Stroke Prediction Model Report

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Contents

1 Introduction

According to the CDC, strokes are a leading cause of death in the US, and are a major cause of serious disability for adults. Nearly 800,000 people in the US have a stroke each year.

This report presents a modeling process designed to predict stroke events and assess stroke risk in patients. The data set used can be found here. It consists of 5110 observations, each one containing a patient's clinical features, a unique ID number, and whether or not they have had a stroke. The clinical features include gender, age, hypertension, heart disease, work type, residence type, marriage status, average glucose level, body mass index, and smoking status.

The goal of this project is to build a model that predicts stroke events with as much accuracy as possible given the predictors with which we are working. However, raw accuracy is not a useful metric because we can achieve over 95% accuracy by simply predicting "no" for all cases. This is because stroke events are rare, occurring in less than 5% of all observations. In light of this, we use the receiver operating characteristic (ROC) curve as our metric for accuracy. By maximizing the area under the ROC curve (AUC) for our model, we ensure that it will produce both high sensitivity and high specificity, and thus a high balanced accuracy. We aim to achieve results with comparable sensitivity and specificity, with slight favor towards sensitivity, as we prefer false positives to false negatives.

First, we download and lightly clean our data set. Next, we explore the data, looking for trends in the variables. We examine the total distributions of each variable, as well as the stroke event rates within each variable. This provides insight on how best to approach the modeling process, particularly the benefits of using class weights and analyzing ROC curves to determine optimal probability thresholds for classification.

After data exploration, we perform some preprocessing to impute missing data and transform categorical variables into numerical ones using one hot encoding. We also create an alternate version of the data where the continuous variables are stratified into categorical intervals, producing a categorical matrix. This categorical matrix is used to build one final model after using the caret package to build several others.

Once our data is ready, we divide it into training and test sets, and begin building our models. Ideally, we would further subdivide our training set into a training and test set, reserving our initial test set solely for final validation. However, due to the small size of our data set, further division of the training set will drastically curtail the accuracy of our model. Instead, we simulate a final validation set by randomly sampling 10,000 observations from our full data set and using this for our final test. We replicate this process 5 times and average the results for evaluation of our final model.

After our final test, we create a risk assessment aspect for our model using 4 probability threshold markers. This divides all observations into 5 categories of risk ranging from very low to very high. We assign risk levels to our full data set, and observe the results.

Finally, we divide our data into prediction categories of true and false positives and negatives, and compare variable distributions for these 4 categories against each other and the full data set in order to gain further insight into the performance of our model.

2 Data exploration

2.1 Getting started

We begin by downloading our data set and loading the necessary libraries:

```
library("tidyverse")
library("readr")
library("varhandle")
library("caret")
library("e1071")
library("pROC")
library("RANN")
library("randomForest")
library("ranger")
library("rpart")
library("gbm")
library("nnet")
```

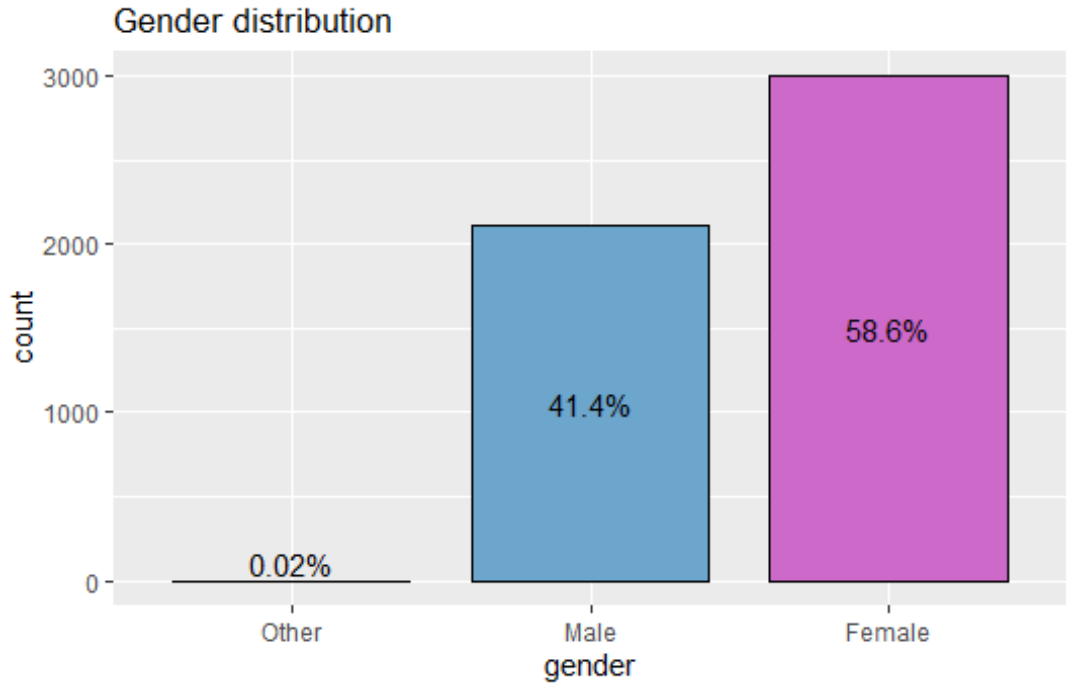
We read in the .csv file to an .rda and examine its structure. We lightly clean the data by removing the id column, converting the body mass index (BMI) column from character to numeric, and converting the stroke column to a factor. Our data structure now looks like this:

variable	class	first_values
gender	character	Male, Female, Male, Female
age	numeric	67, 61, 80, 49
hypertension	numeric	0, 0, 0, 0
heart_disease	numeric	1, 0, 1, 0
ever_married	character	Yes, Yes, Yes, Yes
work_type	character	Private, Self-employed, Private, Private
Residence_type	character	Urban, Rural, Rural, Urban
avg_glucose_level	numeric	228.69, 202.21, 105.92, 171.23
bmi	numeric	36.6, NA, 32.5, 34.4
smoking_status	character	formerly smoked, never smoked, never smoked, smokes
stroke	factor	1, 1, 1, 1

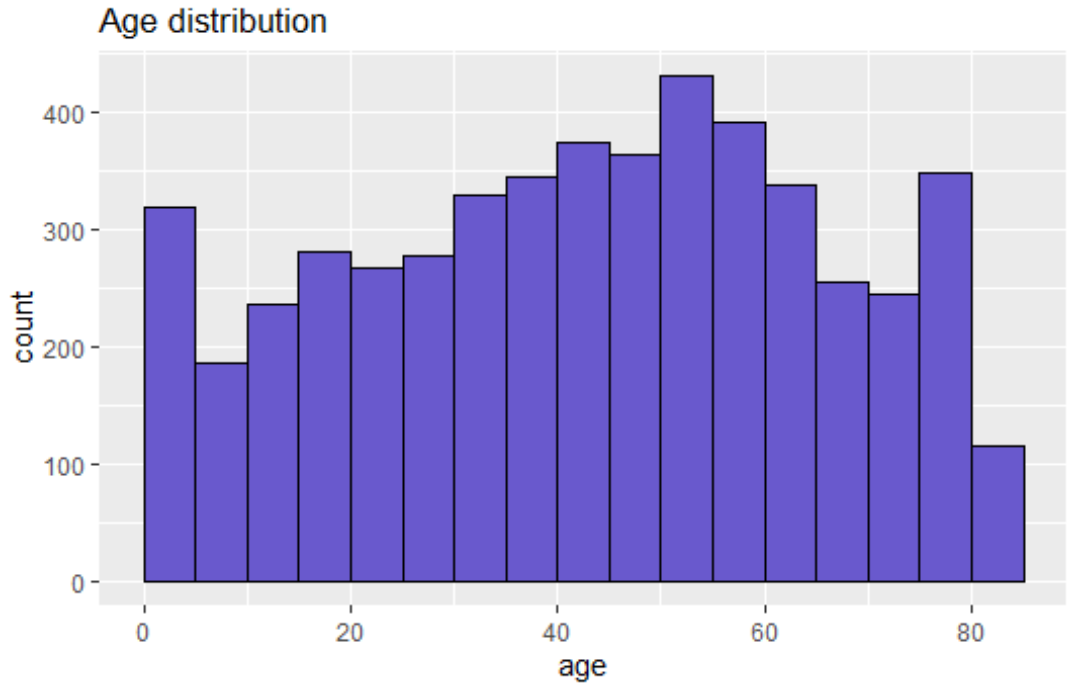
We notice there is at least one missing data point. We count the number of NA's in each column and find there are 201 NA's, all in the bmi column. We leave them as is for now:

	number_of_NAs
gender	0
age	0
hypertension	0
heart_disease	0
ever_married	0
work_type	0
Residence_type	0
avg_glucose_level	0
bmi	201
smoking_status	0
stroke	0

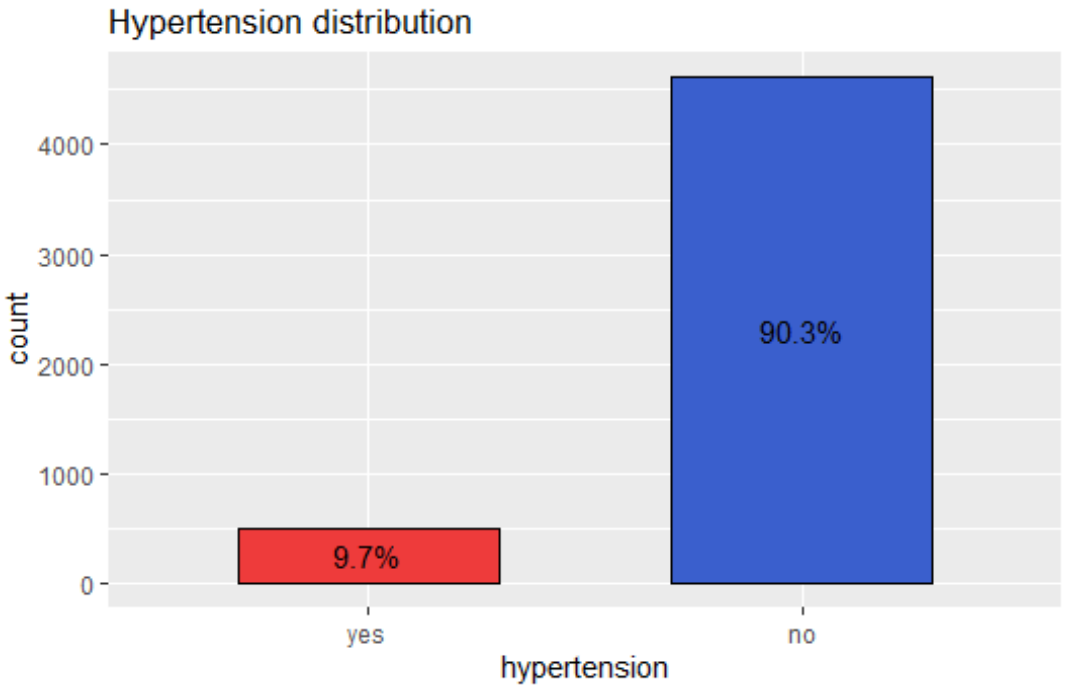
2.2 Examine variable distributions



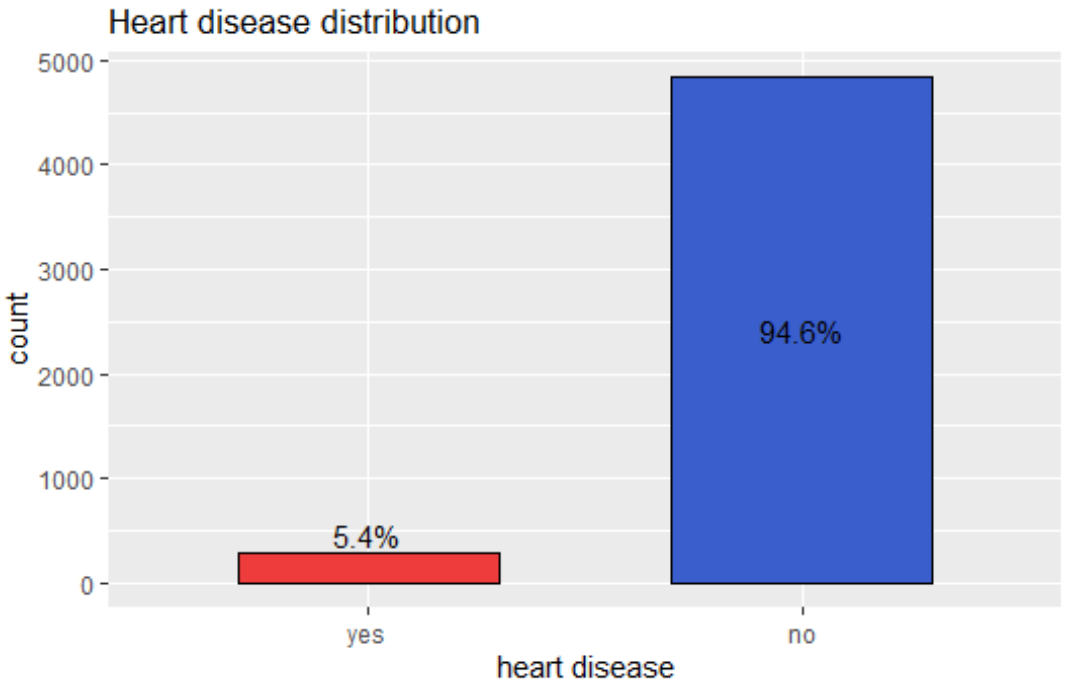
We notice a higher percentage of females, and 1 observation with gender "Other".



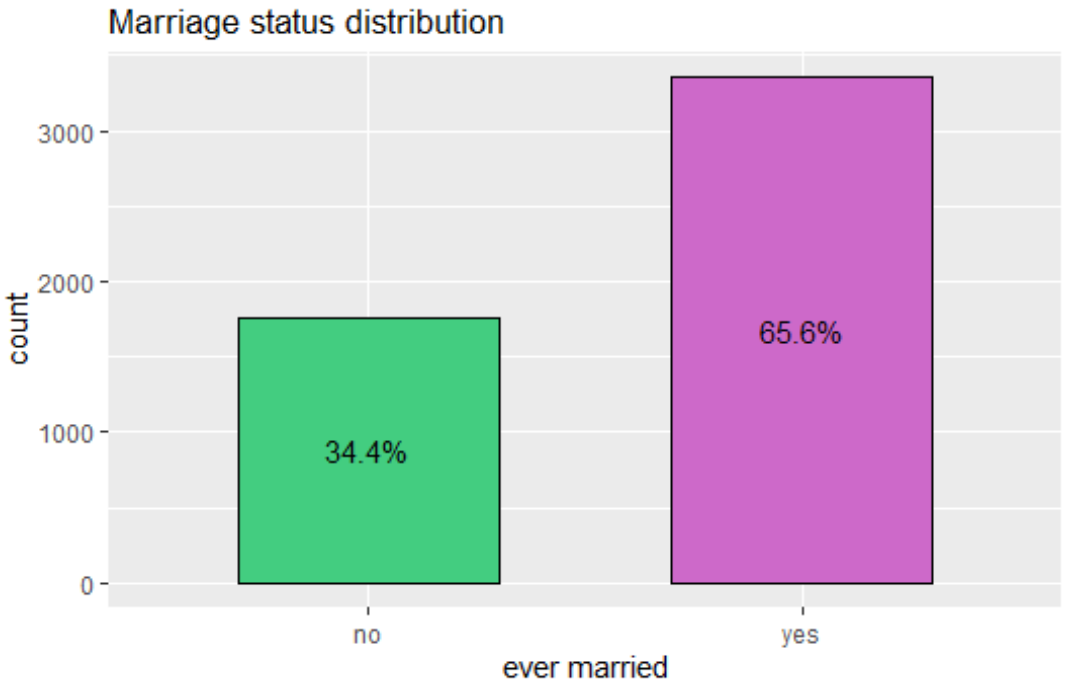
We notice that all age groups are represented fairly well, with the highest age being 82.



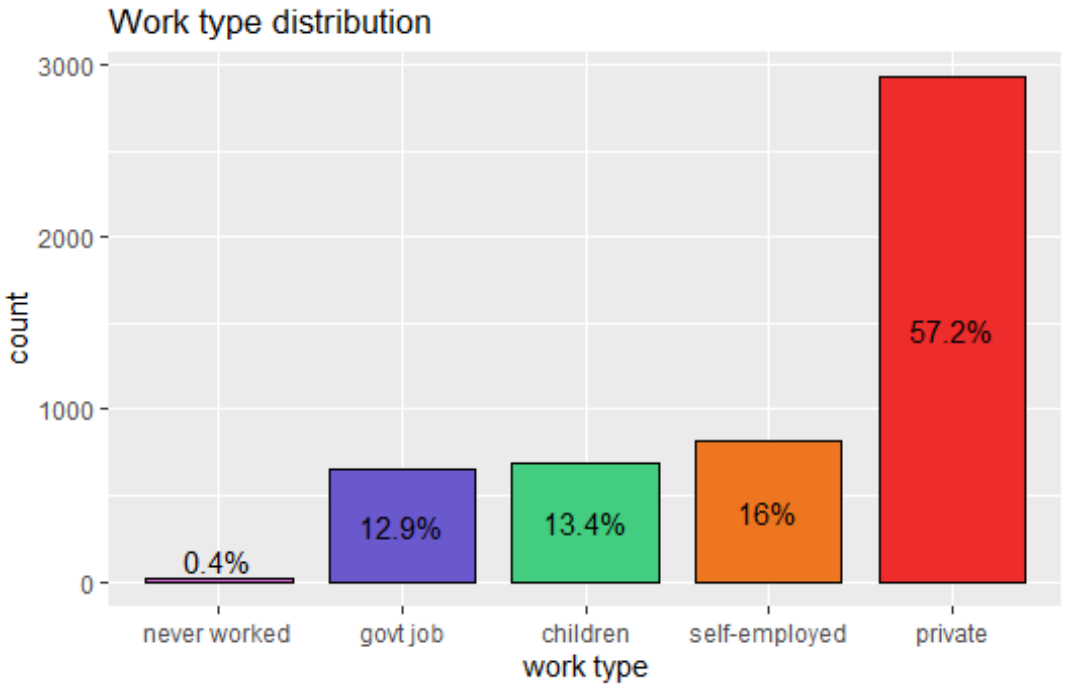
We note that just under 10% of our observations have high blood pressure.



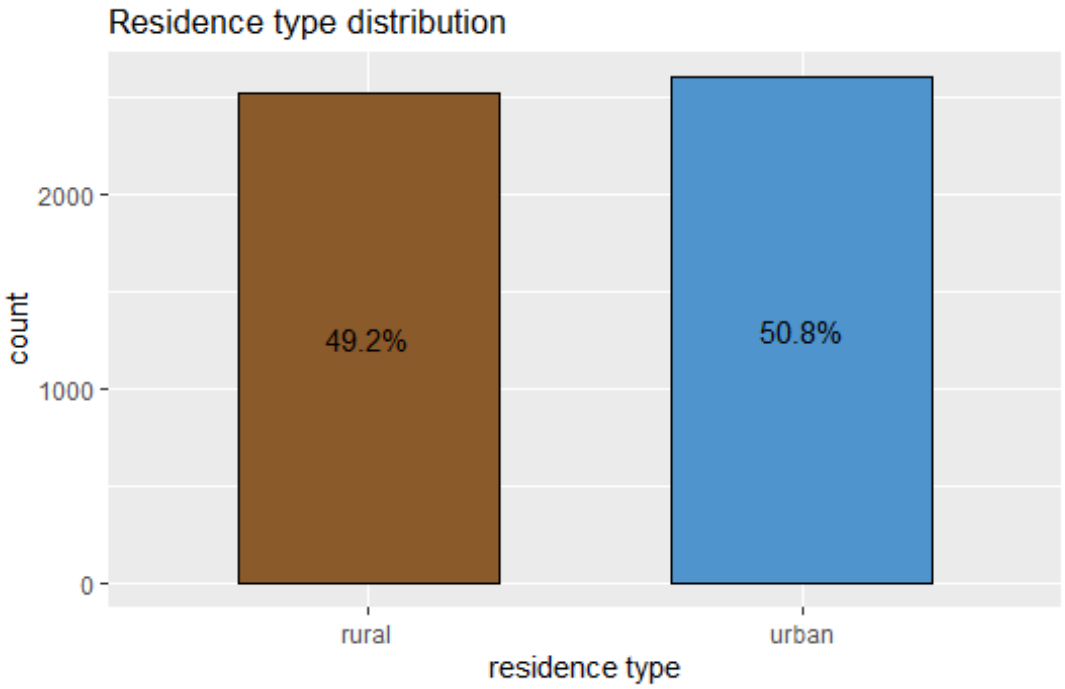
While just over 5% of our observations have heart disease.



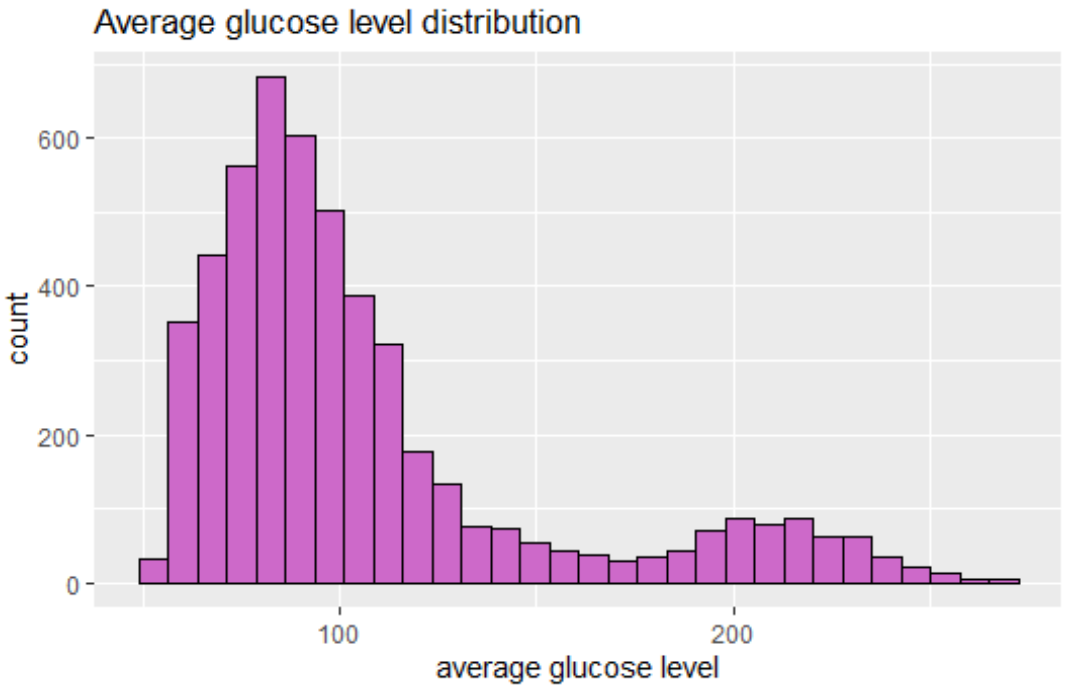
We see about 2/3 of our observations have been married before.



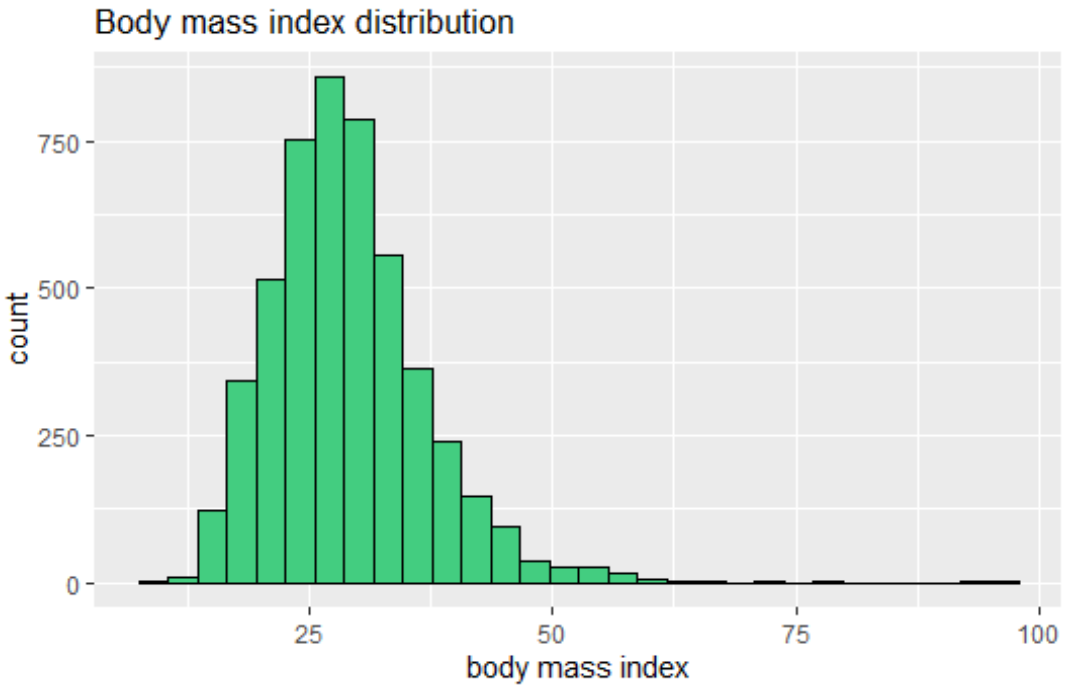
We see that the majority of our observations work in the private sector, while very few have never worked.



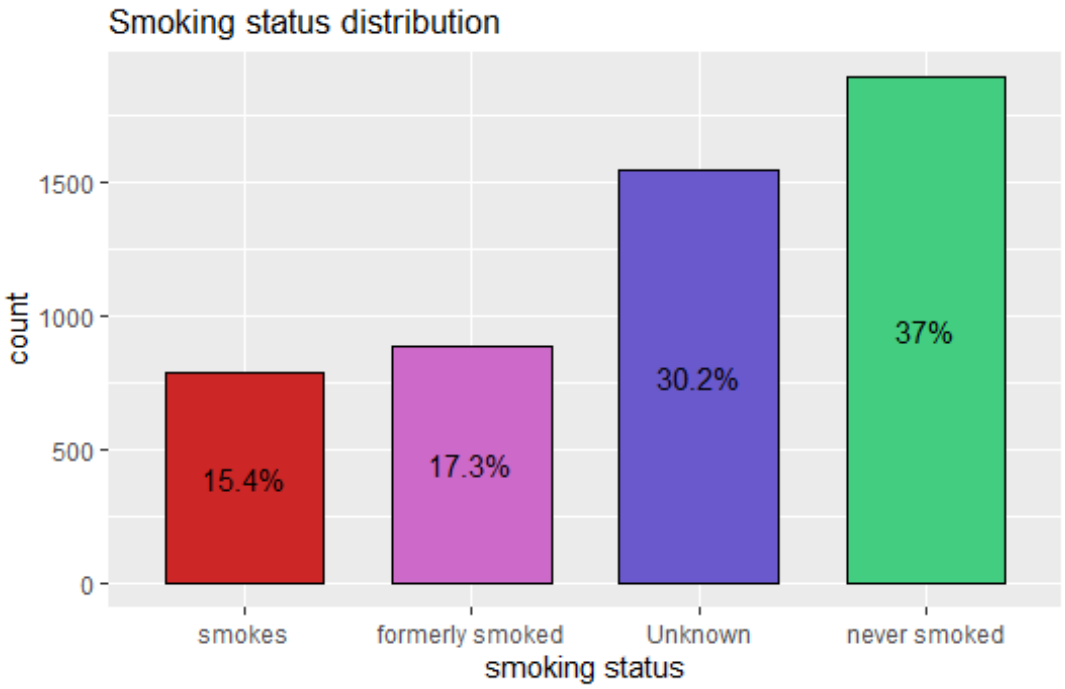
We see a pretty even split between urban and rural residence types.



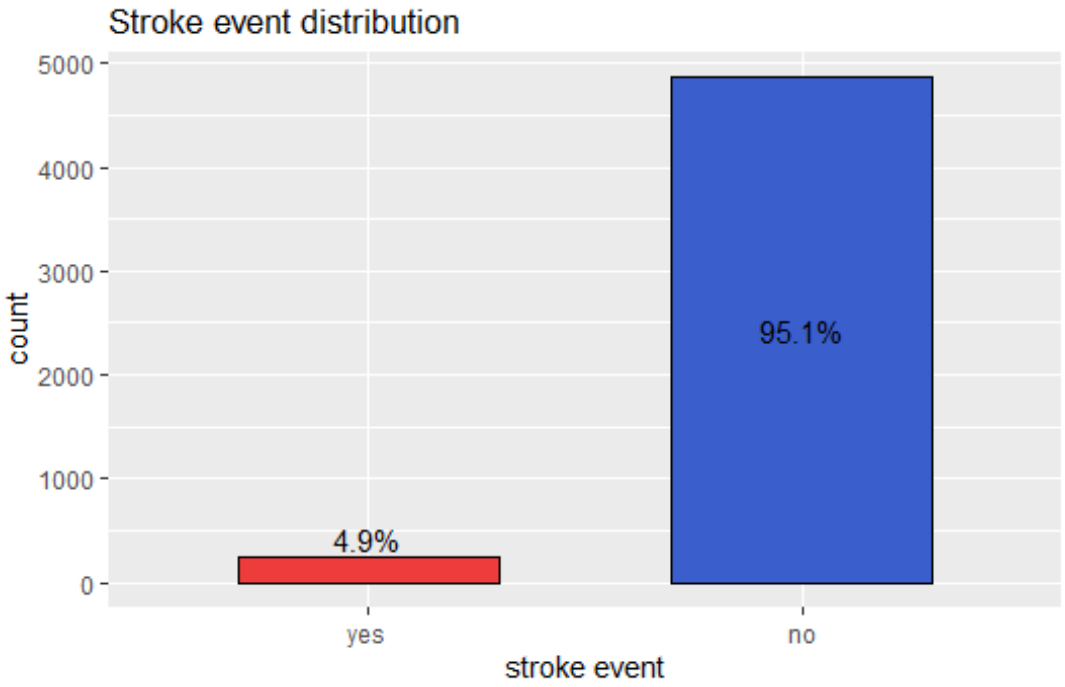
We see a bimodal average glucose distribution with a tall peak in the healthy range and a much shorter peak in the diabetic range.



We see a mostly normal distribution for body mass index with a fatter tail on the high end.

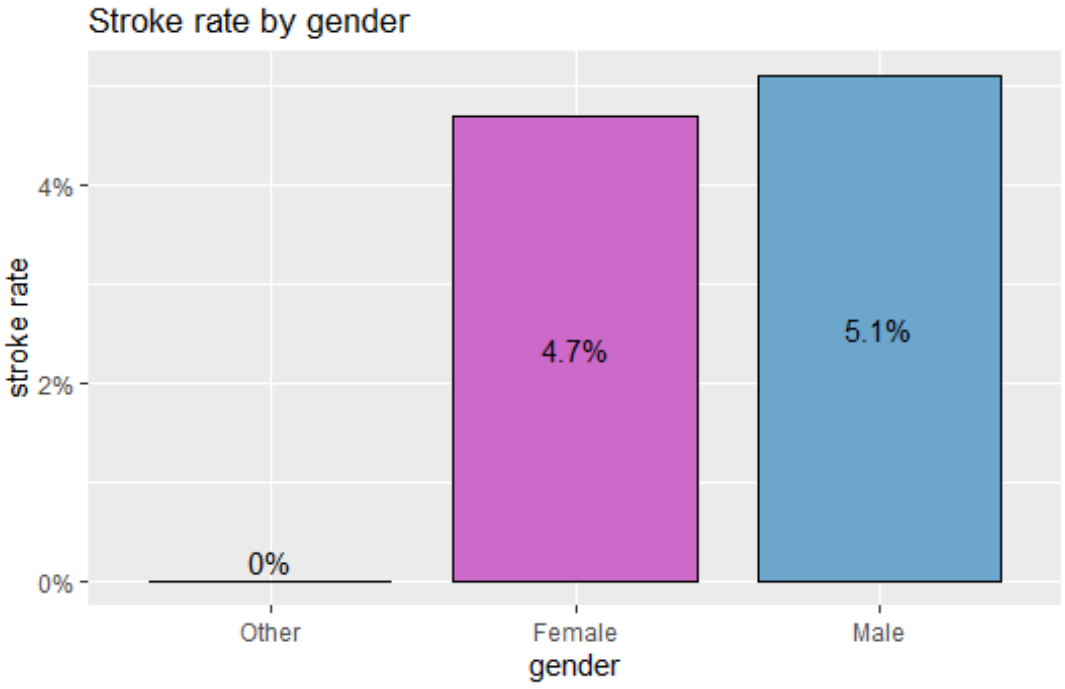


We see that over 1/3 of our cases have never smoked, and over 30% have unknown smoking status.

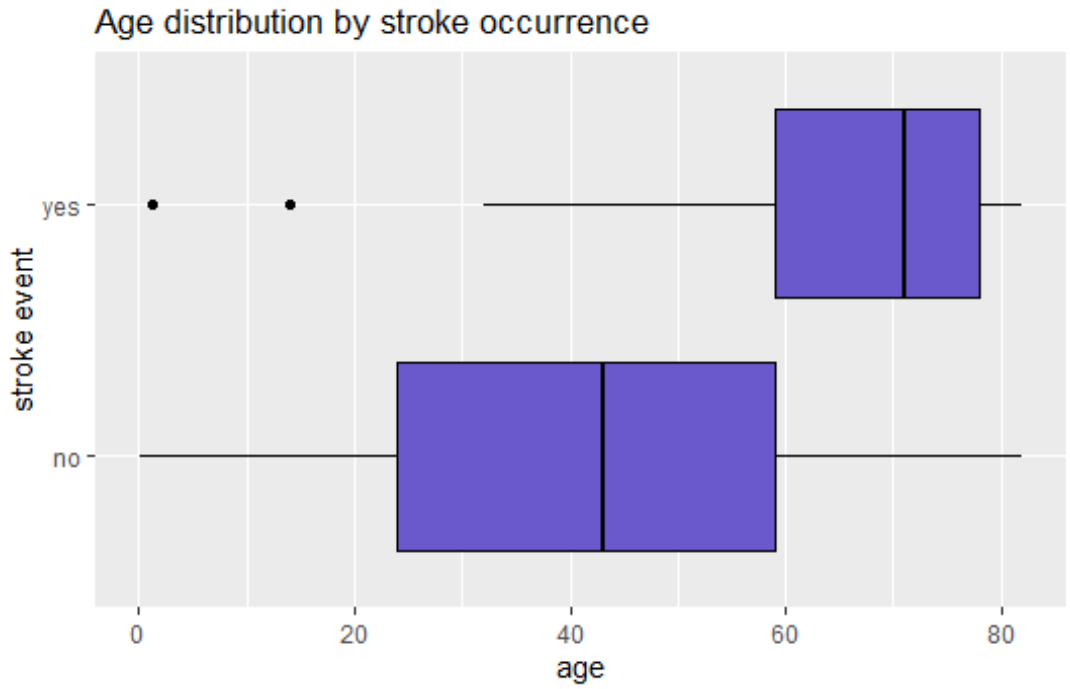


We see that just under 5% of our observations have had a stroke event.

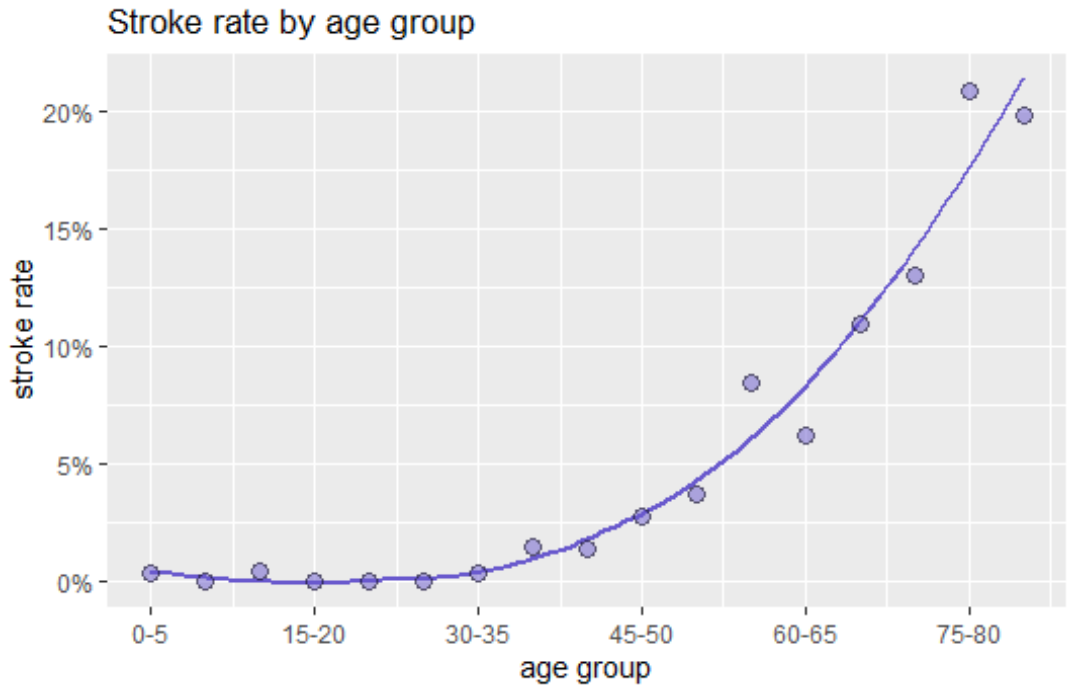
2.3 Examine correlations between variables and stroke events



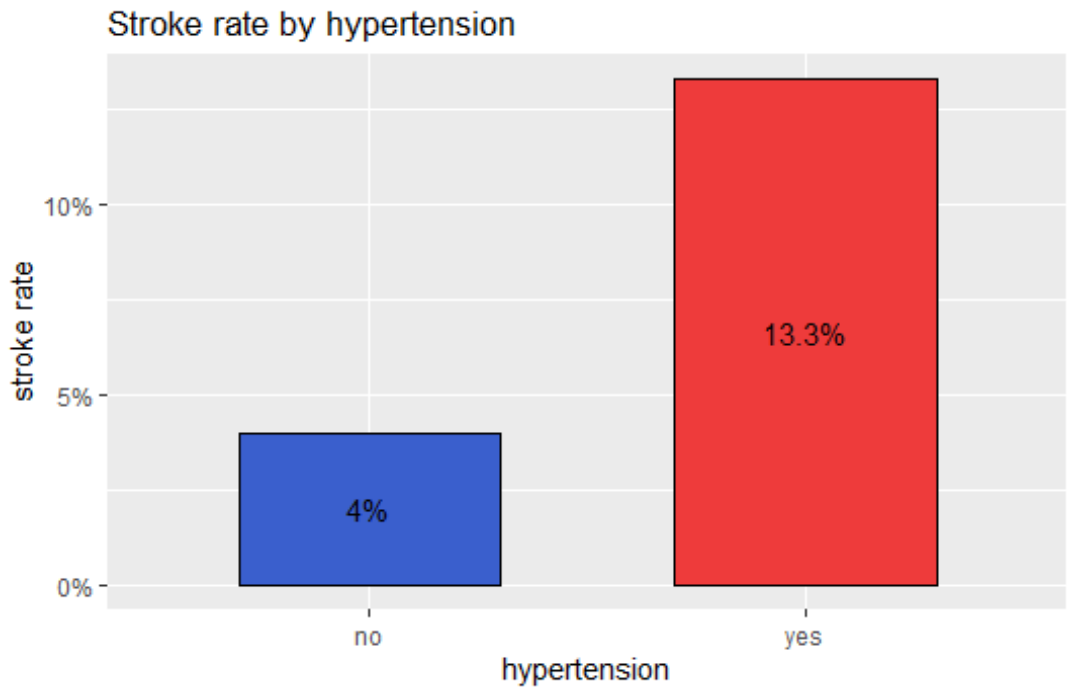
We notice the stroke rate for males is slightly above average while the stroke rate for females is slightly below average.



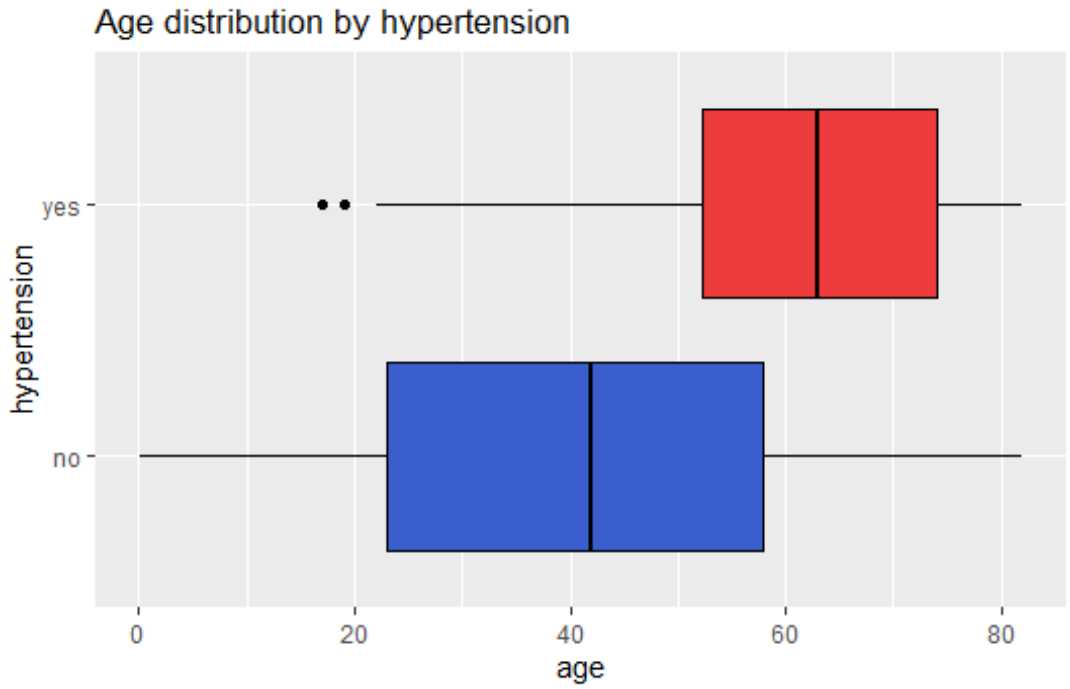
We see the age distribution for observations with stroke events is much higher than for those without, with virtually no overlap in the interquartile ranges. Note only 2 cases under age 30 had strokes.



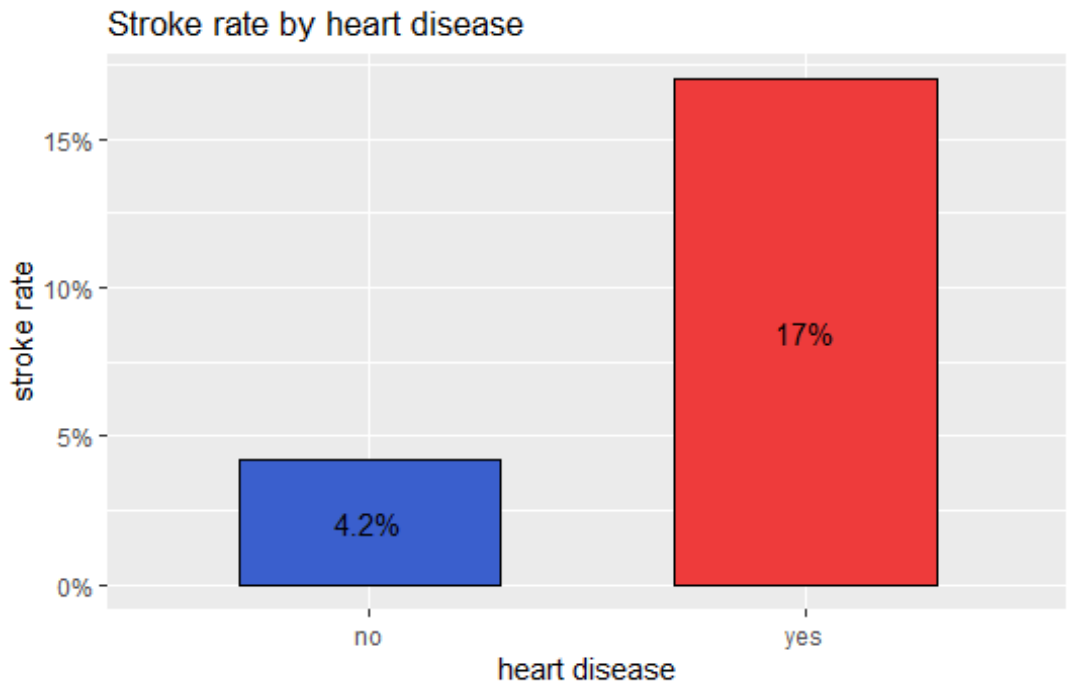
We see the stroke rate increases dramatically with age once people are into their 50's and 60's.



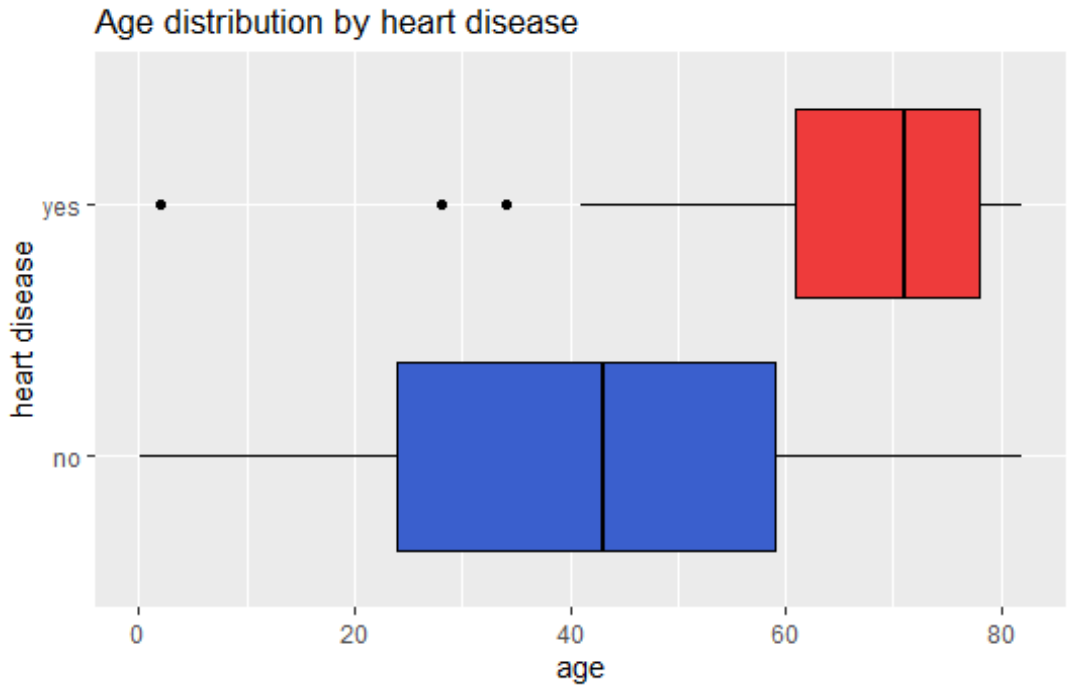
We see that people with high blood pressure have a much higher stroke rate than those without.



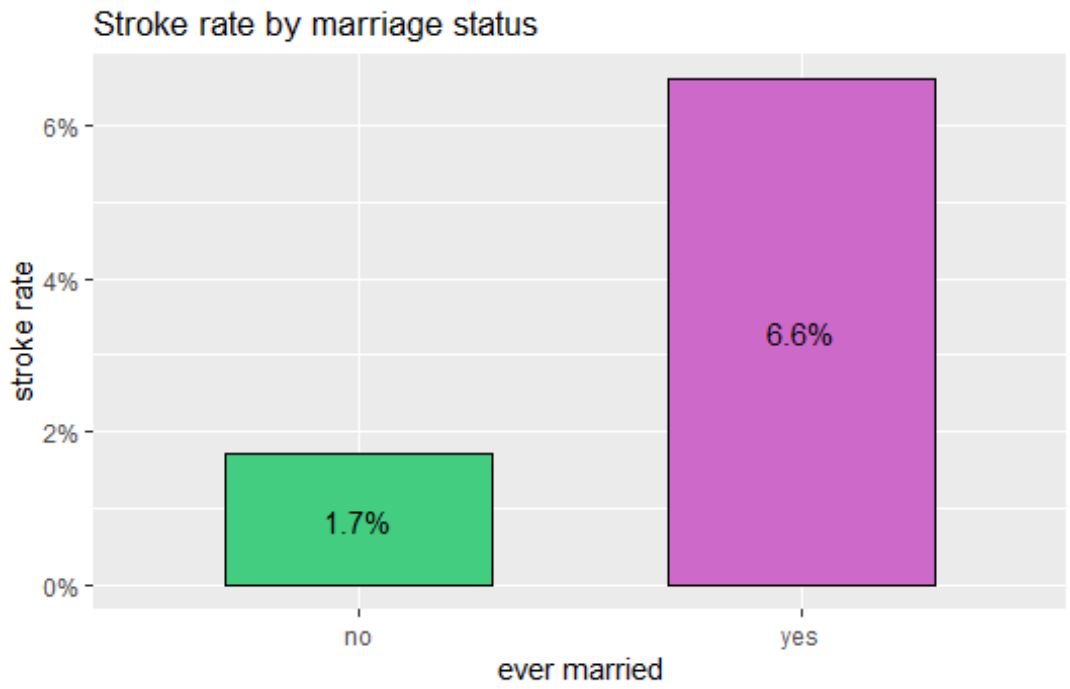
Note that when we plot age distribution by hypertension status, we see that those with hypertension tend to be older than those without. So at least some of the disparity can be attributed to correlation with age here.



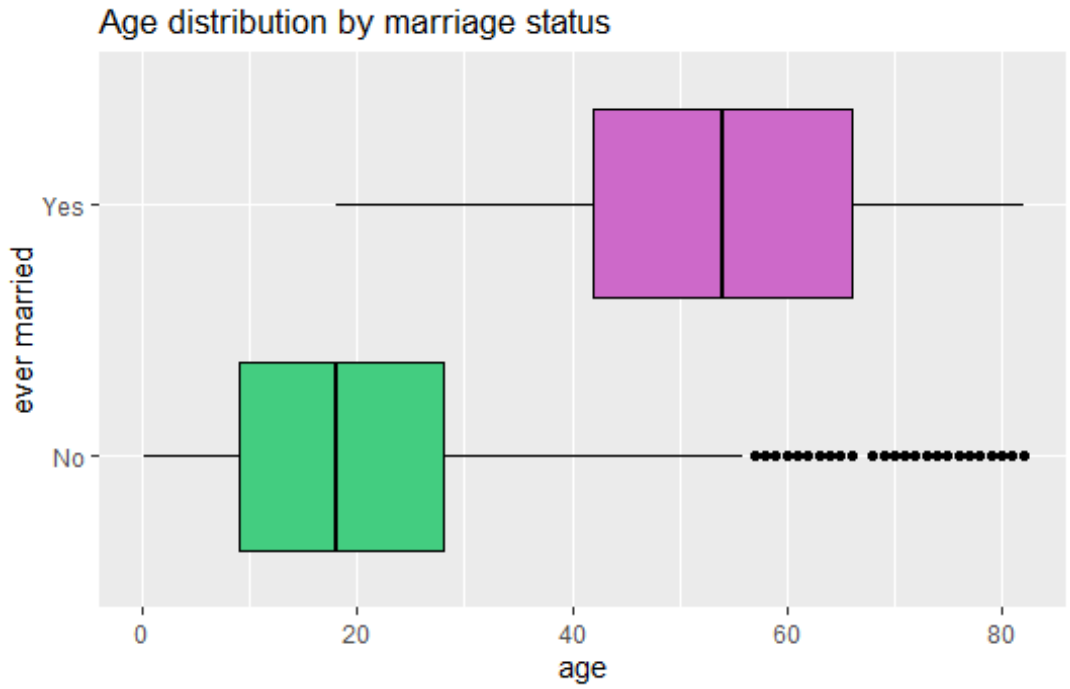
Those with heart disease also have a much higher stroke rate than those without.



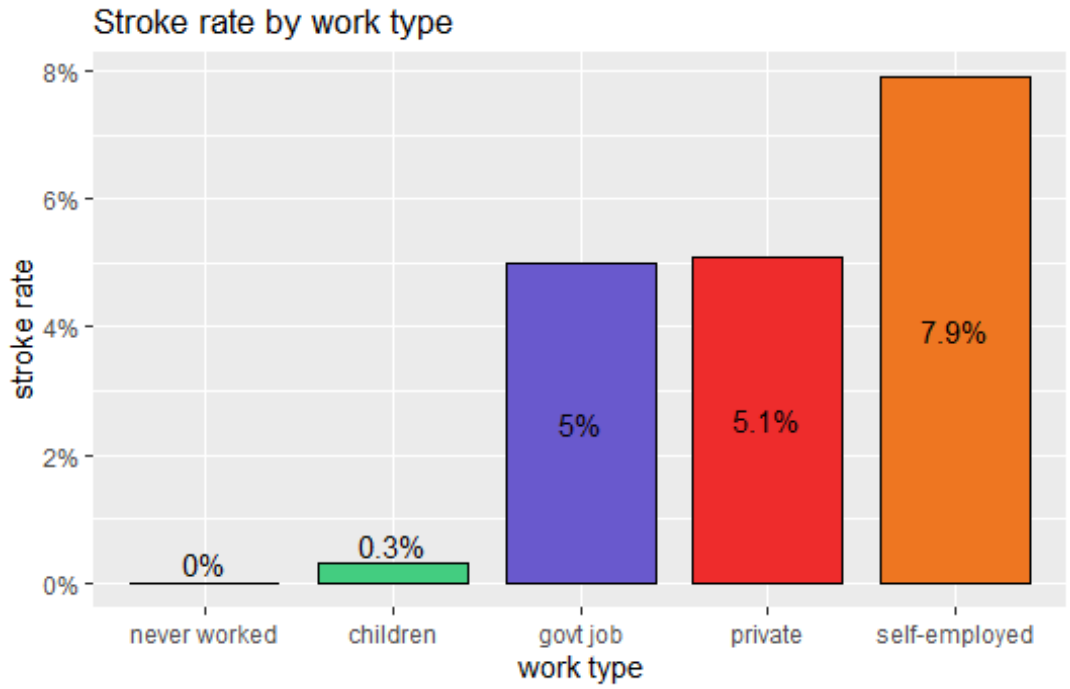
Again, when we plot age distribution by heart disease status, we see that those with heart disease tend to be much older than those without. This indicates that we can attribute some of the increase in rate to age.



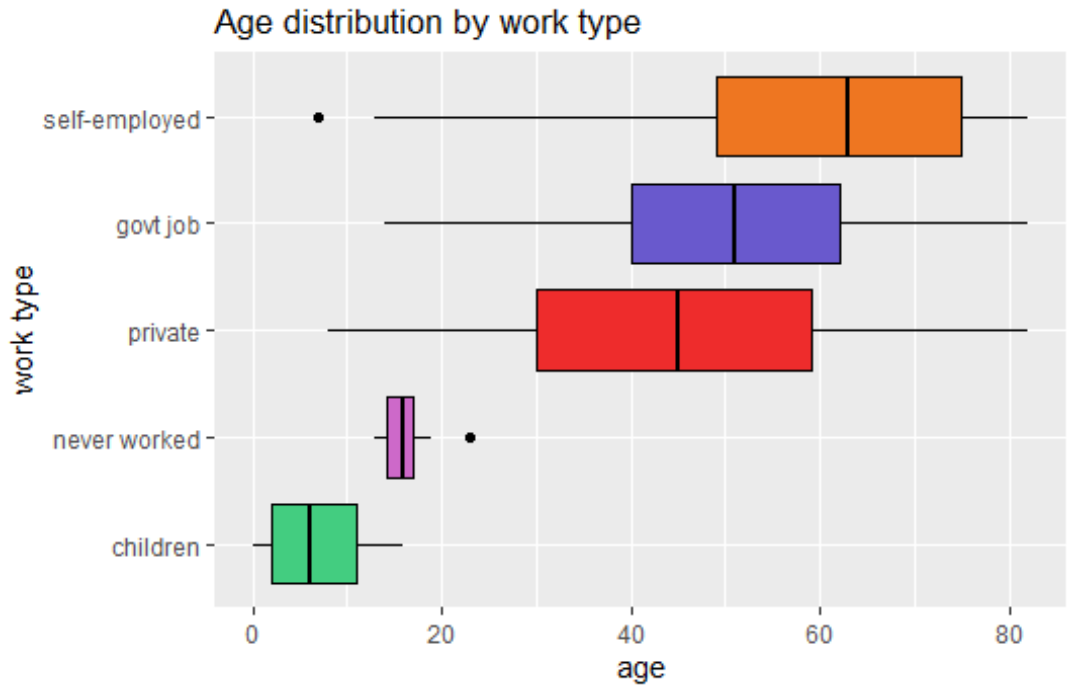
We see that people who have been married have a higher stroke rate than those who have not.



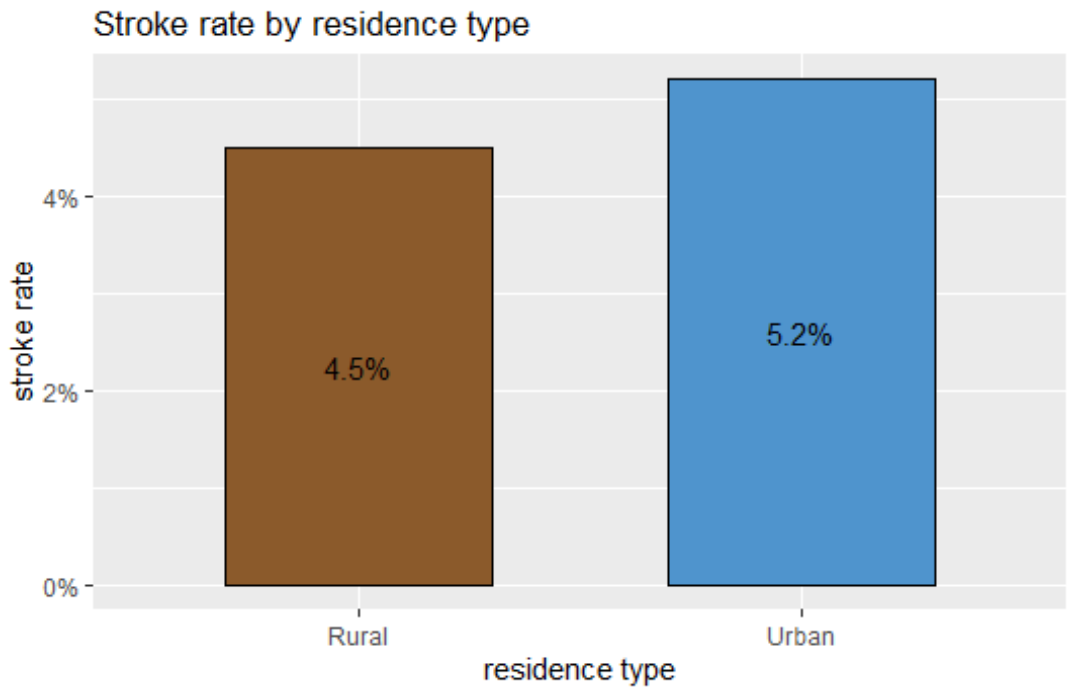
Again, looking at age distribution by marriage status, we see that people who have been married are generally much older than those who have not.



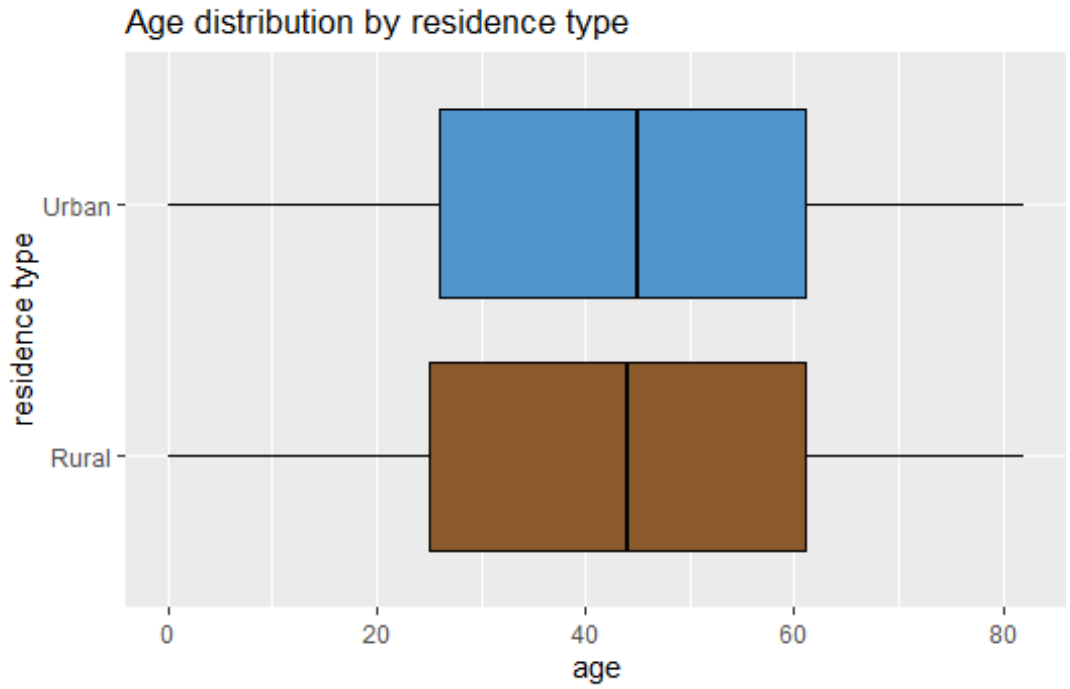
We observe that people who are self-employed have a higher stroke rate than those who are not, while children and those who have never worked have extremely low stroke rates.



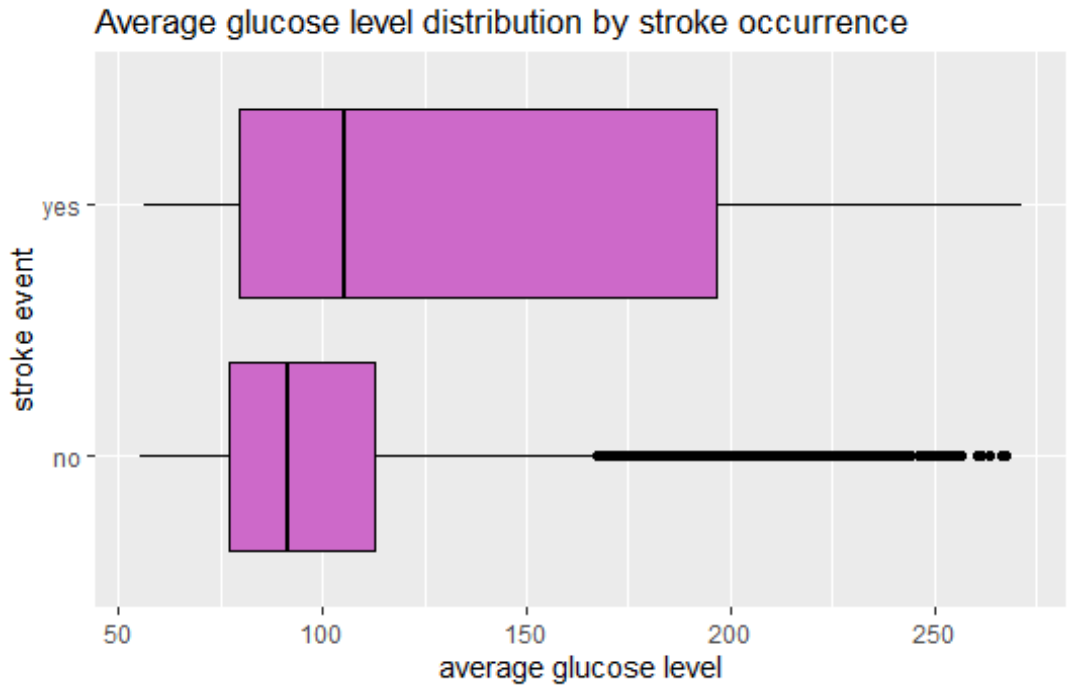
Again, we notice that these categories exhibit a respective correlation with age.



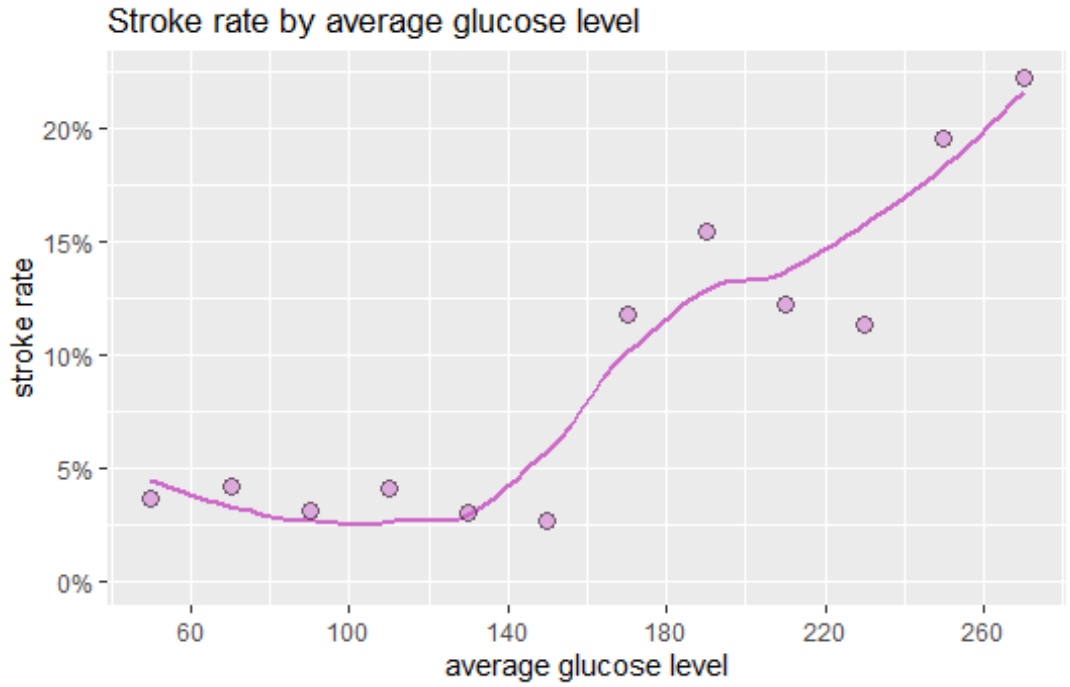
We see the stroke rate for urban dwellers is slightly above average while the stroke rate for rural dwellers is slightly below average.



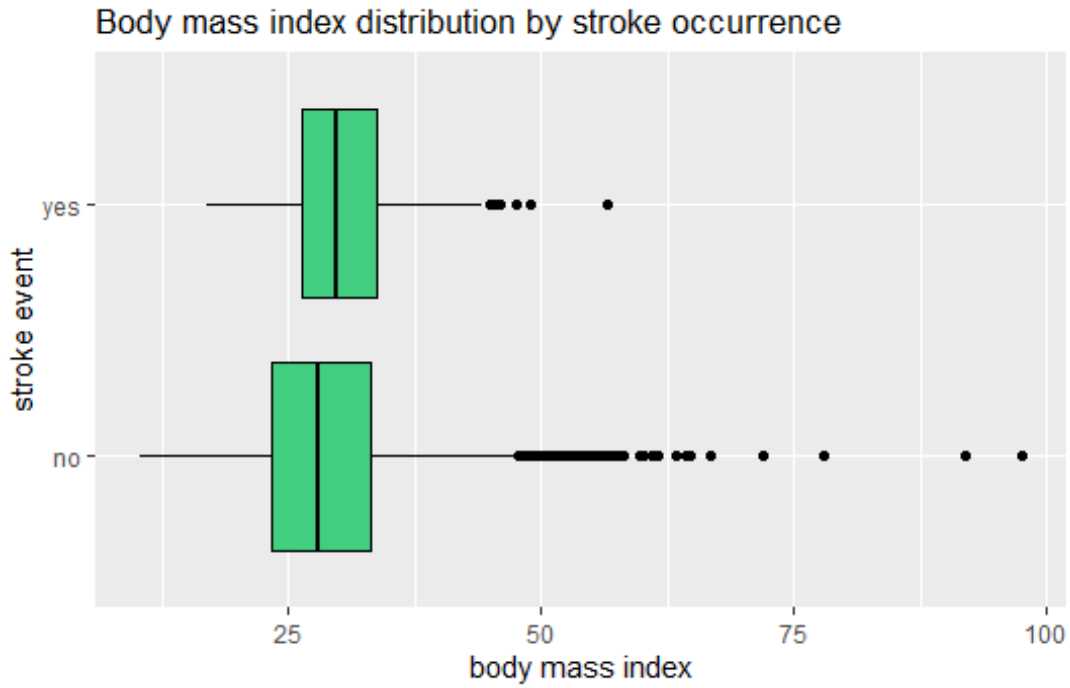
We see the age distributions for each residence type are nearly identical, indicating that the variation here cannot be attributed to a correlation with age.



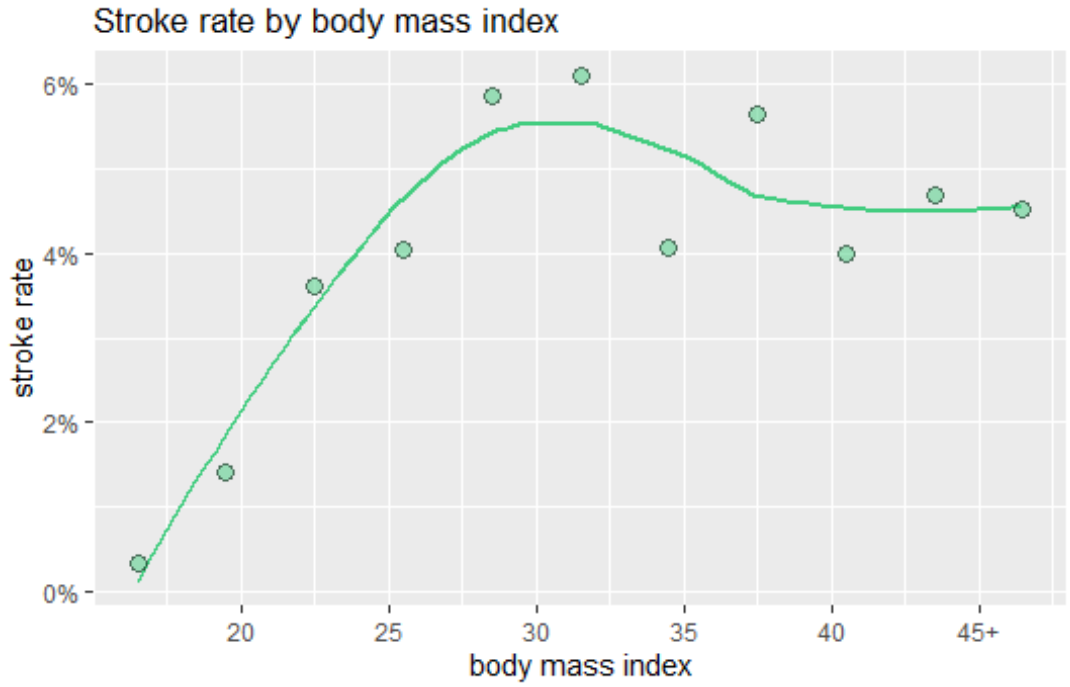
We see that people who have had strokes tend to have higher average glucose levels than those who have not had strokes.



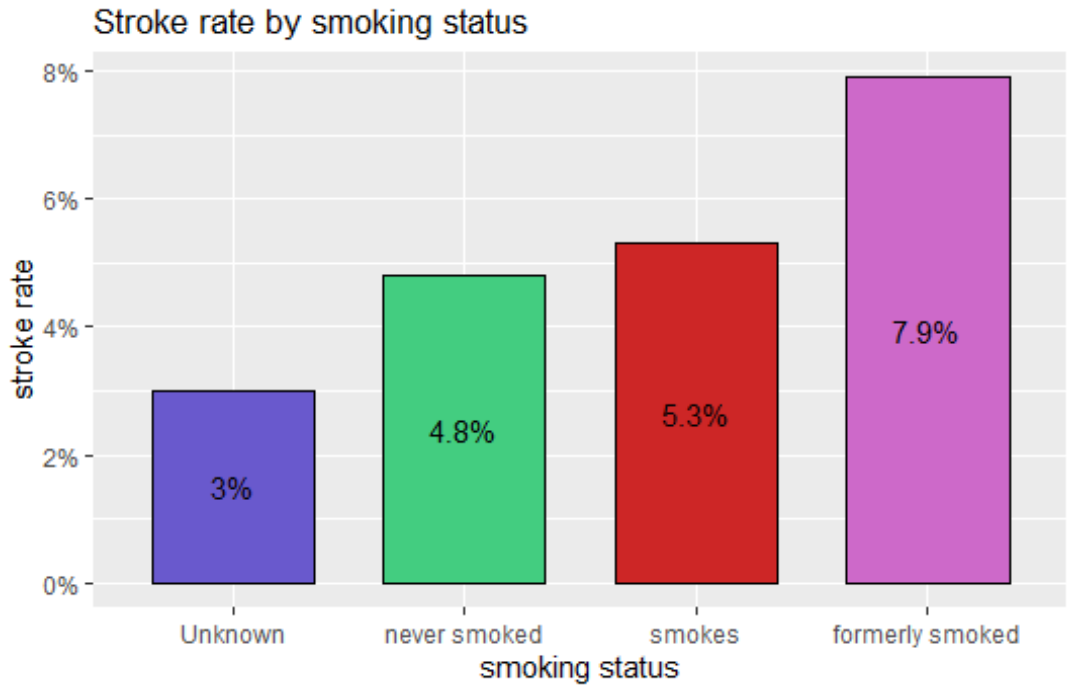
We see the stroke rate increases dramatically when average glucose levels surpass 160, indicating prediabetes. We note a weak positive correlation between age and average glucose levels (coefficient = 0.238), indicating that some of the increase can be attributed to age.



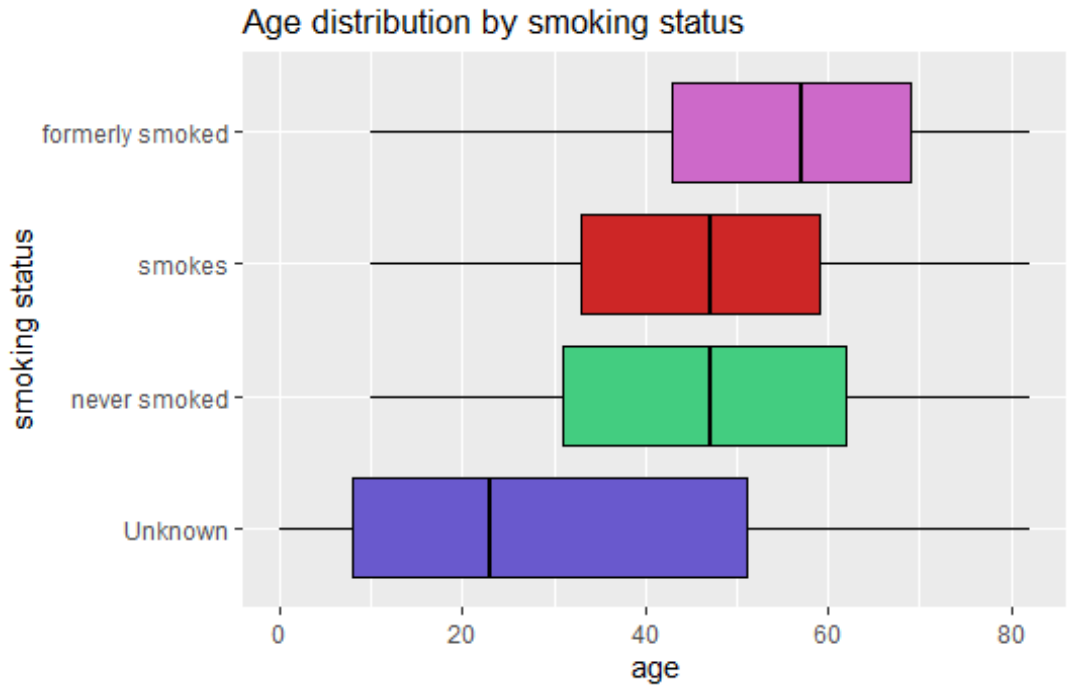
We see that people who have had strokes tend to have a slightly higher body mass index than those who have not had strokes.



We observe the stroke rate increases with BMI , topping out at 6% around a BMI of 30, and varying between 4% and 6% after that. We note a weak correlation between age and BMI (coefficient = 0.337), again indicating that some of the increase can be attributed to age. Keep in mind we are missing 201 data points in the BMI column, which may be distorting our analysis.



We see that people who used to smoke have the highest stroke rate, while those with unknown status have the lowest. People who smoke have an above average stroke rate, while people who never smoked have a below average stroke rate.



Once again, we observe some age correlations that can account for some of the variation here.

3 Model the data

3.1 Preprocess the data

Before we can begin building our models, we need to perform some preprocessing on our data. The first step in this regard is deciding what to do with our 201 missing data points in the BMI column. Exploring these observations, we find that 40 of them are cases with stroke events, representing over 16% of our total stroke events. We also note that the age in these observations tends to be higher than average. As these observations represent a significant portion of our data, we use the `bagImpute` method in the `preProcess()` function of the **caret** package, along with the **RANN** package, to guess these values based on the values of the other variables in each observation.

Next, we arbitrarily set the gender to "Male" for the case where gender is input as "Other," as this one observation will offer no statistical significance in our modeling. Then we convert all of our categorical variables to factors.

Here we create two different versions of our data, one for building a model ourselves, and one for building models with the **caret** package.

Version 1: We stratify our continuous variables (age, average glucose level, BMI) and consolidate any outlying tails into a single stratum. This reduces outlier distortion in our data by ensuring that each stratum has more than a handful of observations. We stratify age by every 5 years, average glucose level by every 20 points, and BMI by every 3 points. For the sake of ease, we change our stroke factor levels from "0" and "1" to "yes" and "no."

Version 2: We employ one hot encoding on our categorical variables. This produces an all numeric matrix with our categorical variables represented by 0's and 1's. Again, we change the stroke factor levels to "yes" and "no."

3.2 Partition the data

Our data is almost ready for training and building models. We use the `createDataPartition()` function from the **caret** package to split the data into training and test sets, using a 90/10 split. Ideally we would partition the training set further into smaller training and test sets, reserving the initial test set solely for final validation of our model. However, the data set is a bit small for this, and doing so would significantly reduce our model accuracy. We will instead simulate a final test by randomly sampling 10,000 observations from our full data set before making predictions with our model. We will replicate this process 5 times and average the results for our final evaluation.

3.3 Train the models

3.3.1 rf model

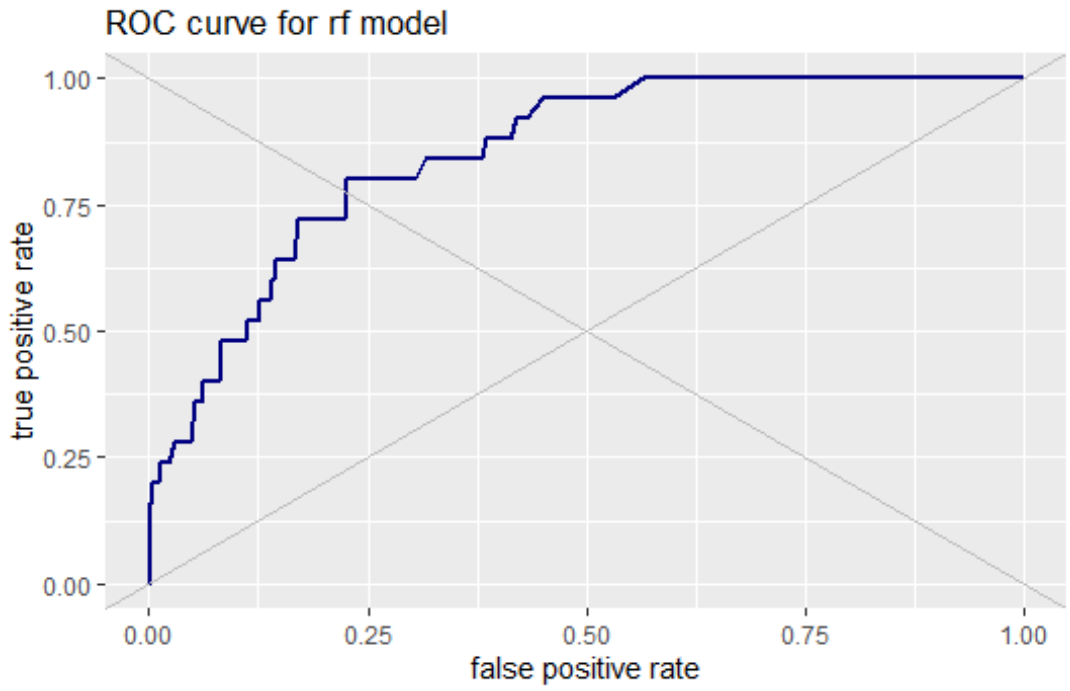
We use the `train()` function from the **caret** package with the `rf` method from the **randomForest** package to train a random forest model on our training set. We set up our train control function to perform 5 fold cross validation repeated 3 times. We use `twoClassSummary` as our summary function and set `classProbs = TRUE`. We use `metric = "ROC"` so that our model will maximize the area under the ROC curve and optimize independently of probability threshold, favoring a high balanced accuracy over raw accuracy. We can achieve over 95% accuracy by guessing "no" for all observations because of the class imbalance of our data, but this produces a balanced accuracy of only 50%.

We train our model and look at the 6 most important variables:

	Importance
avg_glucose_level	100.000000
bmi	81.690205
age	70.020054
Residence_type.Urban	10.524579
gender.Male	9.899484
smoking_status.never.smoked	9.082047

We make predictions on our test set using the `predict()` function from the **stats** package and find that our model predicted "no" for every observation. This is not helpful. We explore to see what has happened.

We use the `roc()` and `auc()` functions from the **pROC** package to extract data from our model for plotting the ROC curve and calculating the AUC, which we find to be 0.8489:



We see from the ROC curve that we can adjust the probability threshold of our model to obtain equal sensitivity and specificity close to 80%.

We use the `predict()` function again, this time using the argument `type = "probs"` to obtain from our model the predicted probability of a positive outcome, stroke = "yes", for each observation. Looking at the distribution of these probabilities for the cases where stroke = "yes", we see:

	min	Q1	median	mean	Q3	max
p | stroke = "yes"	0.004	0.074	0.138	0.18088	0.274	0.41

The distribution of probabilities for cases where stroke = "no":

	min	Q1	median	mean	Q3	max
p | stroke = "no"	0	0	0.008	0.0460821	0.057	0.428

We see that all of the probabilities are less than 0.5. This is why our model predicted "no" for all observations. Adjusting the probability threshold will allow us to greatly improve the performance of our model.

Comparing the distributions, we see that a probability threshold between 0.057 and 0.074 will produce sensitivity and specificity above 75%. Setting the threshold to 0.07, we obtain:

model	balanced_accuracy	sensitivity	specificity
rf_07	0.7870637	0.8	0.7741273

3.3.2 ranger model with weights

We saw that once we adjusted the probability threshold of our `rf` model, it performed relatively well. For our next model, we will again use a random forest, this time introducing class weights into the training function. This will impose a heavier cost for false negative predictions and improve model performance with a probability threshold of 0.5.

To determine the class weights, we divide 1 by the number of occurrences of each class in the training set, and divide that by 2. This ensures that the ratio of the weights is equal to the ratio of the prevalence of each class, and that the weights all add to 1.

$$w_{yes} = \frac{1}{2N_{yes}}$$

$$w_{no} = \frac{1}{2N_{no}}$$

We assign the weights to each observation and we are ready to set up and train our next model.

We use the `ranger` method from the **ranger** package for our model. After some preliminary testing, we set up the tune grid and use the same train control function from our first model. We use the argument `importance = "permutation"` in the `train()` function so that a variable's importance will be determined by its ability to improve prediction accuracy, rather than how often it is used to split a node. This will prevent variable importance from being biased towards the continuous variables due to the larger number of split points they contain. We continue to use the ROC curve as the metric for optimization.

We train our model and look at the 6 most important variables:

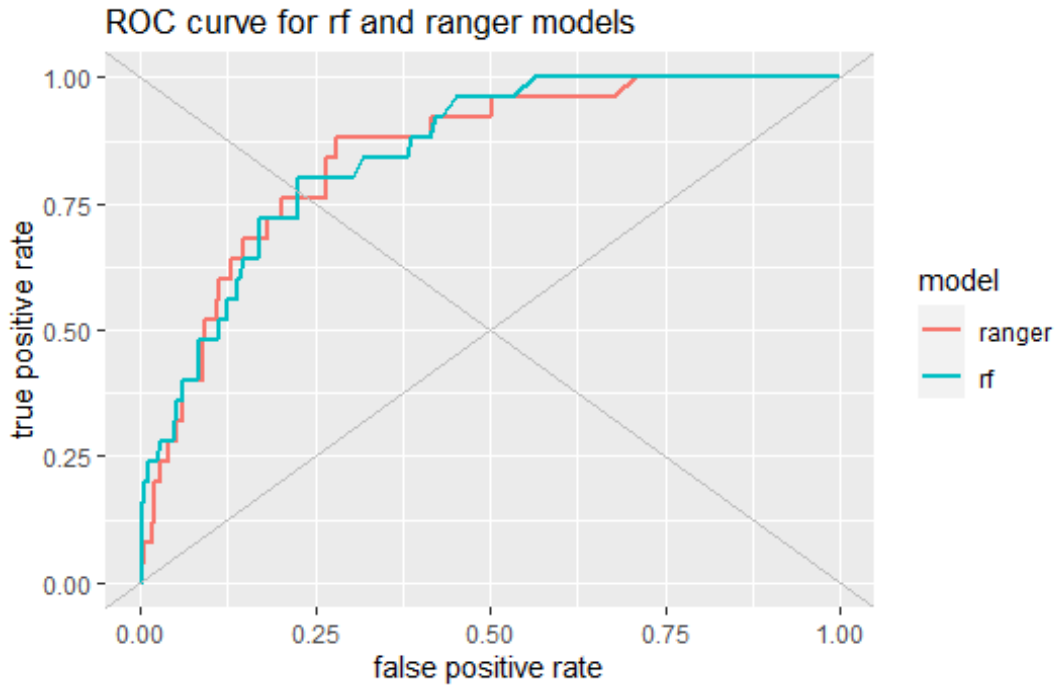
	Importance
ever_married.Yes	100.00000
work_type.Self.employed	88.13214
hypertension.1	79.59358
smoking_status.never.smoked	79.04657
gender.Male	77.03248
Residence_type.Urban	74.78742

We notice that our continuous variables, which were the 3 most important in our last model, are no longer in the top 6.

We make predictions on the test set and find a slight improvement from our first model using the default probability threshold of 0.5:

model	balanced_accuracy	sensitivity	specificity
ranger	0.5707598	0.16	0.9815195

We plot the ROC curve alongside the first model, and calculate an AUC of 0.8448:



We see the 2 models criss-cross each other in performance. The ranger model falls behind right where sensitivity and specificity meet, right where we want our model to perform well.

We use the `predict()` function again to obtain probabilities instead of predictions so we can adjust the threshold, and we observe the following distribution for "yes" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "yes"	0.002	0.1618969	0.277119	0.2921362	0.3914503	0.6857945

We observe the following distribution for "no" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "no"	0	0.0001782	0.0214826	0.0859074	0.128611	0.6924349

Setting the probability threshold to 0.16, we obtain:

model	balanced_accuracy	sensitivity	specificity
ranger_16	0.7763039	0.76	0.7926078

Setting the probability threshold to 0.12, we obtain:

model	balanced_accuracy	sensitivity	specificity
ranger_12	0.7665298	0.8	0.7330595

3.3.3 rpart model with weights

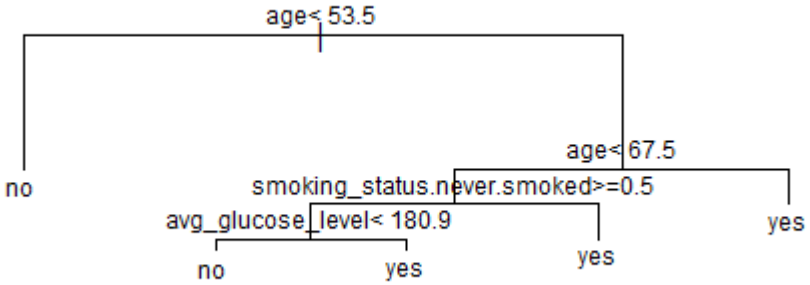
For the next model, we use a single classification tree using the `rpart` method from the **rpart** package. This allows us to plot a decision tree and see what decisions are driving the classification.

This is a much simpler training process, so we increase the number of folds in the cross validation from 5 to 10, and increase the number of repeats from 3 to 5. We again use class weights and use the ROC curve for the model metric. We explore a bit to set up our tune grid, and we train our model.

Observing the 6 most important variables, we see:

	Importance
age	100.000000
avg_glucose_level	33.886949
ever_married.Yes	25.223585
hypertension.1	20.238997
heart_disease.1	17.631490
bmi	5.216388

We plot the decision tree for the final model:

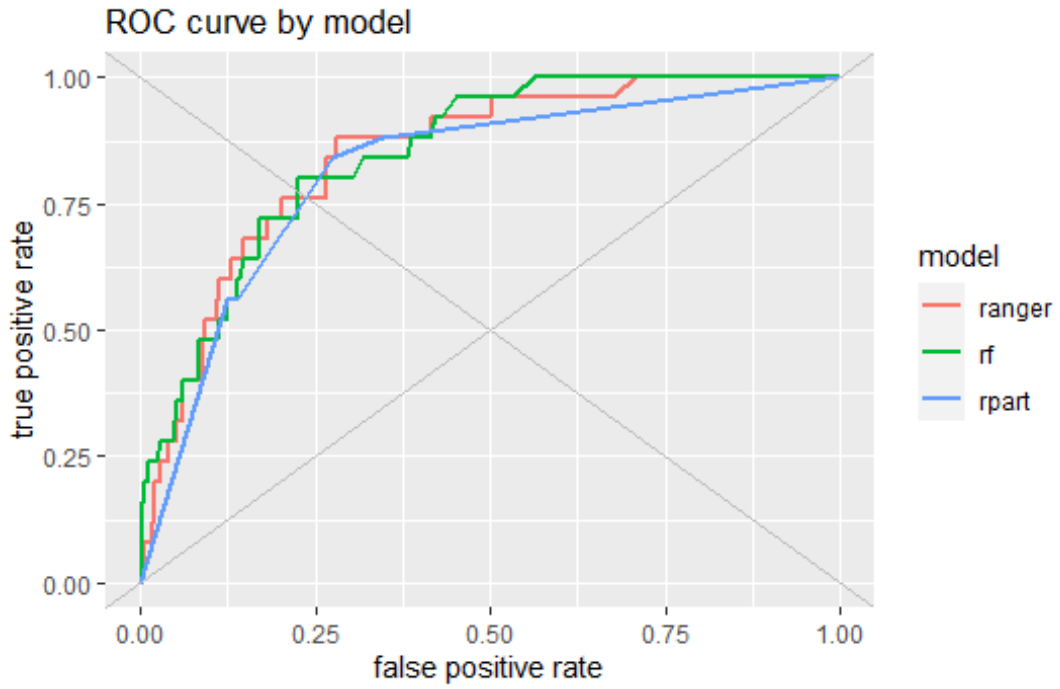


We see that age, never smoking, and average glucose level are the only factors in the final model. Anyone under 53.5 years of age is predicted "no". Anyone under age 67.5 who never smoked and has average glucose level below 180.9 is also predicted "no". Everyone else is predicted "yes".

We make predictions on the test set and find that our model performs well with the default probability threshold of 0.5:

model	balanced_accuracy	sensitivity	specificity
rpart	0.7834497	0.84	0.7268994

We plot the ROC curve alongside our previous models, and calculate an AUC of 0.8145:



We can see from the ROC curve that we cannot do any better with this model by adjusting the probability threshold. We can verify this by inspecting the probability distribution for "yes" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "yes"	0.1588581	0.6600096	0.8029311	0.6627204	0.8029311	0.8029311

Observing the probability distribution for "no" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "no"	0.1588581	0.1588581	0.1588581	0.3187604	0.6600096	0.8029311

If we table all of the probabilities, we see there are no probabilities between 0.24 and 0.66:

probs_rpart	frequency
0.158858139028113	321
0.230331753554503	37
0.66000958619588	72
0.668875522479356	8
0.802931122164537	74

Adjusting the threshold past either one of these points would drastically reduce our model's performance.

3.3.4 gbm model with weights

For the next model, we use stochastic gradient boosting with the `gbm` method from the **gbm** package. We use the same train control function from our last model. We continue to use class weights and use the ROC

curve as our metric. We use the `nTrain` argument to set the model to train on 80% of the data while using the other 20% to compute out-of-sample estimates of the loss function. We explore a bit to set up our tune grid, and we train our model.

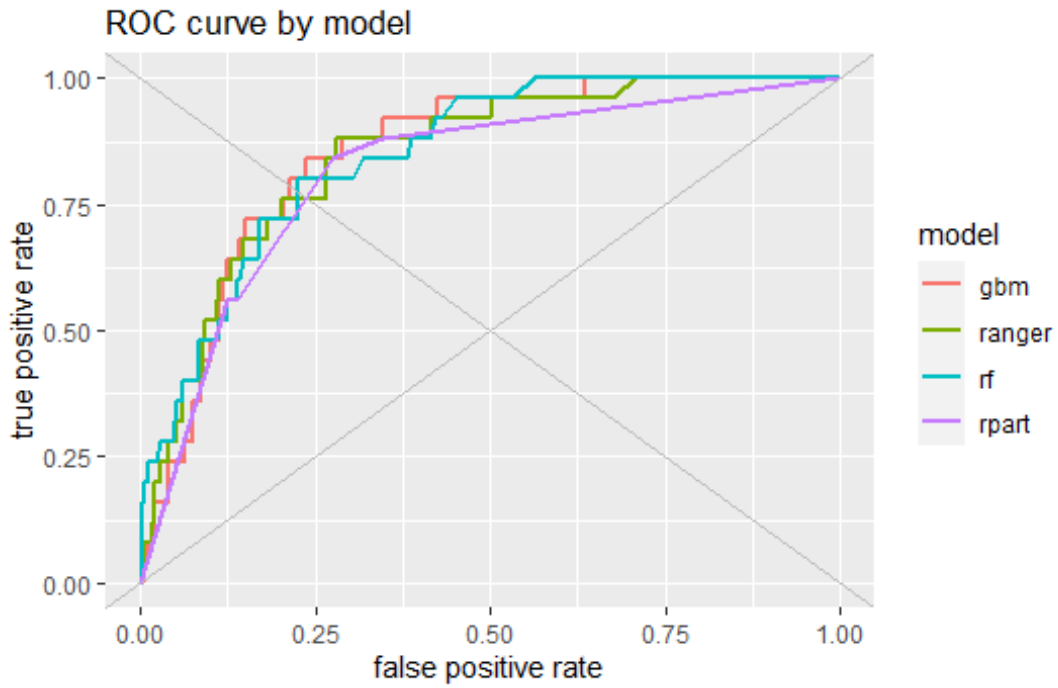
Observing the 6 most important variables, we see:

	Importance
age	100.0000000
bmi	6.4206889
avg_glucose_level	5.9836741
hypertension.1	0.7266712
smoking_status.never.smoked	0.5583898
work_type.Self.employed	0.2865357

We make predictions on the test set and obtain the following results:

model	balanced_accuracy	sensitivity	specificity
gbm	0.7751951	0.92	0.6303901

We plot the ROC curve alongside our previous models, and calculate an AUC of 0.8508:



We see from the ROC curve that the `gbm` model outperforms our previous 3 models right where we want it to. The 2 steps above where sensitivity and specificity meet tell us that we can achieve both 80% and 84% sensitivity while keeping the specificity above 75%.

We use the `predict()` function again to obtain probabilities instead of predictions so we can adjust the threshold, and we observe the following distribution for "yes" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "yes"	0.1717739	0.6428948	0.7026554	0.6706299	0.75294	0.7809987

We observe the following distribution for "no" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "no"	0.158578	0.1625443	0.3056777	0.3836658	0.6181581	0.7810848

Setting the probability threshold to 0.63, we obtain:

model	balanced_accuracy	sensitivity	specificity
gbm_63	0.7839836	0.8	0.7679671

Setting the probability threshold to 0.62, we obtain:

model	balanced_accuracy	sensitivity	specificity
gbm_62	0.7967967	0.84	0.7535934

3.3.5 nnet model with weights

For the next model, we use the `nnet` method from the **nnet** package to build a neural network. This method is a bit computationally intensive, so we reduce our cross validation folds back down to 5 and reduce the number of repeats back down to 3. We continue to use class weights and use the ROC curve as our metric. We use the default tune grid and train the model.

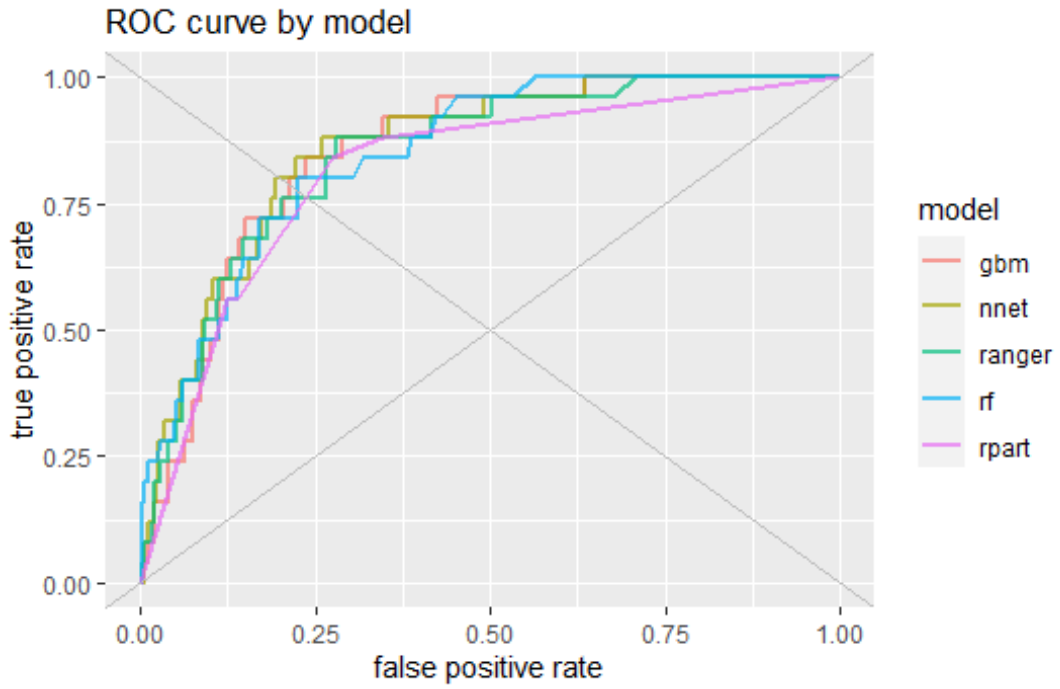
Observing the 6 most important variables, we see:

	Importance
work_type.Self.employed	100.00000
work_type.Govt_job	96.81965
hypertension.1	86.67313
age	67.73404
work_type.Private	56.78913
bmi	46.99077

We make predictions on the test set and obtain the following results:

model	balanced_accuracy	sensitivity	specificity
nnet	0.7952361	0.88	0.7104723

We plot the ROC curve alongside our previous models, and calculate an AUC of 0.8576:



We see from the ROC curve that the `nnet` model outperforms our previous 4 models right where we want it to. The 2 steps above where sensitivity and specificity meet tell us that we can achieve 84% sensitivity while keeping the specificity above 75%, and achieve 88% sensitivity while keeping the specificity just below 75%.

We use the `predict()` function again to obtain probabilities instead of predictions so we can adjust the threshold, and we observe the following distribution for "yes" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "yes"	0.054866	0.6375171	0.7561446	0.6807712	0.8072145	0.8496775

We observe the following distribution for "no" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "no"	0.0156221	0.0275296	0.1998112	0.3018179	0.5649308	0.8543277

Setting the probability threshold to 0.59, we obtain:

model	balanced_accuracy	sensitivity	specificity
nnet_59	0.809117	0.84	0.7782341

Setting the probability threshold to 0.54, we obtain:

model	balanced_accuracy	sensitivity	specificity
nnet_54	0.8106366	0.88	0.7412731

3.3.6 multinom model with weights

For the next model, we use the `multinom` method from the **nnet** package to implement penalized multinomial regression. This method isn't as computationally intensive, so we increase our cross validation folds back up to 10 and increase the number of repeats back up to 5. We continue to use class weights and use the ROC curve as our metric. We use the default tune grid and train the model.

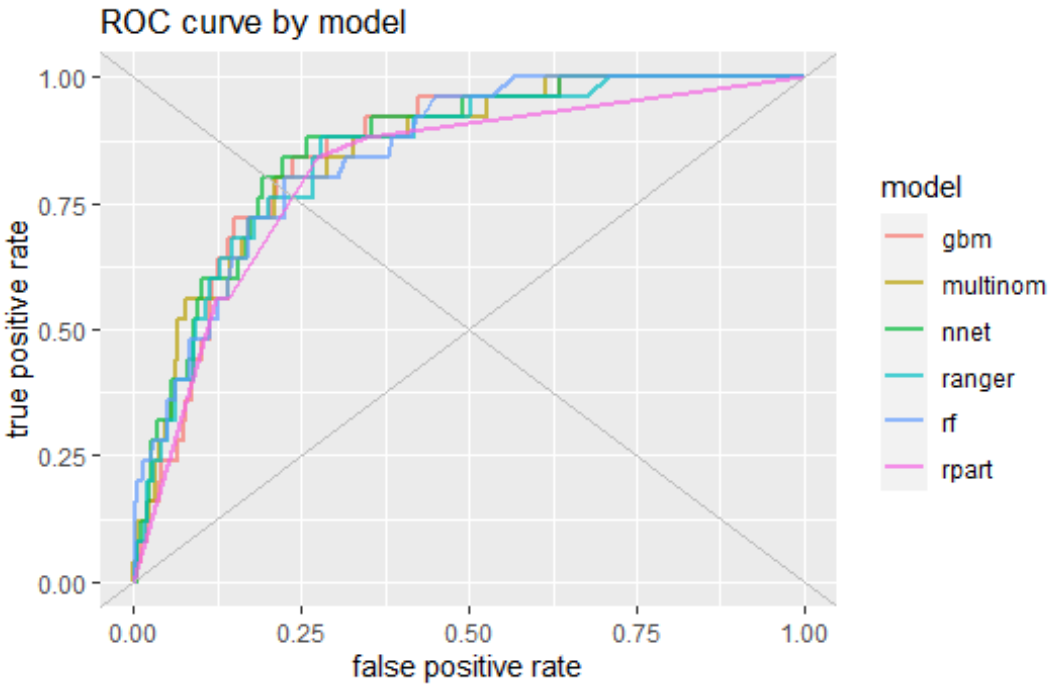
Observing the 6 most important variables, we see:

	Importance
work_type.Self.employed	100.00000
work_type.Govt_job	94.82870
work_type.Private	81.24281
hypertension.1	36.56733
work_type.Never_worked	25.25288
smoking_status.never.smoked	22.16010

We make predictions on the test set and obtain the following results:

model	balanced_accuracy	sensitivity	specificity
multinom	0.7675565	0.8	0.7351129

We plot the ROC curve alongside our previous models, and calculate an AUC of 0.8490:



We see from the ROC curve that the `multinom` model performs relatively well, but not quite as well as the `gbm` and `nnet` models. The step right where sensitivity and specificity meet tells us that we can achieve both sensitivity and specificity around 80%.

We use the `predict()` function again to obtain probabilities instead of predictions so we can adjust the threshold, and we observe the following distribution for "yes" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "yes"	0.1151354	0.5625081	0.77139	0.6708046	0.8204472	0.9335351

We observe the following distribution for "no" cases:

	min	Q1	median	mean	Q3	max
p | stroke = "no"	0.0147428	0.065347	0.2219902	0.3051128	0.5131708	0.9290975

Setting the probability threshold to 0.56, we obtain:

model	balanced_accuracy	sensitivity	specificity
multinom_56	0.7942505	0.8	0.788501

3.3.7 Build a risk assessment model

For our final model, we build a risk assessment system using the version of our data in which we stratified the 3 continuous variables. This allows us to group the data by each variable and calculate the various stroke rates for each value of that variable. For each group, we take the stroke rate for the group, subtract the risk factors we have already calculated for each observation, average the results, and subtract the average stroke rate for the entire training set. This produces the risk factor value for that particular group. We repeat this process until we have calculated risk factors for all values of all variables.

Once we have all the values, we can assign a total risk value to each observation in our data by adding all the respective risk factors for that observation's entries to μ, the total average stroke rate of the training set. We examine the distributions of the risk values with respect to stroke events, and determine an appropriate threshold for stroke prediction.

We walk through the first few steps to see this more clearly.

First we calculate μ, and find it to be 0.0487.

Next, we calculate the gender risk factor, r_g, for each gender:

$$r_g = \frac{1}{N}\sum_{i=1}^{N} y_{g,i} - \mu$$

N is the number of observations for gender g. $y_{g,i}$ is equal to 1 if the ith observation for gender g has had a stroke, and equal to 0 if not.

Next, we calculate the age risk factor, r_a, for each age stratum:

$$r_a = \frac{1}{N}\sum_{i=1}^{N}(\frac{1}{N}\sum_{i=1}^{N} y_{a,i} - r_{g,i}) - \mu$$

N is the number of observations for age stratum a. $y_{a,i}$ is equal to 1 if the ith observation for age stratum a has had a stroke, and equal to 0 if not. $r_{g,i}$ is the risk factor associated with the gender g of the ith observation for age stratum a

We calculate the hypertension risk factor, r_{ht}:

$$r_{ht} = \frac{1}{N}\sum_{i=1}^{N}(\frac{1}{N}\sum_{i=1}^{N} y_{ht,i} - r_{g,i} - r_{a,i}) - \mu$$

We repeat this process for the remaining predictors, and we obtain risk factors for each value of each variable.

We can now calculate the total risk factor for any observation by adding μ to the risk factors associated with that observation's gender, age stratum, hypertension status, heart disease status, marriage status, work type, residence type, average glucose level stratum, BMI stratum, and smoking status:

$$r_{total} = \mu + r_g + r_a + r_{ht} + r_{hd} + r_m + r_w + r_r + r_{ag} + r_b + r_s$$

We perform this first on the training set and examine the distribution of values for cases where stroke = "yes":

	min	Q1	median	mean	Q3	max
r | stroke = "yes"	-0.0160338	0.0903728	0.1507879	0.1508836	0.2132771	0.3585435

We observe the distribution for cases where stroke = "no":

	min	Q1	median	mean	Q3	max
r | stroke = "no"	-0.0516655	-0.0020705	0.0147211	0.0434847	0.0706298	0.3341246

We examine the lowest total risk factor values greater than 0.071 for "yes" cases:

values
0.0728096
0.0755615
0.0785302
0.0788291
0.0802367
0.0825614

We make predictions on the training set with a threshold of 0.072 and observe the following:

model	balanced_accuracy	sensitivity	specificity
risk_train_072	0.7850254	0.8169643	0.7530864

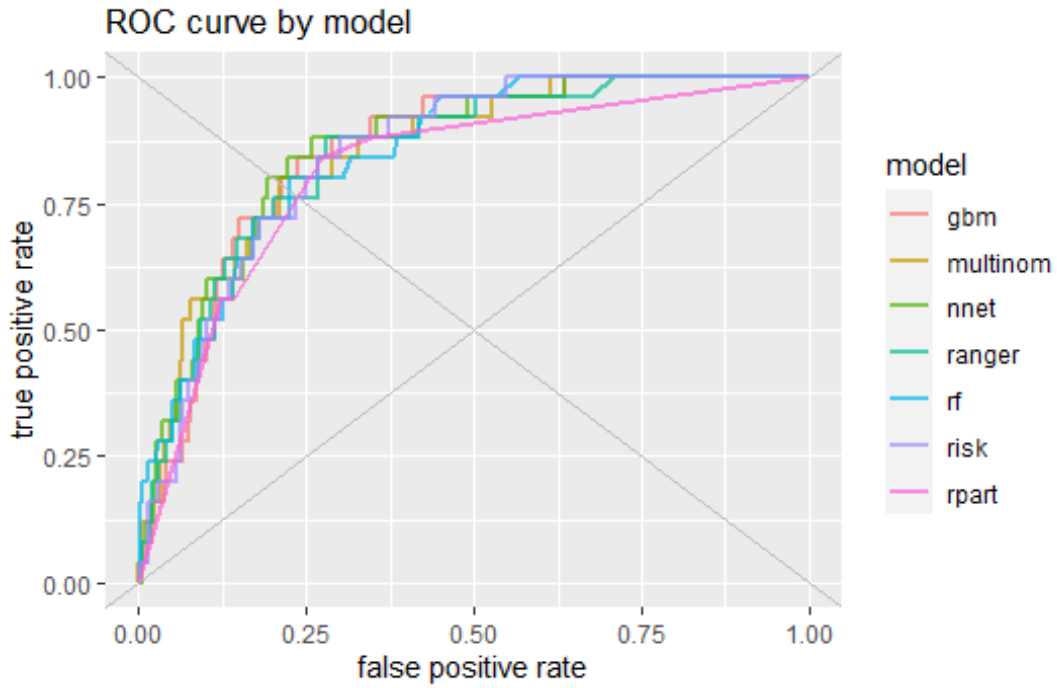
The model performed well on the training set. We make predictions on the test set with a threshold of 0.072 and observe the following:

model	balanced_accuracy	sensitivity	specificity
risk_072	0.7716632	0.8	0.7433265

For this model we need to create the data for the ROC curve and calculate the AUC manually. To do this, we find the maximum and minimum values for the total risk factors on the test set, round them to 4 digits,

add 0.0001 to the max, and subtract 0.0001 from the min. We then make a sequence of values between the max and min, stepping down 0.0001 each time. We use these values to calculate the false positive and true positive rates generated by setting them as the threshold for our predictions on the test set.

Starting with the max value, the model predicts "no" for all observations, producing true positive and false positive rates of 0. Ending with the min value, the model predicts "yes" for all observations, producing true positive and false positive rates of 1. The points in between plot out the ROC curve for the model:



To calculate the AUC, we calculate the area of the trapezoids between all points of the curve and take their sum. The widths of these trapezoids are the differences between consecutive false positive rate values, and the average heights are the averages of consecutive true positive rate values. We multiply width by average height, take their sum, and we calculate and AUC of 0.8464.

3.4 Determine the best model

Sorting the AUC results for our different models, we find the **nnet** model to have the highest AUC:

model	AUC
rpart	0.8145
ranger	0.8448
risk	0.8464
rf	0.8489
multinom	0.8490
gbm	0.8508
nnet	0.8576

Sorting the accuracy summaries for our different models by balanced accuracy, we find the **nnet_54** model performs the best overall:

model	balanced_accuracy	sensitivity	specificity
rf	0.5000	0.00	1.0000
ranger	0.5708	0.16	0.9815
ranger_12	0.7665	0.80	0.7331
multinom	0.7676	0.80	0.7351
risk_072	0.7717	0.80	0.7433
gbm	0.7752	0.92	0.6304
ranger_16	0.7763	0.76	0.7926
rpart	0.7834	0.84	0.7269
gbm_63	0.7840	0.80	0.7680
rf_07	0.7871	0.80	0.7741
multinom_56	0.7943	0.80	0.7885
nnet	0.7952	0.88	0.7105
gbm_62	0.7968	0.84	0.7536
nnet_59	0.8091	0.84	0.7782
nnet_54	0.8106	0.88	0.7413

3.5 Compare probability distributions between test and train sets

As we do not have any fresh data to use for a final validation test of our model, we simulate the test by randomly selecting observations from the full data set with replacement, and making predictions on them. Before we proceed, we compare the probability distributions for the train and test sets, separated by stroke event, to make sure our model is not overly fitted to the train set. We observe the following:

	min	Q1	median	mean	Q3	max
p_test | stroke = "yes" |	0.0548660	0.6375171	0.7561446	0.6807712	0.8072145	0.8496775
p_train | stroke = "yes"	0.0210501	0.6357917	0.7523655	0.6877351	0.8121712	0.8637727
p_test | stroke = "no"	0.0156221	0.0275296	0.1998112	0.3018179	0.5649308	0.8543277
p_train | stroke = "no"	0.0148618	0.0300742	0.2109020	0.3058056	0.5619038	0.8626878

The distributions are quite comparable. We proceed with the final test.

3.6 Simulate final validation test

For the final test, we randomly select 10,000 observations from the full data set with replacement, and make predictions on them. We repeat this process 5 times, each time calculating the sensitivity, specificity, and balanced accuracy. We then take the averages of these values and observe:

model	balanced_accuracy	sensitivity	specificity
final test nnet_54	0.7963	0.8596	0.7329

3.7 Establish risk level thresholds

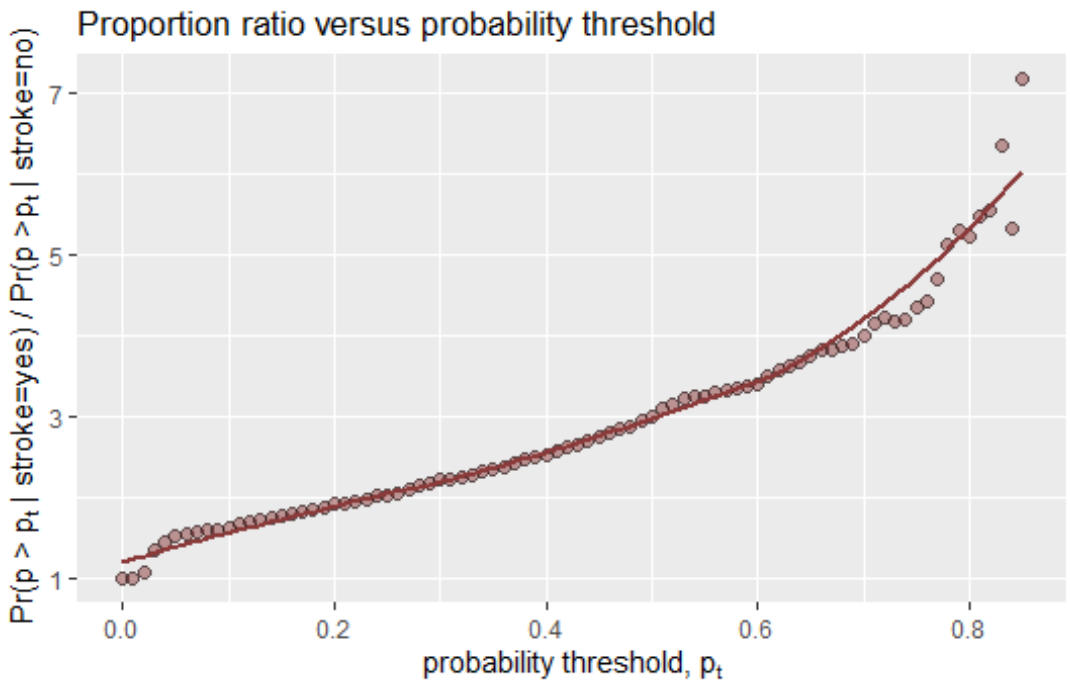
The final aspect we add to our model is a risk level assessment that places each observation into 1 of 5 categories ranging from "very low" risk to "very high" risk of stroke. We use the probabilities predicted by the **nnet** model on the full data set to determine the probability thresholds for each category.

To determine these thresholds, we first find the largest probability value predicted by our model for a case

where stroke = "no" and make a sequence of thresholds from 0 up to but not exceeding that max value in steps of 0.01. For each threshold, p_t, in the sequence, we calculate the ratio of the proportion of probabilities that exceed that threshold when stroke = "yes" to the proportion of probabilities that exceed that threshold when stroke = "no":

$$\frac{Pr(p > p_t|stroke = yes)}{Pr(p > p_t|stroke = no)}$$

We use this ratio as a metric to determine the increase in risk as we surpass each threshold. Plotting this ratio versus probability threshold, p_t, we observe:



Next we determine which values of this ratio we wish to use as markers for categorizing stroke risk level. We first set the marker that delineates high risk to the ratio corresponding to our stroke prediction probability threshold of 0.54, which we find to be 3.24. We set the other markers to ratios of 1.1, below which is considered very low risk, 2, below which is considered low risk, and 5, above which is considered very high risk. We find the probability thresholds that correspond to these markers to be the following:

$$very.low \leq 0.03 < low \leq 0.24 < moderate \leq 0.54 < high \leq 0.78 < very.high$$

We assess the risk level for each observation of the full data set, and our model is complete.

4 Results

4.1 Risk level distributions by stroke event

We now explore the results of our risk level model to see how it performed. Note we are still using the full data set here.

Selecting the observations where a stroke occurred and counting the number of instances of each stroke risk level, we observe:

	very_low	low	moderate	high	very_high
n | stroke = "yes"	1	11	24	107	106

We see that there is 1 observation in the "very low" risk category where a stroke occurred. It is a 16 month old female with no indicators of high risk.

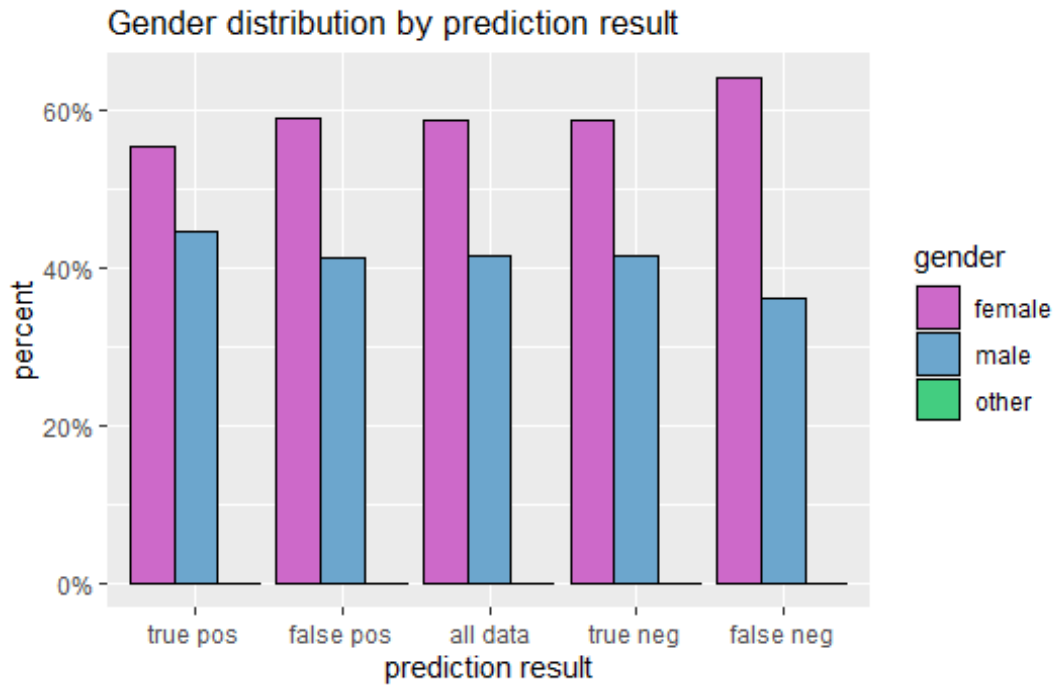
Counting the number of instances of each stroke risk level for observations where a stroke did not occur:

	very_low	low	moderate	high	very_high
n | stroke = "no"	1222	1331	1026	877	405

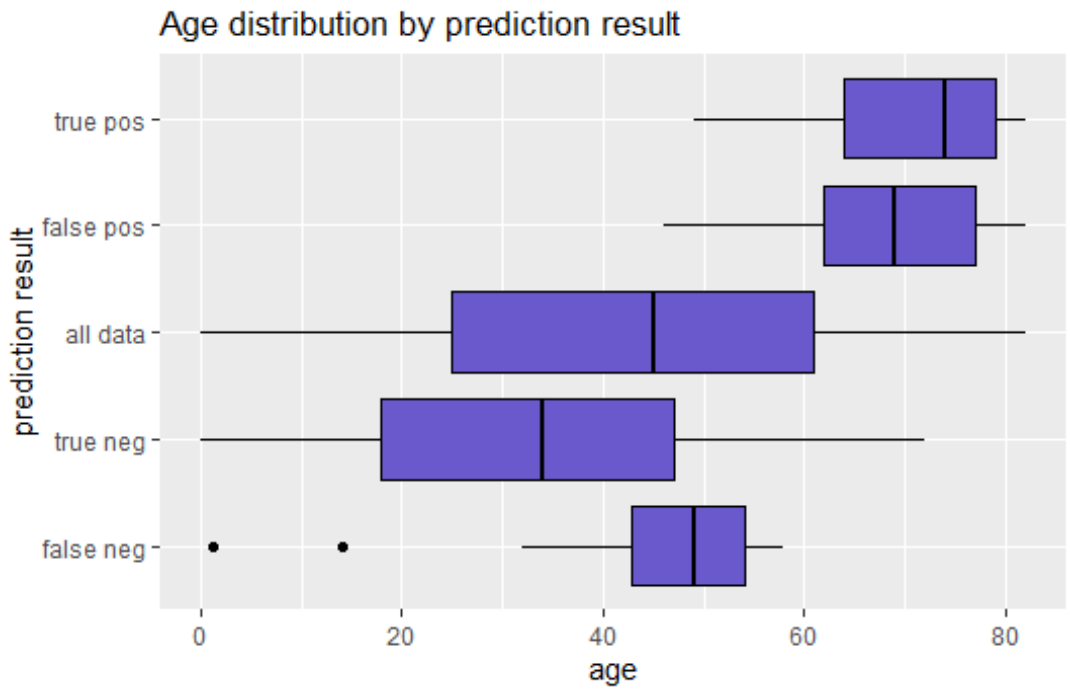
We see there are 1282 observations in the "high" or "very high" risk categories. This means that if our model is accurate, 26.4%, or roughly 1 in 4, of all observations where a stroke has not yet occurred have a high or very high risk of stroke.

4.2 Variable distributions by prediction results

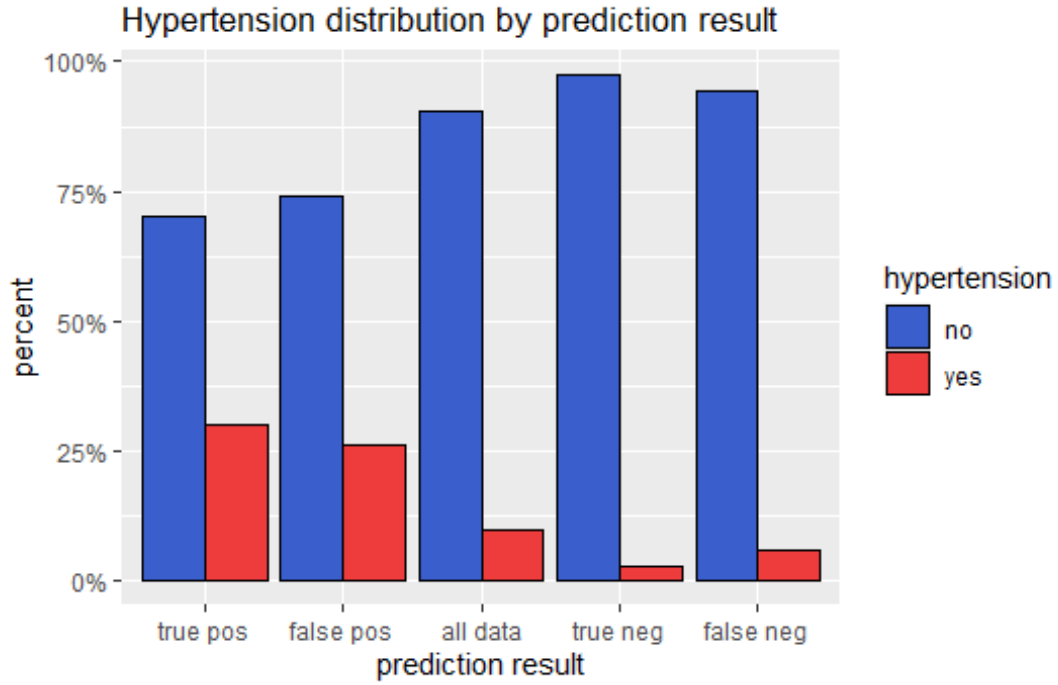
In order to gain insight into our model's prediction performance, we now group the observations into 4 categories: true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN). We then plot each variable's distributions for each group and compare them to each other as well as the variable's distribution for the full data set:



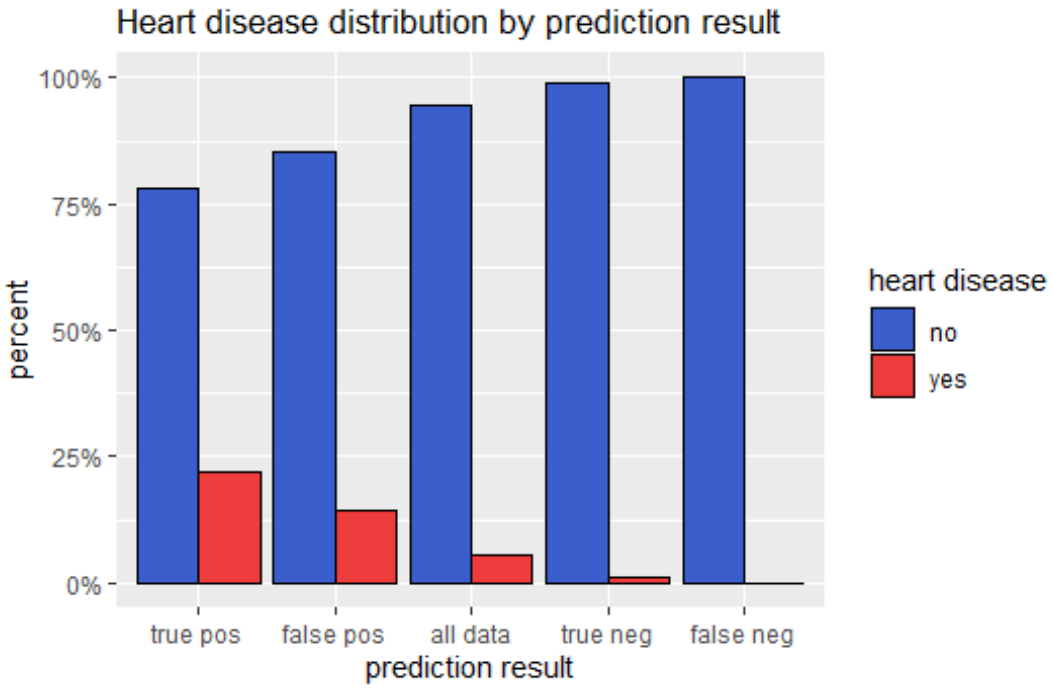
The distributions for gender are similar. We see slightly more males in the TP's, and slightly more females in the FN's. It appears our model may be slightly biased towards predicting male stroke events. It is not statistically significant, however, and could just be random variation.



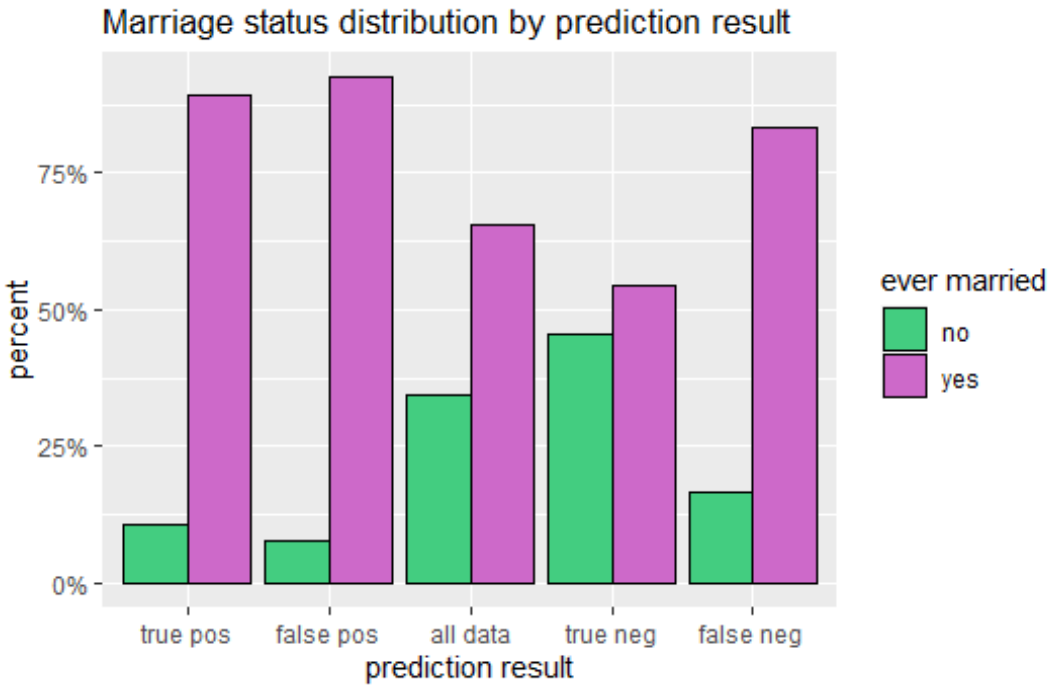
We see in the age distributions that the TP's and the FP's are similarly high in age, reflecting the importance of age as an indicator. We see the TN's tended to be a bit younger. The FN's tended to be middle aged, showing us that these are the challenging stroke events for our model to predict. All but 2 of the FN's are over age 30.



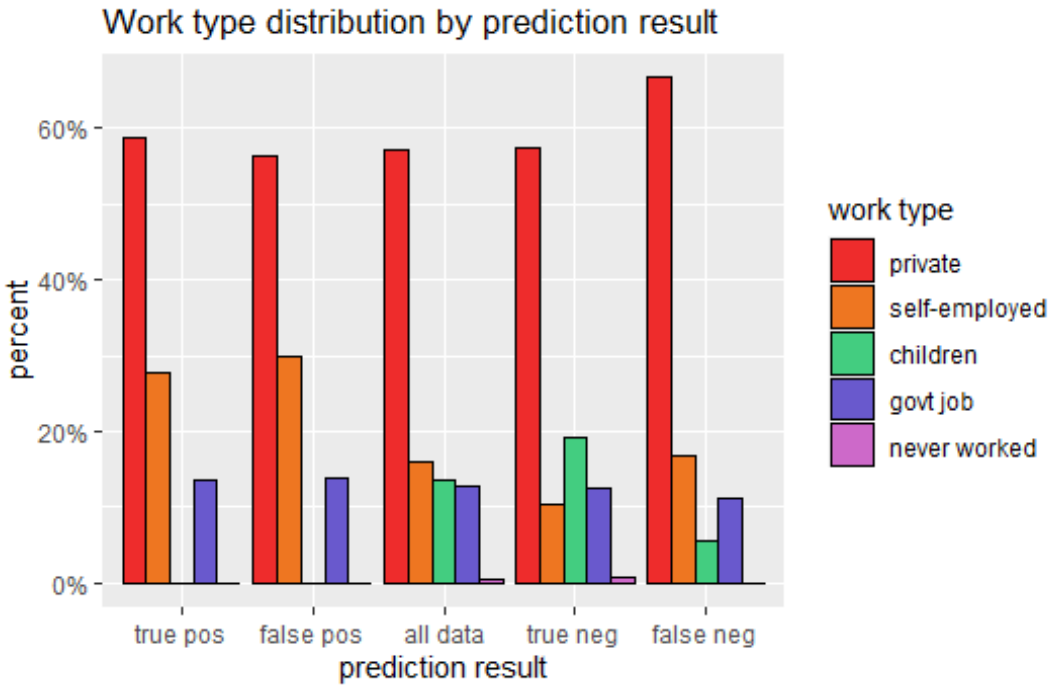
We observe higher rates of hypertension in the TP's and FP's, and lower rates in the TN's and FN's, reflecting its importance as an indicator. Recall a weak correlation between hypertension and age.



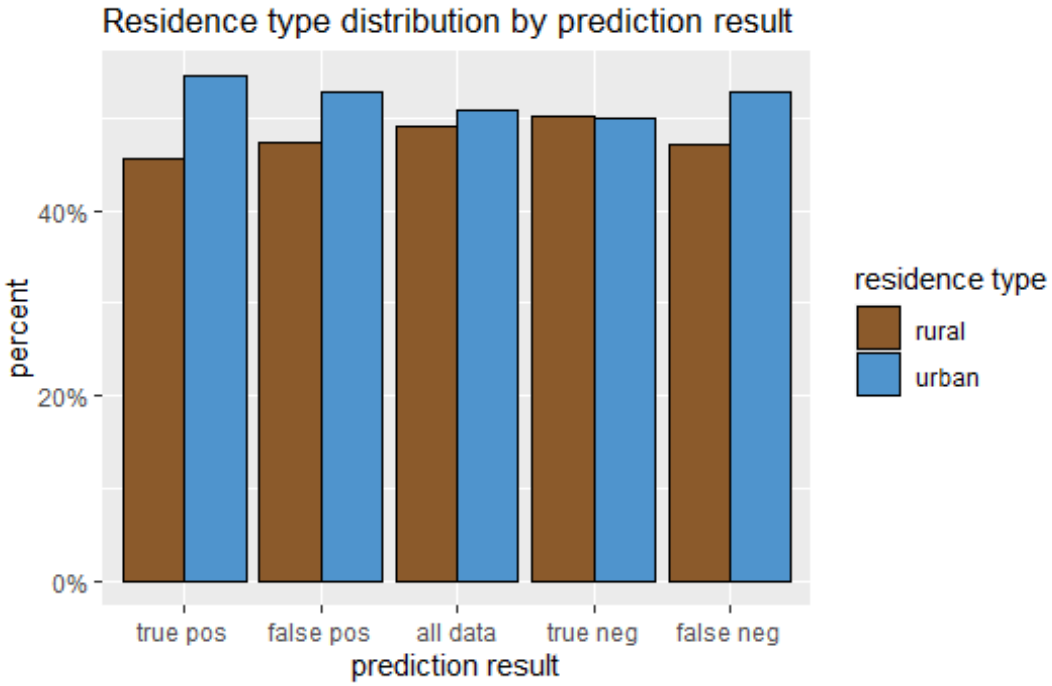
We also observe higher rates of heart disease in the TP's and FP's, and lower rates in the TN's and FN's, reflecting its importance as an indicator. Recall a weak correlation between heart disease and age.



We see that the TP's and FP's have a much higher prevalence of people who have been married before, while the TN's have a much lower prevalence and the FN's are somewhere in between. Recall the high degree of correlation between age and marriage status and notice the similarity between their distributions here.

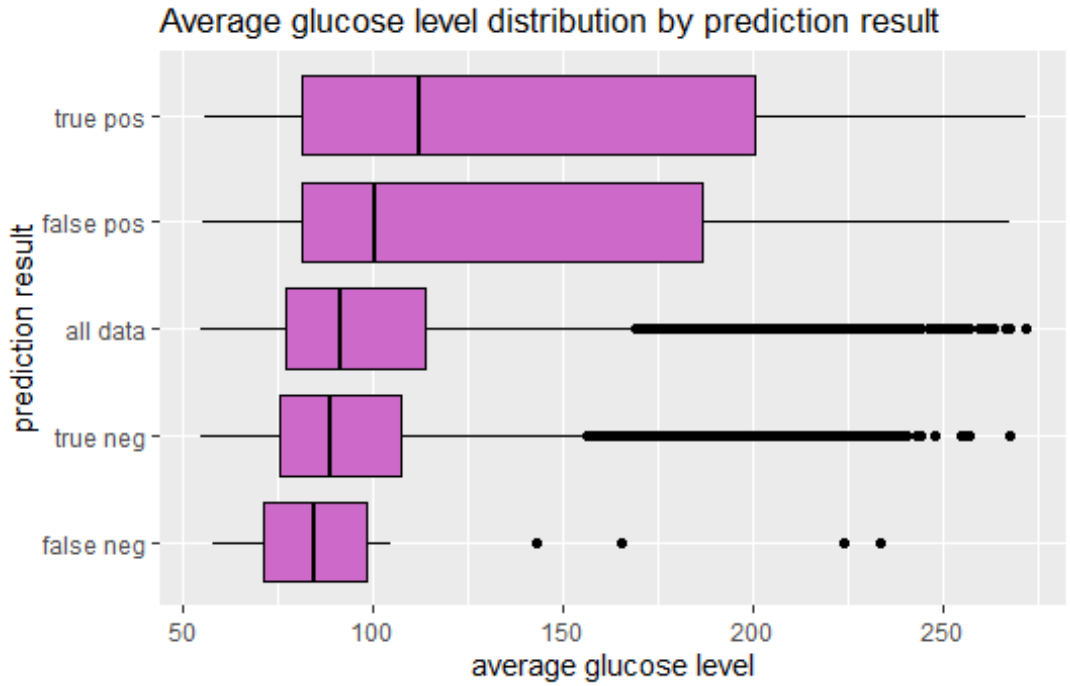


We see that children and those who never worked fall entirely into the TN's and FN's. The self-employed are more prevalent in the TP's and FP's. Those with government jobs show up relatively equally. Those who work in the private sector are more prevalent in the FN's. This partially reflects the age distributions associated with these groups. Children and those who never worked are all very young. The self-employed tend to be older. Those who work government jobs tend to be middle aged, which is where we saw more FN's. It appears our model may be better at predicting strokes for those who work government jobs and not quite as good at predicting strokes for those who work in the private sector.



We see a slightly higher prevalence of urban dwellers in the TP's, FP's, and FN's, with a slightly lower

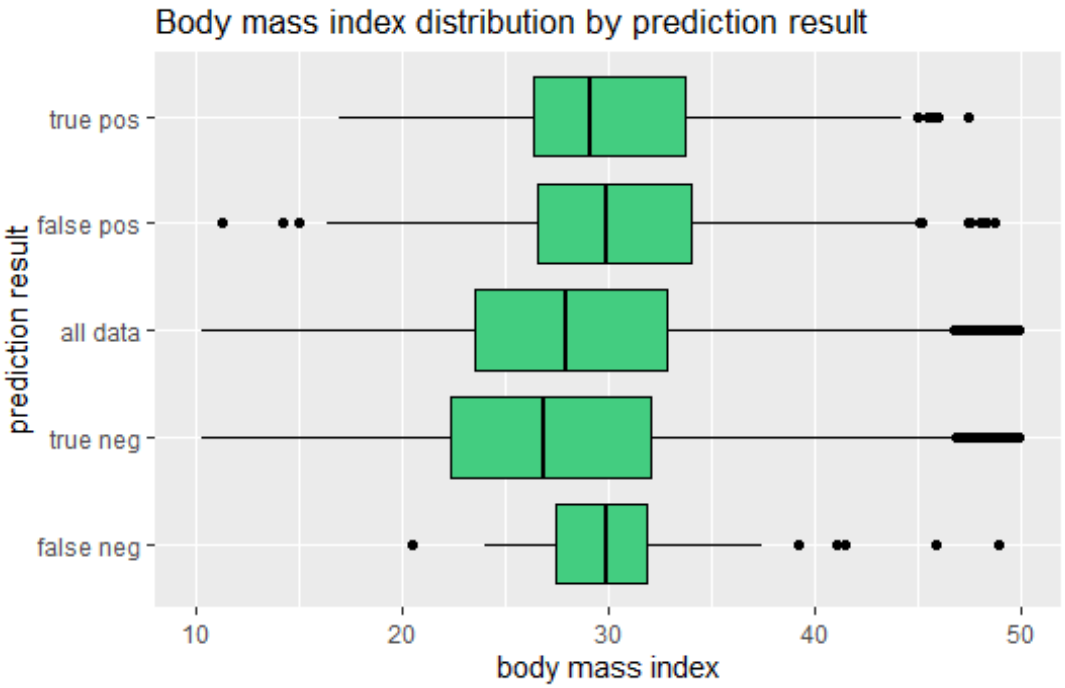
prevalence in the TN's. This partially reflects the importance of this variable in our model. We would expect a lower prevalence of urban dwellers in the FN's based on the variable importance. Keep in mind there are only 36 FN's, so random variation will affect this category considerably.



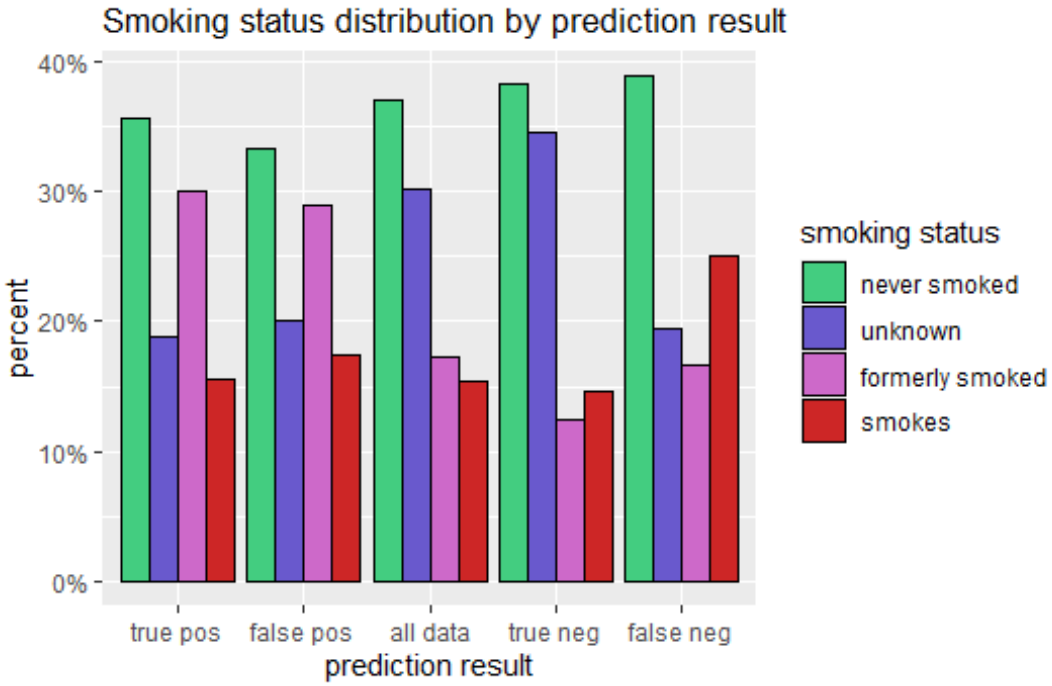
We observe average glucose levels tend to be higher in the TP's and FP's, near average in the TN's, and slightly lower in the FN's, indicating that the stroke events with lower average glucose levels were more difficult for our model to predict.

We see with the BMI distributions that the outliers compress the graph making it difficult to see, so we reset

the limits to crop them out:



We see BMI values tend to be slightly higher in the TP's, FP's, and FN's, and just below average in the TN's. Very low and very high BMI values were almost all predicted to not have stroke events. Most of the morbidly obese observations fall into the TN's. Keep in mind that 201 of our BMI values were guessed by imputation and are in observations that contain 40 of the 249 stroke events. This may be distorting our results.



We see that those who formerly smoked show up more in the TP's and FP's, reflecting their tendency to be higher in age. Those with unknown smoking status show up less in the TP's and FP's, reflecting their

tendency to be lower in age. We see that smokers show up more in the FN's, indicating it may be more difficult for our model to predict stroke events in smokers. Those who have never smoked show up slightly less in the TP's and FP's, and slightly more in the TN's and FN's, reflecting the variable importance (40.8) in our model.

5 Conclusion

Analyzing 5000+ observations of clinical features, we determined the trends and tendencies associated with stroke events. We saw that age is a key factor, and that strokes tend to occur after people move into their 50's and 60's. We saw that stroke rates increase as average glucose levels rise. We saw that stroke rates are higher for those with higher body mass index. We saw that those with hypertension and heart disease have much higher stroke rates, and that males and urban dwellers have slightly higher stroke rates than females and rural folks.

We do not know how much of these tendencies is causal and how much of them is correlation with other variables, as we saw a lot of correlations between age and other variables in particular. Future work could involve isolating out each variable to determine its pure influence, selecting observations with the same values/strata for all other variables and analyzing the variation. This would require more data points to ensure large enough numbers to acquire meaningful statistics.

We trained several stroke prediction models using different methods in the **caret** package, and we built one model ourselves by calculating risk factors based on stroke rates for each variable's categories. The models all generated predictions with balanced accuracy rates over 75%, with the best models pushing 80%. The final test of our final model produced a sensitivity of 86% and a specificity of 73%.

After testing our final model, we augmented it with a risk level assessment, categorizing each observation into 1 of 5 categories ranging from very low to very high. This placed all of our false positive predictions into the high and very high risk categories, while distributing all true negative predictions into the moderate, low, and very low risk categories based on the probability scores generated by our model and their relative prevalence among observations with stroke events. As our false positive rate was around 25%, this implies that roughly 1 in 4 observations could be at high or very high risk of a stroke event.

While our model is insightful and provides a good foundation for stroke prediction, it is limited by the amount of data. Taking the model further would require many more observations in order to fine tune and effectively validate its ability to pass muster, especially concerning the missing data points in the body mass index and smoking status columns. Other variables such as genetic predisposition, stress chemical levels, and mental/emotional well being might also be explored as predictors. An ensemble of multiple models could also be explored as a way to improve model performance.

Even when strokes are not fatal, they often lead to serious long-term disability. Knowing the factors and being able to reduce one's own risk of stroke can help to reduce the vast negative impact that strokes impart on people's lives in society.