Stroke Prediction

Divya Veligandla
May 12th, 2024

Project Summary

This project aims to create a predictive model that reliably identifies people at risk of stroke based on their health characteristics. This classification problem predicts whether a person has a stroke or not with a good amount of accuracy.

I followed the 10 steps of Data Mining for this project. To accomplish this, I used two data mining techniques: Logistic regression and Decision trees. The methods provide special benefits and insights into the predictive modeling process. The one with the better accuracy is our final model.

Our response variable is non-numeric. It is categorical with two classes: stroke/no stroke. Logistic Regression computes its propensity for each class in the output. This interpretability and transparency offered by logistic regression make it easy to identify the classification manually, too. Logistic regression will be hereby referred to as the first method. Logistic regression is used to deal with categorical data. Logistic regression finds a function of the predictor variables that relates them to a 0/1 outcome. It is a fundamental statistical technique for tasks involving binary categorization. We can determine the relevance of each predictor variable in the predictive model and evaluate its influence on the chance of stroke by fitting the logistic regression model to the dataset.

Decision trees are a popular method, relatively straightforward as the output is a set of rules represented by tree diagrams, making it easy to interpret. Decision Trees will be hereby referred to as the second method. Decision trees are available for both classification and prediction. Classification Trees are used for classification, and for prediction, Regression Trees are used. As our output is categoric, Classification trees are used in this case. A classification tree divides the predictor variables into discrete groups that best define the two classes for stroke prediction, where the response variable is binary (stroke/no stroke). It provides a clear visual representation of the decision-making process, with each leaf node representing the predicted class (stroke or no stroke) and each internal node representing a decision based on a predictor variable. Similar to logistic regression, by looking at the splits and choices made inside the tree, we can determine the significance of each predictor variable in the classification model and how these variables affect the chance of stroke. Healthcare providers and other stakeholders can gain actionable insights using decision trees, which offer interpretable rules for detecting high-risk individuals.

Our data mining efforts showed that the predictive model identified individuals with stroke risk with a significant degree of accuracy. In conclusion, this project demonstrates the effectiveness of data mining techniques in predicting stroke events by health metrics. By leveraging machine learning algorithms and comprehensive data analysis, early detection and intervention strategies can be refined, resulting in improved patient outcomes and a reduction in stroke-related disease and mortality.

Main Chapter

Chapter 1: Introduction/Understanding of the Project

Problem Statement: The challenge is to devise an efficient method for identifying individuals at risk of stroke, and facilitating early intervention strategies to mitigate stroke-related morbidity and mortality.

Purpose: Our aim is to develop a comprehensive predictive model for recognizing stroke events. It will provide insights and a predictive model to help identify at-risk individuals. This model will give healthcare professionals practical insights to enable early intervention and prevention. Our research aims to improve understanding of the factors contributing to stroke risk, thus improving patient outcomes and healthcare delivery of a stroke.

Stakeholders: Patients, physicians, healthcare providers, insurance companies, and technology developers all have an interest in the outcomes of this study. They will apply the findings in a diverse way. Here are some ways the results of the analysis are relevant to end users.

- Patients and their families gain from early stroke risk detection. Families can help the patient by enabling preventive actions and lifestyle modifications.
- Healthcare providers gain from immediate intervention and stroke risk reduction for their patients. Medical professionals may quickly identify high-risk patients and take appropriate action to lower the occurrence of strokes
- Healthcare institutions gain from the findings of the study. They can modify staffing, preventive care, and resource allocation policies to enhance patient care.
- Insurance companies gain from improved risk assessments and improved policy formulation.

- Technology developers gain from incorporating stroke prediction algorithms into health tech solutions.

Effects of the results: Improved risk detection and intervention strategies can result in better patient outcomes, reduced expenditures on healthcare, improved resource allocation, and advancements in health technology .

Data: The dataset used in this project comes from Kaggle. Specifically, it comes from the "Stroke prediction Dataset" that Fedesoriano provides. This dataset includes a variety of data points, including demographics (e.g. age, gender, marital status) and health indicators (e.g., high blood pressure, heart disease, smoking status).

Is the analysis a one shot effort or an ongoing procedure?: This analysis is a standalone project to develop the predictive model.

However, the application and refinement of the model can become an ongoing procedure in future. In order to make sure the model stays useful and relevant over time, it could be required to update the model with new data on a regular basis and optimize the algorithms.

Chapter 2: Obtain data for analysis.

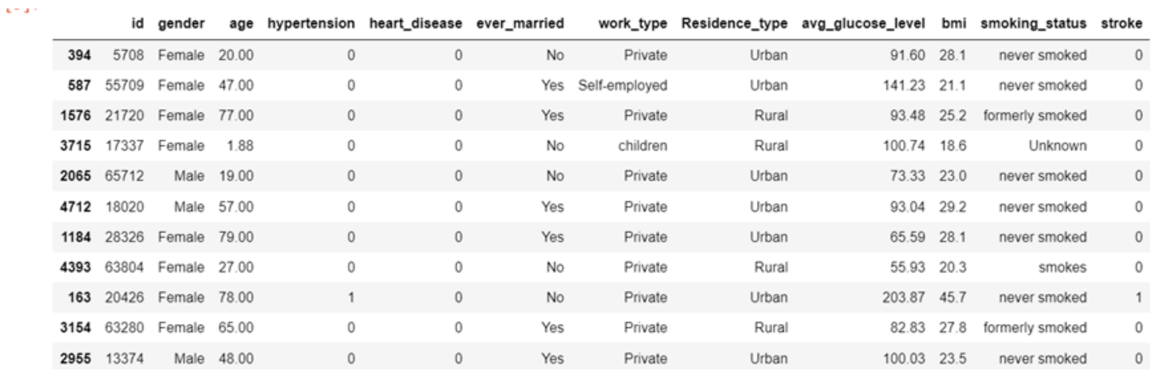
The dataset used in this project comes from Kaggle. Specifically, it comes from the "Stroke prediction Dataset". The goal is to predict the patient's susceptibility to a stroke based on information such as Age, Gender, Hypertension, Heart disease, Ever married, Work type, Residence type, Average Glucose level, BMI, and Smoking status. The dataset contains 11 variables (we have considered 10 predictor variables and excluded the ID column), and the outcome (response variable) is the Stroke.

The table below describes each of the predictors and the outcome:

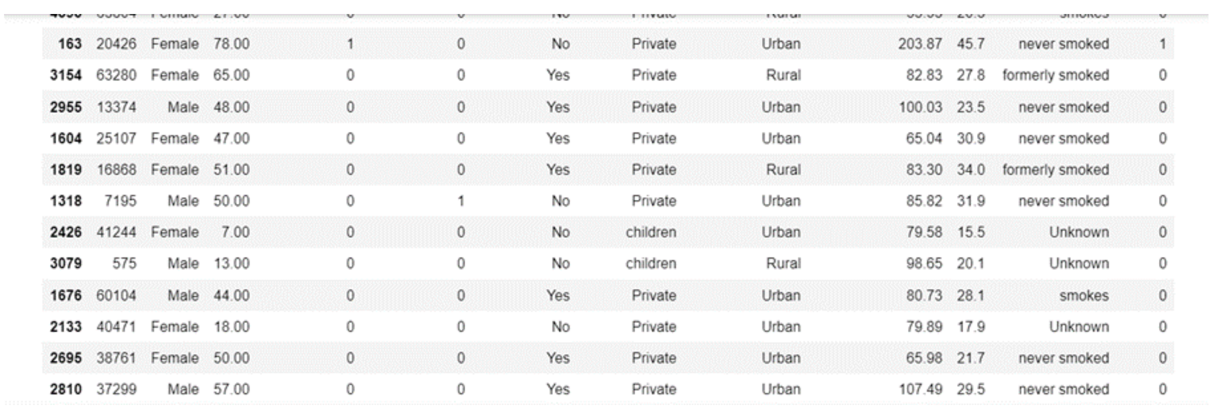
Variables	**Description of Variables**
ID	Patients ID
GENDER	Gender of the patients ('Male', 'Female').
AGE	Age of the Patients.
HYPERTENSION	Patients with Hypertension ("1"-if they had hypertension,"0"-if otherwise)
HEART_DISEASE	Patients with Heart disease ("1"-if they had any heart disease,"0"-if otherwise)
EVER_MARRIED	Marital Status ("Yes"-if they were married, "No"-if otherwise)
WORK_TYPE	Work type of the patients ("Children"," Self-employed", "Private"," Never worked"," Govt job")
RESIDENCE_TYPE	Area where the Patients lived ("Rural"," Urban")
AVG_GLUCOSE_LEVEL	Average level of glucose of each patient.
BMI	Basal Metabolic Index of each patient.
SMOKING_STATUS	("Formerly smoked", "Never smoked"," Smokes"," Unknown")
STROKE	Stroke rate ("1"-if they had a stroke,"0"-had no stroke)

I wanted to obtain a sample of a subset of records for DM modeling.

The sample() function selects a random sample from the data set. Below are the 20 randomly selected records.



	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	stroke
394	5708	Female	20.00	0	0	No	Private	Urban	91.60	28.1	never smoked	0
587	55709	Female	47.00	0	0	Yes	Self-employed	Urban	141.23	21.1	never smoked	0
1576	21720	Female	77.00	0	0	Yes	Private	Rural	93.48	25.2	formerly smoked	0
3715	17337	Female	1.88	0	0	No	children	Rural	100.74	18.6	Unknown	0
2065	65712	Male	19.00	0	0	No	Private	Urban	73.33	23.0	never smoked	0
4712	18020	Male	57.00	0	0	Yes	Private	Urban	93.04	29.2	never smoked	0
1184	28326	Female	79.00	0	0	Yes	Private	Urban	65.59	28.1	never smoked	0
4393	63804	Female	27.00	0	0	No	Private	Rural	55.93	20.3	smokes	0
163	20426	Female	78.00	1	0	No	Private	Urban	203.87	45.7	never smoked	1
3154	63280	Female	65.00	0	0	Yes	Private	Rural	82.83	27.8	formerly smoked	0
2955	13374	Male	48.00	0	0	Yes	Private	Urban	100.03	23.5	never smoked	0

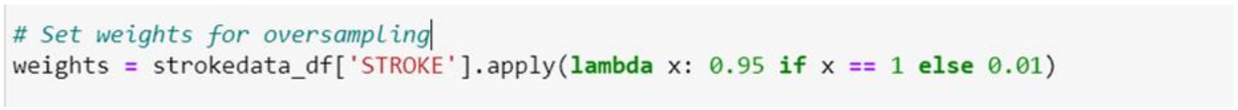


	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	stroke
163	20426	Female	78.00	1	0	No	Private	Urban	203.87	45.7	never smoked	1
3154	63280	Female	65.00	0	0	Yes	Private	Rural	82.83	27.8	formerly smoked	0
2955	13374	Male	48.00	0	0	Yes	Private	Urban	100.03	23.5	never smoked	0
1604	25107	Female	47.00	0	0	Yes	Private	Urban	65.04	30.9	never smoked	0
1819	16868	Female	51.00	0	0	Yes	Private	Rural	83.30	34.0	formerly smoked	0
1318	7195	Male	50.00	0	1	No	Private	Urban	85.82	31.9	never smoked	0
2426	41244	Female	7.00	0	0	No	children	Urban	79.58	15.5	Unknown	0
3079	575	Male	13.00	0	0	No	children	Rural	98.65	20.1	Unknown	0
1676	60104	Male	44.00	0	0	Yes	Private	Urban	80.73	28.1	smokes	0
2133	40471	Female	18.00	0	0	No	Private	Urban	79.89	17.9	Unknown	0
2695	38761	Female	50.00	0	0	Yes	Private	Urban	65.98	21.7	never smoked	0
2810	37299	Male	57.00	0	0	Yes	Private	Urban	107.49	29.5	never smoked	0

We can see from the 20 samples that the occurrence of stroke (stroke=1) is a rare event.

If we want to create a model that detects the probability of stroke in people with maximum attainable accuracy (without overfitting), we need to do an oversampling of data.

We will give 95% weightage to those records with stroke=1 and 5% weightage to stroke=0 records.



```
# Set weights for oversampling
weights = strokedata_df['STROKE'].apply(lambda x: 0.95 if x == 1 else 0.01)
```

To maintain a proper flow of programming, we have implemented this step after data cleaning.

Chapter 3: Explore, Clean, and Preprocess Data; Reduce Data Dimension

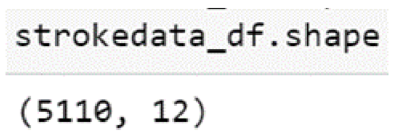
3a. Explore

To explore data, the CSV file must be read by Python and stored in the data frame strokedata_df.

During the exploration phase, we worked on the raw data set.

Data is explored to understand:

- The number of rows and columns – The function shape() is passed on the data frame strokedata_df, which returns the number of rows and columns in a tuple as displayed below. Here, the Data Frame has 5110 rows and 12 columns.

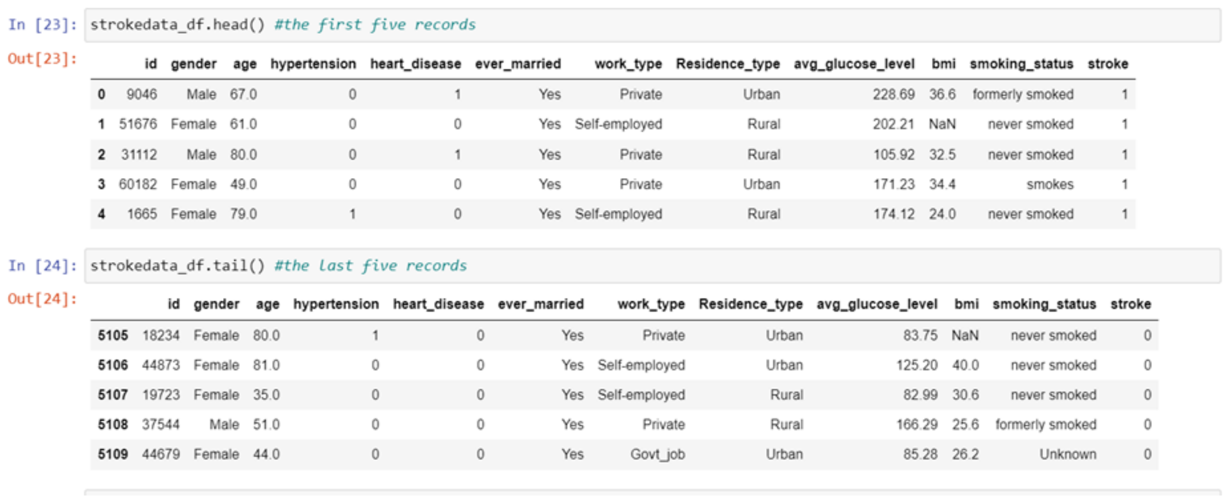


```
strokedata_df.shape
```

```
(5110, 12)
```

- The structure and view of the data type of variables – help us observe the data and do the necessary clean-up operations, such as reviewing column names or changing variables types as needed.

We use the head() function that returns the first five records. We use the tail() function that returns the last five records in the data frame.


In [23]: `strokedata_df.head() #the first five records`

Out[23]:

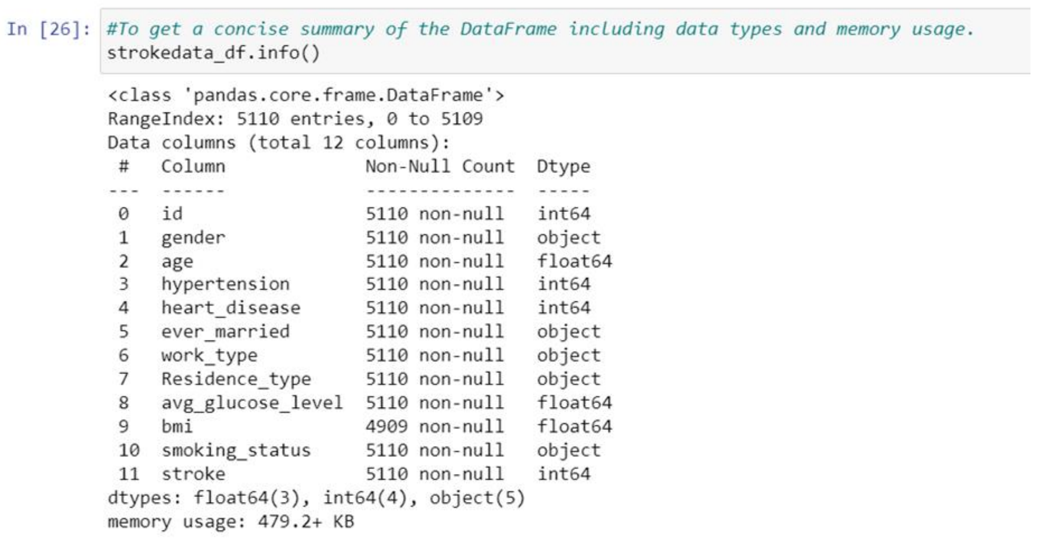
	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	stroke
0	9046	Male	67.0	0	1	Yes	Private	Urban	228.69	36.6	formerly smoked	1
1	51676	Female	61.0	0	0	Yes	Self-employed	Rural	202.21	NaN	never smoked	1
2	31112	Male	80.0	0	1	Yes	Private	Rural	105.92	32.5	never smoked	1
3	60182	Female	49.0	0	0	Yes	Private	Urban	171.23	34.4	smokes	1
4	1665	Female	79.0	1	0	Yes	Self-employed	Rural	174.12	24.0	never smoked	1

In [24]: `strokedata_df.tail() #the last five records`

Out[24]:

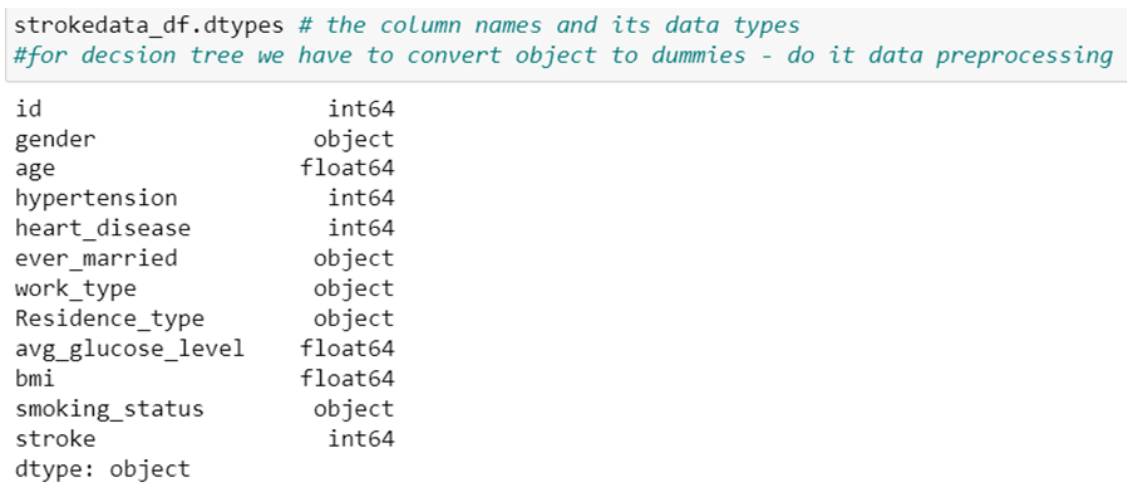
	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	stroke
5105	18234	Female	80.0	1	0	Yes	Private	Urban	83.75	NaN	never smoked	0
5106	44873	Female	81.0	0	0	Yes	Self-employed	Urban	125.20	40.0	never smoked	0
5107	19723	Female	35.0	0	0	Yes	Self-employed	Rural	82.99	30.6	never smoked	0
5108	37544	Male	51.0	0	0	Yes	Private	Rural	166.29	25.6	formerly smoked	0
5109	44679	Female	44.0	0	0	Yes	Govt_job	Urban	85.28	26.2	Unknown	0

We use info() to get a summary of the variable types and memory usage.


In [26]:
```
#To get a concise summary of the DataFrame including data types and memory usage.
strokedata_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5110 entries, 0 to 5109
Data columns (total 12 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   id                 5110 non-null   int64  
 1   gender             5110 non-null   object 
 2   age                5110 non-null   float64
 3   hypertension       5110 non-null   int64  
 4   heart_disease      5110 non-null   int64  
 5   ever_married       5110 non-null   object 
 6   work_type          5110 non-null   object 
 7   Residence_type     5110 non-null   object 
 8   avg_glucose_level  5110 non-null   float64
 9   bmi                4909 non-null   float64
 10  smoking_status     5110 non-null   object 
 11  stroke             5110 non-null   int64  
dtypes: float64(3), int64(4), object(5)
memory usage: 479.2+ KB
```

We can also separately look at the columns and their data types using dtypes().

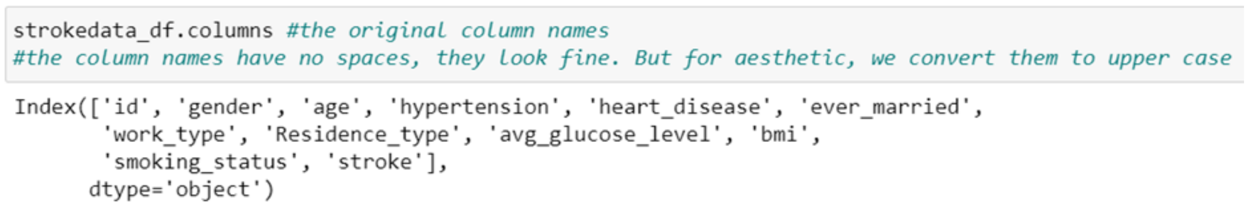


```
strokedata_df.dtypes # the column names and its data types
#for decsion tree we have to convert object to dummies - do it data preprocessing
```

```
id                     int64
gender                object
age                  float64
hypertension           int64
heart_disease          int64
ever_married          object
work_type             object
Residence_type        object
avg_glucose_level    float64
bmi                  float64
smoking_status        object
stroke                 int64
dtype: object
```

For logistic regression and decision trees we are going to convert object data type to category type and then to dummy values. This also needs to be handled in the data cleaning step.

We can also look at the column names separately using columns()



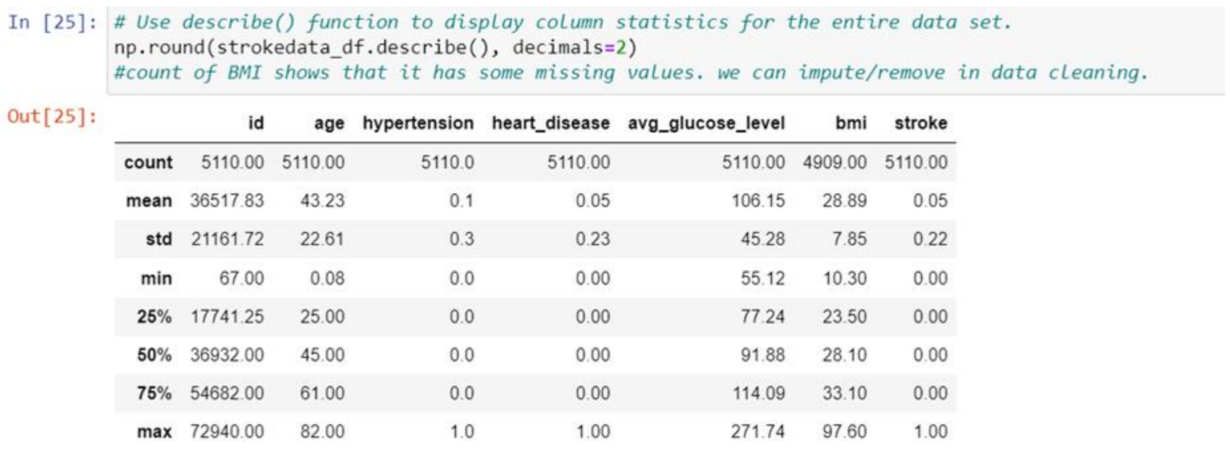
```
strokedata_df.columns #the original column names
#the column names have no spaces, they look fine. But for aesthetic, we convert them to upper case
```

```
Index(['id', 'gender', 'age', 'hypertension', 'heart_disease', 'ever_married',
       'work_type', 'Residence_type', 'avg_glucose_level', 'bmi',
       'smoking_status', 'stroke'],
      dtype='object')
```

The column names do not have spaces. They do not need to be renamed. In data cleaning step, we can change the column names to upper case for aesthetic reasons.

- Identify Numeric measures of data – such as count, mean, median, maximum, minimum, 1st quartile, 3rd quartile, standard deviation. Observing these values gives us information about missing data, helps detect outliers

We use the function describe() to display column statistics of the data set.



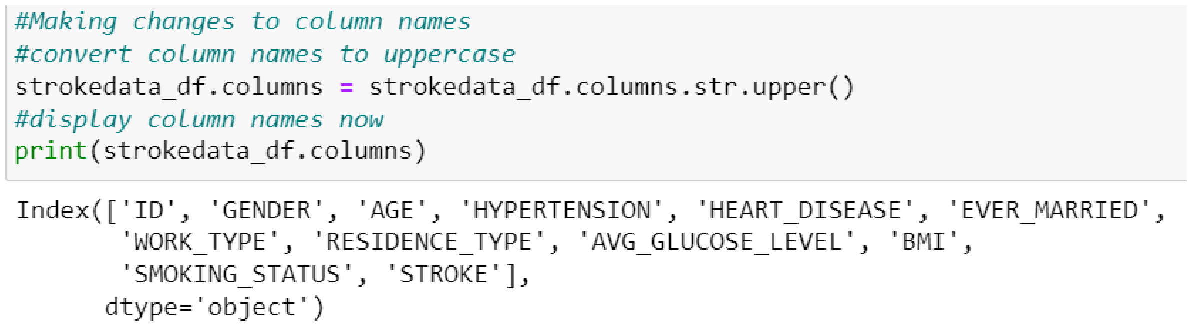
```
In [25]: # Use describe() function to display column statistics for the entire data set.
         np.round(strokedata_df.describe(), decimals=2)
         #count of BMI shows that it has some missing values. we can impute/remove in data cleaning.
Out[25]:
```

	id	age	hypertension	heart_disease	avg_glucose_level	bmi	stroke
count	5110.00	5110.00	5110.0	5110.00	5110.00	4909.00	5110.00
mean	36517.83	43.23	0.1	0.05	106.15	28.89	0.05
std	21161.72	22.61	0.3	0.23	45.28	7.85	0.22
min	67.00	0.08	0.0	0.00	55.12	10.30	0.00
25%	17741.25	25.00	0.0	0.00	77.24	23.50	0.00
50%	36932.00	45.00	0.0	0.00	91.88	28.10	0.00
75%	54682.00	61.00	0.0	0.00	114.09	33.10	0.00
max	72940.00	82.00	1.0	1.00	271.74	97.60	1.00

Count returns the number of values for each column in the data set. If there are records with a value ‘NA’ it is not counted. ‘NA’ or ’N/A’ or blank indicate that there is a missing value. Here, we know the total number of rows is 5110 .The value of count for variable ‘bmi’ says 4909.00 which means that ‘bmi’ column contains some missing values. And these need to be handled either by dropping the records with missing values or performing imputation in the data cleaning step.

3b. Data Cleaning:

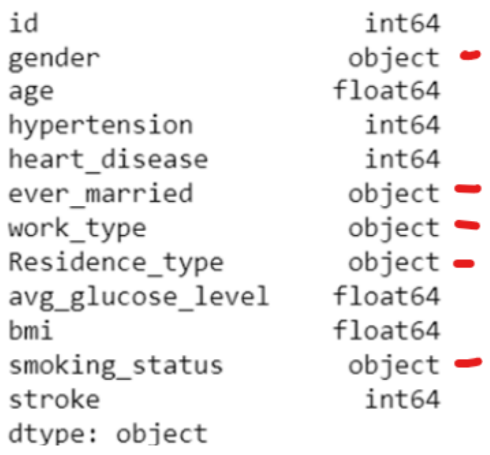
1) Rename the column names – Modifying all the column names to uppercase. The new column names are:



```
#Making changes to column names
#convert column names to uppercase
strokedata_df.columns = strokedata_df.columns.str.upper()
#display column names now
print(strokedata_df.columns)
```

```
Index(['ID', 'GENDER', 'AGE', 'HYPERTENSION', 'HEART_DISEASE', 'EVER_MARRIED',
       'WORK_TYPE', 'RESIDENCE_TYPE', 'AVG_GLUCOSE_LEVEL', 'BMI',
       'SMOKING_STATUS', 'STROKE'],
      dtype='object')
```

2) Converting object type variables to dummy variables and dropping one of their classes to prevent multicollinearity. The object type variables are marked with red ticks.



```
id                     int64
gender                object
age                  float64
hypertension           int64
heart_disease          int64
ever_married          object
work_type             object
Residence_type        object
avg_glucose_level    float64
bmi                  float64
smoking_status        object
stroke                 int64
dtype: object
```

For example, for variable gender, it has 3 classes: male, female, and other. We dropped ‘other’ class. This means when gender_male = 0 and gender_female=0, the value of gender is ‘other.’ The new variable names and their classes are:

```
Variable names and their category levels:
GENDER Index(['Female', 'Male', 'Other'], dtype='object')
EVER_MARRIED Index(['No', 'Yes'], dtype='object')
WORK_TYPE Index(['Govt_job', 'Never_worked', 'Private', 'Self-employed', 'children'], dtype='object')
RESIDENCE_TYPE Index(['Rural', 'Urban'], dtype='object')
SMOKING_STATUS Index(['Unknown', 'formerly smoked', 'never smoked', 'smokes'], dtype='object')

Index(['AGE', 'HYPERTENSION', 'HEART_DISEASE', 'AVG_GLUCOSE_LEVEL', 'BMI',
       'STROKE', 'GENDER_Female', 'GENDER_Male', 'EVER_MARRIED_Yes',
       'WORK_TYPE_Govt_job', 'WORK_TYPE_Never_worked', 'WORK_TYPE_Private',
       'WORK_TYPE_Self-employed', 'RESIDENCE_TYPE_Urban',
       'SMOKING_STATUS_formerly smoked', 'SMOKING_STATUS_never smoked',
       'SMOKING_STATUS_smokes'],
      dtype='object')
```

3) Handling missing data – We observed that some records have bmi values missing. The number of records with STROKE = 1 are less.We do not want to lose records with STROKE=1, we impute BMI missing values with median value of BMI = 28.

   We used median and not mean because median is not affected by large or small values unlike mean.

   When STROKE= 0,and BMI is missing we can drop those records.

```
# Remove rows where "BMI" is missing and "STROKE" is 0
strokedata_df = strokedata_df.dropna(subset=['BMI'], how='all')  # Remove rows where "bmi" is missing
strokedata_df = strokedata_df[~((strokedata_df['BMI'].isna()) & (strokedata_df['STROKE'] == 0))]

# Impute median stroke value (28) where "BMI" is missing and "STROKE" is 1
median_stroke_value = 28
missing_bmi_mask = (strokedata_df['BMI'].isna()) & (strokedata_df['STROKE'] == 1)
strokedata_df.loc[missing_bmi_mask, 'BMI'] = median_stroke_value
```

   After dropping records with missing BMI values where STROKE = 0 , the shape of the data set is (4909,17) – 4909 rows and 17 columns. The total number of records with STROKE = 1 is 209.

```
Shape of data (4909, 17)
Number of records with stroke=1 are 209
```

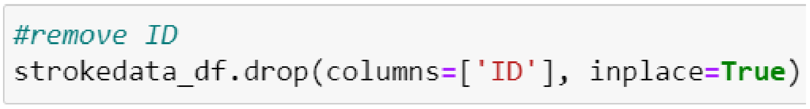
3c. Data Reduction-

We performed two operations of data reduction in data cleaning:

1. Drop irrelevant columns (ID).
2. Drop missing value records.

3. Oversampling - This is not a step in data reduction but for this project involved reduction of data during oversampling to maintain data balance.

- Removing irrelevant columns - The column ID does not have relevant data for stroke prediction. Hence, it is dropped.

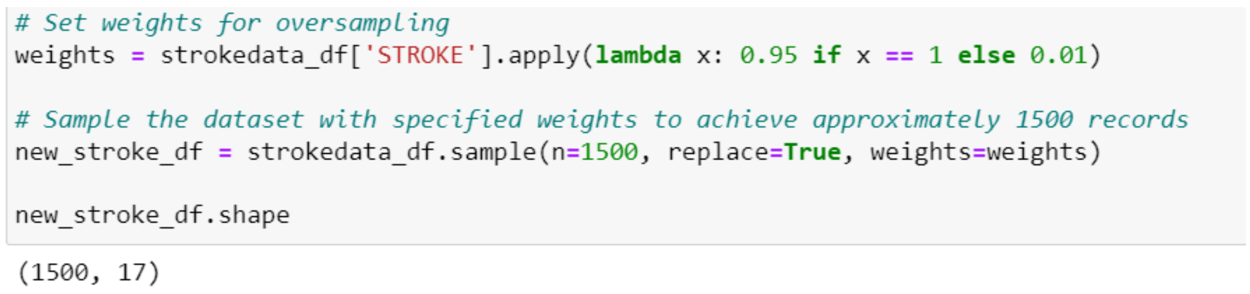


```
#remove ID
strokedata_df.drop(columns=['ID'], inplace=True)
```

- When we were handling missing data, we reduced the number of rows by dropping records with missing BMI values as explained in the data cleaning step (point 3). We did not perform imputation on all records with missing BMI values. Imputation was only performed on Stroke = 1 records.

<u>Oversampling</u>

We oversample 95% of STROKE = 1 data. The rest 5% are STROKE = 0. We have more than 5000 records. There is a clear imbalance in the data set . Therefore, we reduce the number of rows to 1500 which is enough for creating a good predictive model and to main a balance. This will give us 12 to 13% of STROKE = 1 data.



```
# Set weights for oversampling
weights = strokedata_df['STROKE'].apply(lambda x: 0.95 if x == 1 else 0.01)

# Sample the dataset with specified weights to achieve approximately 1500 records
new_stroke_df = strokedata_df.sample(n=1500, replace=True, weights=weights)

new_stroke_df.shape
```

```
(1500, 17)
```

'new_stroke_df' is the cleaned data set that we train on to create our stroke prediction model. This data set has 1500 rows and 17 columns.

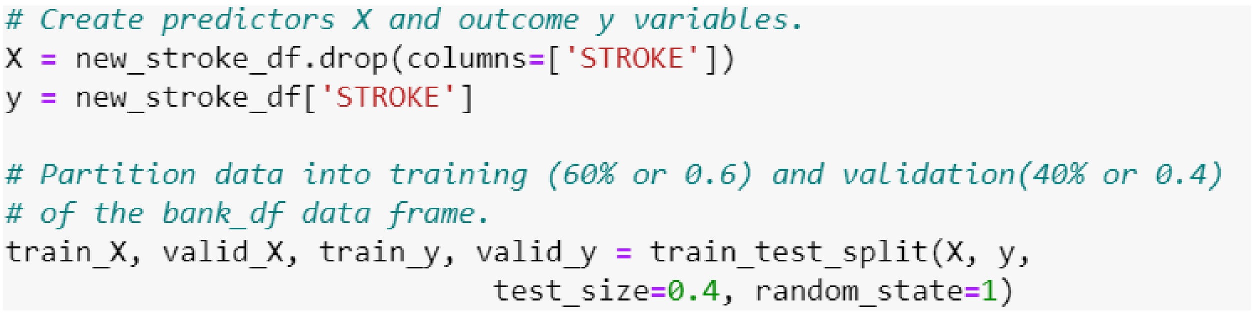
Chapter 4: DETERMINE THE DATA MINING TASK

The outcome variable is Stroke, which has classes 1 and 0 or Yes and No. It is a classification problem. We can use any of the classification models, such as KNN, Neural Networks, Logistic Regression, and Decision Trees. We have used Logistic Regression and Decision Trees for our analysis.

- Logistic regression is a statistical approach used for binary classification problems, where the goal is to predict a binary outcome (such as yes/no, true/false, 0/1) based on input data. In our case, the target variable y is binary. It can take two possible values, as no stroke-0 or stroke-1, in logistic regression.
- The Decision tree algorithm is used for classification and prediction tasks both.
  It works by dividing the datasets into smaller subsets by implying a set of rules
  in order to reach the final prediction of the target variable.

Chapter 5: PARTITION DATA

We should not train the whole data set. Then there will be overfitting. The model will not generalize well to unseen data. We partition into 60% Training Data and 40% Validation Data Set. We partition data to prevent overfitting. The model trains on the training data set and it is evaluated on the validation data set.

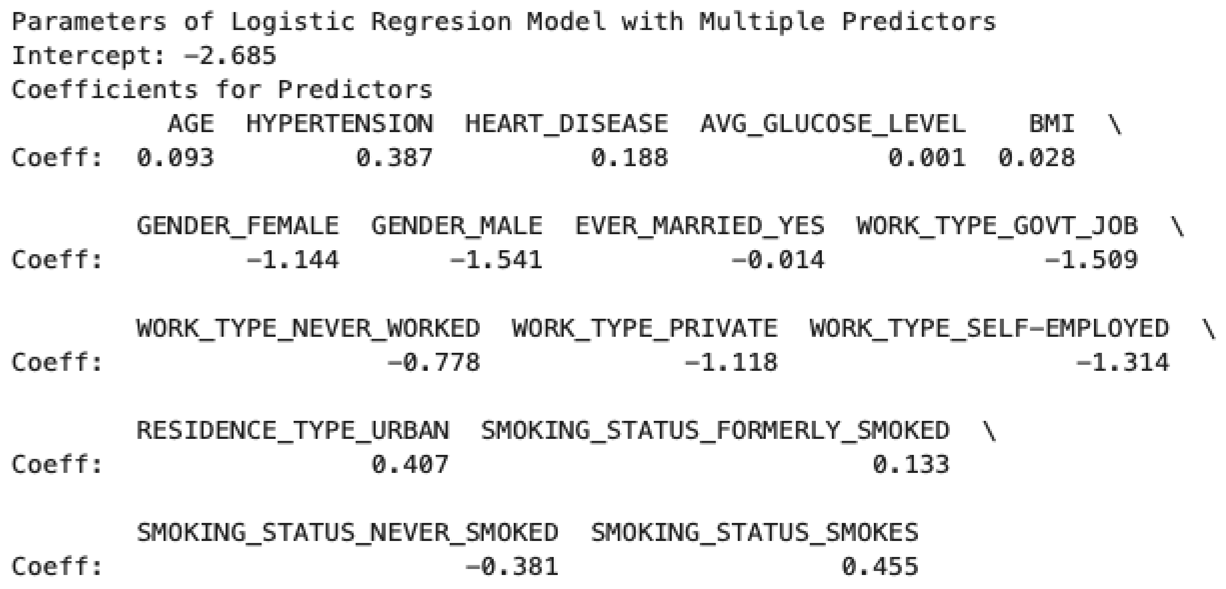


```python
# Create predictors X and outcome y variables.
X = new_stroke_df.drop(columns=['STROKE'])
y = new_stroke_df['STROKE']

# Partition data into training (60% or 0.6) and validation(40% or 0.4)
# of the bank_df data frame.
train_X, valid_X, train_y, valid_y = train_test_split(X, y,
                                     test_size=0.4, random_state=1)
```

Chapter 6: Data Mining Techniques and Algorithms -Method 1 - Logistic Regression

Intercept and Regression Coefficients

The intercept and regression coefficients of the trained logistic regression model are presented below:



```
Parameters of Logistic Regresion Model with Multiple Predictors
Intercept: -2.685
Coefficients for Predictors
          AGE  HYPERTENSION  HEART_DISEASE  AVG_GLUCOSE_LEVEL    BMI  \
Coeff:  0.093         0.387          0.188              0.001  0.028

        GENDER_FEMALE  GENDER_MALE  EVER_MARRIED_YES  WORK_TYPE_GOVT_JOB  \
Coeff:         -1.144       -1.541            -0.014              -1.509

        WORK_TYPE_NEVER_WORKED  WORK_TYPE_PRIVATE  WORK_TYPE_SELF-EMPLOYED  \
Coeff:                  -0.778             -1.118                   -1.314

        RESIDENCE_TYPE_URBAN  SMOKING_STATUS_FORMERLY_SMOKED  \
Coeff:                 0.407                           0.133

        SMOKING_STATUS_NEVER_SMOKED  SMOKING_STATUS_SMOKES
Coeff:                       -0.381                  0.455
```

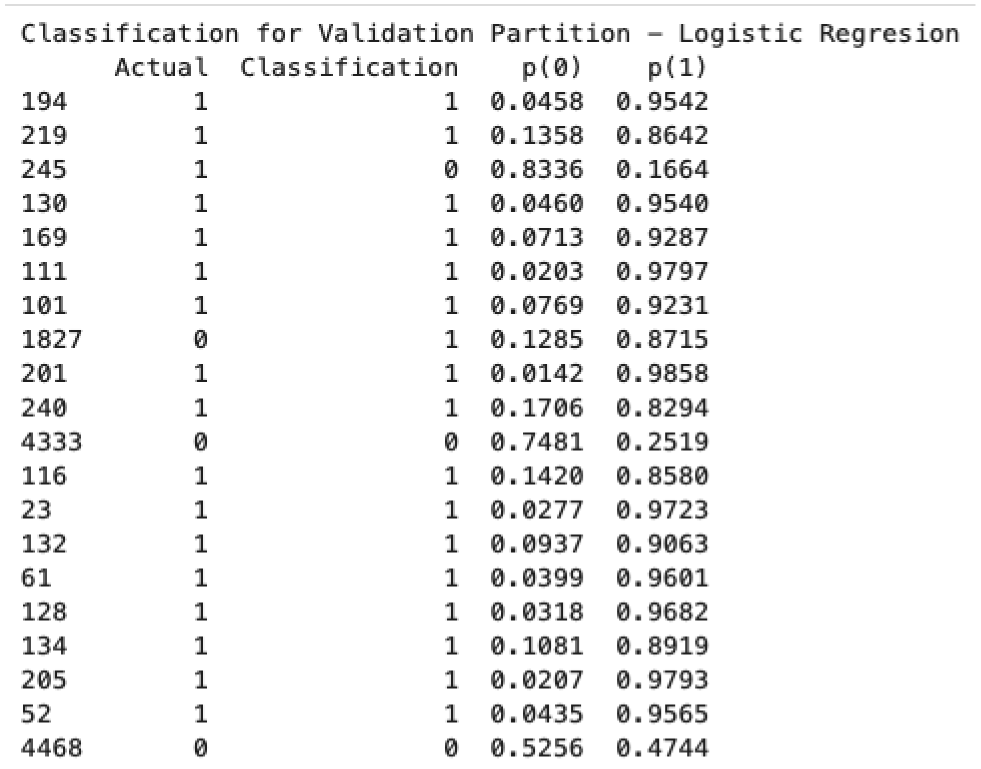
The mathematical equation of the logistic model is the following:

Logit = -2.685 + 0.093 AGE + 0.387 HYPERTENSION + 0.188 HEART_DISEASE + 0.001 AVG_GLUCOSE_LEVEL + 0.028 BMI - 1.144 GENDER_FEMALE - 1.541 GENDER_MALE - 0.014 EVER_MARRIED_YES - 1.509 WORK_TYPE_GOVT_JOB - 0.778 WORK_TYPE_NEVER_WORKED - 1.118 WORK_TYPE_PRIVATE - 1.314 WORK_TYPE_SELF-EMPLOYED + 0.407 RESIDENCE_TYPE_URBAN + 0.133

SMOKING_STATUS_FORMERLY_SMOKED - 0.381

SMOKING_STATUS_NEVER_SMOKED + 0.455 SMOKING_STATUS_SMOKES

The table with the actual and classification results and associated probabilities for the first 20 records in the validation partition are presented below.

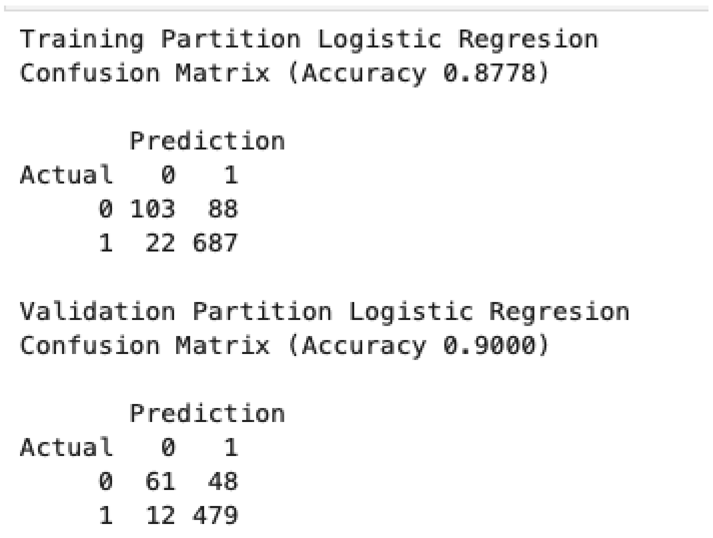


```
Classification for Validation Partition - Logistic Regresion
      Actual  Classification    p(0)    p(1)
194        1               1  0.0458  0.9542
219        1               1  0.1358  0.8642
245        1               0  0.8336  0.1664
130        1               1  0.0460  0.9540
169        1               1  0.0713  0.9287
111        1               1  0.0203  0.9797
101        1               1  0.0769  0.9231
1827       0               1  0.1285  0.8715
201        1               1  0.0142  0.9858
240        1               1  0.1706  0.8294
4333       0               0  0.7481  0.2519
116        1               1  0.1420  0.8580
23         1               1  0.0277  0.9723
132        1               1  0.0937  0.9063
61         1               1  0.0399  0.9601
128        1               1  0.0318  0.9682
134        1               1  0.1081  0.8919
205        1               1  0.0207  0.9793
52         1               1  0.0435  0.9565
4468       0               0  0.5256  0.4744
```

Most of the above validation records are correctly classified as 1 (‘had a stroke’). Two out of the first 20 records with indexes 245, and 1827 are misclassified. Row #245 has the actual stroke value as 1(‘had stroke’), but the logistic regression model misclassified them as 0 (‘had no stroke’), because the probability of 0 is 0.8336, and #1827 has the actual stroke value as 0 (‘had no stroke’), but the logistic regression model misclassified them as 1 (‘had stroke’), because the probability of 1 is 0.8715. Whichever probability is more, will be the final prediction classification.

Confusion Matrices for the Logistic Regression

The confusion matrices for the training is 87.78 % and validation partitions show a very high accuracy of 90 %. The trained logistic regression model fits well into the validation data set and can be used for classification of the stroke. The misclassification rate for the training partition is 1-0.8778 = 0.1222 = 12.22%, and for the validation partition 1-0.9000 = 0.1 or 10%. The accuracy of the model for the validation records is higher than the accuracy for the training records, and therefore, there is no overfitting in this case.

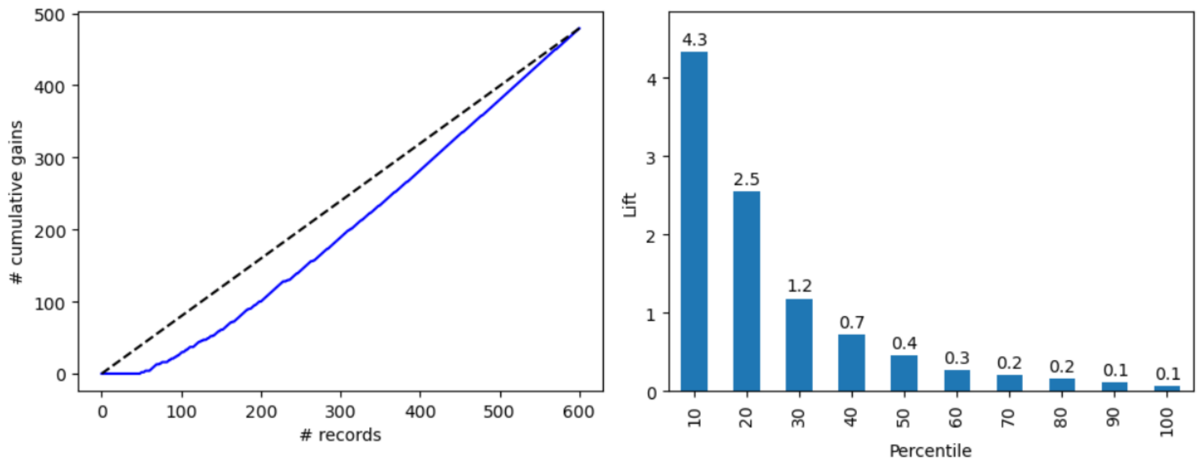


```
Training Partition Logistic Regresion
Confusion Matrix (Accuracy 0.8778)

       Prediction
Actual   0   1
     0 103  88
     1  22 687

Validation Partition Logistic Regresion
Confusion Matrix (Accuracy 0.9000)

       Prediction
Actual   0   1
     0  61  48
     1  12 479
```

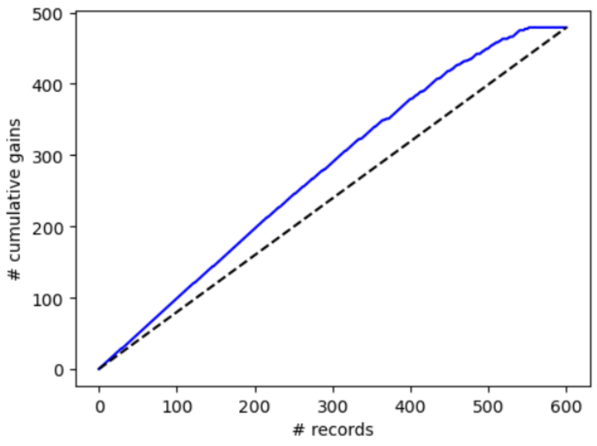
Gain chart and lift chart

Gain chart and lift chart are two graphical tools commonly used in predictive modeling and data analysis, particularly in the context of binary classification problems. Below is what each chart represents:

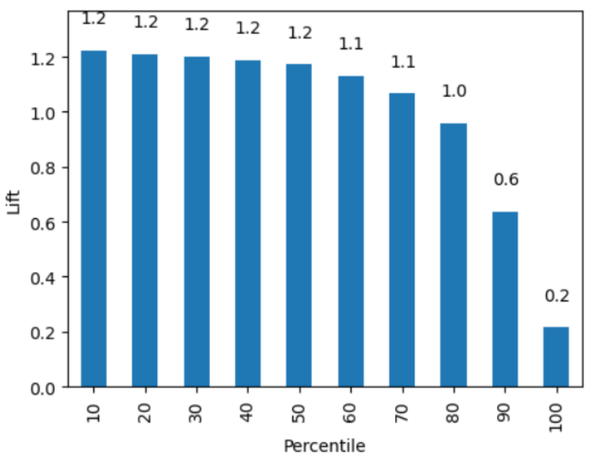
P(0): The lift chart for the ‘had no stroke’ stroke status shows the ratio of the proportion of classifications as 0(‘had no stroke’) using the model vs. proportion of the ‘had no stroke’ stroke status taken randomly for different percentiles in the validation partition. For the top 10% of the data most probable to be 0, the logistic model provides a 4.3 times higher chance of 0 than the proportion of 0’s taken randomly.



P(1): The lift chart for the ‘had stroke’ stroke status shows the ratio of the proportion of classifications as 1(‘had stroke’) using the model vs. proportion of the ‘had stroke’ stroke status taken randomly for different percentiles in the validation partition. For the top 10% of the data most probable to be 1, the logistic model provides a 1.2 times higher chance of 1 than the proportion of 1’s taken randomly.



# cumulative gains
# records
0
100
200
300
400
500
600

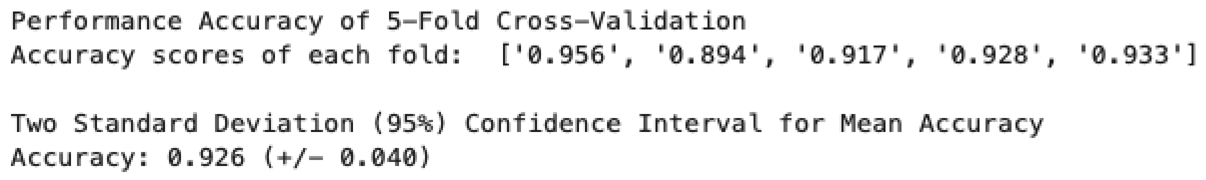


Lift
Percentile
1.2
1.2
1.2
1.2
1.2
1.1
1.1
1.0
0.6
0.2

Chapter 7: Data Mining Techniques and Algorithms - Method 2- Decision Tree

<u>Algorithm: K-Fold</u>

As our outcome is categorical, we have used a Classification Tree. To ensure, we can obtain a more robust estimate of a model's performance compared to simply splitting the data into a training set and a separate test set, we have used Cross Validation here. The model here is trained in K=5 times, each time using K-1 = 4 folds for training and the remaining fold for validation. This means that in each iteration, a different fold is used as the validation set while the remaining 4 folds are used for training. By using K-fold cross-validation. Here are the results of 5-fold Cross Validation.



```
Performance Accuracy of 5-Fold Cross-Validation
Accuracy scores of each fold:  ['0.956', '0.894', '0.917', '0.928', '0.933']

Two Standard Deviation (95%) Confidence Interval for Mean Accuracy
Accuracy: 0.926 (+/- 0.040)
```

Results:

Mean Accuracy: The mean accuracy across all folds is 0.926

95% Confidence Interval for Mean Accuracy: The mean accuracy of 0.926 is associated with a 95% confidence interval of (+/- 0.020). This means that we are 95% confident that the true mean accuracy of the model lies within the range of 0.894 to 0.956.

Overall, as evaluated by 5-fold cross-validation, the model's performance indicates high accuracy, with a mean accuracy of 0.926 and a narrow confidence interval, suggesting that the estimate is quite precise.

GridSearchCV

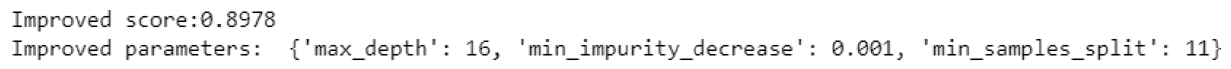
The GridSearchCV function is applied to search through various combinations of hyperparameters. It uses 5-fold cross-validation (cv=5) and parallel processing (n_jobs=1) for efficiency. Here is the range of parameters used.

max_depth: A list of values from 2 to 19.

min_impurity_decrease: Three specific values - 0, 0.0005, and 0.001.

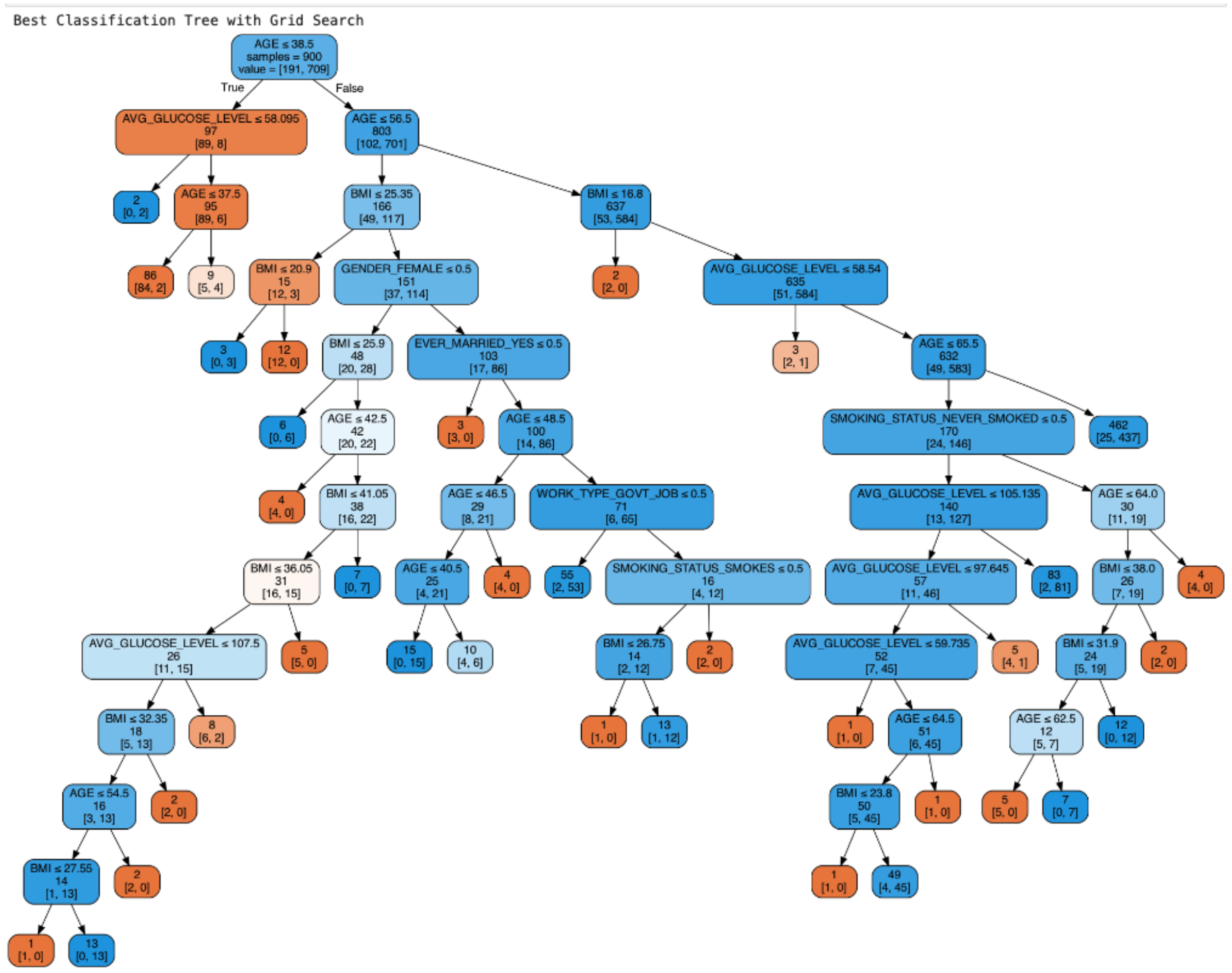
min_samples_split: A list of values from 10 to 29

After fitting the model to the training data (train_X, train_y), the code prints out the best score achieved (gridSearch.best_score_) and the corresponding best parameters (gridSearch.best_params_) as below:



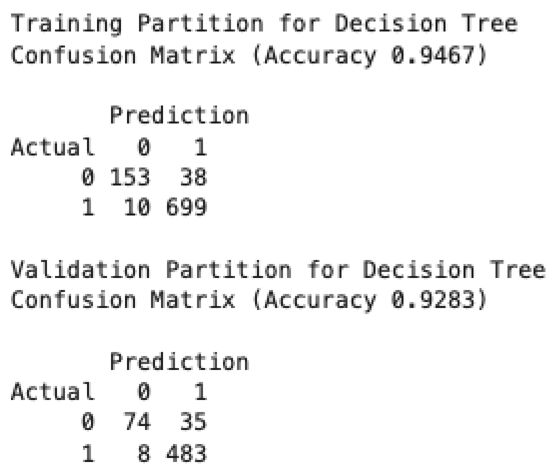
```
Improved score:0.8978
Improved parameters:  {'max_depth': 16, 'min_impurity_decrease': 0.001, 'min_samples_split': 11}
```

Displaying Classification Tree based on Improved Parameters.



```
Best Classification Tree with Grid Search
```

Confusion Matrices



```
Training Partition for Decision Tree
Confusion Matrix (Accuracy 0.9467)

       Prediction
Actual   0   1
     0 153  38
     1  10 699

Validation Partition for Decision Tree
Confusion Matrix (Accuracy 0.9283)

       Prediction
Actual   0   1
     0  74  35
     1   8 483
```

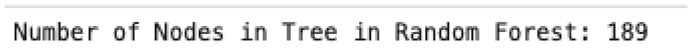
In the training partition, out of 191 instances of class 0 (Actual 0), 153 were correctly classified as 0, and 38 were incorrectly classified as 1. Out of 709 instances of class 1 (Actual 1), 699 were correctly classified as 1, and 10 were incorrectly classified as 0. The misclassification rate of Training Partition is 5.33% (1-0.9467)

In Validation Partition, out of 109 instances of class 0 (Actual 0), 74 were correctly classified as 0, 35 were incorrectly classified as 1 and out of 491 instances of class 1 (Actual 1), 483 were correctly classified as 1, and 8 were incorrectly classified as 0. The misclassification rate of Validation Partition is 7.17% (1-0.9283).

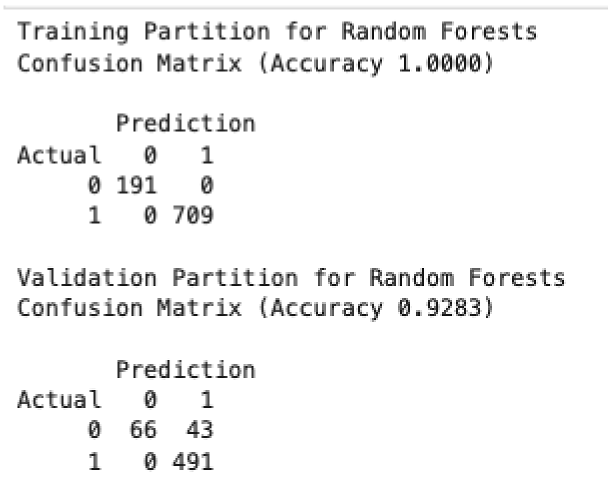
These confusion matrices provide a detailed breakdown of the model's performance on both the training and validation partitions. The accuracy scores indicate that the model performs well on both partitions, with a slightly higher accuracy on the training data compared to the validation data, which is expected.

Random Forest-

Random Forest takes an average of multiple estimates (models), which is more reliable than just using a single estimate. When we use the Random Forest Algorithm, the Validation Partition accuracy remains the same at 92.83 %. The misclassification Rate is 7.17%. But it must be noted that, the misclassified records for actual stroke is 0. It is 100% accurately predicting stroke. But the misclassified records for no stroke increased.



```
Number of Nodes in Tree in Random Forest: 189
```



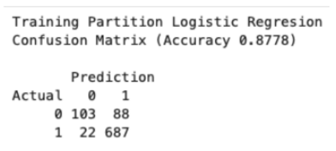
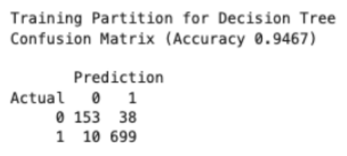
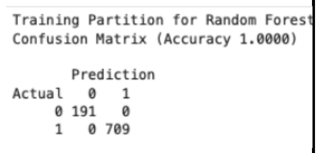
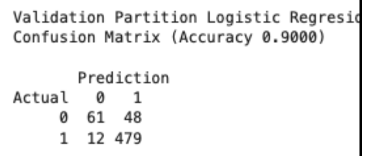
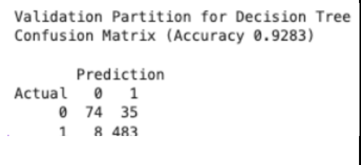
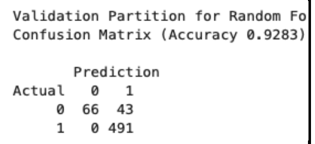
```
Training Partition for Random Forests
Confusion Matrix (Accuracy 1.0000)

       Prediction
Actual   0   1
     0 191   0
     1   0 709

Validation Partition for Random Forests
Confusion Matrix (Accuracy 0.9283)

       Prediction
Actual   0   1
     0  66  43
     1   0 491
```

It must also be taken into account that the training data set for random forests is 100% accurate .

The model learned the data set very well.

Conclusion-

Please see below the comparison of models on accuracy measures.

	Logistic Regression	Decision Trees - Grid Search	Decision Trees - Random Forest
Accuracy of Training Partition	 Training Partition Logistic Regresion Confusion Matrix (Accuracy 0.8778) Prediction Actual 0 1 0 103 88 1 22 687	 Training Partition for Decision Tree Confusion Matrix (Accuracy 0.9467) Prediction Actual 0 1 0 153 38 1 10 699	 Training Partition for Random Forest Confusion Matrix (Accuracy 1.0000) Prediction Actual 0 1 0 191 0 1 0 709
Accuracy of Validation Partition	 Validation Partition Logistic Regresi Confusion Matrix (Accuracy 0.9000) Prediction Actual 0 1 0 61 48 1 12 479	 Validation Partition for Decision Tree Confusion Matrix (Accuracy 0.9283) Prediction Actual 0 1 0 74 35 1 8 483	 Validation Partition for Random Fo Confusion Matrix (Accuracy 0.9283) Prediction Actual 0 1 0 66 43 1 0 491
Misclassification Rate Validation Set	10 %	7.17%	7.17%
Overfitting	No	No	No

All the three models generalize well to unseen data. There isn't overfitting in any of them. The accuracy for Decision trees is comparatively better than the Logistic Regression model (92.83%

vs 90%). Among both the Decision tree models, we recommend **Random Forest** for the following reasons-

- As the model works on training through different subsets of the dataset, this prevents trees from getting closely tied to any specific feature. This helps in generalization and hence, we see that there is no scope for overfitting in the model.
- The misclassification rate for stroke=1 (had stroke) is 0. This indicates that the chances of missing any patient to provide the necessary care are 0. Hence, minimizing the risks of false negatives.
- As the model works on different subsets, it can easily handle the large and complex datasets by easily scaling them. Hence, for future add-ups to the data, a Random Forest would be appropriate.

Bibliography-

- Dr Zinovy's Presentation slides
- Kaggle Dataset
  https://www.kaggle.com/datasets/fedesoriano/stroke-prediction-dataset/data
- Random Forest-
  https://medium.com/@Ambarish_224/random-forests-the-go-to-algorithm-for-complex-data-sets-aacbfaef57a2https://medium.com/@Ambarish_224/random-forests-the-go-to-algorithm-for-complex-data-sets-aacbfaef57a2