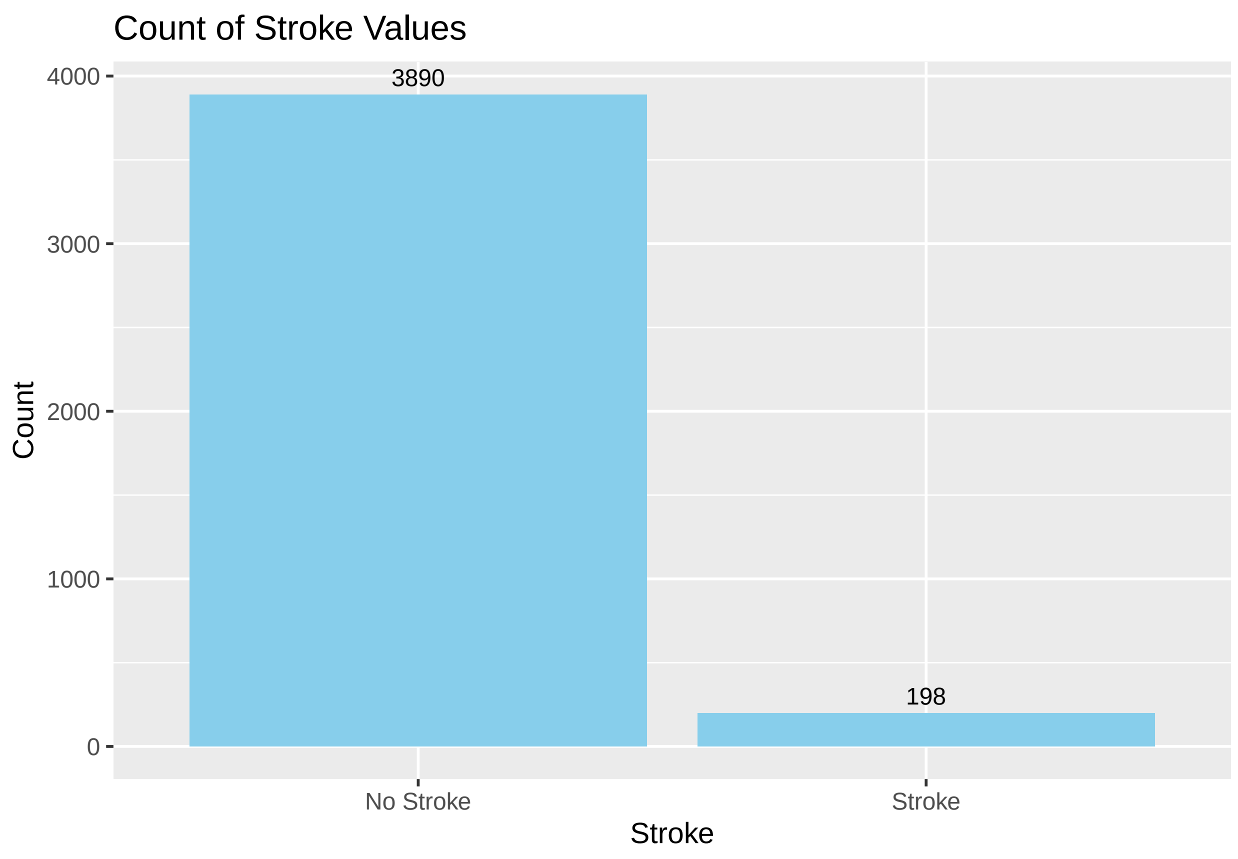
```
# Test
testData_ready <- cbind(testData_dummy, testData_selected)
testData_ready <- testData_ready %>%
  mutate(across(all_of(c("hypertension", "heart_disease", "stroke")), as.factor))
names(testData_ready) <- gsub("\\.", "_", names(testData_ready))
names(testData_ready) <- gsub("_Yes", "", names(testData_ready))
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": 2 1 1 1 1 2 2 2 1 2 ...
##  $ ever_married                  : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 1 2 2 ...
##  $ work_type_Govt_job            : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 2 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": 2 1 2 1 1 1 1 1 2 2 ...
##  $ work_type_Self_employed       : Factor w/ 2 levels "0","1": 1 2 1 2 2 2 2 1 1 1 ...
##  $ Residence_type_Urban          : Factor w/ 2 levels "0","1": 1 1 1 1 2 1 2 2 2 1 ...
##  $ smoking_status_formerly_smoked: Factor w/ 2 levels "0","1": 1 1 1 1 1 1 2 1 2 1 ...
##  $ smoking_status_never_smoked   : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 1 2 1 2 ...
##  $ smoking_status_smokes         : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ age                           : num  80 79 81 50 52 80 80 48 63 76 ...
##  $ hypertension                  : Factor w/ 2 levels "0","1": 1 2 2 2 2 1 1 1 1 2 ...
##  $ heart_disease                 : Factor w/ 2 levels "0","1": 2 1 1 1 1 1 2 1 1 1 ...
##  $ avg_glucose_level             : num  105.9 174.1 80.4 167.4 233.3 ...
##  $ bmi                           : num  32.5 24 29.7 30.9 48.9 ...
##  $ stroke                        : Factor w/ 2 levels "X0","X1": 2 2 2 2 2 2 2 2 2 2 ...
```

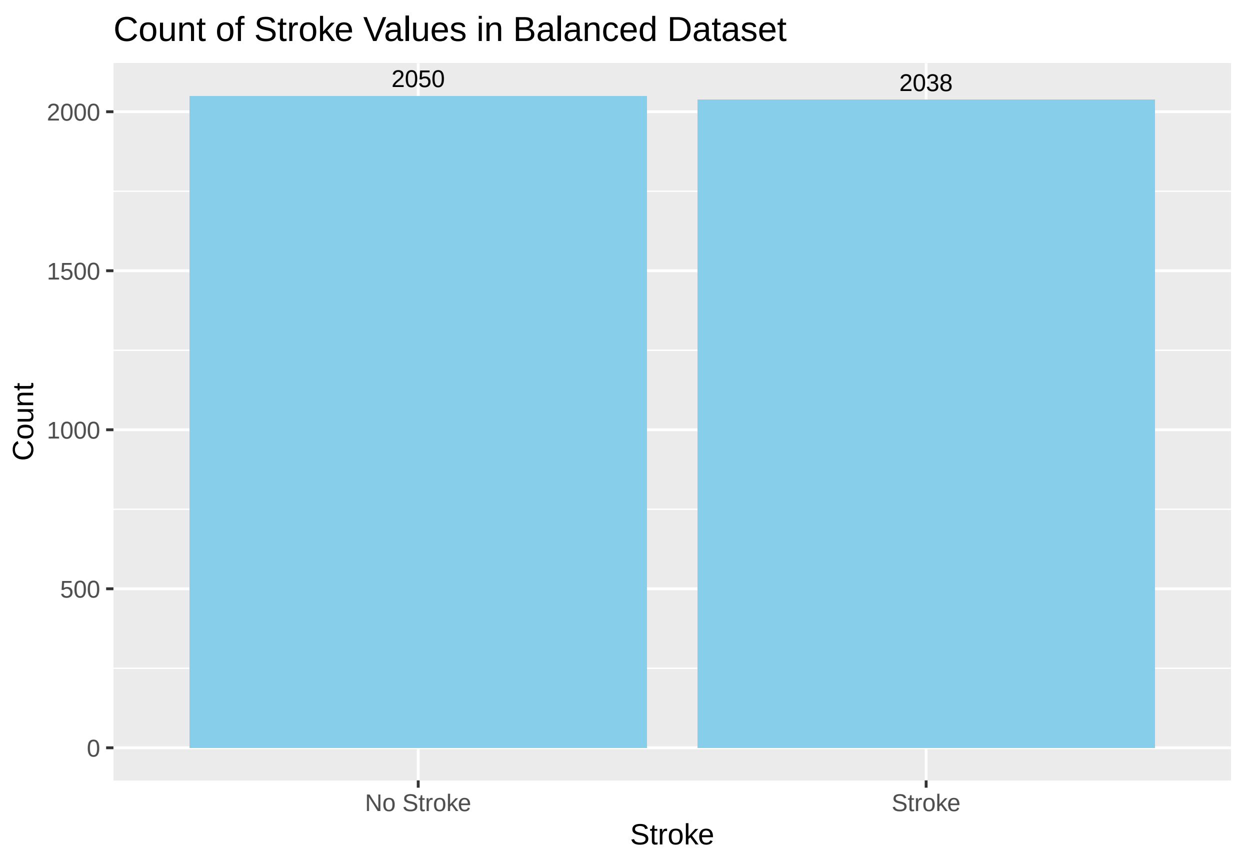
### Class Imbalance (ROSE Method)

```
# 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)) +
```

```r
  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
```



```r
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)                    -3.660e+00  2.903e-01 -12.606  < 2e-16 ***
## gender_Male1                   -3.688e-01  8.355e-02  -4.414 1.01e-05 ***
## ever_married1                   3.268e-01  1.253e-01   2.607 0.009126 **
## work_type_Govt_job1            -1.269e+00  3.323e-01  -3.819 0.000134 ***
## work_type_Never_worked1        -1.137e+01  1.879e+02  -0.060 0.951759
## work_type_Private1             -9.997e-01  3.199e-01  -3.125 0.001780 **
## work_type_Self_employed1       -1.320e+00  3.367e-01  -3.921 8.82e-05 ***
## Residence_type_Urban1           2.210e-01  7.961e-02   2.776 0.005505 **
## smoking_status_formerly_smoked1  4.485e-01  1.240e-01   3.618 0.000296 ***
## smoking_status_never_smoked1   -2.937e-02  1.139e-01  -0.258 0.796570
## smoking_status_smokes1          4.335e-01  1.308e-01   3.314 0.000919 ***
## age                             6.697e-02  2.854e-03  23.461  < 2e-16 ***
## hypertension1                   4.910e-01  1.062e-01   4.623 3.79e-06 ***
## heart_disease1                  6.163e-01  1.317e-01   4.680 2.87e-06 ***
## avg_glucose_level               5.250e-03  7.211e-04   7.280 3.33e-13 ***
## bmi                            -8.352e-03  5.905e-03  -1.414 0.157245
## ---
## 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: 3946.2  on 4072  degrees of freedom
## AIC: 3978.2
##
## Number of Fisher Scoring iterations: 12
```

## 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
##   0.8426977  0.7256911  0.810274
```

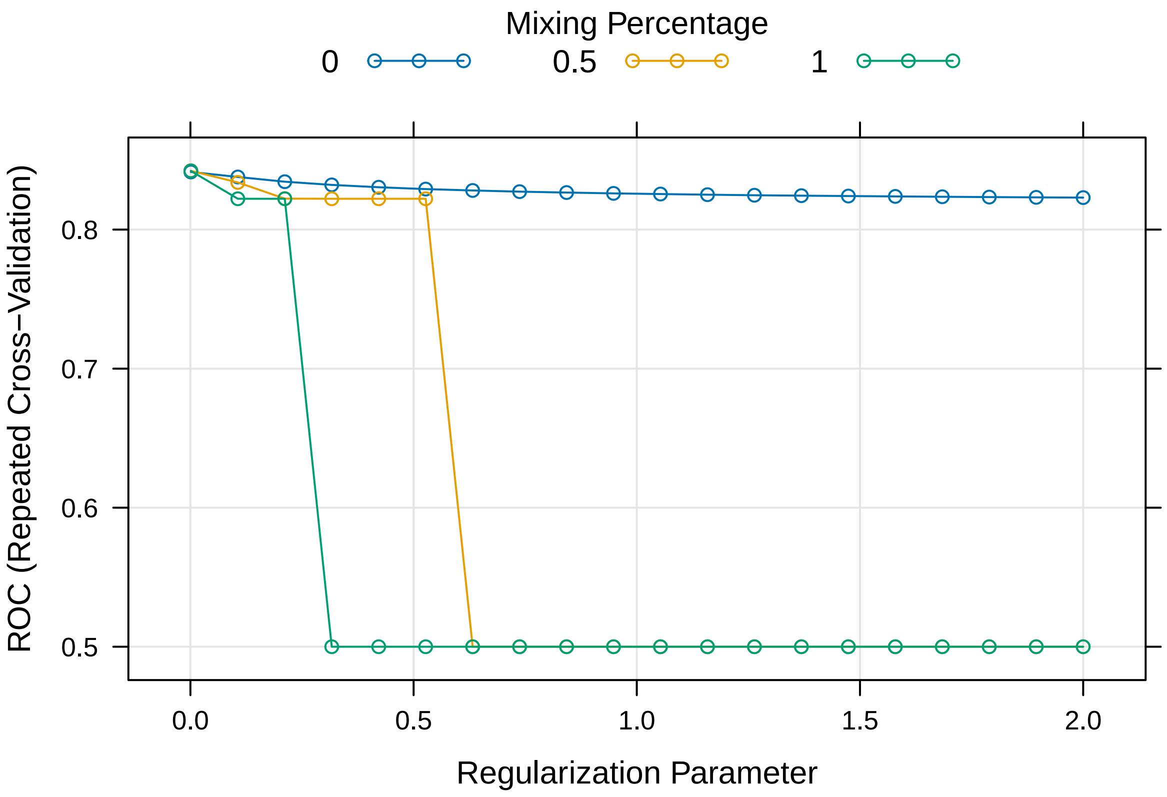
```
ldaCM_stroke <- confusionMatrix(ldaFit_stroke, norm = "none")
ldaCM_stroke
```

```
## Cross-Validated (5 fold, repeated 3 times) Confusion Matrix
##
## (entries are un-normalized aggregated counts)
##
##           Reference
## Prediction   X0   X1
##         X0 4463 1160
##         X1 1687 4954
##
##  Accuracy (average) : 0.7679
```

### 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,
```

```r
                    preProc = c('center', 'scale'),
                    metric = 'ROC',
                    trControl = ctrl)

plot(plrFit_stroke)
```



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

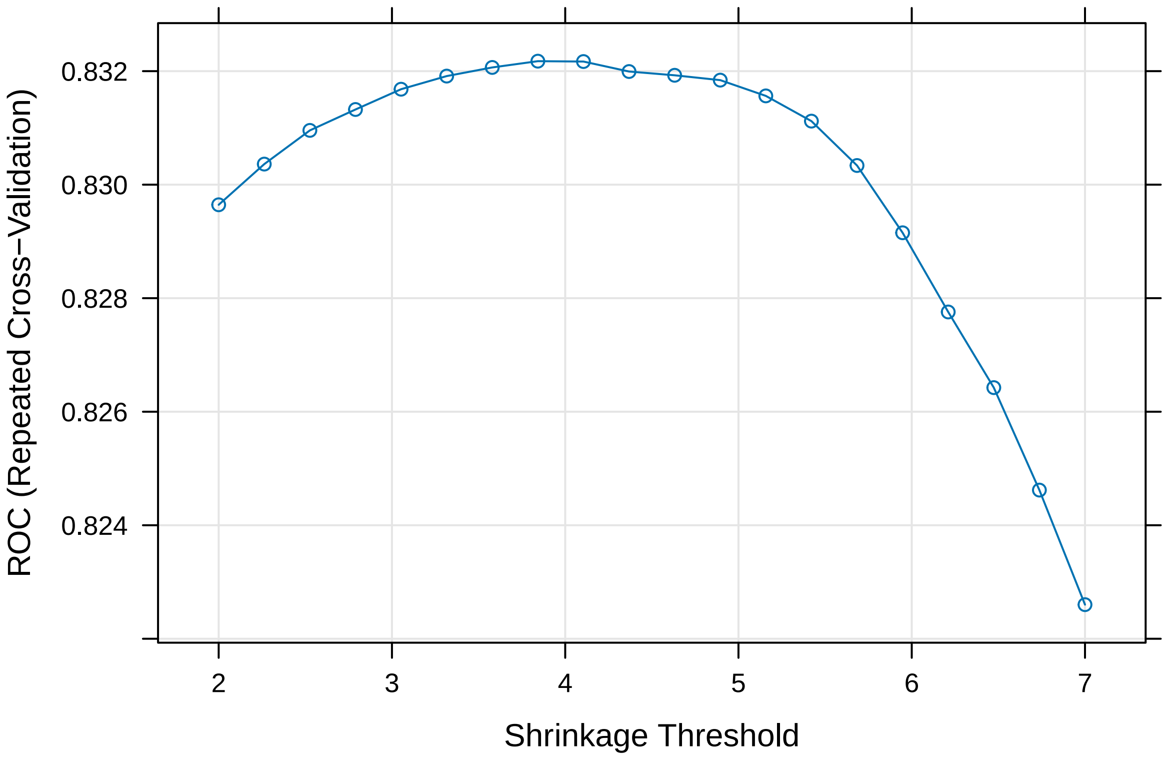
```
## [1] "Best Alpha and Lambda tuning parameters for Penalized Logistic Regression: 0.5,0.001"
```

**Model #3 - Nearest Shrunken Centroids**

```r
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
```

```
plot(nscFit_stroke)
```

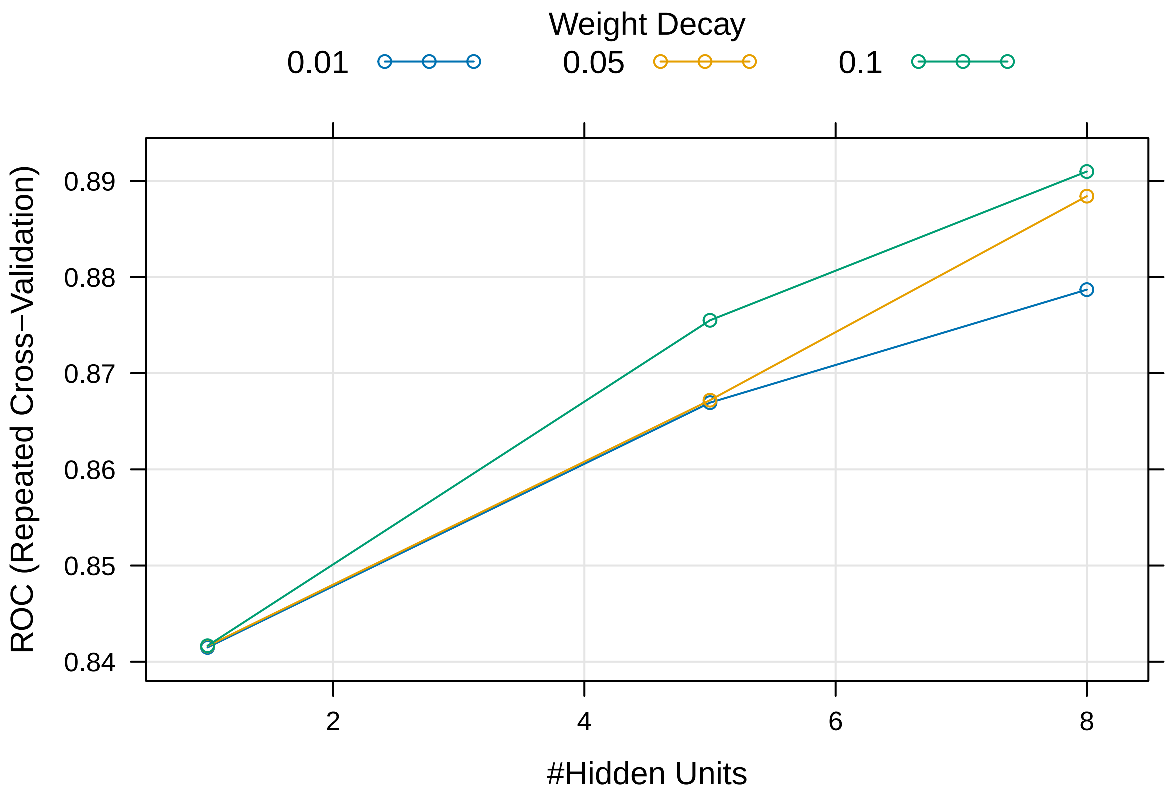


```
# Best tuning parameters
optimal_nsc_tune <- nscFit_stroke$bestTune
print(paste('Best threshold tuning parameter for Nearest Shrunken Centroids:', paste(optimal_nsc_tune,
```

```
## [1] "Best threshold tuning parameter for Nearest Shrunken Centroids: 3.84210526315789"
```

**Model #4 - Neural Network**

```
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)
```



```r
# 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
```

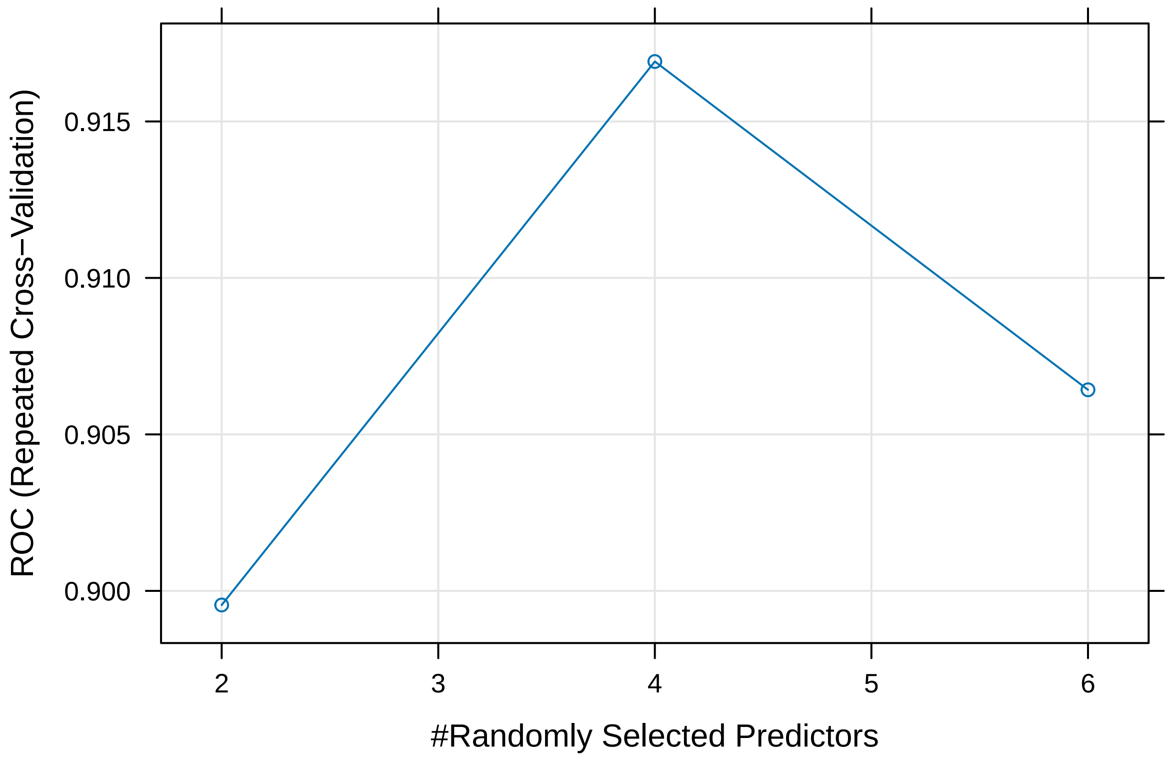
```
## [1] "Best Size and Decay tuning parameters for Neural Network: 8,0.1"
```

**Model #5 - Random Forest**

```r
# 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)
```



```
# 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 | 0.779 | 0.752 | 0.804 |
| Neural Network | 0.763 | 0.736 | 0.789 |
| Penalized Logistic Regression | 0.755 | 0.728 | 0.781 |
| Linear Discriminant Analysis | 0.747 | 0.719 | 0.773 |
| Nearest Shrunken Centroids | 0.710 | 0.681 | 0.738 |

**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)
```

```r
# 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
```

```r
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

```r
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 | 0.763 | 0.736 | 0.789 |
| Penalized Logistic Regression | 0.755 | 0.728 | 0.781 |
| Linear Discriminant Analysis | 0.747 | 0.719 | 0.773 |
| Nearest Shrunken Centroids | 0.710 | 0.681 | 0.738 |