Stroke Factors: Classification & Predictive Analytics

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Dataset: removed NAs, removed outliers

Converted cat variables into num

No PCA analysis

Read dataset

```
stroke <- read.csv(file="stroke_1_raw.csv",header=T, sep=",")
```

Exploratory Analytics and Data Cleaning

```
# Descriptive analysis
str(stroke)
```

```
## 'data.frame':    5110 obs. of  12 variables:
##  $ id               : int  9046 51676 31112 60182 1665 56669 53882 10434 27419 60491 ...
##  $ gender           : chr  "Male" "Female" "Male" "Female" ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : int  0 0 0 0 1 0 1 0 0 0 ...
##  $ heart_disease    : int  1 0 1 0 0 0 1 0 0 0 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Self-employed" "Private" "Private" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Rural" "Urban" ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : chr  "36.6" "N/A" "32.5" "34.4" ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "never smoked" "smokes" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

```
summary(stroke)
```

```
##        id           gender               age          hypertension
##  Min.   :   67   Length:5110        Min.   : 0.08   Min.   :0.00000
##  1st Qu.:17741   Class :character   1st Qu.:25.00   1st Qu.:0.00000
##  Median :36932   Mode  :character   Median :45.00   Median :0.00000
##  Mean   :36518                      Mean   :43.23   Mean   :0.09746
##  3rd Qu.:54682                      3rd Qu.:61.00   3rd Qu.:0.00000
##  Max.   :72940                      Max.   :82.00   Max.   :1.00000
##  heart_disease     ever_married        work_type          Residence_type
##  Min.   :0.00000   Length:5110        Length:5110        Length:5110
##  1st Qu.:0.00000   Class :character   Class :character   Class :character
##  Median :0.00000   Mode  :character   Mode  :character   Mode  :character
##  Mean   :0.05401
##  3rd Qu.:0.00000
##  Max.   :1.00000
##  avg_glucose_level     bmi            smoking_status         stroke
##  Min.   : 55.12    Length:5110        Length:5110        Min.   :0.00000
##  1st Qu.: 77.25    Class :character   Class :character   1st Qu.:0.00000
##  Median : 91.89    Mode  :character   Mode  :character   Median :0.00000
##  Mean   :106.15                                          Mean   :0.04873
##  3rd Qu.:114.09                                          3rd Qu.:0.00000
##  Max.   :271.74                                          Max.   :1.00000
```

```
# Convert 'N/A's (strings) in dataset to NA
is.na(stroke) <- stroke == "N/A"
# Count number of NAs in dataset
sum(is.na(stroke))
```

```
## [1] 201
```

```
# Count number of NAs in all columns
colSums(is.na(stroke))
```

```
##                id            gender               age      hypertension
##                 0                 0                 0                 0
##     heart_disease      ever_married         work_type    Residence_type
##                 0                 0                 0                 0
## avg_glucose_level               bmi    smoking_status            stroke
##                 0               201                 0                 0
```

```
# Count number of 'Unknown's in all columns
colSums(stroke == "Unknown")
```

```
##                id            gender               age      hypertension
##                 0                 0                 0                 0
##     heart_disease      ever_married         work_type    Residence_type
##                 0                 0                 0                 0
## avg_glucose_level               bmi    smoking_status            stroke
##                 0                NA              1544                 0
```

```
# Remove first column 'id'; irrelevant to data analysis
stroke <- stroke[2:12]

# Check attribute levels and convert data types to numeric
# For binary "Yes"/"No" values, "Yes" = 1 and "No" = 2
str(stroke)
```

```
## ’data.frame’:    5110 obs. of  11 variables:
```

```
##  $ gender           : chr  "Male" "Female" "Male" "Female" ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : int  0 0 0 0 1 0 1 0 0 0 ...
##  $ heart_disease    : int  1 0 1 0 0 0 1 0 0 0 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Self-employed" "Private" "Private" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Rural" "Urban" ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : chr  "36.6" NA "32.5" "34.4" ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "never smoked" "smokes" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

```r
unique(stroke$gender)
```

```
## [1] "Male"   "Female" "Other"
```

```r
stroke$gender <- gsub("Male", 1, stroke$gender)
stroke$gender <- gsub("Female", 2, stroke$gender)
stroke$gender <- gsub("Other", 3, stroke$gender)
stroke$gender <- as.numeric(stroke$gender)
unique(stroke$gender)
```

```
## [1] 1 2 3
```

```r
unique(stroke$ever_married)
```

```
## [1] "Yes" "No"
```

```r
stroke$ever_married <- gsub("Yes", 1, stroke$ever_married)
stroke$ever_married <- gsub("No", 0, stroke$ever_married)
stroke$ever_married <- as.numeric(stroke$ever_married)
unique(stroke$ever_married)
```

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

```r
unique(stroke$work_type)
```

```
## [1] "Private"       "Self-employed" "Govt_job"      "children"
## [5] "Never_worked"
```

```r
stroke$work_type <- gsub("Private", 1, stroke$work_type)
stroke$work_type <- gsub("Self-employed", 2, stroke$work_type)
stroke$work_type <- gsub("Govt_job", 3, stroke$work_type)
stroke$work_type <- gsub("children", 4, stroke$work_type)
stroke$work_type <- gsub("Never_worked", 5, stroke$work_type)
stroke$work_type <- as.numeric(stroke$work_type)
unique(stroke$work_type)
```

```
## [1] 1 2 3 4 5
```

```r
unique(stroke$Residence_type)
```

```
## [1] "Urban" "Rural"
```

```r
stroke$Residence_type <- gsub("Urban", 1, stroke$Residence_type)
stroke$Residence_type <- gsub("Rural", 2, stroke$Residence_type)
stroke$Residence_type <- as.numeric(stroke$Residence_type)
unique(stroke$Residence_type)
```

```
## [1] 1 2
```

```r
stroke$bmi <- as.numeric(stroke$bmi)

unique(stroke$smoking_status)
```

```
## [1] "formerly smoked" "never smoked"    "smokes"          "Unknown"
```

```r
stroke$smoking_status <- gsub("formerly smoked", 1, stroke$smoking_status)
stroke$smoking_status <- gsub("never smoked", 2, stroke$smoking_status)
stroke$smoking_status <- gsub("smokes", 3, stroke$smoking_status)
stroke$smoking_status <- gsub("Unknown", 4, stroke$smoking_status)
stroke$smoking_status <- as.numeric(stroke$smoking_status)
unique(stroke$smoking_status)
```

```
## [1] 1 2 3 4
```

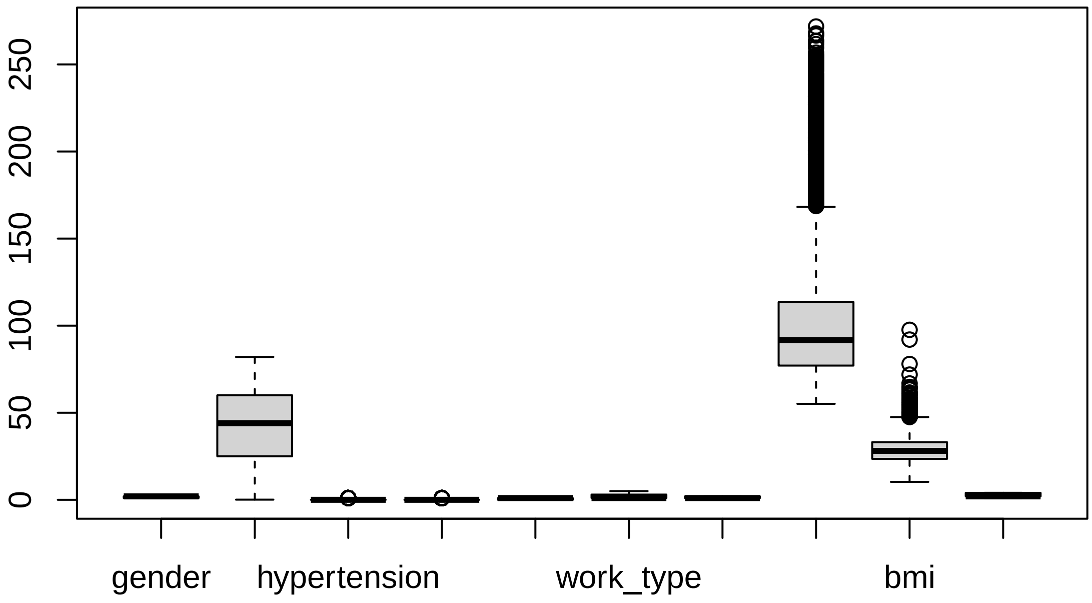
```r
# Assign "No Stroke" and "Stroke" labels for Stroke attribute
stroke$stroke <- ifelse(stroke$stroke == 0, "No Stroke", "Stroke")
# Assign Stroke values as factor levels
stroke$stroke <- as.factor(stroke$stroke)

# Check that all attributes are now numeric data types
str(stroke)
```

```
## ’data.frame’:    5110 obs. of  11 variables:
##  $ gender           : num  1 2 1 2 2 1 1 2 2 2 ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : int  0 0 0 0 1 0 1 0 0 0 ...
##  $ heart_disease    : int  1 0 1 0 0 0 1 0 0 0 ...
##  $ ever_married     : num  1 1 1 1 1 1 1 0 1 1 ...
##  $ work_type        : num  1 2 1 1 2 1 1 1 1 1 ...
##  $ Residence_type   : num  1 2 2 1 2 1 2 1 2 1 ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : num  36.6 NA 32.5 34.4 24 29 27.4 22.8 NA 24.2 ...
##  $ smoking_status   : num  1 2 2 3 2 1 2 2 4 4 ...
##  $ stroke           : Factor w/ 2 levels "No Stroke","Stroke": 2 2 2 2 2 2 2 2 2 2 ...
```

```
# Deal with NAs
# Method 1: remove NAs
stroke_noNAs <- stroke[complete.cases(stroke), ]
# Method 2: replace NAs with values using k-NN algorithm?

# Deal with outliers
# Box plot to visualize outliers
boxplot(as.matrix(stroke_noNAs[1:10]))
```



```
# Excluding categorical variables, avg_glucose_level
# And bmi have several outliers
# Remove outliers using interquartile range values
agl_outliers <- boxplot(stroke$avg_glucose_level, plot = FALSE)$out
bmi_outliers <- boxplot(stroke$bmi, plot = FALSE)$out
stroke_noNAs_noOL <- stroke_noNAs
stroke_noNAs_noOL <- stroke_noNAs_noOL[-which(stroke_noNAs_noOL$avg_glucose_level %in% agl_outliers),]
stroke_noNAs_noOL <- stroke_noNAs_noOL[-which(stroke_noNAs_noOL$bmi %in% bmi_outliers),]

# Examine correlations between all Independent Variables
cor(stroke_noNAs_noOL[1:10])
```

```
##                           gender          age  hypertension heart_disease
## gender              1.0000000000  0.047163661 -0.0181116010  -0.087077746
## age                 0.0471636606  1.000000000  0.2492046322   0.236193434
## hypertension       -0.0181116010  0.249204632  1.0000000000   0.106065206
## heart_disease     -0.0870777462  0.236193434  0.1060652062   1.000000000
## ever_married       0.0508315382  0.687498881  0.1488340141   0.105364898
## work_type         -0.0758616230 -0.439614390 -0.0721676438  -0.041084225
## Residence_type    -0.0003523739 -0.009598891  0.0038834139   0.014064422
## avg_glucose_level -0.0305248091 -0.023924488 -0.0009078475   0.004947325
## bmi                0.0054726191  0.378683833  0.1515384482   0.054618944
## smoking_status    -0.0590370218 -0.385509590 -0.1155068859  -0.057584935
##                    ever_married   work_type Residence_type avg_glucose_level
## gender             0.0508315382 -0.07586162  -0.0003523739     -0.0305248091
## age                0.6874988811 -0.43961439  -0.0095988913     -0.0239244877
## hypertension       0.1488340141 -0.07216764   0.0038834139     -0.0009078475
## heart_disease      0.1053648985 -0.04108422   0.0140644220      0.0049473252
## ever_married       1.0000000000 -0.39116104   0.0004186879     -0.0083602287
## work_type         -0.3911610411  1.00000000  -0.0155902656      0.0109823333
## Residence_type     0.0004186879 -0.01559027   1.0000000000      0.0145557947
## avg_glucose_level -0.0083602287  0.01098233   0.0145557947      1.0000000000
## bmi                0.3756328526 -0.38386175  -0.0110487374      0.0017839920
## smoking_status    -0.3177225122  0.33765019  -0.0042874498      0.0178261247
##                            bmi smoking_status
## gender             0.005472619    -0.05903702
## age                0.378683833    -0.38550959
## hypertension       0.151538448    -0.11550689
## heart_disease      0.054618944    -0.05758493
## ever_married       0.375632853    -0.31772251
## work_type         -0.383861746     0.33765019
## Residence_type    -0.011048737    -0.00428745
## avg_glucose_level  0.001783992     0.01782612
## bmi                1.000000000    -0.26338455
## smoking_status    -0.263384550     1.00000000
```

```
# Normalize continuous numeric variables
# Such as age, avg_blood_glucose, and bmi
# Using z-score methods
stroke_noNAs_noOL$age <- (stroke_noNAs_noOL$age - mean(stroke_noNAs_noOL$age))/sd(stroke_noNAs_noOL$age
stroke_noNAs_noOL$avg_glucose_level <- (stroke_noNAs_noOL$avg_glucose_level - mean(stroke_noNAs_noOL$av
stroke_noNAs_noOL$bmi <- (stroke_noNAs_noOL$bmi - mean(stroke_noNAs_noOL$bmi))/sd(stroke_noNAs_noOL$bmi
```

Classification

Predictive Analytics: Logistic Regression

```
# Split dataset into 70% training, 30% testing sets
stroke_index1 <- sample(1:nrow(stroke_noNAs_noOL), 0.7 * nrow(stroke_noNAs_noOL))

# Assign selected sample as training set
# Assign leftover dataset as test set
train.set1 <- stroke_noNAs_noOL[stroke_index1,]
test.set1 <- stroke_noNAs_noOL[-stroke_index1,]

# Logistic regression model for prediction
glm_model1 <- glm(formula = stroke~., data = train.set1, family = "binomial")
summary(glm_model1)
```

```
##
## Call:
## glm(formula = stroke ~ ., family = "binomial", data = train.set1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9005  -0.2596  -0.1512  -0.0885   3.5382
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -4.057543   0.680977  -5.958 2.55e-09 ***
## gender            -0.108863   0.226937  -0.480  0.63144
## age                1.345140   0.166815   8.064 7.40e-16 ***
## hypertension       0.783931   0.278063   2.819  0.00481 **
## heart_disease      0.269928   0.364550   0.740  0.45903
## ever_married       0.008993   0.338160   0.027  0.97878
## work_type         -0.078070   0.148471  -0.526  0.59901
## Residence_type     0.122204   0.220478   0.554  0.57939
## avg_glucose_level -0.020754   0.109962  -0.189  0.85030
## bmi               -0.162565   0.139428  -1.166  0.24364
## smoking_status    -0.069109   0.107976  -0.640  0.52215
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 821.19  on 2981  degrees of freedom
## Residual deviance: 683.22  on 2971  degrees of freedom
## AIC: 705.22
##
## Number of Fisher Scoring iterations: 8
```

Evaluation Metrics

```r
predicted1 <- predict(glm_model1, test.set1, type = "response")
# Setting 0.5 as threshold - binary prediction
predicted_class1 <- ifelse(predicted1 >= 0.5, "Stroke", "No Stroke")
ConfusionMatrix1 <- table(actual = test.set1$stroke, predicted = predicted_class1)
ConfusionMatrix1
```

```
##            predicted
## actual      No Stroke
##   No Stroke      1235
##   Stroke           44
```

Abysmal predictions using only logistic regression applied to dataset with NAs removed (from BMI column) and outliers removed. No strokes are predicted at all