```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import sklearn.datasets
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

Data Collection and Preprocessing

```
# loading the data from sklearn
breast_cancer_dataset = sklearn.datasets.load_breast_cancer()
```

```
print(breast_cancer_dataset)
```

```
{'data': array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01, 4.601e-01,
         1.189e-01],
        [2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
         8.902e-02],
        [1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
         8.758e-02],
        ...,
        [1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
         7.820e-02],
        [2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
         1.240e-01],
        [7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
         7.039e-02]]), 'target': array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1,
        0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0,
        0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0,
        1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 0, 0,
        1, 1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 1, 0, 1,
        1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0,
        0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1,
        1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1,
        1, 0, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 0, 0,
        0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0,
        1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 0, 1, 1, 0, 0, 1, 0, 1, 1,
        1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
        0, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1,
        1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1,
        1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0,
        0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0,
        0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0,
        1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 1,
        1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0,
        1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1,
        1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0,
        1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
        1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1,
        1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
        1, 1, 1, 1, 1, 0, 1, 0, 0, 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, 0, 0, 0, 0, 1]), 'frame': None, 'target_names': array(['malignant', 'benign'], dtype='<U9'
        'mean smoothness', 'mean compactness', 'mean concavity',
        'mean concave points', 'mean symmetry', 'mean fractal dimension',
        'radius error', 'texture error', 'perimeter error', 'area error',
        'smoothness error', 'compactness error', 'concavity error',
        'concave points error', 'symmetry error',
        'fractal dimension error', 'worst radius', 'worst texture',
        'worst perimeter', 'worst area', 'worst smoothness',
        'worst compactness', 'worst concavity', 'worst concave points',
        'worst symmetry', 'worst fractal dimension'], dtype='<U23'), 'filename': 'breast_cancer.csv', 'data_module': 'sklearn.datasets.data'
```

```
data_frame = pd.DataFrame(breast_cancer_dataset.data, columns = breast_cancer_dataset.feature_names)
```

```
data_frame.head()
```

mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst radius	worst texture	worst perimeter	worst area	worst smoothness	worst compactness	worst concavity	worst concave points
0.27760	0.3001	0.14710	0.2419	0.07871	...	25.38	17.33	184.60	2019.0	0.1622	0.6656	0.7119	0.2654
0.07864	0.0869	0.07017	0.1812	0.05667	...	24.99	23.41	158.80	1956.0	0.1238	0.1866	0.2416	0.1860
0.15990	0.1974	0.12790	0.2069	0.05999	...	23.57	25.53	152.50	1709.0	0.1444	0.4245	0.4504	0.2430
0.28390	0.2414	0.10520	0.2597	0.09744	...	14.91	26.50	98.87	567.7	0.2098	0.8663	0.6869	0.2575
0.13280	0.1980	0.10430	0.1809	0.05883	...	22.54	16.67	152.20	1575.0	0.1374	0.2050	0.4000	0.1625

What can I help you build?

```
# adding the 'target' column to the data frame
data_frame['label'] = breast_cancer_dataset.target
```

```
data_frame.tail()
```

an ss	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst texture	worst perimeter	worst area	worst smoothness	worst compactness	worst concavity	worst concave points	wors symmetr
00	0.11590	0.24390	0.13890	0.1726	0.05623	...	26.40	166.10	2027.0	0.14100	0.21130	0.4107	0.2216	0.206
30	0.10340	0.14400	0.09791	0.1752	0.05533	...	38.25	155.00	1731.0	0.11660	0.19220	0.3215	0.1628	0.257
55	0.10230	0.09251	0.05302	0.1590	0.05648	...	34.12	126.70	1124.0	0.11390	0.30940	0.3403	0.1418	0.221
30	0.27700	0.35140	0.15200	0.2397	0.07016	...	39.42	184.60	1821.0	0.16500	0.86810	0.9387	0.2650	0.408
63	0.04362	0.00000	0.00000	0.1587	0.05884	...	30.37	59.16	268.6	0.08996	0.06444	0.0000	0.0000	0.287

```
data_frame.shape
```

```
(569, 31)
```

```
data_frame.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   mean radius              569 non-null    float64
 1   mean texture             569 non-null    float64
 2   mean perimeter           569 non-null    float64
 3   mean area                569 non-null    float64
 4   mean smoothness          569 non-null    float64
 5   mean compactness         569 non-null    float64
 6   mean concavity           569 non-null    float64
 7   mean concave points      569 non-null    float64
 8   mean symmetry            569 non-null    float64
 9   mean fractal dimension   569 non-null    float64
 10  radius error             569 non-null    float64
 11  texture error            569 non-null    float64
 12  perimeter error          569 non-null    float64
 13  area error               569 non-null    float64
 14  smoothness error         569 non-null    float64
 15  compactness error        569 non-null    float64
 16  concavity error          569 non-null    float64
 17  concave points error     569 non-null    float64
 18  symmetry error           569 non-null    float64
 19  fractal dimension error  569 non-null    float64
 20  worst radius             569 non-null    float64
 21  worst texture            569 non-null    float64
 22  worst perimeter          569 non-null    float64
 23  worst area               569 non-null    float64
 24  worst smoothness         569 non-null    float64
 25  worst compactness        569 non-null    float64
 26  worst concavity          569 non-null    float64
 27  worst concave points     569 non-null    float64
 28  worst symmetry           569 non-null    float64
 29  worst fractal dimension  569 non-null    float64
 30  label                    569 non-null    int64  
dtypes: float64(30), int64(1)
memory usage: 137.9 KB
```

```
#checking for missing values
data_frame.isnull().sum()
```

	0
mean radius	0
mean texture	0
mean perimeter	0
mean area	0
mean smoothness	0
mean compactness	0
mean concavity	0
mean concave points	0
mean symmetry	0
mean fractal dimension	0
radius error	0
texture error	0
perimeter error	0
area error	0
smoothness error	0
compactness error	0
concavity error	0
concave points error	0
symmetry error	0
fractal dimension error	0
worst radius	0
worst texture	0
worst perimeter	0
worst area	0
worst smoothness	0
worst compactness	0
worst concavity	0
worst concave points	0
worst symmetry	0
worst fractal dimension	0
label	0

dtype: int64

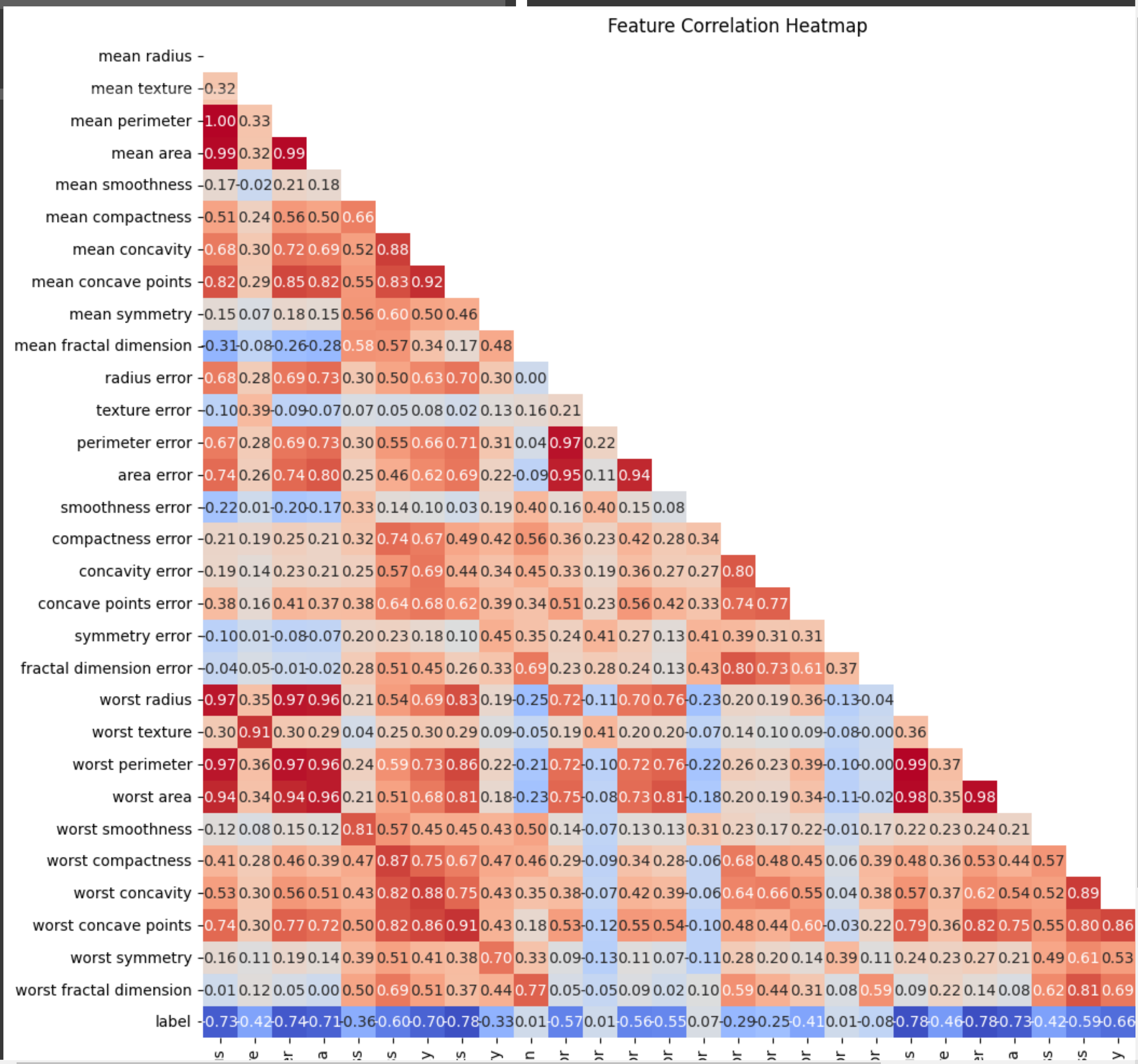
```
data_frame.describe()
```

ean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst texture	worst perimeter	worst area	worst smoothness	wc compactr
9.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	...	569.000000	569.000000	569.000000	569.000000	569.000
4.889104	0.096360	0.104341	0.088799	0.048919	0.181162	0.062798	...	25.677223	107.261213	880.583128	0.132369	0.254
1.914129	0.014064	0.052813	0.079720	0.038803	0.027414	0.007060	...	6.146258	33.602542	569.356993	0.022832	0.157
3.500000	0.052630	0.019380	0.000000	0.000000	0.106000	0.049960	...	12.020000	50.410000	185.200000	0.071170	0.027
0.300000	0.086370	0.064920	0.029560	0.020310	0.161900	0.057700	...	21.080000	84.110000	515.300000	0.116600	0.147
1.100000	0.095870	0.092630	0.061540	0.033500	0.179200	0.061540	...	25.410000	97.660000	686.500000	0.131300	0.211
2.700000	0.105300	0.130400	0.130700	0.074000	0.195700	0.066120	...	29.720000	125.400000	1084.000000	0.146000	0.339
1.000000	0.163400	0.345400	0.426800	0.201200	0.304000	0.097440	...	49.540000	251.200000	4254.000000	0.222600	1.058

Correlation Heatmap to check feature interdependencies

```
plt.figure(figsize=(16,12))
corr = data_frame.corr()
mask = np.triu(np.ones_like(corr, dtype=bool))
sns.heatmap(corr, mask=mask, annot=True, fmt=".2f", cmap='coolwarm'
```

```
plt.title('Feature Correlation Heatmap')
```



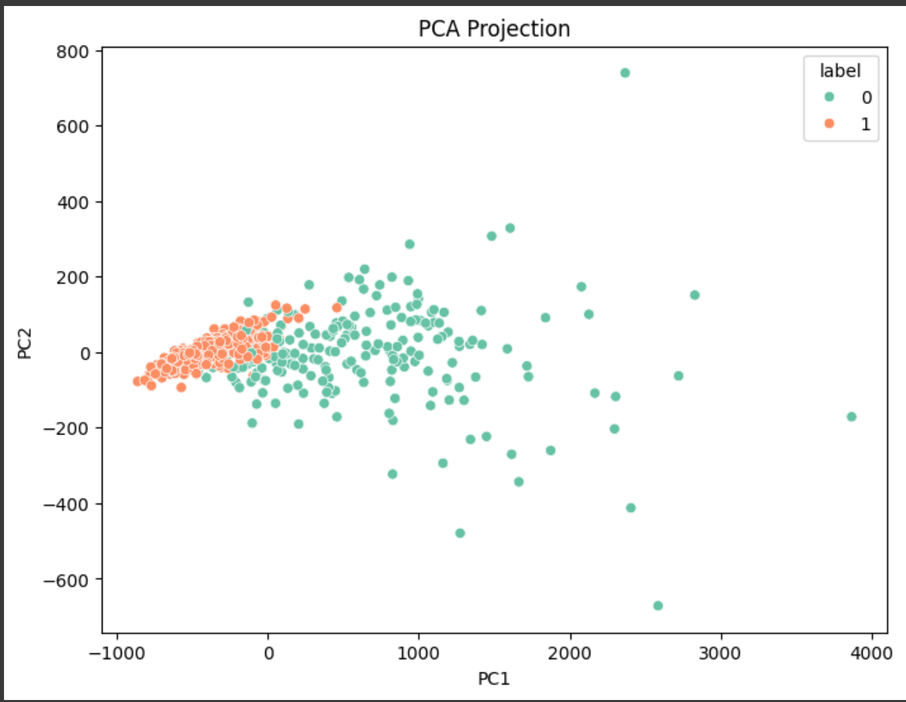

```
data_frame['label'].value_counts() #1->Benign[B] & 0->Malignant[M]
```

label	count
1	357
0	212

dtype: int64

```
from sklearn.decomposition import PCA

pca = PCA(n_components=2)
X_pca = pca.fit_transform(X)

plt.figure(figsize=(8,6))
sns.scatterplot(x=X_pca[:,0], y=X_pca[:,1], hue=Y, palette="Set2")
plt.title("PCA Projection")
plt.xlabel("PC1")
plt.ylabel("PC2")
```

```
plt.show()
```




```
data_frame.groupby('label').mean()
```

label	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst radius	wor textu
0	17.462830	21.604906	115.365377	978.376415	0.102898	0.145188	0.160775	0.087990	0.192909	0.062680	...	21.134811	29.3182
1	12.146524	17.914762	78.075406	462.790196	0.092478	0.080085	0.046058	0.025717	0.174186	0.062867	...	13.379801	23.5150

2 rows × 30 columns

```
#Sperations of features and target
X = data_frame.drop(columns='label', axis=1)
Y = data_frame['label']
```

```
print(X)
```

```
565          0.10340         0.14400            0.09791         0.1752
566          0.10230         0.09251            0.05302         0.1590
567          0.27700         0.35140            0.15200         0.2397
568          0.04362         0.00000            0.00000         0.1587

     mean fractal dimension  ...  worst radius  worst texture  \
0                   0.07871  ...        25.380          17.33
1                   0.05667  ...        24.990          23.41
2                   0.05999  ...        23.570          25.53
3                   0.09744  ...        14.910          26.50
4                   0.05883  ...        22.540          16.67
..                      ...  ...           ...            ...
564                 0.05623  ...        25.450          26.40
565                 0.05533  ...        23.690          38.25
```

```
3             0.6869                0.2575          0.6638
4             0.4000                0.1625          0.2364
..               ...                   ...             ...
564           0.4107                0.2216          0.2060
565           0.3215                0.1628          0.2572
566           0.3403                0.1418          0.2218
567           0.9387                0.2650          0.4087
568           0.0000                0.0000          0.2871

     worst fractal dimension
0                    0.11890
1                    0.08902
2                    0.08758
3                    0.17300
4                    0.07678
..                       ...
564                  0.07115
565                  0.06637
566                  0.07820
567                  0.12400
568                  0.07039

[569 rows x 30 columns]
```

```
print(Y)
```

```
0      0
1      0
2      0
3      0
4      0
      ..
564    0
565    0
566    0
567    0
568    1
Name: label, Length: 569, dtype: int64
```

```
#splitting data into training data and testing data
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=2)
print(X.shape, X_train.shape, X_test.shape)
```

```
(569, 30) (455, 30) (114, 30)
```

Model Training (Logistic Regression)

```
model = LogisticRegression()
model.fit(X_train, Y_train) # training the Logistic Regression model using Training data
```

```
▾ LogisticRegression
LogisticRegression()
```

```
X_train_prediction = model.predict(X_train)
training_data_accuracy = accuracy_score(Y_train, X_train_prediction) #training data accuracy
print('Accuracy on training data = ', training_data_accuracy)
```

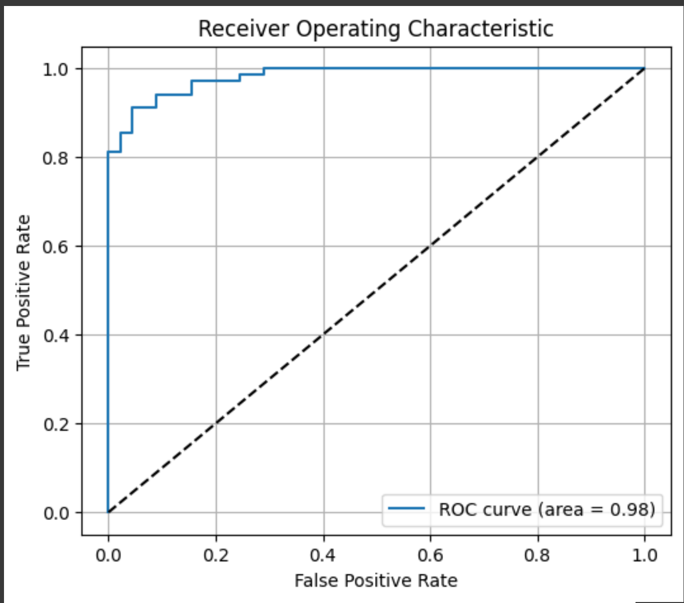
```
Accuracy on training data =  0.9494505494505494
```

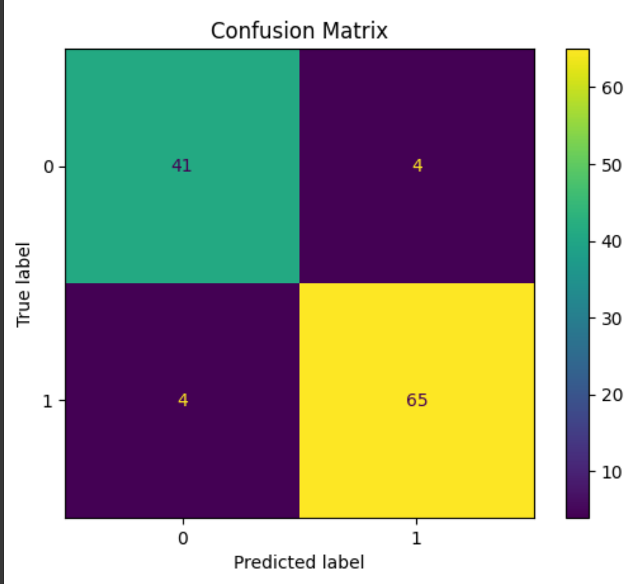
```
X_test_prediction = model.predict(X_test)
test_data_accuracy = accuracy_score(Y_test, X_test_prediction)# accuracy on test data
print('Accuracy on test data = ', test_data_accuracy)
```

```
Accuracy on test data =  0.9298245614035088
```

```
from sklearn.metrics import roc_curve, auc, confusion_matrix, ConfusionMatrixDisplay

# ROC Curve
from sklearn.metrics import roc_auc_score

y_probs = model.predict_proba(X_test)[:,1]
fpr, tpr, _ = roc_curve(Y_test, y_probs)
roc_auc = auc(fpr, tpr)

plt.figure(figsize=(6,5))
plt.plot(fpr, tpr, label='ROC curve (area = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], 'k--')
plt.title('Receiver Operating Characteristic')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend(loc="lower right")
plt.grid()
plt.show()

# Confusion Matrix
```

```
cm = confusion_matrix(Y_test, model.predict(X_test))
disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=model.classes_)
disp.plot()
plt.title("Confusion Matrix")
plt.show()
```





Prediction

```
input_data = (17.2, 15.8, 110.0, 910.2, 0.1023, 0.1304, 0.1505, 0.0894, 0.1901, 0.0623,
              0.4201, 1.250, 3.150, 30.21, 0.00955, 0.0201, 0.0359, 0.01501, 0.0212, 0.0032,
              18.8, 21.5, 120.7, 1100.0, 0.155, 0.2301, 0.3205, 0.175, 0.3152, 0.0895)

# change the input data to a numpy array
input_data_as_numpy_array = np.asarray(input_data)

# reshape the numpy array as we are predicting for one datapoint
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = model.predict(input_data_reshaped)
print(prediction)

if (prediction[0] == 0):
  print('The Breast cancer is Malignant')

else:
  print('The Breast Cancer is Benign')
```

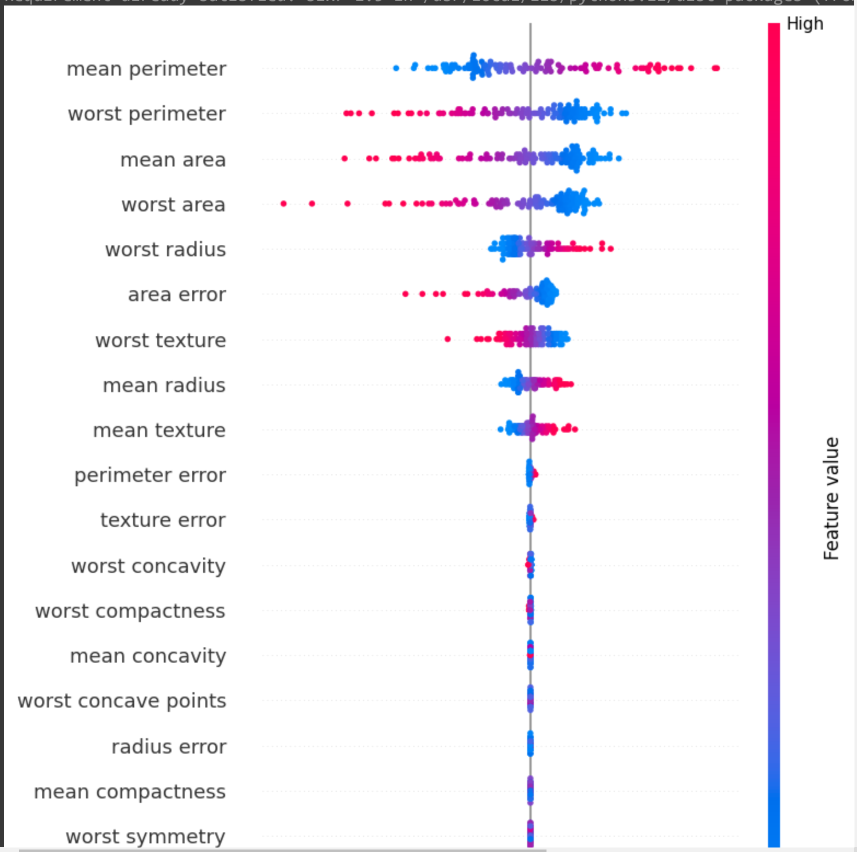
```
[0]
The Breast cancer is Malignant
```

Shap Integration

```
# SHAP Explanation
```

```
# SHAP Explanation
!pip install shap

import shap

# Create an explainer for the trained model
explainer = shap.Explainer(model, X_test)

# Get SHAP values for the test set
shap_values = explainer(X_test)

# Plot global feature importance
shap.summary_plot(shap_values, X_test)
```

```
Requirement already satisfied: shap in /usr/local/lib/python3.11/dist-packages (0.48.0)
Requirement already satisfied: numpy in /usr/local/lib/python3.11/dist-packages (from s
Requirement already satisfied: scipy in /usr/local/lib/python3.11/dist-packages (from s
Requirement already satisfied: scikit-learn in /usr/local/lib/python3.11/dist-packages
Requirement already satisfied: pandas in /usr/local/lib/python3.11/dist-packages (from
Requirement already satisfied: tqdm>=4.27.0 in /usr/local/lib/python3.11/dist-packages
Requirement already satisfied: packaging>20.9 in /usr/local/lib/python3.11/dist-package
Requirement already satisfied: slicer==0.0.8 in /usr/local/lib/python3.11/dist-packages
Requirement already satisfied: numba>=0.54 in /usr/local/lib/python3.11/dist-packages (
Requirement already satisfied: cloudpickle in /usr/local/lib/python3.11/dist-packages (
Requirement already satisfied: typing-extensions in /usr/local/lib/python3.11/dist-pack
Requirement already satisfied: llvmlite<0.44,>=0.43.0dev0 in /usr/local/lib/python3.11/
Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.11/dist
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.11/dist-packages
Requirement already satisfied: tzdata>=2022.7 in /usr/local/lib/python3.11/dist-package
Requirement already satisfied: joblib>=1.2.0 in /usr/local/lib/python3.11/dist-packages
Requirement already satisfied: threadpoolctl>=3.1.0 in /usr/local/lib/python3.11/dist-p
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.11/dist-packages (fro
```



What This Plot Shows Each dot is one instance (patient).

X-axis: SHAP value — how much that feature pushed the model toward malignant or benign.

Y-axis: Feature names (sorted by overall importance).