EK 125 Project

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```
clear all;
close all;
```

Section: Introduction

Strokes are the 2nd leading cause of death globally, according to the World Health Organization (WHO). Over 10% of total deaths are the result of a stroke (Fedesoriano). The WHO has called the stroke, the 'incoming epidemic of the 21st century' (Sarikaya, Ferro & Arnold, 2015). A stroke occurs when blood supply to part of the brain is cut off or reduced, preventing oxygen and nutrients from reaching brain cells. Without oxygen or nutrients brain cells begin to die after just minutes. Many strokes are preventable (Guzik & Bushnell, 2017). Some risk factors leaving one more susceptible to a stroke include hypertension (high blood pressure), smoking, diabetes mellitus (which results in elevated levels of blood glucose), a previous stroke, and obesity (Guzik & Bushnell, 2017). If there was a way to predict the likelihood of a patient developing a stroke, how many lives would we be able to save with effective medical interventions and/or lifestyle changes? Our selected dataset outlines this potentially relevant patient information to predict if a patient is more prone to have a stroke.

References

Fedesoriano (Ed.). (2021, January 26). Stroke prediction dataset. Retrieved April 04, 2021, from https://www.kaggle.com/fedesoriano/stroke-prediction-dataset

Guzik, A., & Bushnell, C. (2017). Stroke Epidemiology and Risk Factor Management. Continuum (Minneapolis, Minn.), 23(1, Cerebrovascular Disease), 15–39. https://doi.org/10.1212/CON.0000000000000416

Sarikaya, H., Ferro, J., & Arnold, M. (2015). Stroke prevention--medical and lifestyle measures. European neurology, 73(3-4), 150–157. https://doi.org/10.1159/000367652

Section: Loading Data

Importing the Data and Brief Overview of the Data

Loading in the "*healthcare-dataset-stroke-data.csv*" data.

Section: Goals and Hypotheses

The goal of our script is to identify the attributes that affect a person's risk of stroke. With that we can then focus on attempting to cluster the attributes to find the patients with these attributes that most effectively might yield a successful predictor of future strokes. Since strokes are preventable, the people who fit into a highly predictive cluster could be alerted that they are at a high risk for stroke. Then they could be informed of any preventative steps they could take to decrease this risk. Based on our preliminary research, we hypothesize that people who have any of the following are at a higher risk for stroke: history of hypertension or heart disease, a history of or a status of currently smoking, a high average glucose level and a high BMI. Furthermore, if they have more than one of these risk factors, then their risk for having a stroke increases even more. We will graph each of these risk factors individually to compare the number of patients who had a stroke with those who did not to be able to reinforce our preliminary research findings. We will then be able to use machine learning to pass these different attributes to the program which will return if it thinks that a person is likely to have a stroke or not.

It is important to remember that only 249 patients in this study had a stroke, compared to the almost 5,000 who did not have a stroke, so coming to any significant conclusions based on this dataset might be hard. That is only a small percentage of patients who had a stroke. But we can compare the lifestyles of the patients within that group to try to come to conclusions about potential risk factors.

Make sure to **(1)** have the CSV *file in the working directory* and **(2)** *match the file name* used above (or change it below) to ensure this code will load the data.

```
%This version of the "readtable" call only reads in a subset of the file
%{
Commented this out cause we don't really need it

strokedata_sample = readtable("healthcare-dataset-stroke-data.csv",'Range','A1:L5');

%}
```

```
%This version of the "readtable" call loads in the entire stroke dataet
strokedata = readtable("healthcare-dataset-stroke-data.csv");
```

A little overview of the information loaded in "strokedata"

Fields - *Total of 12*

1. "id" - A list of integers to identify the patients
2. "gender" - Male or Female
3. "age" - Integers
4. "hypertension" - Binary
5. "heart_disease" - Binary
6. "ever_married" - Yes/No
7. "work_type" - Categorical information - strings
8. "Residence_type" - Categorical (urban or rural)
9. "avg_glucose_level" - Float value
10. "bmi" - Float, Int, or N/A
11. "smoking_status" - Categorical
12. "stroke" - Binary

Setting up a short preview section, including a function that loads any choice of rows and fields.

(NOTE: There is no content here that is relevent to our project unless you would like to preview some of the data for some reason. This was useful early on in our project but did not contribute to our general goals.)

Select the fields you want - enter 1 to extract the field or 0 to ignore the field

```
id_f                =  0;
gender_f            =  0;
age_f               =  1;
hypertension_f      =  0;
heart_disease_f     =  0;
ever_married_f      =  0;
work_type_f         =  0;
```

```
Residence_type_f    =  0;
avg_glucose_level_f =  0;
bmi_f               =  1;
smoking_status_f    =  0;
stroke_f            =  1;

%creating the vector passed to the function preview_data
log_vec = logical([id_f, gender_f, age_f, hypertension_f,heart_disease_f, ever_married_f, work_
```

Select the rows you want.

There are **two approachs you can use to extract rows.**

(1) Select specific rows - *see bullet points below*

- Sections of rows can be passed via colon notation (e.g., 10:1:100)
- The rows will be extracted in numerical order - e.g. if [10, 2, 100, 2000, 60] are requested the rows will be returned in the order [2, 10, 60, 100, 2000].

(2) Select all rows

```
% Enter selected method for extracting rows
% "all rows" = 1
% "specific rows" = 2
choice = 2;

% Enter the specific rows you want below
rowrange = [1:10];  % enter the row numbers in the vector

preview_table = preview_data(strokedata,log_vec,choice,rowrange);
%struct displays below

% PREVIEW DISPLAYS HERE
%disp(preview_table)
% Just clearing up some memory.
% No need to keep these variables.
clearvars id_f gender_f age_f hypertension_f heart_disease_f ever_married_f work_type_f Resider
clearvars log_vec rowrange choice preview_table;
```

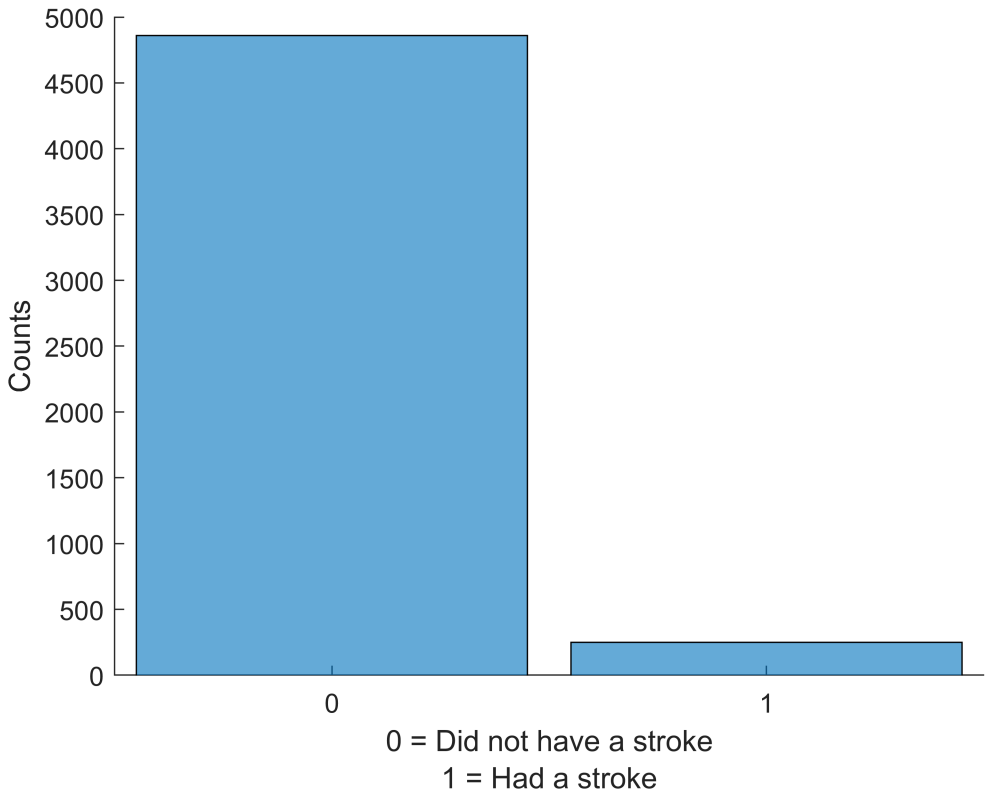
Section: Exploratory Data Analysis

First, let's look at what portion of the patients in the study had a stroke or didn't have a stroke.

It is good sampling practice and good for predictive models to consider both people who did and did not have a stroke. Individuals who had a stroke provide insight into common lifestyle choices that may lead to strokes. Meanwhile, the subjects who did not have strokes offer a baseline of comparison. While we may find a common lifestyle choice among subjects who had a stroke, this factor may also be common among people who did not have a stroke (and generally common among the collective participants in the study). This comparison will be valuable in determining predictive factors for strokes.

Since it will be beneficial to compare the two groups of stroke patients, the distribution of these patients will be examined first.

```
% Grabbing the "stroke" column of the table
stroke_col_array = strokedata.stroke;

stroke_dist_figure = figure(1);
clf(stroke_dist_figure)
hold on

stoke_dist = histogram(categorical(stroke_col_array),{'0','1'});
xlabel(["0 = Did not have a stroke","1 = Had a stroke"]);
ylabel("Counts")

hold off
```




```
% That count is really low. Determining the exact number of people who had
% a stroke
num_strokes = length(stroke_col_array(stroke_col_array == 1));
fprintf("There are %d individuals in the dataset who had a stroke.",num_strokes)
```

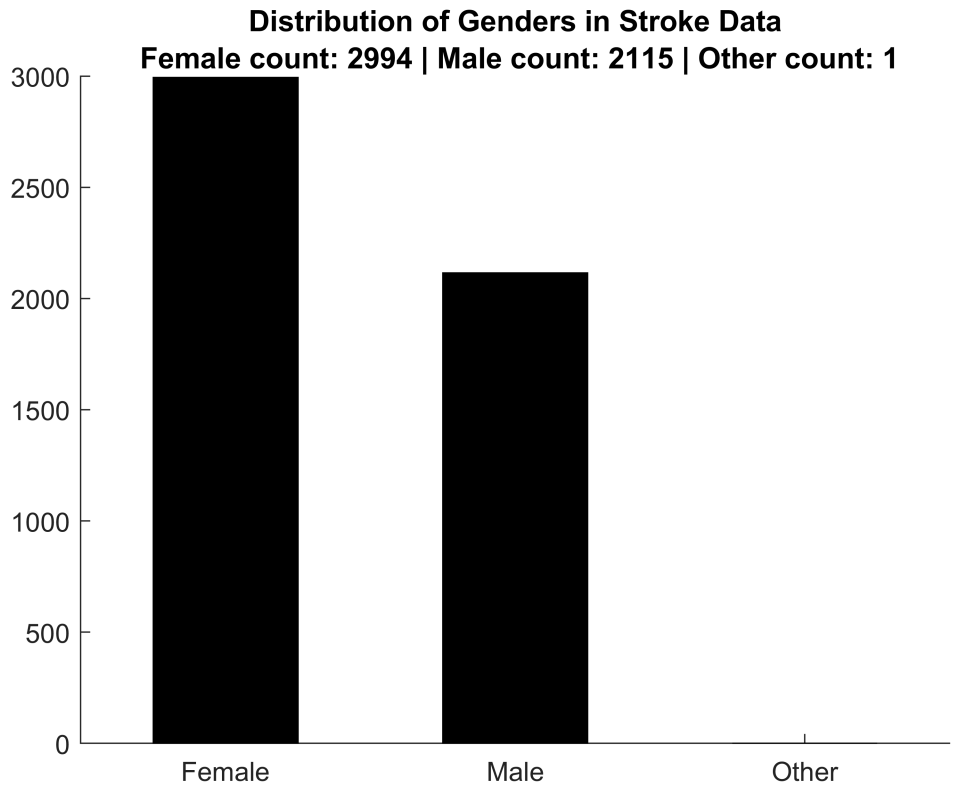
```
There are 249 individuals in the dataset who had a stroke.
```

```
clearvars num_strokes stroke_col_array
```

Clearly, more patients were surveyed for this study that did not have a stroke compared to the small group of 249 poeple that did have a stroke. The sample size of patients with a history of stroke is small compared to the entire collection of people interviewed, which limits, to some degree, the value of any conclusions about strokes that we may develop from this data. The sample is probably a bit small to be able to generate robust predictions about a perosn's chances of having a s.troke. However, the primary focus here is to identify lifestyle features that correlate with risk of stroke. The large sample size of non-stroke patients means that any risk factor or lifestyle choice that clearly distinguishes the group of patients with a stroke from the rest of the patients is highly likely to be predictive of a stroke.

Second, basic statistics about gender. Only one piece of information is available: how many males and how many females.

```
% Gotta grab the only information about gender.
gender_array = strokedata.gender;

% Determining all of the unique entries in this data
entry_types = unique(gender_array);
% Now that we know what we are looking at, let's get a distribution of
% these entries
gender_categories = categorical({'Female','Male','Other'});
sort_gender_categories = reordercats(gender_categories,{'Female','Male','Other'});
gender_dist_plot = figure(2);
clf(gender_dist_plot) %note: this just clears the figure so changes can be made and the old one
hold on
% grabbing the plotting values
gender_dist = histcounts(categorical(gender_array),sort_gender_categories);
%plotting the information
bar(sort_gender_categories,gender_dist,0.5,'k');
%interesting title for the plot
gender_plot_title = sprintf("Distribution of Genders in Stroke Data\n Female count: %d | Male c
                            gender_dist(1),gender_dist(2),gender_dist(3));
title(gender_plot_title);
hold off
```



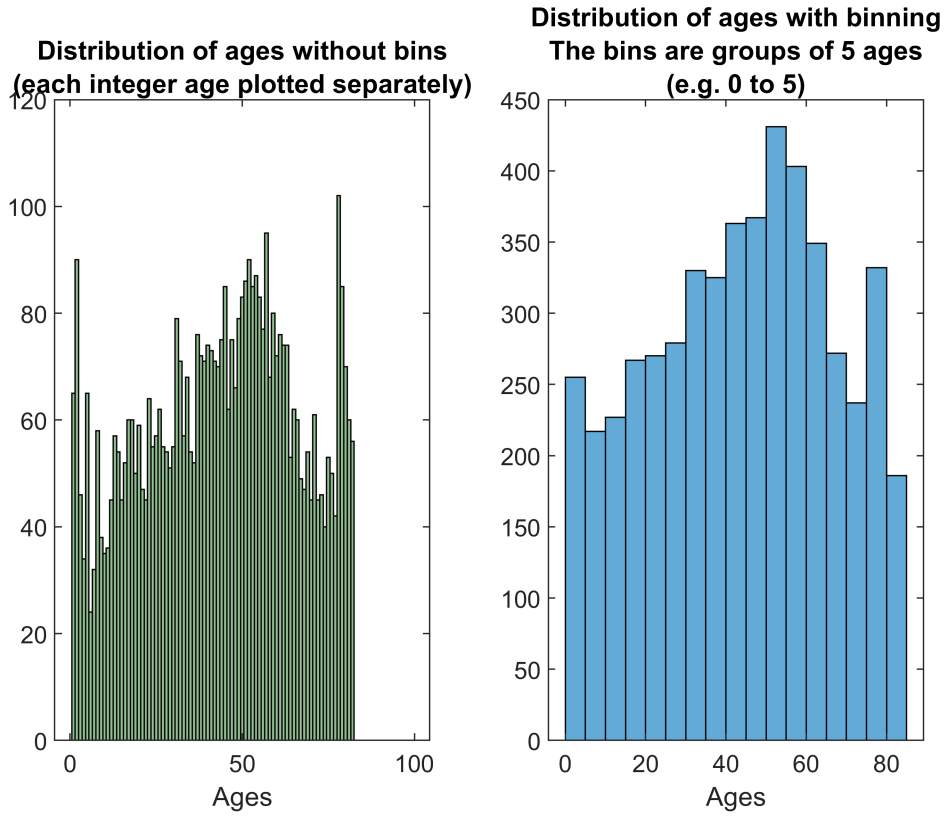

```
clearvars gender_plot_title gender_dist gender_categories sort_gender_categories entry_types; %
```

The participants in the study are actually mostly listed as male or female, despite the other category, which simplifies working with this gender data. The general distribution of males and females is nearly 50/50 and nothing substantial stands out about the gender distribution that would suggest there needs to be concerns about working with this data.

Third, basic statistics about age. An examination of the distribution of ages.

```
%grabbing the age data
age_array = strokedata.age;

%Going to do a subplot
% Subplot 1: All ages ... no binning
% Subplot 2: All ages ... binned within a range
%   (ex. bins of 5 years, 21-25 | 26-30 | 31-35 etc.)

age_distribution_plot = figure(3);
clf(age_distribution_plot)

hold on
subplot(1,2,1);
% PLOT 1 Script
no_bins_edges = [0.5:1:99.5]; %Should indicate to "histogram" function what values we want in t
```

```
age_no_bins_hist = histogram(age_array,no_bins_edges,'FaceColor',[0.3, .6, 0.3]);
%Modifying histogram
titleforsubplot1 = sprintf("Distribution of ages without bins\n(each integer age plotted separa
title(titleforsubplot1);
xlabel("Ages");

%PLOT 2 Script
subplot(1,2,2);
%going to use features of "historgram" function to do binning
age_bins_hist = histogram(age_array,'BinMethod','auto');

titleforsubplot2 = sprintf("Distribution of ages with binning\nThe bins are groups of %d ages\n
                           (age_bins_hist.BinEdges(2)-age_bins_hist.BinEdges(1)),...
                            age_bins_hist.BinEdges(1), age_bins_hist.BinEdges(2));
title(titleforsubplot2)
xlabel("Ages")

hold off
```




```
clearvars age_no_bins_hist titleforsubplot1 titleforsubplot1 no_bins_edges ages_no_stroke ages_
clearvars ages_distribution_plot ages_distribution_stroke_conditional; %freeing up computer spa
```

The age distributions reveal some deviations from a normal data distrbitution. Age does not seem like a feature that would generally follow a normal distribution, but it's still important to keep of the trends in this data among the subjects.

In particular, it is interesting that the distribution of all ages has large spikes at very high and very low ages. The age 1 bin has nearly 100 subjects from the study. The study was conducted among patients in a hospital,

so seeing 100 babies in a hospital is not unexpected since they likely make far more visits to doctors than the average healthy adult, but this group may need to be separated out when it comes to using this data for predicting strokes. **It is unlikely that babies and young children can effectively provide information about predicting the potential for a stroke.**

Next, we will extract the number of patients who have hypertension and look to see how many of them also had a stroke.

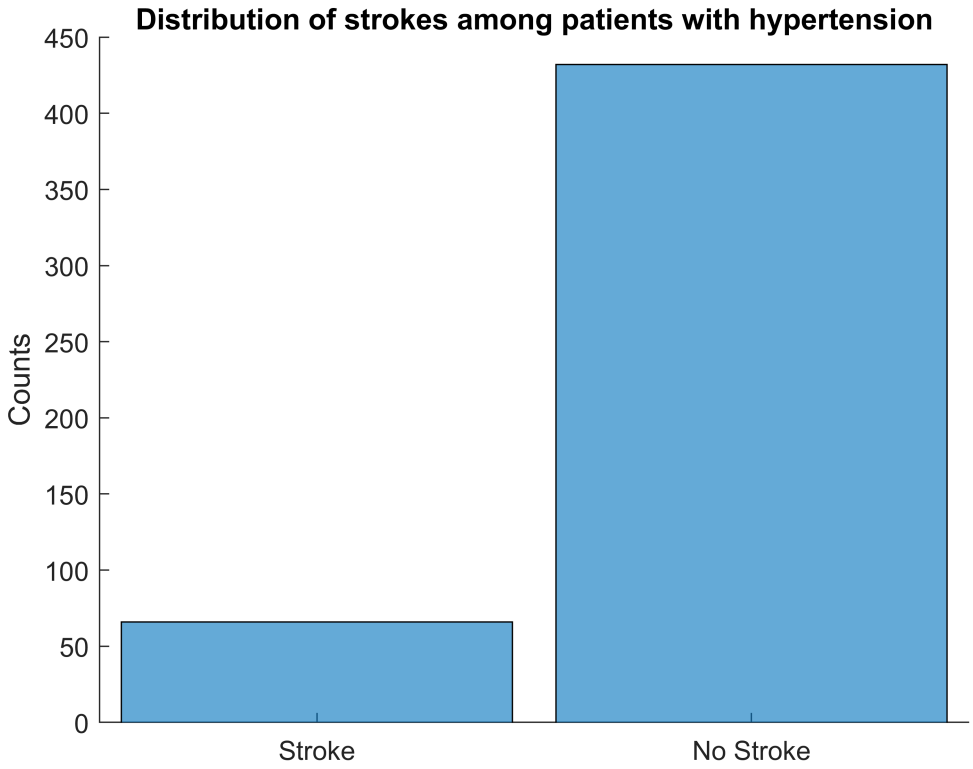
```
% Exploring the distribution of patients who had a stroke and hypertension

hypertension_mask = (strokedata.hypertension == 1);         % Extract a logical of patients who
count_hypertension = sum(hypertension_mask);                % total number of people who had a
hypertension_positive  = strokedata(hypertension_mask,:);   % table including only patients who
stroke_mask = (hypertension_positive.stroke==1);            % Further extracting parts of the t
count_stroke = sum(stroke_mask);


percent_hypertension_stroke = (count_stroke/count_hypertension)*100;

fprintf("There were %d particiants who have a history of hypertension and %d of them also suffe
```

```
There were 498 particiants who have a history of hypertension and 66 of them also suffered a stroke.
```

```
fprintf("This means that %.2f%% of the participants who have hypertension also suffered a strok
```

```
This means that 13.25% of the participants who have hypertension also suffered a stroke.
```

```
y1 = count_stroke;
y2 = count_hypertension - count_stroke;
figure(21);
clf(21);
hold on


histogram('Categories',{'Stroke','No Stroke'},'BinCounts',[y1, y2])
title("Distribution of strokes among patients with hypertension")
ylabel("Counts")

hold off
```



This data is simply meant to help demonstrate the distribution of patients with hypertension. There are significantly more patients who did not have a stroke than who did, so it is not surprising to see far more non-stroke patients with hypertension. Therea are two helpful observations that you can make from this data though. First, a relatively low number of patients (only around 10%) reported having hypertension. Second, while the number of stroke patients with hypertension is a low total, more than 20% of the stroke patients had hypertension. It is not definitive information, but there does appear to be a higher rate of hypertension among the stroke patients (more than 20%) compared to the general collection of patients (about 10%).

Now, we will extract the number of patients who have a history of heart disease and look to see how many of them also had a stroke.

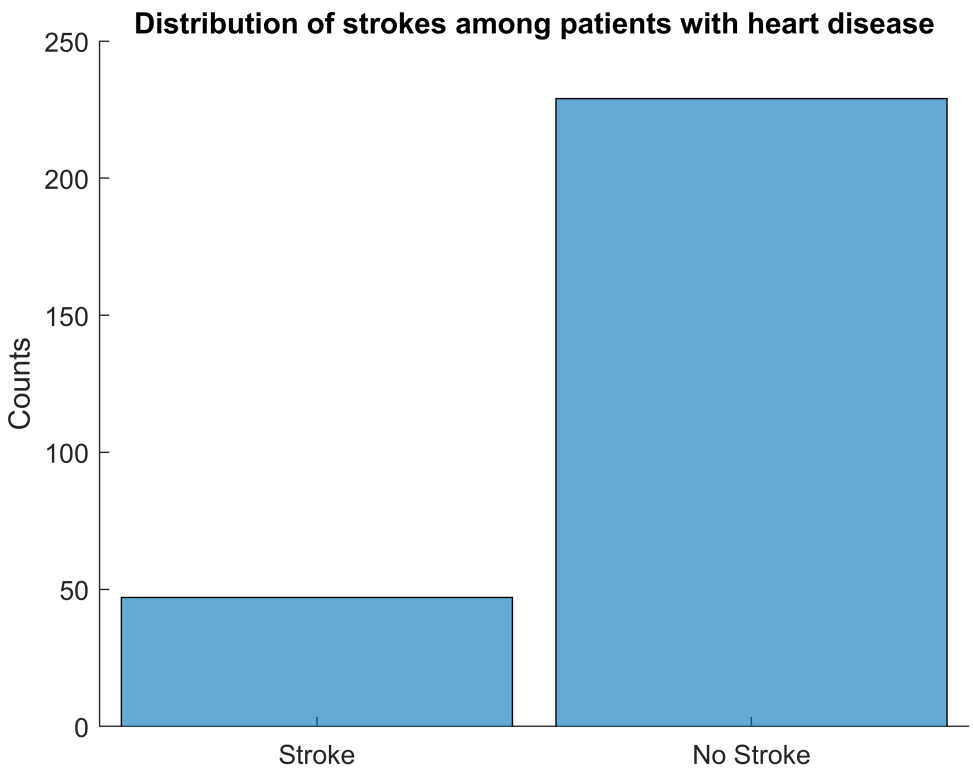
```
heart_mask = strokedata.heart_disease == 1;
count_heart = sum(heart_mask);
heart_positive  = strokedata(heart_mask,:);
heart_mask = heart_positive.stroke==1;
count_heart_stroke = sum(heart_mask);


percent_heart_disease_stroke = (count_heart_stroke/count_heart)*100;

fprintf("There were %d particiants have a history of heart disease and %d of them also suffered
```

```
There were 276 particiants have a history of heart disease and 47 of them also suffered a stroke.
```

```
fprintf("This means that %.2f%% of the participants who have hypertension also suffered a strok
```

This means that 17.03% of the participants who have hypertension also suffered a stroke.

```
yhd1 = count_heart_stroke;
yhd2 = count_heart - count_heart_stroke;

figure(22);
clf(22);
hold on

histogram('Categories',{'Stroke','No Stroke'},'BinCounts',[yhd1, yhd2])
title("Distribution of strokes among patients with heart disease")
ylabel("Counts")

hold off
```




```
clearvars count_heart count_heart_stroke heart_mask heart_positive
```

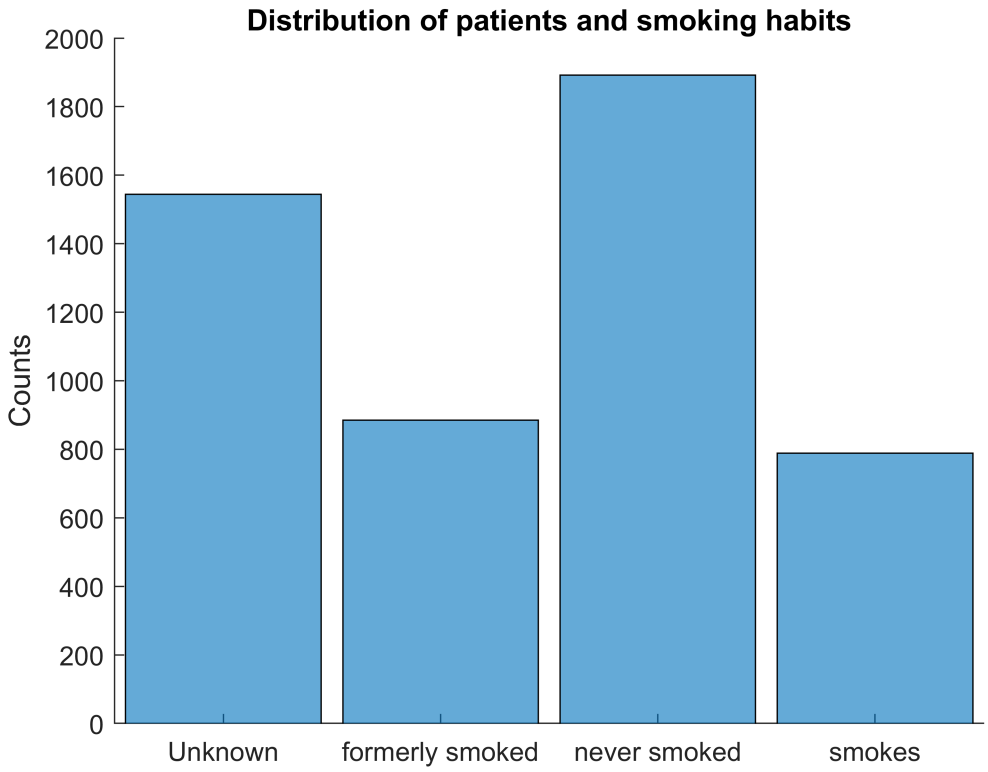
This data is simply meant to help demonstrate the distribution of patients with heart disease. There are significantly more patients who did not have a stroke than who did, so it is not surprising to see far more non-stroke patients with heart disease. There are helpful observations that you can make from this data though. First, a relatively low number of patients (only around 5%) reported having heart disease. Second, while the number of stroke patients with heart disease is a low total, more than about 20% of the stroke patients had heart disease. It is not definitive information, but there does appear to be a higher rate of heart disease among the stroke patients.

Next, the distribution of strokes among smokers and non-smokers

```
smoking_col_from_table = strokedata.smoking_status;
smoking_array_entries = unique(smoking_col_from_table); % just returns all the categories that
[counts, order_of_counts] = histcounts(categorical(smoking_col_from_table),smoking_array_entrie
for i = 1:length(counts)
    fprintf("%s: %d counts\n",order_of_counts{i},counts(i))
end
```

```
Unknown: 1544 counts
formerly smoked: 885 counts
never smoked: 1892 counts
smokes: 789 counts
```

```
figure(23);
clf(23);
hold on
histogram('Categories',order_of_counts,'BinCounts',counts)
title("Distribution of patients and smoking habits")
ylabel("Counts")
hold off
```




```
[smoking_col_stroke_pos, smoking_col_stroke_neg] = bin_conditional_extract(strokedata,"smoking_

[counts2, order_of_counts2] = histcounts(categorical(smoking_col_stroke_pos),smoking_array_entr
```

```
[counts3, order_of_counts3] = histcounts(categorical(smoking_col_stroke_neg),smoking_array_entr

fprintf("There were %d particiants who formerly or currently smoke and %d of them also suffered
```

```
There were 1674 particiants who formerly or currently smoke and 112 of them also suffered a stroke.
```

```
fprintf("This means that %.2f%% of the participants who have formerly or currrently smoked also
                                                                    (counts2(2) + counts2(4)
```

```
This means that 6.69% of the participants who have formerly or currrently smoked also suffered a stroke.
```

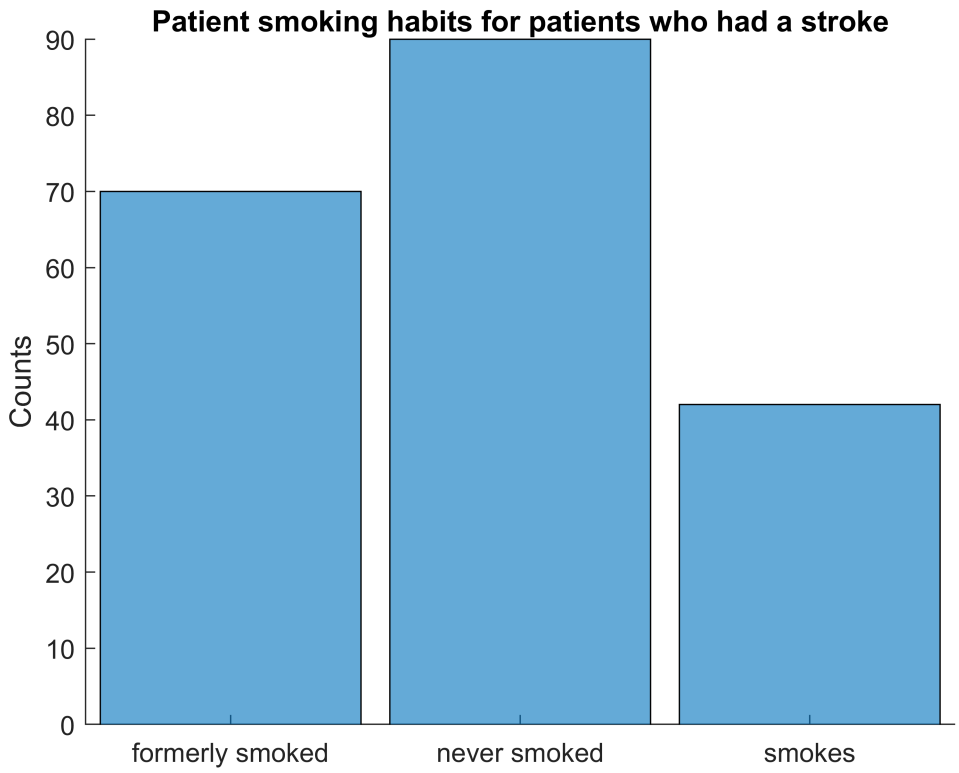
```
fprintf("There were %d particiants who never smoked and %d of them also suffered a stroke./n",
```

```
There were 1892 particiants who never smoked and 90 of them also suffered a stroke./n
```

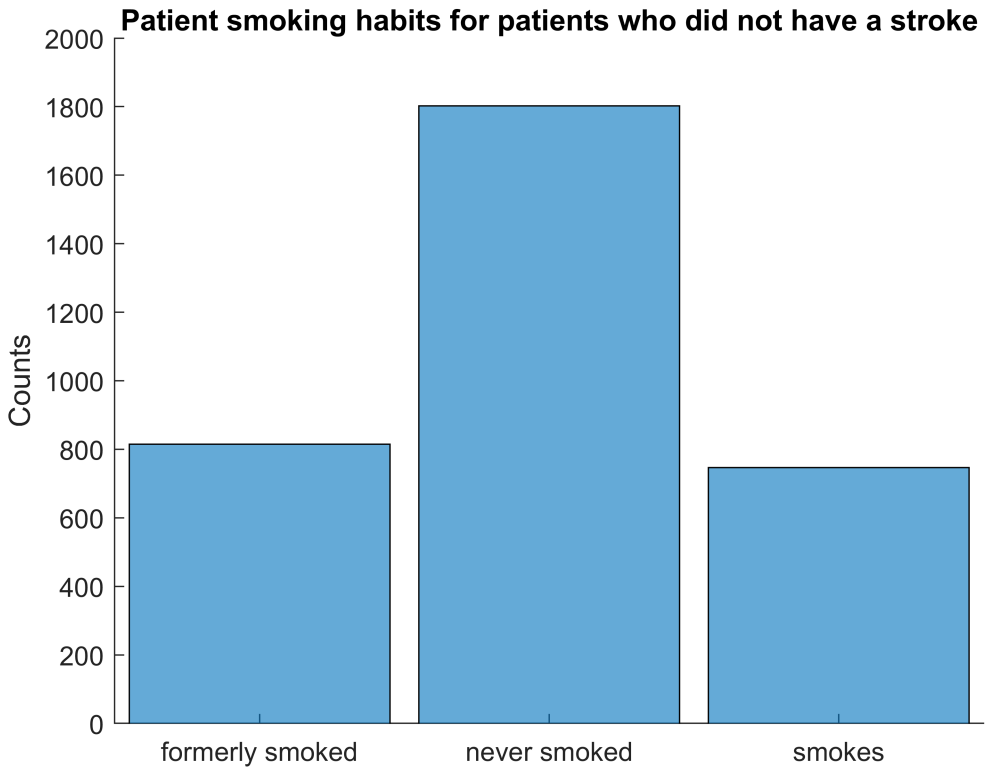
```
fprintf("This means that %.2f%% of the participants who have never smoked also suffered a strok
```

```
This means that 4.76% of the participants who have never smoked also suffered a stroke./n
```

```
%Now, here is the information plotted

smoking_and_stroke_1 = figure(24);
%smoking_and_stroke_subplot.Position = [800 500 560 420] --- Ignore this
clf(24);
hold on
histogram('Categories',order_of_counts2(2:4),'BinCounts',counts2(2:4))
title("Patient smoking habits for patients who had a stroke")
ylabel("Counts")
hold off
```



```
smoking_and_stroke_2 = figure(25);
clf(25);
hold on
histogram('Categories',order_of_counts3(2:4),'BinCounts',counts3(2:4))
title("Patient smoking habits for patients who did not have a stroke")
ylabel("Counts")
hold off
```




```
formated_print = "Among stroke patients, %d patients of %d total are smokers (%.2f%%).\n\nAmong
fprintf(formated_print,counts2(2) + counts2(4), sum(counts2), sum(counts2([2,3]))/sum(counts2)*
```

```
Among stroke patients, 112 patients of 249 total are smokers (64.26%).

Among non-stroke patients, 1562 patients of 4861 total are non-smokers (53.84%).

Note: These numbers include those patients who reported as being 'unknown'.
```

```
clearvars smoking_array_entries percent_heart_disease_stroke title_subplot2 titleforsubplot2 ti
clearvars order_of_counts order_of_counts2 order_of_counts3 smoking_col_from_table smoking_col_
```

An initial observation about this data is the large number of unknown entries among the patients. More than 20% of the participants are listed as "unknown," which makes it challenging to use this attribute of the data to make predictions about a person's chance of stroke.

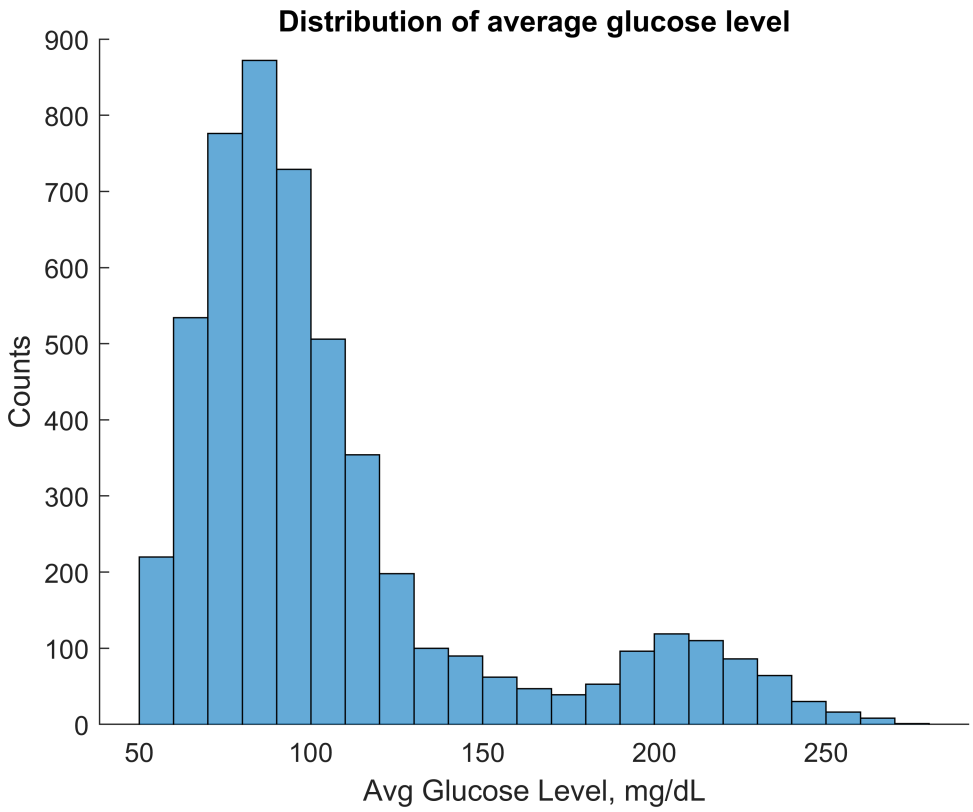
Ideally, the data could be used without any of these subjects. However, the smoking patients available are already a small portion of the data, and their other data is valuable. *While performing some data cleaning before*

proceeding to analysis, some of the "unknown" subjects may be removed, but these individuals were generally treated as "never smoking." This decision errors on the side of indicating that smoking is not a factor that leads to strokes; a conclusion drawn based on the distributions of stroke and non-stroke patients (above), where the proportion of non-smokers is much higher among the patients who have not had a stroke.

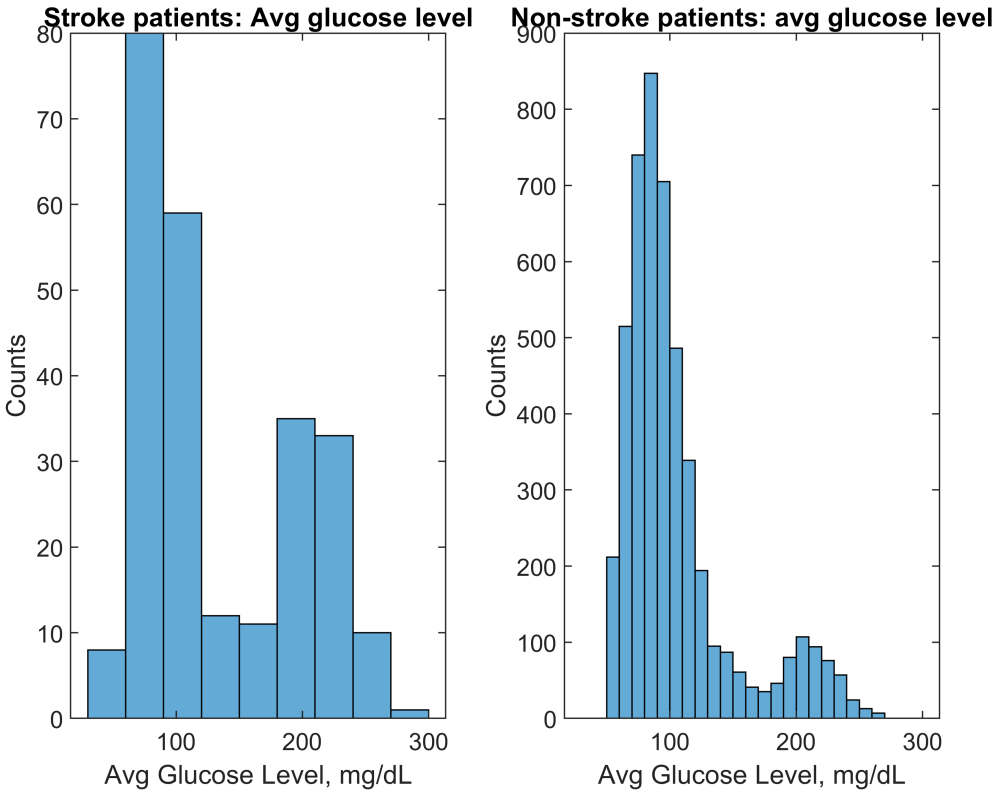
Additionally, there does not appear to be a significant variation in smoking patterns in the distributions of stroke patients and non-stroke patients. The relationships of the smokers ("formerly smoked" and "smokes") and non-smokers ("never smoked") in the plot above are not exactly identical, which would indicate no difference at all. The total counts of smokers and non-smokers is approximately equal among the samples of stroke and non-stroke patients. As a model is developed to predict the chance of someone having a stroke, the model will be given this data, and it will be allowed to learn to use this information appropriately even if it turns out that the smoking data does not have a significant impact on its ability to predict that someone is likely to have a stroke.

Next up, distribution of average glucose level among the study patients

```
f1 = figure(27);
clf(f1);
hold on
histogram(strokedata.avg_glucose_level,'BinMethod',"auto");

title("Distribution of average glucose level")
xlabel("Avg Glucose Level, mg/dL")
ylabel("Counts")
hold off
```




```
[avg_glucose_stroke, avg_glucose_no_stroke] = bin_conditional_extract(strokedata,"avg_glucose_l
f2 = figure(28);
clf(f2);
hold on

subplot(1,2,1)
h1 = histogram(avg_glucose_stroke,'BinMethod',"auto");
title("Stroke patients: Avg glucose level")
xlabel("Avg Glucose Level, mg/dL")
ylabel("Counts")

subplot(1,2,2)
h2 = histogram(avg_glucose_no_stroke,'BinMethod',"auto");
h2.BinLimits = [30, 300];
title("Non-stroke patients: avg glucose level")
xlabel("Avg Glucose Level, mg/dL")
ylabel("Counts")
```




```
clearvars f1 f2 h1 h2 avg_glucose_no_stroke avg_glucose_stroke;
```

From the plots, nothing substantial jumps out about the stroke patients. The distributions have similar shaps, indicating that there isn't a dramatic shift in average glucose level among the stroke or non-stroke patients. This piece of information is a fairly complex piece of data to use because context is important. Glucose levels vary dramatically throughout the day. It was not explicitly stated with the data, but it is presumed that this daily variation is the reason the data was provided as an average (over the course of a day). This addresses one contextual issue, but glucose levels are heavily influenced by a number of health factors, like having diabetes for example. It would take substantial effort and experience to parse out what this distribution of average glucose level might provide about the health of these patients. Instead, the data was provided as is to the classification learner as is, with all of the underlying information included, to allow the high-level statistical model to try to parse out if the information provided by this data is effective in providing infromation about stroke rates.

Finally, distribution of BMI among the study patients

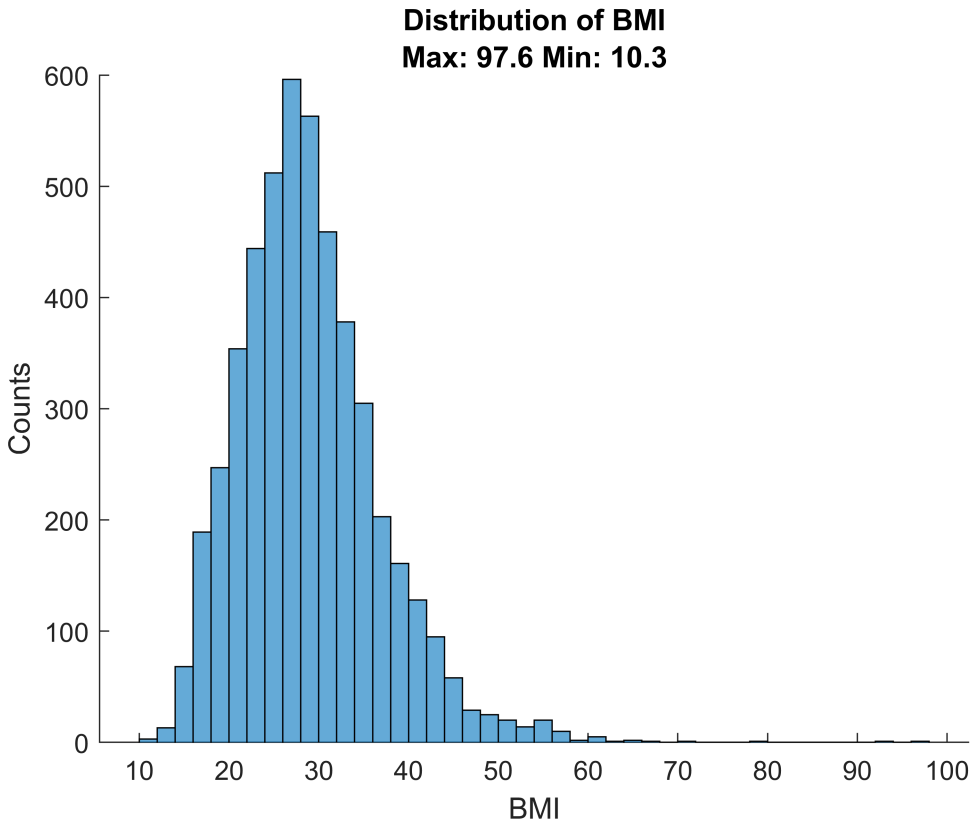
BMI is a convenient composite feature to have available in this analysis. It is a representative attribute of a person's height and weight, and plenty of work has been done with the feature already. BMI classification with regards to health has been done as follows:

- <18.5 --- "Underweight"
- 18.5 to <25 --- "Normal"

- 25.0 to <30 --- "Overweight"
- >30.0 --- "Obese"

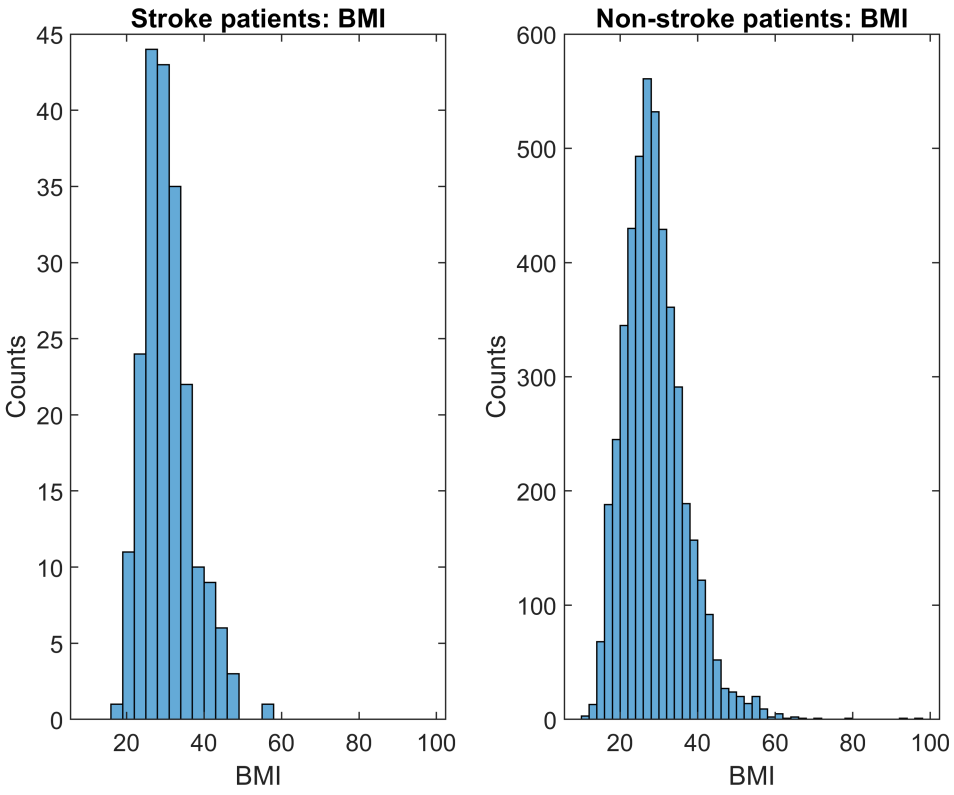
These classifications are helpful context, but the reality is that they can be innaccurate classifications for some. For example, people with large muscle mass, like large atheletes, may not be unhealthy but likely fall into the "overweight" or "obese" category. For this reason, the BMI data was used as a value rather than a classification. The classifications might be inaccurate, but the value of BMI itself still provides helpful information about a persons' general body and health that might be useful in identifying strokes.

```
f1 = figure(30);
clf(f1);
hold on
histogram(strokedata.bmi,'BinMethod',"auto");
titlef1 = sprintf("Distribution of BMI\nMax: %.1f Min: %.1f",max(strokedata.bmi),min(strokedata
title(titlef1)
xlabel("BMI")
ylabel("Counts")
hold off
```




```
[bmi_stroke, bmi_no_stroke] = bin_conditional_extract(strokedata,"bmi","stroke",1);
f2 = figure(31);
clf(f2);
hold on

subplot(1,2,1)
```

```
h1 = histogram(bmi_stroke,'BinMethod',"auto");
h1.BinLimits = [10,98];
title("Stroke patients: BMI")
xlabel("BMI")
ylabel("Counts")

subplot(1,2,2)
h2 = histogram(bmi_no_stroke,'BinMethod',"auto");
title("Non-stroke patients: BMI")
xlabel("BMI")
ylabel("Counts")
```




```
clearvars f1 titlef1 f2 h2 h1;
```

For the BMI data, there does not appear to be much of a shift in the distribution, which would be expected if any substantial correlation occured between BMI and stroke rate. These plots do not demonstrate a significant exploration and statistical understanding of the distribution. The data was provided to the classification learning model for further anlaysis and assessment of significance.

Section: Data Scrubbing and Preparation

In the Data Analysis section below, some preliminary analysis has indicated that extracting only adults from "strokedata" will yield more accurate information about people who are at risk for strokes. The section of code below will be used to extract a table of only patients above the age of 18 that can be used for the majority of our data analysis.

```
strokedata_18plus = strokedata([strokedata.age >= 18],["gender","age","hypertension","heart_dis
                                                       "Residence_type","avg_glucose_level","bm
%NOTE: Some variables from "strokedata" were removed.
% "id" & "ever_married" were not extracted
```

From the preliminary exploration of the data, most attributes provided on the patients in this study did not provide a strong basis to extract the stroke patients. In other words, when separating the stroke patients from non-stroke patients in EDA, very few of the attributes extracted a significant portion of the 249 stroke patients while extracting very few of the non-stroke patients. In particular, three commonly linked risk factors for health complications, (1) heart disease, (2) hypertension, and (3) smoking did not show an obvious percentage increase in the stroke patients compared to the overall patient sample. As noted with hypertension in particular, there might be a slight, and still useful, shift caused by these risk factors. Thus, some feature engineering was done to translate these binary pieces of information ("smoking status" was translated to two groups: (1) smoked at any point and (2) never smoked at all or unknown) to a four point scale that generally represents medical risk factors for the patients in the study.

In the section below, the three features "heart_disease", "hypertension", and "smoking_status" were redesigned to fit on a four point scale. The four point scale was added back to the table to replace these three attributes in a new attribute that was named "medical_risk." A short outline of what was done is provided below before the new feature was created.

- No risk factors (i.e. not a smoker, no heart disease, and no hypertension) === 0
- 1 risk factor === 1
- 2 risk factors === 2
- All risk factors === 3

The model was passed only the "medical_risk" attribute, not any of the three attributes that contribute to it, with the idea that the group of information is likely a better predictor of stroke than any of the individual attributes. While MATLAB's machine learning model may have been able to come to the same conclusion or may have come to a slightly different conclusion, this approach seemed to be the most tangible and informative all in one.

```
%starting with the data table created above --- strokedata_18plus

%Going to remove "Residence_type" now because it has not been an attribute
%that we are interested in (will remove by not extracting through really

%Using a function to perform the feature creation and preparation of a new
%table because I did not want to clutter this script more than necessary

%INPUTS: strokedata_18plus
strokedata_prepped = datacleanandprep(strokedata_18plus);
```

The new table "strokedata_prepped" has 7 columns. These columns are listed below.

1. "gender"
2. "age"
3. "Work_type"
4. "avg_glucose_level"
5. "bmi"
6. "stroke"
7. "medical_risk"

These attributes will be provided to the classification learner in MATLAB in order to develop a model that accurately predicts stroke from this information. The "stroke" column of the table will be the response that the model is trying to classify. It will be using the other 6 features provided as predictors that classify subjects as likely or not to have a stroke.

Section: Data Analysis

The work in this section was dominated by trying to understand and use the classification learner to make stroke predictions from the risk factor data. However, from the exploration of the data, it was clear that age distribution shifted dramatically when looking at stroke patients, so this distribution was analyzed a bit and cleaned up to provide better information for developing a stroke prediction model.

Further exploration of age distribution based on other qualifying factors.

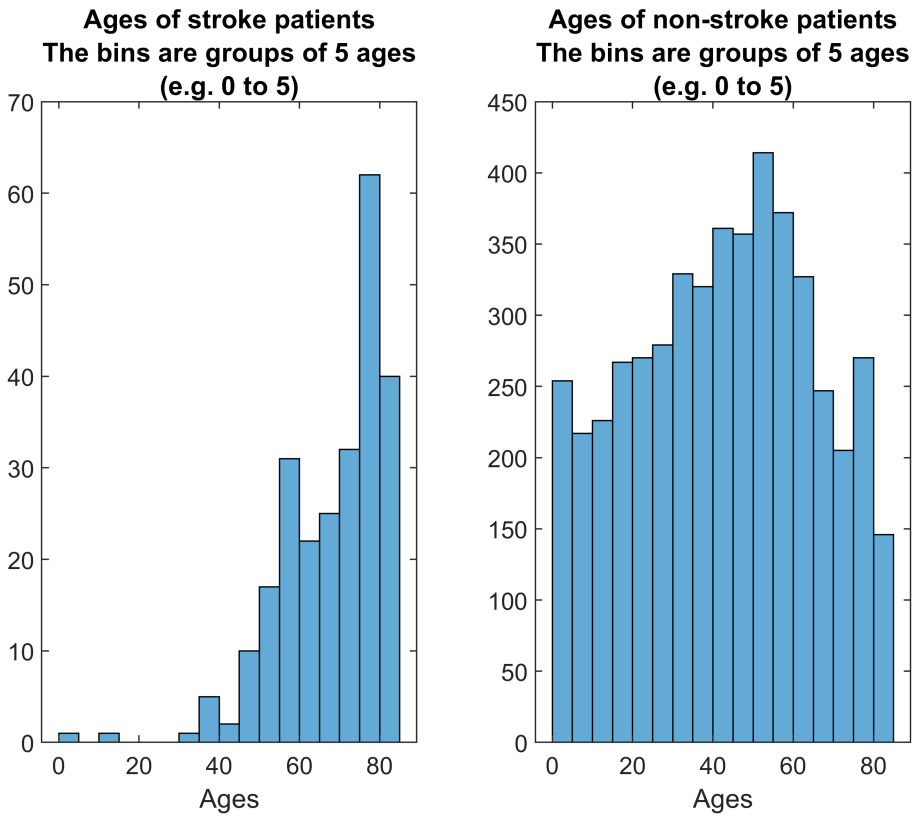
Age is an important qualifier in the context of lifestyle choices effecting a person's chances of having a stroke. It is likely at younger ages that strokes are frequently a result of other medical conditions rather than a child's lifestyle choices, which is what we are generally considering with this dataset. Similarly, elderly subjects in the study are more likely to have additional medical conditions that may play a role in their chances of having a stroke. The next step was to briefly investigate the age distributions of certain attributes (like whether or not someone had a stroke) based on ages.

```
% This line uses "bin_conditional_extract" (read: "Binary Conditional
% Extract") to extract the ages (in a vector) of people who had a stroke
[ages_with_stroke, ages_no_stroke] = bin_conditional_extract(strokedata,"age","stroke",1);
```

Now that the ages have been separated into two groups, it is time to look at how ages are distributed for stroke patients compared to non-stroke patients.

```
age_distribution_stroke_conditional = figure(20); %20 is a random figure number
```

```
clf(age_distribution_stroke_conditional)

subplot(1,2,1)
%going to use features of "historgram" function to do binning
ages_stroke_patients = histogram(ages_with_stroke,'BinMethod','auto');

title_subplot1 = sprintf("Ages of stroke patients\nThe bins are groups of %d ages\n(e.g. %d to
                          (ages_stroke_patients.BinEdges(2)-ages_stroke_patients.BinEdges(1)
                           ages_stroke_patients.BinEdges(1), ages_stroke_patients.BinEdges(2
title(title_subplot1)
xlabel("Ages")


subplot(1,2,2)
ages_no_stroke_pats = histogram(ages_no_stroke,'BinMethod','auto');

title_subplot2 = sprintf("Ages of non-stroke patients\nThe bins are groups of %d ages\n(e.g. %d
                         (ages_no_stroke_pats.BinEdges(2)-ages_no_stroke_pats.BinEdges(1)),...
                         ages_no_stroke_pats.BinEdges(1), ages_no_stroke_pats.BinEdges(2));
title(title_subplot2)
xlabel("Ages")

hold off
```



Based on the plots above, it certainly looks like there is a correlation between age and a person's chances of having a stroke. This is useful information with regard to our end goal, understanding what risk factors can be

used to predict a person's chances of having a stroke, and will come up later as we try to find a way to predict a person's chances of having a stroke.

However, most importantly, this age information provides some valuable underlying context to the rest of our data analysis: young children and babies, who do not have useful inputs for many of the attributes investigated (like smoking status, BMI, hypertension, etc.), probably do not contribute helpful information about how these risk factors effect a person's chances of having a stroke. **Moving forward, it will likely be helpful to look at only patients in the age range 18+ becasue they are full grown adults that are more responsible for their lifestyle choices and accurate information about the relationships between the risk factors and stroke rates. The patients under 18 perhaps suffered a stroke due to other issues unrelated to lifestyle, such as other illnesses or having the genetic tendency for a stroke.**

Before proceeding to remove a set of ages in the data, a test of significance was done on the two distributions above to test our hypothesis that the distribution of ages among stroke patients is signficantly different than distribution of all patients in the study.

In other words,

- A two sample t-test was done to determine if the two populations in the plot above represent the same normal distribution of people (Null hypothesis). Alternatively, if there is a significant difference between the distributions, then the test will indicate that there is a signficant difference in the data sets, which are soley different based on the condition that one group is former stoke patients.
- Null hypothesis (returns 0 for no significant difference): The two distributions are from the same population of people. In other words, the fact that one group is only stroke patients does not significantly effect the distribution of ages.

```
[h, p] = ttest2(ages_with_stroke,ages_no_stroke);
fprintf("The t-test returned h = %d. The chance that these distributions represent the same pop
```

```
The t-test returned h = 1. The chance that these distributions represent the same populations of ages is 0.000%.
```

The test supports the conclusion that stroke patients have a signficantly different age distribution, which can be seen graphically as being higher ages among stroke patients. Now, the stroke data will be re-extracted but will only consider patients who are 18+ in age.

```
clearvars ages_no_stroke ages_with_stroke; %clearing some space first
```

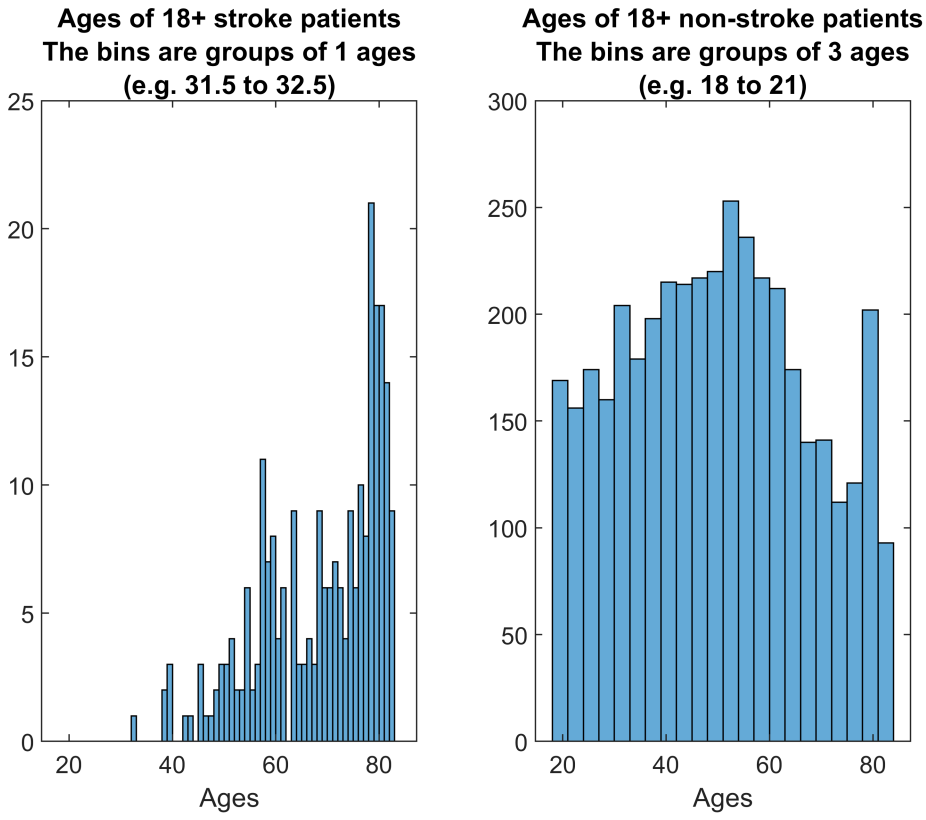
NOTE: The 18+ patients were extracted into a new table to use for data analysis in the Data Scrubbing and Extraction section above.

The 18+ patients have been extracted to **"strokedata_18plus."**

Now, the age distributions will be displayed briefly for the new data.

```
[ages_stroke, ages_no_stroke] = bin_conditional_extract(strokedata_18plus,"age","stroke",1);

age_distribution_stroke_conditional = figure(26); %26 is a random figure number
clf(age_distribution_stroke_conditional)
```

```
subplot(1,2,1)
%going to use features of "historgram" function to do binning
ages_stroke_patients = histogram(ages_stroke,'BinMethod','auto');

title_subplot1 = sprintf("Ages of 18+ stroke patients\nThe bins are groups of %d ages\n(e.g. %.
                          (ages_stroke_patients.BinEdges(2)-ages_stroke_patients.BinEdges(1)
                           ages_stroke_patients.BinEdges(1), ages_stroke_patients.BinEdges(2
title(title_subplot1)
ages_stroke_patients.BinLimits = [18, 84];
xlabel("Ages")



subplot(1,2,2)
ages_no_stroke_pats = histogram(ages_no_stroke,'BinMethod','auto');

title_subplot2 = sprintf("Ages of 18+ non-stroke patients\nThe bins are groups of %d ages\n(e.g
                         (ages_no_stroke_pats.BinEdges(2)-ages_no_stroke_pats.BinEdges(1)),..
                         ages_no_stroke_pats.BinEdges(1), ages_no_stroke_pats.BinEdges(2));
title(title_subplot2)
ages_no_stroke_pats.BinLimits = [18, 84];
xlabel("Ages")

hold off
```




```
clearvars h p ages_stroke ages_no_stroke;
```

The data extracted in this section was further modified during feature development, so the data strokedata_18plus was not actually used to develop the stroke model - a variation of this data table was used though.

Data Analysis: Using the Classification Learner to Develop a Stroke Prediction Model

Some scripting and data display is done here, but the remainder of the project (analysis and images of our work) is primarily completed in attached documentation.

Below displays some information about the best prediction model identified (Model 1.1 - Fine Type Tree Class) - named "FineTreeTypeStrokePrediction"

```
load("FineTreeTypeStrokePredictionModel.mat") %should load Model 1.1 using the "Fine Tree" clas

fprintf("\n%s\n\n",FineTreeTypeStrokePrediction.About)
```

```
This struct is a trained model exported from Classification Learner R2020b.
```

```
fprintf("\n%s\n\n",FineTreeTypeStrokePrediction.HowToPredict)
```

```
To make predictions on a new table, T, use:
  yfit = c.predictFcn(T)
replacing 'c' with the name of the variable that is this struct, e.g. 'trainedModel'.

The table, T, must contain the variables returned by:
  c.RequiredVariables
Variable formats (e.g. matrix/vector, datatype) must match the original training data.
Additional variables are ignored.

For more information, see How to predict using an exported model.
```

The section below is meant to demonstrate how predictions can be made with the model. The assessment was done within the classification learner app, so all data has been used for training or assessment by the model, rendering additional predictions on the data as redundant useage. Thus, this demonstration of predictions and comparison to the true results is just to demonstrate how the model is used.

```
randvec = randi([1,4200],1,20);
random_strokedata = strokedata_prepped(randvec,["gender","age","work_type","avg_glucose_level",

predictions = FineTreeTypeStrokePrediction.predictFcn(random_strokedata);

comparisontable = strokedata_prepped(randvec,"stroke");
comparisontable.stroke_modelprediction = predictions;

disp(comparisontable)
```

stroke	stroke_modelprediction

```
0               0
0               0
0               0
0               0
1               0
0               0
0               0
0               0
0               0
0               0
1               0
0               0
0               0
0               0
1               1
0               0
0               0
0               0
0               0
0               0
```

It's gonna be a lot of zeros ... which was basically the problem dicussed in much of our analysis.

Data Analysis: Using the Classification Learner to Develop a Stroke Prediction Model

At this point, the strokedata_prepped table was used to develop a machine learning model. The entire table was passed to the application. This was done with the knowledge that the application is capable of performing a self-assessment of itself. The model application was instructed to separate 15% of the data in "strokedata_prepped" to use as an assessment tool. As models were developed, this randomly separated data was used to assess the accuracy of each model iteration.

Once again, the medical risk is based on smoking history, heart disease, hypertension and the scores are as follows:

- No risk factors (i.e. not a smoker, no heart disease, and no hypertension) === 0
- 1 risk factor === 1
- 2 risk factors === 2
- All risk factors === 3

Now, some brief additional context to outline what was provided to the classification learner. The data table mentioned above was the only data provided. As just noted, a section of this data was separated out of assessment. The “gender”, “age”, “work_type”, “avg_glucose_level”, “bmi”, and “medical_risk” features were all provided as “predictors” - the data being used to predict which classification a subject should receive. The “response” that the model was trying to classify subjects into was the “stroke” column of the table.

With little experience and understanding of the classification learner models, the data was used to train a couple functions that were capable of handling the type of information provided. Given the mixture of categorical and numerical data, there were a limited number of models capable of properly using both. Also, options may have been limited because principle component analysis (PCA) was enabled, which will be discussed more shortly.

The “All Quick-To-Train” option was used to train three models that could handle the data. All three were variations of decision tree models. With limited experience, it was challenging to understand exactly what options to select to get the best modeling results. Training more than one model was recommended and was useful in showing how slightly different models yield different outputs from the same data. Additionally, the decision was made to enable PCA. It was slightly unclear if there would be any repercussions of this decision (since PCA does not work with categorical features), it was an understood concept that would seemingly simplify the relationship of data to the classification output. The only downside of enabling the feature was a reduced understanding of how the model related the inputs and outputs. However, the model functionality was already a bit of a mystery, so modifying the analysis process to include PCA did not seem unreasonable. The use of the categorical data, which was a concern when deciding how to prepare models, seems to have not been an issue since the model descriptions reported “All 2 categorical predictors are used in the model. PCA is not applied to categoricals.”

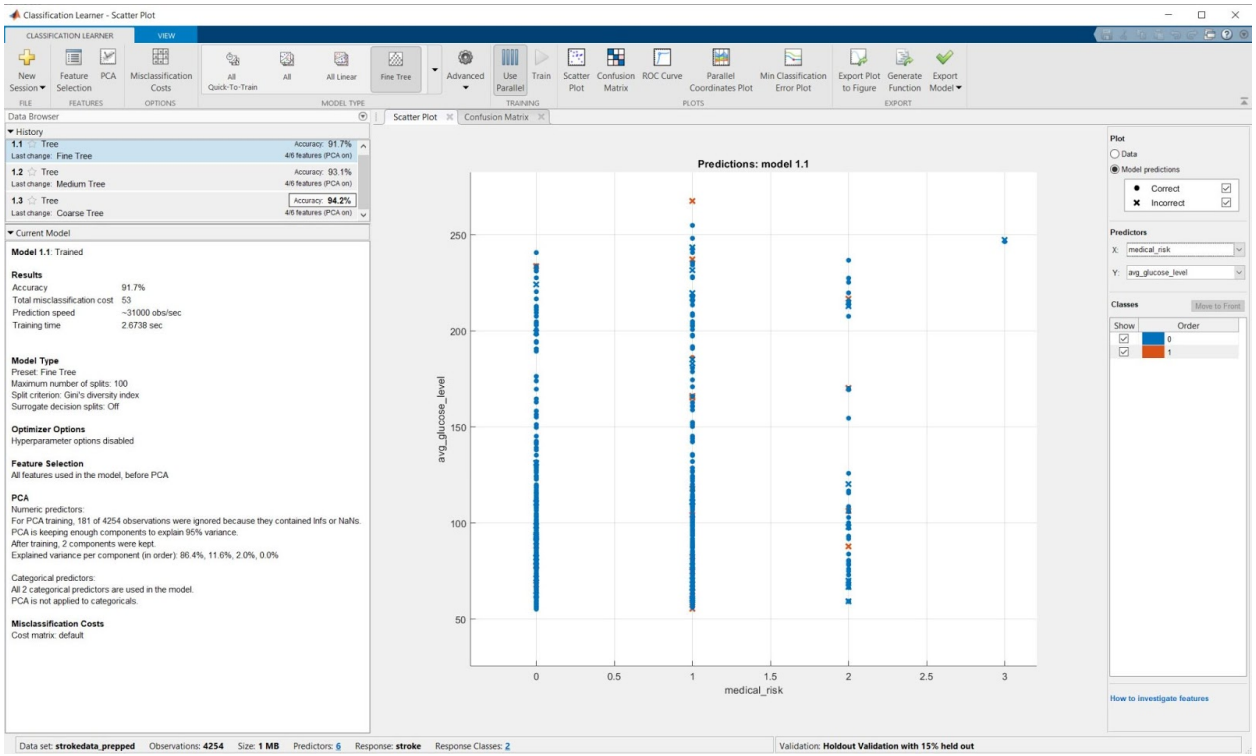
The data was provided and options desired for our model were selected. Now, the provided data was used to train the models with our data with the goal of predicting the stroke response data. According to MATLAB the accuracy is high, for all three tree models (91.7% Fine Tree, 93.1% Medium Tree, 94.2% Coarse Tree). At first glance, it seemed the data yielded positive results for our work. Perfect prediction would have been great, but given the basic data provided to the model 90% seemed exceptional. The next step was looking at the assessment tools for each model that provided more context about these accuracy percentages. This was where it became clear that the models trained were not quite as valuable as the accuracy number had presented.

The assessment information of each model will be explained in more detail. In short, the models predicted non-stroke patients very well, but generally failed to actually predict strokes. The Fine Tree model, which had the lowest accuracy, predicted the most strokes from assessment data set, but it was only 3 patients who fell into this category among the more than 600 subjects that were used for assessment. While looking through the models and assessing them, which will follow this, was valuable, it was quickly apparent that the general conclusion from this work was that the data available was not appropriate for trying to predict if a person is likely to have a stroke.

Intuition might be “predicting someone to have a stroke from lifestyle choices alone would be much too convenient” to not have been discovered already. Whether or not this is true, the failure in this case seemed to be far more dependent on the data used. As noted early on in the data exploration, there were not many patients in the study who suffered a stroke. There was only a small chance that the data available could be used to decisively group these few patients from the rest of the group of non-stroke patients which had significantly more room for variation. It might be unlikely that the risk factors provided here could ever be used to consistently predict strokes. Strokes are a complex occurrence in the body, and the data analyzed here is not even directly linked to the response itself. With a significantly larger dataset, it might be possible to find a general cluster of stroke patients according to the features assessed in this work. Even if the accuracy of the model was much lower, it would still be a

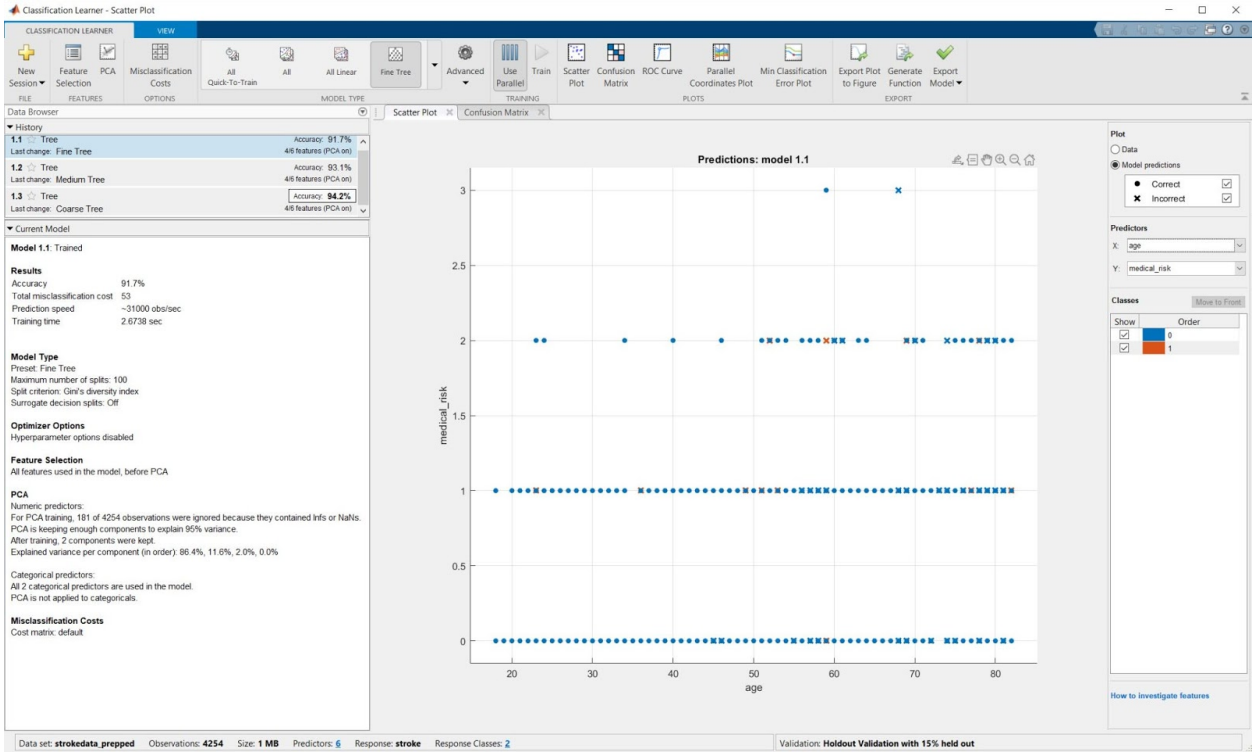
valuable tool for identifying a significantly smaller subset of the general population that should consider making changes to their lifestyle for their health. Thus, the conclusion for this set of data is more inconclusive than failure, and the approach might be valuable with more information.

After addressing the experience of using the classification learner overall, the intricacies of assessing the models will be examined in more detail.

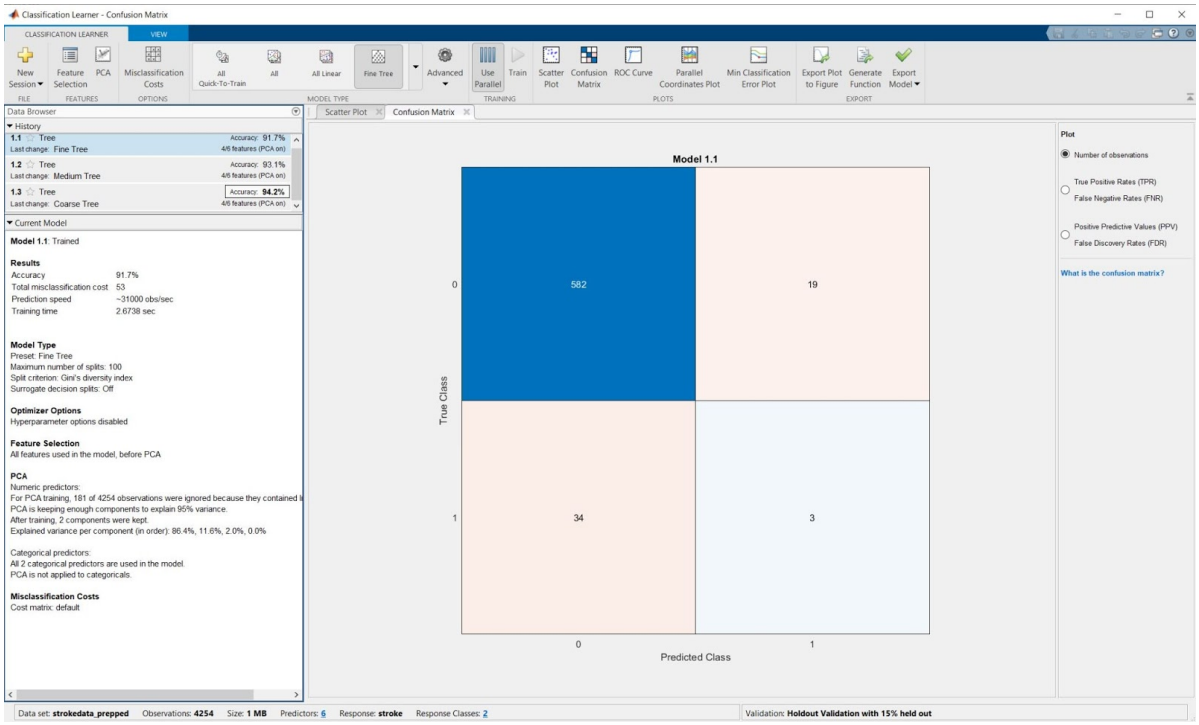


The plot of medical risk by the average glucose level was used to try to predict if a patient gets a stroke or not, since smoking, heart disease, hypertension and elevated glucose levels are believed to cause strokes. The screenshot above is the predictions model based on those factors. A red mark, or a 1, is indicative of someone having a stroke. Further, a red ‘o’ is a correct prediction, meaning the patient was expected to have a stroke and in fact did have a stroke, while a red ‘x’ is an incorrect prediction, meaning the patient was expected to have a stroke, but did not. A blue mark, or a 0 is indicative of someone not having a stroke. A blue ‘o’ is a correct prediction, meaning the patient was not expected to have a stroke and did not have one, while a blue ‘x’ is an incorrect prediction, meaning the patient was not predicted to have a stroke and still had one. Based on our research, the points where the medical risk score and the average glucose level are both higher, we would expect to see more occurrences of strokes, or red ‘o’s. That is not what we see.

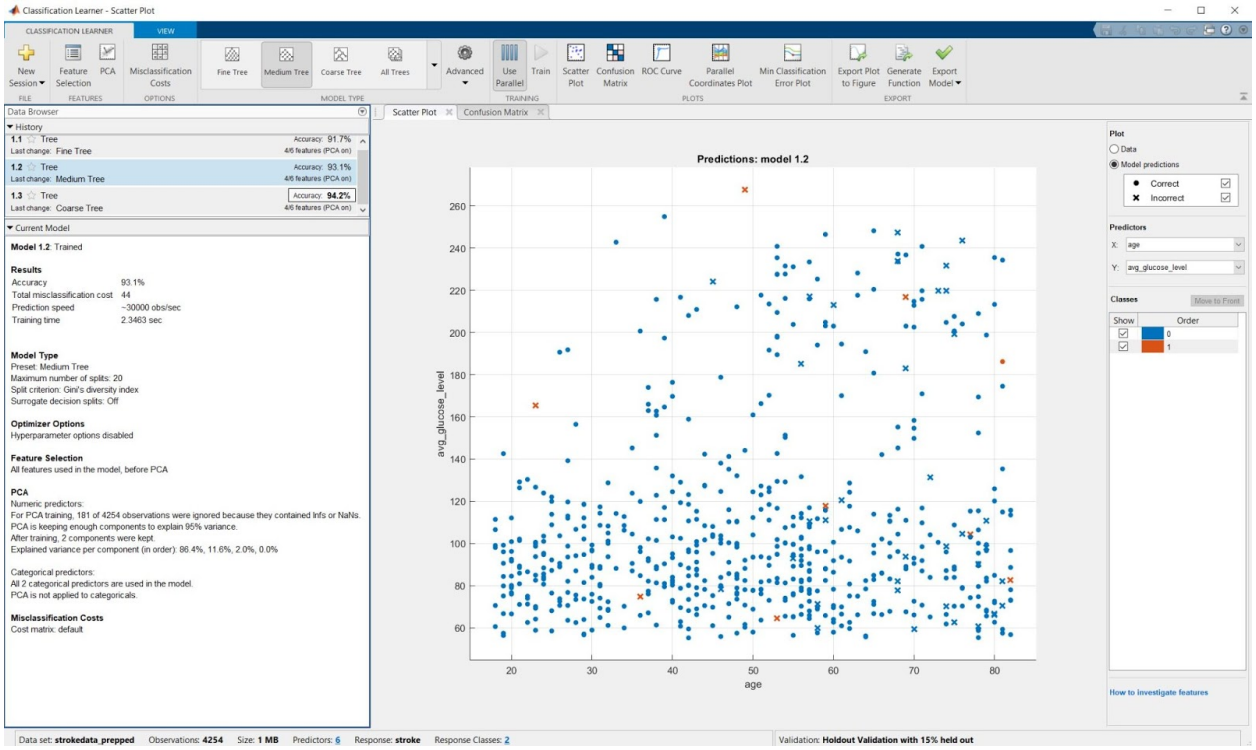
We then graphed medical risk by age, shown below, to see if being at an older age and having a higher medical risk would lead to more strokes, as one would predict based on our preliminary research. Once again, we saw a MATLAB accuracy in the 90th percentile. However, visually it does not look to be that accurate.

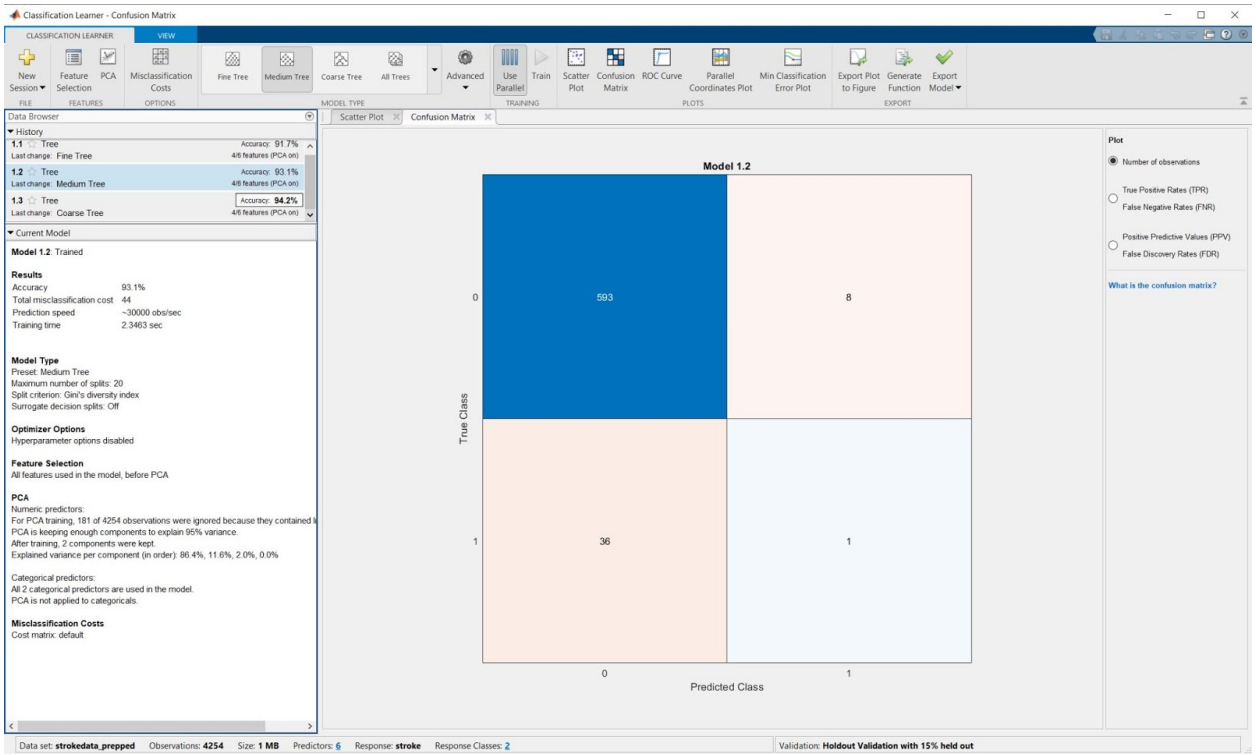


We wanted to see if we could easily quantify visually those results above. In order to do that we looked at a different plot type. We looked at the corresponding ‘Confusion Matrix’ (shown below) which displays the number of correct predictions, i.e. predicted class: 0, true class: 0, 582 predictions, and predicted class: 1, true class: 1, 3 predictions. It also displays the number of false positives, where a patient was predicted to have a stroke, but did not, predicted class: 1, true class: 0, 19 predictions, and the number of false negatives, where a patient was predicted not to have a stroke, but did, predicted class: 0, true class: 1, 34 predictions. This shows that even though according to MATLAB there is a high accuracy, the numbers of false positives and false negatives is quite high compared to the number of correct positives. This indicates that the model did not accurately predict the number of people who would have a stroke.

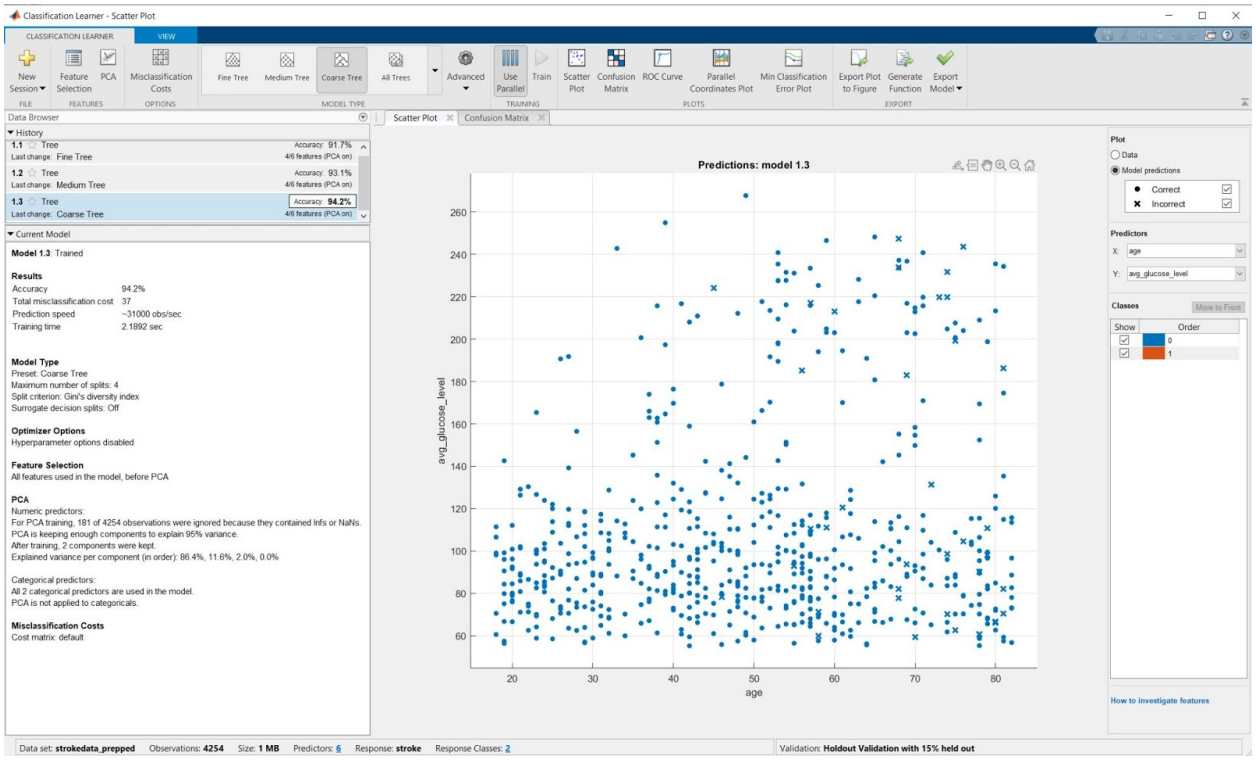


We next plotted average glucose level by age to determine how well those factors would predict stroke. We would predict, based on our preliminary research, that a high average glucose level and an older age would result in more strokes. Here we looked at the Medium Tree model which has a 93.1% accuracy according to MATLAB. However, when we look at the corresponding Confusion Matrix we see 36 false negatives and 19 false positives, with only 3 true positives. The Confusion Matrix shown below, once again shows that the model did not very accurately predict the number of strokes within the patient population based on average glucose level and age.


Classification Learner - Scatter Plot
Predictions: model 1.2
avg_glucose_level
age
Plot
Data
Model predictions
Correct
Incorrect
Predictors
X: age
Y: avg_glucose_level
Classes
Show
Order
0
1
How to investigate features
Data set: strokedata_prepped Observations: 4254 Size: 1 MB Predictors: 6 Response: stroke Response Classes: 2
Validation: Holdout Validation with 15% held out


Classification Learner - Confusion Matrix
Model 1.2
593
8
36
1
True Class
Predicted Class
Plot
Number of observations
True Positive Rates (TPR)
False Negative Rates (FNR)
Positive Predictive Values (PPV)
False Discovery Rates (FDR)
What is the confusion matrix?
Data set: strokedata_prepped Observations: 4254 Size: 1 MB Predictors: 6 Response: stroke Response Classes: 2
Validation: Holdout Validation with 15% held out

Finally we looked at the Coarse Tree model for predicting stroke based on average glucose level and age. The accuracy came back for the Coarse Tree model at 94.2% which is a very good accuracy measure. However, on the graph we do not see any red marks. Perhaps this is because the red data points are behind the blue data points.



Using the “All Quick-To-Train” method, three decision tree models were produced for the trained data. When we plotted the different risk factors of having a stroke (age, medical risk (smoking, heart disease, hypertension), average glucose level) in the classification learner to try to predict if someone has a stroke or not, MATLAB returned the decision tree models with an accuracy above 90% for all 3. This would indicate that our risk factors are indeed good predictors if someone is likely to have a stroke. However, when we looked at the Confidence Matrix produced by these different pairings, the number of false positives was high compared to the number of true positives. The number of false negatives compared to true negatives was a better ratio. This would indicate that the model does have trouble accurately predicting the likelihood of someone having a stroke based on risk factors such as their average glucose level, age, medical risk (including smoking history, heart disease, hypertension). In conclusion, according to MATLAB our model could be used with over 90% accuracy to predict if someone is likely to have a stroke. It is important though to keep in mind that false positives and false negatives still occur. However, if people are at high risk for a stroke, i.e. have any combination of the following risk factors: hypertension, history of smoking or heart disease, high average glucose level, high BMI, it would be beneficial for their health to try to change their lifestyle in someway to reduce the risk of stroke.

Biased Article

Why We Need Accountable Algorithms by Cathy O'Neil

Algorithms separate people into different groups of "winners and losers", based on factors such as class, gender, race. Why is that? It is because algorithms are trained. They are trained on curated historical data, historical information of successes and failures. They examine data, but there are two major problems with data. Data can be very messy, so one has to make sure it is clean and relevant because issues such as spelling errors or vague information can drastically change how the data is read. Another issue with data is that information is not equally distributed. People in the minority and people on welfare or people with criminal records will have more data in the system then others. Recidivism risk scores for example are used by courts to compare a criminal defendant's profile to another's to see if they are expected to return to prison. A higher score can equate to a longer term. Criminal defendants have no way to protest or understand how their scores are determined. Just one example of how algorithms compare people as just data points, and not as human beings. It's also important to keep track of the trade-off between the number of false positives and the number of false negatives produced from data algorithms. In an ideal world these trade-offs would be made clear and errors would be kept track of, O'Neil believes these errors are not given the attention they should be.

Our history is overwhelmingly filled with racism, sexism and xenophobia, so O'Neil states we must assume algorithms inherently contain the same unethical biases. Data science is just codifying these prejudices, making them less visible to the human eye, but behind the curtain, they're more apparent in society than ever. Ethical nondiscriminatory constraints are expensive. It's expensive to add layers and to keep monitoring layers of the algorithm. No one wants to be the company at a competitive disadvantage when it comes to profit margins, so they all use similar algorithms that are inherently prejudiced. O'Neil believes that unless there are standards for anti-discrimination and fairness laws, we will not be able to move forward into a ethically-just and fair world.

Citation:

O'Neil, C. (2017, August 7). *Why We Need Accountable Algorithms*. Cato Unbound. https://www.cato-unbound.org/2017/08/07/cathy-oneil/why-we-need-accountable-algorithms.