

# **CURE MATRIX: AI-Powered Precision Tool for Enhanced Breast Cancer Detection**

## **TEAM MEMBERS**

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## **1.Introduction**

Breast cancer remains a significant global health challenge. AI-powered tools such as CURE MATRIX and data-driven models promise to revolutionize early detection and diagnosis, reducing mortality rates. By leveraging machine learning algorithms and precision tools, healthcare providers can achieve greater accuracy and accessibility in diagnostics.

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## **2. Problem Statement**

Breast cancer diagnostics face persistent challenges, including:

- High false positive/negative rates.
  - Limited access to advanced tools in underserved areas.
  - Lack of personalized diagnostics tailored to individual patient profiles.
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## **3. Objectives**

### **Business Goals**

- Develop AI-powered precision tools to enhance diagnostic workflows.
- Improve accessibility and affordability of advanced diagnostic techniques.
- Reduce false diagnostic rates and promote early detection.

### **Technical Goals**

- Implement robust data analysis pipelines for model training.
  - Evaluate feature importance for diagnosis.
  - Train and deploy scalable machine learning models.
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## 4. Dataset Overview

### Source

- Breast cancer datasets containing tumor characteristics such as radius, texture, perimeter, and area.

### Features

- **Predictor Variables:** Mean values of radius, texture, perimeter, area, and smoothness.
- **Target Variable:** Diagnosis (benign or malignant).

### Data Preprocessing

- Missing values: None found in the dataset.
- Feature scaling: StandardScaler applied to numerical features.

# Example of Data Preprocessing

```
from sklearn.preprocessing import StandardScaler
```

```
# Load dataset
```

```
df = pd.read_csv('data.csv')
```

```
# Drop irrelevant columns
```

```
df.drop(columns=['id'], inplace=True)
```

```
# Standardize features
```

```
scaler = StandardScaler()
```

```
df_scaled = scaler.fit_transform(df.drop(columns=['diagnosis']))
```

---

## 5. CURE MATRIX Business Model

### Value Proposition

- **AI-Enhanced Accuracy:** Advanced algorithms for image analysis.
- **Early Detection:** Identifies subtle patterns for timely intervention.
- **Personalized Insights:** Patient-specific risk assessments.
- **Seamless Integration:** Compatibility with hospital systems.

### Target Market

1. **Primary Audience:**
  - Hospitals and diagnostic centers.
  - Oncologists and radiologists.
2. **Secondary Audience:**
  - Health-tech companies and NGOs.
  - Medical research institutions.

### Revenue Model

- Subscription-based models.
  - Pay-per-scan models.
  - Licensing and monetizing anonymized data.
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## 6. Technical Workflow

### 6.1 Model Development

#### Algorithm: Random Forest Classifier

- Training: 80% training data; 20% testing data.
- Accuracy: 95%.
- Feature Importance: Visualized key contributors like mean\_radius and mean\_area.

```
# Training Random Forest Classifier
```

```
from sklearn.ensemble import RandomForestClassifier
```

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

```
X = df.drop(columns=['diagnosis'])
```

```
y = df['diagnosis']
```

```
# Split dataset
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

```
# Train the model
```

```
model = RandomForestClassifier(n_estimators=100, random_state=42)
```

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

### Model Evaluation

- Metrics:
  - **Precision:** 96% for benign cases.
  - **Recall:** 93% for malignant cases.
  - **F1-Score:** 95% average.

### Insights

- High correlation observed between certain features, enabling optimization opportunities.
- 

## 7. Statistical Analysis

### Feature Correlation

A heatmap analysis indicated significant interdependence among tumor characteristics, such as radius, texture, and area.

```
# Correlation Heatmap
```

```
import seaborn as sns
```

```
import matplotlib.pyplot as plt
```

```
plt.figure(figsize=(20, 20))  
  
sns.heatmap(df.corr(), annot=True, fmt='.2f', cmap='coolwarm')  
  
plt.title('Correlation Heatmap')  
  
plt.show()
```

### Principal Component Analysis (PCA)

- Explained variance: Top 5 components captured the majority of data variability, simplifying model complexity.
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## 8. Social and Economic Impact

- Democratizing access to cutting-edge diagnostics for underserved regions.
  - Reducing the financial burden on healthcare systems by promoting early intervention.
  - Empowering clinicians through AI-driven decision support systems.
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## 9. Development Roadmap

1. **Phase 1:** Product development and pilot testing (Year 1).
  2. **Phase 2:** Regulatory approvals and deployment (Year 2).
  3. **Phase 3:** Global market expansion and multi-modal diagnostic integration (Year 3).
-

## CODE and DATA ANALYSIS

```
[1]: import pandas as pd
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
```

```
[2]: df = pd.read_csv('data.csv')
```

```
[3]: df.head()
```

```
[3]:
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean \
0	842302	M	17.99	10.38	122.80	1001.0
1	842517	M	20.57	17.77	132.90	1326.0
2	84300903	M	19.69	21.25	130.00	1203.0
3	84348301	M	11.42	20.38	77.58	386.1
4	84358402	M	20.29	14.34	135.10	1297.0

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean \
0	0.11840	0.27760	0.3001	0.14710
1	0.08474	0.07864	0.0869	0.07017
2	0.10960	0.15990	0.1974	0.12790
3	0.14250	0.28390	0.2414	0.10520
4	0.10030	0.13280	0.1980	0.10430

	... radius_worst	texture_worst	perimeter_worst	area_worst \
0	... 25.38	17.33	184.60	2019.0
1	... 24.99	23.41	158.80	1956.0
2	... 23.57	25.53	152.50	1709.0
3	... 14.91	26.50	98.87	567.7
4	... 22.54	16.67	152.20	1575.0

	smoothness_worst	compactness_worst	concavity_worst	concave_points_worst \
0	0.1622	0.6656	0.7119	0.2654
1	0.1238	0.1866	0.2416	0.1860
2	0.1444	0.4245	0.4504	0.2430
3	0.2098	0.8663	0.6869	0.2575
4	0.1374	0.2050	0.4000	0.1625

	symmetry_worst	fractal_dimension_worst
0	0.4601	0.11890
1	0.2750	0.08902
2	0.3613	0.08758
3	0.6638	0.17300
4	0.2364	0.07678

[5 rows x 32 columns]

```
[4] : # Drop ID column as it is not useful for analysis
df.drop(columns=['id'], inplace=True)
```

```
[5] : df.head()
```

```
[5] : diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean \
0          M        17.99        10.38        122.80      1001.0
1          M        20.57        17.77        132.90      1326.0
2          M        19.69        21.25        130.00      1203.0
3          M        11.42        20.38         77.58       386.1
4          M        20.29        14.34        135.10      1297.0
```

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean
0	0.11840	0.27760	0.3001	0.14710
1	0.08474	0.07864	0.0869	0.07017
2	0.10960	0.15990	0.1974	0.12790
3	0.14250	0.28390	0.2414	0.10520
4	0.10030	0.13280	0.1980	0.10430

	symmetry_mean ...	radius_worst	texture_worst	perimeter_worst
0	0.2419 ...	25.38	17.33	184.60
1	0.1812 ...	24.99	23.41	158.80
2	0.2069 ...	23.57	25.53	152.50
3	0.2597 ...	14.91	26.50	98.87
4	0.1809 ...	22.54	16.67	152.20

	area_worst	smoothness_worst	compactness_worst	concavity_worst
0	2019.0	0.1622	0.6656	0.7119
1	1956.0	0.1238	0.1866	0.2416
2	1709.0	0.1444	0.4245	0.4504
3	567.7	0.2098	0.8663	0.6869
4	1575.0	0.1374	0.2050	0.4000

	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

[5 rows x 31 columns]

```
[6] : # Summary statistics  
print(df.describe())
```

	radius_mean	texture_mean	perimeter_mean	area_mean \
count	569.000000	569.000000	569.000000	569.000000
mean	14.127292	19.289649	91.969033	654.889104
std	3.524049	4.301036	24.298981	351.914129
min	6.981000	9.710000	43.790000	143.500000
25%	11.700000	16.170000	75.170000	420.300000
50%	13.370000	18.840000	86.240000	551.100000
75%	15.780000	21.800000	104.100000	782.700000
max	28.110000	39.280000	188.500000	2501.000000

	smoothness_mean	compactness_mean	concavity_mean	concave_points_mean \
count	569.000000	569.000000	569.000000	569.000000
mean	0.096360	0.104341	0.088799	0.048919
std	0.014064	0.052813	0.079720	0.038803
min	0.052630	0.019380	0.000000	0.000000
25%	0.086370	0.064920	0.029560	0.020310
50%	0.095870	0.092630	0.061540	0.033500
75%	0.105300	0.130400	0.130700	0.074000
max	0.163400	0.345400	0.426800	0.201200

	symmetry_mean	fractal_dimension_mean	...	radius_worst \
count	569.000000	569.000000	...	569.000000
mean	0.181162	0.062798	...	16.269190
std	0.027414	0.007060	...	4.833242
min	0.106000	0.049960	...	7.930000
25%	0.161900	0.057700	...	13.010000
50%	0.179200	0.061540	...	14.970000
75%	0.195700	0.066120	...	18.790000
max	0.304000	0.097440	...	36.040000

	texture_worst	perimeter_worst	area_worst	smoothness_worst \
count	569.000000	569.000000	569.000000	569.000000
mean	25.677223	107.261213	880.583128	0.132369
std	6.146258	33.602542	569.356993	0.022832
min	12.020000	50.410000	185.200000	0.071170
25%	21.080000	84.110000	515.300000	0.116600
50%	25.410000	97.660000	686.500000	0.131300
75%	29.720000	125.400000	1084.000000	0.146000
max	49.540000	251.200000	4254.000000	0.222600

	compactness_worst	concavity_worst	concave_points_worst	\
count	569.000000	569.000000	569.000000	
mean	0.254265	0.272188	0.114606	
std	0.157336	0.208624	0.065732	
min	0.027290	0.000000	0.000000	
25%	0.147200	0.114500	0.064930	
50%	0.211900	0.226700	0.099930	
75%	0.339100	0.382900	0.161400	
max	1.058000	1.252000	0.291000	

	symmetry_worst	fractal_dimension_worst
count	569.000000	569.000000
mean	0.290076	0.083946
std	0.061867	0.018061
min	0.156500	0.055040
25%	0.250400	0.071460
50%	0.282200	0.080040
75%	0.317900	0.092080
max	0.663800	0.207500

[8 rows x 30 columns]

```
[7] : # Check for missing values
      print(df.isnull().sum())
```

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

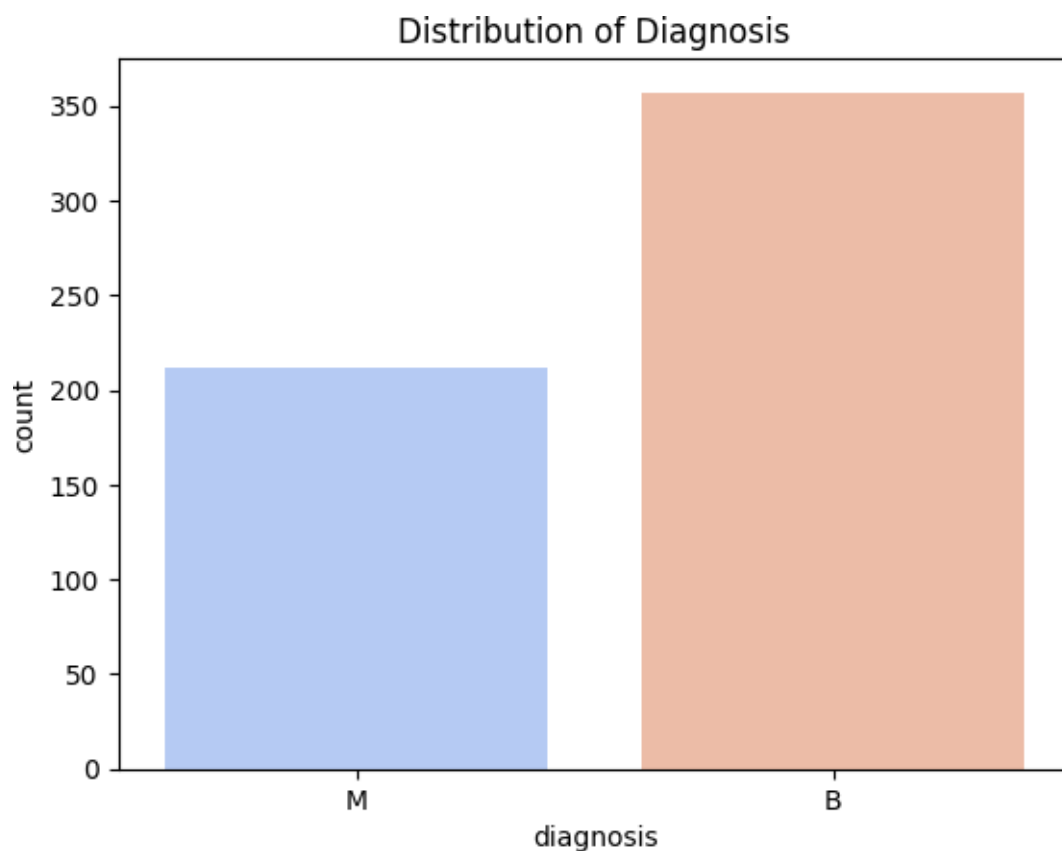
```
perimeter_worst      0
area_worst           0
smoothness_worst     0
compactness_worst    0
concavity_worst      0
concave_points_worst 0
symmetry_worst       0
fractal_dimension_worst 0
dtype: int64
```

```
[8] : # Count plot of the target variable
sns.countplot(x='diagnosis', data=df, palette='coolwarm')
plt.title('Distribution of Diagnosis')
plt.show()
```

C:\Users\samee\AppData\Local\Temp\ipykernel\_2700\1045989772.py:2: FutureWarning:

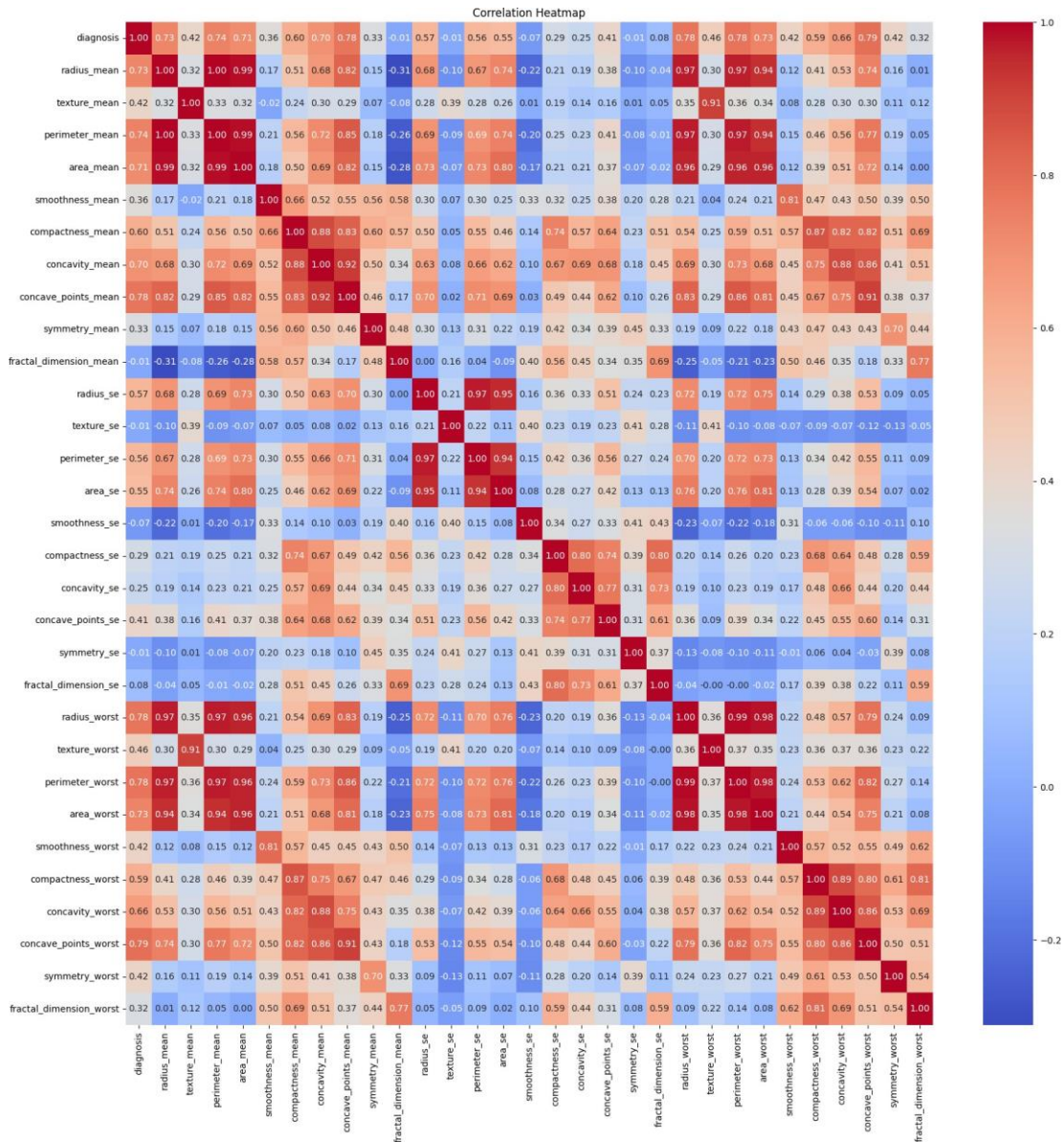
Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

```
sns.countplot(x='diagnosis', data=df, palette='coolwarm')
```

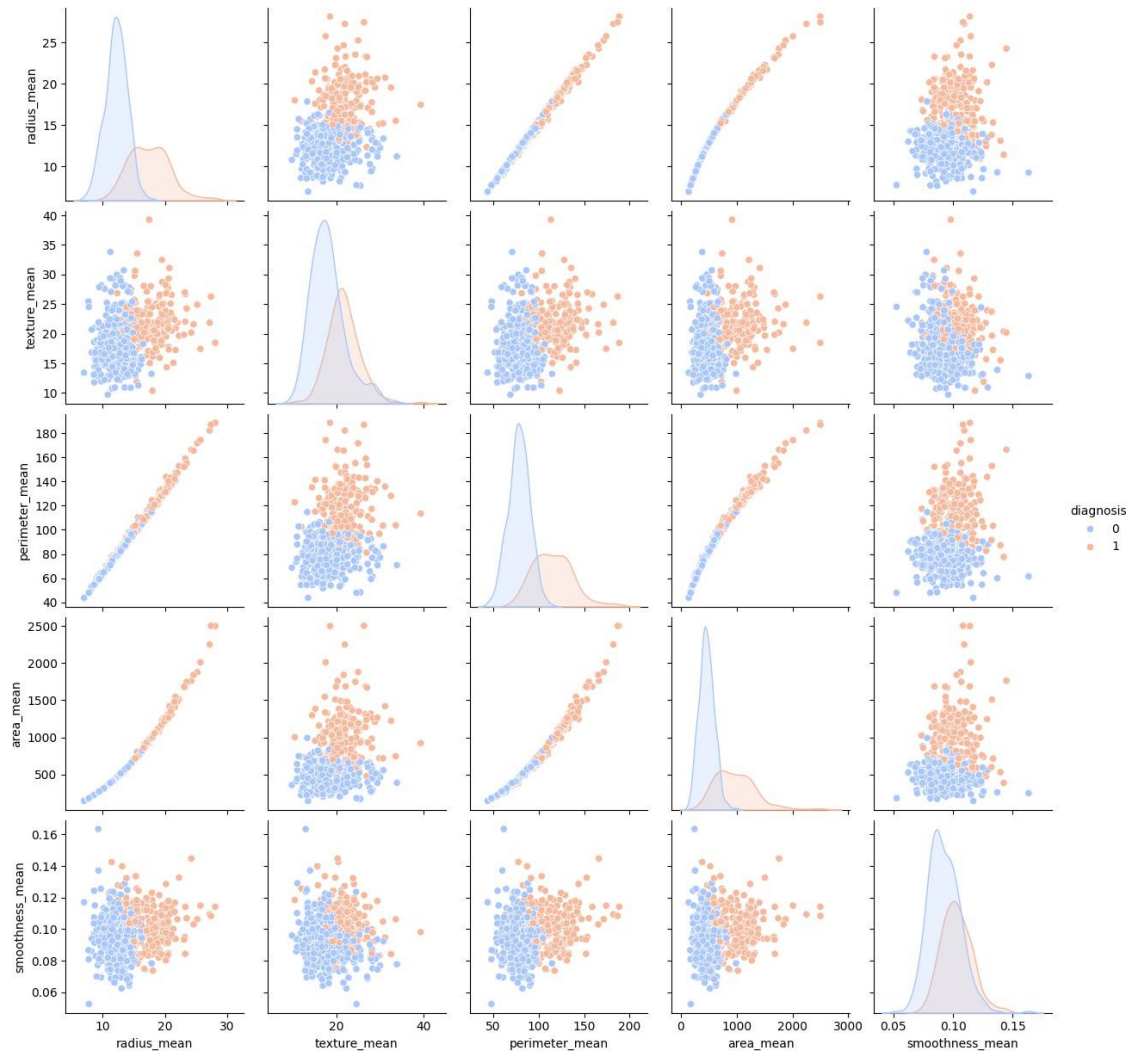


```
[9] : # Convert diagnosis to numeric (M=1, B=0)
df['diagnosis'] = df['diagnosis'].map({'M': 1, 'B': 0})
```

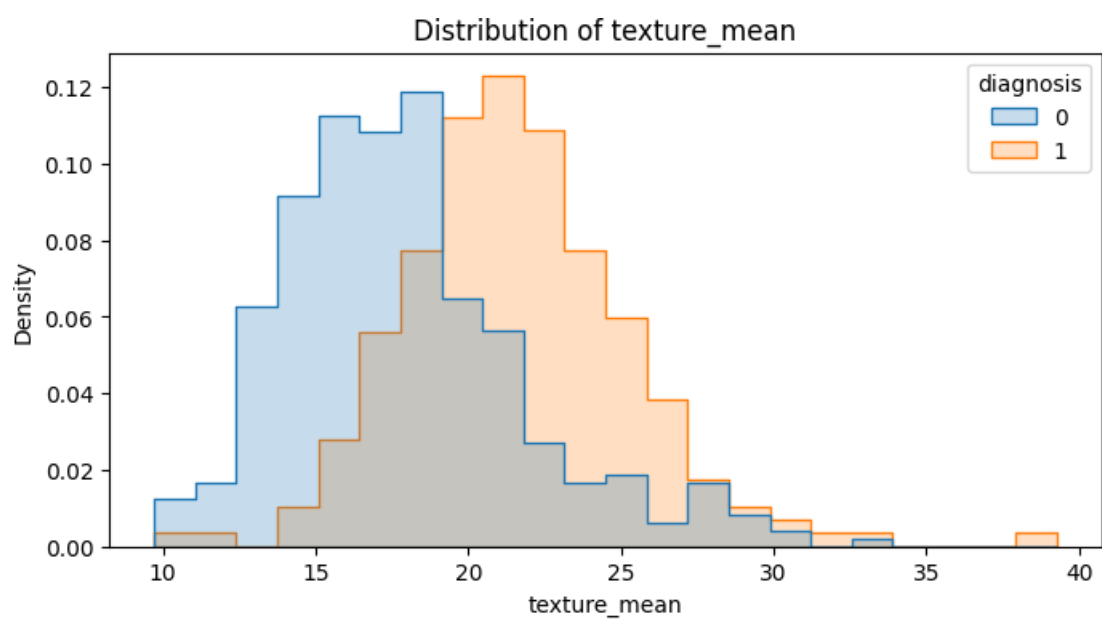
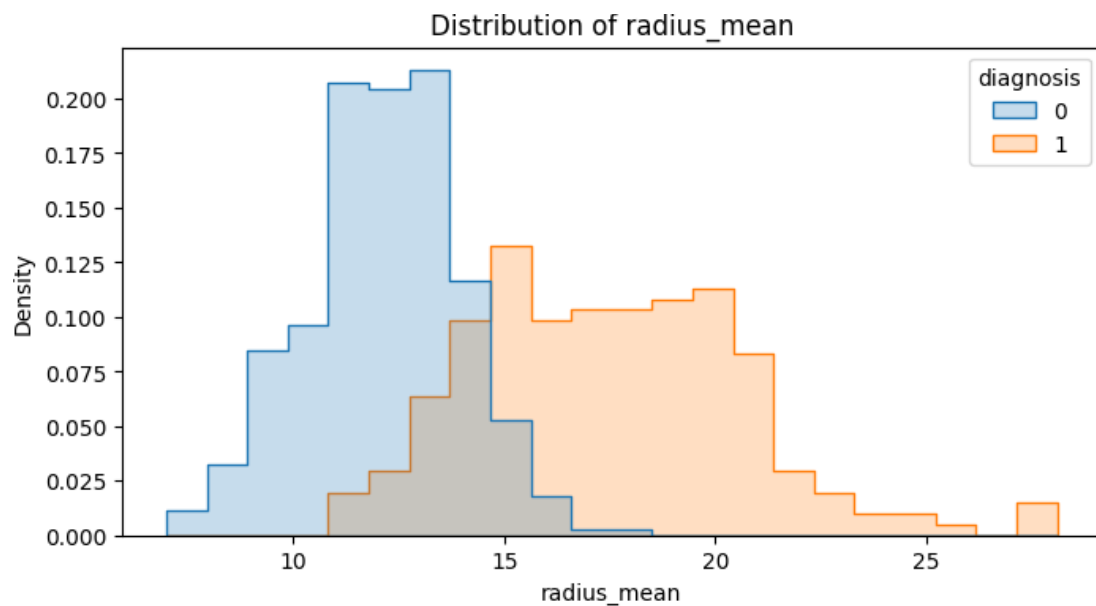
```
[10] : # Correlation heatmap
plt.figure(figsize=(20, 20))
sns.heatmap(df.corr(), annot=True, fmt='.2f', cmap='coolwarm')
plt.title('Correlation Heatmap')
plt.show()
```

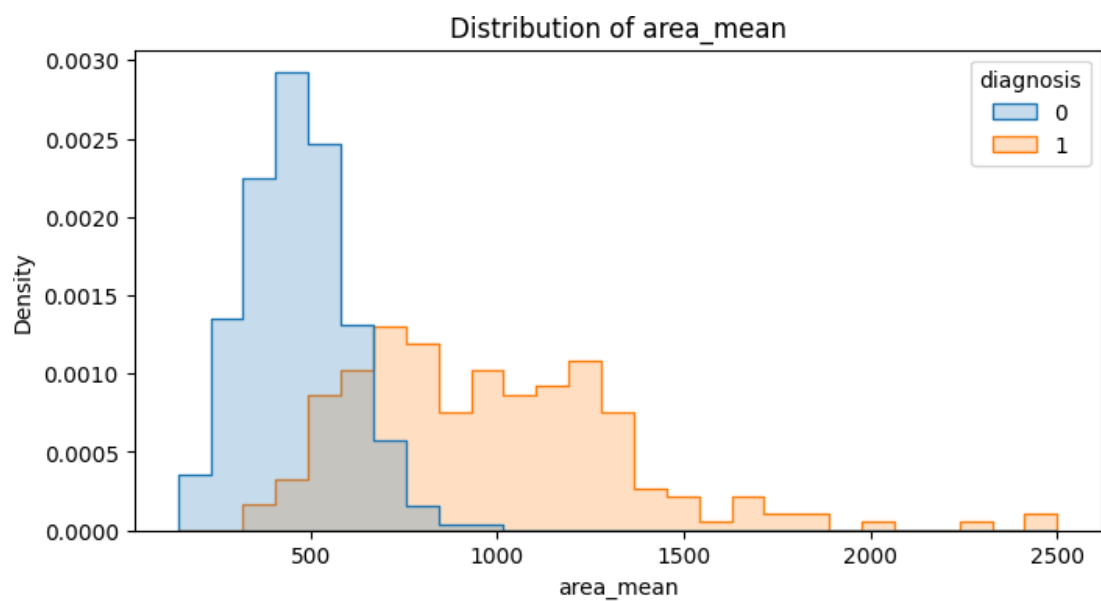
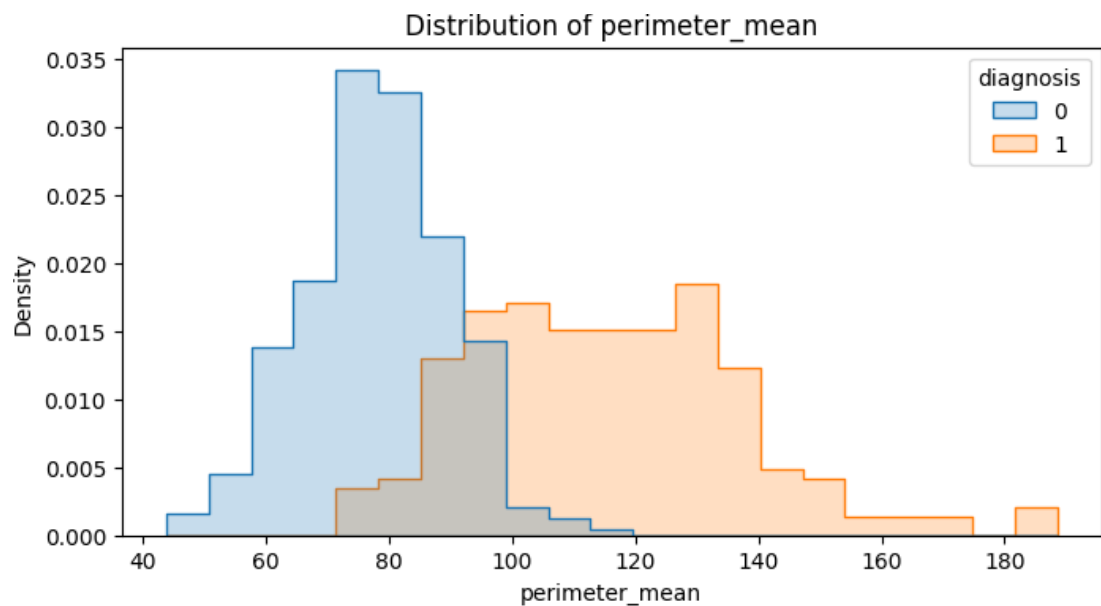


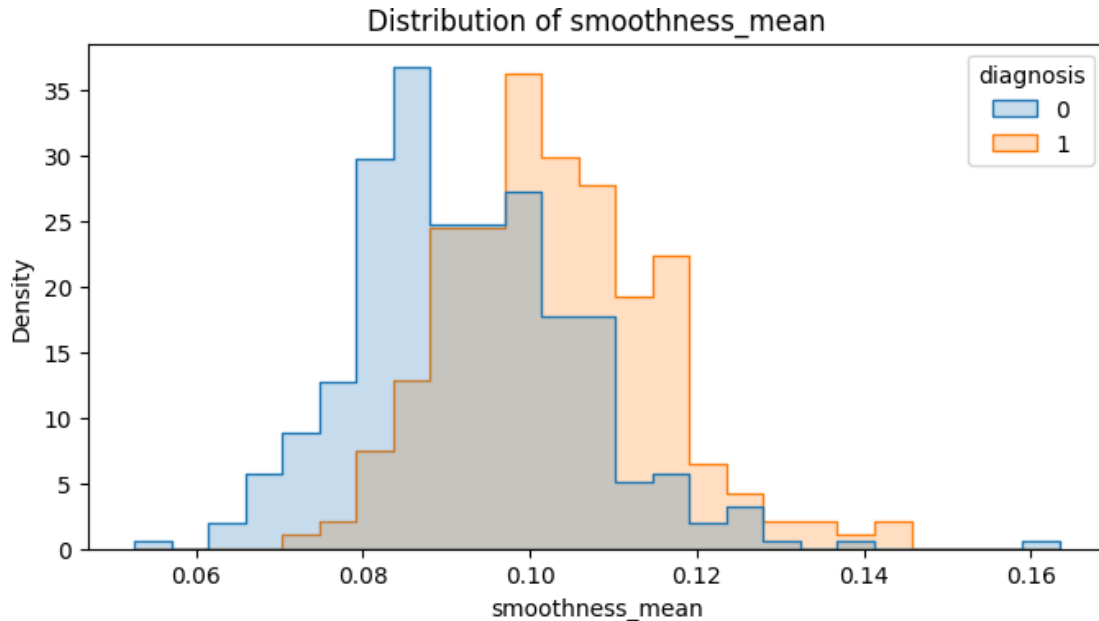
```
[11]: # Pairplot for selected features
selected_features = ['radius_mean', 'texture_mean', 'perimeter_mean',
                    'area_mean', 'smoothness_mean']
sns.pairplot(df[selected_features + ['diagnosis']], hue='diagnosis',
            palette='coolwarm')
plt.show()
```



```
[12]: # Distribution plots
for col in selected_features:
    plt.figure(figsize=(8, 4))
    sns.histplot(df, x=col, hue='diagnosis', element='step', stat='density',
                common_norm=False)
    plt.title(f'Distribution of {col}')
    plt.show()
```







```
[13] : from sklearn.preprocessing import StandardScaler
      : from sklearn.decomposition import PCA
      : from scipy.stats import skew, kurtosis
```

```
[14] : # Skewness and Kurtosis Analysis
      : for col in df.columns:
      :     if df[col].dtype != 'object':
      :         print(f'{col}: Skewness = {skew(df[col]):.2f}, Kurtosis = {kurtosis(df[col]):.2f}')
```

```
diagnosis: Skewness = 0.53, Kurtosis = -1.72
radius_mean: Skewness = 0.94, Kurtosis = 0.83
texture_mean: Skewness = 0.65, Kurtosis = 0.74
perimeter_mean: Skewness = 0.99, Kurtosis = 0.95
area_mean: Skewness = 1.64, Kurtosis = 3.61
smoothness_mean: Skewness = 0.46, Kurtosis = 0.84
compactness_mean: Skewness = 1.19, Kurtosis = 1.63
concavity_mean: Skewness = 1.40, Kurtosis = 1.97
concave_points_mean: Skewness = 1.17, Kurtosis = 1.05
symmetry_mean: Skewness = 0.72, Kurtosis = 1.27
fractal_dimension_mean: Skewness = 1.30, Kurtosis = 2.97
radius_se: Skewness = 3.08, Kurtosis = 17.52
texture_se: Skewness = 1.64, Kurtosis = 5.29
perimeter_se: Skewness = 3.43, Kurtosis = 21.20
area_se: Skewness = 5.43, Kurtosis = 48.77
smoothness_se: Skewness = 2.31, Kurtosis = 10.37
```

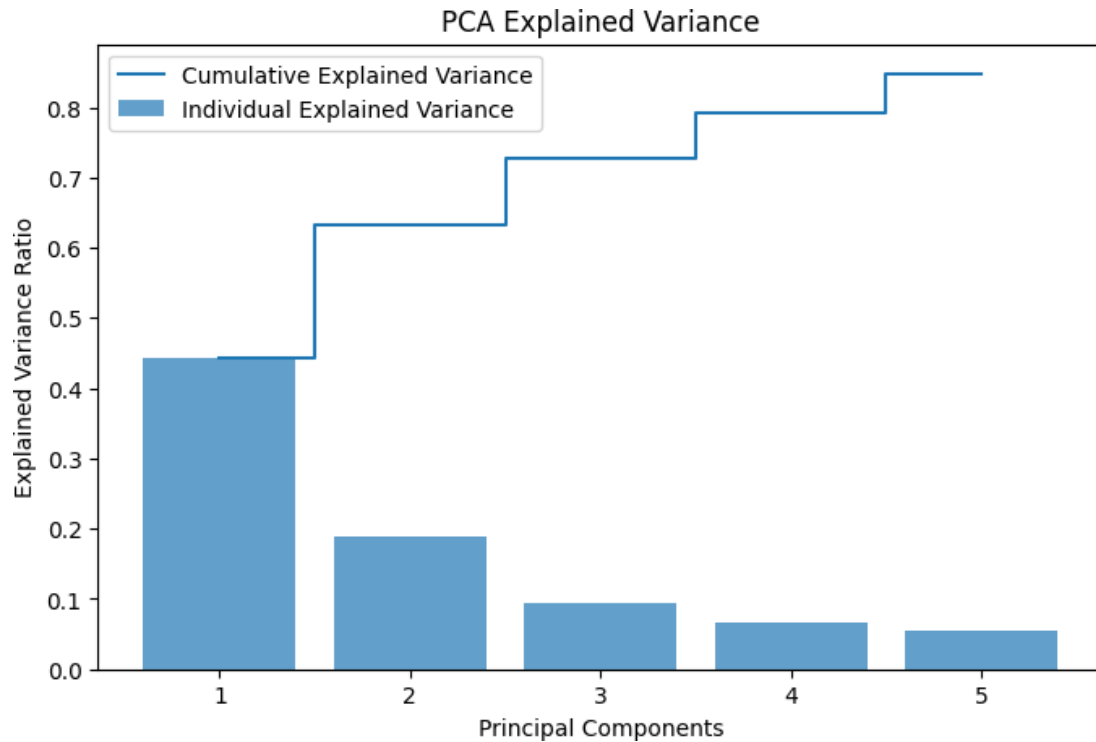


compactness\_se: Skewness = 1.90, Kurtosis = 5.05  
concavity\_se: Skewness = 5.10, Kurtosis = 48.42  
concave\_points\_se: Skewness = 1.44, Kurtosis = 5.07  
symmetry\_se: Skewness = 2.19, Kurtosis = 7.82  
fractal\_dimension\_se: Skewness = 3.91, Kurtosis = 26.04  
radius\_worst: Skewness = 1.10, Kurtosis = 0.93  
texture\_worst: Skewness = 0.50, Kurtosis = 0.21  
perimeter\_worst: Skewness = 1.13, Kurtosis = 1.05  
area\_worst: Skewness = 1.85, Kurtosis = 4.35  
smoothness\_worst: Skewness = 0.41, Kurtosis = 0.50  
compactness\_worst: Skewness = 1.47, Kurtosis = 3.00  
concavity\_worst: Skewness = 1.15, Kurtosis = 1.59  
concave\_points\_worst: Skewness = 0.49, Kurtosis = -0.54  
symmetry\_worst: Skewness = 1.43, Kurtosis = 4.40  
fractal\_dimension\_worst: Skewness = 1.66, Kurtosis = 5.19

```
[15] : # Standardizing the data for PCA
      scaler = StandardScaler()
      df_scaled = scaler.fit_transform(df.drop(columns=['diagnosis']))

[16] : # PCA analysis
      pca = PCA(n_components=5)
      pca_results = pca.fit_transform(df_scaled)
      explained_variance = pca.explained_variance_ratio_

[17] : plt.figure(figsize=(8, 5))
      plt.bar(range(1, 6), explained_variance, alpha=0.7, align='center',
              label='Individual Explained Variance')
      plt.step(range(1, 6), np.cumsum(explained_variance), where='mid',
              label='Cumulative Explained Variance')
      plt.xlabel('Principal Components')
      plt.ylabel('Explained Variance Ratio')
      plt.legend()
      plt.title('PCA Explained Variance')
      plt.show()
```

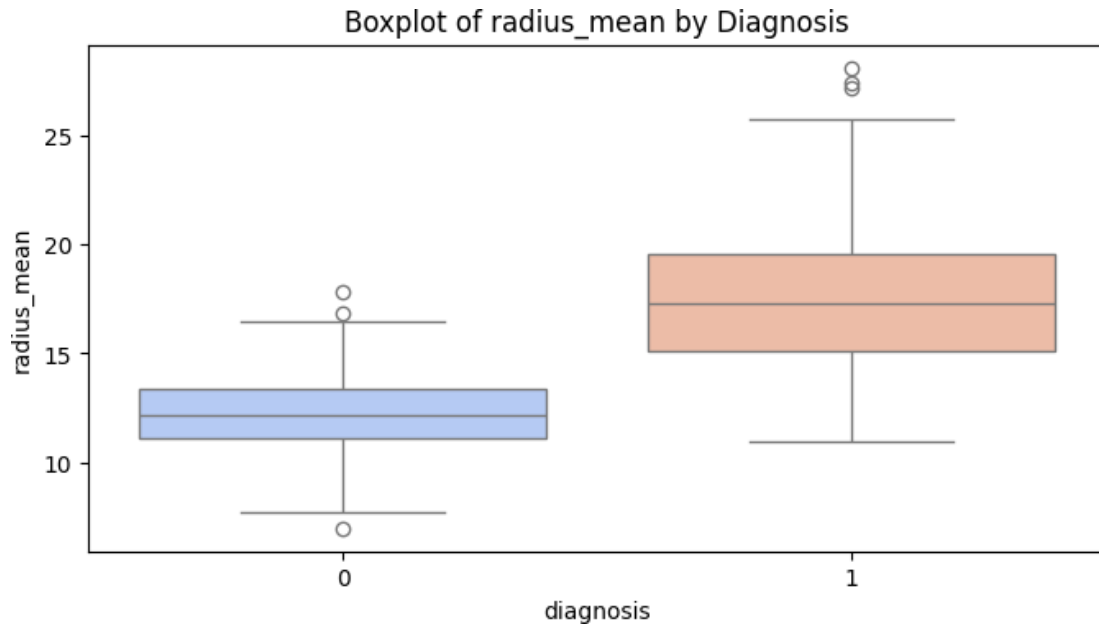


```
[18] : # Boxplots for feature analysis
for col in selected_features:
    plt.figure(figsize=(8, 4))
    sns.boxplot(x='diagnosis', y=col, data=df, palette='coolwarm')
    plt.title(f'Boxplot of {col} by Diagnosis')
    plt.show()
```

C:\Users\samee\AppData\Local\Temp\ipykernel\_2700\767013395.py:4: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

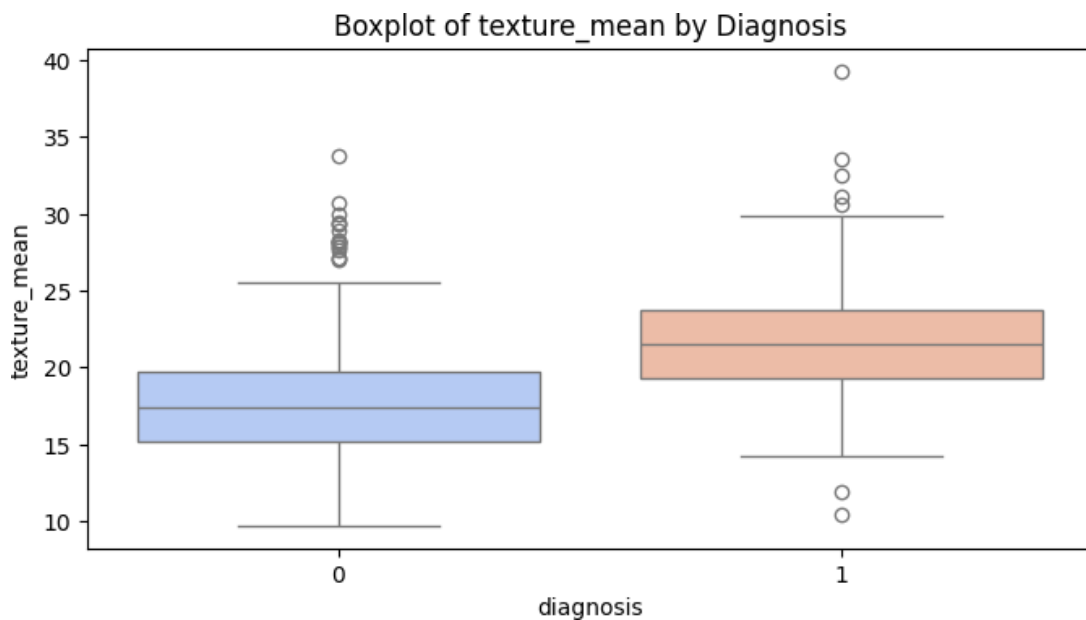
```
sns.boxplot(x='diagnosis', y=col, data=df, palette='coolwarm')
```



C:\Users\samee\AppData\Local\Temp\ipykernel\_2700\767013395.py:4: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

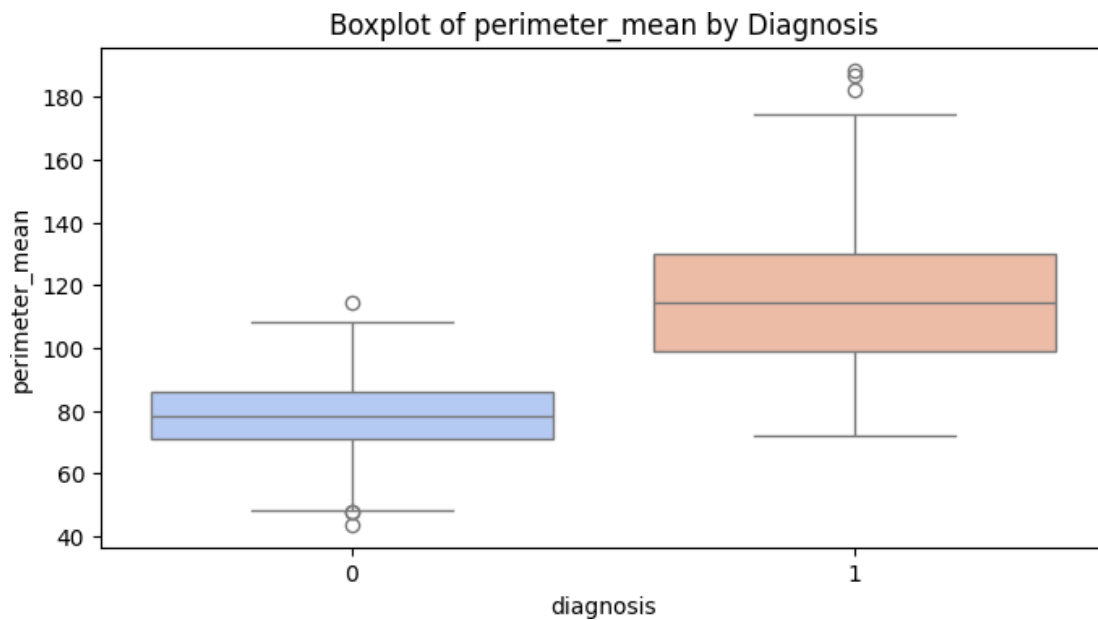
```
sns.boxplot(x='diagnosis', y=col, data=df, palette='coolwarm')
```



C:\Users\samee\AppData\Local\Temp\ipykernel\_2700\767013395.py:4: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

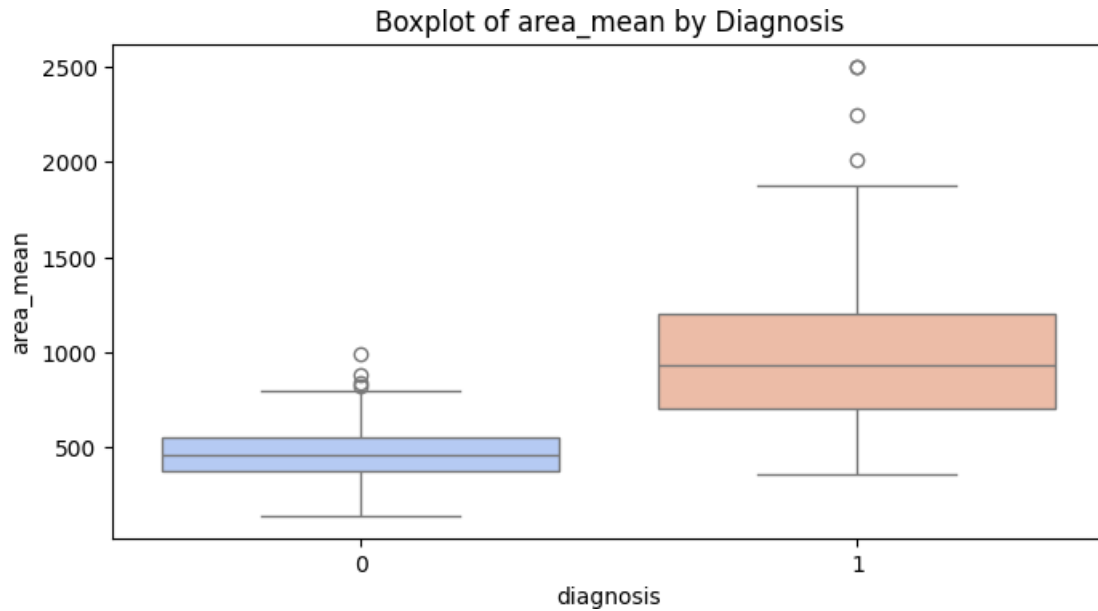
```
sns.boxplot(x='diagnosis', y=col, data=df, palette='coolwarm')
```



C:\Users\samee\AppData\Local\Temp\ipykernel\_2700\767013395.py:4: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

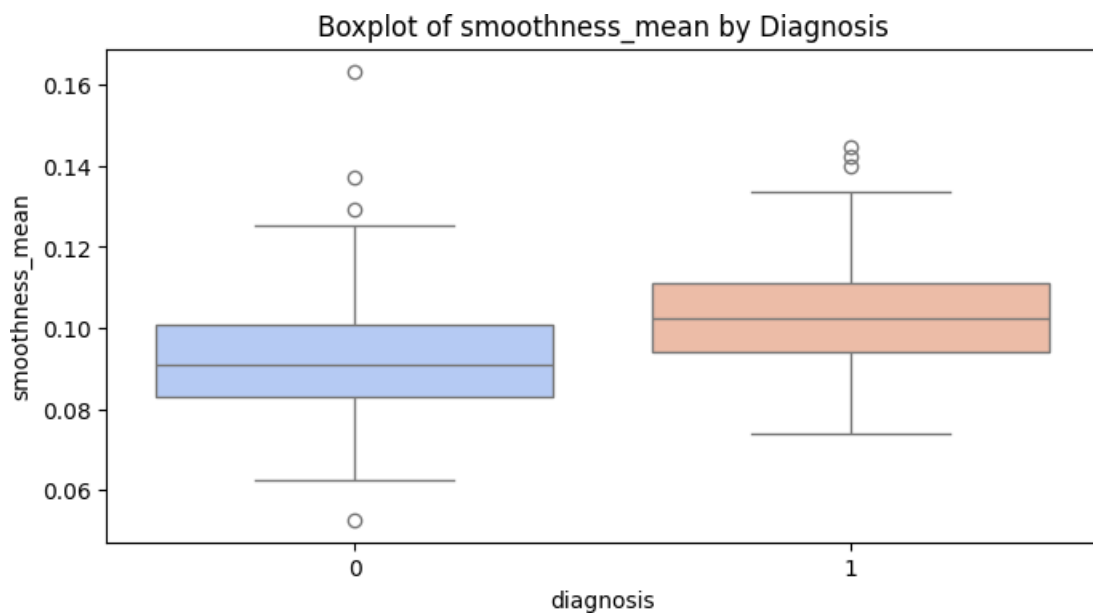
```
sns.boxplot(x='diagnosis', y=col, data=df, palette='coolwarm')
```



C:\Users\samee\AppData\Local\Temp\ipykernel\_2700\767013395.py:4: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

```
sns.boxplot(x='diagnosis', y=col, data=df, palette='coolwarm')
```



```
[19] : from sklearn.model_selection import train_test_split
      from sklearn.ensemble import RandomForestClassifier
      from sklearn.metrics import accuracy_score, classification_report,
      .confusion_matrix

[20] : # Splitting data into training and testing sets
      X = df.drop(columns=['diagnosis'])
      y = df['diagnosis']
      X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
      .random_state=42)

[21] : # Training a RandomForest Classifier
      model = RandomForestClassifier(n_estimators=100, random_state=42)
      model.fit(X_train, y_train)

[21] : RandomForestClassifier(random_state=42)

[22] : #Making predictions
      y_pred = model.predict(X_test)

[23] : # Evaluating the model
      print("Accuracy:", accuracy_score(y_test, y_pred))
      print("Classification Report:\n", classification_report(y_test, y_pred))
      print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred))
```

Accuracy: 0.9649122807017544

Classification Report:

	precision	recall	f1-score	support
0	0.96	0.99	0.97	71
1	0.98	0.93	0.95	43
accuracy			0.96	114
macro avg	0.97	0.96	0.96	114
weighted avg	0.97	0.96	0.96	114

Confusion Matrix:

```
[[70  1]
 [ 3 40]]
```