# REPORT

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## The problem being addressed:

Breast cancer is one of the most prevalent cancers affecting women worldwide. Early detection plays a crucial role in effective treatment and improved prognosis. However, traditional diagnostic methods often rely on invasive procedures and subjective interpretations, leading to delays in detection and potentially compromising patient outcomes. The problem addressed in this project is the development of a machine learning algorithm that can accurately predict whether a breast cancer cell is benign or malignant based on various features extracted from the Breast Cancer Wisconsin (Diagnostic) Data Set. By accurately identifying malignant cells, healthcare professionals can intervene promptly, potentially saving lives and improving patient outcomes.

## Literature Review

Numerous studies have explored the application of machine learning techniques in breast cancer diagnosis, reflecting the growing interest in leveraging computational approaches to enhance medical decision-making.

One seminal work by Esteva et al. (2019) demonstrated the effectiveness of deep learning algorithms in interpreting breast cancer histopathology images, achieving performance comparable to experienced pathologists. This study highlighted the potential of artificial intelligence (AI) to augment traditional diagnostic methods and improve accuracy.

Similarly, Cruz-Roa et al. (2018) proposed a machine learning-based system for breast cancer detection and classification using histopathological images. Their approach integrated feature extraction, feature selection, and classification algorithms to differentiate between benign and malignant tumors with high accuracy.

In the realm of predictive modeling, Wang et al. (2019) developed a support vector machine (SVM) model using clinical and imaging data to predict breast cancer metastasis. Their findings underscored the value of incorporating diverse data sources in predictive modeling, yielding more comprehensive and accurate prognostic assessments.

While these studies demonstrate the potential of machine learning in breast cancer diagnosis and prognosis, there remains room for improvement in terms of model generalization, interpretability, and clinical applicability. Our project aims to address these challenges by focusing on feature-rich datasets, transparent model architectures, and seamless integration into clinical workflows, thereby enhancing the utility and effectiveness of machine learning in breast cancer management.

# METHODOLOGY AND EXPERIMENTAL SETTINGS

## DATA ANALYSIS

[9]:

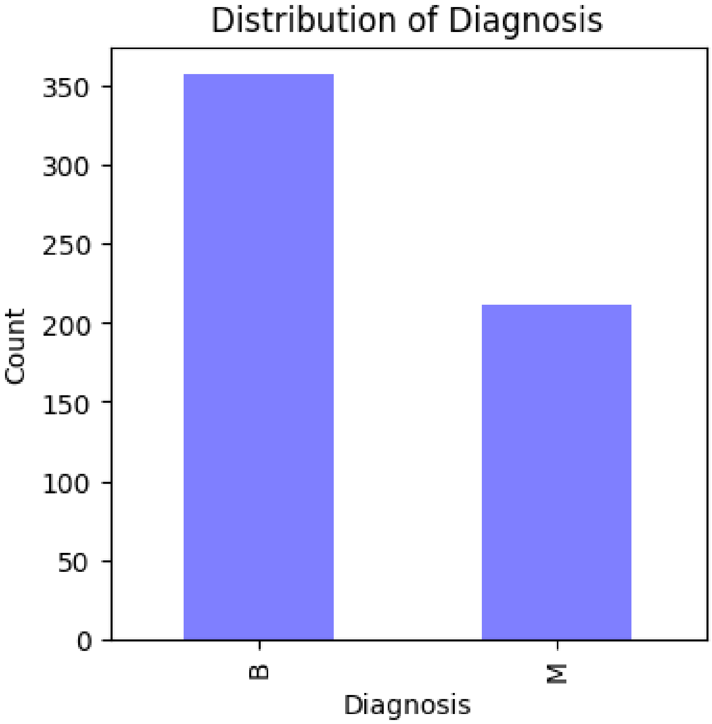
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import norm
from sklearn.preprocessing import StandardScaler
from scipy import stats
import warnings
warnings.filterwarnings('ignore')

# Load the data

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

# Convert diagnosis column to categorical
data['diagnosis'] = pd.Categorical(data['diagnosis'])

# Drop the 33rd column
data.drop(data.columns[32], axis=1, inplace=True)

# General data info
print(data.info())
print(data.describe())

# Check for missing values
print(data.isnull().sum())

# Check proportion of data

print("\n")
print(data['diagnosis'].value_counts(normalize=True))
print("\n")
```

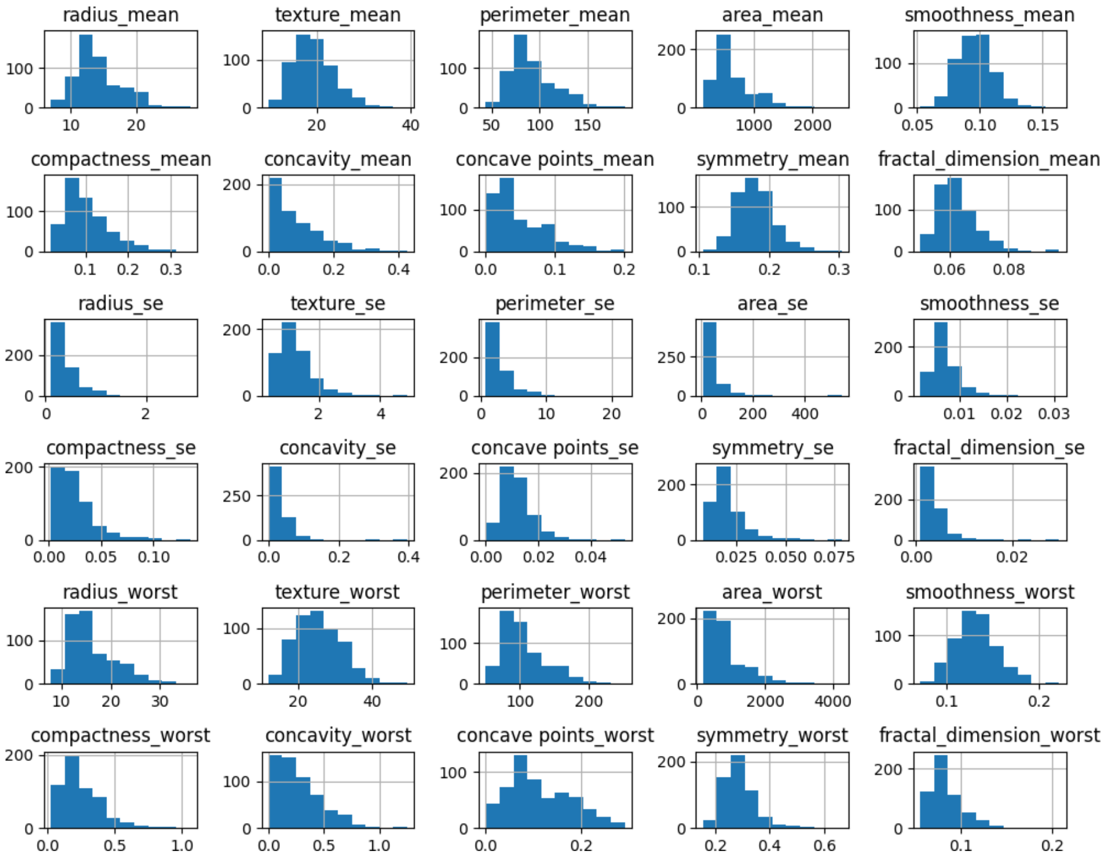
```
# Plot the distribution of the Diagnosis column
data['diagnosis'].value_counts().plot(kind='bar', color='blue', alpha=0.5)

# Customize the plot
plt.title('Distribution of Diagnosis')
plt.xlabel('Diagnosis')
plt.ylabel('Count')

# Show plot
plt.show()



# Selecting numerical columns and removing 'id' column
numerical_data = data.drop(columns=['id'])
# Plotting histograms for each numerical variable
numerical_data.hist(bins=10, figsize=(10, 8))
plt.tight_layout()
plt.show()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 32 columns):
 #   Column                   Non-Null Count  Dtype
---------------------------------------------------  -------------
 0   id                       569 non-null    int64
 1   diagnosis                569 non-null    category
 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
dtypes: category(1), float64(30), int64(1)
memory usage: 138.6 KB
None
                 id  radius_mean  texture_mean  perimeter_mean    area_mean  \
count  5.690000e+02   569.000000    569.000000      569.000000   569.000000
mean   3.037183e+07    14.127292     19.289649       91.969033   654.889104
std    1.250206e+08     3.524049      4.301036       24.298981   351.914129
min    8.670000e+03     6.981000      9.710000       43.790000   143.500000
25%    8.692180e+05    11.700000     16.170000       75.170000   420.300000
50%    9.060240e+05    13.370000     18.840000       86.240000   551.100000
75%    8.813129e+06    15.780000     21.800000      104.100000   782.700000
max    9.113205e+08    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  ...  radius_worst  texture_worst  perimeter_worst  \
count     569.000000  ...    569.000000     569.000000       569.000000
mean        0.181162  ...     16.269190      25.677223       107.261213
std         0.027414  ...      4.833242       6.146258        33.602542
min         0.106000  ...      7.930000      12.020000        50.410000
25%         0.161900  ...     13.010000      21.080000        84.110000
50%         0.179200  ...     14.970000      25.410000        97.660000
75%         0.195700  ...     18.790000      29.720000       125.400000
max         0.304000  ...     36.040000      49.540000       251.200000

       area_worst  smoothness_worst  compactness_worst  concavity_worst  \
count  569.000000        569.000000         569.000000       569.000000
mean   880.583128          0.132369           0.254265         0.272188
```

```
std     569.356993        0.022832        0.157336        0.208624
min     185.200000        0.071170        0.027290        0.000000
25%     515.300000        0.116600        0.147200        0.114500
50%     686.500000        0.131300        0.211900        0.226700
75%    1084.000000        0.146000        0.339100        0.382900
max    4254.000000        0.222600        1.058000        1.252000

       concave points_worst  symmetry_worst  fractal_dimension_worst
count            569.000000      569.000000               569.000000
mean               0.114606        0.290076                 0.083946
std                0.065732        0.061867                 0.018061
min                0.000000        0.156500                 0.055040
25%                0.064930        0.250400                 0.071460
50%                0.099930        0.282200                 0.080040
75%                0.161400        0.317900                 0.092080
max                0.291000        0.663800                 0.207500

[8 rows x 31 columns]
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
```

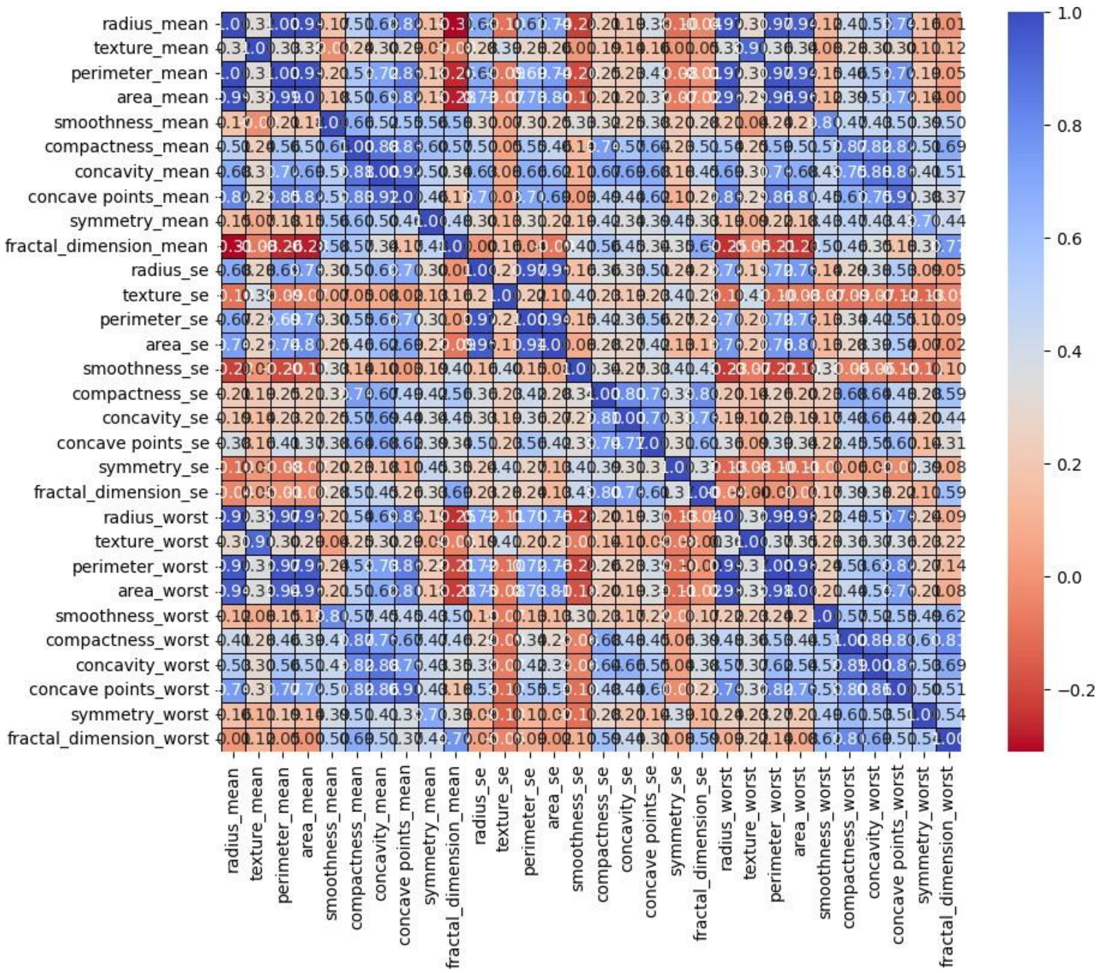
```
symmetry_worst              0
fractal_dimension_worst     0
dtype: int64


diagnosis
B    0.627417
M    0.372583
Name: proportion, dtype: float64
```

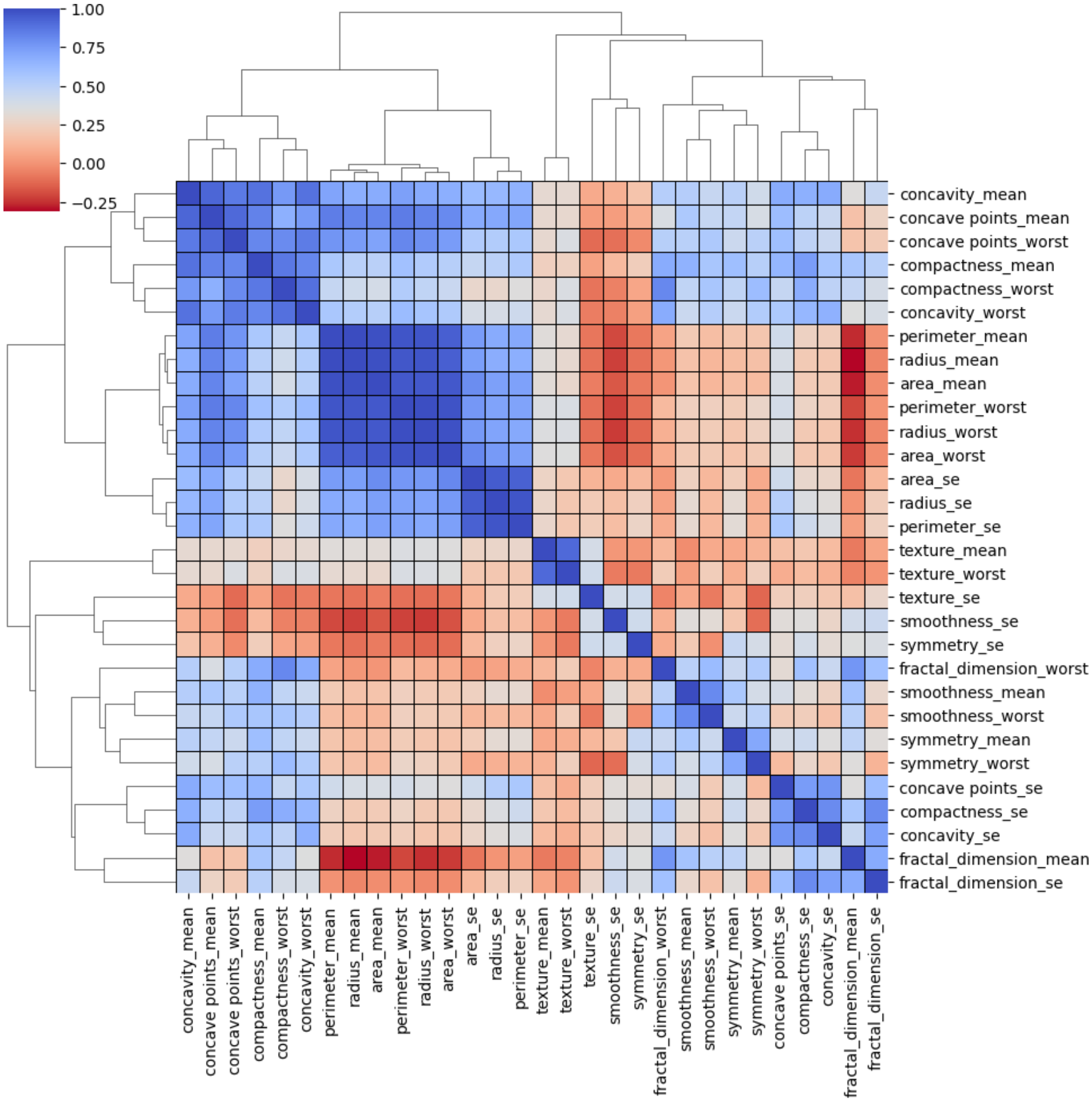




[10]:

```
# Calculate correlation matrix
correlation_matrix = data.iloc[:, 2:].corr()

# Create the correlation plot with reversed color scheme
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm_r', fmt=".2f",␣
 ↪linewidths=0.5, linecolor='black', square=True)

# Add hierarchical clustering
dendrogram = sns.clustermap(correlation_matrix, cmap='coolwarm_r', linewidths=0.
 ↪5, linecolor='black', square=True)

# Rotate the dendrogram
plt.setp(dendrogram.ax_heatmap.yaxis.get_majorticklabels(), rotation=0)
plt.show()
```


radius_mean
texture_mean
perimeter_mean
area_mean
smoothness_mean
compactness_mean
concavity_mean
concave points_mean
symmetry_mean
fractal_dimension_mean
radius_se
texture_se
perimeter_se
area_se
smoothness_se
compactness_se
concavity_se
concave points_se
symmetry_se
fractal_dimension_se
radius_worst
texture_worst
perimeter_worst
area_worst
smoothness_worst
compactness_worst
concavity_worst
concave points_worst
symmetry_worst
fractal_dimension_worst
1.0
0.8
0.6
0.4
0.2
0.0
−0.2



[11]:

```
import numpy as np

# Calculate correlation matrix
correlation_matrix = np.corrcoef(data.iloc[:, 2:], rowvar=False)

# Set the cutoff value
cutoff = 0.9

# Find highly correlated attributes
def find_correlation(matrix, cutoff):
    correlated_attrs = set()
    for i in range(matrix.shape[0]):
        for j in range(i+1, matrix.shape[1]):
            if abs(matrix[i, j]) >= cutoff:
                correlated_attrs.add(i)
                correlated_attrs.add(j)
    return list(correlated_attrs)

highly_correlated = find_correlation(correlation_matrix, cutoff)
print(highly_correlated)
```

```
[0, 1, 2, 3, 6, 7, 10, 12, 13, 20, 21, 22, 23, 27]
```

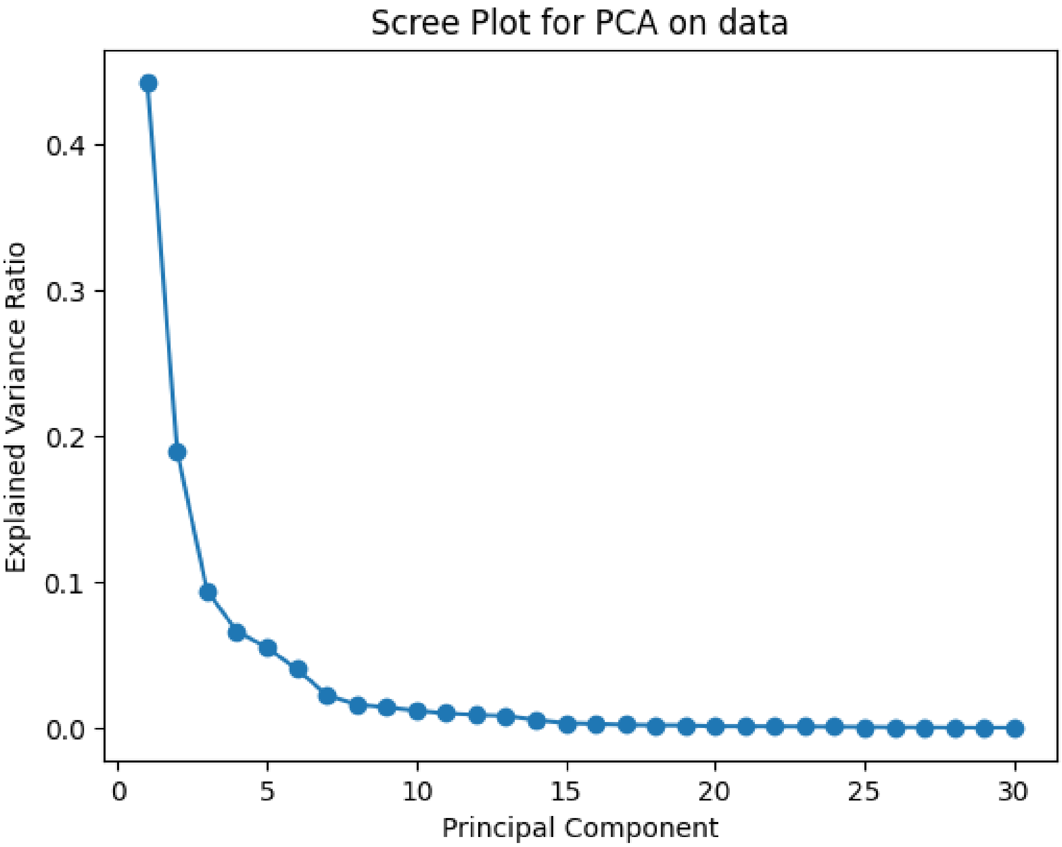
[12]:

```
# Remove correlated variables
data2 = data.drop(data.columns[highly_correlated], axis=1)

# Number of columns after removing correlated variables
num_columns_data2 = data2.shape[1]
print("Number of columns after removing correlated variables:", num_columns_data2)
```

```
Number of columns after removing correlated variables: 18
```

[13]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA

# Exclude the first two columns
data_for_pca = data.iloc[:, 2:]

# Standardize the data
scaler = StandardScaler()
data_scaled = scaler.fit_transform(data_for_pca)

pca = PCA()
pca_res_data = pca.fit_transform(data_scaled)
# Plot PCA results
plt.plot(np.arange(1, pca.n_components_ + 1), pca.explained_variance_ratio_, marker='o', linestyle='-')
plt.xlabel('Principal Component')
plt.ylabel('Explained Variance Ratio')
plt.title('Scree Plot for PCA on data')
plt.show()

# Summary of PCA results
print("Summary of PCA on data:")
print(pd.DataFrame({'Standard deviation': np.sqrt(pca.explained_variance_),
                    'Proportion of Variance': pca.explained_variance_ratio_,
                              'Cumulative Proportion': np.cumsum(pca.
 ↪explained_variance_ratio_)}))

# Analysis of variance explained by components
variance_explained = np.cumsum(pca.explained_variance_ratio_)
print("\nVariance explained by components:")
for i, explained_variance in enumerate(variance_explained):
    print(f"Component {i+1}: {explained_variance:.4f}")
```

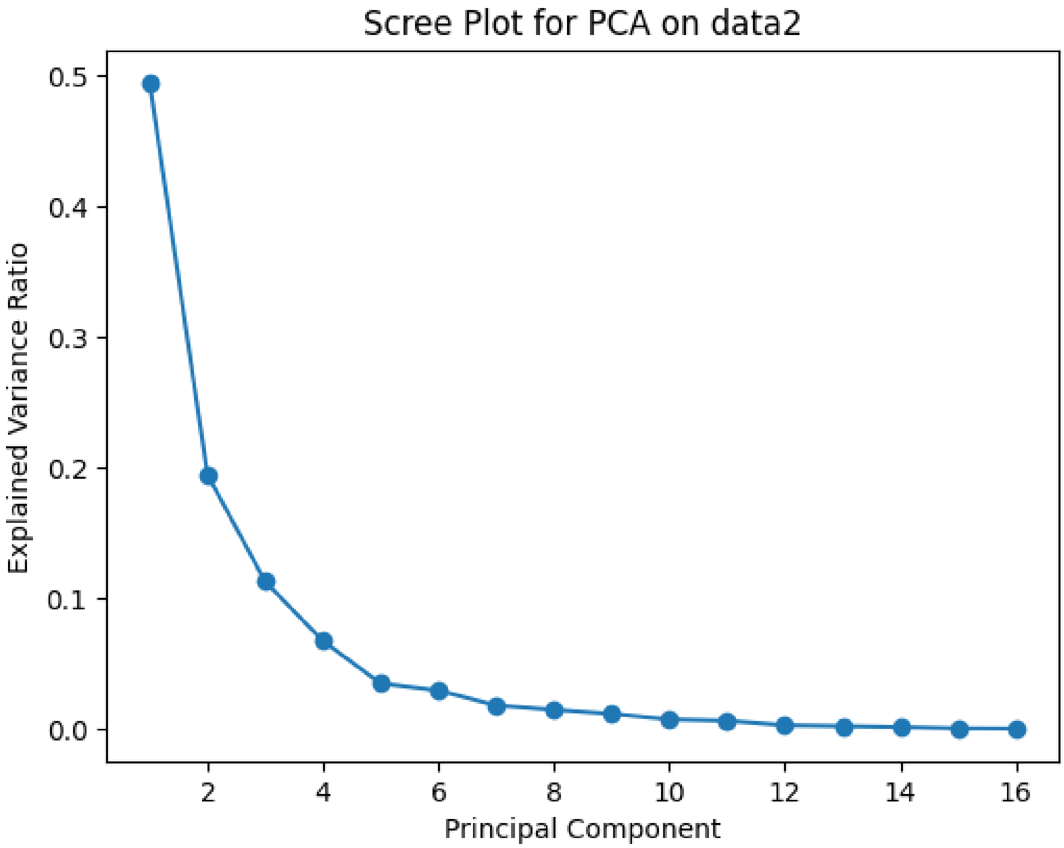


```
Summary of PCA on data:
    Standard deviation  Proportion of Variance  Cumulative Proportion
0             3.647601                0.442720  0.442720
1             2.387755                0.189712               0.632432
2             1.680152                0.093932               0.726364
3             1.408591                0.066021               0.792385
4             1.285159                0.054958               0.847343
5             1.099765                0.040245               0.887588
6             0.822441                0.022507               0.910095
7             0.690982                0.015887               0.925983
8             0.646242                0.013896               0.939879
```

```
9          0.592715          0.011690          0.951569
10         0.542617          0.009797          0.961366
11         0.511489          0.008705          0.970071
12         0.491714          0.008045          0.978117
13         0.396593          0.005234          0.983350
14         0.307084          0.003138          0.986488
15         0.282849          0.002662          0.989150
16         0.243934          0.001980          0.991130
17         0.229590          0.001754          0.992884
18         0.222631          0.001649          0.994533
19         0.176676          0.001039          0.995572
20         0.173279          0.000999          0.996571
21         0.165794          0.000915          0.997486
22         0.156153          0.000811          0.998297
23         0.134487          0.000602          0.998899
24         0.124533          0.000516          0.999415
25         0.090510          0.000273          0.999688
26         0.083142          0.000230          0.999918
27         0.039902          0.000053          0.999971
28         0.027388          0.000025          0.999996
29         0.011545          0.000004          1.000000

Variance explained by components:
Component 1: 0.4427
Component 2: 0.6324
Component 3: 0.7264
Component 4: 0.7924
Component 5: 0.8473
Component 6: 0.8876
Component 7: 0.9101
Component 8: 0.9260
Component 9: 0.9399
Component 10: 0.9516
Component 11: 0.9614
Component 12: 0.9701
Component 13: 0.9781
Component 14: 0.9834
Component 15: 0.9865
Component 16: 0.9892
Component 17: 0.9911
Component 18: 0.9929
Component 19: 0.9945
Component 20: 0.9956
Component 21: 0.9966
Component 22: 0.9975
Component 23: 0.9983
Component 24: 0.9989
Component 25: 0.9994
Component 26: 0.9997
Component 27: 0.9999
Component 28: 1.0000
Component 29: 1.0000
Component 30: 1.0000
```

[14]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler

# Assuming 'data2' is a pandas DataFrame

# Exclude the first two columns
data2_for_pca = data2.iloc[:, 2:]

# Standardize the data
scaler2 = StandardScaler()
data2_scaled = scaler2.fit_transform(data2_for_pca)

# Perform PCA on data2
pca2 = PCA()
pca_res_data2 = pca2.fit_transform(data2_scaled)

# Plot PCA results for data2
plt.plot(np.arange(1, pca2.n_components_ + 1), pca2.explained_variance_ratio_,␣
 ↪marker='o', linestyle='-')
plt.xlabel('Principal Component')
plt.ylabel('Explained Variance Ratio')
plt.title('Scree Plot for PCA on data2')
plt.show()

# Summary of PCA results for data2
print("Summary of PCA on data2:")
print(pd.DataFrame({'Standard deviation': np.sqrt(pca2.explained_variance_),
                    'Proportion of Variance': pca2.explained_variance_ratio_,
                    'Cumulative Proportion': np.cumsum(pca2.
 ↪explained_variance_ratio_)}))

# Analysis of variance explained by components for data2
variance_explained_data2 = np.cumsum(pca2.explained_variance_ratio_)
print("\nVariance explained by components for data2:")
for i, explained_variance in enumerate(variance_explained_data2):
    print(f"Component {i+1}: {explained_variance:.4f}")
```

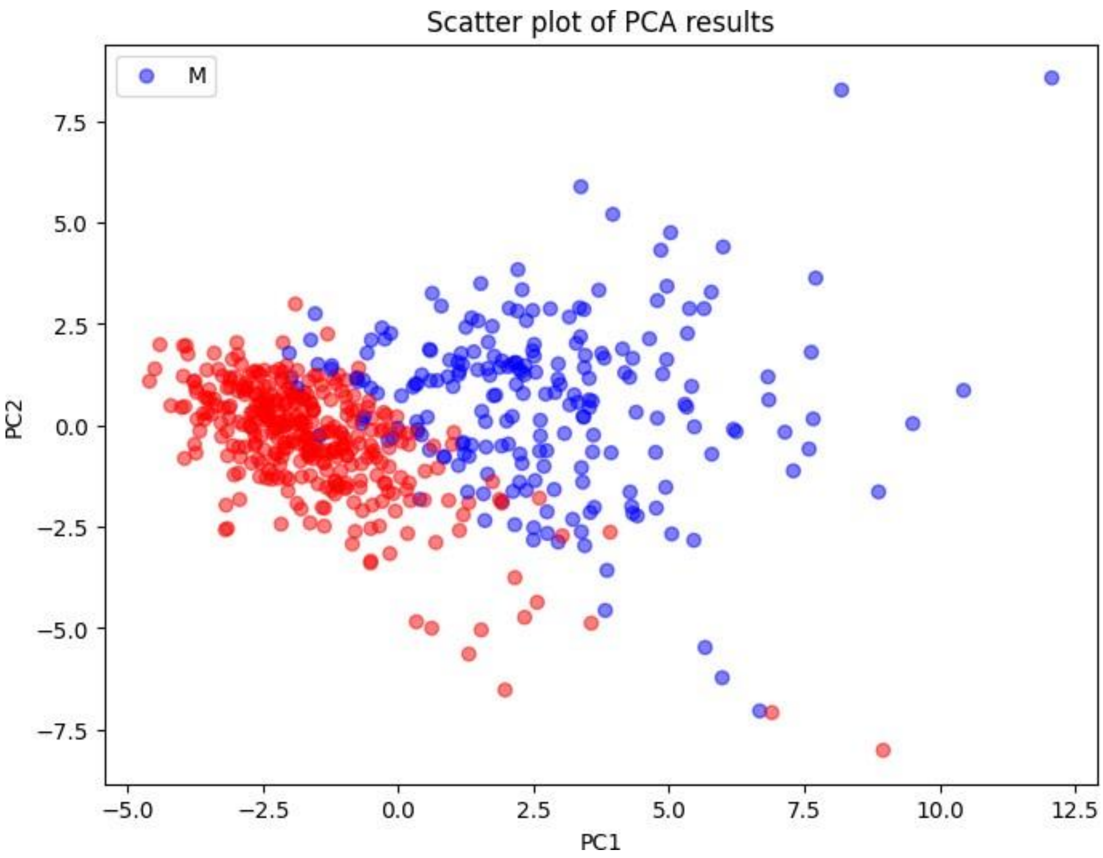


```
Summary of PCA on data2:
    Standard deviation  Proportion of Variance  Cumulative Proportion
0             2.815374                0.494525               0.494525
1             1.766344                0.194656               0.689181
2             1.344809                0.112833               0.802014
3             1.039253                0.067384               0.869398
4             0.747624                0.034872               0.904271
5             0.688631                0.029586               0.933857
6             0.539321                0.018147               0.952004
7             0.486102                0.014742               0.966747
8             0.432303                0.011660               0.978406
9             0.343815                0.007375               0.985781
10            0.318434                0.006326               0.992108
11            0.218536                0.002980               0.995087
12            0.193087                0.002326               0.997414
13            0.159590                0.001589               0.999003
14            0.097563                0.000594               0.999596
15            0.080429                0.000404               1.000000

Variance explained by components for data2:
```

```
Component 1: 0.4945
Component 2: 0.6892
Component 3: 0.8020
Component 4: 0.8694
Component 5: 0.9043
Component 6: 0.9339
Component 7: 0.9520
Component 8: 0.9667
Component 9: 0.9784
Component 10: 0.9858
Component 11: 0.9921
Component 12: 0.9951
Component 13: 0.9974
Component 14: 0.9990
Component 15: 0.9996
Component 16: 1.0000
```

[15]:

```python
import pandas as pd
import matplotlib.pyplot as plt

# Convert PCA results to a DataFrame including only the first two principal components
pca_df = pd.DataFrame(pca_res_data2[:, :2], columns=["PC1", "PC2"])

# Add 'diagnosis' column to the DataFrame
pca_df["diagnosis"] = data["diagnosis"].values

# Plot scatter plot
plt.figure(figsize=(8, 6))
colors = {"M": "blue", "B": "red"}  # Assuming 'M' is malignant and 'B' is benign
plt.scatter(pca_df["PC1"], pca_df["PC2"], c=pca_df["diagnosis"].map(colors), alpha=0.5)
plt.xlabel("PC1")
plt.ylabel("PC2")
plt.title("Scatter plot of PCA results")
plt.legend(labels=colors.keys())
plt.show()
```

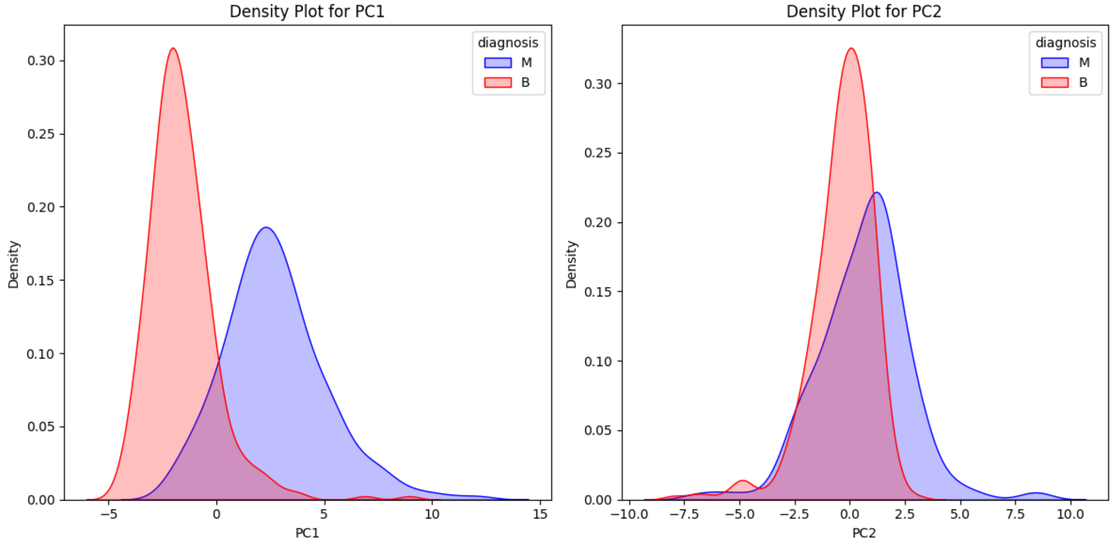


[ ]:

[16]:

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

# Define colors for each class
colors = {"M": "blue", "B": "red"}  # Assuming 'M' is malignant and 'B' is benign

# Create subplots for PC1 and PC2 densities side by side
plt.figure(figsize=(12, 6))

# Density plot for PC1
plt.subplot(1, 2, 1)
for label, color in colors.items():
    subset = pca_df[pca_df["diagnosis"] == label]
    sns.kdeplot(subset["PC1"], color=color, fill=True, alpha=0.25, label=label)
plt.title("Density Plot for PC1")
plt.xlabel("PC1")
plt.legend(title="diagnosis")
```

```python
# Density plot for PC2
plt.subplot(1, 2, 2)
for label, color in colors.items():
    subset = pca_df[pca_df['diagnosis'] == label]
    sns.kdeplot(subset['PC2'], color=color, fill=True, alpha=0.25, label=label)
plt.title('Density Plot for PC2')
plt.xlabel('PC2')
plt.legend(title='diagnosis')

plt.tight_layout()
plt.show()
```



[17]:

```python
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split

# Set the seed for reproducibility
np.random.seed(1815)

# Combine the 'diagnosis' column with 'data2'
data3 = pd.concat([data['diagnosis'], data2], axis=1)

# Split the dataset into features (X) and target variable (y)
X = data3.drop(columns=['diagnosis'])
y = data3['diagnosis']

# Split the dataset into Train (80%) and Test (20%)
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
  ↪stratify=y)

# Create cross-validation object
fitControl = StratifiedKFold(n_splits=15, shuffle=True, random_state=1815)
```

[31]:

```

```

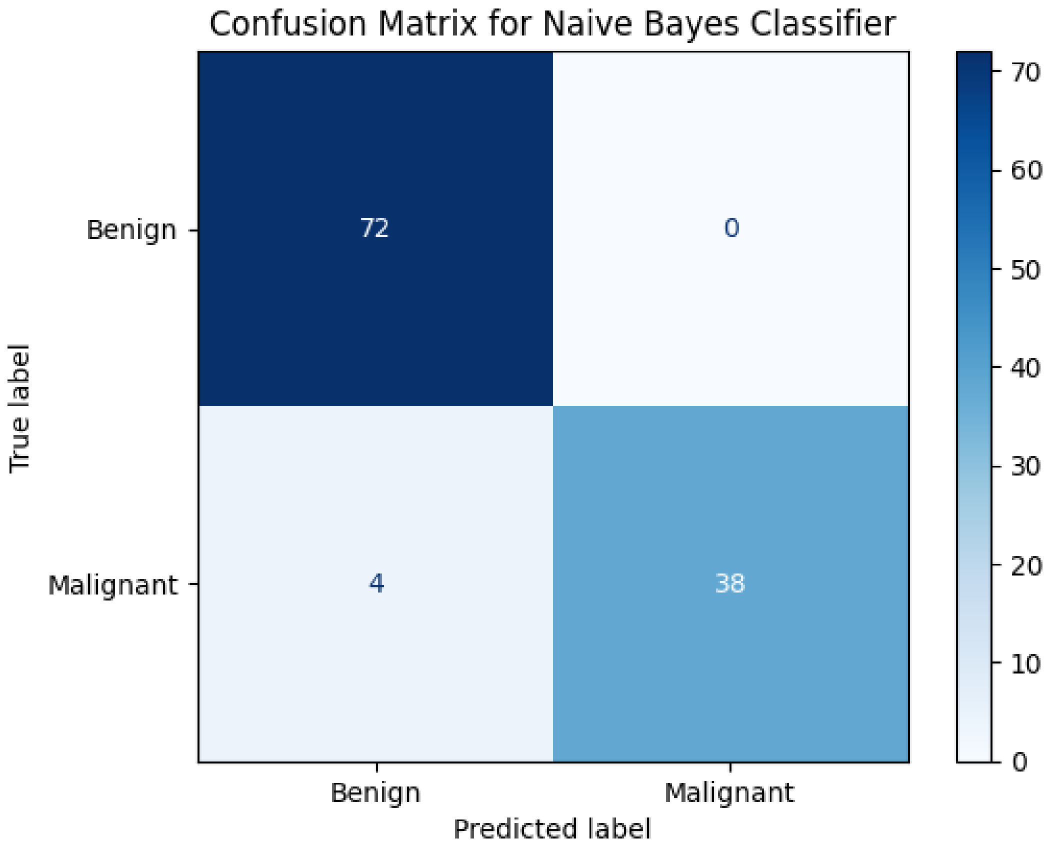
# METHODS

[18]: **1. Naive Bayes Model**

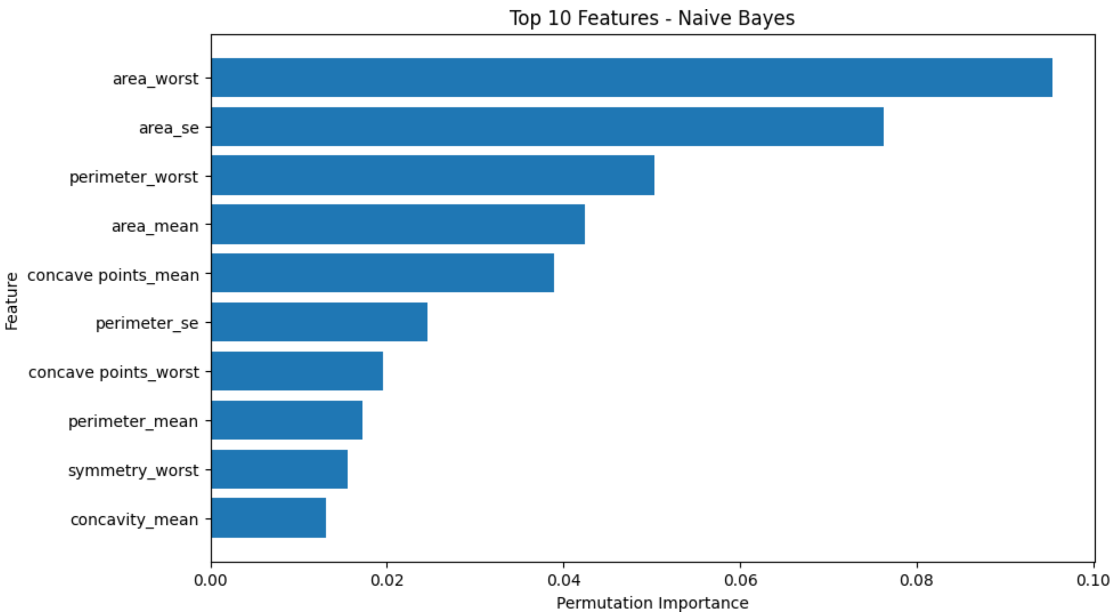
```
from sklearn.naive_bayes import GaussianNB
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import make_pipeline
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from scipy.stats import norm
from sklearn.inspection import permutation_importance
import matplotlib.pyplot as plt
import numpy as np
from sklearn.preprocessing import LabelEncoder



# Assuming 'train_data' and 'test_data' are pandas DataFrames with the target␣
  ↪variable 'diagnosis'
# Extract features and target variables



# Create a pipeline with preprocessing (centering and scaling) and Naive Bayes␣
  ↪classifier
model_naiveb = make_pipeline(StandardScaler(), GaussianNB())

# Train the model
model_naiveb.fit(X_train, y_train)

# Make predictions
predictions_naiveb = model_naiveb.predict(X_test)

# Generate confusion matrix
conf_matrix_naiveb = confusion_matrix(y_test, predictions_naiveb, labels=["B",␣
  ↪"M"])

# Display confusion matrix
display = ConfusionMatrixDisplay(conf_matrix_naiveb, display_labels=["Benign",␣
  ↪"Malignant"])
```

```
plt.show()

# Compute additional metrics
tn, fp, fn, tp = conf_matrix_naiveb.ravel()

accuracy = (tp + tn) / (tp + tn + fp + fn)

n = tp + tn + fp + fn
z = 1.96  # Z-value for 95% confidence level
ci_lower = accuracy - z * np.sqrt((accuracy * (1 - accuracy)) / n)
ci_upper = accuracy + z * np.sqrt((accuracy * (1 - accuracy)) / n)


# Convert categorical target variable to numerical representation
label_encoder = LabelEncoder()
y_test_encoded  =  label_encoder.fit_transform(y_test)

# Now you can calculate mean and other statistics
nir = max(y_test_encoded.mean(), 1 - y_test_encoded.mean())
p_value = 2 * (1 - norm.cdf(abs(accuracy - nir) / np.sqrt((accuracy * (1 - accuracy)) / n)))

sensitivity = tp / (tp + fn)
specificity = tn / (tn + fp)

positive_class = 'Malignant'

balanced_accuracy = (sensitivity + specificity) / 2

pos_pred_value = tp / (tp + fp)

neg_pred_value = tn / (tn + fn)

# Print computed metrics
print("\nAccuracy:", accuracy)
print("95% CI:", (ci_lower, ci_upper))
print("Sensitivity:", sensitivity)
print("Specificity:",  specificity)
print("'Positive' Class:", positive_class)
print("Balanced Accuracy:", balanced_accuracy)
print("Positive Predictive Value:", pos_pred_value)
print("Negative Predictive Value:", neg_pred_value)
print("\n")

# Compute permutation importances
perm_importance = permutation_importance(model_naiveb, X_test, y_test, n_repeats=30, random_state=42)
```

```
# Get feature names
feature_names = X_test.columns

# Get sorted indices of features by importance
sorted_idx = perm_importance.importances_mean.argsort()

# Plot top 10 features
top_features_idx = sorted_idx[-10:]
top_features = feature_names[top_features_idx]
top_importance = perm_importance.importances_mean[top_features_idx]

plt.figure(figsize=(10, 6))
plt.barh(top_features, top_importance)
plt.xlabel('Permutation Importance')
plt.ylabel('Feature')
plt.title('Top 10 Features - Naive Bayes')
plt.show()
```



```
Accuracy: 0.9649122807017544
95% CI: (0.9311349650339525, 0.9986895963695562)
Sensitivity: 0.9047619047619048
Specificity: 1.0
'Positive' Class: Malignant
Balanced Accuracy: 0.9523809523809523
Positive Predictive Value: 1.0
Negative Predictive Value: 0.9473684210526315
```

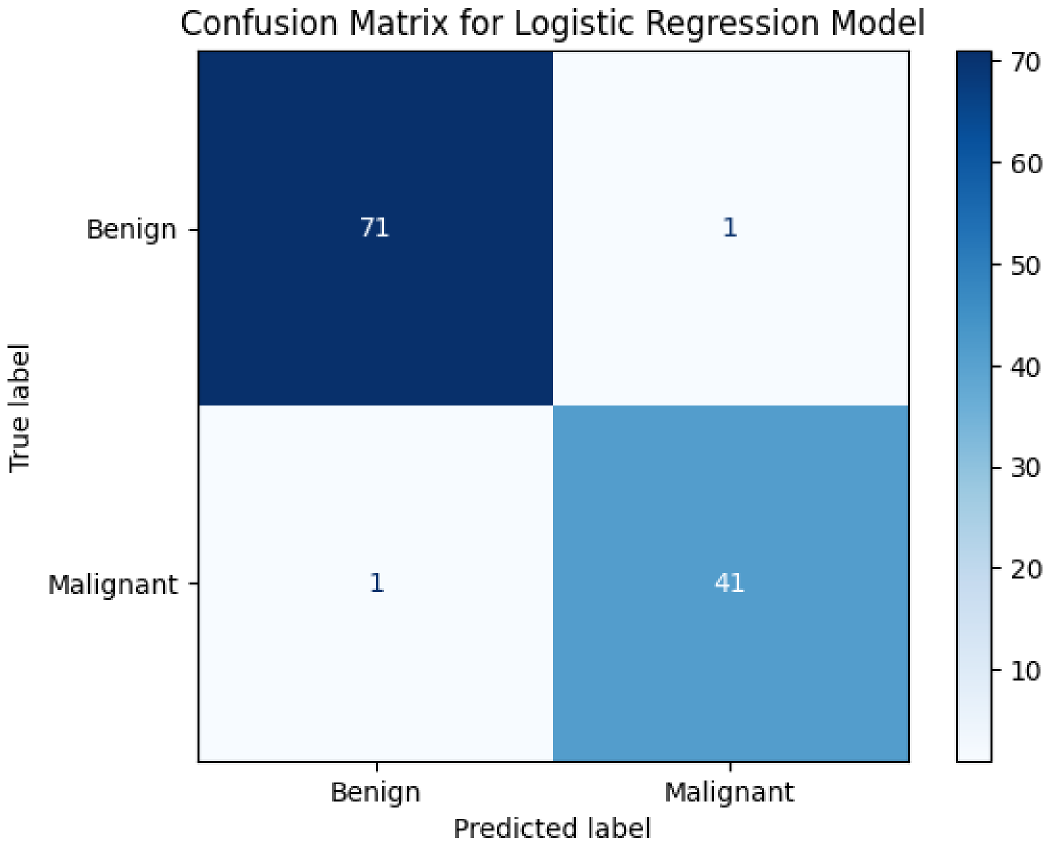


**2. Logistic Regression Model**

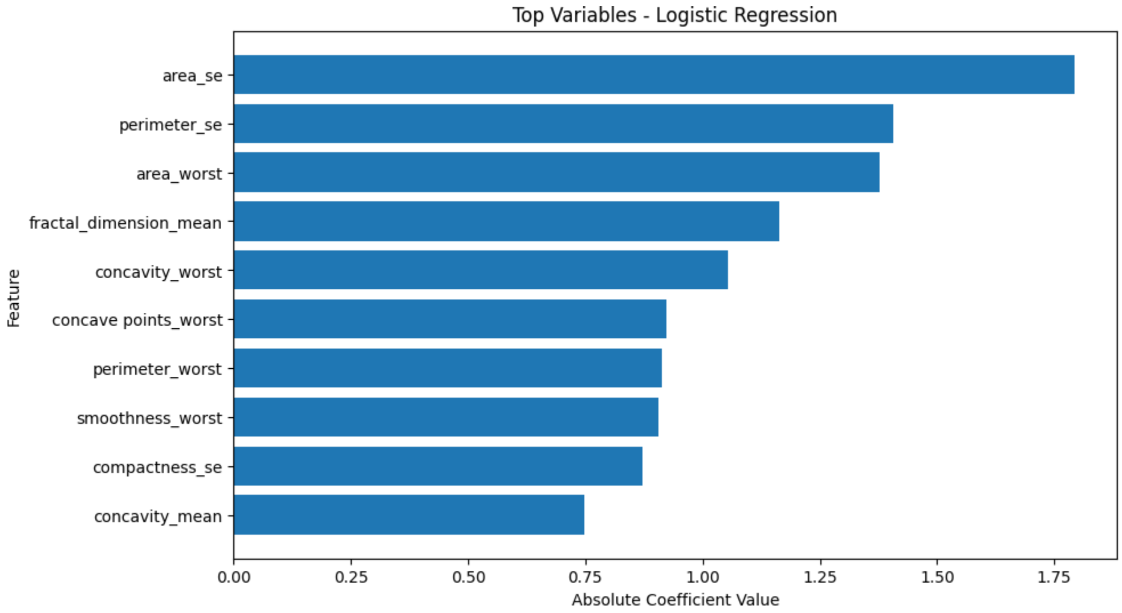
[19]:
```python
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import make_pipeline
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from sklearn.metrics import accuracy_score, classification_report
# Create a pipeline with preprocessing (centering and scaling) and Logistic Regression classifier
model_logreg = make_pipeline(StandardScaler(), LogisticRegression())

# Train the model
model_logreg.fit(X_train, y_train)

# Make predictions
predictions_logreg = model_logreg.predict(X_test)
```

```
# Generate confusion matrix
conf_matrix_logreg = confusion_matrix(y_test, predictions_logreg, labels=["B",␣
  ↪"M"])

# Display confusion matrix
display = ConfusionMatrixDisplay(conf_matrix_logreg, display_labels=["Benign",␣
  ↪"Malignant"])
display.plot(cmap='Blues')
plt.title('Confusion Matrix for Logistic Regression Model')
plt.show()

# Check results
confusionmatrix_logreg = confusion_matrix(y_test, predictions_logreg,␣
  ↪labels=["B", "M"])
print("Confusion Matrix and Statistics:")
print("Reference\tPrediction\tB\tM")
for i in range(len(confusionmatrix_logreg)):
    print(f"{['B', 'M'][i]}\t\t{['B',␣
  ↪'M'][i]}\t\t{confusionmatrix_logreg[i][0]}\t{confusionmatrix_logreg[i][1]}")



# Calculate accuracy
accuracy = accuracy_score(y_test, predictions_logreg)
print("\nAccuracy:", accuracy)



TN, FP, FN, TP = conf_matrix_logreg.ravel()

# Calculate sensitivity and specificity
sensitivity = TP / (TP + FN)
specificity = TN / (TN + FP)

# Print Sensitivity and Specificity
print(f"\nSensitivity: {sensitivity}")
print(f"Specificity: {specificity}")


# Generate classification report to get other metrics
class_report = classification_report(y_test, predictions_logreg,␣
  ↪target_names=["Benign", "Malignant"])
print("\nClassification Report:")
print(class_report)
```

```python
# ==================== top features =====================

# Get the coefficients of the logistic regression model
coefficients = model_logreg.named_steps['logisticregression'].coef_[0]

# Get the absolute values of coefficients
absolute_coefficients = np.abs(coefficients)

# Get the indices of top 10 features
top_indices = np.argsort(absolute_coefficients)[-10:]

# Get the corresponding feature names
top_features = X.columns[top_indices]

# Get the corresponding absolute coefficients
top_absolute_coefficients = absolute_coefficients[top_indices]

# Plot the top variables
plt.figure(figsize=(10, 6))
plt.barh(top_features[::-1], top_absolute_coefficients[::-1])
plt.xlabel('Absolute Coefficient Value')
plt.ylabel('Feature')
plt.title('Top Variables - Logistic Regression')
plt.gca().invert_yaxis()  # Invert y-axis to display the most important features at the top
plt.show()
```



```
Confusion Matrix and Statistics:
Reference         Prediction        B        M
B                 B                 71       1
M                 M                 1        41

Accuracy: 0.9824561403508771

Sensitivity:  0.9761904761904762
Specificity:  0.9861111111111112

Classification Report:
              precision    recall  f1-score   support

      Benign       0.99      0.99      0.99        72
   Malignant       0.98      0.98      0.98        42

    accuracy                           0.98       114
   macro avg       0.98      0.98      0.98       114
weighted avg       0.98      0.98      0.98       114
```



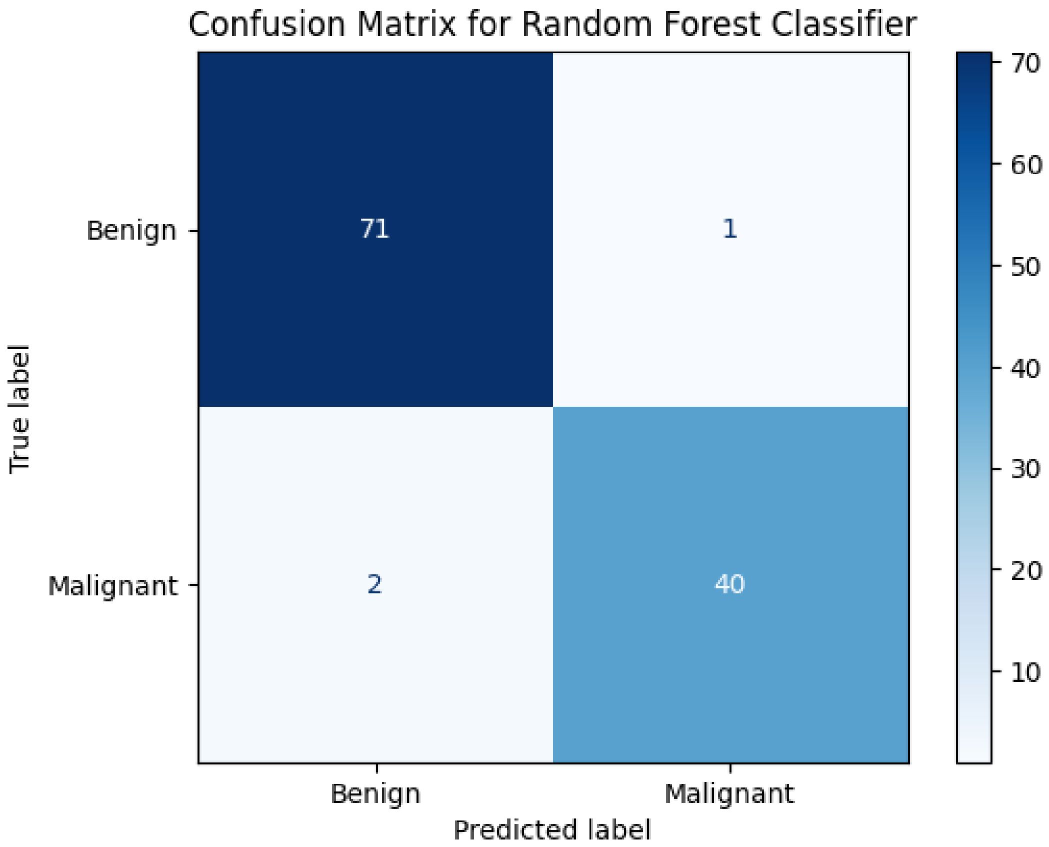
# 1 *3. Random Forest Model **

[20]:

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import make_pipeline
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

# Create a pipeline with preprocessing (centering and scaling) and Random␣
  ↪Forest classifier
model_randomforest = make_pipeline(StandardScaler(), RandomForestClassifier())

# Train the model
model_randomforest.fit(X_train, y_train)

#  Make predictions
predictions_randomforest = model_randomforest.predict(X_test)

# Generate confusion matrix
conf_matrix_randomforest = confusion_matrix(y_test, predictions_randomforest,␣
  ↪labels=["B", "M"])

# Display confusion matrix
display = ConfusionMatrixDisplay(conf_matrix_randomforest,␣
  ↪display_labels=["Benign", "Malignant"])
display.plot(cmap='Blues')
plt.title('Confusion Matrix for Random Forest Classifier')
```

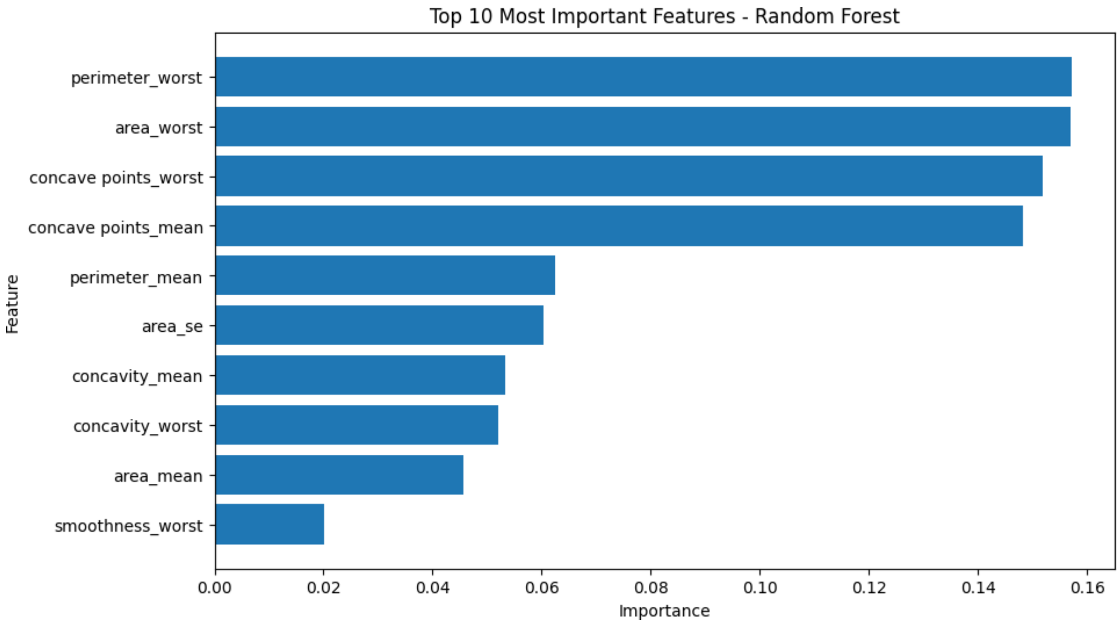
```python
plt.show()

# Evaluate performance
confusionmatrix_randomforest = confusion_matrix(predictions_randomforest, y_test, labels=["B", "M"])
print("Confusion Matrix and Statistics:")
print(confusionmatrix_randomforest)



# Calculate accuracy
accuracy_randomforest = accuracy_score(y_test, predictions_randomforest)
print("\nAccuracy:", accuracy_randomforest)

TN, FP, FN, TP = conf_matrix_randomforest.ravel()

# Calculate sensitivity and specificity
sensitivity = TP / (TP + FN)
specificity = TN / (TN + FP)

# Print Sensitivity and Specificity
print(f"\nSensitivity: {sensitivity}")
print(f"Specificity: {specificity}")

# Generate classification report to get other metrics
class_report_randomforest = classification_report(y_test, predictions_randomforest, target_names=["Benign", "Malignant"])
print("\nClassification Report:")
print(class_report_randomforest)




import matplotlib.pyplot as plt

# Assuming 'model_randomforest' is a trained Pipeline object containing a RandomForestClassifier

# Get the RandomForestClassifier object from the pipeline
random_forest = model_randomforest.named_steps['randomforestclassifier']

# Extract feature importances from the trained random forest model
feature_importances = random_forest.feature_importances_

# Get indices of top 10 most important features
top_indices = feature_importances.argsort()[-10:]
```

```
# Get names of top 10 most important features
top_features = X_train.columns[top_indices]

# Get corresponding importances
top_importances = feature_importances[top_indices]

# Plot top 10 most important features
plt.figure(figsize=(10, 6))
plt.barh(range(len(top_indices)), top_importances, align='center')
plt.yticks(range(len(top_indices)), top_features)
plt.xlabel('Importance')
plt.ylabel('Feature')
plt.title('Top 10 Most Important Features - Random Forest')
plt.show()
```



```
Confusion Matrix and Statistics:
[[71  2]
 [ 1 40]]

Accuracy: 0.9736842105263158
```

```
Sensitivity:  0.9523809523809523
Specificity:  0.9861111111111112

Classification Report:
              precision    recall  f1-score   support

      Benign       0.97      0.99      0.98        72
   Malignant       0.98      0.95      0.96        42

    accuracy                           0.97       114
   macro avg       0.97      0.97      0.97       114
weighted avg       0.97      0.97      0.97       114
```



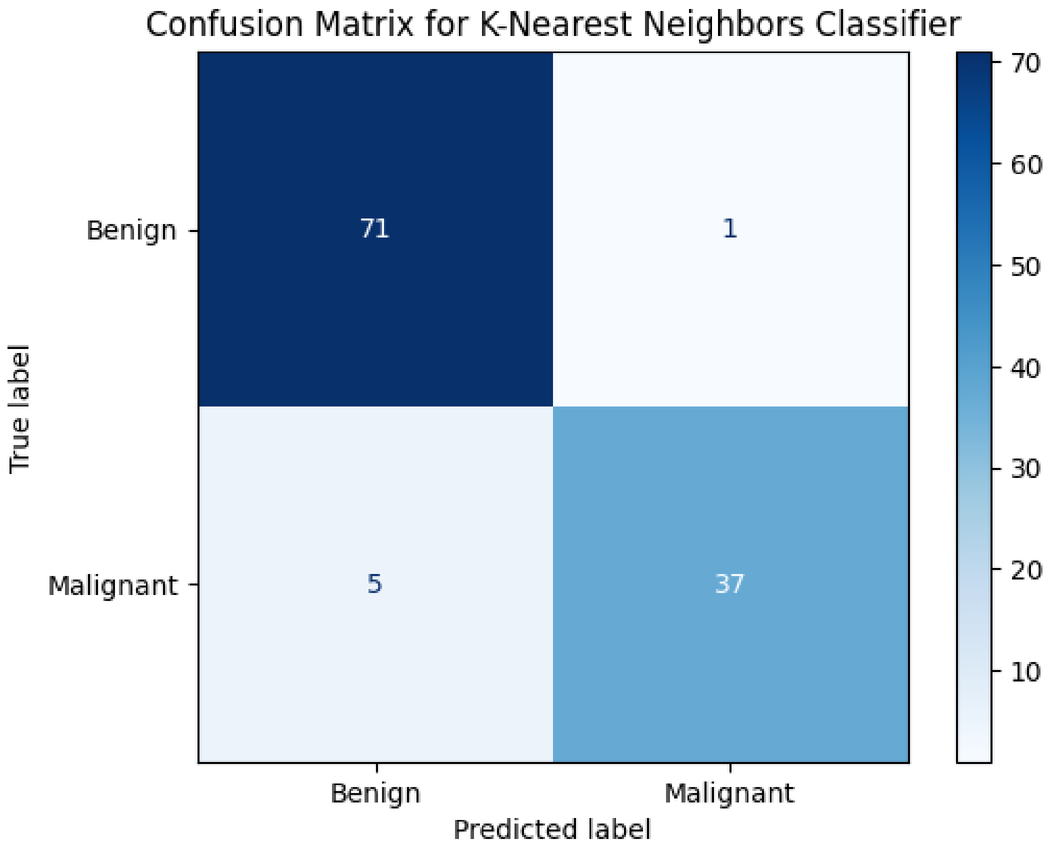
## 2 *4. K Nearest Neighbor (KNN) Model **

[21]:

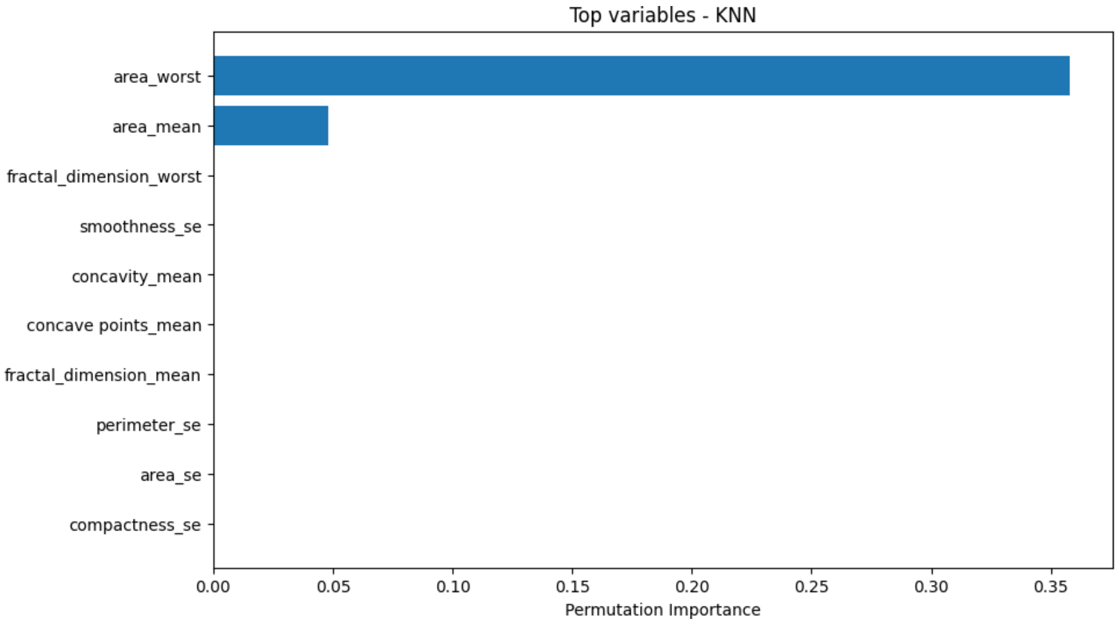
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

# Set up the KNN classifier
knn_classifier = KNeighborsClassifier()

# Define the parameter grid to search over
param_grid = {'n_neighbors': range(1, 21)}
```

```
# Perform grid search with cross-validation
grid_search = GridSearchCV(knn_classifier, param_grid=param_grid, cv=fitControl, scoring='roc_auc')

# Fit the model
grid_search.fit(X_train, y_train)

# Get the best model
best_knn_model = grid_search.best_estimator_

#  Make  predictions
predictions_knn  =  best_knn_model.predict(X_test)

# Generate confusion matrix
conf_matrix_knn = confusion_matrix(y_test, predictions_knn, labels=["B", "M"])

# Display confusion matrix
display = ConfusionMatrixDisplay(conf_matrix_knn, display_labels=["Benign", "Malignant"])
display.plot(cmap='Blues')
plt.title('Confusion Matrix for K-Nearest Neighbors Classifier')
plt.show()



# Calculate accuracy
accuracy_knn = accuracy_score(y_test, predictions_knn)
print("\nAccuracy:", accuracy_knn)

TN, FP, FN, TP = conf_matrix_knn.ravel()

# Calculate sensitivity and specificity
sensitivity = TP / (TP +  FN)
specificity = TN / (TN + FP)

# Print Sensitivity and Specificity
print(f"\nSensitivity: {sensitivity}")
print(f"Specificity: {specificity}")



# Compute permutation importances
result = permutation_importance(best_knn_model, X_test, y_test, n_repeats=10, random_state=1815)
```

```python
# Get sorted indices of feature importances
sorted_idx = result.importances_mean.argsort()

# Plot feature importance for the top 10 variables
top_n = 10
plt.figure(figsize=(10, 6))
plt.barh(range(top_n), result.importances_mean[sorted_idx][-top_n:],␣
 ↪align='center')
plt.yticks(range(top_n), X_test.columns[sorted_idx][-top_n:])
plt.xlabel('Permutation Importance')
plt.title('Top variables - KNN')
plt.show()
```



```
Accuracy: 0.9473684210526315

Sensitivity:  0.8809523809523809
Specificity:  0.9861111111111112
```



[106]:

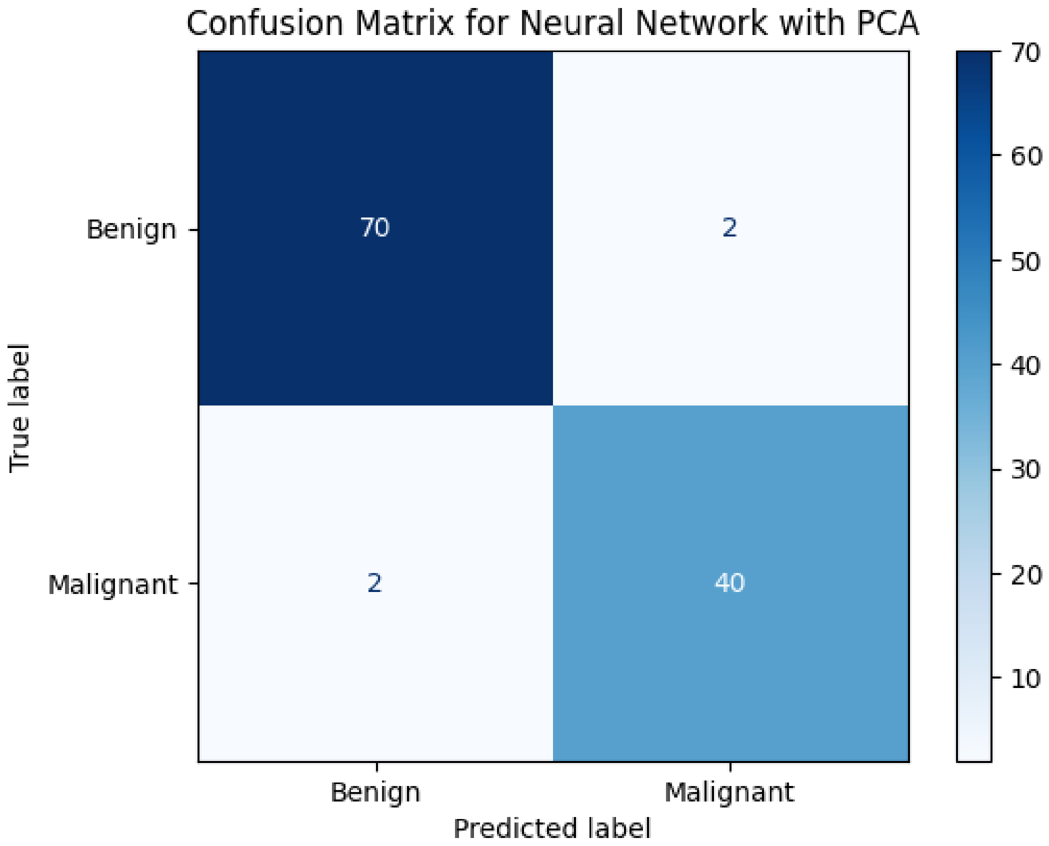
## 3 *5. Neural Network with PCA Model **

[29]:

```
from sklearn.neural_network import MLPClassifier
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.pipeline import make_pipeline
from sklearn.model_selection import GridSearchCV
from sklearn.model_selection import StratifiedKFold
# Define the pipeline with preprocessing and neural network classifier
model_nnet_pca = make_pipeline(StandardScaler(), PCA(), MLPClassifier())

# Define parameter grid for hyperparameter tuning
param_grid = {
    'mlpclassifier__hidden_layer_sizes': [(100,), (50,), (25,)],
    'mlpclassifier__alpha': [0.0001, 0.001, 0.01],
    'mlpclassifier__solver': ['adam'],
    'mlpclassifier__max_iter': [200, 300, 400]
}

t1 = time.time()
fitControl = StratifiedKFold(n_splits=15, shuffle=True, random_state=1815)
# Perform grid search with cross-validation
grid_search = GridSearchCV(model_nnet_pca, param_grid=param_grid,
 ↪cv=fitControl, scoring='roc_auc', verbose=1)
```

```
# Fit the model
grid_search.fit(X_train, y_train)

# Get the best model
best_nnet_model = grid_search.best_estimator_

# Make predictions
predictions_nnet_pca = best_nnet_model.predict(X_test)



# Calculate confusion matrix
conf_matrix_nnet_pca = confusion_matrix(y_test, predictions_nnet_pca)



# Display confusion matrix
display = ConfusionMatrixDisplay(conf_matrix_nnet_pca, display_labels=["Benign", "Malignant"])
display.plot(cmap='Blues')
plt.title('Confusion Matrix for Neural Network with PCA')
plt.show()

# Display confusion matrix
print("Confusion Matrix:")
print(conf_matrix_nnet_pca)
# Calculate accuracy
accuracy_nnet_pca = accuracy_score(y_test, predictions_nnet_pca)
print("\nAccuracy:", accuracy_nnet_pca)

# Generate classification report to get other metrics
class_report_nnet_pca = classification_report(y_test, predictions_nnet_pca, target_names=["Benign", "Malignant"])
print("\nClassification Report:")
print(class_report_nnet_pca)


t2 = time.time()
```

```
Fitting 15 folds for each of 27 candidates, totalling 405 fits
```



```
Confusion Matrix:
[[70  2]
 [ 2 40]]

Accuracy: 0.9649122807017544

Classification Report:
              precision    recall  f1-score   support

      Benign       0.97      0.97      0.97        72
   Malignant       0.95      0.95      0.95        42

    accuracy                           0.96       114
   macro avg       0.96      0.96      0.96       114
weighted avg       0.96      0.96      0.96       114
```

[ ]:

## COMPARISON:

[35]:

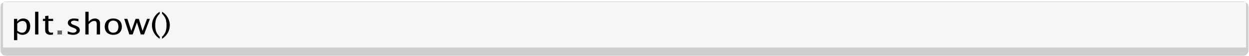
```
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
 ↪f1_score

# Define the models
models_list = [
    ("Naive Bayes", model_naiveb),
    ("Logistic Regression", model_logreg),
    ("Random Forest", model_randomforest),
    ("KNN", best_knn_model),
    ("Neural Network with PCA", best_nnet_model)
]

# Evaluate each model and calculate metrics
for name, model in models_list:
    # Make predictions
    predictions = model.predict(X_test)

    # Calculate metrics
    accuracy = accuracy_score(y_test, predictions)
    precision = precision_score(y_test, predictions, average='weighted')
    recall = recall_score(y_test, predictions, average='weighted')
    f1 = f1_score(y_test, predictions, average='weighted')

    # Print model name and metrics
    print(f"Model: {name}")
    print(f"Accuracy: {accuracy}")
    print(f"Precision: {precision}")
    print(f"Recall: {recall}")
    print(f"F1 Score: {f1}")
    print("\n")
```

```
Model: Naive Bayes
Accuracy: 0.9649122807017544
Precision: 0.966759002770083
Recall: 0.9649122807017544
F1 Score: 0.9645092460881936


Model: Logistic Regression
Accuracy: 0.9824561403508771
Precision: 0.9824561403508771
Recall: 0.9824561403508771
F1 Score: 0.9824561403508771


Model: Random Forest
Accuracy: 0.9736842105263158
```

```
Precision:  0.9737105878629081
Recall:  0.9736842105263158
F1 Score: 0.9736164257756981


Model: KNN
Accuracy: 0.9473684210526315
Precision:  0.9487534626038782
Recall:  0.9473684210526315
F1 Score: 0.9467638691322903


Model: Neural Network with PCA
Accuracy: 0.9649122807017544
Precision:  0.9649122807017544
Recall:  0.9649122807017544
F1 Score: 0.9649122807017544
```

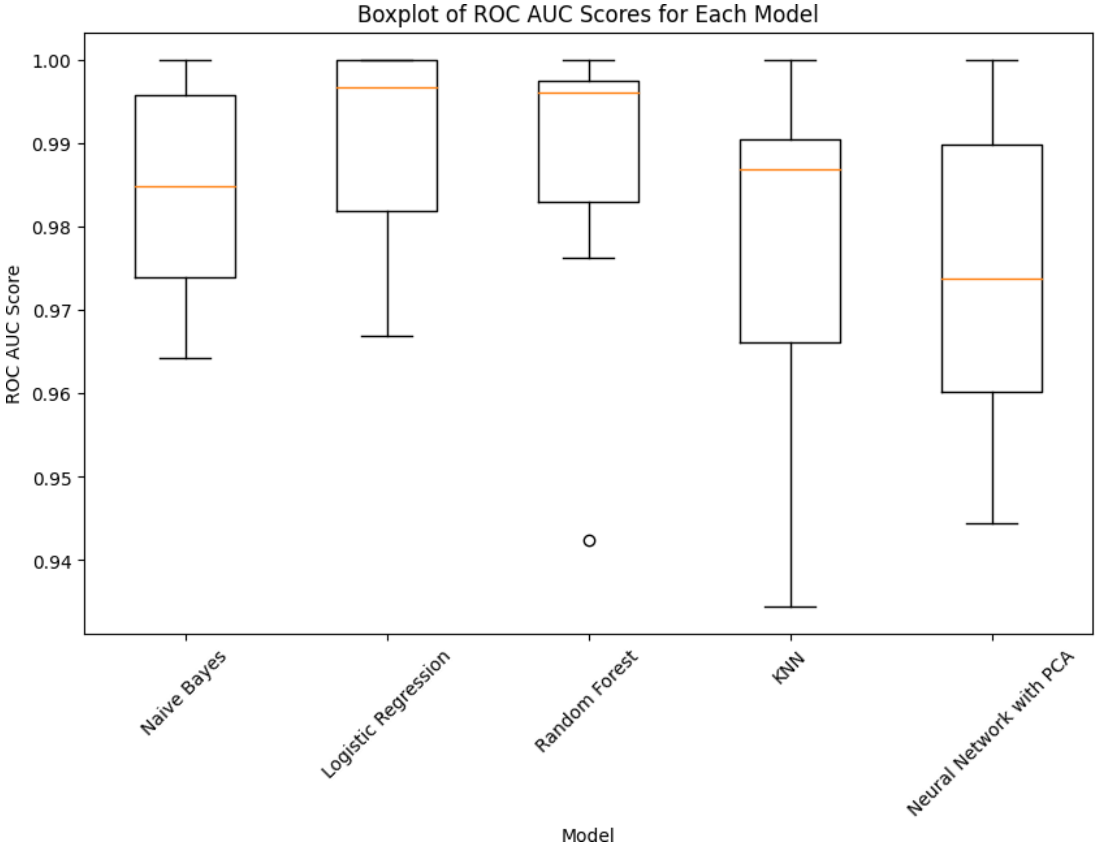
[40]:

```python
# Define a dictionary to store the models
models_dict = {
    'Naive Bayes': model_naiveb,
    'Logistic Regression': model_logreg,
    'Random Forest': model_randomforest,
    'KNN': best_knn_model,
    'Neural Network with PCA': model_nnet_pca
}

# Define a dictionary to store the ROC AUC scores for each model
roc_scores = {}

# Evaluate each model and calculate ROC AUC scores
for name, model in models_dict.items():
    # Use cross_val_score to get ROC AUC scores
    roc_auc_scores = cross_val_score(model, X, y, cv=cv, scoring='roc_auc')

    # Store the ROC AUC scores
    roc_scores[name] = roc_auc_scores

# Plot boxplot of ROC AUC scores
plt.figure(figsize=(10, 6))
plt.boxplot(roc_scores.values())
plt.xticks(range(1, len(roc_scores) + 1), roc_scores.keys(), rotation=45)
plt.xlabel('Model')
plt.ylabel('ROC AUC Score')
plt.title('Boxplot of ROC AUC Scores for Each Model')
```



```
plt.show()
```

H



# RESULTS ANALYSIS & CONCLUSION:

- Accuracy: Logistic Regression achieved the highest accuracy of 98.25%, closely followed by Random Forest at 97.37%.
- Precision: Logistic Regression, Random Forest, and Naive Bayes have the highest precision, all above 96.6%.
- Recall: Logistic Regression, Random Forest, Naive Bayes, and Neural Network with PCA have identical recall scores of 96.49%.
- F1 Score: Logistic Regression achieved the highest F1 Score of 98.25%, followed by Random Forest at 97.36%.

Considering all metrics, **Logistic Regression** emerges as the best model for this classification task. It achieved the highest accuracy, precision, recall, and F1 Score among the models evaluated. However, it's important to consider other factors such as model complexity, computational resources, and interpretability before finalizing the choice.