JOSEPH KINGORI NJIRI

TASK 5 HACKATHON

BREAST CANCER PROGNOSIS USING MACHINE LEARNING SOLUTIONS

Each data has a unique ID as an attribute, the prognosis will give out whether a patient has cancer or not using M(malignant) or B(benign). The data will classify this outcome using the attributes the radius of the infection/lobes, the texture, compactness, area and the perimeter of tumor. The link of the dataset is https://www.kaggle.com/datasets/yasserh/breast-cancer-dataset. I will fine tune the hyper parameters and evaluation metrics of various classifications.

Problem Statement

Breast cancer is the most common cancer amongst women in the world. It accounts for 25% of all cancer cases, and affected over 2.1 Million people in 2015 alone. It starts when cells in the breast begin to grow out of control. These cells usually form tumors that can be seen via X-ray or felt as lumps in the breast area. The key challenges against its detection is how to classify tumors into malignant (cancerous) or benign (non-cancerous). I will use machine learning for analysis and classifying these tumors. Tests such as MRI, mammogram, ultrasound and biopsy are commonly used to diagnose breast cancer performed.

Objectives

1. Identifying the problem and Data Sources
2. Exploratory Data Analysis
3. Pre-Processing the Data
4. Build model to predict whether breast cell tissue is malignant or Benign

Exploratory Data Analysis

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```
# importing the libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

```
df = pd.read_csv('/content/breast-cancer.csv')
df.head(10)
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	radius_worst	te
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	...	25.38	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	...	24.99	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	...	23.57	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	...	14.91	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	...	22.54	
5	843786	M	12.45	15.70	82.57	477.1	0.12780	0.17000	0.15780	0.08089	...	15.47	
6	844359	M	18.25	19.98	119.60	1040.0	0.09463	0.10900	0.11270	0.07400	...	22.88	

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```
df.dtypes
```

```
id                        int64
diagnosis                object
radius_mean            float64
texture_mean           float64
perimeter_mean         float64
area_mean              float64
smoothness_mean        float64
compactness_mean       float64
concavity_mean         float64
concave points_mean    float64
symmetry_mean          float64
fractal_dimension_mean float64
radius_se              float64
texture_se             float64
perimeter_se           float64
area_se                float64
smoothness_se          float64
compactness_se         float64
concavity_se           float64
concave points_se      float64
symmetry_se            float64
fractal_dimension_se   float64
radius_worst           float64
```

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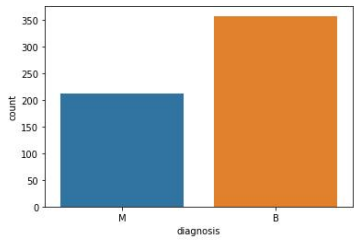
```
[ ]        'compactness_worst', 'concavity_worst', 'concave points_worst',
           'symmetry_worst', 'fractal_dimension_worst'],
          dtype='object')
```

```
[ ] df.drop('id',inplace  =True,axis = 1)
```

```
sns.countplot(data=df,x='diagnosis')
plt.savefig('targetdiagnosis')
```




```
[ ] data=df.describe().T
```

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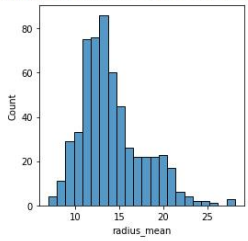
```
[ ] perimeter_worst          84.110000   97.660000   125.400000   251.20000
    area_worst              515.300000  686.500000  1084.000000  4254.00000
    smoothness_worst          0.116600    0.131300     0.146000     0.22260
```

```
plt.figure(figsize=(4,4))
sns.histplot(data = df,x = 'radius_mean')
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f59d75c5590>
```




```
[ ] plt.figure(figsize=(4,4))
    sns.boxplot(data = df,x = 'texture_mean')
```

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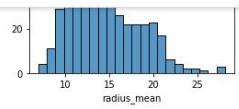
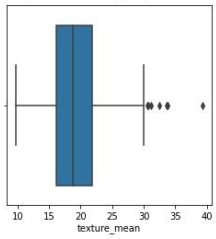



```
plt.figure(figsize=(4,4))
sns.boxplot(data = df,x = 'texture_mean')
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f59d7538c90>
```



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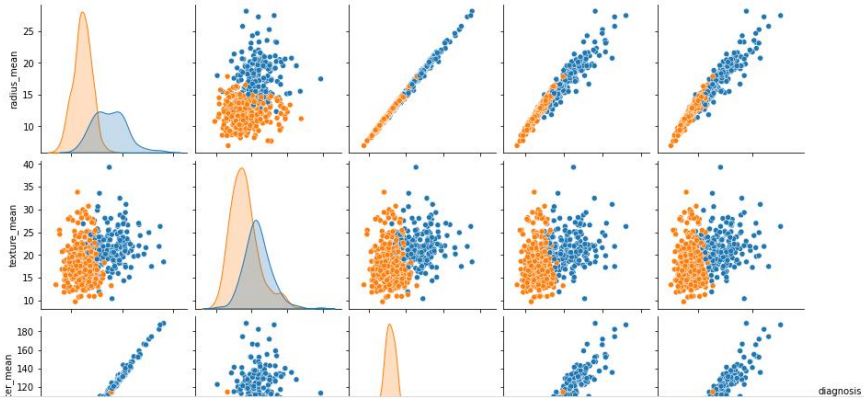
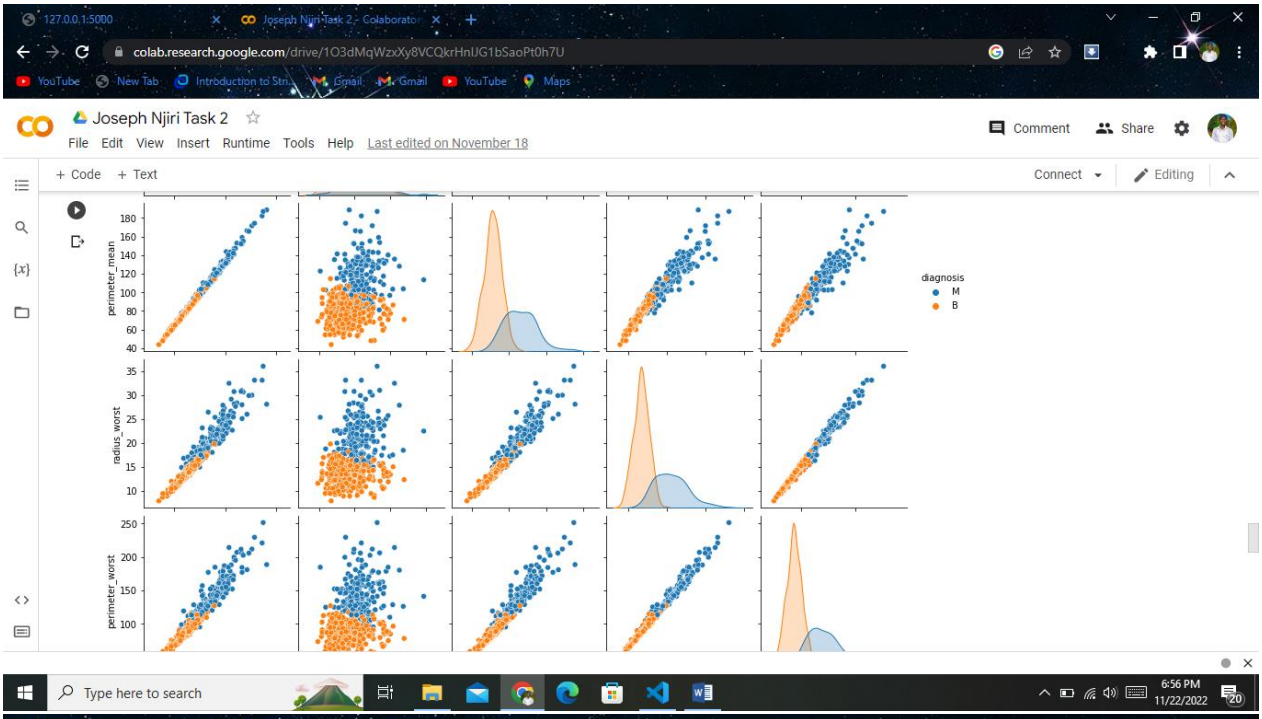
```
sns.pairplot(df, hue="diagnosis", vars=["radius_mean", "texture_mean", "perimeter_mean", "radius_worst", "perimeter_worst"])
plt.show()
```

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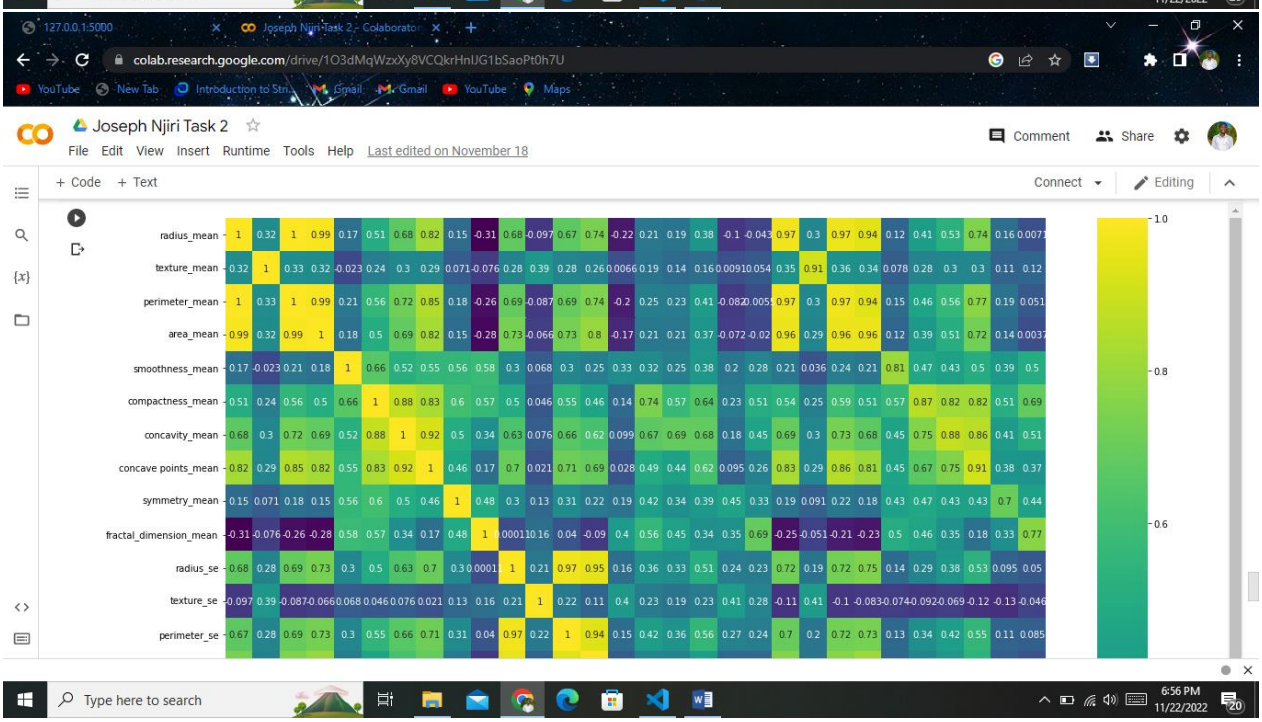
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fractal_dimension_mean
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smoothness_se
compactness_se
concavity_se
concave points_se
symmetry_se
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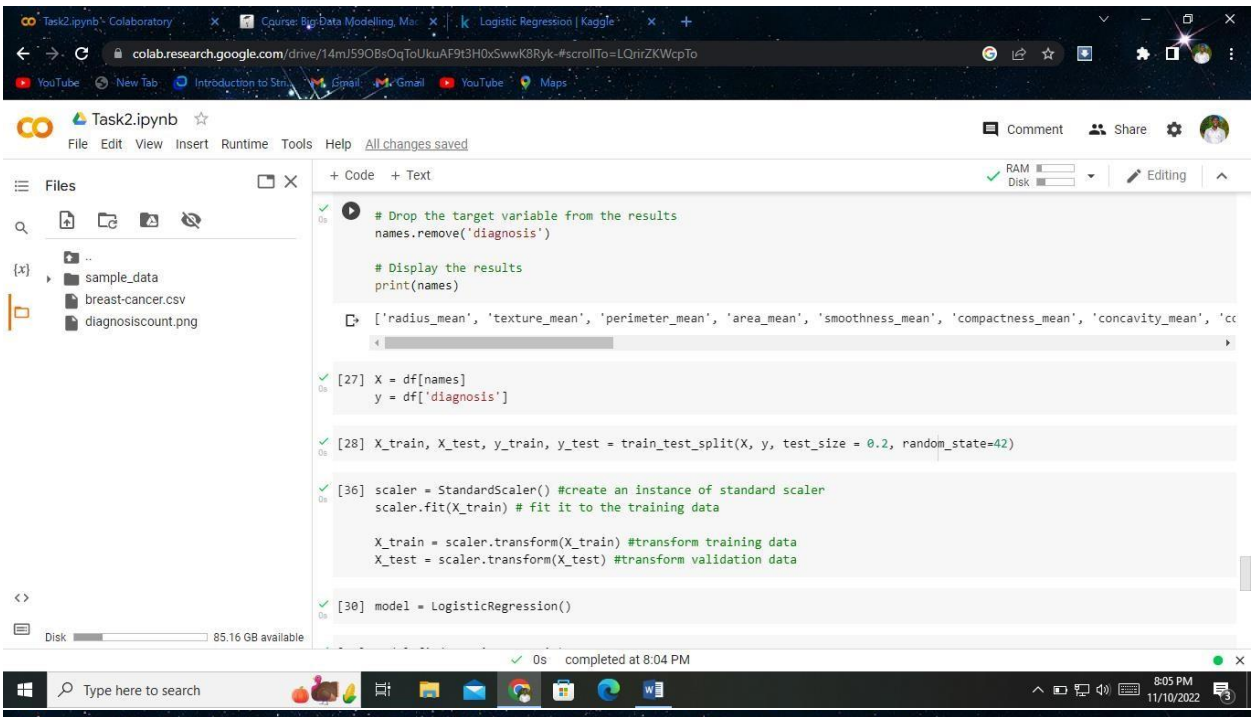
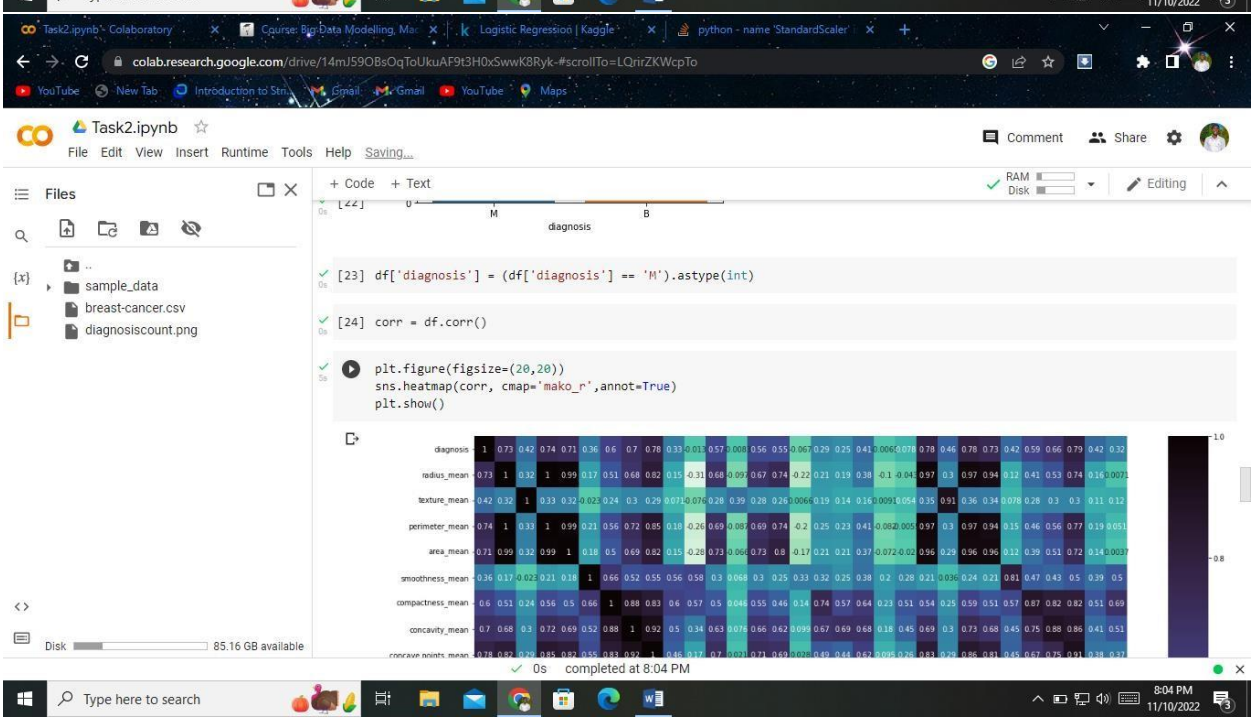
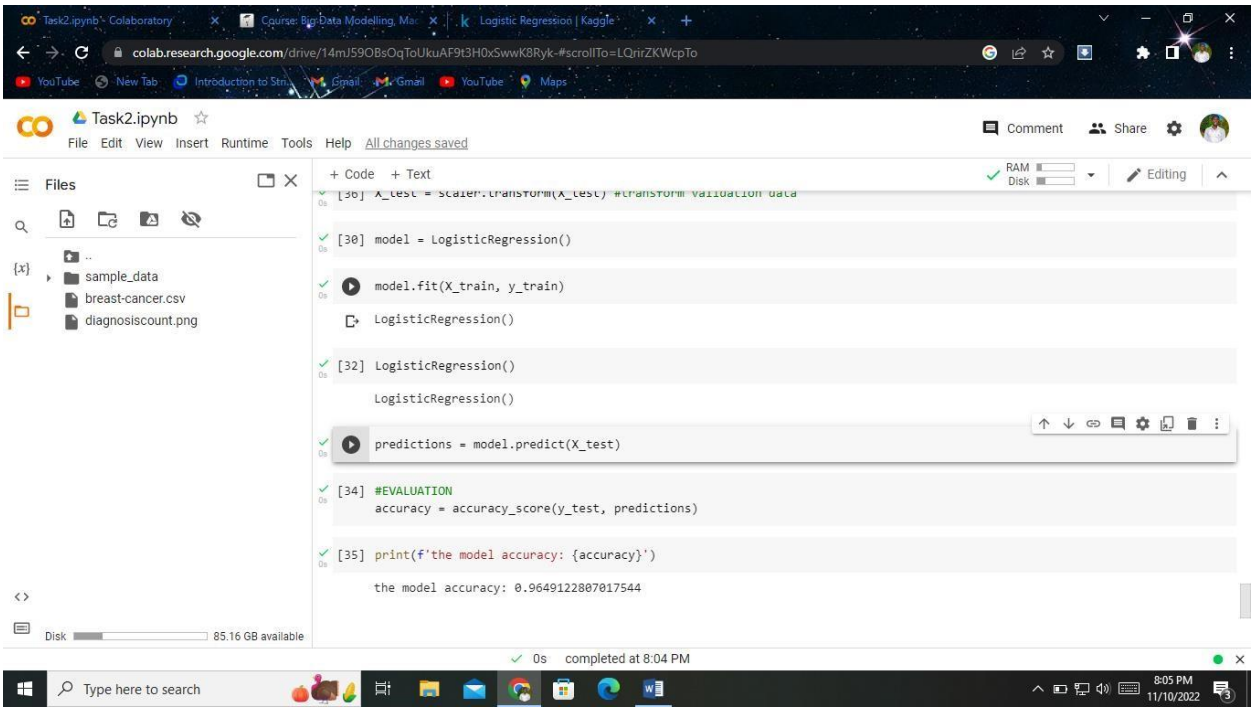
Logistic Regression







SUPPORT VECTOR MACHINES(SVM)

(SVM) support vector machine can be used for both classification or regression challenges. However, it is mostly used in classification problems. In the SVM algorithm, we plot each data item as a point in n-dimensional space (where n is a number of features you have) with the value of each feature being the value of a particular coordinate. Then, we perform classification by finding the hyper-plane that differentiates the two classes very well in this case the benign and the malignant type of cancer it gave the highest accuracy of 0.98/98% thus it's the best machine learning solution for the breast cancer dataset. Support Vectors are simply the coordinates of individual observation. The SVM classifier is a frontier that best segregates the two classes (hyperplane/ line).

Task2.ipynb

```
[42] pred = model.predict(X_test)
```

```
[43] from sklearn.metrics import classification_report,confusion_matrix
```

```
print(classification_report(y_test,pred))
print('\n')

print(confusion_matrix(y_test,pred))
```

```
              precision    recall  f1-score   support

           0       0.97      0.99      0.98        71
           1       0.98      0.95      0.96        43

    accuracy                           0.97       114
   macro avg       0.97      0.97      0.97       114
weighted avg       0.97      0.97      0.97       114


[[70  1]
 [ 2 41]]
```

```
[45] from sklearn.model_selection import GridSearchCV
```

Task2.ipynb

```
[ 2 41]]
```

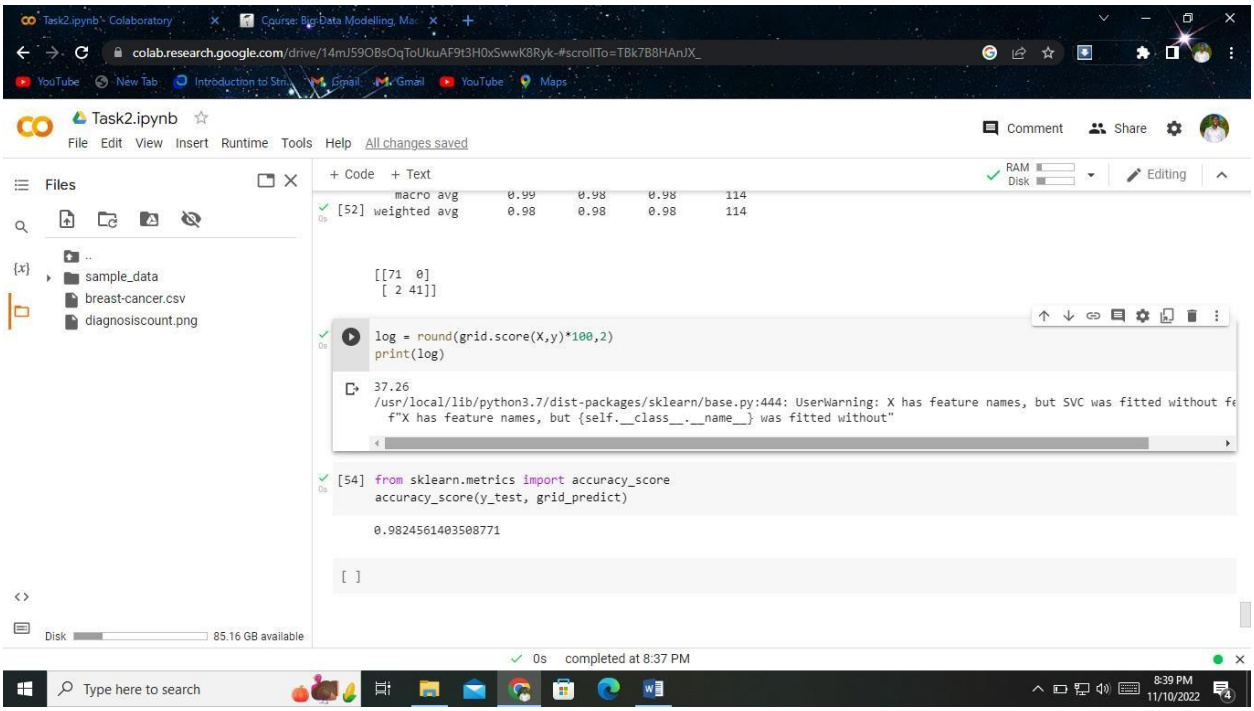
```
[45] from sklearn.model_selection import GridSearchCV
```

```
[46] param_grid = {'C':[0.1,1.1,10,100,1000],'gamma':[1,0.1,0.01,0.001,0.0001]}
```

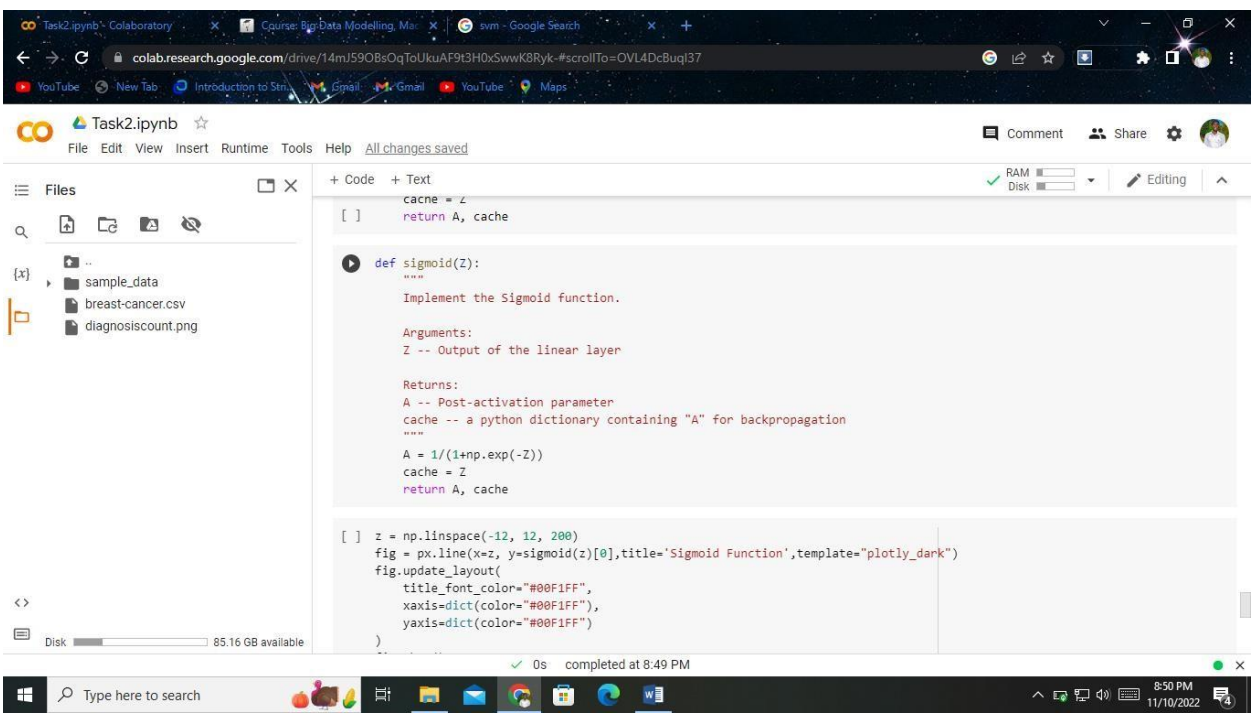
```
[47] grid = GridSearchCV(SVC(),param_grid,verbose=3)
```

```
[48] grid.fit(X_train,y_train)
```

```
Fitting 5 folds for each of 25 candidates, totalling 125 fits
[CV 1/5] END ....................C=0.1, gamma=1;, score=0.637 total time=   0.0s
[CV 2/5] END ....................C=0.1, gamma=1;, score=0.626 total time=   0.0s
[CV 3/5] END ....................C=0.1, gamma=1;, score=0.626 total time=   0.0s
[CV 4/5] END ....................C=0.1, gamma=1;, score=0.626 total time=   0.0s
[CV 5/5] END ....................C=0.1, gamma=1;, score=0.626 total time=   0.0s
[CV 1/5] END .................C=0.1, gamma=0.1;, score=0.912 total time=   0.0s
[CV 2/5] END .................C=0.1, gamma=0.1;, score=0.967 total time=   0.0s
[CV 3/5] END .................C=0.1, gamma=0.1;, score=0.934 total time=   0.0s
[CV 4/5] END .................C=0.1, gamma=0.1;, score=0.934 total time=   0.0s
[CV 5/5] END .................C=0.1, gamma=0.1;, score=0.912 total time=   0.0s
[CV 1/5] END ................C=0.1, gamma=0.01;, score=0.934 total time=   0.0s
[CV 2/5] END ................C=0.1, gamma=0.01;, score=0.923 total time=   0.0s
[CV 3/5] END ................C=0.1, gamma=0.01;, score=0.956 total time=   0.0s
```

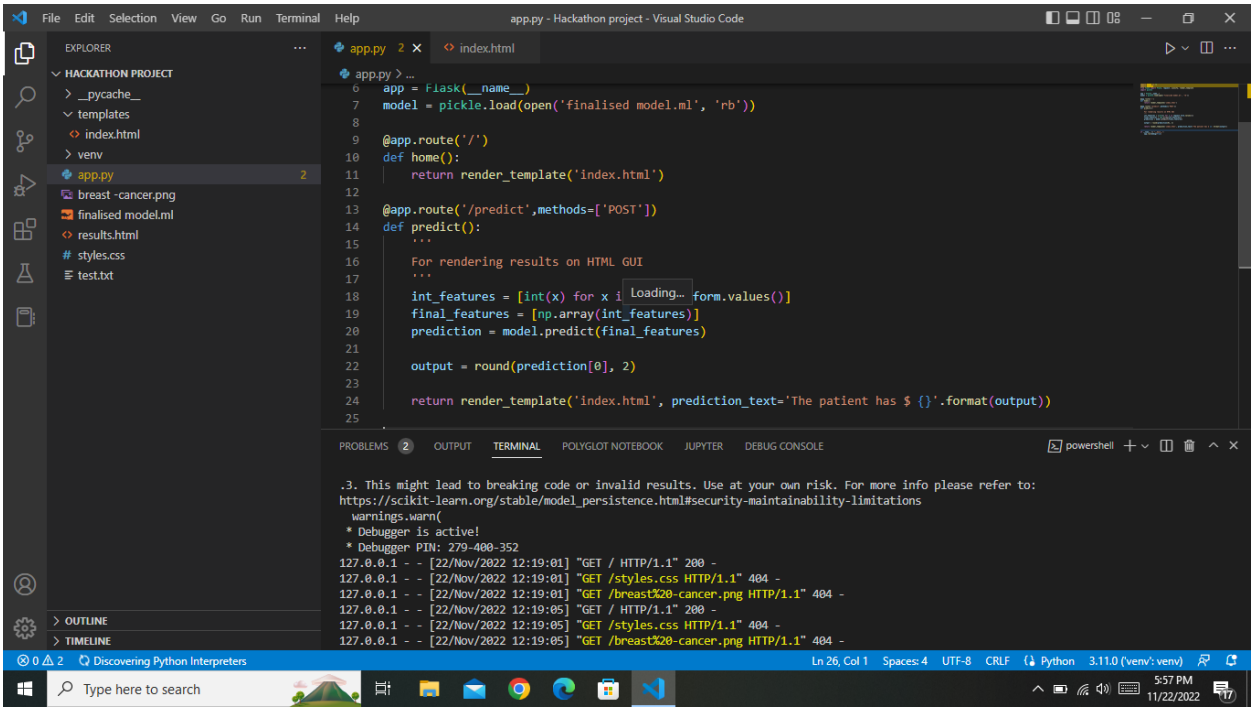


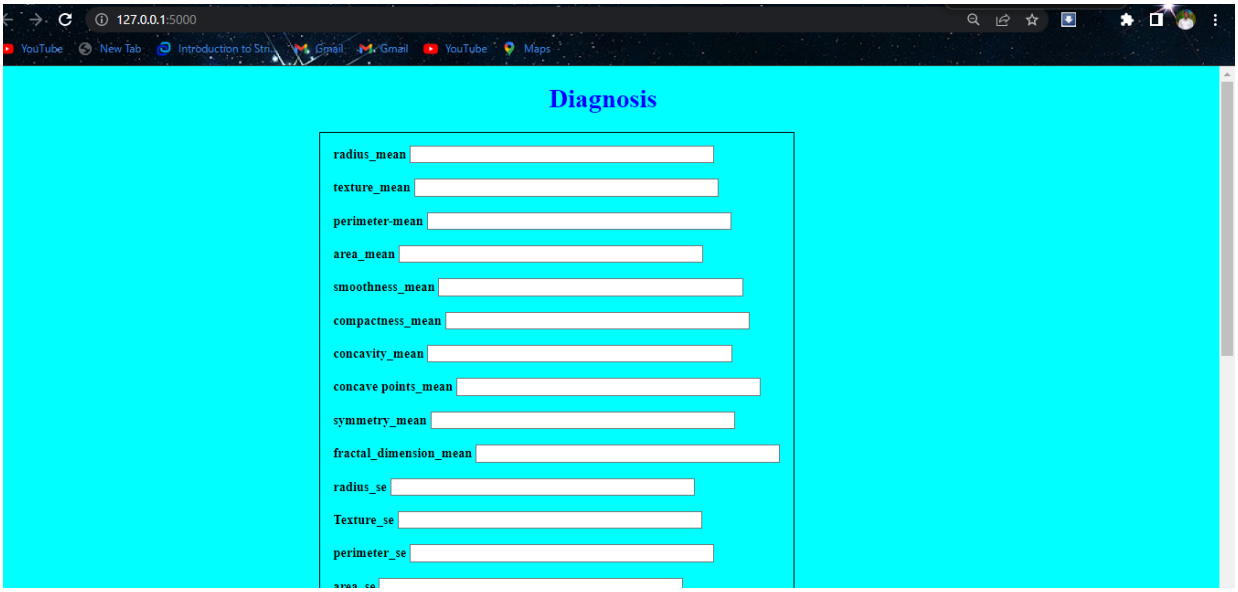
NEURAL NETWORKS

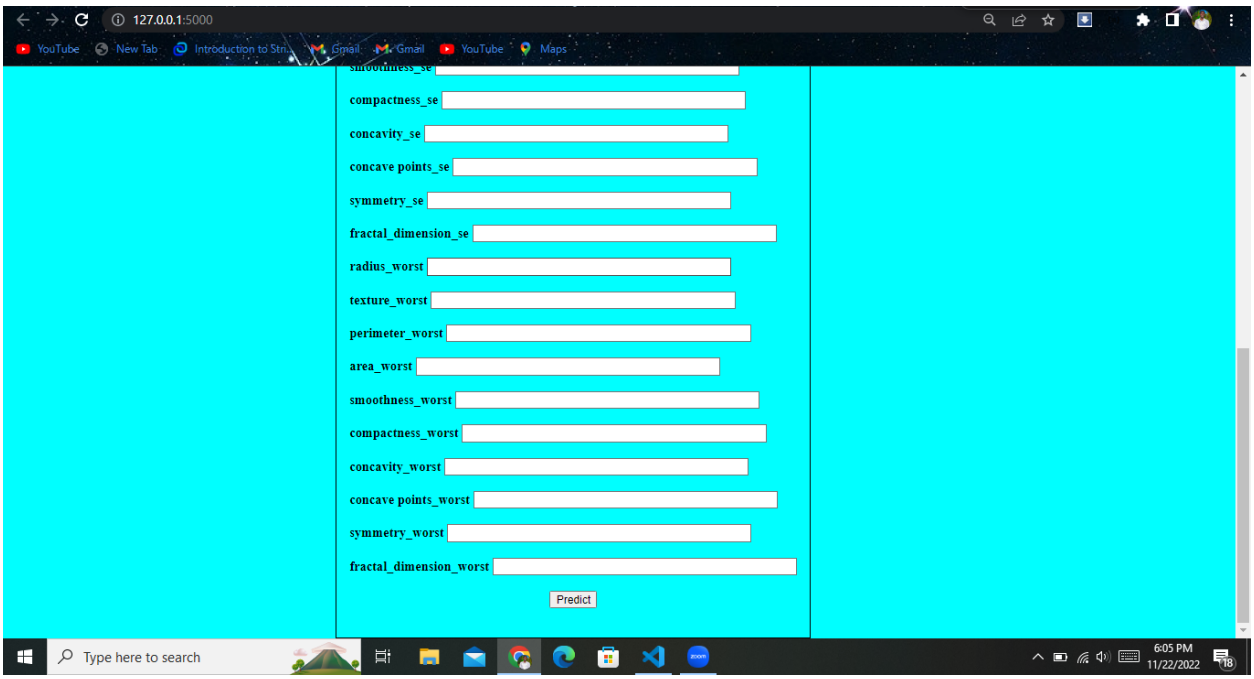


The above machine learning technique gives an accuracy of 0.96. It evaluates the model using the sigmoid function and creating a class neural networks. The process of model evaluation was too long but it gave a lower accuracy compared to support vector machine algorithm svm.

Model Deployment







Given breast cancer results from breast fine needle aspiration (FNA) test (is a quick and simple procedure to perform, which removes some fluid or cells from a breast lesion or cyst (a lump, sore or swelling) with a fine needle similar to a blood sample needle). Since this build a model that can classify a breast cancer tumor using two training classification:

1= Malignant (Cancerous) - Present

0= Benign (Not Cancerous) -Absent

After inputing different types of data a diagnosis will be given in form of text showing whether the cancer is malignant(M) or benign(B).