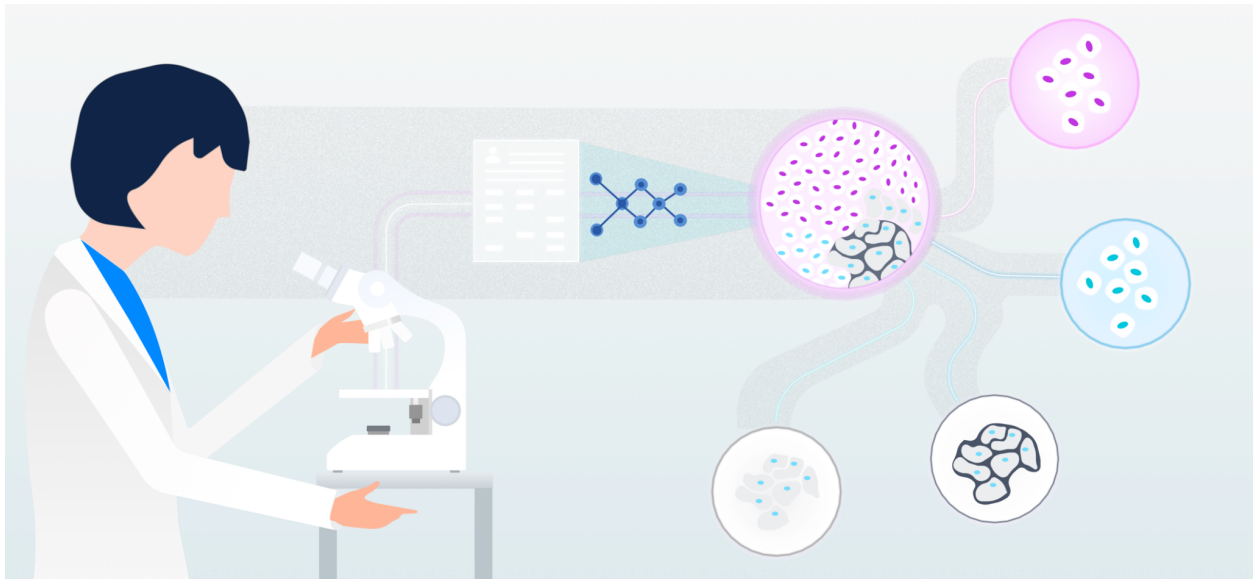


Machine learning

BREAST CANCER PREDICTION



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PROBLEM STATEMENT

The objective of this project is investigating the probability of predicting the chances of breast cancer from the given characteristics of breast mass computed from the dataset.

INTRODUCTION

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 challenge against it's detection is how to classify tumors into malignant (cancerous) or benign(non cancerous).

DATASET INFORMATION

<https://www.kaggle.com/datasets/jainilcoder/breast-cancer-dataset>

The Dataset contains 32 Columns and 570 rows consisting all the parameters used for detecting a Breast Cancer.

The Breast Cancer Wisconsin (Diagnostic) DataSet, obtained from Kaggle, contains features computed from a digitized image of a fine needle aspirate (FNA) of a breast mass and describe characteristics of the cell nuclei present in the image.

Attribute information

- ID number

- Diagnosis (M = malignant, B = benign)
- Ten real-valued features are computed for each cell nucleus:
 - radius (mean of distances from center to points on the perimeter)
 - texture (standard deviation of gray-scale values)
 - perimeter
 - area
 - smoothness (local variation in radius lengths)
 - compactness ($\text{perimeter}^2 / \text{area} - 1.0$)
 - concavity (severity of concave portions of the contour)
 - concave points (number of concave portions of the contour)
 - symmetry
 - fractal dimension ("coastline approximation" - 1)

Input Code :

```
# importing libraries

import numpy as np

import matplotlib.pyplot as plt

import pandas as pd

import seaborn as sns

import sklearn.datasets

from sklearn.model_selection import train_test_split

from sklearn.linear_model import LogisticRegression

from sklearn.metrics import accuracy_score

# reading data from the file

df=pd.read_csv("data.csv")

df.head() #The head() method returns a specified number of rows,
string from the top

df.info() #info() function is used to get a concise summary of the
dataframe

<class 'pandas.core.frame.DataFrame'>
```

RangeIndex: 569 entries, 0 to 568

Data columns (total 33 columns):

#	Column	Non-Null Count	Dtype
---	-----	-----	-----
0	id	569 non-null	int64
1	diagnosis	569 non-null	object
2	radius_mean	569 non-null	float64
3	texture_mean	569 non-null	float64
4	perimeter_mean	569 non-null	float64
5	area_mean	569 non-null	float64
6	smoothness_mean	569 non-null	float64
7	compactness_mean	569 non-null	float64
8	concavity_mean	569 non-null	float64
9	concave points_mean	569 non-null	float64
10	symmetry_mean	569 non-null	float64
11	fractal_dimension_mean	569 non-null	float64
12	radius_se	569 non-null	float64
13	texture_se	569 non-null	float64
14	perimeter_se	569 non-null	float64
15	area_se	569 non-null	float64
16	smoothness_se	569 non-null	float64
17	compactness_se	569 non-null	float64
18	concavity_se	569 non-null	float64
19	concave points_se	569 non-null	float64

20	symmetry_se	569 non-null	float64
21	fractal_dimension_se	569 non-null	float64
22	radius_worst	569 non-null	float64
23	texture_worst	569 non-null	float64
24	perimeter_worst	569 non-null	float64
25	area_worst	569 non-null	float64
26	smoothness_worst	569 non-null	float64
27	compactness_worst	569 non-null	float64
28	concavity_worst	569 non-null	float64
29	concave points_worst	569 non-null	float64
30	symmetry_worst	569 non-null	float64
31	fractal_dimension_worst	569 non-null	float64
32	Unnamed: 32	0 non-null	float64

dtypes: float64(31), int64(1), object(1)

memory usage: 146.8+ KB

return all the columns with null values count

df.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

# remove the column

df=df.dropna(axis=1)

# return the size of dataset after dropping null value

df.shape

(569, 32)

# statistical measures about the data

df.describe()

# checking the distribution of Target Varibale

df['diagnosis'].value_counts()

B      357
M      212
Name: diagnosis, dtype: int64

value_counts = df['diagnosis'].value_counts()

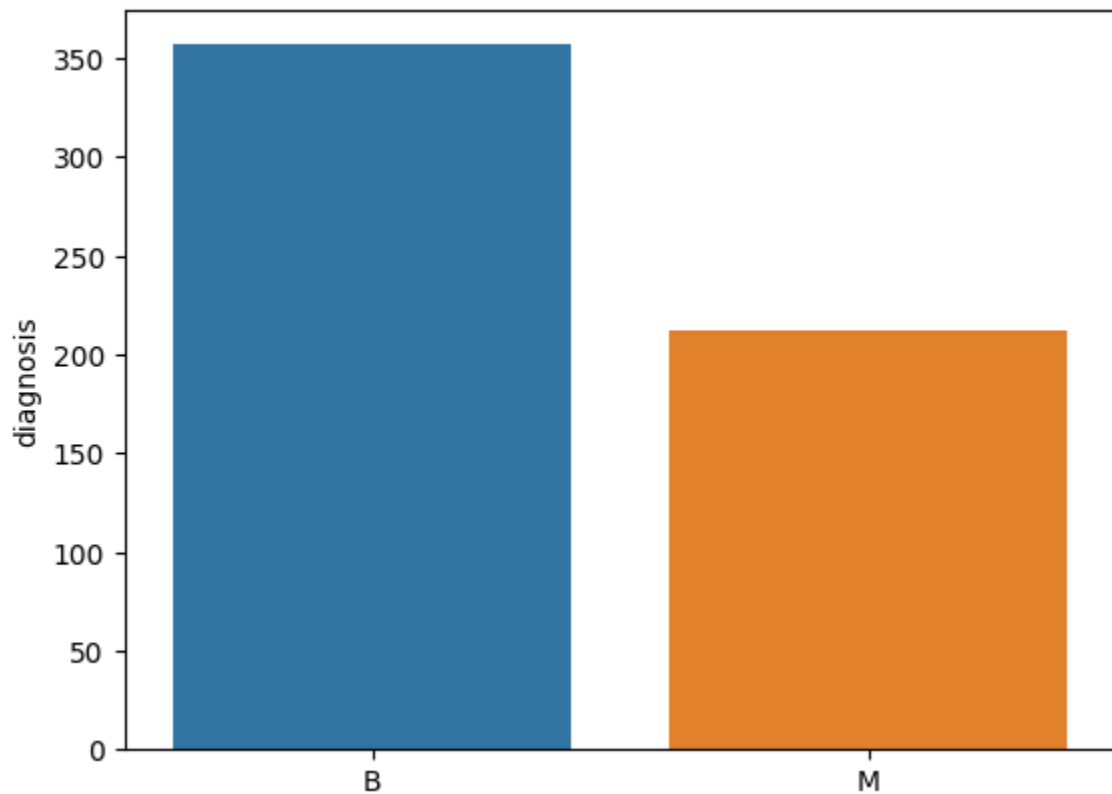
# Plot the counts using a bar plot

sns.barplot(x=value_counts.index, y=value_counts)

# Show the plot

plt.show()

```



```
df.groupby('diagnosis').mean()

#easier to spot differences & patterns between groups

X = df.drop(columns='diagnosis', axis=1)

Y = df['diagnosis']

from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()

scaler.fit(X)

standardized_data = scaler.transform(X)
```



```
print(standardized_data)

[[-0.23640517  1.09706398 -2.07333501 ...  2.29607613  2.75062224
    1.93701461]
 [-0.23640344  1.82982061 -0.35363241 ...  1.0870843  -0.24388967
    0.28118999]
 [ 0.43174109  1.57988811  0.45618695 ...  1.95500035  1.152255
    0.20139121]
 ...
 [-0.23572747  0.70228425  2.0455738  ...  0.41406869 -1.10454895
   -0.31840916]
 [-0.23572517  1.83834103  2.33645719 ...  2.28998549  1.91908301
    2.21963528]
 [-0.24240586 -1.80840125  1.22179204 ... -1.74506282 -0.04813821
   -0.75120669]]
```

```
print(X)
```

	id	radius_mean	texture_mean	perimeter_mean	area_mean
0	842302	17.99	10.38	122.80	1001.0
1	842517	20.57	17.77	132.90	1326.0
2	84300903	19.69	21.25	130.00	1203.0
3	84348301	11.42	20.38	77.58	386.1
4	84358402	20.29	14.34	135.10	1297.0
..
564	926424	21.56	22.39	142.00	1479.0
565	926682	20.13	28.25	131.20	1261.0

566	926954	16.60	28.08	108.30	858.1
567	927241	20.60	29.33	140.10	1265.0
568	92751	7.76	24.54	47.92	181.0

	smoothness_mean	compactness_mean	concavity_mean	concave
points_mean \				

0	0.11840	0.27760	0.30010
0.14710			

1	0.08474	0.07864	0.08690
0.07017			

2	0.10960	0.15990	0.19740
0.12790			

3	0.14250	0.28390	0.24140
0.10520			

4	0.10030	0.13280	0.19800
0.10430			

..
...			

564	0.11100	0.11590	0.24390
0.13890			

565	0.09780	0.10340	0.14400
0.09791			

566	0.08455	0.10230	0.09251
0.05302			

567	0.11780	0.27700	0.35140
0.15200			

568	0.05263	0.04362	0.00000
0.00000			

	symmetry_mean	...	radius_worst	texture_worst
perimeter_worst \				
0	0.2419	...	25.380	17.33
184.60				
1	0.1812	...	24.990	23.41
158.80				
2	0.2069	...	23.570	25.53
152.50				
3	0.2597	...	14.910	26.50
98.87				
4	0.1809	...	22.540	16.67
152.20				
..
...				
564	0.1726	...	25.450	26.40
166.10				
565	0.1752	...	23.690	38.25
155.00				
566	0.1590	...	18.980	34.12
126.70				
567	0.2397	...	25.740	39.42
184.60				
568	0.1587	...	9.456	30.37
59.16				

	area_worst	smoothness_worst	compactness_worst
concavity_worst \			
0	2019.0	0.16220	0.66560
0.7119			

1	1956.0	0.12380	0.18660
0.2416			
2	1709.0	0.14440	0.42450
0.4504			
3	567.7	0.20980	0.86630
0.6869			
4	1575.0	0.13740	0.20500
0.4000			
..
...			
564	2027.0	0.14100	0.21130
0.4107			
565	1731.0	0.11660	0.19220
0.3215			
566	1124.0	0.11390	0.30940
0.3403			
567	1821.0	0.16500	0.86810
0.9387			
568	268.6	0.08996	0.06444
0.0000			

	concave points_worst	symmetry_worst	fractal_dimension_worst
0	0.2654	0.4601	0.11890
1	0.1860	0.2750	0.08902
2	0.2430	0.3613	0.08758
3	0.2575	0.6638	0.17300
4	0.1625	0.2364	0.07678
..

564	0.2216	0.2060	0.07115
565	0.1628	0.2572	0.06637
566	0.1418	0.2218	0.07820
567	0.2650	0.4087	0.12400
568	0.0000	0.2871	0.07039

[569 rows x 31 columns]

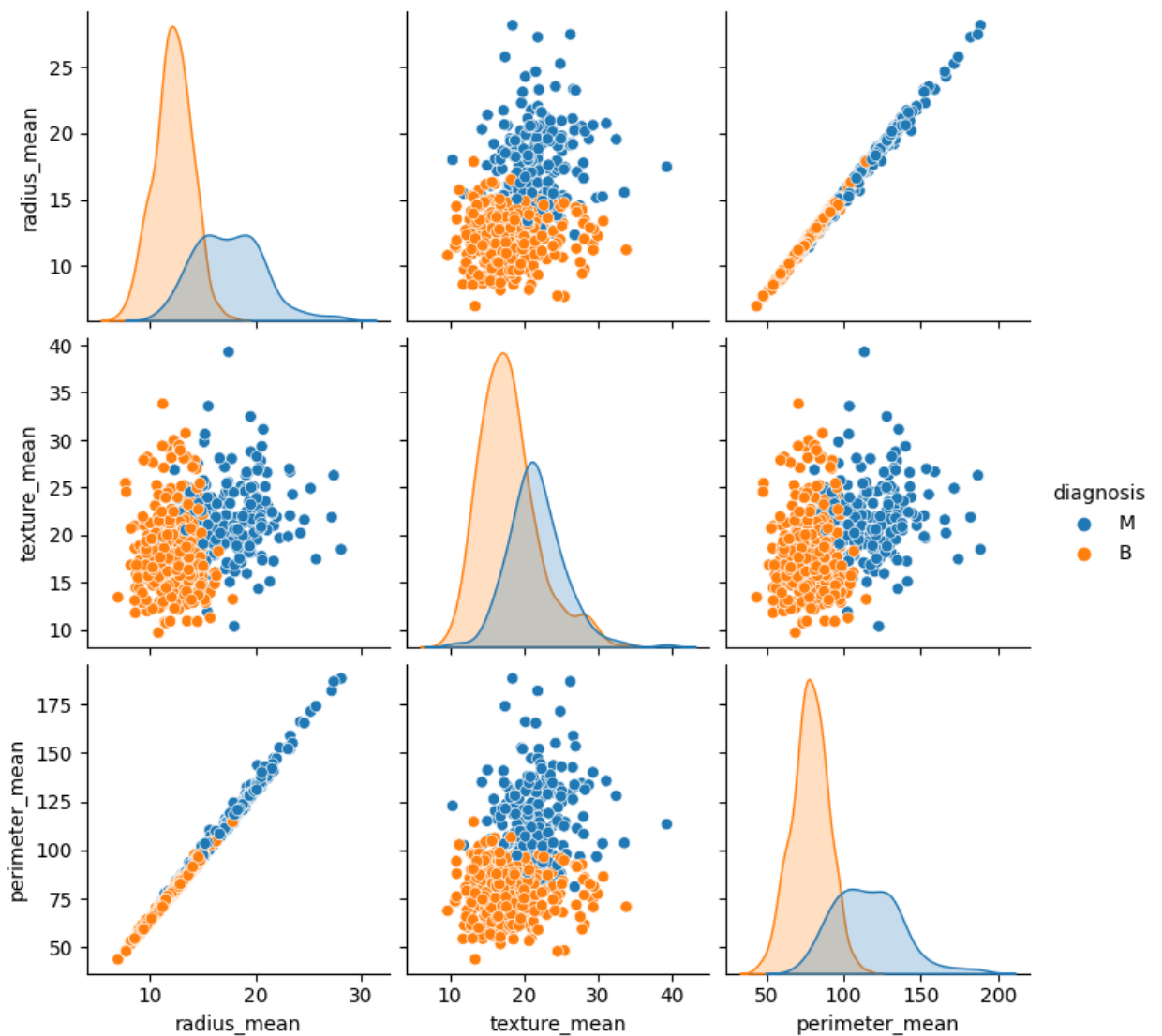
```
print(Y)
```

```
0      M
1      M
2      M
3      M
4      M
      ..
564    M
565    M
566    M
567    M
568    B
```

Name: diagnosis, Length: 569, dtype: object

```
sns.pairplot(df.iloc[:,1:5],hue="diagnosis")
```

<seaborn.axisgrid.PairGrid at 0x7f80ff430040>



```
# get the correlation
```

```
df.iloc[:,1:32].corr()
```

```
# visualize the correlation
```

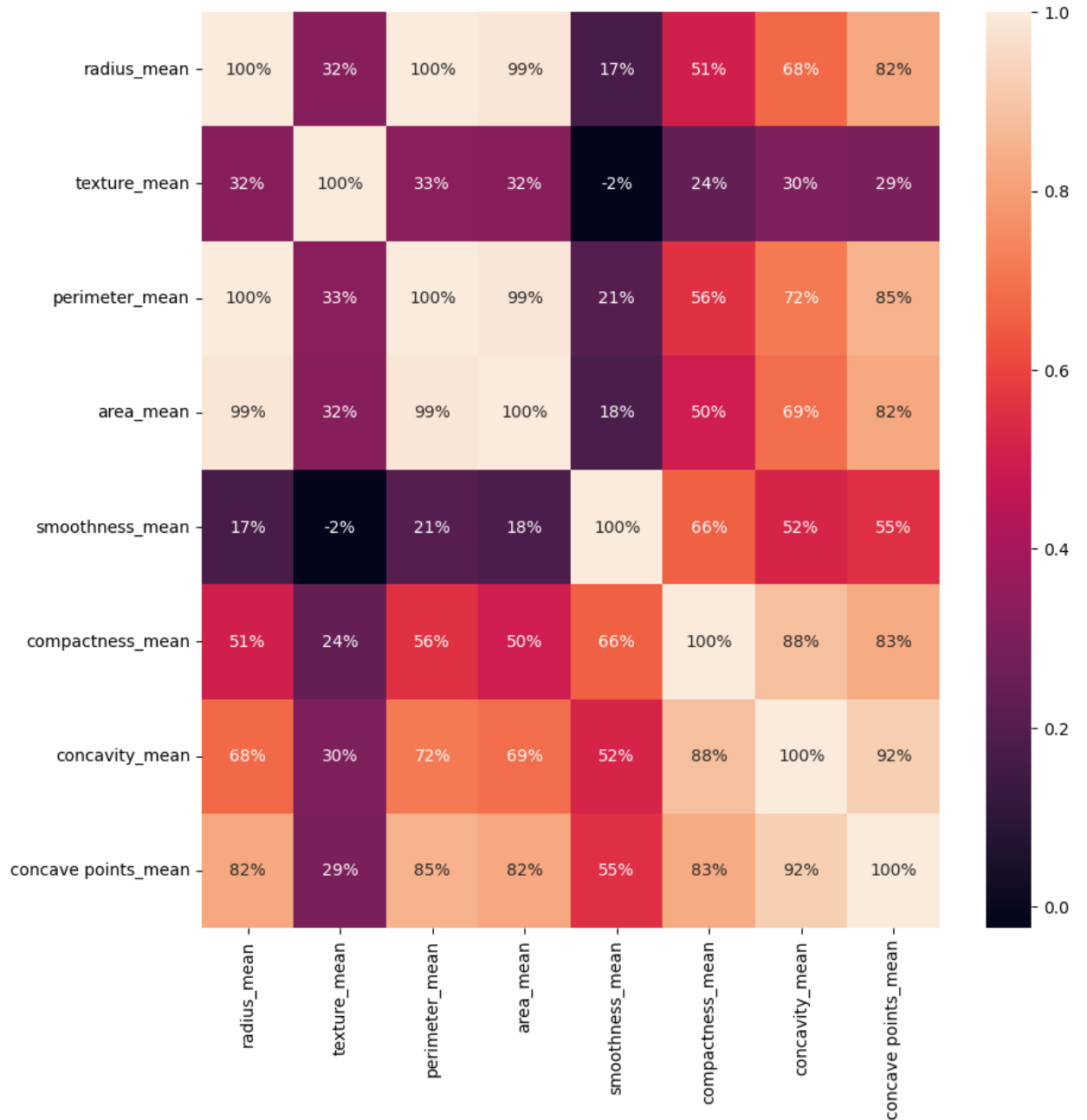
```
plt.figure(figsize=(10,10))
```

```
sns.heatmap(df.iloc[:,1:10].corr(),annot=True,fmt=".0%")
```

<ipython-input-18-a2668557c8b3>:3: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of numeric_only to silence this warning.

```
sns.heatmap(df.iloc[:,1:10].corr(),annot=True,fmt=".0%")
```

<Axes: >



```
# splitting the data into training and test dataset
```

```
from sklearn.model_selection import train_test_split
```

```
X_train,X_test,Y_train,Y_test=train_test_split(X,Y,test_size=0.20,ra
```

```
ndom_state=0)

# feature scaling

from sklearn.preprocessing import StandardScaler

X_train=StandardScaler().fit_transform(X_train)

X_test=StandardScaler().fit_transform(X_test)

# LOGISTIC REGRESSION


from sklearn.linear_model import LogisticRegression

from sklearn.metrics import accuracy_score

from sklearn.metrics import classification_report


# create logistic regression object


model = LogisticRegression()


# train the model using the training sets


model.fit(X_train , Y_train)


X_train_prediction = model.predict(X_train)

training_data_accuracy = accuracy_score(Y_train, X_train_prediction)

print('Accuracy on training data = ', training_data_accuracy)
```



```

# accuracy on test data

X_test_prediction = model.predict(X_test)

# comparing actual response values (y_test) with predicted response
values (X_test_prediction)

test_data_accuracy = accuracy_score(Y_test, X_test_prediction)

print('Accuracy on test data = ', test_data_accuracy)

Accuracy on training data =  0.989010989010989

Accuracy on test data =  0.956140350877193

# models/ Algorithms

def models(X_train,Y_train):

    #Random Forest

    from sklearn.ensemble import RandomForestClassifier

    forest=RandomForestClassifier(random_state=0,criterion="entropy",n_estimators=10)

    forest.fit(X_train,Y_train)

    #Decision Tree

    from sklearn.tree import DecisionTreeClassifier

```

```
tree=DecisionTreeClassifier(random_state=0,criterion="entropy")
```

```
tree.fit(X_train,Y_train)
```

```
print('[0]Random forest  
accuracy:',forest.score(X_train,Y_train))
```

```
print('[1]Decision tree  
accuracy:',tree.score(X_train,Y_train))
```

```
return forest,tree
```

```
model=models(X_train,Y_train)
```

```
[0]Random forest accuracy: 0.9978021978021978
```

```
[1]Decision tree accuracy: 1.0
```

```
# testing the models/result
```

```
from sklearn.metrics import accuracy_score
```

```
from sklearn.metrics import classification_report
```

```
for i in range(len(model)):
```

```
    print("Model",i)
```

```
    print(classification_report(Y_test,model[i].predict(X_test)))
```

```
    print('Accuracy :
```

```
',accuracy_score(Y_test,model[i].predict(X_test)))
```

Model 0

	precision	recall	f1-score	support
B	0.96	1.00	0.98	67
M	1.00	0.94	0.97	47
accuracy			0.97	114
macro avg	0.98	0.97	0.97	114
weighted avg	0.97	0.97	0.97	114

Accuracy : 0.9736842105263158

Model 1

	precision	recall	f1-score	support
B	0.91	0.94	0.93	67
M	0.91	0.87	0.89	47
accuracy			0.91	114
macro avg	0.91	0.91	0.91	114
weighted avg	0.91	0.91	0.91	114

Accuracy : 0.9122807017543859

```
from sklearn import svm
```

```

classifier = svm.SVC(kernel='linear')

#training the support vector Machine Classifier

classifier.fit(X_train, Y_train)

# accuracy score on the training data

X_train_prediction = classifier.predict(X_train)

training_data_accuracy = accuracy_score(X_train_prediction, Y_train)

print('Accuracy score of the training data : ',
      training_data_accuracy)

# accuracy score on the test data

X_test_prediction = classifier.predict(X_test)

test_data_accuracy = accuracy_score(X_test_prediction, Y_test)

print('Accuracy score of the test data : ', test_data_accuracy)

Accuracy score of the training data :  0.989010989010989

Accuracy score of the test data :  0.9649122807017544

from sklearn.preprocessing import StandardScaler

#input_data =
(20.55,20.86,137.8,1308,0.1046,0.1739,0.2085,0.1322,0.2127,0.06251,0
.6986,0.9901,4.706,87.78,0.004578,0.02616,0.04005,0.01421,0.01948,0.
002689,24.3,25.48,160.2,1809,0.1268,0.3135,0.4433,0.2148,0.3077,0.45

```

```
,0.07569)
```

```
input_data = (13.54,14.36,87.46,566.3,0.09779,0.08129,0.06664,0.14  
,0.04781,0.1885,0.05766,0.2699,0.7886,2.058,23.56,0.008462,0.0146,0.  
02387,0.01315,0.0198,0.0023,15.11,19.26,99.7,711.2,0.144,0.1773,0.23  
9,0.1288,0.2977,0.07259)
```

```
# changing the input_data to numpy array
```

```
input_data_as_numpy_array = np.asarray(input_data)
```

```
# reshape the array as we are predicting for one instance
```

```
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
```

```
# standardize the input data
```

```
std_data = scaler.transform(input_data_reshaped)
```

```
prediction = classifier.predict(std_data)
```

```
print(prediction)
```

```
if (prediction[0] == 'M'):
```

```
    print('The Breast cancer is Malignant')#Cancerous cells
```

```
else:
```

```
    print('The Breast Cancer is Benign')#non-cancerous cells
```

```
sns.lmplot(x='area_mean',y='area_worst',data=dataset,hue='diagnosis',  
palette='Set1',fit_reg=True, scatter_kws={"s":50})
```

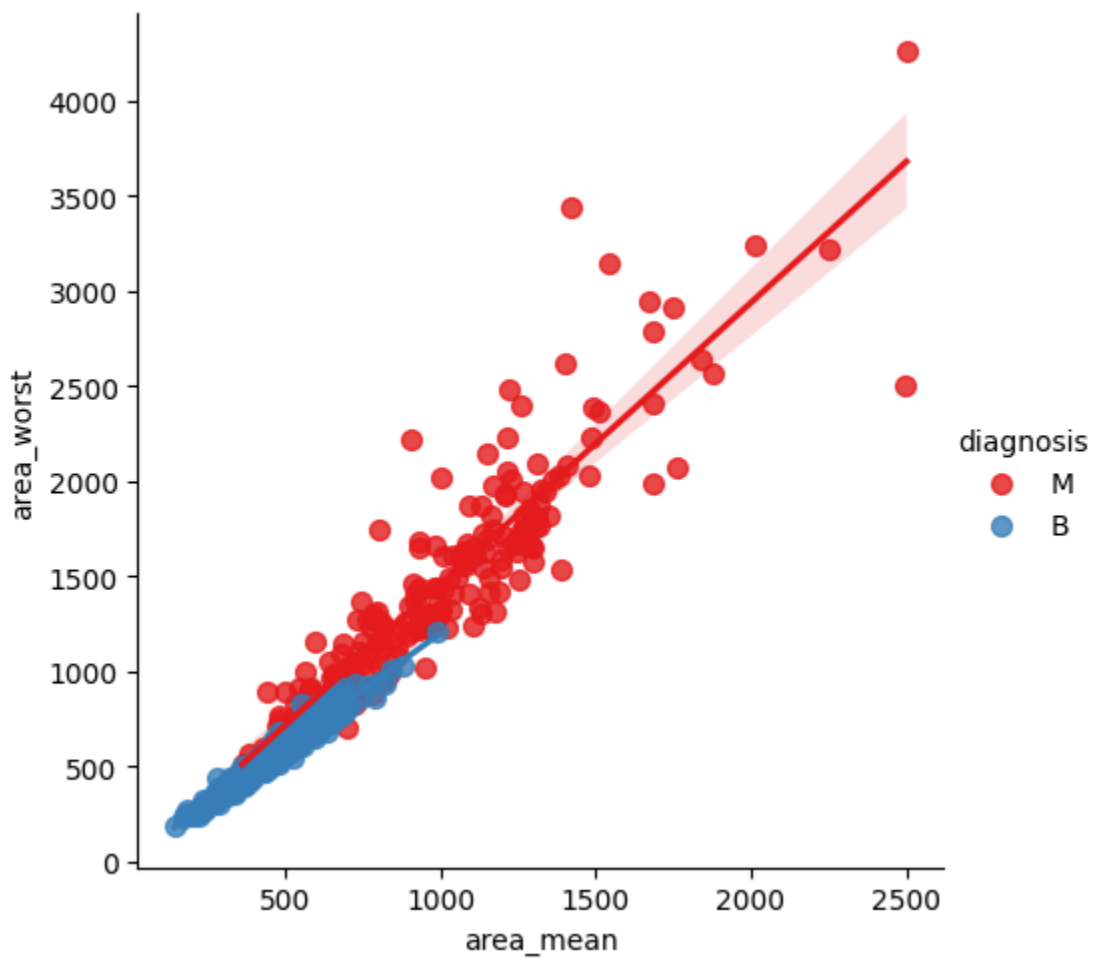
/usr/local/lib/python3.10/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but StandardScaler was fitted with feature names

```
warnings.warn(
```

```
['M']
```

The Breast cancer is Malignant

<seaborn.axisgrid.FacetGrid at 0x7f80f7ac76a0>



CONCLUSION

Breast cancer can be detected in the early stages. It can be treated effectively. Breast cancer when it is most treatable, does not produce any symptoms, therefore be diligent with breast health. Combining multiple risk factors in modeling for breast cancer prediction could help the early diagnosis of the disease with necessary care plans. Collection, storage, and management of different data and intelligent systems based on multiple factors for predicting breast cancer are effective in disease management.

REFERENCES

An official website of the United States government:United States National Library of
Medicine, a branch of the National Institutes of Health.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9175124/>