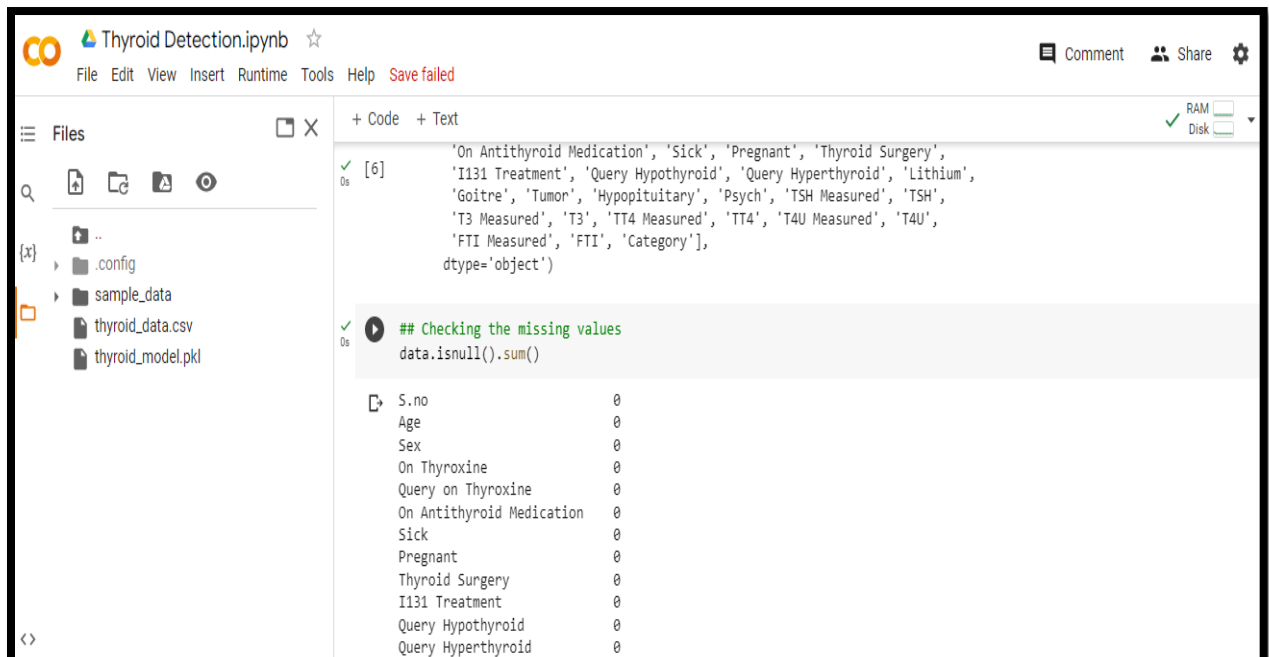
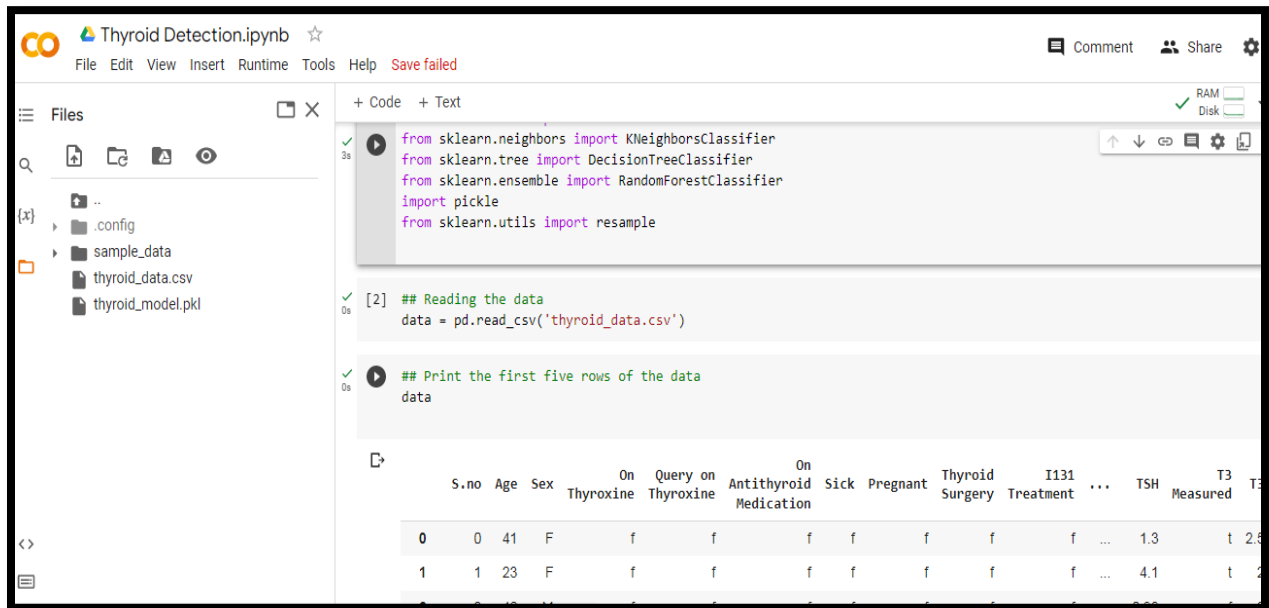


## Thyroid Disease Classification Using ML

## Sample Output



Files

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{x}

..

config

sample\_data

thyroid\_data.csv

thyroid\_model.pkl

+ Code + Text

So, we have replaced all such values with 'nan' values.

```
## Unique Values
for column in data.columns:
    print(column,(data[column].unique()))
```

```
0.015 10 100 0.03 3.2 00 0.02 0.29 3.1 3.3 32
'0.33' '31' '5.8' '0.28' '51' '6.3' '4.4' '9.6' '3.4' '0.09' '24' '0.76'
'42' '25' '10' '4.6' '8.6' '0.66' '6.2' '0.79' '28' '0.86' '9.7' '0.84'
'17' '18' '55' '14' '3.7' '0.87' '6.7' '0.74' '7.6' '0.065' '0.29' '0.37'
'8' '11' '0.48' '44' '7.9' '5' '7.2' '0.89' '0.93' '0.97' '0.12' '6.4'
'33' '0.85' '7.1' '0.73' '199' '8.2' '188' '0.22' '98' '22' '6.6' '5.1'
'0.06' '0.42' '3.8' '35' '4' '0.78' '0.63' '0.52' '60' '0.43' '5.6' '6.9'
'3.6' '29' '0.38' '4.9' '0.41' '9.9' '7.5' '34' '6.5' '4.7' '103' '0.95'
'0.14' '0.35' '4.2' '0.81' '0.54' '0.58' '8.9' '5.5' '0.34' '9.3' '0.13'
'54' '0.39' '8.3' '478' '21' '6.8' '0.32' '0.23' '0.24' '8.1' '0.91'
'5.3' '100' '0.27' '1.01' '58' '41' '183' '18.4' '0.47' '0.17' '12.1'
'0.19' '0.82' '43' '0.44' '70' '7.7' '8.4' '0.69' '8.5' '0.21' '82'
'0.055' '0.96' '0.71' '38' '0.36' '9.8' '7' '0.46' '11.1' '39' '76' '5.7'
'32' '126' '26.4' '0.53' '0.49' '36' '178' '145' '47' '4.8' '10.3' '89'
'7.4' '472' '0.51' '116' '61' '99' '46' '78' '468']
```

The screenshot shows a Jupyter Notebook interface. On the left is a file explorer with a sidebar containing icons for file operations. The main area of the file explorer shows a directory structure with a folder named 'sample\_data' containing two files: 'thyroid\_data.csv' and 'thyroid\_model.pkl'. On the right, a code cell is active, displaying Python code that iterates over columns and creates density plots. The code is as follows:

```
+ Code + Text
for column in columns:
    ax = plt.subplot(3,2,plotnumber)
    sns.distplot(final_df[column])
    plt.xlabel(column,fontsize=10)
    plotnumber+=1
plt.show()
```

Below the code, the output of the execution is shown, consisting of two side-by-side density plots. The left plot has a y-axis labeled 'Density' ranging from 0.0025 to 0.0200. The right plot also has a y-axis labeled 'Density' ranging from 0.02 to 0.08. Both plots show a single, narrow, blue-filled density curve representing the distribution of a specific variable.

Thyroid Detection.ipynb - Colab X | https://naanmudhalvan.smarti... | thyroid disease classification g... | thyroid-disease-detection - Git... | GitHub - pankaj1551/Thyroid - X

colab.research.google.com/drive/1K7NQu4AYCTNPjirpluVjZUuLmvGHjbCQ?scrollTo=KGHGQYZZ-VFW

Thyroid Detection.ipynb ☆

File Edit View Insert Runtime Tools Help Save failed

Comment Share

Files

- ..
- .config
- sample\_data
- thyroid\_data.csv
- thyroid\_model.pkl

Code

```
SVM:
Train Score:0.6165285503462368
Test Score:0.6391284611892873

KNN:
Train Score:0.8651379271199909
Test Score:0.8483885610531094

Decision Tree:
Train Score:0.9162220456351459
Test Score:0.8955969133000454

Random Forest:
Train Score:0.9162220456351459
Test Score:0.9024858102587381
```

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Thyroid-Detection.ipynb | Thyroid-Prediction-....zip

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Thyroid Detection.ipynb - Colab X | https://naanmudhalvan.smarti... | thyroid disease classification g... | thyroid-disease-detection - Git... | GitHub - pankaj1551/Thyroid - X

colab.research.google.com/drive/1K7NQu4AYCTNPjirpluVjZUuLmvGHjbCQ?scrollTo=KGHGQYZZ-VFW

Thyroid Detection.ipynb ☆

File Edit View Insert Runtime Tools Help Save failed

Comment Share

Files

- ..
- .config
- sample\_data
- thyroid\_data.csv
- thyroid\_model.pkl

Code

```
[42] print(accuracies.mean())
0.8971514807553399

[43] import pickle
filename = 'thyroid_model.pkl'
pickle.dump(classifier_forest,open(filename,'wb'))

[44] model = open('thyroid_model.pkl','rb')
forest = pickle.load(model)

[45] y_pred = forest.predict(X_test)

confusion_matrix(y_test, y_pred)
array([[563,  0,  0,  0],
       [ 0, 526,  0, 27],
       [ 21, 48, 423, 40],
       [ 52, 29,  0, 474]])
```

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