

Sneha R
Sai Vidya Institute of Technology
Data Science Intern- @TAS
Innovation

TASK 2: Tea Leaves Disease Prediction

Submitted by
Sneha R



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```
In [2]: import pandas as pd
        from sklearn.model_selection import train_test_split
        from sklearn.linear_model import LinearRegression
        from sklearn.metrics import mean_squared_error
        import numpy as np
        import matplotlib.pyplot as plt
        import seaborn as sns
        from sklearn.model_selection import train_test_split
        from sklearn.linear_model import LinearRegression
        from sklearn.metrics import mean_squared_error, r2_score, accuracy_score
```

```
In [3]: data=pd.read_csv("PlantDisease.csv")
```

```
In [4]: data.head()
```

```
Out[4]:
```

	Anthraco	algal	bird	brown	gray	red	white	healthy
	nose	leaf	eye	blight	light	leaf	spot	
0	1	1	1	0	0	0	0	0
1	0	0	0	1	1	0	0	1
2	0	0	0	0	0	0	1	0
3	1	0	0	0	0	0	0	0
4	1	1	0	0	0	0	1	0

```
In [5]: data.info()
```

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```
In [5]: data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 42 entries, 0 to 41
Data columns (total 8 columns):
#   Column          Non-Null Count  Dtype
---  -
0   Anthracnose      42 non-null    int64
1   algal leaf       42 non-null    int64
2   bird eye spot    42 non-null    int64
3   brown blight     42 non-null    int64
4   gray light       42 non-null    int64
5   red leaf spot    42 non-null    int64
6   white spot       42 non-null    int64
7   healthy          42 non-null    int64
dtypes: int64(8)
memory usage: 2.8 KB
```

```
In [6]: data.shape
```

```
Out[6]: (42, 8)
```

```
In [7]: data.describe
```

```
Out[7]: <bound method NDFrame.describe of      Anthracnose  algal leaf  bird eye spot  brown blight  gray light  \
0              1          1              1          0          0
1              0          0              0          1          1
2              0          0              0          0          0
3              1          0              0          0          0
4              1          1              0          0          0
```



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8	0	0	0	0	0
9	0	0	0	0	0
10	0	0	0	0	0
11	0	0	0	0	0
12	0	0	0	0	0
13	0	0	0	0	0
14	1	0	0	0	0
15	0	0	0	0	0
16	1	1	0	0	0
17	0	1	0	0	0
18	0	0	0	0	0
19	0	0	0	0	0
20	1	0	0	0	0
21	0	0	0	0	0
22	0	0	0	0	0
23	0	0	0	0	0
24	0	0	0	0	0
25	0	0	0	0	0
26	0	0	0	1	0
27	0	0	0	0	0
28	0	0	0	0	0
29	0	0	0	0	0
30	0	0	0	0	0
31	0	0	0	0	0
32	0	0	0	0	0
33	0	0	0	0	0
34	0	0	0	0	0
35	0	0	0	0	0
36	0	0	0	0	0
37	0	1	0	0	0
38	0	0	0	0	0
39	0	1	0	0	0
40	0	1	0	0	0
41	1	1	0	0	0



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```
41          1          1          0          0          0
      red leaf spot white spot healthy
0          0          0          0
1          0          0          1
2          0          1          0
3          0          0          0
4          0          1          0
5          0          0          0
6          0          0          0
7          0          0          0
8          0          0          0
9          0          0          0
10         0          0          0
11         0          0          0
12         0          0          0
13         0          0          0
14         0          0          0
15         0          0          1
16         0          0          0
17         1          0          1
18         0          0          1
19         1          0          0
20         0          0          0
21         0          0          0
22         1          0          0
23         1          0          0
24         0          0          0
25         0          0          1
26         0          0          1
27         0          0          1
28         0          0          0
29         0          0          0
30         0          0          0
--         -          -          -
```



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In [8]:

```
data.corr()
```

Out[8]:

	Anthracnose	algal leaf	bird eye spot	brown blight	gray light	red leaf spot	white spot	healthy
Anthracnose	1.000000	0.433861	0.349215	-0.100000	-0.069843	-1.825742e-01	0.200000	-2.000000e-01
algal leaf	0.433861	1.000000	0.321960	-0.108465	-0.075755	1.485221e-01	0.176256	-5.423261e-02
bird eye spot	0.349215	0.321960	1.000000	-0.034922	-0.024390	-6.375767e-02	-0.034922	-6.984303e-02
brown blight	-0.100000	-0.108465	-0.034922	1.000000	0.698430	-9.128709e-02	-0.050000	5.000000e-01
gray light	-0.069843	-0.075755	-0.024390	0.698430	1.000000	-6.375767e-02	-0.034922	3.492151e-01
red leaf spot	-0.182574	0.148522	-0.063758	-0.091287	-0.063758	1.000000e+00	-0.091287	8.868040e-18
white spot	0.200000	0.176256	-0.034922	-0.050000	-0.034922	-9.128709e-02	1.000000	-1.000000e-01
healthy	-0.200000	-0.054233	-0.069843	0.500000	0.349215	8.868040e-18	-0.100000	1.000000e+00

In [10]:

```
features=data.drop('healthy',axis=1)  
labels=data['healthy']
```

In [11]:

```
X_train,X_test,y_train,y_test=train_test_split(features,labels,test_size=0.2,random_state=100)
```

In [12]:

```
regressor=LinearRegression()
```

In [13]:

```
regressor.fit(X_train,y_train)
```

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In [13]: regressor.fit(X_train,y_train)

Out[13]: LinearRegression()
**In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.**

In [14]: y_pred=regressor.predict(X_test)

In [15]: mse=mean_squared_error(y_test,y_pred)

In [16]: r2=r2_score(y_test,y_pred)

In [18]: print(X_train)

	Anthracnose	algal leaf	bird eye spot	brown blight	gray light	\
36	0	0	0	0	0	
18	0	0	0	0	0	
7	0	0	0	0	0	
39	0	1	0	0	0	
32	0	0	0	0	0	
25	0	0	0	0	0	
28	0	0	0	0	0	
19	0	0	0	0	0	
13	0	0	0	0	0	
1	0	0	0	1	1	
26	0	0	0	1	0	
12	0	0	0	0	0	
31	0	0	0	0	0	

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```
33      0      0      0      0      0
14      1      0      0      0      0
2       0      0      0      0      0
34      0      0      0      0      0
30      0      0      0      0      0
10      0      0      0      0      0
15      0      0      0      0      0
23      0      0      0      0      0
3       1      0      0      0      0
24      0      0      0      0      0
8       0      0      0      0      0

      red leaf spot  white spot
36      0      0
18      0      0
7       0      0
39      1      0
32      0      0
25      0      0
28      0      0
19      1      0
13      0      0
1       0      0
26      0      0
12      0      0
31      0      0
22      1      0
9       0      0
29      0      0
11      0      0
4       0      1
37      0      0
40      0      0
16      0      0
```


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```
3      0      0
24     0      0
8      0      0
```

In [19]: `print(X_test)`

```
      Anthracnose  algal leaf  bird eye spot  brown blight  gray light  \
27              0           0              0              0              0
5               0           0              0              0              0
6               0           0              0              0              0
38              0           0              0              0              0
21              0           0              0              0              0
0               1           1              1              0              0
20              1           0              0              0              0
41              1           1              0              0              0
35              0           0              0              0              0
```

```
      red leaf spot  white spot
27                0           0
5                 0           0
6                 0           0
38                0           0
21                0           0
0                 0           0
20                0           0
41                0           0
35                0           0
```

In [20]: `print(y_train)`

```
36  0
18  1
7   0
```

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In [20]: print(y_train)

```
36 0
18 1
7 0
39 0
32 0
25 1
28 0
19 0
13 0
1 1
26 1
12 0
31 0
22 0
9 0
29 0
11 0
4 0
37 0
40 0
16 0
17 1
33 0
14 0
2 0
34 0
30 0
10 0
15 1
23 0
```



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```
24 0
8 0
Name: healthy, dtype: int64
```

```
In [21]: print(y_test)
```

```
27 1
5 0
6 0
38 0
21 0
0 0
20 0
41 0
35 0
Name: healthy, dtype: int64
```

```
In [22]: print(f"Mean Squared Error:{mse}")
```

```
Mean Squared Error:0.09455985828254297
```

```
In [23]: print(f"R-squared score:{r2}")
```

```
R-squared score:0.04258143488925237
```

```
In [33]: print(y_pred)
```

```
[ 0.13824885  0.13824885  0.13824885  0.13824885  0.13824885  0.07834101
 -0.02419355  0.07834101  0.13824885]
```

```
In [72]: new=[[0,0,1,1,0,1,1]]
```

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```
35 0
    Name: healthy, dtype: int64
```

```
In [22]: print(f"Mean Squared Error:{mse}")
```

```
Mean Squared Error:0.09455985828254297
```

```
In [23]: print(f"R-squared score:{r2}")
```

```
R-squared score:0.04258143488925237
```

```
In [33]: print(y_pred)
```

```
[ 0.13824885  0.13824885  0.13824885  0.13824885  0.13824885  0.07834101
 -0.02419355  0.07834101  0.13824885]
```

```
In [72]: new=[[0,0,1,1,0,1,1]]
```

```
In [76]: predicted= regressor.predict(new)
```

```
C:\ProgramData\anaconda3\Lib\site-packages\sklearn\base.py:439: UserWarning: X does not have valid feature names, but LinearRegression was fitted with feature names
  warnings.warn(
```

```
In [77]: print(f"Prediction: {predicted}")
```

```
Prediction: [0.8859447]
```