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Machine Learning Project

Breast Cancer Prediction Model

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Introduction:

Breast cancer is one of the most prevalent and life-threatening diseases affecting women worldwide. Early detection and accurate diagnosis are crucial in improving the chances of successful treatment and survival. The Breast Cancer Prediction Model is a machine learning-based application developed to aid in the early detection of breast cancer by predicting the likelihood of a patient having malignant (cancerous) or benign (non-cancerous) tumors based on their medical features.

This project leverages advanced classification algorithms to analyze medical data and provide reliable predictions, which can assist healthcare professionals in making informed decisions. The model is trained on the Breast Cancer Wisconsin (Diagnostic) dataset, a widely-used dataset in the medical research community that contains detailed measurements of cell nuclei present in breast cancer biopsies.

The predictive model is deployed within an easy-to-use web application, built using the Flask framework. This web interface allows users to input specific medical features related to breast cancer, and it returns predictions along with informative messages and visual aids to help interpret the results.

The Breast Cancer Prediction Model demonstrates the potential of machine learning in healthcare, showcasing how technology can be harnessed to enhance diagnostic accuracy and support early intervention strategies. By providing a user-friendly platform for breast cancer prediction, this project aims to contribute to the ongoing efforts to improve breast cancer outcomes and save lives through early detection.

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Technologies Used for the Breast Cancer Prediction Model

1. Python

- **Description**: A high-level programming language known for its readability and versatility.
- **Role**: Used for data processing, model training, and application development. Python's extensive libraries facilitate machine learning and web development.

2. Scikit-learn

- **Description**: A powerful machine learning library for Python.
- **Role**: Provides tools for building and training the predictive model. It includes various algorithms for classification, such as support vector machines, decision trees, and ensemble methods.

3. Flask

- **Description**: A lightweight web framework for Python.
- **Role**: Used to build the web application that allows users to interact with the predictive model. Flask handles web requests, routing, and rendering of HTML templates.

4. Pickle

- **Description**: A Python module for serializing and deserializing Python objects.
- **Role**: Used to save the trained machine learning model to a file (`model.pkl`) and load it into the application for making predictions.

5. HTML/CSS

- **Description**: Standard technologies for creating and styling web pages.
- **Role**: HTML is used for structuring the content of the web application, while CSS is used for styling and visual design, including layout and color schemes.

6. Bootstrap

- **Description**: A front-end framework for developing responsive and mobile-first websites.
- **Role**: Provides pre-designed components and styles to create a responsive and visually appealing user interface. Bootstrap simplifies the design process and ensures compatibility across various devices.

7. Jinja2

- **Description**: A templating engine for Python, used with Flask.
- **Role**: Allows dynamic generation of HTML pages by embedding Python code within HTML templates. It helps in rendering data and results from the Flask application into the web pages.

8. NumPy

- **Description**: A fundamental package for scientific computing with Python.
- **Role**: Provides support for large multi-dimensional arrays and matrices. Used to handle and manipulate the input features for prediction.

9. Pandas

- **Description**: A data manipulation and analysis library for Python.
- **Role**: Facilitates data cleaning, transformation, and analysis. It is particularly useful for preprocessing the dataset before training the model.

10. Matplotlib & Seaborn

- **Description**: Libraries for data visualization in Python.
- **Role**: Used to create plots and visualizations that help in analyzing the data and understanding model performance.

CODE AND OUTPUT

```
import numpy as np
import pandas as pd
```

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

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	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	texture_w
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	...	

5 rows × 33 columns

```
breast.shape
```

(569, 33)

```
breast['diagnosis'].value_counts()
```

diagnosis	count
B	357
M	212

dtype: int64

```
breast.info()
```

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```
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
```

```
breast.isnull().sum()
```

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	0
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

```
# Convert 'diagnosis' column to numerical
representation
breast['diagnosis'] = breast['diagnosis'].map({'M': 1,
'B': 0})

# Now calculate correlations
breast.corr()
```

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	id	diagnosis	radius_mean	texture_mean
id	1.000000	0.039769	0.074626	0.099770
diagnosis	0.039769	1.000000	0.730029	0.415185
radius_mean	0.074626	0.730029	1.000000	0.323782
texture_mean	0.099770	0.415185	0.323782	1.000000
perimeter_mean	0.073159	0.742636	0.997855	0.329533
area_mean	0.096893	0.708984	0.987357	0.321086
smoothness_mean	-0.012968	0.358560	0.170581	-0.023389
compactness_mean	0.000096	0.596534	0.506124	0.236702
concavity_mean	0.050080	0.696360	0.676764	0.302418

```
breast.drop('Unnamed: 32', axis=1, inplace=True)
```

```
breast.describe()
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000
mean	3.037183e+07	0.372583	14.127292	19.289649	91.969033	654.889104
std	1.250206e+08	0.483918	3.524049	4.301036	24.298981	351.914129
min	8.670000e+03	0.000000	6.981000	9.710000	43.790000	143.500000
25%	8.692180e+05	0.000000	11.700000	16.170000	75.170000	420.300000
50%	9.060240e+05	0.000000	13.370000	18.840000	86.240000	551.100000
75%	8.813129e+06	1.000000	15.780000	21.800000	104.100000	782.700000
max	9.113205e+08	1.000000	28.110000	39.280000	188.500000	2501.000000

8 rows × 32 columns

```
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
```

```
breast['diagnosis'] =
le.fit_transform(breast['diagnosis'])
```

Splitting Data into Training and Testing Sets

```
from sklearn.model_selection import train_test_split
# Split the data into training and testing sets
X = breast.drop('diagnosis', axis=1)
y = breast['diagnosis']
X_train, X_test, y_train, y_test = train_test_split(X,
y, test_size=0.2, random_state=42)
```

Feature Scaling

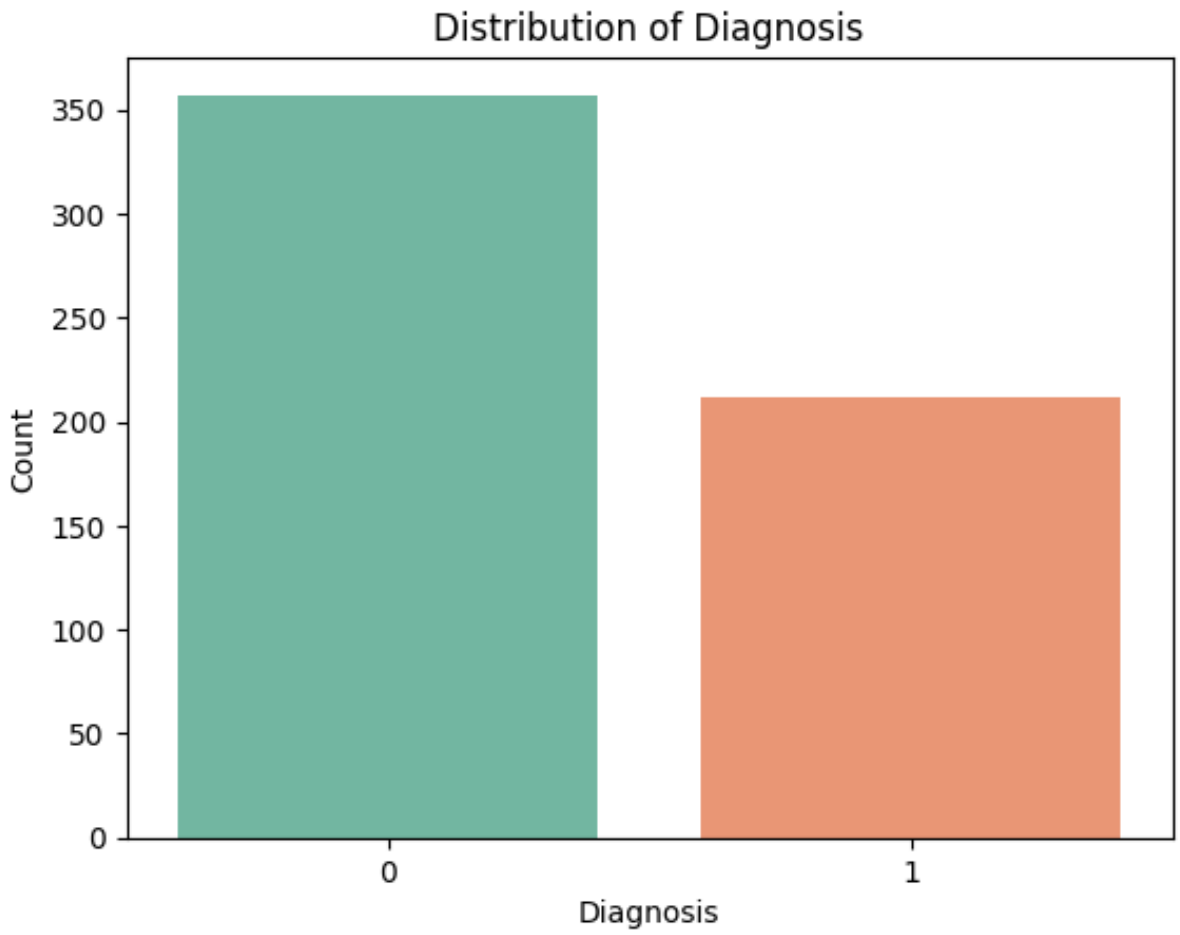
```
from sklearn.preprocessing import StandardScaler
# Scale the features
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

Exploratory Data Analysis (EDA)

```
import seaborn as sns
import matplotlib.pyplot as plt

# Assuming 'breast' is a DataFrame and 'diagnosis' is
the target variable
# Set a specific palette to differentiate the bars
sns.countplot(x=breast['diagnosis'], palette='Set2')
plt.title('Distribution of Diagnosis')
```

```
plt.xlabel('Diagnosis')
plt.ylabel('Count')
plt.show()
```




```
# Correlation Heatmap
plt.figure(figsize=(12, 10))
sns.heatmap(breast.corr(), annot=True, cmap='coolwarm',
fmt=".2f")
plt.title('Correlation Matrix')
plt.show()
```

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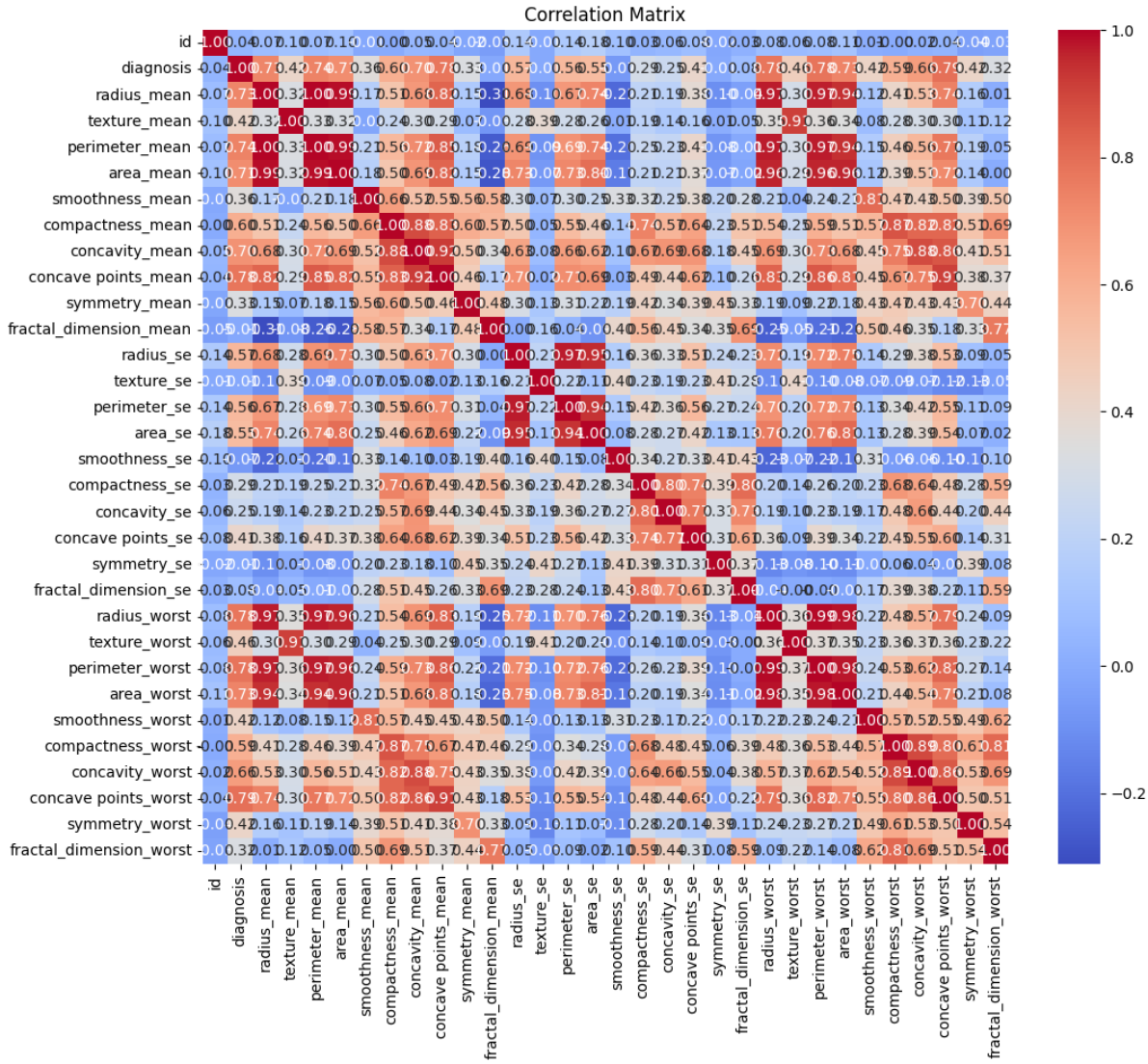
6861
Machine Learning Project




```
# Box Plots for Selected Features
features_to_plot = ['radius_mean', 'texture_mean',
'perimeter_mean', 'area_mean', 'smoothness_mean']
plt.figure(figsize=(15, 10))
for i, feature in enumerate(features_to_plot, 1):
  plt.subplot(2, 3, i)
```

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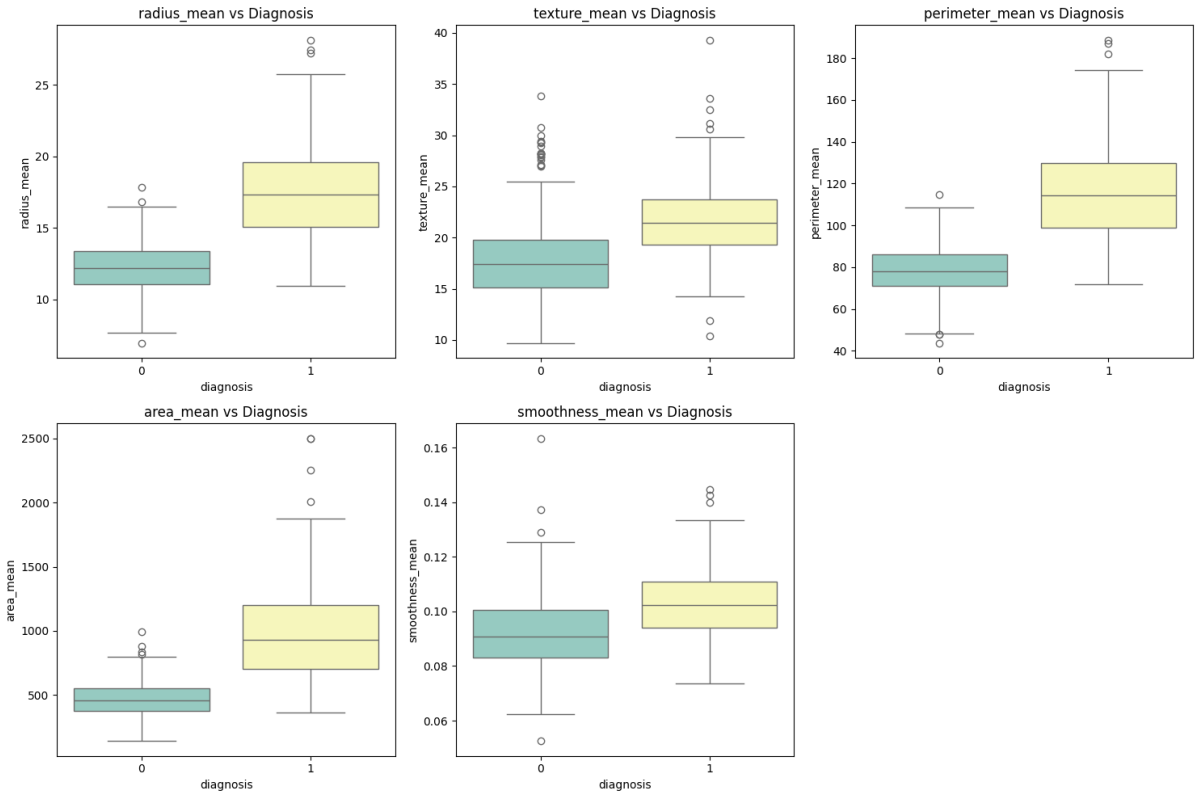
```
  sns.boxplot(x='diagnosis', y=feature, data=breast,
palette='Set3')
  plt.title(f'{feature} vs Diagnosis')
plt.tight_layout()
plt.show()
```




```
# Pairplot for Selected Features
selected_features = ['radius_mean', 'texture_mean',
'perimeter_mean', 'area_mean']
sns.pairplot(breast[selected_features + ['diagnosis']],
hue='diagnosis', palette='husl')
plt.show()
```

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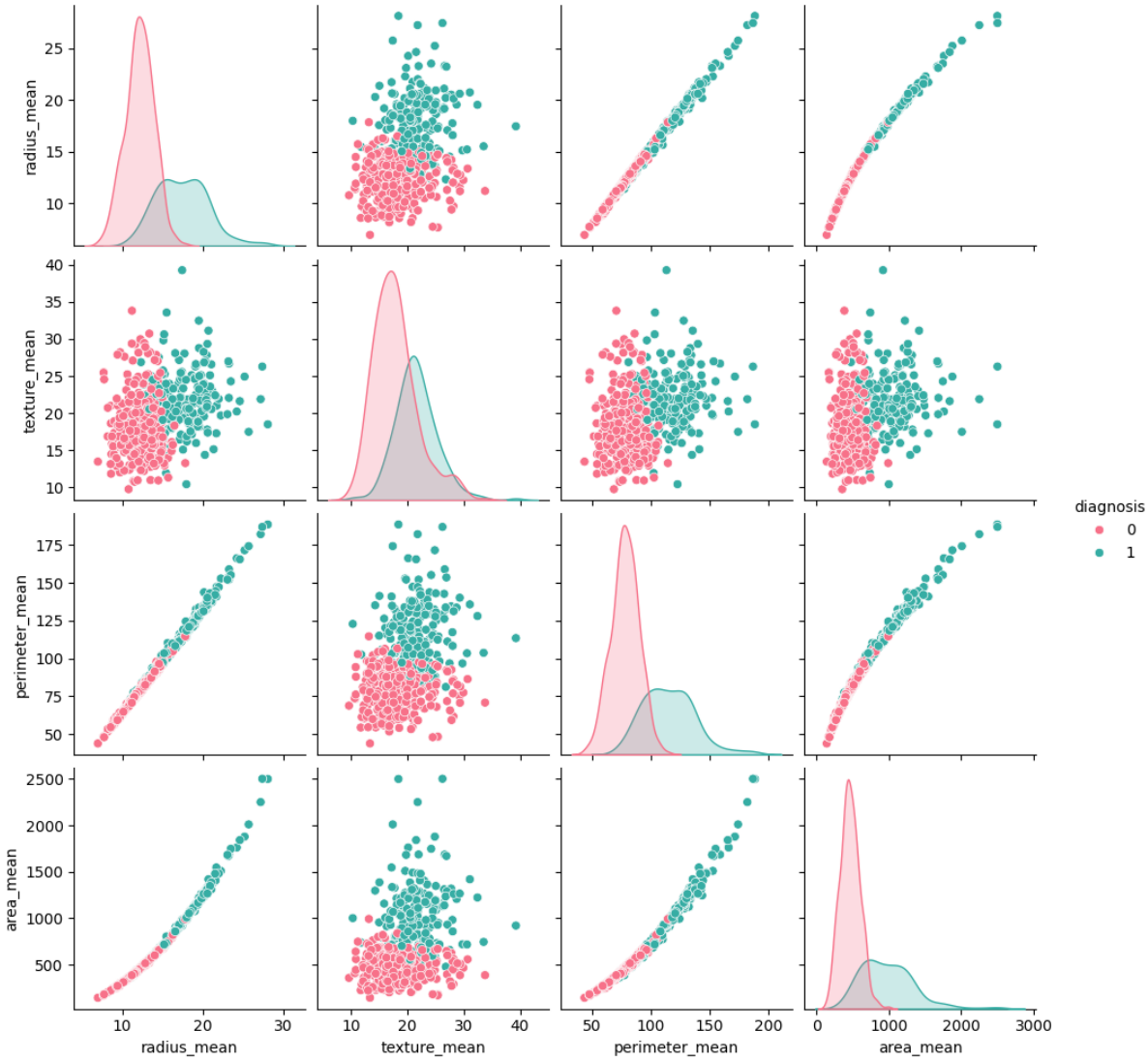


```
# Visualize the correlation matrix
breast.corr()
```

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	id	diagnosis	radius_mean	texture_mean
id	1.000000	0.039769	0.074626	0.099770
diagnosis	0.039769	1.000000	0.730029	0.415185
radius_mean	0.074626	0.730029	1.000000	0.323782
texture_mean	0.099770	0.415185	0.323782	1.000000
perimeter_mean	0.073159	0.742636	0.997855	0.329533
area_mean	0.096893	0.708984	0.987357	0.321086
smoothness_mean	-0.012968	0.358560	0.170581	-0.023389
compactness_mean	0.000096	0.596534	0.506124	0.236702

Training Model

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score

# Train the logistic regression model
lr = LogisticRegression()
lr.fit(X_train, y_train)

# Evaluate the performance on the testing set
y_pred_lr = lr.predict(X_test)
accuracy_lr = accuracy_score(y_test, y_pred_lr)
print('Accuracy:', accuracy_lr)
```

```
Accuracy: 0.9736842105263158
```

```
input_text = (-0.23717126, -0.64487029, -0.11382239, -
0.57427777, -0.60294971,
```

```
    1.0897546, 0.91543814, 0.41448279, 0.09311633,
1.78465117,
    2.11520208, 0.28454765, -0.31910982, 0.2980991,
0.01968238,
    -0.47096352, 0.45757106, 0.28733283, -0.23125455,
0.26417944,
    0.66325388, 0.12170193, 0.42656325, 0.36885508,
0.02065602,
    1.39513782, 2.0973271, 2.01276347, 0.61938913,
2.9421769,
    3.15970842)
np_df = np.asarray(input_text)
# Use 'lr' instead of 'lg' to make the prediction
prediciont = lr.predict(np_df.reshape(1,-1))
if prediciont[0] == 1:
    print("Cancrous")
else:
    print("Not Cancrous")
```

```
Cancrous
```

Prediction System

```
import numpy as np

input_text = (-0.23717126, -0.64487029, -0.11382239, -
0.57427777, -0.60294971,
        1.0897546 ,  0.91543814,  0.41448279,
0.09311633,  1.78465117,
        2.11520208,  0.28454765, -0.31910982,
0.2980991 ,  0.01968238,
       -0.47096352,  0.45757106,  0.28733283, -
0.23125455,  0.26417944,
        0.66325388,  0.12170193,  0.42656325,
0.36885508,  0.02065602,
```

```
        1.39513782,  2.0973271 ,  2.01276347,
0.61938913,  2.9421769 ,
        3.15970842)
np_df = np.asarray(input_text)
pred = lr.predict(np_df.reshape(1,-1))
if pred[0] == 1:
    print("Cancrous")
else:
    print("Not Cancrous")
```

Saving a Machine Learning Model with Pickle

```
import pickle


pickle.dump(lr, open('model.pkl','wb'))  # Now pickle
the 'lg' object
```

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FLASK CODE

App.py

```
from flask import Flask, render_template, request
import numpy as np
import pandas as pd
import pickle

# loading model
model = pickle.load(open('model.pkl', 'rb'))

# flask app
app = Flask(__name__)


@app.route('/')
def home():
    return render_template('index.html')


@app.route('/predict', methods=['POST'])
def predict():
    features = request.form['feature']
    features = features.split(',')
    np_features = np.asarray(features, dtype=np.float32)

    # prediction
    pred = model.predict(np_features.reshape(1, -1))
    message = ['Cancrouse' if pred[0] == 1 else 'Not Cancrouse']
    # print(message[0])
    return render_template('index.html', message=message)


if __name__ == '__main__':
    app.run(debug=True)
```

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INDEX.HTML

```
<!doctype html>
<html lang="en">
  <head>
    <meta charset="utf-8">
    <meta name="viewport" content="width=device-width, initial-scale=1">
    <title>CA 2 FOR MACHINE LEARNING 6861</title>
    <link href="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0-
alpha3/dist/css/bootstrap.min.css" rel="stylesheet" integrity="sha384-
KK94CHFLLe+nY2dmCWGMq91rCGa5gtU4mk92HdvYe+M/SXH301p5ILy+dN9+nJOZ"
crossorigin="anonymous">
  </head>
  <body style="background:black; color:white;">

  <div class="container my-3 mt-3">
      <h1 style="text-align:center">Breast Cancer Prediction Model
(6861)</h1>
      <img style="width:100%; height:160px" src="{{ url_for('static',
filename='images.jpg') }}" alt="My Image">
          <form action="/predict" method="POST">
            <div class="mb-3">
              <label for="text" class="form-label">Input Breast Cancer
Features</label>
              <input type="text" class="form-control" id="number"
name="feature" aria-describedby="emailHelp">
            </div>
            <button type="submit" class="btn btn-primary">Predict</button>
      </form>

         {% for i in message %}
      <p>{{i}}</p>
          {% if i=='Not Cancrouse' %}
            <div class="card my-3 mt-3" style="width: 18rem;">
              <img src="{{url_for('static', filename='img2.jpg')}}"
class="card-img-top" alt="...">
              <div class="card-body">
                <h5 class="card-title">Not Cancrouse</h5>
                <p class="card-text">Don't Worry You don't have Breast
Cancer Disease, Enjoy your life.</p>
              </div>
            </div>
          {% else %}
            <div class="card my-3 mt-3" style="width: 18rem;">
              <img src="{{url_for('static', filename='img1.jpg')}}"
class="card-img-top" alt="...">
              <div class="card-body">
                <h5 class="card-title">Cancrouse</h5>
                <p class="card-text">Alert You have a Breast Cancer
Disease, check yourself by doctor.</p>
              </div>
            </div>
          {% endif %}
        {% endfor %}



</div>
```

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```
    <script
src="https://cdn.jsdelivr.net/npm/@popperjs/core@2.11.7/dist/umd/popper.min
.js" integrity="sha384-
zYPOMqeu1DAVkHiLqWBUTcbYfZ8osu1Nd6Z89ify25QV9guujx43ITvfi12/QExE"
crossorigin="anonymous"></script>
<script src="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0-
alpha3/dist/js/bootstrap.min.js" integrity="sha384-
Y4oOpwW3duJdCWv5ly8SCFYWqFDsfob/3GkgExXKV4idmbt98QcxXYs9UoXAB7BZ"
crossorigin="anonymous"></script>
    <script src="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0-
alpha3/dist/js/bootstrap.bundle.min.js" integrity="sha384-
ENjdO4Dr2bkBIFxQpeoTz1HIcje39Wm4jDKdf19U8gI4ddQ3GYNS7NTKfAdVQSZe"
crossorigin="anonymous"></script>
  </body>
</html>
```

Output

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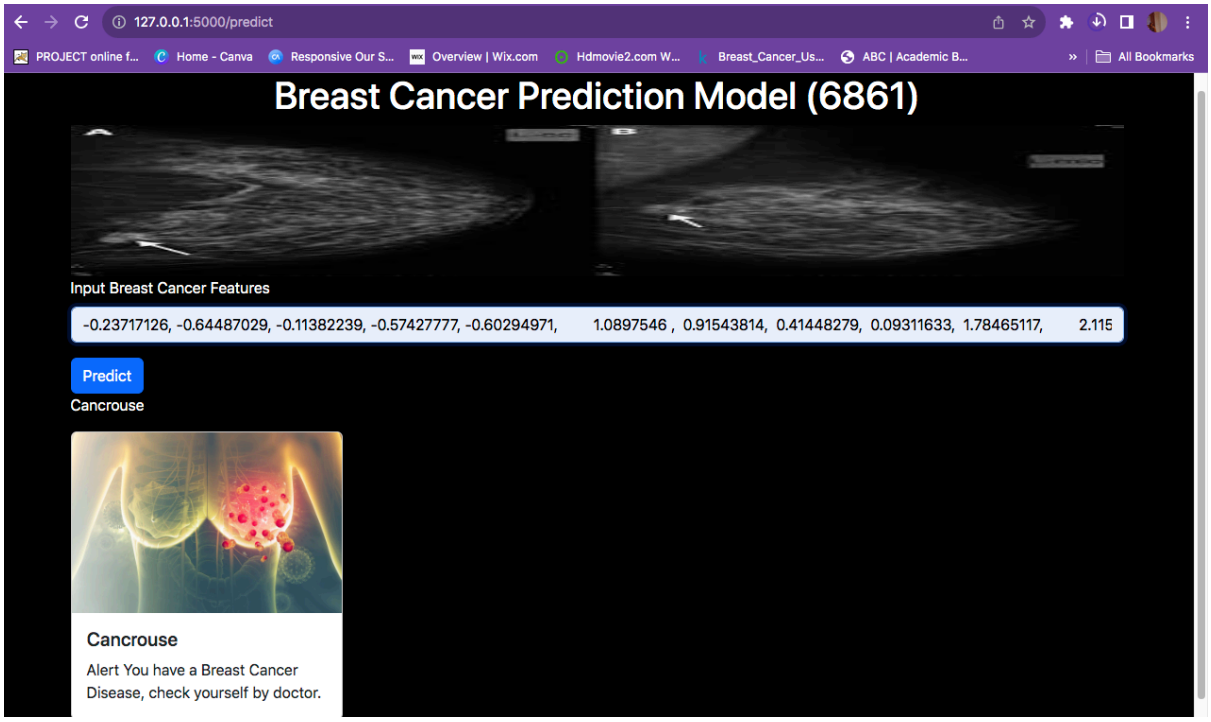

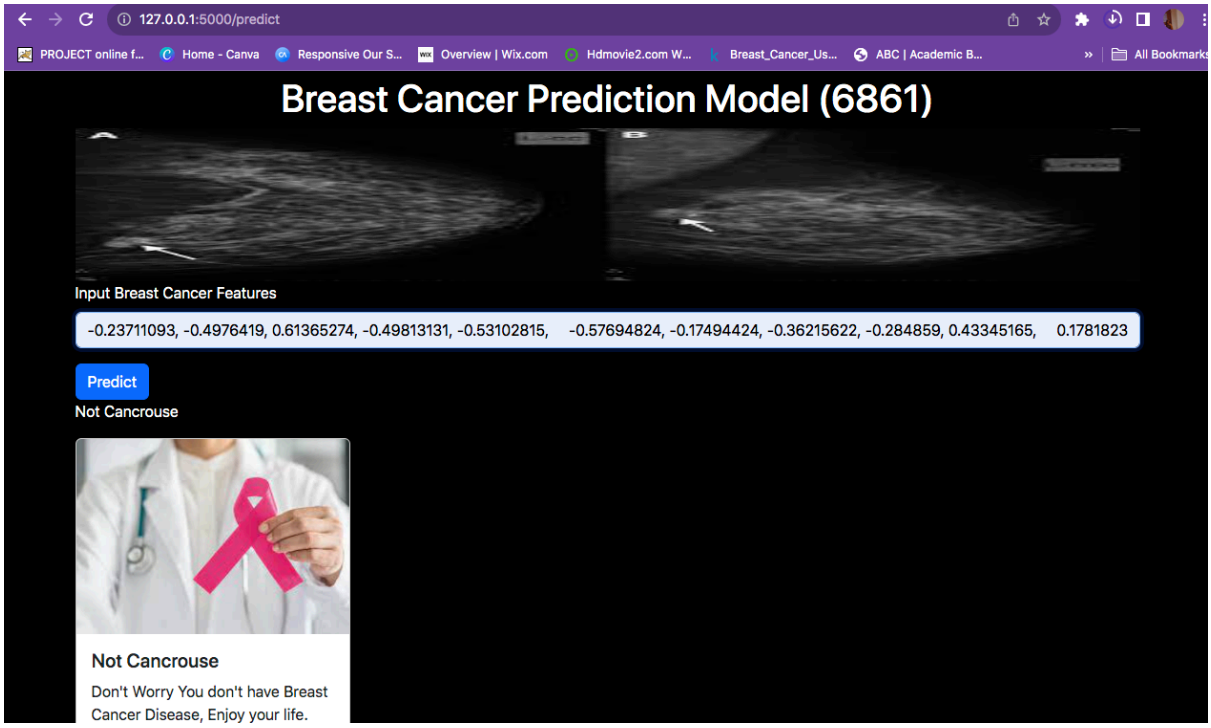

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Conclusion:

The cancer prediction system employs logistic regression to assess key features and predict the likelihood of cancer presence. Achieving an accuracy of approximately 97.37%, the model demonstrates high reliability and precision in generating predictions from input data. This robust performance highlights its potential as an effective tool for early cancer detection, aiding in timely diagnosis and intervention. The system's accuracy underscores its capability to support healthcare professionals in making informed decisions, ultimately contributing to improved patient outcomes and proactive healthcare management.