[2]:	<pre>%matplotlib inline plt.rc("font", size=14) from sklearn.linear_model import train_test_split from sklearn.model_selection import train_test_split from sklearn.linear_model import LogisticRegression from sklearn.metrics import classification_report from sklearn.metrics import roc_curve, roc_auc_score from sklearn.metrics import confusion_matrix import seaborn as sns sns.set(style="white") sns.set(style="whitegrid", color_codes=True) import statsmodels.api as sm</pre> pip install -U imbalanced-learn
[3]:	Requirement already satisfied: imbalanced-learn in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (0.10.1) Requirement already satisfied: threadpoolctl>=2.0.0 in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (from imbalanced-learn) (2.1.0) Requirement already satisfied: joblib>=1.1.1 in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (from imbalanced-learn) (1.2.0) Requirement already satisfied: scikit-learn>=1.0.2 in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (from imbalanced-learn) (1.2.1) Requirement already satisfied: scipy>=1.3.2 in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (from imbalanced-learn) (1.6.2) Requirement already satisfied: numpy>=1.17.3 in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (from imbalanced-learn) (1.6.2) Requirement already satisfied: numpy>=1.17.3 in /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages (from imbalanced-learn) (1.20.1) Note: you may need to restart the kernel to use updated packages. Conda install -c conda-forge imbalanced-learn Collecting package metadata (current_repodata.json): done Solving environment: done
	==> WARNING: A newer version of conda exists. <== current version: 4.14.0 latest version: 23.1.0 Please update conda by running \$ conda update -n base -c conda-forge conda # All requested packages already installed. Retrieving notices:working done Note: you may need to restart the kernel to use updated packages.
[4]: [4]:	Stroke_dataset= pd.read_csv("healthcare-dataset-stroke-data.csv")
5]:	25% 17741.250000 25.000000 0.000000 0.000000 77.245000 23.500000 0.000000 50% 36932.000000 45.000000 0.000000 0.000000 91.885000 28.100000 0.000000 75% 54682.000000 61.000000 0.000000 114.090000 33.100000 0.000000 max 72940.000000 82.000000 1.000000 1.000000 271.740000 97.600000 1.000000 stroke_dataset= pd.read_csv("healthcare-dataset-stroke-data.csv") print(stroke_dataset.columns) Index(['id', 'gender', 'age', 'hypertension', 'heart_disease', 'ever_married', 'work_type', 'Residence_type', 'avg_glucose_level', 'bmi', 'smoking_status', 'stroke'],
	Data Cleansing The stroke_dataset is imported into the Juypter along with all the libraries. For the first step of this project I have done data cleaning. Seleveral steps to data cleaning are: 1. First I have fixed the data type of each column. 2. Secondly, I checked if the data set had any null values.
6]:	<pre>3. In the third step, I handled missing valus by delecting the records. 4. In the fourth step, I checked if there are any duplicate value especially in the id column. 5. I also delected the column 'ever_married' due to multiple missing values. Step1 = stroke_dataset.drop('ever_married', axis=1) print(Step1) convert_dict = {'id': int,</pre>
	'avg_glucose_level': float,
	5106
	5110 rows x 11 columns id int64 int64 gender object age int64 hypertension int64 heart_disease int64 work_type object avg_glucose_level float64 bmi float64 smoking_status object stroke int64 dtype: object objec
7]:	Step2.isnull() step2.isnull().any() Step2.isnull().sum() id 0 gender 0 gender 0 aye 0 hypertension 0 heart_disease 0 work_type 0 Residence_type 0 avg_glucose_level 0 bmi 201 smoking_status 0 stroke 0 0
[8]:	Stroke_df = Step2[Step2['bmi'].notnull()] print(Stroke_df) id gender age hypertension heart_disease work_type \ 0 9046 Male 67 0 1 Private 2 31112 Male 80 0 1 Private 3 60182 Female 49 0 0 Private 4 1665 Female 79 1 0 Self-employed 5 56669 Male 81 0 0 Private
	5108 37544 Male 51 0 0 Private 5109 44679 Female 44 0 0 O Govt_job Residence_type avg_glucose_level bmi smoking_status stroke 0 Urban 228.69 36.6 formerly smoked 1 2 Rural 105.92 32.5 never smoked 1 3 Urban 171.23 34.4 smokes 1 4 Rural 174.12 24.0 never smoked 1 5 Urban 186.21 29.0 formerly smoked 1 1 5104 Rural 103.08 18.6 Unknown 0 5107 Rural 82.99 30.6 never smoked 0 5108 Rural 166.29 25.6 formerly smoked 0 5108 Rural 166.29 25.6 formerly smoked 0<
	Calculate IQR by finding Q1 and Q2 In second step check if there are any outliers Q1 = Stroke_df.quantile(0.25) Q3 = Stroke_df.quantile(0.75) IQR = Q3 - Q1 print(IQR)
.0]:	<pre>id</pre>
	id gender age hypertension heart_disease work_type
	3 Urban 171.23 34.4 smokes 1 4 Rural 174.12 24.0 never smoked 1 5 Urban 186.21 29.0 formerly smoked 1 5064 Rural 193.88 24.3 Unknown 0 5076 Rural 174.37 23.0 never smoked 0 5088 Urban 76.89 30.2 Unknown 0 5091 Rural 95.05 30.9 never smoked 0 5100 Rural 71.97 28.3 never smoked 0 5100 Rural 71.97 28.3 never smoked 0 510this input-10-bb8bdedf4a34>:3: FutureWarning: Automatic reindexing on DataFrame vs Series comparisons is deprecated and will raise ValueError in a future version of left, right = left.align(right, axis=1, copy=False) before e.g. 'left == right' Outliers = Stroke_df [((Stroke_df < Lower_Limit) ((Stroke_df > Upper_Limit))).any(axis=1)] <ipython-input-10-bb8bdedf4a34>:3: FutureWarning: Automatic reindexing on DataFrame vs Series comparisons is deprecated and will raise ValueError in a future version of left, right = left.align(right, axis=1, copy=False) before e.g. 'left == right' Outliers = Stroke_df [((Stroke_df < Lower_Limit) ((Stroke_df > Upper_Limit))).any(axis=1)] <ip>Cipython-input-10-bb8bdedf4a34>:3: FutureWarning: Automatic reindexing on DataFrame vs Series comparisons is deprecated and will raise ValueError in a future version of left, right = left.align(right, axis=1, copy=False) before e.g. 'left == right'</ip></ipython-input-10-bb8bdedf4a34>
.1]:	Outliers = Stroke_df [((Stroke_df < Lower_Limit) ((Stroke_df > Upper_Limit))).any(axis=1)] Stroke_df.isnull().sum() Stroke_df.shape Stroke_df.duplicated(['id']) 0 False 2 False 3 False 4 False 5 False 5104 False 5106 False 5107 False
.2]:	5107 False 5108 False 5109 False Length: 4909, dtype: bool Select columns bmi, age and avg_glucose_level and create box plots Num_columns = Stroke_df[["bmi", "age", "avg_glucose_level"]] print(Num_columns) bmi age avg_glucose_level 0 36.6 67 228.69 2 32.5 80 105.92 3 34.4 49 171.23
	4 24.0 79 174.12 5 29.0 81 186.21
.3]:	1. Created box plots to show the data distribution. 2. Box-Plot for age, bmi and average_glucose_level Num_columns.plot(kind = "box", title = "Box-Plot for age, bmi and average_glucose_level") <a).plot(kind="bar")<="" ,="" columns="stroke" count")="" group_gender.pivot(index="gender" href="mailto:AxesSubplot:title={'center': 'Box-Plot for age, bmi and average_glucose_level'}> Box-Plot for age, bmi and average_glucose_level 250 200 200 200 200 200 200 200 200 20</td></tr><tr><td></td><td>1. The bmi in above box plot is above 25. This could be related to stroke and bmi above 25 is considered over weight. 2. The age is between 25 and 70. The age shows adult category therefore this could be our predictor. 3. The blood sugar level from the box plot is between 70 to 130 which is normal level for before and after meal. This probabbly is not a good predictor for stroke.</td></tr><tr><td>.4]:</td><td>Used group by function to group variables. Used count function to count number of stroke cases in each subgroups. 1. Created bar charts and clustered bar charts for gender, work_type, Residence_type, smoking_status, heart_disease, hypertension columns to show the stroke cases. group_gender = Stroke_df.groupby(['gender', 'stroke'])['stroke'].count().reset_index(name=" print(group_gender)="" stacked="True," td="" title="stroke cases by gender type" values="count">
.4]:	gender stroke count 0 Female 0 2777 1 Female 1 120 2 Male 0 1922 3 Male 1 89 4 Other 0 1
	Female has more stroke cases than male. The clustered bar chart shows that the geneder could be good predictor for stroke.
.5]:	<pre>group_work = Stroke_df.groupby(["work_type", "stroke"])["stroke"].count().reset_index(name="count") print(group_work) group_work.pivot(index = 'work_type', columns = 'stroke', values = 'count').plot(kind = 'bar', title = 'stroke cases by job type') work_type stroke count 0 Govt_job 0 602 1 Govt_job 1 28 2 Never_worked 0 22 3 Private 0 2684 4 Private 1 127 5 Self-employed 0 722 6 Self-employed 0 722 6 Self-employed 1 53 7 children 0 670 8 children 1 1</pre>
.5]:	<pre><axessubplot:title={'center':'stroke by="" cases="" job="" type'},="" xlabel="work_type"> stroke cases by job type 2500 2000 1500 1000</axessubplot:title={'center':'stroke></pre>
.6]:	There is huge variation of stroke cases in work_type. Therefore, work_type could be our predictor. group_Residence_type = Stroke_df.groupby(["Residence_type", "stroke"])["stroke"].count().reset_index(name="count") print(group_Residence_type)
.6]:	group_Residence_type.pivot(index = 'Residence_type', columns = 'stroke', values = 'count').plot(kind = 'bar', title = 'stroke cases by Residence type') Residence_type stroke count Rural 0 2319 Rural 1 100 Urban 0 2381 Urban 1 109 <axessubplot:title={'center':'stroke by="" cases="" residence="" type'},="" xlabel="Residence_type"> stroke cases by Residence type stroke cases by Residence type stroke cases by Residence type</axessubplot:title={'center':'stroke>
	The Residence_type do not show much difference between rural and urban living areas. This probabbly is not our
.7]:	<pre>group_smoking_status = Stroke_df.groupby(["smoking_status", "stroke"])["stroke"].count().reset_index(name="count") print(group_smoking_status) group_smoking_status.pivot(index = 'smoking_status', columns = 'stroke', values = 'count').plot(kind = 'bar', title = 'stroke cases by smoking_status') smoking_status stroke count 0</pre>
.7]:	<pre>7 smokes 1 39 </pre> <pre><axessubplot:title={'center':'stroke by="" cases="" smoking_status'},="" xlabel="smoking_status"></axessubplot:title={'center':'stroke></pre>
	The stroke case is different in the people with different smoking habits. The smoking_status could be a predictor for stroke.
.8]: .8]:	group_heart_disease = Stroke_df.groupby(['heart_disease', 'stroke'])['stroke'].count().reset_index(name="count") print(group_heart_disease) group_heart_disease.pivot(index = 'heart_disease', columns = 'stroke', values = 'count').plot(kind = 'bar', title = 'stroke cases by heart_disease') heart_disease stroke count 0
	3000 2000 1000 heart_disease
	From the above bar chart we can see that people without the heart disease tend to have more stroke cases than the people with the heart disease. group_hypertension = Stroke_df.groupby(['hypertension', 'stroke'])['stroke'].count().reset_index(name="count") print(group_hypertension) group_hypertension.pivot(index = 'hypertension', columns = 'stroke', values = 'count').plot(kind = 'bar', title = 'stroke cases by hypertension') hypertension stroke count 0 0 0 4309 1 0 1 149 2 1 0 391 3 1 1 60 <axessubplot:title={'center':'stroke by="" cases="" hypertension'},="" xlabel="hypertension"></axessubplot:title={'center':'stroke>
	stroke cases by hypertension
	Above bar chart shows that people who do not have hypertension tend to have higher cases of stroke. Created dummy variables In this section, I have created dummy variables for columns like smoking status to convert categorical values into numerical values.
20]:	categorical_vars=['gender','work_type','Residence_type','smoking_status', 'hypertension', 'heart_disease'] for var in categorical_vars: categorical_list='var'+'_'+var categorical_list = pd.get_dummies(Stroke_df[var], prefix=var) data1=Stroke_df.join(categorical_list) Stroke_df=data1 categorical_vars=['gender','work_type','Residence_type','smoking_status', 'hypertension', 'heart_disease'] data_vars=Stroke_df.columns.values.tolist() to_keep=[i for i in data_vars if i not in categorical_vars] Final Columns to keep
	data_final=Stroke_df[to_keep] data_final.columns.values array(['id', 'age', 'avg_glucose_level', 'bmi', 'stroke', 'gender_Female',
22]:	Dropped Columns Removed columns that are unnecessary for the analysis. data_final.drop(['id'], axis = 1, inplace = True) /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages/pandas/core/frame.py:4308: SettingWithCopyWarning: A value is trying to be set on a copy of a slice from a DataFrame See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy return super().drop(data final.columns
:[د	<pre>data_final.columns data_final.head() data_final = data_final.drop(['gender_Female', 'gender_Other', 'hypertension_1', 'heart_disease_1',</pre>
	Creating Training Data and Test Data Divided the final data into x values (Independent variables) and y values (Depedent variables) for the test. X = data_final.loc[:, data_final.columns != 'stroke'] y = data_final.loc[:, data_final.columns == 'stroke'] from imblearn.over_sampling import SMOTE os = SMOTE(random_state=0) X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=0) Columns = X_train.columns os_data_X,os_data_y=os.fit_resample(X_train, y_train)
35]:	os_data_X = pd.DataFrame(data=os_data_X,columns=columns) os_data_y= pd.DataFrame(data=os_data_y,columns=['stroke']) # we can Check the numbers of our data print("length of oversampled data is ",len(os_data_X)) print("Number of no stroke in oversampled data",len(os_data_y[os_data_y['stroke']==0])) print("Number of stroke",len(os_data_y[os_data_y['stroke']==1])) print("Proportion of no stroke data in oversampled data is ",len(os_data_y[os_data_y['stroke']==0])/len(os_data_X)) print("Proportion of stroke data in oversampled data is ",len(os_data_y[os_data_y['stroke']==1])/len(os_data_X)) length of oversampled data is 6564 Number of no stroke in oversampled data 3282 Number of stroke 3282 Proportion of no stroke data in oversampled data is 0.5 Proportion of stroke data in oversampled data is 0.5
35]: 36]: 37]:	<pre>#y_data = data_final['stroke'] #x_data = data_final.drop('stroke', axis = 1) #from sklearn.model_selection import train_test_split #x_training_data, x_test_data, y_training_data, y_test_data = train_test_split(x_data, y_data, test_size = 0.3) from sklearn.linear_model import LogisticRegression</pre>
	Training the Logistic Regression Model Created a model by instantiating an instance of the LogisticRegression. Called fit method and passed in x values and y values. Created a variable called predictions and used model logistic regression model to make predictions. Used the model to calculate the performance metrics for our logistic regression.
89]: 10]:	<pre>#model = LogisticRegression() from sklearn.linear_model import LogisticRegression from sklearn import metrics X_train, X_test, y_train, y_test = train_test_split(os_data_X, os_data_y, test_size=0.3, random_state=0) logreg = LogisticRegression() logreg.fit(X_train, y_train) /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d array expected. Please change the shape of y to (n_samples,), for example using ravel().</pre>
•0]:	<pre>y = column_or_1d(y, warn=True) /Users/divyabastola/opt/anaconda3/lib/python3.8/site-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge (status=1): STOP: TOTAL NO. of ITERATIONS REACHED LIMIT. Increase the number of iterations (max_iter) or scale the data as shown in: https://scikit-learn.org/stable/modules/preprocessing.html Please also refer to the documentation for alternative solver options: https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression n_iter_i = _check_optimize_result(*LogisticRegression LogisticRegression()</pre> y_pred = logreg.predict(X_test)
:1]: :2]:	<pre>print('Accuracy of logistic regression classifier on test set: {:.2f}'.format(logreg.score(X_test, y_test))) Accuracy of logistic regression classifier on test set: 0.90 from sklearn.metrics import confusion_matrix confusion_matrix = confusion_matrix(y_test, y_pred) print(confusion_matrix) [[889 94] [110 877]] from sklearn.metrics import classification_report print(classification_report(y_test, y_pred))</pre>
	precision recall f1-score support 0 0.89 0.90 0.90 983 1 0.90 0.89 0.90 987 accuracy macro avg 0.90 0.90 0.90 1970 weighted avg 0.90 0.90 0.90 1970 Our model has calculated the accuracy as 90%.
	Interpretation: Of the entire test set, 90% of the stroke cases are predicted by the dependent variables.
:]: :]:	