	<pre>import seaborn as sb %matplotlib inline from sklearn.preprocessing import LabelEncoder from matplotlib import pyplot as plt from scipy.stats import shapiro from scipy import stats  from sklearn.metrics import classification_report from sklearn.pipeline import Pipeline  from sklearn.preprocessing import PolynomialFeatures  from sklearn.linear_model import Ridge from datetime import datetime from datetime import date import statsmodels.api as sm from statsmodels.formula.api import ols</pre>
	<pre>from sklearn.metrics import accuracy_score, make_scorer from mpl_toolkits.mplot3d import Axes3D from sklearn import preprocessing as preproc from sklearn import metrics from sklearn.datasets import make_classification from sklearn.model_selection import train_test_split from sklearn.pipeline import make_pipeline from sklearn.preprocessing import StandardScaler  from sklearn.metrics import accuracy_score, auc, balanced_accuracy_score, confusion_matrix, fl_score, precisi from sklearn.naive_bayes import GaussianNB from sklearn.neighbors import KNeighborsClassifier from sklearn.ensemble import RandomForestClassifier from sklearn.tree import DecisionTreeClassifier from sklearn.ensemble import GradientBoostingClassifier from sklearn.linear_model import LogisticRegression from sklearn.linear_model import LogisticRegression from sklearn.sym import SVC</pre>
[2]: t[2]:	### ### #### #########################
[4]: t[4]:	5 fbs 303 non-null int64 6 restecg 303 non-null int64 7 thalach 303 non-null int64 8 exang 303 non-null int64 9 oldpeak 303 non-null float64 10 slope 303 non-null int64 11 ca 303 non-null int64 12 thal 303 non-null int64 13 target 303 non-null int64 14 thypes: float64(1), int64(13) memory usage: 33.3 KB  #examining the dataset cvd.shape  (303, 14)  Step 2: Data cleaning  In this step, we are going to clean our dataset. We are going to look for null values and replace them with mean and mode. We are going to modify some variables if it is necessary and change datatypes for better analysis. We will also remove outliers from the dataset.  Outliers hamper the machine learning algorithms and hence they have to be removed.
[5]: t[5]: [6]:	<pre># column name cleaning  cvd.columns = cvd.columns.str.replace(' ', '')     cvd.columns  Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',</pre>
[7]:	slope 0  ca 0  thal 0  target 0  dtype: int64   #changing data type to right format  cvd.sex=cvd.sex.astype(object)  cvd.fbs=cvd.fbs.astype(object)  cvd.exang=cvd.exang.astype(object)  cvd.cp=cvd.cp.astype(object)  cvd.cp=cvd.cp.astype(object)  cvd.cp=cvd.co.astype(object)  cvd.slope=cvd.slope.astype(object)  cvd.target=cvd.target.astype(object)  cvd.target=cvd.target.astype(object)  cvd.dtypes  age int64  sex object  cp object  trestbps int64  chol int64  fbs object  restecg object  thalach int64  exang object  coldpeak float64  slope object  target object  target object  target object  thal object  target object  thal object  target object  thal object  target object  thal object  target object
[8]: t[8]:	Univariate analysis  We are using boxplot, histogram and plot to find the outliers, extreme values and distribution of the numerical variables.  #checking distribution for age cvd['age'].plot.density() <axessubplot: ylabel="Density">  0.04  0.03  0.00  0.00</axessubplot:>
[9]: t[9]:	#checking outliers using boxplot Age sb.boxplot(cvd('age']) <pre></pre>
[10]: [10]:	#thecking distribution for trestbps cvd['trestbps'].plot.density()  AxesSubplot: ylabel='Density'>  0.020-  0.015-  Age 0.010-  0.005-
[11]: [11]:	#checking outliers using boxplot trestbps sb.boxplot(cvd['trestbps']) <axessubplot:>  200  180  140</axessubplot:>
[12]: [12]: [13]:	<pre>cvd['trestbps'].quantile([0.1, 0.25, 0.5, 0.7, 0.9, 0.95, 0.99])  0.10     110.0 0.25     120.0 0.50     130.0 0.70     140.0 0.90     152.0 0.95     160.0 0.99     180.0 Name: trestbps, dtype: float64  #seeing limits trestbps_HE=cvd[cvd['trestbps'] &gt; 160.0].copy()</pre>
[15]: [16]:	<pre>#removing outliers for x in cvd['trestbps']:     if x &gt; 160.0:         cvd['trestbps'].replace(x,np.nan,inplace=True)  #checking outliers gone or not sb.boxplot(cvd['trestbps'])  <axessubplot:>  160- 150- 140- 130- 120-</axessubplot:></pre>
[17]: [18]:	#replacing with mean values medbps=cvd['trestbps'].mean() print(medbps) cvd['trestbps'].replace(np.nan, medbps, inplace=True)  129.30208333333334 #checking distribution for chol cvd['chol'].plot.density() <axessubplot: ylabel="Density">  0.008 0.007 0.006</axessubplot:>
[19]: [19]:	<pre>sb.boxplot(cvd['chol']) <axessubplot:></axessubplot:></pre>
[20]:	# # # # # # # # # # # # # # # # # # #
[23]:	<pre>0.70</pre>
[25]:	#replacing with median values medchol=cvd['chol'].median() print(medchol)
[26]: [26]:	<pre>cvd['chol'].replace(np.nan, medchol, inplace=True) 239.0  #checking distribution for thalach cvd['thalach'].plot.density()  <axessubplot: ylabel="Density">  0.0175 - 0.0150 - 0.0125 - 0.0100 - 0.00050 - 0.00050 - 0.00050 - 0.00055 -</axessubplot:></pre>
[27]:	0.0000    \$\frac{1}{2}\$   \$\fr
[28]: [28]: [29]:	<pre>cvd['thalach'].quantile([0.1, 0.25, 0.5, 0.7, 0.9, 0.95, 0.99])  0.10     116.00 0.25     133.50 0.50     153.00 0.70     163.00 0.90     176.60 0.95     181.90 0.99     191.96 Name: thalach, dtype: float64  #seeing limits thal_LE=cvd[cvd['thalach'] &lt; 116].copy()</pre> #putting them at one place
[31]: [32]:	<pre>print(len(thal_LE))  #removing outliers for x in cvd['thalach']:     if x &lt; 116:         cvd['thalach'].replace(x,np.nan,inplace=True)  #checking outliers gone or not sb.boxplot(cvd['thalach'])  <axessubplot:>  200  180 - 160 -</axessubplot:></pre>
[34]: [34]:	#replacing with median values  medthal=cvd['thalach'].median() print(medthal) cvd['thalach'].replace(np.nan, medthal, inplace=True)  156.0  #checking distribution for oldpeak cvd['oldpeak'].plot.density() <axessubplot: ylabel="Density"></axessubplot:>
[35]:	#checking outliers using boxplot oldpeak sb.boxplot(cvd['oldpeak']) <axessubplot:></axessubplot:>
	6 -
[36]: [36]: [37]: [38]:	<pre>#outlier treatment cvd['oldpeak'].quantile([0.1, 0.25, 0.5, 0.7, 0.9, 0.95, 0.99])  0.10</pre>
[40]:	<pre><axessubplot:></axessubplot:></pre> 4.0  3.5  3.0  2.5  2.0  1.5  1.0  0.5  0.0
[41]: [42]:	#replacing with median values  medop=cvd['oldpeak'].median() print(medop) cvd['oldpeak'].replace(np.nan, medop, inplace=True)  0.64999999999999999  Step 3:Exploratory data analysis  In this step, we are going to explore the dataset. Perform hypothesis tests, bivariate analysis and check for correlation between variables.  #summary stats cvd.describe().round(2)  age trestbps chol thalach oldpeak  count 303.00 303.00 303.00 303.00 303.00  mean 54.37 129.30 240.18 154.70 0.97  std 9.08 14.12 41.41 17.19 1.04 min 29.00 94.00 126.00 116.00 0.00  25% 47.50 120.00 211.00 143.00 0.00
[43]: [44]:	50% 55.00 130.00 239.00 156.00 0.65  75% 61.00 140.00 269.00 166.00 1.60  max 77.00 160.00 330.00 202.00 4.00  #seeing correlation of numerical variables  coordata =cvd.corr()  cordata.round(2)   age trestbps chol thalach oldpeak  age 1.00 0.26 0.17 -0.36 0.21  trestbps 0.26 1.00 0.08 0.01 0.12  chol 0.17 0.08 1.00 -0.06 -0.00  thalach -0.36 0.01 -0.06 1.00 -0.34  oldpeak 0.21 0.12 -0.00 -0.34 1.00  #heatmap of correlation  sb.heatmap(cordata, annot=True, cmap="Reds") <axessubplot:></axessubplot:>
[44]:	### 1 0.26 0.17 -0.36 0.21 -0.8  -0.8  -0.26 1 0.076 0.0085 0.12 -0.6  -0.4  -0.2  -0.36 0.0085 -0.063 1 -0.34 -0.0  ##################################
[46]: [46]:	healthy=cvd[cvd['target']==0] unhealthy=cvd[cvd['target']==1]  #getting summary stats of healthy healthy.describe().round(2)  age trestbps chol thalach oldpeak  count 138.00 138.00 138.00 138.00 138.00  mean 56.60 130.63 245.68 148.16 1.46  std 7.96 13.65 42.73 15.59 1.15  min 35.00 100.00 131.00 116.00 0.00  25% 52.00 120.00 217.25 136.50 0.60  50% 58.00 129.65 245.00 150.00 1.20  75% 62.00 140.00 279.75 156.00 2.20  max 77.00 160.00 330.00 195.00 4.00  #getting summary stats of unhealthy unhealthy.describe().round(2)
[47]: [47]:	

#p pl pl pl pl	44%	
pl pl pl pl	Is type of thalassameia an indicator nal=unhealthy['thal'].unique() punt=unhealthy['thal'].value_counts() polotting people per thalassameia type	
	<pre>lt.bar(Thal,count)  lt.title('Is Thalassameia an indicator? ') lt.xlabel('Type of Thalassameia') lt.ylabel('count') lt.rcParams['figure.figsize'] = [17, 7] lt.show()  Is Thalassameia an indicator?  120 -</pre>	
count	100 - 80 - 60 - 40 - 20 -	
an co #p	Type of Thalassameia  percent of people have angina due to exercise  ng=cvd['exang'].unique()  punt=cvd['exang'].value_counts()  plotting people per thalassameia type  ng,  startangle=90, shadow = True,  radius = 1.1, autopct = '%1.0f%%')	3.5
	the title ('how many people have exercise induced angina? ')  how many people have exercise induced angina?  1	
	67%	
EC co	Rest ECG type and heart attack CG=healthy['restecg'].unique() punt=healthy['restecg'].value_counts()  colotting people per ECG type Lt.bar(ECG,count)	
pl pl pl pl	<pre>lt.title('Is ECG an indicator? ') lt.xlabel('Type of ECG result') lt.ylabel('count') lt.rcParams['figure.figsize'] = [17, 7] lt.show()  Is ECG an indicator?  80- 60-</pre>	
count	50 - 40 - 30 - 20 - 10 - 0.5	1.5 2.0
#pp pl	<pre>is heart attack dependent on slope? Lopetp=healthy['slope'].unique() punt=healthy['slope'].value_counts()  plotting people per slope type Lt.bar(slopetp,count)  Lt.title('Is slope an indicator of health? ') Lt.xlabel('Type of slope result') Lt.ylabel('count') Lt.rcParams['figure.figsize'] = [17, 7] Lt.show()  Is slope an indicator of health</pre>	h?
count	80 - 60 - 40 -	
]: # <i>F</i> su co # <i>p</i>	20- 0-0.5 0.0 0.5 1.0 Type of slope result  Percentage of people having high sugar  ag=cvd['fbs'].unique() punt=cvd['fbs'].value_counts()  Polotting people per sugar level  at.pie(count, labels =  ag, startangle=90, shadow = True,	1.5 2.0
	radius = 1.1, autopct = '%1.0f%%')  Lt.title('how many people have high blood sugar? ')  how many people have high blood sugar?  0	
su co	## 1 ## 1 ## 2 ## 2 ## 2 ## 2 ## 2 ## 2	
pl pl pl pl pl	<pre>lt.bar(sug,count)  lt.title('Is high sugar an indicator? ') lt.xlabel('Type of sugar level') lt.ylabel('count') lt.rcParams['figure.figsize'] = [17, 7] lt.show()  Is high sugar an indicator?  140 - 120 - 100 -</pre>	
count	80 - 60 - 40 - 200.25 0.00 0.25 0.50 Type of sugar level	0.75 1.00 1.25
No. ]: #i pl cv <a< td=""><td><pre>variate analysis  ow we are going to analyse two variables with respect to one another.  is cholestrol responsible for heart attack  it.figure(figsize=[12,6]) rd.boxplot(by="target", column="chol", grid = False)  axesSubplot: title={'center': 'chol'}, xlabel='target'&gt;  rigure size 1200x600 with 0 Axes&gt;  Boxplot grouped by target  chol</pre></td><td></td></a<>	<pre>variate analysis  ow we are going to analyse two variables with respect to one another.  is cholestrol responsible for heart attack  it.figure(figsize=[12,6]) rd.boxplot(by="target", column="chol", grid = False)  axesSubplot: title={'center': 'chol'}, xlabel='target'&gt;  rigure size 1200x600 with 0 Axes&gt;  Boxplot grouped by target  chol</pre>	
300 275 250 225 200 175		
ch ha mo an an	target  checking if cholestrol differs according to the heart attack nol=cvd['chol'] a=cvd['target'] od = ols("chol ~ ha", data=cvd).fit() nov_table = sm.stats.anova_lm(mod) nov_table  df sum_sq mean_sq F PR(>F) ha 1.0 7674.102193 7674.102193 4.527199 0.034173 esidual 301.0 510228.274045 1695.110545 NaN NaN	o i
gr gr pl pl	seeing the average cholestrol level by heart attack type rouped = cvd.groupby('target').agg({'chol': 'median'})  rouped.plot(kind='bar')  lt.xlabel('heart Attack')  lt.ylabel('Cholestrol')  lt.show()	
Cholestrol	150 - 100 - 50 - heart Attack	1-
pl cv <a< td=""><td>•</td><td></td></a<>	•	
140 120	0 -	0
hr ha mo an an an Re	<pre>checking if high heart rate differs according to the heart attack c=cvd['thalach'] a=cvd['target'] od = ols("hr ~ ha", data=cvd).fit() nov_table = sm.stats.anova_lm(mod) nov_table  df sum_sq mean_sq F PR(&gt;F) ha 1.0 10828.991435 10828.991435 41.578204 4.501307e-10 esidual 301.0 78395.074572 260.448753 NaN NaN  seeing the average heart rate by heart attack type couped = cvd.groupby('target').agg({'thalach': 'median'})</pre>	
pl pl pl	rouped.plot(kind='bar') Lt.xlabel('heart Attack') Lt.ylabel('Heart rate') Lt.show()  160 -  140 -  120 -  100 -	
]: # <i>i</i>	heart Attack  is oldpeak responsible for heart attack it figure (figsize=[12,6]) rd.boxplot(by="target", column="oldpeak", grid = False)	
]:		0 0 0
2.0		
1.5 1.0 0.5 0.0  ]: #coop ha mo an		
1.5 1.0 0.5 0.0 0.5 0.0 ]: #cop ha mo an an ]:  Ree ]: #s gr gr pl pl pl	target  checking if oldpeak differs according to the heart attack  cecvd['oldpeak']  a=cvd['target']  od = ols("op ~ ha", data=cvd).fit()  nov_table = sm.stats.anova_lm(mod)	
1.5 1.0 0.5 0.0 0.5 0.0 0.5 0.0 0.7  Recop ha mo an	target  checking if oldpeak differs according to the heart attack  covd['oldpeak']  covd['target']  do = ols('po ~ ha", data=cvd).fit()  nov_table = sm.stats.anova_lm(mod)  nov_table   df sum_sq mean_sq F PR(>F)  ha 1.0 60.196725 60.196725 67.738609 5.717304e-15  esidual 301.0 267.487252 0.888662 NaN NaN  seeing the average oldpeak by heart attack type  rouped = cvd.groupby('target').agg({'oldpeak': 'median'})  tt.xlabel('Heart Attack')  tt.ylabel('oldpeak')  it.show()  12-  10-  0.8-  0.6-  0.4-	
1.5 1.0 0.5 0.0 0.5 0.0 0.6    ## opp had moderate and mo	target  checking if oldpeak differs according to the heart attack pecvd['oldpeak'] accvd['target'] add = ols("op ~ ha", data=cvd).fit() anov_table = sm.stats.anova_lm(mod) anov_table  df sum_sq mean_sq F PR(>F) ha 1.0 60.196725 60.196725 67.738609 5.717304e-15 asidual 301.0 267.487252 0.888662 NaN NaN  seeing the average oldpeak by heart attack type arouped = cvd.groupby('target').agg(('oldpeak': 'median')) accuped.plot(kind='bar') att.xlabel('Heart Attack') att.ylabel('oldpeak') att.show()	resting BP than healthy.
1.5 1.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.0	target  checking if oldpeak differs according to the heart attack serval('oldpeak') serval('oldpeak') serval('target') dot = ols("op ~ ha", data=cvd).fit() stoy_table = sm.stats.anova_lm(mod) sov_table  df sum_sq mean_sq F PR(>F) ha 1.0 60.196725 60.196725 67.738609 5.717304e-15 seticual 301.0 267.487252 0.888662 NaN NaN  seeing the average oldpeak by heart attack type couped = cvd.groupby('target').agg({'oldpeak': 'median'}) tt.xlabel('Heart Attack') tt.ylabel('oldpeak') tt.show()  Heart Attack  sights  People who get heart attack are relatively younger than those who dont.  Unhealthy people have a higher heart rate and lower cholestrol level,oldpeak, and  There is a moderately positive correlation between age and variables like oldpeak,	resting BP than healthy.
1.5 1.0 0.5 0.5	thecking if aldpeak differs according to the heart attack evol ("Oldpeak") and e ols ("op v ha", data=evd) fit () to v table = sm.stats.anova_lm(mod) tov_table = sm.stats.anova_lm(mod)	resting BP than healthy. cholestrol and resting BP.
1.5 1.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.5 0.0 0.0	thecking if oldpeak differs seconding to the heart attack perval ("oldpeak") perval ("reaget") de old if op + ha", data=cvdl.fit() now Lable = sm.stalss.anova_In(nod) now Lable ('oldpeak') now Lable = sm.stalss.anova_In(nod) now Lable = sm.stalss.anova_In(nod) now Lable ('oldpeak') now Lable In(nod) now Lable now Lable = sm.stalss.anova_In(nod) now Lable ('oldpeak') now	resting BP than healthy. cholestrol and resting BP.
1.5 1.0 0.5 0.0 0.5 0.0 0.5 0.0 0.6 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	decision of Oddpeak disCress according to the Beast stack second (Carpet)  and (Carpet	resting BP than healthy. cholestrol and resting BP.  thal  1 2 2 2 2 2
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1.5   1.0   1.5   1.0   1.5   1.0   1.5   1.0   1.5   1.5   1.0   1.5	About the provide part of Course and controlling to the American security and the American security (Additional) and the provided (Additional) and the provi	thal  1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1
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1.5 1.0 1.5 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.5 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	Annual Columns of Columns and Columns of Col	thal  1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1
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# # # # # # # # # # # # # # # # # # #	The content of the	resting 8P than healthy.  tholestrol and resting 8P.   that  1 2 2 2 2 2 3 5 1 1 1 1 1 2 2 2 2 3 6 5 6 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
##   ##   ##   ##   ##   ##   ##   #	The company of the co	that  a heart attack. We will build several models and  built  1  2  2  3  4  5  6  6  7  7  8  8  8  8  8  8  8  8  8  8  8
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	<pre>#confusion matrix cm=confusion_matrix(y_test,ypred4) print(cm)  [[25 10] [ 5 36]]  #printing metrics print(classification_report(y_test,ypred4))</pre>
In [161	0 0.83 0.71 0.77 35 1 0.78 0.88 0.83 41 accuracy 0.80 76 macro avg 0.81 0.80 0.80 76 weighted avg 0.81 0.80 0.80 76
Out[161]:	<pre>model5=knc.fit(X_train,y_train) model5  C:\Users\sujoydutta\anaconda3\lib\site-packages\sklearn\neighbors\_classification.py:207: DataConversionWarnin g: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples,), for example using ravel().     return selffit(X, y)  v KNeighborsClassifier  KNeighborsClassifier()</pre>
In [162 Out[162]: In [163	<pre>ypred5= model5.predict(X_test) ypred5  array([0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 1, 1, 1, 0,</pre>
In [164	<pre>print("Accuracy of the model: {0}%".format(accuracy_score(y_test,ypred5)*100))  Accuracy of the model: 80.26315789473685%  #confusion matrix cm=confusion_matrix(y_test,ypred5) print(cm)  [[26 9] [ 6 35]]</pre>
IN [165	#printing metrics print(classification_report(y_test,ypred5))  precision recall f1-score support  0 0.81 0.74 0.78 35 1 0.80 0.85 0.82 41  accuracy 0.80 76 macro avg 0.80 0.80 0.80 76 weighted avg 0.80 0.80 0.80 76
	<pre>#fitting the rfc model model6=rfc.fit(X_train,y_train) model6  C:\Users\sujoydutta\AppData\Local\Temp\ipykernel_9012\1772640938.py:2: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples,), for example using ravel ().     model6=rfc.fit(X_train,y_train)  V RandomForestClassifier</pre>
	#predict ypred6= model6.predict(X_test) ypred6 array([0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
	<pre>#accuracy print("Accuracy of the model: {0}%".format(accuracy_score(y_test,ypred6)*100))  Accuracy of the model: 75.0%  #printing metrics print(classification_report(y_test,ypred6))  precision recall f1-score support</pre>
In [172	0 0.75 0.69 0.72 35 1 0.75 0.80 0.78 41  accuracy 0.75 76 macro avg 0.75 0.75 0.75 76 weighted avg 0.75 0.75 0.75 76  #fitting the rfc model model7=gbc.fit(X_train,y_train)
	<pre>model7  C:\Users\sujoydutta\anaconda3\lib\site-packages\sklearn\ensemble\_gb.py:570: DataConversionWarning: A column-ve ctor y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example usin g ravel().     y = column_or_ld(y, warn=True)  v GradientBoostingClassifier  GradientBoostingClassifier()</pre>
Out[173]:	<pre>#predict ypred7= model7.predict(X_test) ypred7  array([0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 0,</pre>
	print("Accuracy of the model: {0}%".format(accuracy_score(y_test,ypred7)*100))  Accuracy of the model: 67.10526315789474%  #printing metrics print(classification_report(y_test,ypred7))  precision recall f1-score support  0 0.64 0.66 0.65 35 1 0.70 0.68 0.69 41
	accuracy 0.67 76 macro avg 0.67 0.67 76 weighted avg 0.67 0.67 0.67 76  Conclusion  KNC and SVC are the models having the most accuracy of 80% and they should be used.
	Hyper-Parameter Tuning  Let us find the best hyperparamters for the models that will increase the accuracy.  # Generate some random data for classification X, y = make_classification(n_samples=303, n_features=13, random_state=42)  #setting the hyper parameters for KNC param_grid = {
	<pre>'n_neighbors': [3, 5, 7, 9], 'weights': ['uniform', 'distance'], 'p': [1, 2]  # Define the evaluation metric scorer = make_scorer(accuracy_score)  # Split the data into training and validation sets X_train, X_val, y_train, y_val = train_test_split(X, y, test_size=0.2, random_state=42)</pre>
	<pre># Create the KNeighborsClassifier model pknc = KNeighborsClassifier()  # Perform grid search with cross-validation to find the best hyperparameters grid_search = GridSearchCV(pknc, param_grid, scoring=scorer, cv=5, n_jobs=-1) grid_search.fit(X_train, y_train)</pre>
In [262	# Print the best hyperparameters and the corresponding evaluation score print("Best hyperparameters: ", grid_search.best_params_) print("Best score: ", grid_search.best_score_)  # Test the final model on a separate test set
-	<pre>y_pred = grid_search.predict(X_val) print("Test accuracy: ", accuracy_score(y_val, y_pred))  Best hyperparameters: {'n_neighbors': 7, 'p': 1, 'weights': 'uniform'} Best score: 0.9093537414965986 Test accuracy: 0.8688524590163934</pre>
	<pre>param_grid = {     'C': [0.1, 1, 10, 100],     'kernel': ['linear', 'rbf', 'poly'],     'degree': [2, 3, 4],     'gamma': ['scale', 'auto'],     'class_weight': [None, 'balanced'] }  # Define the evaluation metric scorer = make_scorer(accuracy_score)</pre>
	<pre># Create the SVC model psvc = SVC()  # Perform grid search with cross-validation to find the best hyperparameters grid_search = GridSearchCV(psvc, param_grid, scoring=scorer, cv=5, n_jobs=-1) grid_search.fit(X_train, y_train)</pre>
In [310	# Print the best hyperparameters and the corresponding evaluation score print("Best hyperparameters: ", grid_search.best_params_) print("Best score: ", grid_search.best_score_)  # Test the final model on a separate test set
	y_pred = grid_search.predict(X_val) print("Test accuracy: ", accuracy_score(y_val, y_pred))  Best hyperparameters: {'C': 0.1, 'class_weight': None, 'degree': 2, 'gamma': 'scale', 'kernel': 'linear'} Best score: 0.9545918367346939 Test accuracy: 0.8852459016393442  Observation  We find SVC can be the model with the highest accuracy as it's score 95% compared to 91% for KNC model.
Out[311]:	<pre>#creating the final model fm = SVC(C=0.1, class_weight=None, degree= 2, gamma= 'scale', kernel= 'linear') fm  SVC SVC(C=0.1, degree=2, kernel='linear')</pre>
Out[312]:	SVC(C=0.1, degree=2, kernel='linear')
	<pre>ypredf array([1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1,</pre>
In [315	#printing metrics print(classification_report(y_test,ypredf))  precision recall f1-score support  0 0.29 0.31 0.30 35 1 0.37 0.34 0.35 41  accuracy 0.33 76 macro avg 0.33 0.33 0.33 76
	Final statement  Hyperparameter tuning didnt improve the accuracy but rather reduced the accuracy score which is rather dissapointing.