HarvardX PH125.9x Data Science: Capstone Stroke Prediction System

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Contents

1. INTRODUCTION

In a healthy individual, our veins and arteries carry blood and nutrients throughout our body, including to our brain. A stroke is a medical emergency that occurs when this blood supply to the brain is interrupted or stops moving through the vascular system to the brain. According to the National Institute of Neurological Disorders and Stroke, the United States sees more than 795,000 stroke cases annually, which is the fifth leading cause of death in the country.[1] The CDC stated that in 2018, 1 in every 6 deaths from cardiovascular disease was due to stroke. Furthermore, every 40 seconds, someone in the United States has a stroke, and every 4 minutes, someone dies of stroke.[2]

The two main types of stroke are **ischemic**, where blood clots or fatty deposits called plaque block the blood vessels, and **hemorrhagic**, where blood vessels bust in the brain causing blood to pool up and damage surrounding tissue. Many factors increase the risk of having one of these two types of stroke, including being overweight (or obese), being physically inactive, heavy (or binge) drinking, use of illegal drugs, high blood pressure, smoking, high cholesterol, diabetes, obstructive sleep apnea, cardiovascular disease, family history of stroke or heart attack, and COVID-19 infection.[3]

This project focuses on creating a stroke prediction system using a synthetic dataset[4] uploaded by user Dhiren Dommeti to the well-known public code & data repository website, Kaggle. This is to fulfill the the "IDV Learners" portion of the **HarvardX: PH125.9x Data Science: Capstone** course.

This project report will step through the process of programmatically obtaining and analyzing the stroke data file, creating and analyzing the necessary datasets, building and testing multiple machine learning algorithms, and will conclude with commenting on the final model and its results. Using supervised machine learning methodologies, coded in the R programming language[5], the following algorithms will be used to predict the likelihood of a stroke based on variables in the dataset:

1. Generalized Linear Model (GLM)
2. Naive Bayes
3. Linear Discriminant Analysis (LDA)
4. Classification and Regression Trees (CART)
5. Random Forest
6. k-Nearest Neighbor (KNN)

The resultant highest accuracy score was found with the Classification and Regression Trees (CART) model at 0.997.

[1] https://www.stroke.nih.gov/materials/needtoknow.htm
[2] https://www.cdc.gov/stroke/facts.htm
[3] https://www.mayoclinic.org/diseases-conditions/stroke/symptoms-causes/syc-20350113
[4] https://www.kaggle.com/dhirendommeti/stroke
[5] https://www.r-project.org/

2. PREREQUISITES

This project and its code has minimum requirements in order to duplicate the environment necessary to successfully run in R Studio. It will be assumed that all required R packages and applications are current as of the date of this report (found on the cover page), and that the computer has Internet access.

Current RStudio Version Output:

```
##                _
## platform       x86_64-w64-mingw32
## arch           x86_64
## os             mingw32
## system         x86_64, mingw32
## status
## major          4
## minor          1.0
## year           2021
## month          05
## day            18
## svn rev        80317
## language       R
## version.string R version 4.1.0 (2021-05-18)
## nickname       Camp Pontanezen
```

2.1 Required Packages

In order for the R code to run properly, the below packages are required. In the event that they are not available at runtime, the R code will download, install, and load them first.

Package Loading Code Snippet:

```
# Download and install the necessary packages for this project.
if(!require(tidyverse)) +
  install.packages("tidyverse", repos = "http://cran.us.r-project.org")
if(!require(caret)) +
  install.packages("caret", repos = "http://cran.us.r-project.org")
if(!require(data.table)) +
  install.packages("data.table", repos = "http://cran.us.r-project.org")
if(!require(scales)) +
  install.packages("scales", repos = "http://cran.us.r-project.org")
if(!require(corrplot)) +
  install.packages("corrplot", repos = "http://cran.us.r-project.org")
if(!require(dplyr)) +
  install.packages("dplyr", repos = "http://cran.us.r-project.org")
if(!require(grid)) +
  install.packages("gridExtra", repos = "http://cran.us.r-project.org")
if(!require(grid)) +
  install.packages("gridExtra", repos = "http://cran.us.r-project.org")
```

```r
if(!require(kableExtra)) +
  install.packages("kableExtra", repos = "http://cran.us.r-project.org")
if(!require(stats))
  install.packages("stats", repos = "http://cran.us.r-project.org")

# Load the necessary libraries for this project.
library(tidyverse)
library(caret)
library(data.table)
library(scales)
library(corrplot)
library(dplyr)
library(grid)
library(gridExtra)
library(kableExtra)
library(stats)
```

2.2 Required Data

The stroke dataset used for this project is originally from the Kaggle website. Since Kaggle requires each user to log into their site before being able to download any data files, the 314KB **Stroke-Data.csv** file was previously downloaded and pushed to the GitHub repository this RStudio project was created in.

Dataset Download Code Snippet:

```r
# Download the Stroke-Data.csv file from GitHub, create the data frame "rawdata",
# and fill it with the 12 columns of data that were in the  file, labeling them
# id, gender, age, hypertension, heart_disease, ever_married, work_type,
# Residence_type, bmi, avg_glucose_level, smoking_status, and stroke,
# respectively.
rawdata <- read.csv("https://raw.githubusercontent.com/rwalscheid/HarvardX-Capstone-CYO/main/Strok
                    quote = "",
                    row.names = NULL,
                    stringsAsFactors = FALSE)
```

The .csv file will automatically be downloaded to your computer's temporary directory and read into a data frame, which contains the necessary records for this project.

3. STROKE-DATA.CSV DATA FILE

With the required R packages loaded and the `Stroke-Data.csv` data file downloaded and ingested into a data frame, reviewing this file within an appropriate editor (e.g. Microsoft Excel, OpenOffice Calc, Google Drive, etc.) would be beneficial in understanding its full contents for this project. Only a few of the predictors found in this dataset are directly-related health-based factors that impact a person's risk of stroke, while others are surrounding environmental factors.

1. **id** (class=integer): A unique identification number for each person.
2. **gender** (class=character): The person's gender, as male or female.
3. **age** (class=numeric): The person's age in years.
4. **hypertension** (class=integer): Yes/No (as 1/0) entry for whether the person has hypertension.
5. **heart_disease** (class=integer): Yes/No (as 1/0) entry for whether the person has heart disease.
6. **ever_married** (class=character): Yes/No entry for whether the person has ever been married.
7. **work_type** (class=character): Category of work the person is in (or whether they are a child).
8. **Residence_type** (class=character): Rural/Urban entry for where the person lives.
9. **bmi** (class=character): The person's body mass index (BMI).
10. **avg_glucose_level** (class=numeric): The person's average blood sugar level.
11. **smoking_status** (class=character): Category for whether the person is/was a smoker.
12. **stroke** (class=integer): Yes/No (as 1/0) entry for whether the person has had a stroke.

A basic analysis of this dataset once created is shown below.

rawdata Object Summary:

```
# Summary information of the "rawdata" dataset
summary(rawdata)
```

```
##        id            gender                age          hypertension
##  Min.   :   67   Length:5110        Min.   : 0.08   Min.   :0.00000
##  1st Qu.:11980   Class :character   1st Qu.:25.00   1st Qu.:0.00000
##  Median :32702   Mode  :character   Median :45.00   Median :0.00000
##  Mean   :33831                      Mean   :43.23   Mean   :0.09746
##  3rd Qu.:52644                      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
##      bmi            avg_glucose_level smoking_status         stroke
##  Length:5110        Min.   : 55.12    Length:5110        Min.   :0.00000
##  Class :character   1st Qu.: 77.25    Class :character   1st Qu.:0.00000
##  Mode  :character   Median : 91.89    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
```

rawdata Data Structure:

```
# Structure of the "rawdata" dataset
str(rawdata)
```

```
## 'data.frame':    5110 obs. of  12 variables:
##  $ id                : int  9046 9047 9048 9049 9050 9051 9052 9053 9054 9055 ...
##  $ 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" ...
##  $ bmi               : chr  "36.6" "N/A" "32.5" "34.4" ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ smoking_status    : chr  "formerly smoked" "never smoked" "never smoked" "smokes" ...
##  $ stroke            : int  1 1 1 1 1 1 1 1 1 1 ...
```

4. DATA PREPARATION & ANALYSIS

4.1 `rawdata` Dataset

With the `rawdata` dataset now created, the previous basic analysis showed the data frame consists of 5,110 rows and 12 columns (`id`, `gender`, `age`, `hypertension`, `heart_disease`, `ever_married`, `work_type`, `Residence_type`, `bmi`, `avg_glucose_level`, `smoking_status`, and `stroke`).

Each variable with multiple categories will need to be reviewed, as they will be changed to factors with levels (the variable's categories) for easier plotting and analysis throughout this project report. This will also help determine upfront as to whether there are outliers that may be discarded to minimize confounding.

```
# View the multiple categories for each applicable variable to determine factor levels
# to convert to.
unique(rawdata$gender)
```

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

```
unique(rawdata$ever_married)
```

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

```
unique(rawdata$work_type)
```

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

```
unique(rawdata$Residence_type)
```

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

```
unique(rawdata$smoking_status)
```

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

Variable Conversion to Factors with Levels

Out of the 5,110 rows in the dataset, there is a single non-female/male entry in the gender category labeled `Other`.

```
# View the gender count for the category "Other".
rawdata %>% filter(gender %in% "Other") %>% group_by(gender) %>% summarize(n=n())
```

```
## # A tibble: 1 x 2
##   gender     n
##   <chr>  <int>
## 1 Other      1
```

The count of `Other` entries above shows only one person listed. This single entry will be removed when the cleansed dataset is created in the next section for simplicity since 1 entry out of 5,110 in this particular dataset is not considered statistically significant. This will leave only two levels for the `gender` factor when converted: `Male` and `Female`.

To make plotting charts and performing summary analysis throughout this report easier to read and identify, the variables below will be converted to factors, then relabeled and re-ordered (if necessary) as follows:

Variables	Factor Levels
gender	Male
	Female
hypertension	wo_hypertension = 0
	w_hypertension = 1
heart_disease	wo_heart_disease = 0
	w_heart_disease = 1
ever_married	Yes
	No
work_type	Underage_child = children
	Never_worked
	Self-employed
	Private_company = Private
	Govt_job
Residence_type	Rural
	Urban
smoking_status	never smoked
	formerly smoked
	smokes
	Unknown
stroke	no_stroke = 0
	stroke = 1

When examining the structure of the `rawdata` data frame in Section 3, it was noted that the `bmi` vector is of class `character`. Since the body mass index (`bmi`) is numeric, this variable will need to be converted.

4.2 `stroke_data` Dataset

With the variable categories laid out and the factor level order, labels, and levels determined, a new clean dataset named `stroke_data` will be created with all of the changes listed in Section 4.1 above. This new data frame will contain 5,109 rows with 12 columns.

```
# Remove the single "Other" gender row to not skew results, convert the BMI to numeric,
# and convert "gender", "hypertension", "heart_disease", "ever_married", "work_type",
# "Residence_type", "smoking_status", and "stroke" all to factors with their respective
# levels.
stroke_data <- rawdata %>% filter(gender!="Other") %>%
  mutate(gender = factor(gender, levels = c("Male", "Female")),
         hypertension = factor(hypertension,
```

```
                            labels = c("wo_hypertension", "w_hypertension"),
                            levels = c("0","1")),
        heart_disease = factor(heart_disease,
                             labels = c("wo_heart_disease", "w_heart_disease"),
                             levels = c("0","1")),
        ever_married = factor(ever_married,
                            labels = c("never_married", "is_or_was_married"),
                            levels = c("No","Yes")),
        work_type = factor(work_type,
                           labels = c("Underage_child",
                                      "Never_worked",
                                      "Self-employed",
                                      "Private_company",
                                      "Govt_job"),
                           levels = c("children",
                                      "Never_worked",
                                      "Self-employed",
                                      "Private",
                                      "Govt_job")),
        Residence_type = factor(Residence_type,
                                levels = c("Rural", "Urban")),
        bmi = as.numeric(bmi),
        smoking_status = factor(smoking_status,
                                levels = c("never smoked",
                                           "formerly smoked",
                                           "smokes",
                                           "Unknown")),
        stroke = factor(stroke,
                        labels = c("no_stroke", "stroke"),
                        levels = c("0","1")))
```

A basic analysis of this dataset once created is shown below.

stroke_data Object Summary:

```
# Summary information of the "stroke_data" dataset
summary(stroke_data)
```

```
##        id            gender          age                 hypertension
##  Min.   :   67   Male  :2115   Min.   : 0.08   wo_hypertension:4611
##  1st Qu.:11973   Female:2994   1st Qu.:25.00   w_hypertension : 498
##  Median :32687                 Median :45.00
##  Mean   :33826                 Mean   :43.23
##  3rd Qu.:52619                 3rd Qu.:61.00
##  Max.   :72940                 Max.   :82.00
##
##           heart_disease             ever_married            work_type
##  wo_heart_disease:4833   never_married    :1756   Underage_child : 687
```

```
##  w_heart_disease : 276   is_or_was_married:3353   Never_worked   :  22
##                                                  Self-employed  : 819
##                                                  Private_company:2924
##                                                  Govt_job       : 657
##
##
##  Residence_type      bmi        avg_glucose_level         smoking_status
##  Rural:2513     Min.   :10.30   Min.   : 55.12    never smoked   :1892
##  Urban:2596     1st Qu.:23.50   1st Qu.: 77.24    formerly smoked: 884
##                 Median :28.10   Median : 91.88    smokes         : 789
##                 Mean   :28.89   Mean   :106.14    Unknown        :1544
##                 3rd Qu.:33.10   3rd Qu.:114.09
##                 Max.   :97.60   Max.   :271.74
##                 NA's   :201
##        stroke
##  no_stroke:4860
##  stroke   : 249
##
##
##
##
##
```

stroke_data Data Structure:

```
# Structure of the "stroke_data" dataset
str(stroke_data)
```

```
## 'data.frame':    5109 obs. of  12 variables:
##  $ id                : int  9046 9047 9048 9049 9050 9051 9052 9053 9054 9055 ...
##  $ gender            : Factor w/ 2 levels "Male","Female": 1 2 1 2 2 1 1 2 2 2 ...
##  $ age               : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension      : Factor w/ 2 levels "wo_hypertension",..: 1 1 1 1 2 1 2 1 1 1 ...
##  $ heart_disease     : Factor w/ 2 levels "wo_heart_disease",..: 2 1 2 1 1 1 2 1 1 1 ...
##  $ ever_married      : Factor w/ 2 levels "never_married",..: 2 2 2 2 2 2 2 1 2 2 ...
##  $ work_type         : Factor w/ 5 levels "Underage_child",..: 4 3 4 4 3 4 4 4 4 4 ...
##  $ Residence_type    : Factor w/ 2 levels "Rural","Urban": 2 1 1 2 1 2 1 2 1 2 ...
##  $ bmi               : num  36.6 NA 32.5 34.4 24 29 27.4 22.8 NA 24.2 ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ smoking_status    : Factor w/ 4 levels "never smoked",..: 2 1 1 3 1 2 1 1 4 4 ...
##  $ stroke            : Factor w/ 2 levels "no_stroke","stroke": 2 2 2 2 2 2 2 2 2 2 ...
```

In the `rawdata` structure output in Section 3, it can be seen that the system generating the `Stroke-Data.csv` data replaced any null (empty) `bmi` fields with the characters "`N/A`". When the `stroke_data` dataset converted those "`N/A`" character entries to numeric format, `NA`'s were introduced in their place by coercion.

bmi "NA" Quantity & Percentage Calculations:

```
# Calculate the number of bmi N/A entries as a percentage of the total.
bmi_na_num <- sum(is.na(stroke_data$bmi))
bmi_na_num
```

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

```
bmi_na_pct_tot <- (bmi_na_num/NROW(stroke_data$bmi))*100
bmi_na_pct_tot
```

```
## [1] 3.934234
```

With the resulting quantity of `bmi` `NA`'s being 201 (accounting for almost 4% of the entire dataset), the number of entries justifies looking into the statistical impact against the overall outcome. With the outcome being stratified into `no_stroke` or `stroke` results, determining the stroke-negative and stroke-positive percentages these `NA`'s have will show whether they can be excluded from further calculations.

bmi "NA" Stroke/No-Stroke Percentage Calculations:

```
# Calculate statistical significance the stroke-positive vs. stroke-negative NA's
# would have on the predictability.
bmi_na_pct_stroke <-
  (length(which(is.na(stroke_data$bmi) & stroke_data$stroke == "stroke"))/
     NROW(stroke_data$bmi))*100
bmi_na_pct_stroke #Stroke-Positive Percentage
```

```
## [1] 0.7829321
```

```
bmi_na_pct_nostroke <-
  (length(which(is.na(stroke_data$bmi) & stroke_data$stroke == "no_stroke"))/
     NROW(stroke_data$bmi))*100
bmi_na_pct_nostroke #Stroke-Negative Percentage
```

```
## [1] 3.151302
```

As shown above, the `NA` entries in the `bmi` variable have a 0.7829% and 3.1513% impact to the predictability of a `stroke` vs. `no_stroke` result, respectively. If this difference had been closer to a 50%/50% split, we could possibly omit the `NA` `bmi` entries since their presence would not impact the overall correlation of `bmi` value to a `stroke`/`no_stroke` outcome. The `NA`'s instead will be replaced with the mean `bmi` values for `stroke`/`no_stroke` results, accordingly.

bmi "NA" Replacement:

```
# Calculate the mean bmi in the dataset for all non-"NA" bmi entries that were also
# stroke-negative.
ns_bmi_mu <- as.numeric(stroke_data %>% filter(!is.na(bmi) & stroke=="no_stroke") %>%
  summarize(bmi_mu=mean(bmi)))

# Calculate the mean bmi in the dataset for all non-"NA" bmi entries that were also
# stroke-positive.
s_bmi_mu <- as.numeric(stroke_data %>% filter(!is.na(bmi) & stroke=="stroke") %>%
  summarize(bmi_mu=mean(bmi)))

# Replace all bmi "NA" entries with the stroke-positive or stroke-negative mean bmi
# values, accordingly.
stroke_data <- stroke_data %>%
  mutate(bmi = case_when(is.na(bmi) & stroke == "stroke" ~ s_bmi_mu,
                         is.na(bmi) & stroke == "no_stroke" ~ ns_bmi_mu,
                         TRUE ~ bmi))
```

4.2.1 `stroke_data_num` Dataset

While the factor variables in the `stroke_data` dataset allow for easier graphical analysis, correlation coefficient functions like `cor()`, `cor.test()`, and `corrplot()` will be used in later sections for analyzing variable importance. This requires that the factors be converted into numeric format. The `stroke_data` dataset will be copied into a new dataset called `stroke_data_num` with the exception of the `id` column, since that variable is not necessary for this purpose, and all necessary variables will be converted accordingly.

```
# Create the fully-numeric "stroke_data_num" dataset, copying the original
# "stroke_data" dataset and convert all factor variables.
stroke_data_num <- stroke_data %>% mutate(gender=as.numeric(gender),
                                          hypertension=as.numeric(hypertension),
                                          heart_disease=as.numeric(heart_disease),
                                          ever_married=as.numeric(ever_married),
                                          work_type=as.numeric(work_type),
                                          Residence_type=as.numeric(Residence_type),
                                          smoking_status=as.numeric(smoking_status),
                                          stroke=as.numeric(stroke)) %>%
  select(-id) #Leave out the "id" column as it is not needed for correlation analysis
```

stroke_data_num Data Structure:

```
# Structure of the "stroke_data_num" dataset
str(stroke_data_num)
```

```
## 'data.frame':    5109 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     : num  1 1 1 1 2 1 2 1 1 1 ...
##  $ heart_disease    : num  2 1 2 1 1 1 2 1 1 1 ...
##  $ ever_married     : num  2 2 2 2 2 2 2 1 2 2 ...
##  $ work_type        : num  4 3 4 4 3 4 4 4 4 4 ...
##  $ Residence_type   : num  2 1 1 2 1 2 1 2 1 2 ...
##  $ bmi              : num  36.6 30.5 32.5 34.4 24 ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ smoking_status   : num  2 1 1 3 1 2 1 1 4 4 ...
##  $ stroke           : num  2 2 2 2 2 2 2 2 2 2 ...
```

4.3 `stroke_final_train` and `stroke_validation` Datasets

Now that the data is ready for model development, the `stroke_data` data frame will be split with a 80%/20% ratio into a final training subset called `stroke_final_train` (4,087 rows) and a final hold-out validation subset called `stroke_validation` (1,022 rows), respectively. These datasets will only be used to create further training and test subsets for use during model development, and for final training and validation of the final model. the split percentage chosen is one of the most commonly used in data science, and should suffice for this smaller dataset.

stroke_final_train and stroke_validation Subset Creation Code Snippet:

```
# The training dataset, "stroke_final_train", and validation test dataset,
# "stroke_validation", will be created from an 80%/20% split of the
# "stroke_data" data frame, respectively.
set.seed(1, sample.kind="Rounding")
test_index <- createDataPartition(y = stroke_data$stroke, times = 1, p = 0.2, list = FALSE)
stroke_final_train <- stroke_data[-test_index,]
stroke_validation <- stroke_data[test_index,]
rm(test_index) #Clean up temporary variables.
```

stroke_final_train and stroke_validation Object Summary:

```
# Summary information for the "stroke_final_train" dataset.
summary(stroke_final_train)
```

```
##        id           gender          age                hypertension
##  Min.   :   67   Male  :1685   Min.   : 0.08   wo_hypertension:3699
##  1st Qu.:12102   Female:2402   1st Qu.:25.00   w_hypertension : 388
##  Median :32840                 Median :44.00
##  Mean   :33777                 Mean   :42.94
##  3rd Qu.:52540                 3rd Qu.:60.00
##  Max.   :72940                 Max.   :82.00
##           heart_disease             ever_married            work_type
##  wo_heart_disease:3871   never_married    :1421   Underage_child : 560
##  w_heart_disease : 216   is_or_was_married:2666   Never_worked   :  15
##                                                   Self-employed  : 649
##                                                   Private_company:2330
##                                                   Govt_job       : 533
```

```
##
##  Residence_type      bmi        avg_glucose_level         smoking_status
##  Rural:2023     Min.   :10.30   Min.   : 55.22    never smoked   :1494
##  Urban:2064     1st Qu.:23.80   1st Qu.: 77.46    formerly smoked: 714
##                 Median :28.50   Median : 92.23    smokes         : 640
##                 Mean   :28.92   Mean   :106.40    Unknown        :1239
##                 3rd Qu.:32.80   3rd Qu.:114.09
##                 Max.   :97.60   Max.   :267.76
##        stroke
##  no_stroke:3888
##  stroke   : 199
##
##
##
##
```

```
# Summary information for the "stroke_validation" dataset.
summary(stroke_validation)
```

```
##        id           gender         age                hypertension
##  Min.   :   91   Male  :430   Min.   : 0.16   wo_hypertension:912
##  1st Qu.:11776   Female:592   1st Qu.:26.00   w_hypertension :110
##  Median :32480                Median :46.00
##  Mean   :34023                Mean   :44.41
##  3rd Qu.:53333                3rd Qu.:63.00
##  Max.   :72867                Max.   :82.00
##           heart_disease            ever_married           work_type
##  wo_heart_disease:962   never_married    :335   Underage_child :127
##  w_heart_disease : 60   is_or_was_married:687   Never_worked   :  7
##                                                 Self-employed  :170
##                                                 Private_company:594
##                                                 Govt_job       :124
##
##  Residence_type      bmi        avg_glucose_level         smoking_status
##  Rural:490      Min.   :13.00   Min.   : 55.12    never smoked   :398
##  Urban:532      1st Qu.:23.50   1st Qu.: 76.20    formerly smoked:170
##                 Median :28.10   Median : 90.28    smokes         :149
##                 Mean   :28.83   Mean   :105.10    Unknown        :305
##                 3rd Qu.:33.08   3rd Qu.:113.93
##                 Max.   :78.00   Max.   :271.74
##        stroke
##  no_stroke:972
##  stroke   : 50
##
##
##
##
```

4.3.1 `stroke_train` and `stroke_test` Modeling Datasets

The final hold-out test dataset (`stroke_validation`) will only be used for evaluating and testing the accuracy of the final algorithm, and not during model development. Since 20% of the entire `stroke_data` dataset has already been allocated to the final hold-out (`stroke_validation`), the `stroke_final_train` dataset itself will be split into an additional 80% training data subset (`stroke_train`) and 20% test subset (`stroke_test`), with 3,269 and 818 rows, respectively. They will be used to build and test algorithms in the Modeling section of this report.

The analysis and charting in the next section (Section 4.4) will use the larger `stroke_data` dataset, while the modeling section (Section 5) will use the smaller `stroke_train`/`stroke_test` datasets for model development.

stroke_train and stroke_test Subset Creation Code Snippet:

```
# The training dataset, "stroke_train", and validation test dataset,
# "stroke_test", will be created from an 80%/20% split of the
# "stroke_final_train" data frame, respectively.
set.seed(1, sample.kind="Rounding")
test_index <- createDataPartition(y = stroke_final_train$stroke, times = 1, p = 0.2, list = FALSE)
stroke_train <- stroke_final_train[-test_index,]
stroke_test <- stroke_final_train[test_index,]
rm(test_index) #Clean up temporary variables.
```

stroke_train and stroke_test Object Summary:

```
# Summary information for the "stroke_train" dataset.
summary(stroke_train)
```

```
##        id            gender          age                hypertension
##  Min.   :   67   Male  :1332   Min.   : 0.08   wo_hypertension:2954
##  1st Qu.:11872   Female:1937   1st Qu.:25.00   w_hypertension : 315
##  Median :32563                 Median :45.00
##  Mean   :33643                 Mean   :43.04
##  3rd Qu.:52593                 3rd Qu.:61.00
##  Max.   :72915                 Max.   :82.00
##           heart_disease             ever_married            work_type
##  wo_heart_disease:3093   never_married    :1124   Underage_child : 455
##  w_heart_disease : 176   is_or_was_married:2145   Never_worked   :  11
##                                                   Self-employed  : 522
##                                                   Private_company:1849
##                                                   Govt_job       : 432
##
##  Residence_type      bmi         avg_glucose_level         smoking_status
##  Rural:1597     Min.   :10.30   Min.   : 55.22    never smoked   :1173
##  Urban:1672     1st Qu.:23.90   1st Qu.: 77.52    formerly smoked: 576
##                 Median :28.50   Median : 92.81    smokes         : 509
##                 Mean   :28.94   Mean   :106.96    Unknown        :1011
```

```
##                 3rd Qu.:32.70   3rd Qu.:114.84
##                 Max.   :97.60   Max.   :267.76
##        stroke
##  no_stroke:3110
##  stroke   : 159
##
##
##
##
```

```
# Summary information for the "stroke_test" dataset.
summary(stroke_test)
```

```
##        id           gender         age                 hypertension
##  Min.   :   77   Male  :353   Min.   : 0.08   wo_hypertension:745
##  1st Qu.:13160   Female:465   1st Qu.:26.00   w_hypertension : 73
##  Median :33567                Median :44.00
##  Mean   :34313                Mean   :42.52
##  3rd Qu.:52413                3rd Qu.:59.75
##  Max.   :72940                Max.   :82.00
##          heart_disease            ever_married           work_type
##  wo_heart_disease:778   never_married    :297   Underage_child :105
##  w_heart_disease : 40   is_or_was_married:521   Never_worked   :  4
##                                                 Self-employed  :127
##                                                 Private_company:481
##                                                 Govt_job       :101
##
##  Residence_type      bmi        avg_glucose_level         smoking_status
##  Rural:426      Min.   :11.30   Min.   : 55.72    never smoked   :321
##  Urban:392      1st Qu.:23.70   1st Qu.: 76.94    formerly smoked:138
##                 Median :28.30   Median : 89.92    smokes         :131
##                 Mean   :28.88   Mean   :104.17    Unknown        :228
##                 3rd Qu.:33.00   3rd Qu.:111.69
##                 Max.   :66.80   Max.   :263.56
##        stroke
##  no_stroke:778
##  stroke   : 40
##
##
##
##
```

4.4 Dataset Analysis

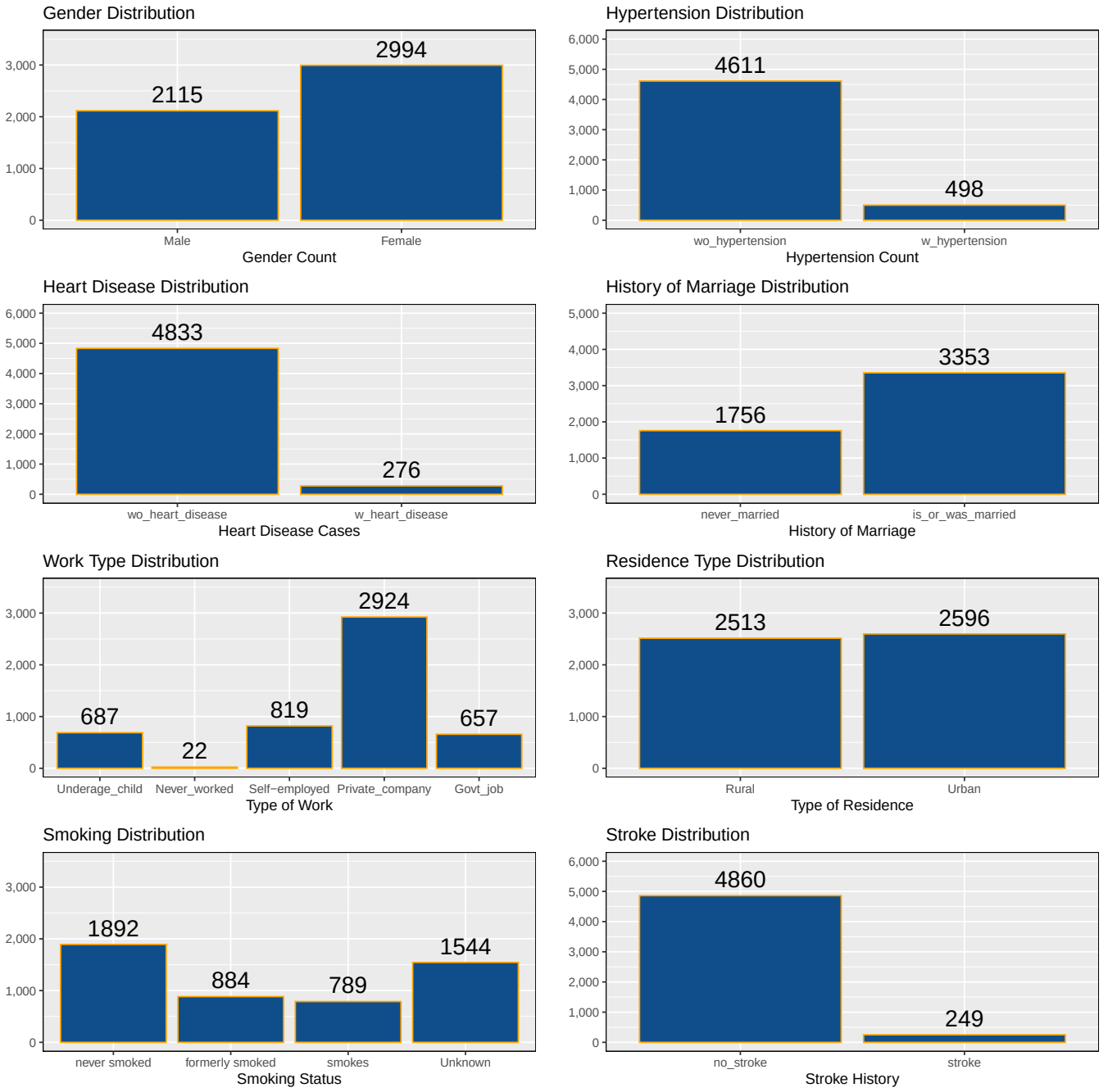
Reviewing the datasets in raw format, along with creating correlative visual aids is necessary when comparing and contrasting the data. Basic analysis of each dataset has been done following their creation in previous sections. This section will focus on studying the data itself and any correlations that can aid in model selection.

stroke_data Object Glimpse:

```
# Get a quick glimpse of the data in stroke_data.
glimpse(stroke_data, width=80)
```

```
## Rows: 5,109
## Columns: 12
## $ id                <int> 9046, 9047, 9048, 9049, 9050, 9051, 9052, 9053, 9054~
## $ gender            <fct> Male, Female, Male, Female, Female, Male, Male, Fema~
## $ age               <dbl> 67, 61, 80, 49, 79, 81, 74, 69, 59, 78, 81, 61, 54, ~
## $ hypertension      <fct> wo_hypertension, wo_hypertension, wo_hypertension, w~
## $ heart_disease     <fct> w_heart_disease, wo_heart_disease, w_heart_disease, ~
## $ ever_married      <fct> is_or_was_married, is_or_was_married, is_or_was_marr~
## $ work_type         <fct> Private_company, Self-employed, Private_company, Pri~
## $ Residence_type    <fct> Urban, Rural, Rural, Urban, Rural, Urban, Rural, Urb~
## $ bmi               <dbl> 36.60000, 30.47129, 32.50000, 34.40000, 24.00000, 29~
## $ avg_glucose_level <dbl> 228.69, 202.21, 105.92, 171.23, 174.12, 186.21, 70.0~
## $ smoking_status    <fct> formerly smoked, never smoked, never smoked, smokes,~
## $ stroke            <fct> stroke, stroke, stroke, stroke, stroke, stroke, stro~
```

In **Figure 4.4.1** below, a grid of eight bar graphs shows a graphical breakdown of all factors and their individual category (level) quantities. The Male/Female ratio is split fairly close at 41% to 59%, respectively. The distribution of individuals diagnosed with hypertension, heart_disease, and/or stroke is very imbalanced, which will require further correlative review among the other predictors to determine any statistical significance. The `smoking_status` factor has a fairly large quantity of individuals in the `Unknown` category (where their status was unavailable at time of entry), which could skew the correlation coefficient between it and `stroke`. The residence type is split almost 50/50 between `Rural` and `Urban`, which means that predictor will have little to no impact on the prediction model.



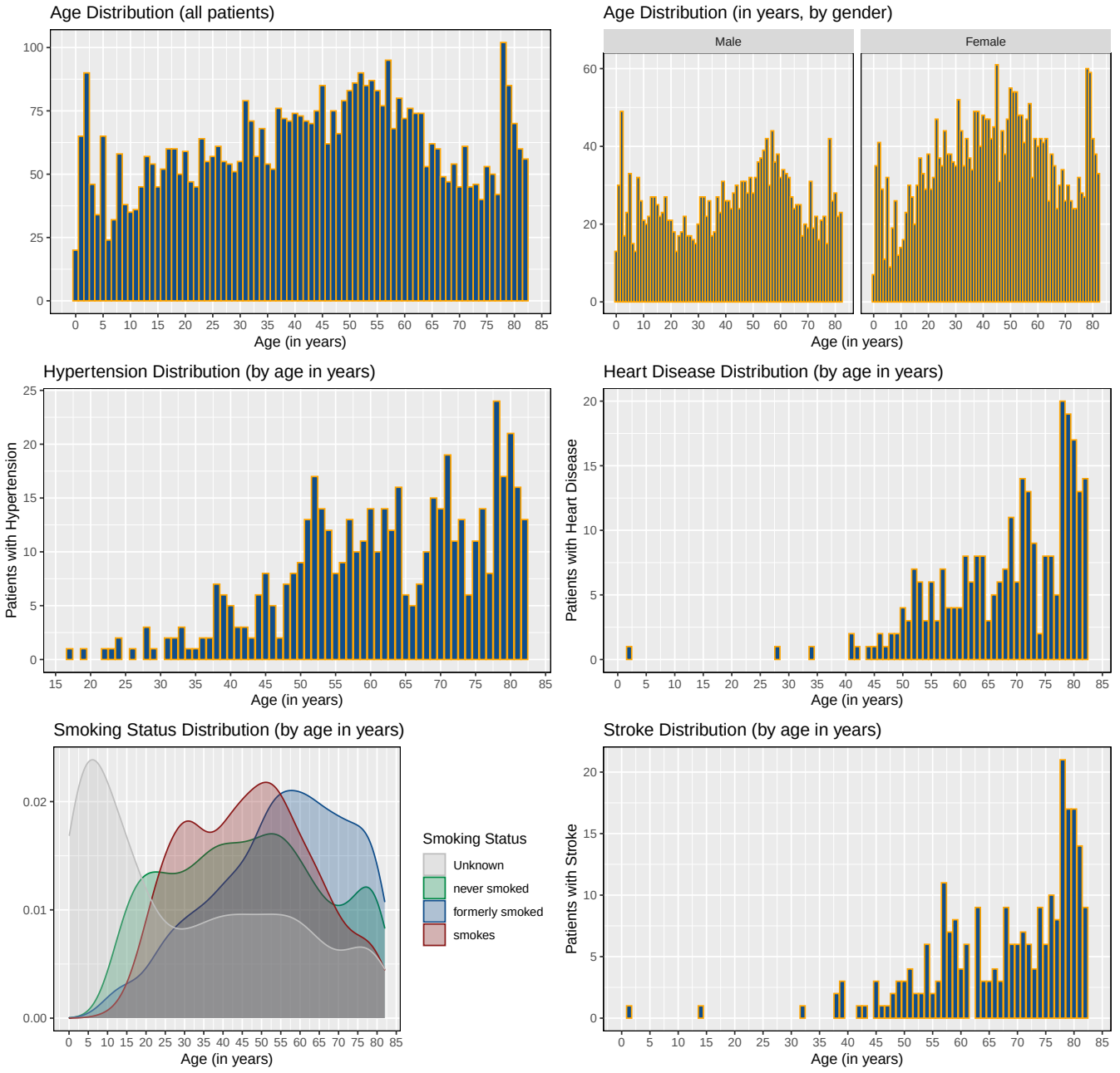
Source Data: stroke_data

Figure 4.4.1

In **Figure 4.4.2** below, a grid of six charts shows a graphical comparison of various predictors as they relate to patient age. When reviewing the charts showing hypertension, heart disease, and history of stroke as it relates to patient age, those predictors have little prevalence in patients under 35 years old.

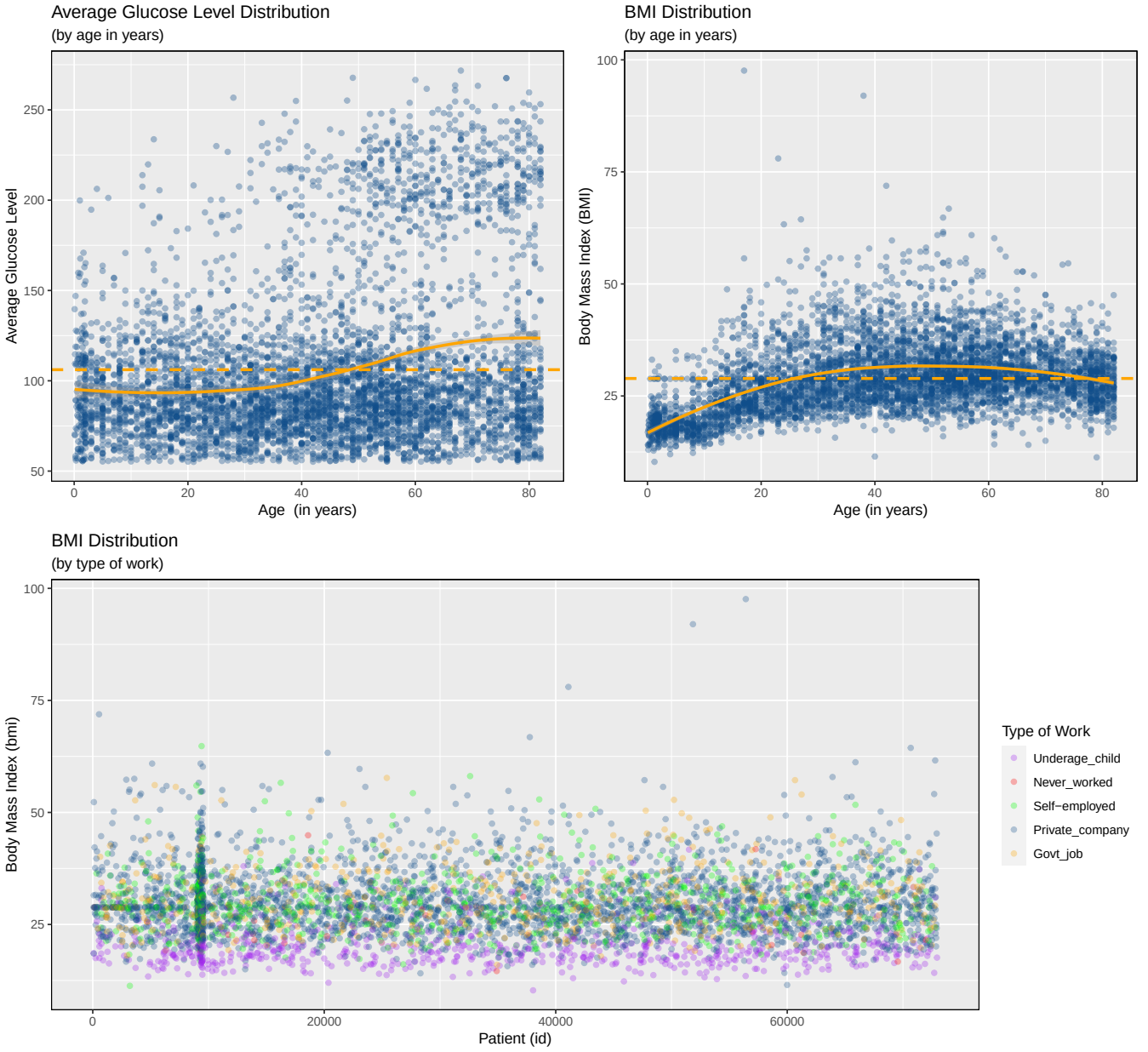
The `Unknown` smoking status category, when stratified by age, shows a trend in minors that can be explained by the parent/guardian of the patient viewing the smoking section of the doctor's/hospital admission forms as "not applicable". The relevant age of the `smoking_status` predictor, unlike hypertension and heart disease, starts around age 15 as that is when the `smokes` category increases rapidly.

The age distribution by gender shows a similar curve between Male/Female from ages 30 and up, but there are more Male patients that are minors.



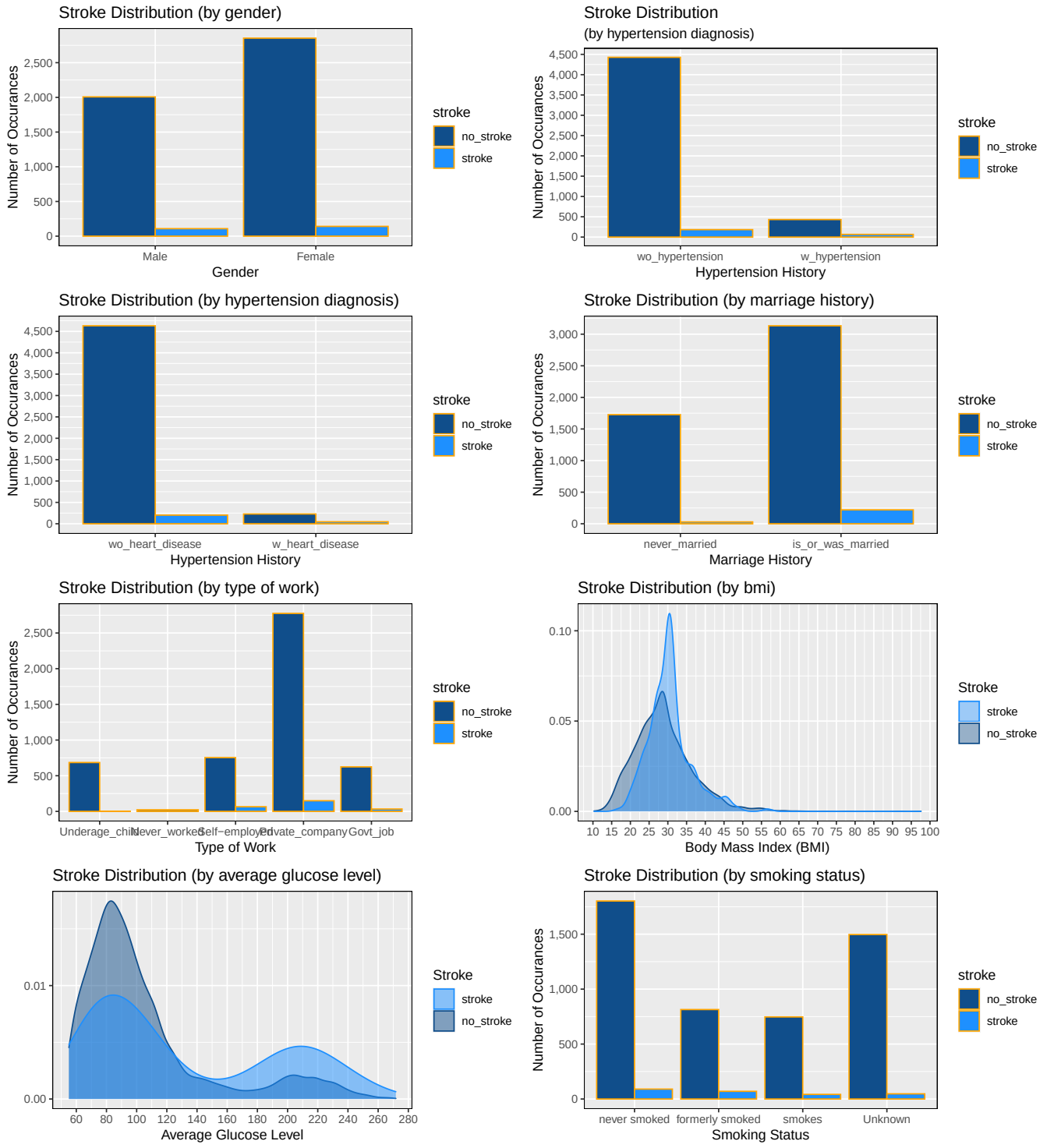
Source Data: stroke_data
Figure 4.4.2

The average blood sugar (glucose) level and BMI distribution charts (**Figure 4.4.3 below**) both show anticipated trends (though both are fairly flat) where the body's ability to manage blood sugar lowers over time (causing the average levels to increase with age), and the BMI increases as you reach middle-age, then lowers a little in the very late stages of life.



Source Data: stroke_data
Figure 4.4.3

In **Figure 4.4.4** below, a grid of eight charts shows a graphical comparison of various predictors as they relate to stroke occurrence. Since **Figure 4.4.1** showed a stroke count of only 249, out of a possible 5109, it is unsurprising that they appear highly imbalanced. All charts show an evenly-scaled distribution of stroke/no_stroke occurrences among each predictor (not previously charted) or its categories.

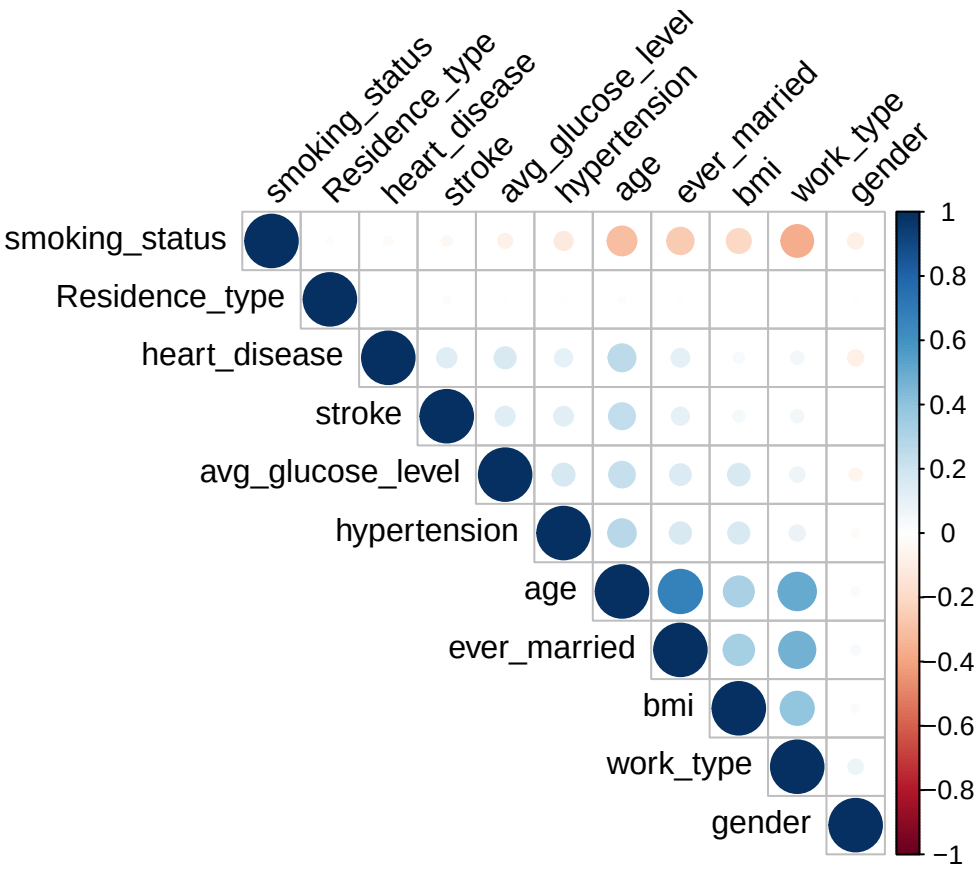


Source Data: stroke_data

Figure 4.4.4

While the charts allow the ability to correlate the predictors to the outcome by sight, it is as (if not more) important to confirm statistically what can be surmised visually. Using the `corrplot` package, a visual representation of actual correlation coefficient data can be maintained:

Correlation Coefficient Chart




```
# Create correlation variables for each correlation coefficient's output
cor_gender <- cor(stroke_data_num$gender, stroke_data_num$stroke)
cor_age <- cor(stroke_data_num$age, stroke_data_num$stroke)
cor_hypertension <- cor(stroke_data_num$hypertension, stroke_data_num$stroke)
cor_heart_disease <- cor(stroke_data_num$heart_disease, stroke_data_num$stroke)
cor_ever_married <- cor(stroke_data_num$ever_married, stroke_data_num$stroke)
cor_work_type <- cor(stroke_data_num$work_type, stroke_data_num$stroke)
cor_Residence_type <- cor(stroke_data_num$Residence_type, stroke_data_num$stroke)
cor_bmi <- cor(stroke_data_num$bmi, stroke_data_num$stroke)
cor_avg_glucose_level <- cor(stroke_data_num$avg_glucose_level, stroke_data_num$stroke)
cor_smoking_status <- cor(stroke_data_num$smoking_status, stroke_data_num$stroke)

# Create a table title variable with the list of dataset variable names
cor_table_titles <- c("gender","age","hypertension","heart_disease","ever_married",
                      "work_type","Residence_type","bmi","avg_glucose_level",
                     "smoking_status")
```

```
# Create a variable with a list of dataset correlation coefficient results.
cor_table_coeffs <- c(cor_gender,cor_age,cor_hypertension,cor_heart_disease,
                      cor_ever_married,cor_work_type,cor_Residence_type,cor_bmi,
                      cor_avg_glucose_level,cor_smoking_status)
# Create a table with the "cor_table_titles" contents in the left column, and
# the "cor_table_coeffs" contents in the right column.
kable(tibble(cor_table_titles, cor_table_coeffs),
      col.names = c("Variable Name", "Correlation Coefficient to Stroke")) %>%
  row_spec(0,background="#104E8B", color="white") %>%
  column_spec(2, bold=TRUE) %>%
  kable_styling(bootstrap_options="bordered",
                full_width=FALSE,
                position="center",
                latex_options="HOLD_position")
```

Variable Name	Correlation Coefficient to Stroke
gender	**-0.0090806**
age	**0.2452388**
hypertension	**0.1278913**
heart_disease	**0.1349048**
ever_married	**0.1082993**
work_type	**0.0573656**
Residence_type	**0.0154146**
bmi	**0.0460594**
avg_glucose_level	**0.1319912**
smoking_status	**-0.0366669**

The table above shows the correlation coefficient amounts for each applicable variable. The `id` column was removed during the `stroke_data_num` dataset creation since there is no direct correlation with that field, and running the `cor()` command against the `stroke` variable would always be 1, so it was not added to the table.

The data shows that the `age`, `heart_disease`, `avg_glucose_level`, and `hypertension` are the most relevant predictors to `stroke`.

5. MODELING

Throughout the data analysis performed above, some data point comparisons show the possibility of higher correlations while others appear they would have little impact to the overall predictability, and thus the model. To determine the impact of each predictor, various models will be tested, starting with logistic regression and then including Naive Bayes, linear discriminant analysis, classification and regression trees, random forest, and k-Nearest Neighbor. Each resultant accuracy calculation will be summarized in a list with previous results as to make it easy to compare all results and determine which model performs the best (having the highest accuracy score).

Cross-Validation Training Options Code Snippet:

```
# Model cross-validation training options variable creation.
fitControl <- trainControl(method = "cv",  #cross-validation
                           number = 10)    #10-fold cross-validation
```

Model 1: Logistic Regression (GLM)

The logistic regression is a very basic and frequently used machine learning model where independent variables determine a binary outcome, such as the stroke prediction in this dataset. The conditional probability can be modeled as:

$$g\{Pr(Y = 1|X = x)\} = \beta_0 + \beta_1$$

```
set.seed(1, sample.kind = "Rounding")
# Train the logistic regression model with the generalized linear model (GLM)
# method, using the fitControl tuning parameters.
model1_fit <- train(stroke ~ ., data = stroke_train,
                    method = "glm",
                    preProcess=c("center", "scale"),
                    trControl = fitControl)
model1_fit
```

```
## Generalized Linear Model
##
## 3269 samples
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2942, 2942, 2943, 2942, 2942, 2942, ...
## Resampling results:
##
##   Accuracy  Kappa
##   0.946773  0.1373651
```

```r
# Predict the outcome from the stroke_test dataset
model1_preds <- predict(model1_fit, stroke_test)

# Calculate the accuracy of the model against the stroke_test dataset.
model1_accuracy <- confusionMatrix(model1_preds, stroke_test$stroke)$overall["Accuracy"]
model1_accuracy
```

```
##  Accuracy
## 0.9425428
```

Using the `stroke_test` data, the accuracy for this model is calculated to be 0.9425428.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**

Model 2: Naive Bayes

The Naive Bayes model, based on Bayes Theorem[6], estimates the outcome by estimating the conditional distribution of the predictors, which also assumes independence among the predictors. The naive model can be written as:

$$p(x) = Pr(Y = 1|X = x) = \frac{f_{X|Y=1}(X)Pr(Y = 1)}{f_{X|Y=0}(X)Pr(Y = 0) + f_{X|Y=1}(X)Pr(Y = 1)}$$

With $f_{X|Y=1}$ and $f_{X|Y=0}$ representing the distribution functions of the predictor X for the two classes $Y = 1$ and $Y = 0$.

```r
set.seed(1, sample.kind = "Rounding")
# Train the Naive Bayes model using the fitControl tuning parameters.
model2_fit <- train(stroke ~ ., data = stroke_train,
                    method = "naive_bayes",
                    preProcess=c("center", "scale"),
                    trControl = fitControl)
model2_fit
```

```
## Naive Bayes
##
## 3269 samples
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2942, 2942, 2943, 2942, 2942, 2942, ...
```

[6]https://rafalab.github.io/dsbook/

```
## Resampling results across tuning parameters:
##
##   usekernel  Accuracy   Kappa
##   FALSE      0.8286927  0.305134
##    TRUE      0.9620701  0.347350
##
## Tuning parameter 'laplace' was held constant at a value of 0
## Tuning
##  parameter 'adjust' was held constant at a value of 1
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were laplace = 0, usekernel = TRUE
##  and adjust = 1.
```

```
# Predict the outcome from the stroke_test dataset
model2_preds <- predict(model2_fit, stroke_test)

# Calculate the accuracy of the model against the stroke_test dataset.
model2_accuracy <- confusionMatrix(model2_preds, stroke_test$stroke)$overall["Accuracy"]
model2_accuracy
```

```
##  Accuracy
## 0.9547677
```

Using the `stroke_test` data, the accuracy for this model is calculated to be 0.9547677.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**
Model 2: Naive Bayes	**0.9547677**

Model 3: Linear Discriminant Analysis (LDA)

The linear discriminant analysis model improved upon Naive Bayes by using a dimensionality reduction technique that estimates the probability that a new set of inputs belongs to every class. The resultant output class is the one that has the highest probability (the prediction).

```
set.seed(1, sample.kind = "Rounding")
# Train the LDA model using the fitControl tuning parameters.
model3_fit <- train(stroke ~ ., data = stroke_train,
                    method = "lda",
                    preProcess=c("center", "scale"),
                    trControl = fitControl)
model3_fit
```

```
## Linear Discriminant Analysis
##
```

```
## 3269 samples
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2942, 2942, 2943, 2942, 2942, 2942, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.9510544  0.2251664
```

```
# Predict the outcome from the stroke_test dataset
model3_preds <- predict(model3_fit, stroke_test)

# Calculate the accuracy of the model against the stroke_test dataset.
model3_accuracy <- confusionMatrix(model3_preds, stroke_test$stroke)$overall["Accuracy"]
model3_accuracy
```

```
##  Accuracy
## 0.9425428
```

Using the `stroke_test` data, the accuracy for this model is calculated to be 0.9425428.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**
Model 2: Naive Bayes	**0.9547677**
Model 3: Linear Discriminant Analysis (LDA)	**0.9425428**

Model 4: Classification and Regression Trees Model (CART)

Classification (decision) trees build up a set of decision rules that "branch out" to form a tree structure, similar to a flow chart. This branching helps predict an outcome based on the input data.

$$\text{Gini}(j) = \sum_{k=1}^{K} \hat{p}_{j,k}(1 - \hat{p}_{j,k})$$

The Gini Index (above) or Entropy (below) can be used as a metric for classifiers in the classification tree method.

$$entropy(j) = -\sum_{k=1}^{K} \hat{p}_{j,k} \log(\hat{p}_{j,k}), \text{ with 0 x log(0) defined as 0}$$

```
set.seed(1, sample.kind = "Rounding")
# Train the Decision Tree model, setting the tuning parameters.
model4_fit <- train(stroke ~ ., data = stroke_train,
                    method = "rpart",
```

```
                  preProcess=c("center", "scale"),
                  tuneGrid = data.frame(cp = seq(0.0, 0.1, len = 25)))
model4_fit
```

```
## CART
##
## 3269 samples
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 3269, 3269, 3269, 3269, 3269, 3269, ...
## Resampling results across tuning parameters:
##
##   cp           Accuracy   Kappa
##   0.000000000  0.9961171  0.9573652
##   0.004166667  0.9961503  0.9577363
##   0.008333333  0.9962164  0.9585633
##   0.012500000  0.9962833  0.9594410
##   0.016666667  0.9961486  0.9580374
##   0.020833333  0.9961458  0.9584712
##   0.025000000  0.9963118  0.9603148
##   0.029166667  0.9963118  0.9603148
##   0.033333333  0.9963120  0.9602990
##   0.037500000  0.9963113  0.9604555
##   0.041666667  0.9963449  0.9608063
##   0.045833333  0.9963449  0.9608063
##   0.050000000  0.9963449  0.9608063
##   0.054166667  0.9963449  0.9608063
##   0.058333333  0.9963449  0.9608063
##   0.062500000  0.9963449  0.9608063
##   0.066666667  0.9963449  0.9608063
##   0.070833333  0.9963449  0.9608063
##   0.075000000  0.9963449  0.9608063
##   0.079166667  0.9963449  0.9608063
##   0.083333333  0.9965416  0.9631052
##   0.087500000  0.9965416  0.9631052
##   0.091666667  0.9965416  0.9631052
##   0.095833333  0.9965416  0.9631052
##   0.100000000  0.9965416  0.9631052
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.1.
```

```
# Predict the outcome from the stroke_test dataset
model4_preds <- predict(model4_fit, stroke_test)
```

```r
# Calculate the accuracy of the model against the stroke_test dataset.
model4_accuracy <- confusionMatrix(model4_preds, stroke_test$stroke)$overall["Accuracy"]
model4_accuracy
```

```
##  Accuracy
## 0.9963325
```

Using the `stroke_test` data, the accuracy for this model is calculated to be 0.9963325.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**
Model 2: Naive Bayes	**0.9547677**
Model 3: Linear Discriminant Analysis (LDA)	**0.9425428**
Model 4: Classification and Regression Trees Model (CART)	**0.9963325**

Model 5: Random Forest

With the CART model being prone to over-fitting, the random forest model compensates for this by using decision trees to generate many predictors, and then averages them until a final prediction is made based on the averages. The trade-off for its performance gain is the loss of interpret ability of the data.

This model uses the `Rborist` method, which a high-performance implementation of random forest.

```r
set.seed(1, sample.kind = "Rounding")
# Train the Random Forest model using the "Rborist" method.  Set basic decision tree
# tuning parameters.
model5_fit <- train(stroke ~ ., data = stroke_train,
                    method = "Rborist",
                    preProcess=c("center", "scale"),
                    tuneGrid = expand.grid(predFixed = seq(1,4), minNode = 2))
model5_fit
```

```
## Random Forest
##
## 3269 samples
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 3269, 3269, 3269, 3269, 3269, 3269, ...
## Resampling results across tuning parameters:
##
##   predFixed  Accuracy   Kappa
##   1          0.9519816  0.0000000
```

```
##   2          0.9659864  0.4410448
##   3          0.9925190  0.9131642
##   4          0.9961114  0.9570753
##
## Tuning parameter 'minNode' was held constant at a value of 2
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were predFixed = 4 and minNode = 2.
```

```
# Predict the outcome from the stroke_test dataset
model5_preds <- predict(model5_fit, stroke_test)

# Calculate the accuracy of the model against the stroke_test dataset.
model5_accuracy <- confusionMatrix(model5_preds, stroke_test$stroke)$overall["Accuracy"]
model5_accuracy
```

```
## Accuracy
##  0.99511
```

Using the `stroke_test` data, the accuracy for this model is calculated to be 0.99511.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**
Model 2: Naive Bayes	**0.9547677**
Model 3: Linear Discriminant Analysis (LDA)	**0.9425428**
Model 4: Classification and Regression Trees Model (CART)	**0.9963325**
Model 5: Random Forest	**0.9951100**

Model 6: k-Nearest Neighbor (kNN)

The k-nearest neighbor model searches its neighboring data, assuming that similar data points exist close by. The most similar data points to the ones you have to predict are found by averaging the neighboring values, or by most frequent class. Decreasing the value of K yields less accurate predictions, and increasing it too high produces errors which also yields less accurate predictions.

```
set.seed(1, sample.kind = "Rounding")
# Train the k-Nearest Neighbors model, setting the k-value tuning parameters.
model6_fit <- train(stroke ~ ., data = stroke_train,
                    method = "knn",
                    preProcess=c("center", "scale"),
                    tuneGrid = data.frame(k = seq(1,100,5)))
model6_fit
```

```
## k-Nearest Neighbors
##
## 3269 samples
```

```
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 3269, 3269, 3269, 3269, 3269, 3269, ...
## Resampling results across tuning parameters:
##
##   k   Accuracy   Kappa
##    1  0.9242739   1.657514e-01
##    6  0.9391311   8.624354e-02
##   11  0.9491857   3.850397e-02
##   16  0.9507189   2.310222e-02
##   21  0.9510189   1.189415e-02
##   26  0.9511871   5.580644e-03
##   31  0.9514525   3.943574e-03
##   36  0.9516845   3.239779e-03
##   41  0.9517838   3.335000e-03
##   46  0.9518497  -2.571048e-04
##   51  0.9519153  -1.300634e-04
##   56  0.9519487  -6.459928e-05
##   61  0.9519816   0.000000e+00
##   66  0.9519816   0.000000e+00
##   71  0.9519816   0.000000e+00
##   76  0.9519816   0.000000e+00
##   81  0.9519816   0.000000e+00
##   86  0.9519816   0.000000e+00
##   91  0.9519816   0.000000e+00
##   96  0.9519816   0.000000e+00
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 96.
```

```r
# Predict the outcome from the stroke_test dataset
model6_preds <- predict(model6_fit, stroke_test)

# Calculate the accuracy of the model against the stroke_test dataset.
model6_accuracy <- confusionMatrix(model6_preds, stroke_test$stroke)$overall["Accuracy"]
model6_accuracy
```

```
##  Accuracy
## 0.9511002
```

Using the `stroke_test` data, the accuracy for this model is calculated to be 0.9511002.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**
Model 2: Naive Bayes	**0.9547677**
Model 3: Linear Discriminant Analysis (LDA)	**0.9425428**
Model 4: Classification and Regression Trees Model (CART)	**0.9963325**
Model 5: Random Forest	**0.9951100**
Model 6: k-Nearest Neighbor (kNN)	**0.9511002**

6. RESULTS

Having done all of the initial data analysis in section 4 and pinpointing which factors may contribute to (or at least warrant a model to test) an accurate stroke prediction system, stepping through six (6) different models yielded the most accurate results with the use of the Classification and Regression Trees Model (CART) model.

While testing the various performance tuning options of each model a few models ended up having extended compute-intensive time frames (up to 2 hours on an 8-core hyperthreaded processor with 64GB RAM). The final tests with the parameters used in this report only took around 30 minutes to complete from start to finish.

The final accuracy results table below shows the summary list of all prediction models tested for a stroke prediction system using the stroke_train and stroke_test datasets.

Model	Accuracy
Model 1: Logistic Regression (GLM)	**0.9425428**
Model 2: Naive Bayes	**0.9547677**
Model 3: Linear Discriminant Analysis (LDA)	**0.9425428**
Model 4: Classification and Regression Trees Model (CART)	**0.9963325**
Model 5: Random Forest	**0.9951100**
Model 6: k-Nearest Neighbor (kNN)	**0.9511002**

The final hold-out testing of this model using the initial `stroke_final_train` and `stroke_validation` datasets yielded the following final accuracy score:

```
set.seed(1, sample.kind = "Rounding")
# Train the selected final model.
final_model_fit <- train(stroke ~ ., data = stroke_final_train,
                    method = "rpart",
                    preProcess=c("center", "scale"),
                    tuneGrid = data.frame(cp = seq(0.0, 0.1, len = 25)))
final_model_fit
```

```
## CART
##
## 4087 samples
##   11 predictor
##    2 classes: 'no_stroke', 'stroke'
##
## Pre-processing: centered (16), scaled (16)
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 4087, 4087, 4087, 4087, 4087, 4087, ...
## Resampling results across tuning parameters:
##
##   cp           Accuracy   Kappa
```

```
##   0.000000000  0.9971477  0.9693575
##   0.004166667  0.9971477  0.9693575
##   0.008333333  0.9970670  0.9683095
##   0.012500000  0.9970135  0.9678374
##   0.016666667  0.9968814  0.9664043
##   0.020833333  0.9968036  0.9656196
##   0.025000000  0.9965630  0.9632909
##   0.029166667  0.9965364  0.9630492
##   0.033333333  0.9966426  0.9642094
##   0.037500000  0.9965629  0.9633829
##   0.041666667  0.9965625  0.9637581
##   0.045833333  0.9964822  0.9629492
##   0.050000000  0.9964288  0.9624573
##   0.054166667  0.9964022  0.9621480
##   0.058333333  0.9964022  0.9621480
##   0.062500000  0.9964289  0.9624559
##   0.066666667  0.9964289  0.9624559
##   0.070833333  0.9965363  0.9635234
##   0.075000000  0.9965363  0.9635234
##   0.079166667  0.9965363  0.9635234
##   0.083333333  0.9965363  0.9635234
##   0.087500000  0.9965363  0.9635234
##   0.091666667  0.9965363  0.9635234
##   0.095833333  0.9965363  0.9635234
##   0.100000000  0.9965363  0.9635234
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.004166667.
```

```r
# Predict the outcome from the stroke_test dataset
final_model_preds <- predict(final_model_fit, stroke_validation)

# Calculate the accuracy of the model against the stroke_test dataset.
final_model_accuracy <- confusionMatrix(final_model_preds, stroke_validation$stroke)$overall["Accu
final_model_accuracy
```

```
##  Accuracy
## 0.9970646
```

Model	Accuracy
FINAL MODEL: Classification and Regression Trees Model (CART)	**0.9970646**

7. CONCLUSION

The purpose of this project was to create a stroke prediction system using a public dataset from Kaggle, and building multiple machine learning models, selecting the one with the highest accuracy as the final model. From initial GitHub repository creation, to data wrangling, dataset analysis, data visualizations, and model development, the knowledge and techniques learned throughout the entire course series has been used.

Both the logistic regression, Naive Bayes, and linear discriminant models all performed their calculations very quickly, and all used the same tuning parameters with results that were all still very high (0.9425428, 0.9547677, and 0.9425428, respectively). The Random Forest and k-Nearest Neighbors tuning parameters were more difficult to test as the calculation times would get extended, and the CPU resources would be locked to the process until completed each time.

After testing 6 different predictive models, using their respective calculated accuracy scores as the success indicator for each, the Classification and Regression Trees Model (CART) model yielded the highest score of 0.9963325. Comparing this accuracy score to the initial Logistic Regression model (0.9425428), there was an improvement of approximately 5.707%.

While the dataset contained many of the health factors that were considered risks by the Centers for Disease Control (CDC) and the National Institute of Neurological Disorders and Stroke (NINDS), as indicated in the Introduction, limitations to the model included several other missing predictors that could be added to future tests, such as Race, geographic location, alcohol drinking habits, drug use, cholesterol level, etc. Being able to inform both the patient and their doctor of their risk of stroke could lead to proactive treatment, better life choices, and a prolonged life span. The data in this particular dataset showed `age`, `heart_disease`, `avg_glucose_level`, and `hypertension` are the most relevant predictors to `stroke`.

Further improvements and future work include an expanded dataset with more samples, additional performance tuning on all of the models in the future (especially in the event that additional factors get added). Additional models, such as the ensemble method, could be developed and tuned to test whether further accuracy can be achieved.

8. REFERENCES

1. Data Science textbook by Rafael Irizarry, https://rafalab.github.io/dsbook.
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3. National Institute of Neurological Disorders and Stroke (NINDS), https://www.stroke.nih.gov/materials/needtoknow.htm
4. Centers for Disease Control (CDC), https://www.cdc.gov/stroke/facts.htm
5. Mayo Clinic, https://www.mayoclinic.org/diseases-conditions/stroke/symptoms-causes/syc-20350113