Exploratory Data Analysis: Which genes and their expression levels may be associated with developing familial alzheimer's disease?

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Introduction

This document aims to explore, analyse and explain the data set being used in answering the following research question: “Given 10 attributes, how do they compare in predicting the chances of a person’s risk of a stroke?”. As the res earch question implies, the data set consists of 10 attributes. This project has the goal of comparing those attributes, so that the most likely predictors for a stroke may be deduced. Some attributes affect each other, while others may not. Analysis of these correlations can help in finding the rankings of the attr ibutes.

To get a feel for what the scope and attributes of the data set consists of, it will be loaded and the first 10 results will be displayed.

```
main <- read.csv("../data/stroke-data.csv")
head(main)
```

```
##      id gender age hypertension heart_disease ever_married     work_type
## 1  9046   Male  67            0             1          Yes       Private
## 2 51676 Female  61            0             0          Yes Self-employed
## 3 31112   Male  80            0             1          Yes       Private
## 4 60182 Female  49            0             0          Yes       Private
## 5  1665 Female  79            1             0          Yes Self-employed
## 6 56669   Male  81            0             0          Yes       Private
##   Residence_type avg_glucose_level  bmi   smoking_status stroke
## 1          Urban            228.69 36.6 formerly smoked      1
## 2          Rural            202.21  N/A    never smoked      1
## 3          Rural            105.92 32.5    never smoked      1
## 4          Urban            171.23 34.4          smokes      1
## 5          Rural            174.12   24    never smoked      1
## 6          Urban            186.21   29 formerly smoked      1
```

```
nrow(main)
```

```
## [1] 5110
```

There are 12 attributes, 10 of which will be used in the analysis: Gender, age hypertension, heart_disease, ever_married, work_type, residence_type, avg_gluco se_level, bmi and smoking_status. The last column indicates whether the person has already experienced a prior stroke. This can be used to the train the machine learning model which will be utilized to answer the research question.

There are 5110 entries in this data set. This is also why the row numbers will not be replaced with the id’s, because there is no order in the id numbers. They exceed the number 5110.

The attributes and their units can be seen in the code book on the next page.

Codebook

```
knitr::kable(codebook)
```

Column	Unit	Description
ID	Number	Unique patient identifier
Gender	Text	“Male”, “Female” or “Other”
Age	Number	Age of patient
Hypertension	Boolean	Whether patient has hypertension
Heart_disease	Boolean	Whether patient has a heart disease
Ever_married	Boolean	Whether patient has ever been married
Work_type	Text	Occupation status of patient
Residence_type	Text	Patient living enviroment
Avg_glucose_level	Number	Average glucose level in blood
BMI	Number	Body mass index of patient
Smoking_status	Boolean	Whether patient smokes or not
Stroke	Boolean	Whether patient has ever experienced a stroke

Initial Data and Attributes

In this section, the attributes will be examined individually. What these attri butes could mean for the research question will be discussed. Correlations will be observed in a later section. Any preprocessing or cleanup required will also be performed in this section.

ID

This column is neither noteworthy for analysis or data structure. This column will therefore be dropped, because the dataframe used already has row numbers and this makes the ID redundant.

```
main <- main[2:12]
```

Age

The age of the patient. At first sight, it might look redundant for this data to be stored as a float, since most of the data consists of a rounded age number. Some of the entries contain very young patients. The younger a patient is, the more important the specifity of the age is, since the age difference is still significant at that point. It is for that reason that any patient under the age of 2 will contain a float number, with two decimal numbers. A couple of those instances will be shown in vector format below:

```
head(c(main[main$age < 2, 2]))
```

```
## [1] 1.32 0.64 0.88 1.80 0.32 1.08
```

The likelihood of a person experiencing a stroke increases with age. This will therefore be an important attribute in the analysis.

Hypertension

This indicates with a 0 or 1 whether the patient is affected by hypertension. The first attribute which is relevant to the heart status of a patient. These types of attributes will always be important, because any heart condition tends to come with an increased risk of experiencing a stroke. Since this is a boolean, the patient either has hypertension, which is indicated with a 1, or not, which is indicated with a 0. This could be a harder type for the later machine learning model to work with. Correlations will probably be found between hypertension and the other attributes. No further cleanup is required here.

Heart Disease

Similar to the previous attribute, this is also an important element when trying to predict stroke risk. The previous observation also applies to this attribute.

Ever married

This displays whether the patient has ever been married in their lifetime. This will most likely not bet detrimental in predicting the stroke risks of patients. But this is part of the dataset, so it will therefore be compared with the other attributes, to see where it ranks with it's prediction.

Work Type

A similar attribute to the prior one. Will most likely not be a good predictor for stroke risk. But it may rank higher than the marriage attribute. Some sector s could theoretically expose a person to environments where strokes are more likely.

Residence Type

Considering that some types of residency might be healthier than others, this attribute may be slightly important in determining the stroke risk of a person.

Average Glucose Level

This may be more important than the prior three attributes, especially when these levels are unusually low or high. The literature concerning glucose levels and their connection to strokes is still being debated. Some papers conclude that it is not detrimental when observed in non-diabetic people.

BMI

The body mass index is an indicator for how a person's weight/height ratio. Age and gender also being taken into consideration for the calculation. Both extreme ends of this attribute could be important to the stroke risk of a person. Higher BMIs are also associated with developing heart disease. Glucose levels may also be affected. Several other attributes are most likely going to have a correlation to this attribute.

Smoking Status

Whether a patient is smoking will most likely affect some of the other attribute s in this data set. Whether these significant correlations will need to be tested. The smoking status is unknown for some of the patients.

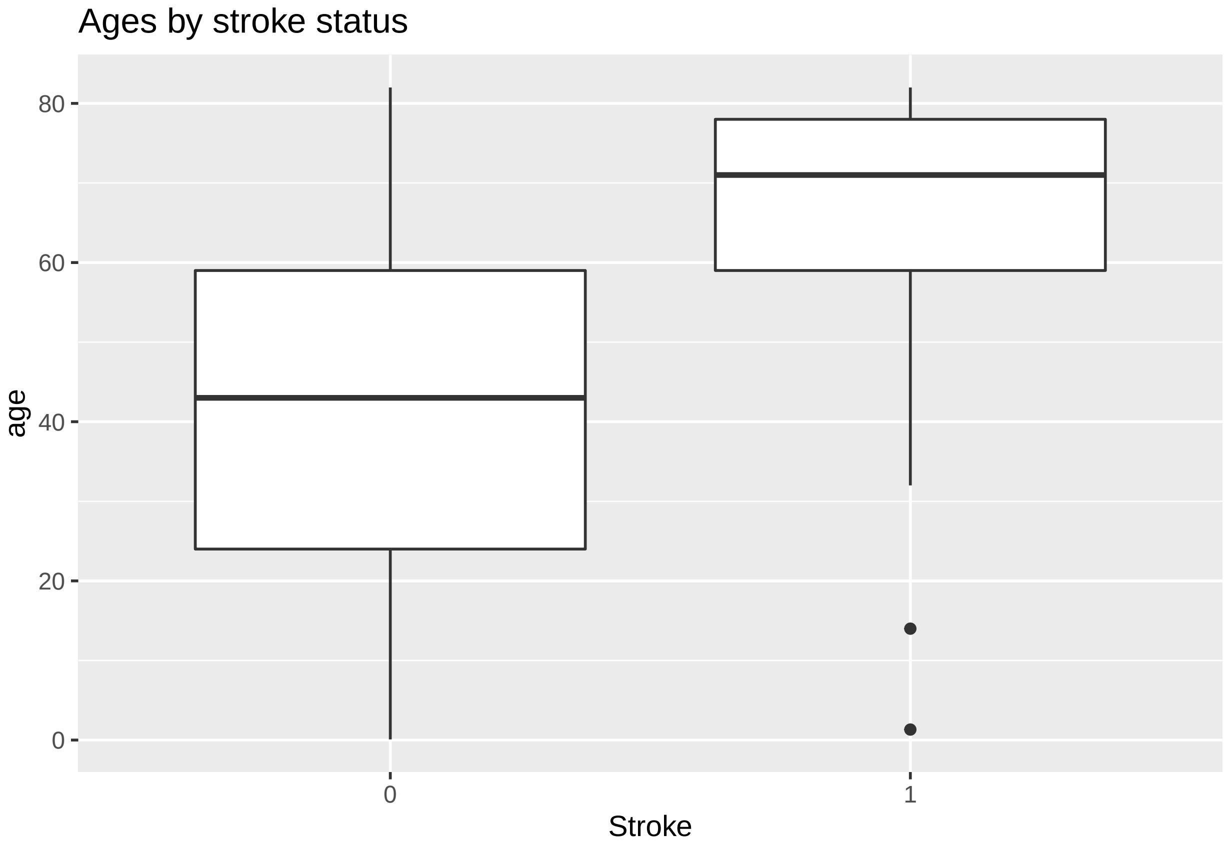
Stroke

The column indicating whether the patient has ever had a stroke. This will be used to train a machine learning model in the actual journal.

Correlations

Following the examination of the intial values and attributes, they may now be compared so that trends and correlations can be observed. Starting with the first attribute, which will most likely be important in determining stroke rist, age. By plotting the summaries of patients who had a stroke, and those who did not, maybe a link can be seen between the two.

```
no_stroke <- main[main$stroke == 0,]
stroke <- main[main$stroke == 1,]
ggplot(main, aes(x=factor(stroke), y=age))+geom_boxplot()+ggtitle("Ages by stroke status")+
  xlab("Stroke")
```



This plot shows that the group of people who have had strokes are, on average, older than the group who has not experienced a stroke. This may also be observed with a summary

```
summary(no_stroke$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.08   24.00   43.00   41.97   59.00   82.00
```

```
summary(stroke$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.32   59.00   71.00   67.73   78.00   82.00
```

It is worth noting that the no stroke group does contain plenty of patients of higher age.

Now, a t-test may be performed to determine whether age is a significant difference between the two groups. A one sample t-test is most appropriate here, considering that every patient's risk is independent from another

```
t.test(no_stroke$age, stroke$age)[3]
```

```
## $p.value
## [1] 2.115685e-95
```

Without considering the other attributes, it seems that with that p-value, the two age means are significantly different.

These tests may be performed for all of the other attributes too. Showing them all individually would be redundant, since the correlations between having a stroke and the other attributes relating to the heart already have literature confirming them.

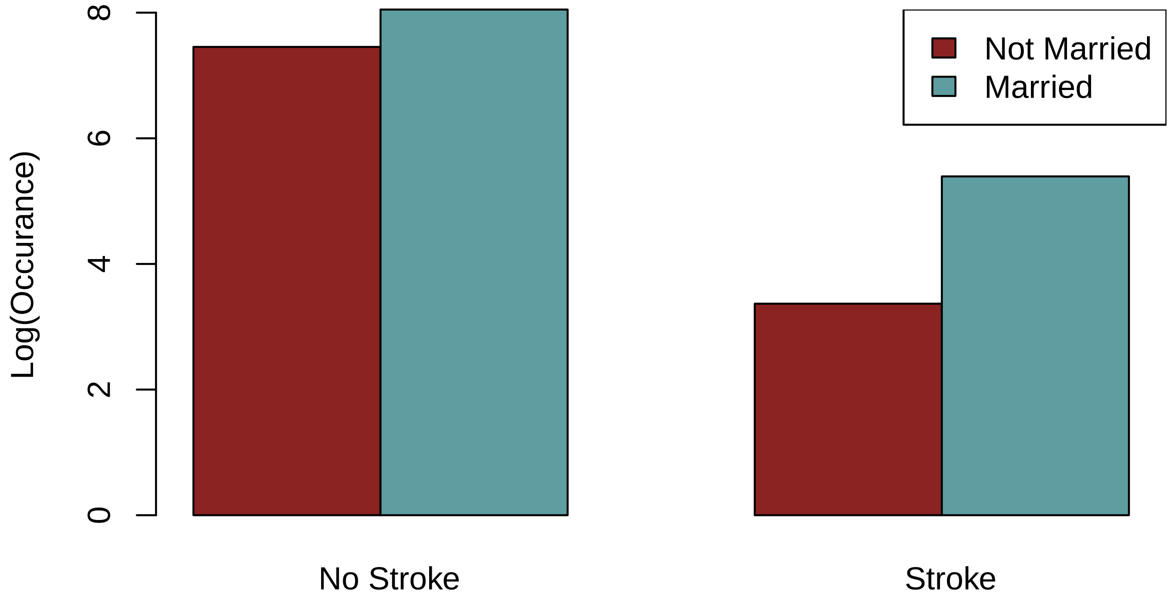
The attributes, which may seem less influential at first would be worth checking manually. The marriage status being the first one to consider. This column is not a boolean number, even though it is comparable to the other 1 or 0 columns. For consistency, yes will become 1 and no will become 0.

```
main[main$ever_married == "Yes",]$ever_married <- 1
main[main$ever_married == "No",]$ever_married <- 0
no_stroke <- main[main$stroke == 0,]
stroke <- main[main$stroke == 1,]

no_s_table <- log(table(no_stroke$ever_married))
s_table <- log(table(stroke$ever_married))

vec <- c(no_s_table[1], no_s_table[2], s_table[1], s_table[2])

barplot(vec, space = c(0,0,1,0), col = c("brown4", "cadetblue"),
        names.arg = c("                       No Stroke","",
                      "                       Stroke",""), ylab = "Log(Occurance)")
legend("topright", c("Not Married", "Married"), fill = c("brown4", "cadetblue"))
```



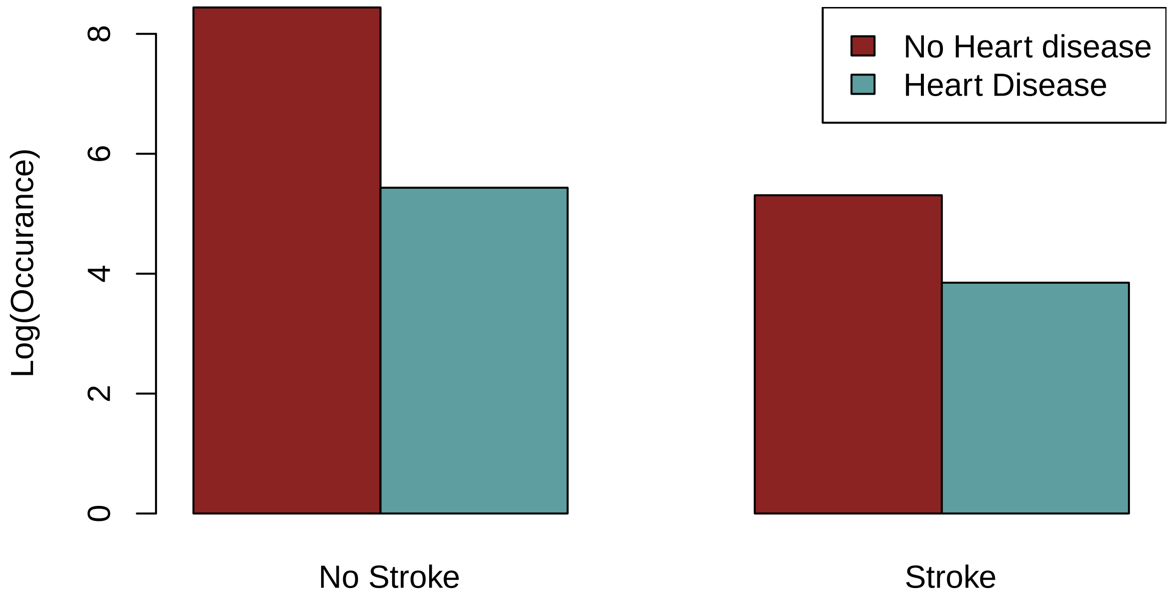
The data has been normalized, so that it may be properly displayed. The group of people with no stroke quite lower than the other group. This plot shows that for both groups, the amount of people who have ever been married is bigger than the not married group. It makes sense for there to be proportionally more people who have married than less when looking at the stroke bars. This is because people who have had a stroke are on average older than the other group. It is also safe to assume that the older a person is, the more likely that they have ever been married in their life.

Now, it is possible to make a similar plot, but with a more relevant attribute. Heart disease would be a good choice.

```
no_s_table <- log(table(no_stroke$heart_disease))
s_table <- log(table(stroke$heart_disease))

vec <- c(no_s_table[1], no_s_table[2], s_table[1], s_table[2])

barplot(vec, space = c(0,0,1,0), col = c("brown4", "cadetblue"),
        names.arg = c("                        No Stroke","",
                      "                        Stroke",""), ylab = "Log(Occurance)")
legend("topright", c("No Heart disease", "Heart Disease"),
       fill = c("brown4", "cadetblue"))
```



The assumption would be that a heart disease has a correlation with having a stroke. The bar plot above does not show anything out of the ordinary. It might be difficult to find any correlation by just looking at these bar plots. Calculating the differing odds between two groups could help.

```
ratio1 <- as.vector(table(no_stroke$heart_disease)[2])/nrow(no_stroke)
ratio2 <- as.vector(table(stroke$heart_disease)[2])/nrow(stroke)
ratio1
```

```
## [1] 0.04710965
```

```
ratio2
```

```
## [1] 0.188755
```

In this case, it does appear that the ratio is different. A calculation can be made to determine how much more likely patients with heart conditions may get a stroke.

```
ratio2/ratio1
```

```
## [1] 4.006717
```

Judging by that simple calculation, a patient with a heart condition has 4 times the likelihood of getting a stroke than someone without a heart condition.

A bar plot showing the correlation between BMI and other attributes could also show correlations. Before doing that however, it seems that the BMI column consists of characters, not numbers. This must first be changed.

```
typeof(main$bmi)
```

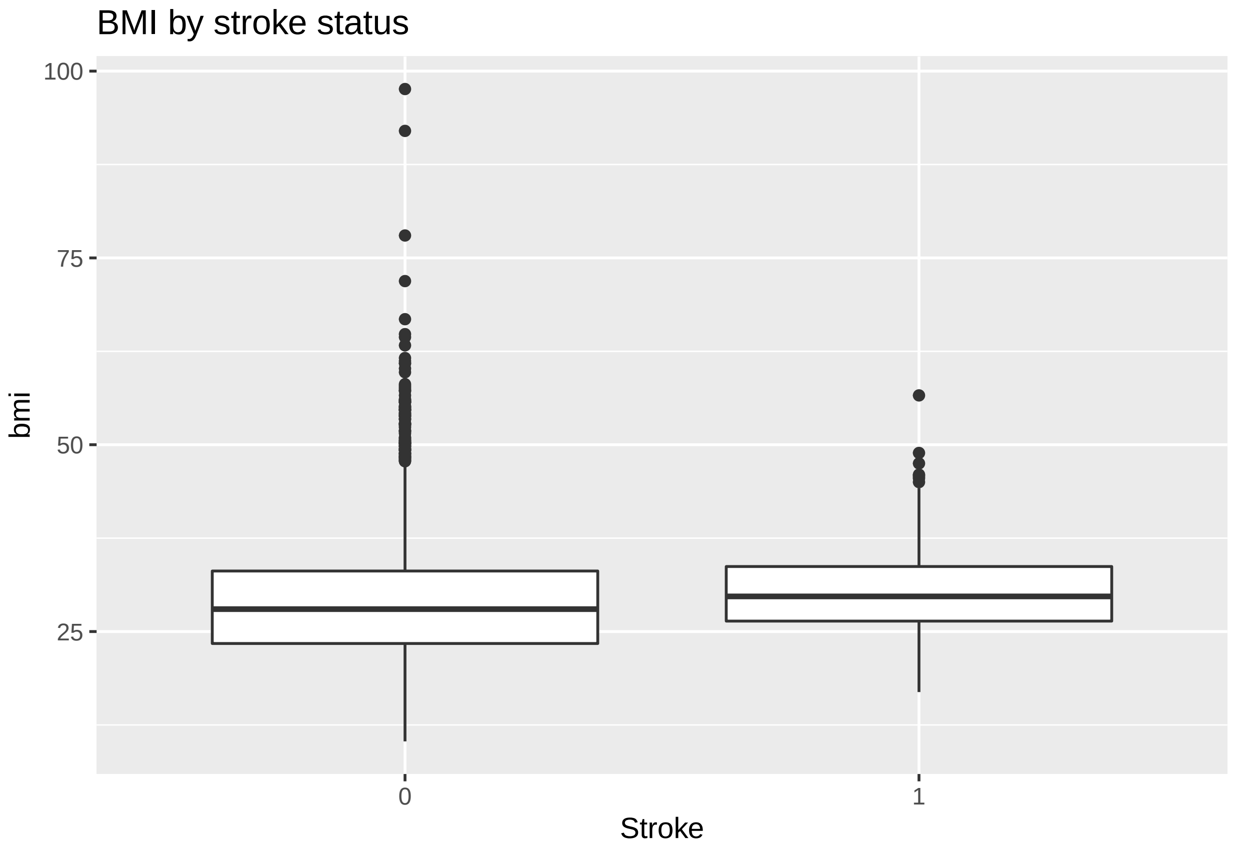
```
## [1] "character"
```

```
main$bmi <- as.numeric(main$bmi)
```

```
## Warning: NAs introduced by coercion
```

```
ggplot(main, aes(x=factor(stroke), y=bmi))+geom_boxplot()+ggtitle("BMI by stroke status")+
  xlab("Stroke")
```

```
## Warning: Removed 201 rows containing non-finite values (stat_boxplot).
```



There are around 200 NA entries, which were not taken into consideration when creating the plots.