R Notebook

This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

```
if (!require(caret)) install.packages("caret", dependencies=TRUE)
```

```
## Loading required package: caret
```

```
## Loading required package: ggplot2
```

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

```
if (!require(corrplot)) install.packages("corrplot", dependencies=TRUE)
```

```
## Loading required package: corrplot
```

```
## corrplot 0.95 loaded
```

```
library(ggplot2)
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
```

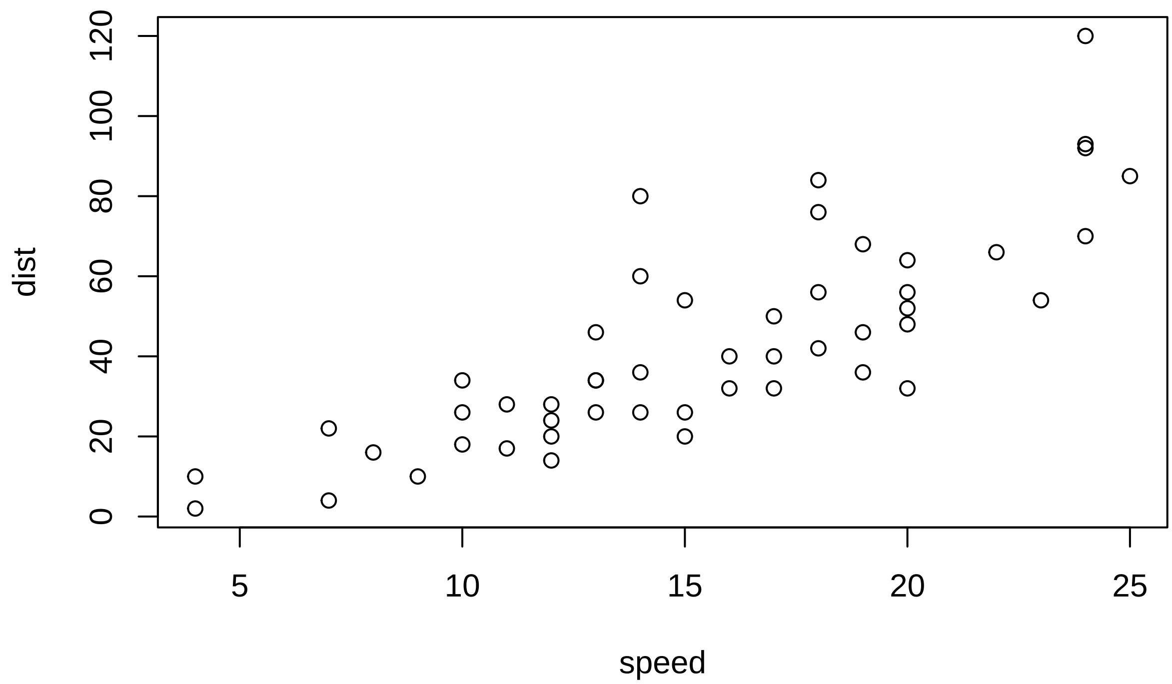
```
library(caret)
library(randomForest)
```

```
## randomForest 4.7-1.2
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'

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

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

```r
library(corrplot)
library(reshape2)



plot(cars)
```



1: Data Processing # 2: Exploratory Data Analysis(EDA) # 3: Train-test split # 4: Modeling # 5: Evaluation

Load the dataset

```
stroke_data <- read.csv("healthcare-dataset-stroke-data.csv")
```

Remove 'id' column as it is not useful for prediction

```
stroke_data <- stroke_data[, !names(stroke_data) %in% "id"]
```

Check for missing values

```
sum(is.na(stroke_data))
```

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

Replace non-numeric values in 'bmi' with NA and impute missing values with mean

```
stroke_data$bmi <- as.numeric(gsub("[^0-9.]", "", stroke_data$bmi))
stroke_data$bmi[is.na(stroke_data$bmi)] <- mean(stroke_data$bmi, na.rm = TRUE)
```

#Imputing missing values in 'bmi' with mean

```
stroke_data$bmi[is.na(stroke_data$bmi)] <- mean(stroke_data$bmi, na.rm = TRUE)
```

Convert categorical variables to factors

```
cat_cols <- c("gender", "hypertension", "heart_disease", "ever_married",
              "work_type", "Residence_type", "smoking_status", "stroke")
stroke_data[cat_cols] <- lapply(stroke_data[cat_cols], as.factor)
```

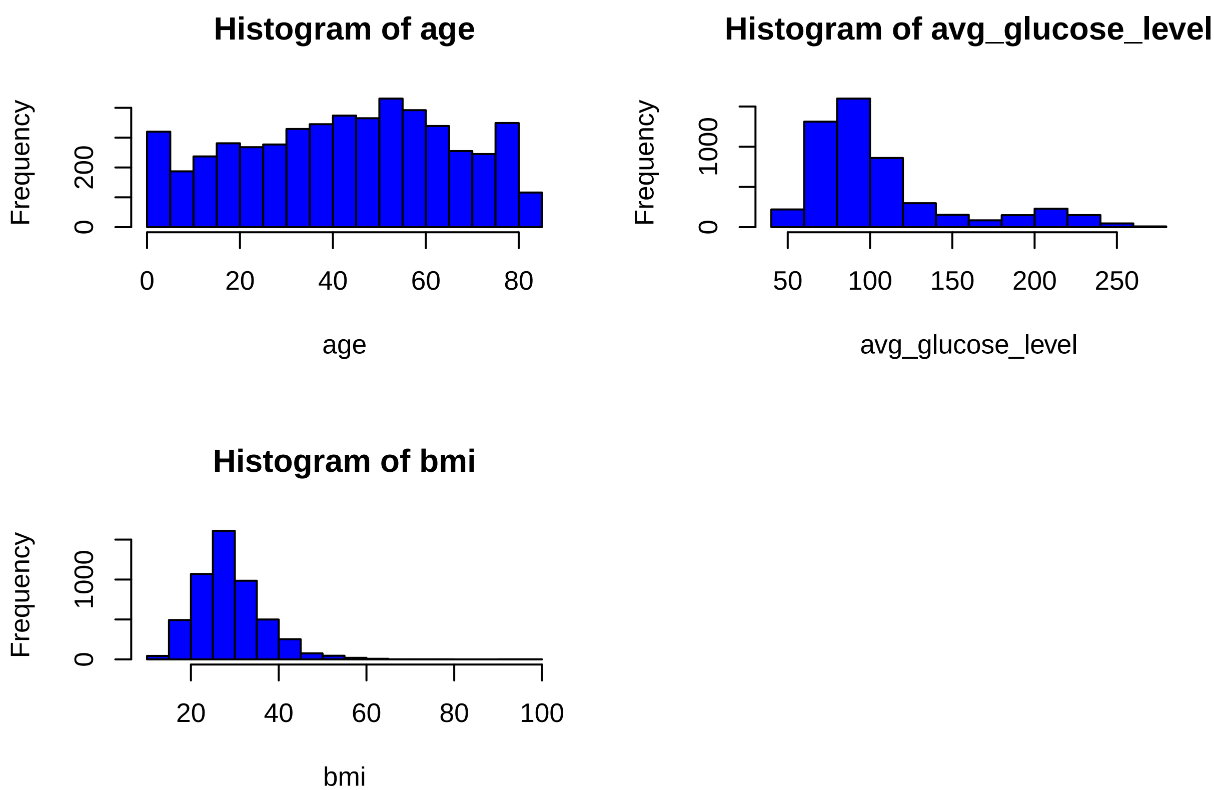
Distribution of Numerical Features

```
numeric_features <- stroke_data[, sapply(stroke_data, is.numeric)]
par(mfrow = c(2,2))
lapply(names(numeric_features), function(col) hist(numeric_features[[col]],
     main = paste("Histogram of", col), xlab = col, col = "blue"))
```

```
## [[1]]
## $breaks
##  [1]  0  5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
##
## $counts
##  [1] 320 187 237 281 268 277 329 345 374 365 431 392 339 255 245 349 116
##
## $density
##  [1] 0.012524462 0.007318982 0.009275930 0.010998043 0.010489237 0.010841487
##  [7] 0.012876712 0.013502935 0.014637965 0.014285714 0.016868885 0.015342466
## [13] 0.013268102 0.009980431 0.009589041 0.013659491 0.004540117
##
## $mids
##  [1]  2.5  7.5 12.5 17.5 22.5 27.5 32.5 37.5 42.5 47.5 52.5 57.5 62.5 67.5 72.5
## [16] 77.5 82.5
##
## $xname
## [1] "numeric_features[[col]]"
##
## $equidist
## [1] TRUE
##
## attr(,"class")
## [1] "histogram"
##
## [[2]]
## $breaks
##  [1]  40  60  80 100 120 140 160 180 200 220 240 260 280
##
## $counts
##  [1]  220 1312 1599  860  298  153   85  149  229  150   46    9
##
## $density
##  [1] 2.152642e-03 1.283757e-02 1.564579e-02 8.414873e-03 2.915851e-03
##  [6] 1.497065e-03 8.317025e-04 1.457926e-03 2.240705e-03 1.467710e-03
## [11] 4.500978e-04 8.806262e-05
##
## $mids
##  [1]  50  70  90 110 130 150 170 190 210 230 250 270
##
## $xname
## [1] "numeric_features[[col]]"
##
## $equidist
## [1] TRUE
##
## attr(,"class")
## [1] "histogram"
##
## [[3]]
## $breaks
##  [1]  10  15  20  25  30  35  40  45  50  55  60  65  70  75  80  85  90  95 100
##
## $counts
```

```
##  [1]   44  493 1070 1610  985  500  253   76   46   20    8    1    1    1    0
## [16]    0    1    1
##
## $density
##  [1] 1.722114e-03 1.929550e-02 4.187867e-02 6.301370e-02 3.855186e-02
##  [6] 1.956947e-02 9.902153e-03 2.974560e-03 1.800391e-03 7.827789e-04
## [11] 3.131115e-04 3.913894e-05 3.913894e-05 3.913894e-05 0.000000e+00
## [16] 0.000000e+00 3.913894e-05 3.913894e-05
##
## $mids
##  [1] 12.5 17.5 22.5 27.5 32.5 37.5 42.5 47.5 52.5 57.5 62.5 67.5 72.5 77.5 82.5
## [16] 87.5 92.5 97.5
##
## $xname
## [1] "numeric_features[[col]]"
##
## $equidist
## [1] TRUE
##
## attr(,"class")
## [1] "histogram"
```

```r
par(mfrow = c(1,1))
```

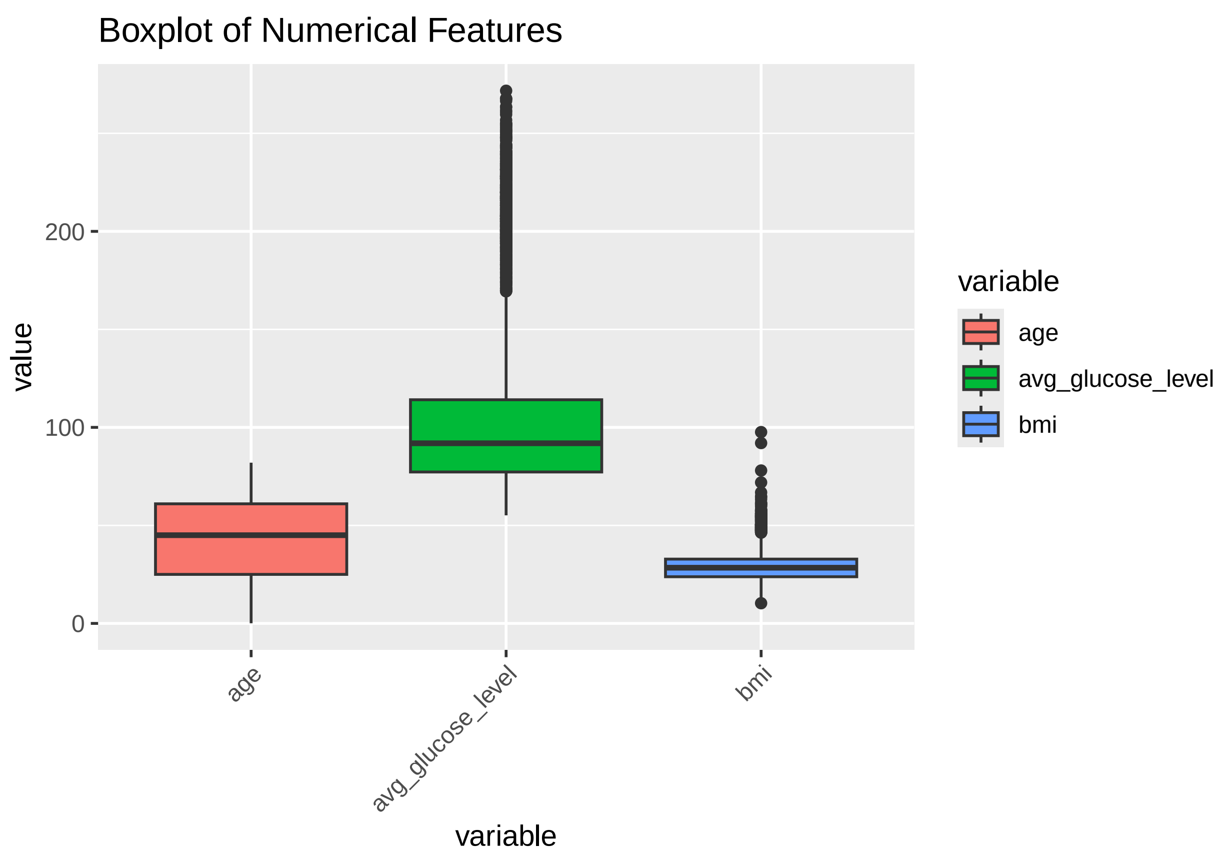


Convert numeric features to long format explicitly

```
numeric_features_long <- melt(numeric_features, id.vars = NULL, measure.vars = names(numeric_features))
```

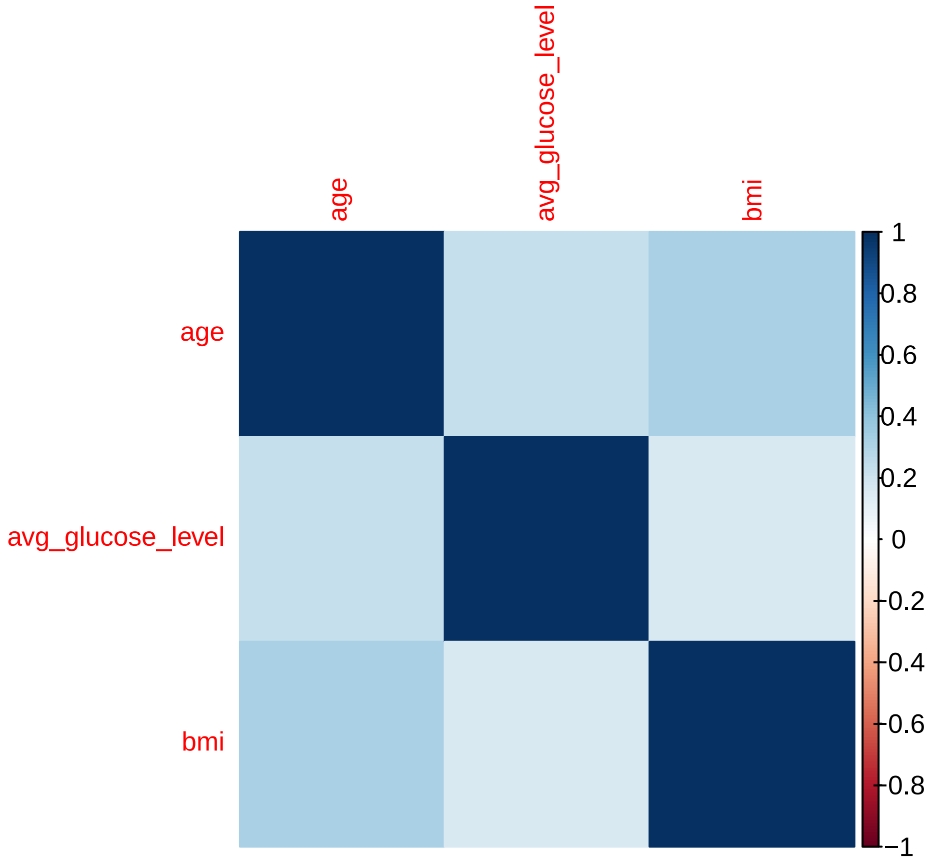
Boxplot for Outlier Detection

```
ggplot(numeric_features_long, aes(x = variable, y = value)) +
  geom_boxplot(aes(fill = variable)) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  ggtitle("Boxplot of Numerical Features")
```



Correlation matrix

```
cor_matrix <- cor(numeric_features, use = "complete.obs")
corrplot(cor_matrix, method = "color", tl.cex = 0.8)
```



Outlier Detection and Removal (Using IQR)

```
outlier_removal <- function(x) {
  Q1 <- quantile(x, 0.25, na.rm = TRUE)
  Q3 <- quantile(x, 0.75, na.rm = TRUE)
  IQR <- Q3 - Q1
  x[x < (Q1 - 1.5 * IQR) | x > (Q3 + 1.5 * IQR)] <- NA
  return(x)
}

stroke_data[names(numeric_features)] <- lapply(stroke_data[names(numeric_features)], outlier_removal)
stroke_data <- na.omit(stroke_data)
```

Standardization (Scaling Numeric Features)

```
stroke_data[names(numeric_features)] <- scale(stroke_data[names(numeric_features)])
```

Splitting data into training and testing sets

```r
set.seed(123)
train_index <- createDataPartition(stroke_data$stroke, p = 0.8, list = FALSE)
train_data <- stroke_data[train_index, ]
test_data <- stroke_data[-train_index, ]
```

Logistic Regression Model

```r
stroke_model <- glm(stroke ~ ., data = train_data, family = binomial)
pred_probs <- predict(stroke_model, test_data, type = "response")
pred_labels <- ifelse(pred_probs > 0.5, 1, 0)
conf_matrix <- confusionMatrix(factor(pred_labels, levels = levels(test_data$stroke)), test_data$stroke
print(conf_matrix)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 845  33
##          1   0   0
##
##                Accuracy : 0.9624
##                  95% CI : (0.9476, 0.974)
##     No Information Rate : 0.9624
##     P-Value [Acc > NIR] : 0.5461
##
##                   Kappa : 0
##
##  Mcnemar's Test P-Value : 2.54e-08
##
##             Sensitivity : 1.0000
##             Specificity : 0.0000
##          Pos Pred Value : 0.9624
##          Neg Pred Value :    NaN
##              Prevalence : 0.9624
##          Detection Rate : 0.9624
##    Detection Prevalence : 1.0000
##       Balanced Accuracy : 0.5000
##
##        'Positive' Class : 0
##
```

Decision Tree Model

```r
tree_model <- train(stroke ~ ., data = train_data, method = "rpart")
tree_pred <- predict(tree_model, test_data)
```

```r
tree_conf_matrix <- confusionMatrix(tree_pred, test_data$stroke)
print(tree_conf_matrix)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 845  33
##          1   0   0
##
##                Accuracy : 0.9624
##                  95% CI : (0.9476, 0.974)
##     No Information Rate : 0.9624
##     P-Value [Acc > NIR] : 0.5461
##
##                   Kappa : 0
##
##  Mcnemar's Test P-Value : 2.54e-08
##
##             Sensitivity : 1.0000
##             Specificity : 0.0000
##          Pos Pred Value : 0.9624
##          Neg Pred Value :    NaN
##              Prevalence : 0.9624
##          Detection Rate : 0.9624
##    Detection Prevalence : 1.0000
##       Balanced Accuracy : 0.5000
##
##        'Positive' Class : 0
##
```

Random Forest Model

```r
rf_model <- randomForest(stroke ~ ., data = train_data, ntree = 100)
rf_pred <- predict(rf_model, test_data)
rf_conf_matrix <- confusionMatrix(rf_pred, test_data$stroke)
print(rf_conf_matrix)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 845  32
##          1   0   1
##
##                Accuracy : 0.9636
##                  95% CI : (0.9489, 0.9749)
##     No Information Rate : 0.9624
##     P-Value [Acc > NIR] : 0.4755
##
```

```
##                   Kappa : 0.0567
##
##  Mcnemar's Test P-Value : 4.251e-08
##
##             Sensitivity : 1.0000
##             Specificity : 0.0303
##          Pos Pred Value : 0.9635
##          Neg Pred Value : 1.0000
##              Prevalence : 0.9624
##          Detection Rate : 0.9624
##    Detection Prevalence : 0.9989
##       Balanced Accuracy : 0.5152
##
##        'Positive' Class : 0
##
```