APSIT SKILLS INTERNSHIP – PROJECT REPORT

PO COMPUTER

Project Batch: B1

Team Members Names:

Team Leader: - Rahul J. Bhiwande

Member 1: - Saurabh V. Yadav

Member 2: - Urvi V. Aryamane

Technology Selected:

Python

Project Topic Name:

Breast Cancer Classification using Machine Learning

Problem statement:

During their life, among 8% of women are diagnosed with Breast cancer (BC), after lung cancer, BC is the second popular cause of death in both developed and undeveloped worlds. BC is characterized by the mutation of genes, constant pain, changes in the size, color(redness), skin texture of breasts. Today, Machine Learning (ML) techniques are being broadly used in the breast cancer classification problem. They provide high classification accuracy and effective diagnostic capabilities. The early diagnosis of BC can improve the prognosis and chance of survival significantly, as it can promote timely clinical treatment to patients. Further accurate classification of benign tumors can prevent patients undergoing unnecessary treatments. To observe which features are most helpful in predicting malignant or benign cancer and to see general trends that may aid us in model selection. The goal is to classify whether the breast cancer is benign or malignant.

Detailed Workflow:

- Functions/modules used for the program:
    1. NumPy
    2. Pandas
    3. Matplotlib
    4. Scikit learn

- Flow of the code:

Step 1: Data Preparation

We will use the UCI Machine Learning Repository for breast cancer dataset.

Step 2: Data Exploration

We will import the necessary libraries and use the library functions to examine the available data.

Step 3: Handling the Categorical Data

The data in the dataset is not always in the numeric form. Further processing requires the data to be in numeric form. Hence, in this step, we will convert the non-numeric data into numeric data.

Step 4: Splitting the dataset

The data we use is usually split into training data and test data. The training set contains a known output and the model learns on this data in order to be generalized to other data later on. We have the test dataset (or subset) in order to test our model's prediction on this subset.

Step 5: Feature Scaling

Most of the times, the data will be varying over a large range. Hence, this data is needed to be brought in a lower range using normalization.

Step 6: Model Selection, classification and visualization

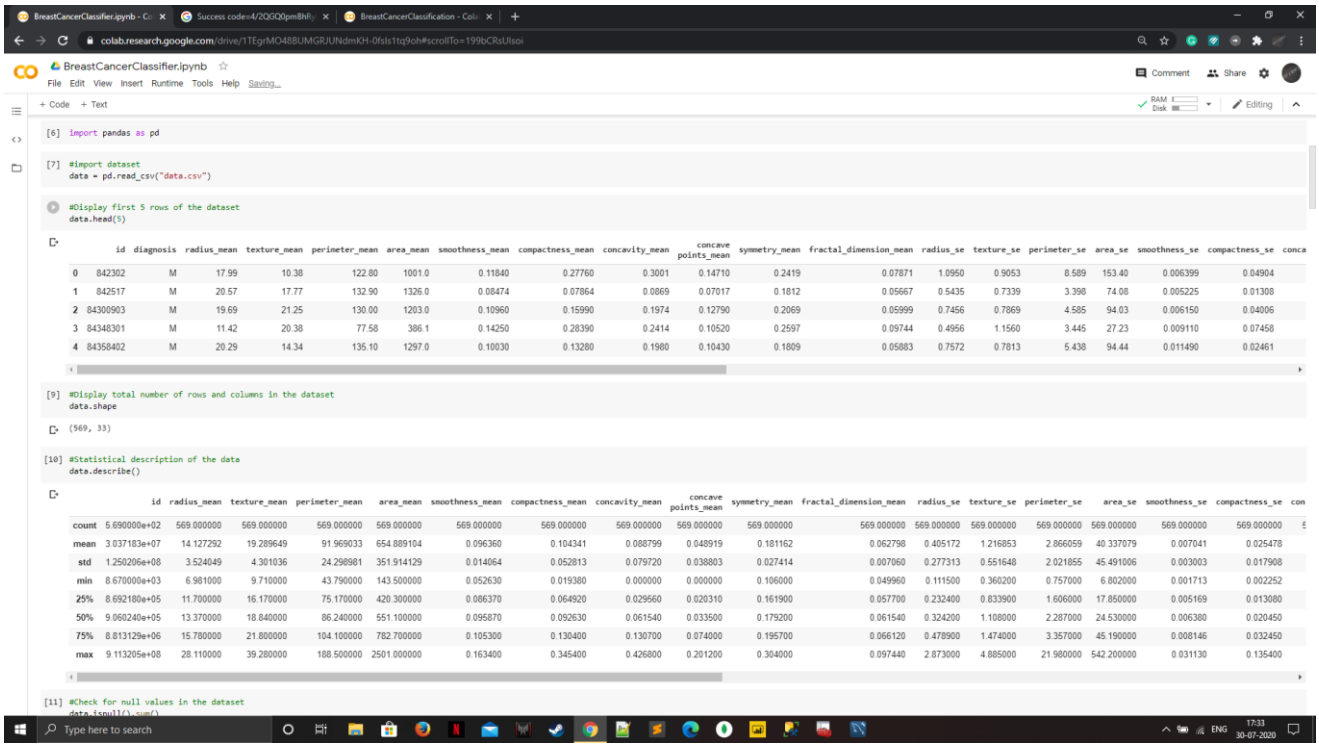
We will be using various classification models. In our dataset we have the outcome variable or Dependent variable i.e. Y having only two set of values, either M (Malign) or B(Benign). So, we will use Classification algorithm of supervised learning. Also, the data will be visualized in the form of graphs, using python libraries.

GitHub / Drive link of project code:

Data model:
https://colab.research.google.com/drive/1TEgrMO48BUMGRJUNdmKH-0fsIs1tq9oh

Output Screenshots:

Data Model:



BreastCancerClassifier.ipynb

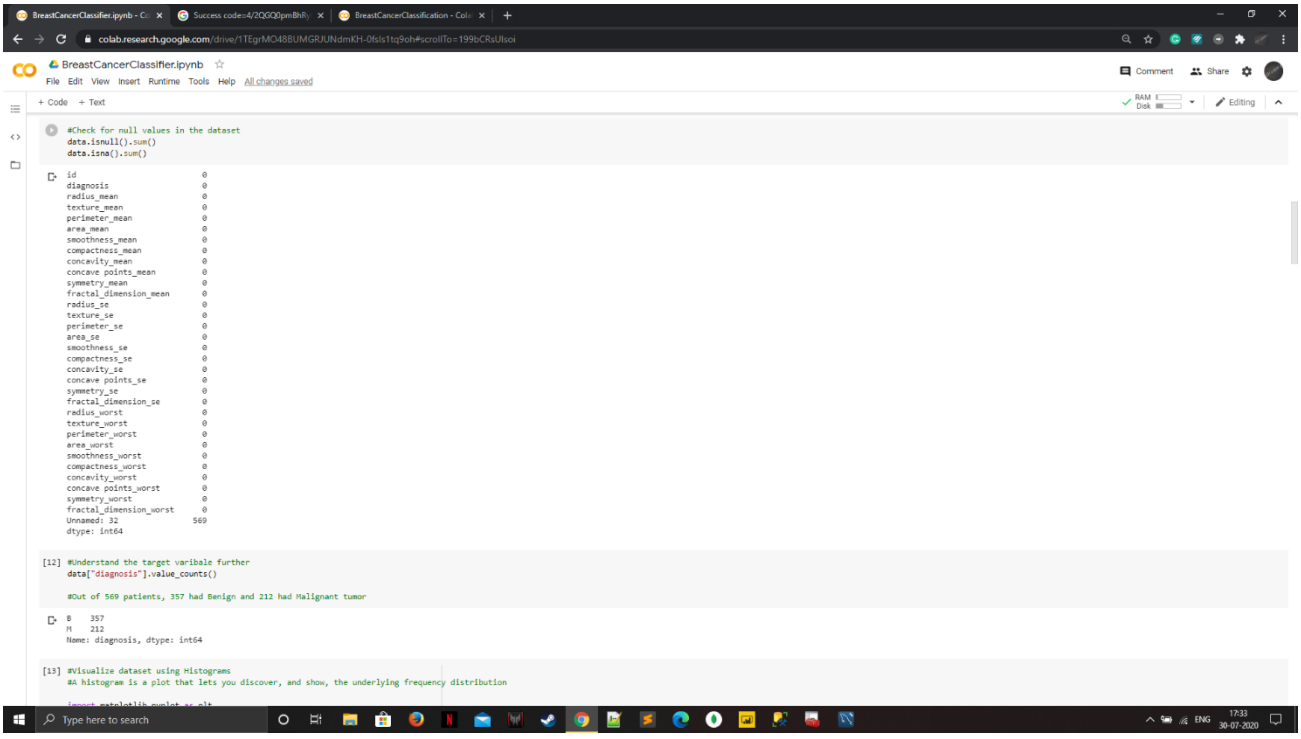
```
[6] import pandas as pd

[7] #import dataset
    data = pd.read_csv("data.csv")

    #Display first 5 rows of the dataset
    data.head(5)
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	fractal_dimension_mean	radius_se	texture_se	perimeter_se	area_se	smoothness_se	compactness_se	conca
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	1.0950	0.9053	8.589	153.40	0.006399	0.04904	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	0.5435	0.7339	3.398	74.08	0.005225	0.01308	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	0.7456	0.7869	4.585	94.03	0.006150	0.04006	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	0.4956	1.1560	3.445	27.23	0.009110	0.07458	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	0.7572	0.7813	5.438	94.44	0.011490	0.02461	

```
[9] #Display total number of rows and columns in the dataset
    data.shape

    (569, 33)

[10] #Statistical description of the data
     data.describe()
```

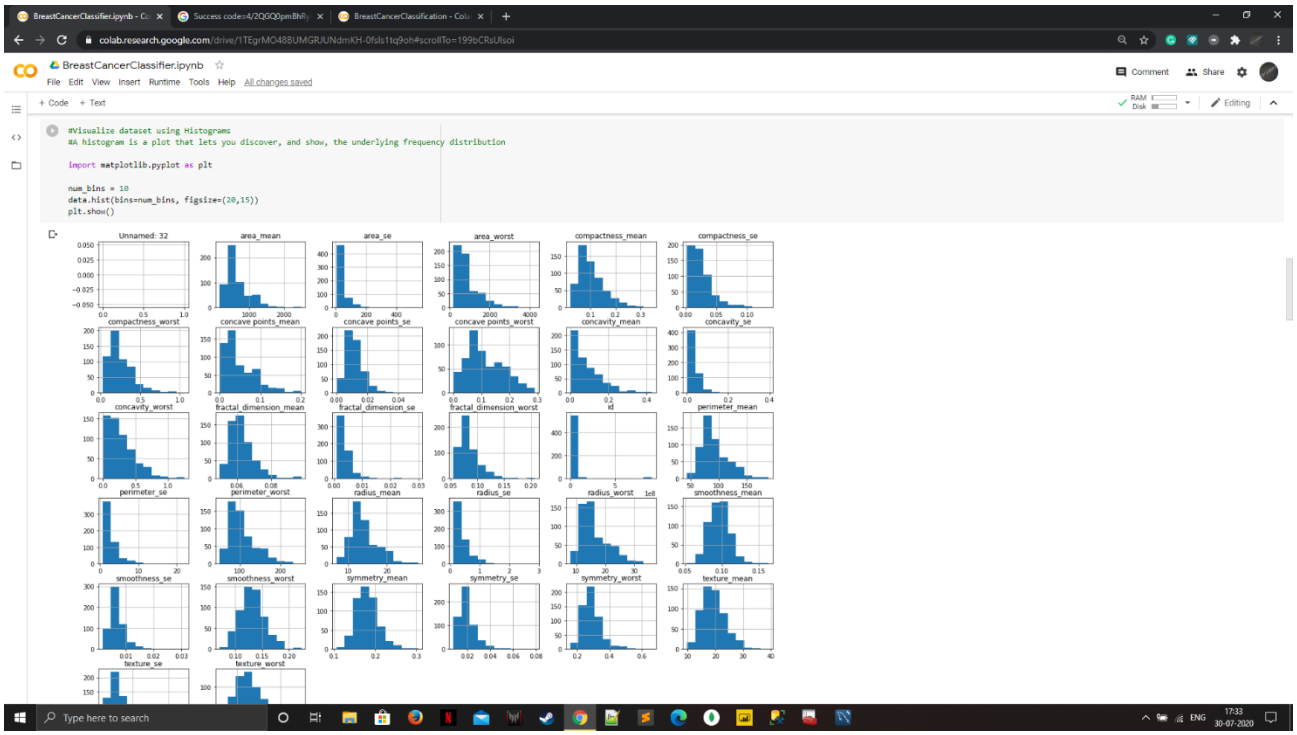
	id	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	fractal_dimension_mean	radius_se	texture_se	perimeter_se	area_se	smoothness_se	compactness_se	con
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	0.181162	0.062798	0.405172	1.216853	2.866059	40.337079	0.007041	0.025478	
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.079720	0.038803	0.027414	0.007060	0.277313	0.551648	2.021855	45.491006	0.003003	0.017908	
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	0.106000	0.049960	0.111500	0.360200	0.757000	6.802000	0.001713	0.002252	
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	0.161900	0.057700	0.232400	0.833900	1.606000	17.850000	0.005169	0.013080	
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	0.179200	0.061540	0.324200	1.108000	2.287000	24.530000	0.006380	0.020450	
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	0.195700	0.066120	0.478900	1.474000	3.357000	45.190000	0.008146	0.032450	
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	0.304000	0.097440	2.873000	4.885000	21.980000	542.200000	0.031130	0.135400	

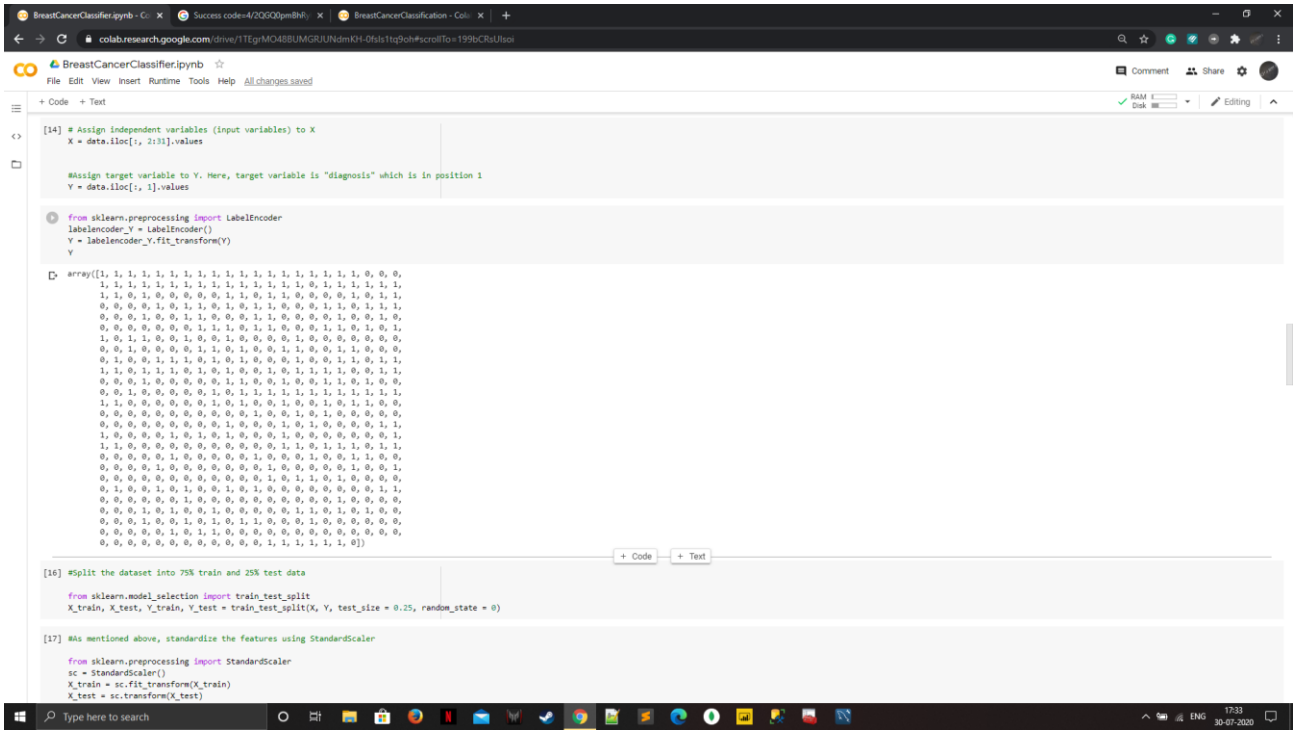
```
[11] #Check for null values in the dataset
     data.isnull().sum()
```



BreastCancerClassifier.ipynb

```
#Check for null values in the dataset
data.isnull().sum()
data.isna().sum()

id                         0
diagnosis                  0
radius_mean                0
texture_mean               0
perimeter_mean             0
area_mean                  0
smoothness_mean            0
compactness_mean           0
concavity_mean             0
concave points_mean        0
symmetry_mean              0
fractal_dimension_mean     0
radius_se                  0
texture_se                 0
perimeter_se               0
area_se                    0
smoothness_se              0
compactness_se             0
concavity_se               0
concave points_se          0
symmetry_se                0
fractal_dimension_se       0
radius_worst               0
texture_worst              0
perimeter_worst            0
area_worst                 0
smoothness_worst           0
compactness_worst          0
concavity_worst            0
concave points_worst       0
symmetry_worst             0
fractal_dimension_worst    0
Unnamed: 32                569
dtype: int64

[12] #Understand the target varibale further
     data["diagnosis"].value_counts()

     #Out of 569 patients, 357 had Benign and 212 had Malignant tumor

B    357
M    212
Name: diagnosis, dtype: int64

[13] #Visualize dataset using Histograms
     #A histogram is a plot that lets you discover, and show, the underlying frequency distribution
```


BreastCancerClassifier.ipynb
File Edit View Insert Runtime Tools Help All changes saved
+ Code + Text
#Visualize dataset using Histograms
#A histogram is a plot that lets you discover, and show, the underlying frequency distribution
import matplotlib.pyplot as plt
num_bins = 10
data.hist(bins=num_bins, figsize=(20,15))
plt.show()
Unnamed: 32
area_mean
area_se
area_worst
compactness_mean
compactness_se
compactness_worst
concave points_mean
concave points_se
concave points_worst
concavity_mean
concavity_se
concavity_worst
fractal_dimension_mean
fractal_dimension_se
fractal_dimension_worst
id
perimeter_mean
perimeter_se
perimeter_worst
radius_mean
radius_se
radius_worst
smoothness_mean
smoothness_se
smoothness_worst
symmetry_mean
symmetry_se
symmetry_worst
texture_mean
texture_se
texture_worst


BreastCancerClassifier.ipynb
File Edit View Insert Runtime Tools Help All changes saved
[14] # Assign independent variables (input variables) to X
X = data.iloc[:, 2:31].values
#Assign target variable to Y. Here, target variable is "diagnosis" which is in position 1
Y = data.iloc[:, 1].values
from sklearn.preprocessing import LabelEncoder
labelencoder_Y = LabelEncoder()
Y = labelencoder_Y.fit_transform(Y)
Y
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
0, 0, 1, 0, 0, 1, 1, 1, 0, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1,
0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0,
0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0, 1,
1, 0, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
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1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1, 1, 0, 0,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0,
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0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1,
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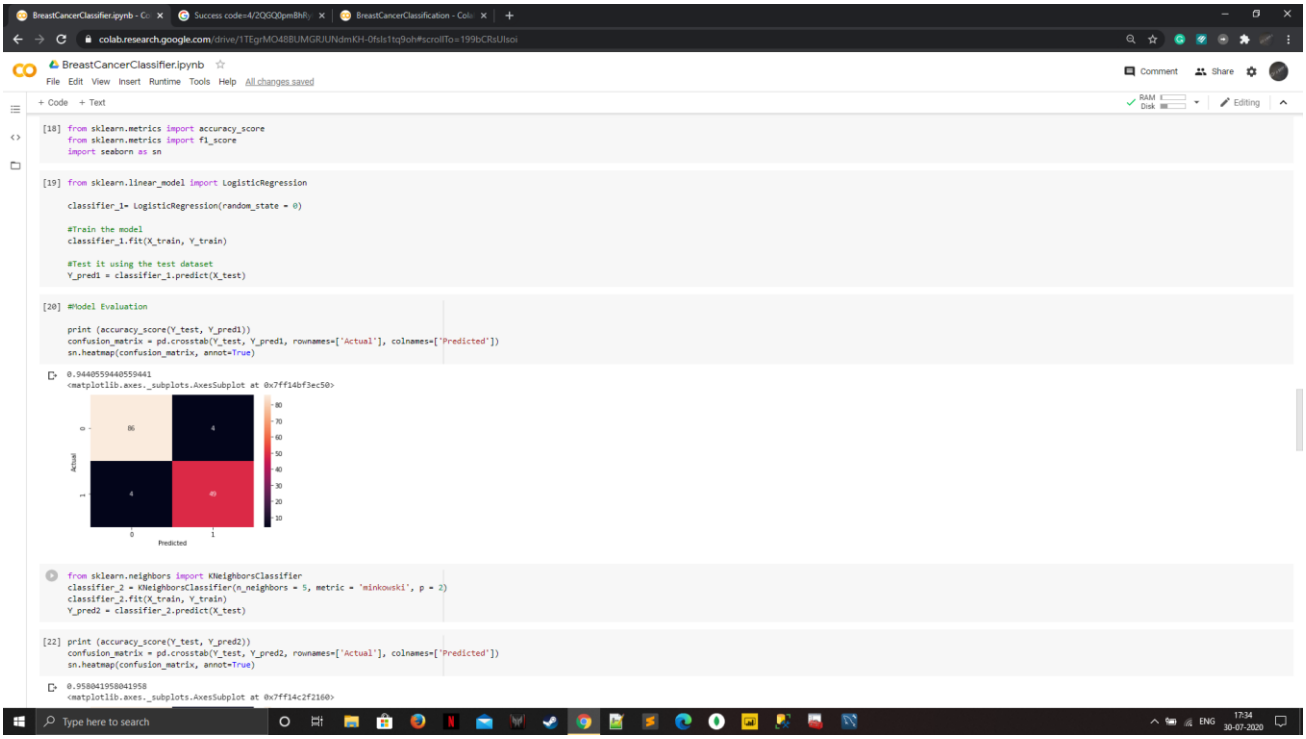
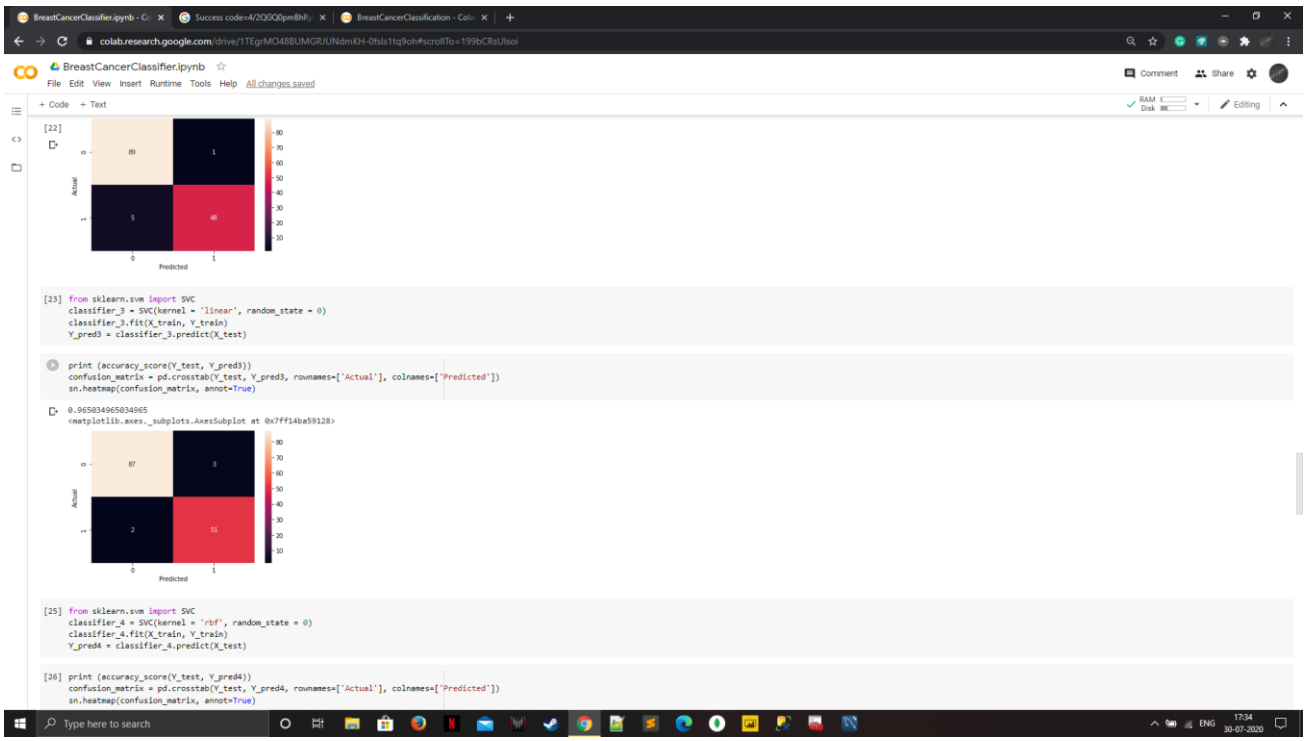
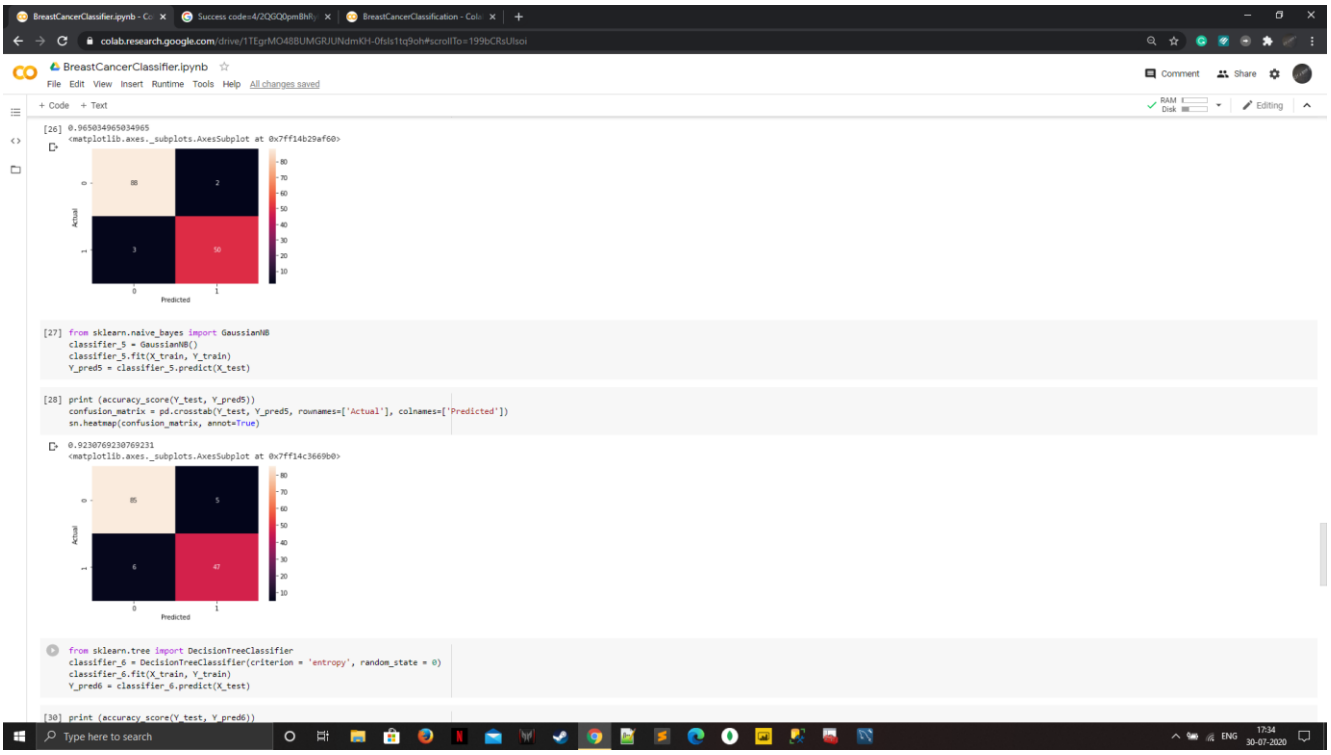
0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 0])
+ Code + Text
[16] #Split the dataset into 75% train and 25% test data
from sklearn.model_selection import train_test_split
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.25, random_state = 0)
[17] #As mentioned above, standardize the features using StandardScaler
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)

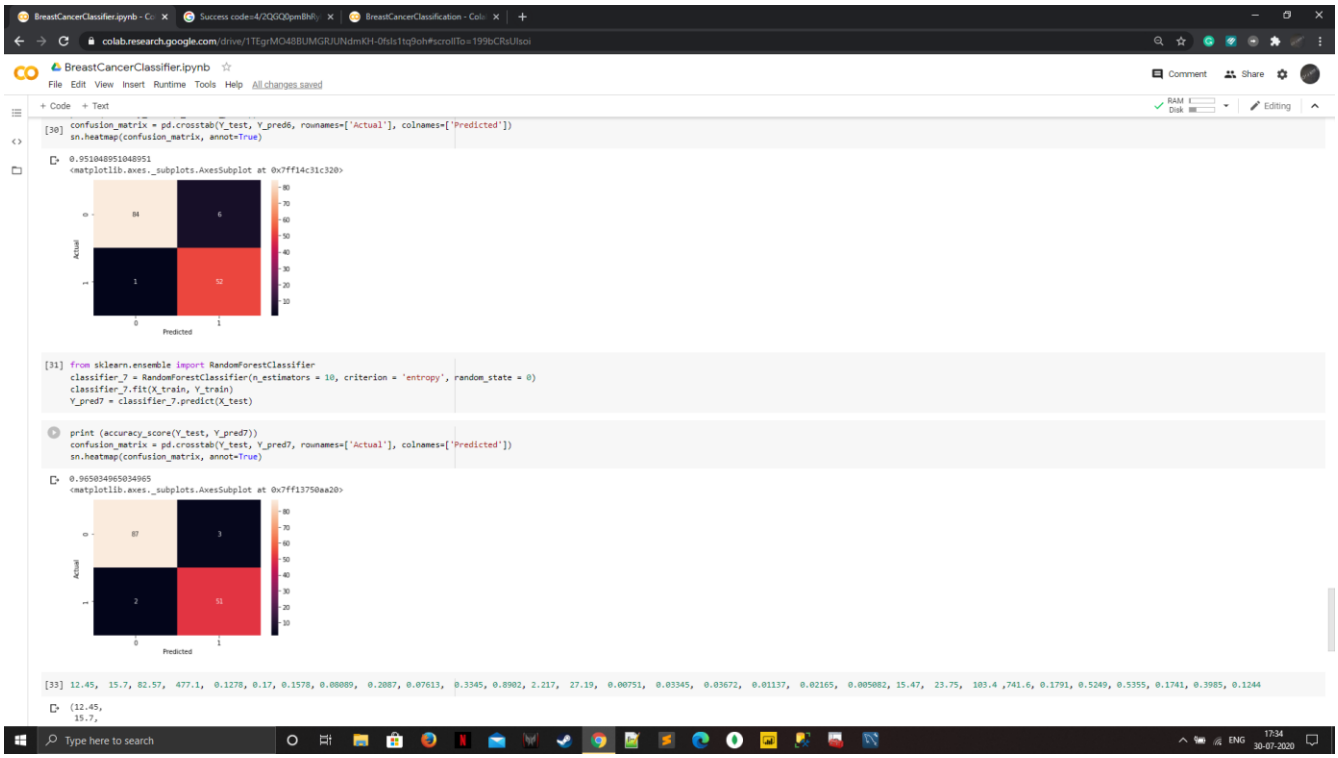


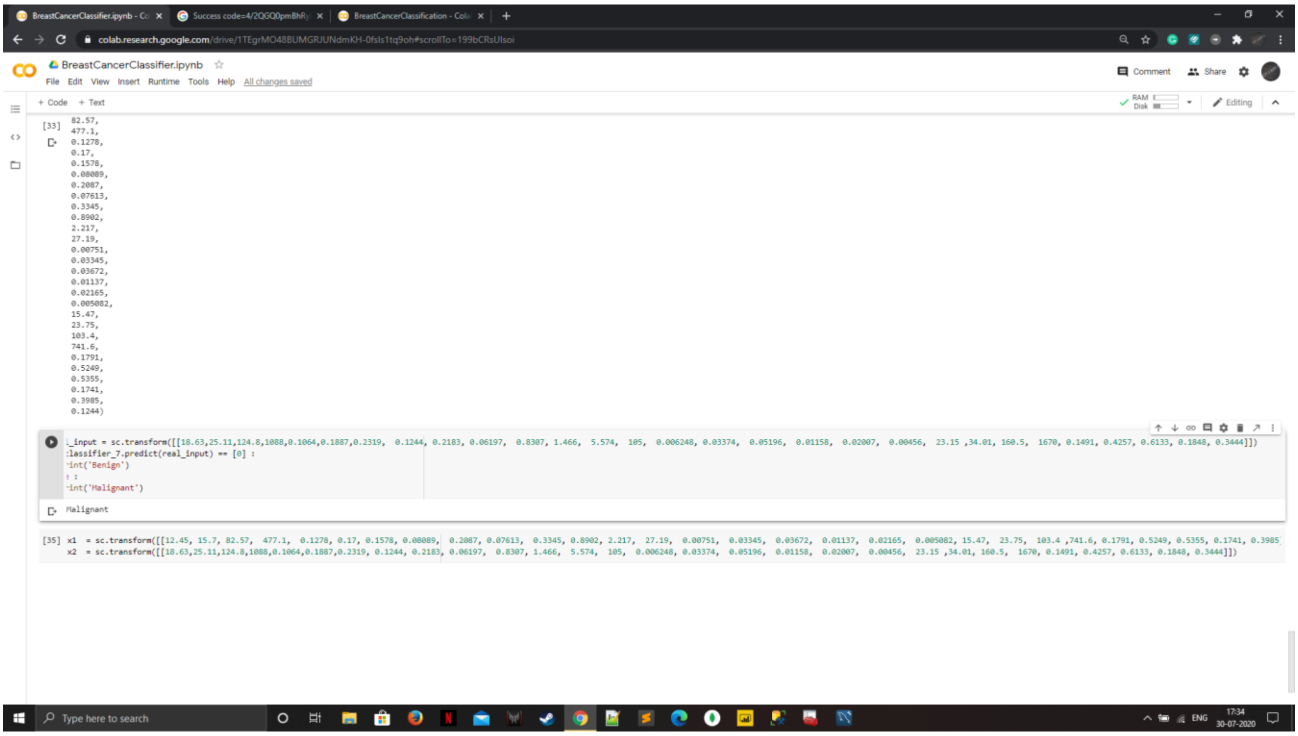
```
[18] from sklearn.metrics import accuracy_score
     from sklearn.metrics import f1_score
     import seaborn as sn

[19] from sklearn.linear_model import LogisticRegression

     classifier_1= LogisticRegression(random_state = 0)

     #Train the model
     classifier_1.fit(X_train, Y_train)

     #Test it using the test dataset
     Y_pred1 = classifier_1.predict(X_test)

[20] #Model Evaluation

     print (accuracy_score(Y_test, Y_pred1))
     confusion_matrix = pd.crosstab(Y_test, Y_pred1, rownames=['Actual'], colnames=['Predicted'])
     sn.heatmap(confusion_matrix, annot=True)

     0.9440559440559441
     <matplotlib.axes._subplots.AxesSubplot at 0x7ff14bf3ec50>

     from sklearn.neighbors import KNeighborsClassifier
     classifier_2 = KNeighborsClassifier(n_neighbors = 5, metric = 'minkowski', p = 2)
     classifier_2.fit(X_train, Y_train)
     Y_pred2 = classifier_2.predict(X_test)

[22] print (accuracy_score(Y_test, Y_pred2))
     confusion_matrix = pd.crosstab(Y_test, Y_pred2, rownames=['Actual'], colnames=['Predicted'])
     sn.heatmap(confusion_matrix, annot=True)

     0.958041958041958
     <matplotlib.axes._subplots.AxesSubplot at 0x7ff14c2f2160>
```

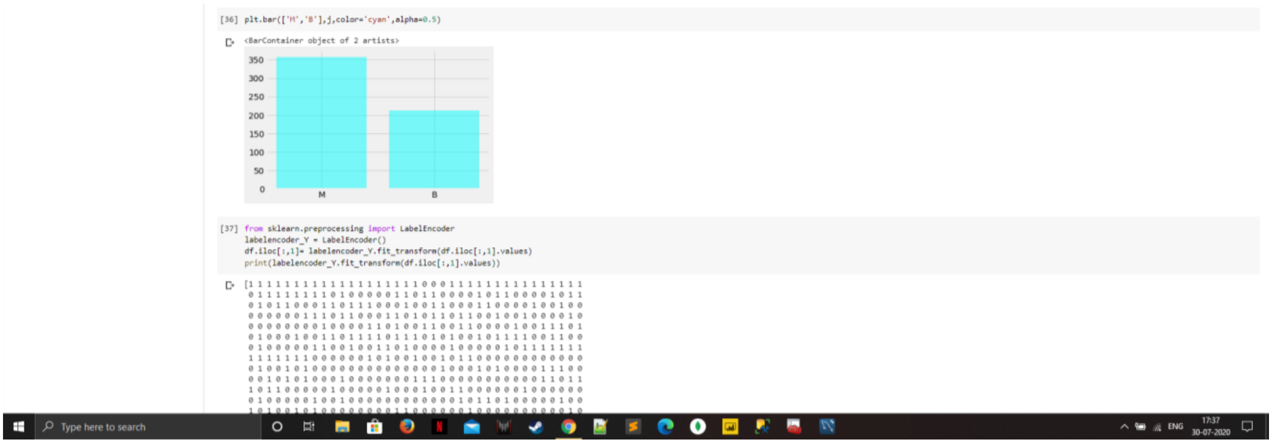


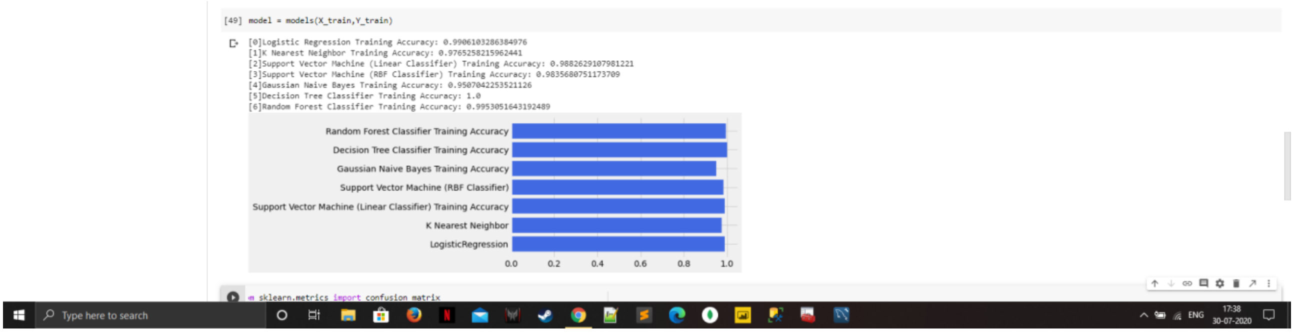
```
[22]
     <matplotlib.axes._subplots.AxesSubplot at 0x7ff14ba59128>

[23] from sklearn.svm import SVC
     classifier_3 = SVC(kernel = 'linear', random_state = 0)
     classifier_3.fit(X_train, Y_train)
     Y_pred3 = classifier_3.predict(X_test)

     print (accuracy_score(Y_test, Y_pred3))
     confusion_matrix = pd.crosstab(Y_test, Y_pred3, rownames=['Actual'], colnames=['Predicted'])
     sn.heatmap(confusion_matrix, annot=True)

     0.965034965034965
     <matplotlib.axes._subplots.AxesSubplot at 0x7ff14ba59128>

[25] from sklearn.svm import SVC
     classifier_4 = SVC(kernel = 'rbf', random_state = 0)
     classifier_4.fit(X_train, Y_train)
     Y_pred4 = classifier_4.predict(X_test)

[26] print (accuracy_score(Y_test, Y_pred4))
     confusion_matrix = pd.crosstab(Y_test, Y_pred4, rownames=['Actual'], colnames=['Predicted'])
     sn.heatmap(confusion_matrix, annot=True)
```

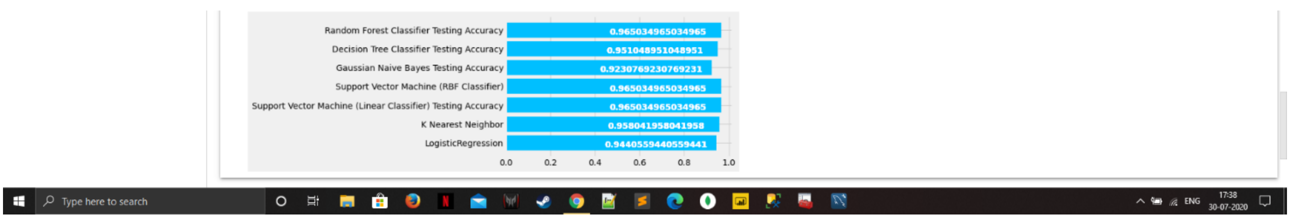

BreastCancerClassifier.ipynb
File Edit View Insert Runtime Tools Help All changes saved
+ Code + Text
[26] 0.965034965034965
<matplotlib.axes._subplots.AxesSubplot at 0x7ff14b29af60>
Actual
Predicted
[27] from sklearn.naive_bayes import GaussianNB
classifier_5 = GaussianNB()
classifier_5.fit(X_train, Y_train)
Y_pred5 = classifier_5.predict(X_test)
[28] print (accuracy_score(Y_test, Y_pred5))
confusion_matrix = pd.crosstab(Y_test, Y_pred5, rownames=['Actual'], colnames=['Predicted'])
sn.heatmap(confusion_matrix, annot=True)
0.9230769230769231
<matplotlib.axes._subplots.AxesSubplot at 0x7ff14c3669b0>
from sklearn.tree import DecisionTreeClassifier
classifier_6 = DecisionTreeClassifier(criterion = 'entropy', random_state = 0)
classifier_6.fit(X_train, Y_train)
Y_pred6 = classifier_6.predict(X_test)
[30] print (accuracy_score(Y_test, Y_pred6))


BreastCancerClassifier.ipynb
File Edit View Insert Runtime Tools Help All changes saved
+ Code + Text
[30] confusion_matrix = pd.crosstab(Y_test, Y_pred6, rownames=['Actual'], colnames=['Predicted'])
sn.heatmap(confusion_matrix, annot=True)
0.951048951048951
<matplotlib.axes._subplots.AxesSubplot at 0x7ff14c31c320>
Actual
Predicted
[31] from sklearn.ensemble import RandomForestClassifier
classifier_7 = RandomForestClassifier(n_estimators = 10, criterion = 'entropy', random_state = 0)
classifier_7.fit(X_train, Y_train)
Y_pred7 = classifier_7.predict(X_test)
print (accuracy_score(Y_test, Y_pred7))
confusion_matrix = pd.crosstab(Y_test, Y_pred7, rownames=['Actual'], colnames=['Predicted'])
sn.heatmap(confusion_matrix, annot=True)
0.965034965034965
<matplotlib.axes._subplots.AxesSubplot at 0x7ff13750aa20>
Actual
Predicted
[33] 12.45, 15.7, 82.57, 477.1, 0.1278, 0.17, 0.1578, 0.08089, 0.2087, 0.07613, 0.3345, 0.8902, 2.217, 27.19, 0.00751, 0.03345, 0.03672, 0.01137, 0.02165, 0.005082, 15.47, 23.75, 103.4 ,741.6, 0.1791, 0.5249, 0.5355, 0.1741, 0.3985, 0.1244
(12.45,
15.7,


BreastCancerClassifier.ipynb
File Edit View Insert Runtime Tools Help All changes saved
[33]
0.1244)
_input = sc.transform([[18.63,25.11,124.8,1088,0.1064,0.1887,0.2319, 0.1244, 0.2183, 0.06197, 0.8307, 1.466, 5.574, 105, 0.006248,
lassifier_7.predict(real_input) == [0] :
int('Benign')
int('Malignant')
Malignant
[35] x1 = sc.transform([[12.45, 15.7, 82.57, 477.1, 0.1278, 0.17, 0.1578, 0.08089, 0.2087, 0.07613, 0.3345, 0.8902, 2.217, 27.19,
x2 = sc.transform([[18.63,25.11,124.8,1088,0.1064,0.1887,0.2319, 0.1244, 0.2183, 0.06197, 0.8307, 1.466, 5.574, 105, 0.006248,
Type here to search


[36] plt.bar(['M','B'],j,color='cyan',alpha=0.5)
<BarContainer object of 2 artists>
350
300
250
200
150
100
50
0
M
B
[37] from sklearn.preprocessing import LabelEncoder
labelencoder_Y = LabelEncoder()
df.iloc[:,1]= labelencoder_Y.fit_transform(df.iloc[:,1].values)
print(labelencoder_Y.fit_transform(df.iloc[:,1].values))
Type here to search


[49] model = models(X_train,Y_train)
[0]Logistic Regression Training Accuracy: 0.9906103286384976
[1]K Nearest Neighbor Training Accuracy: 0.9765258215962441
[2]Support Vector Machine (Linear Classifier) Training Accuracy: 0.9882629107981221
[3]Support Vector Machine (RBF Classifier) Training Accuracy: 0.9835680751173709
[4]Gaussian Naive Bayes Training Accuracy: 0.9507042253521126
[5]Decision Tree Classifier Training Accuracy: 1.0
[6]Random Forest Classifier Training Accuracy: 0.9953051643192489
Random Forest Classifier Training Accuracy
Decision Tree Classifier Training Accuracy
Gaussian Naive Bayes Training Accuracy
Support Vector Machine (RBF Classifier)
Support Vector Machine (Linear Classifier) Training Accuracy
K Nearest Neighbor
LogisticRegression
0.0 0.2 0.4 0.6 0.8 1.0
m sklearn.metrics import confusion matrix
Type here to search


Random Forest Classifier Testing Accuracy 0.965034965034965
Decision Tree Classifier Testing Accuracy 0.951048951048951
Gaussian Naive Bayes Testing Accuracy 0.9230769230769231
Support Vector Machine (RBF Classifier) 0.965034965034965
Support Vector Machine (Linear Classifier) Testing Accuracy 0.965034965034965
K Nearest Neighbor 0.958041958041958
LogisticRegression 0.9440559440559441
0.0 0.2 0.4 0.6 0.8 1.0
Type here to search

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Reference:

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