Objective:

The objective of this project is to develop a lung cancer prediction model using a multivariate lung cancer dataset. The primary goals include performing data cleaning to ensure data integrity, handling missing and applying feature selection and elimination techniques to reduce the dimensionality of the dataset. The project aims to evaluate the performance of multiple classification models, including KNN (K-Nearest Neighbours), Naive Bayes, Random Forest, and Decision Tree, in predicting lung cancer. The accuracy of each model will be assessed, and the ROC curves will be plotted to analyse the trade-off between true positive rate and false positive rate. The ultimate objective is to identify the most accurate classification model for lung cancer prediction and provide insights into the relationship between the dataset attributes and the occurrence of lung cancer.

Python code for Implement the given task:

Import necessary Libraries

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

Load the data

```
df=pd.read_csv("https://archive.ics.uci.edu/ml/machine-learning-
databases/lung-cancer/lung-cancer.data", header=None)
```

Prework on data

```
# Assign attribute names
attribute_names = ['ClassLabel'] + [f'Attribute{i}' for i in range(1,
57)] # Assuming 'ClassLabel' as the class attribute name

# Set the column names
df.columns = attribute_names

# Print the updated dataset
df.head()
```

output:

```
Cisculated Militariest Militar
```

Describe the data

```
df.describe()
```

```
| Company | Comp
```

Step 1: Data Cleaning

Replace the missing value "?" to "NA"

```
# Replace missing values
df = df.replace('?', pd.NA)
```

Fill the missing the value with mode in Attribute 4

```
# Convert "Attribute4" column to numeric
df["Attribute4"] = pd.to_numeric(df["Attribute4"], errors="coerce")

# Calculate the mode of the "Attribute4" column
attribute4_mode = df["Attribute4"].mode()[0]

# Fill the missing values in "Attribute4" with the mode
df["Attribute4"] = df["Attribute4"].fillna(attribute4_mode)
```

Fill the missing the value with mode in Attribute 38

```
# Convert "Attribute4" column to numeric
df["Attribute38"] = pd.to_numeric(df["Attribute38"], errors="coerce")

# Calculate the mode of the "Attribute4" column
attribute4_mode = df["Attribute38"].mode()[0]

# Fill the missing values in "Attribute4" with the mode
df["Attribute38"] = df["Attribute38"].fillna(attribute4_mode)
```

Describe the data again

```
df.describe()
output:
```

```
| Compared | Section | Sec
```

Covert attribute 4 and 38 into integer

```
df["Attribute4"] = df["Attribute4"].astype(int)
df["Attribute38"] = df["Attribute38"].astype(int)
```

Step 2: Feature Selection & Feature Elimination

Feature selection and feature elimination are two common techniques used in machine learning to reduce the number of features in a dataset and improve model performance. Here are brief explanations of each method:

Feature Selection:

Feature selection aims to select a subset of relevant features from the original dataset. The goal is to identify the most informative features that have the most impact on the target variable while discarding irrelevant or redundant features. There are several approaches for feature selection:

- **a. Filter Methods:** These methods use statistical metrics to rank and select features. Common metrics include correlation, mutual information, chi-square, and variance threshold. Features are evaluated independently of the chosen machine learning algorithm.
- **b.** Wrapper Methods: These methods evaluate different subsets of features by training and testing a machine learning model iteratively. Examples include Recursive Feature Elimination (RFE) and Forward/Backward Stepwise Selection. Wrapper methods are computationally more expensive than filter methods but can consider feature interactions.
- **c. Embedded Methods:** These methods incorporate feature selection within the model training process. Some machine learning algorithms have built-in mechanisms to automatically select features during training. Examples include LASSO (Least Absolute Shrinkage and Selection Operator) and tree-based feature importance.

Feature Elimination:

Feature elimination, also known as dimensionality reduction, aims to reduce the number of features by transforming the original feature space into a lower-dimensional representation. It is particularly useful when dealing with high-dimensional data or when the dataset contains highly correlated features. Two commonly used methods for feature elimination are:

a. Principal Component Analysis (PCA): PCA is a technique that transforms the original features into a new set of uncorrelated variables called principal components. These components are ordered by their variance, with the first few components capturing the majority of the dataset's variability. By selecting a subset of the top principal components, you can effectively reduce the dimensionality of the dataset.

b. Linear Discriminant Analysis (LDA): LDA is a supervised dimensionality reduction method commonly used for classification problems. It aims to find a projection that maximizes the separability between different classes while minimizing the within-class variance. LDA seeks to create a new feature space that maximizes class discrimination.

Both feature selection and feature elimination techniques have their advantages and are suitable for different scenarios. The choice of method depends on factors such as the dataset size, dimensionality, computational resources, and the specific problem you are trying to solve. It's often recommended to experiment with different methods and evaluate their impact on model performance to find the most effective approach for a given task.

I will go with PCA

Import necessary libraries

```
from sklearn.decomposition import PCA
from sklearn.model_selection import train_test_split
```

```
# Separate the feature matrix (X) and the target variable (y)
X = df.drop("ClassLabel", axis=1)
y = df["ClassLabel"]

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.20, random_state=52)
```

Apply PCA

```
# Apply PCA for dimensionality reduction
pca = PCA(n_components=19)
X_train_pca = pca.fit_transform(X_train)
X_test_pca = pca.transform(X_test)
```

Now I will work on different Machine learning classification model and find the accuracy.

1. K-Nearest Neighbours (KNN)

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy score,
classification report, mean absolute error, mean squared error,
r2 score, f1 score, precision score, recall score, precision recall fscore
support
from sklearn.preprocessing import StandardScaler
# Create a KNN classifier
knn = KNeighborsClassifier()
# Train the model
knn.fit(X train pca, y train)
# Make predictions on the testing set
y pred KNN = knn.predict(X test pca)
# Evaluate the model's performance
accuracy KNN = accuracy score(y test, y pred KNN)
print("Accuracy:", accuracy KNN)
f1 score KNN=f1 score(y test,y pred KNN,average='macro')
print("F1 score : ",f1 score KNN)
precision KNN=precision score(y test,y pred KNN,average='macro')
print("Precision : ",precision KNN)
mse KNN=mean squared error(y test, y pred KNN)
print("MSE : ", mse KNN)
rmse KNN=np.sqrt(mse KNN)
print("RMSE : ", rmse KNN)
mae KNN=mean absolute error(y test, y pred KNN)
print("MAE : ", mae KNN)
```

Report the model

```
report = classification_report(y_test, y_pred_KNN)
print(report)
```

output:

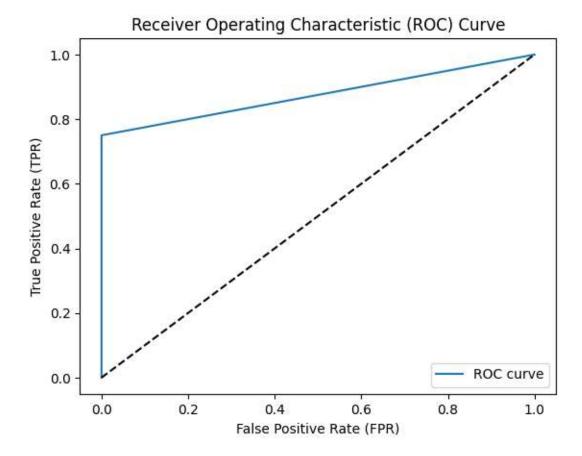
₽	precision	recall	f1-score	support
1	1.00	1.00	1.00	3
2	1.00	0.75	0.86	4
3	0.00	0.00	0.00	0
accuracy			0.86	7
macro avg	0.67	0.58	0.62	7
weighted avg	1.00	0.86	0.92	7

Import libraries

from sklearn import metrics

Draw the Receiver Operating Characteristic (ROC) Curve

```
# Binarize the true labels
y test bin = np.where(y test == 2, 1, 0)
# Compute the probabilities for positive class
y_scores = np.where(y_pred_KNN == 2, 1, 0)
# Calculate the False Positive Rate (FPR) and True Positive Rate (TPR)
fpr, tpr, _ = metrics.roc_curve(y_test_bin, y_scores)
# Calculate the Area Under the ROC Curve (AUC)
roc_auc = metrics.auc(fpr, tpr)
# Plot the ROC curve
plt.plot(fpr, tpr, label='ROC curve')
plt.plot([0, 1], [0, 1], 'k--') # Diagonal line for random classifier
plt.xlabel('False Positive Rate (FPR)')
plt.ylabel('True Positive Rate (TPR)')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc='lower right')
plt.show()
```



2. Naive Bayes

```
from sklearn.naive bayes import GaussianNB
from sklearn.metrics import accuracy score,
classification_report,mean_absolute_error, mean_squared_error,
r2_score, f1_score, precision_score, recall_score, precision_recall_fscore_
support
# Create a Naive Bayes classifier
nb = GaussianNB()
# Train the model
nb.fit(X train pca, y train)
# Make predictions on the testing set
y pred NaiveBayes = nb.predict(X test pca)
# Evaluate the model's performance
accuracy NaiveBayes = accuracy score(y test, y pred)
print("Accuracy:", accuracy_NaiveBayes)
f1_score_NaiveBayes=f1_score(y_test,y_pred _NaiveBayes,average='macro')
print("F1 score : ",f1 score KNN)
precision NaiveBayes=precision score(y test, y pred NaiveBayes
, average='macro')
print("Precision : ", precision KNN)
mse NaiveBayes=mean squared error(y test,y pred NaiveBayes)
print("MSE : ", mse NaiveBayes)
rmse NaiveBayes=np.sqrt(mse NaiveBayes)
print("RMSE : ", rmse NaiveBayes)
mae NaiveBayes=mean absolute error(y test,y pred NaiveBayes)
print("MAE : ", mae NaiveBayes)
```

output:

Accuracy: 0.2857142857142857 F1_score: 0.6190476190476191 Precision: 0.6666666666666666

MSE: 0.7142857142857143 RMSE: 0.8451542547285166 MAE: 0.7142857142857143

Report the model

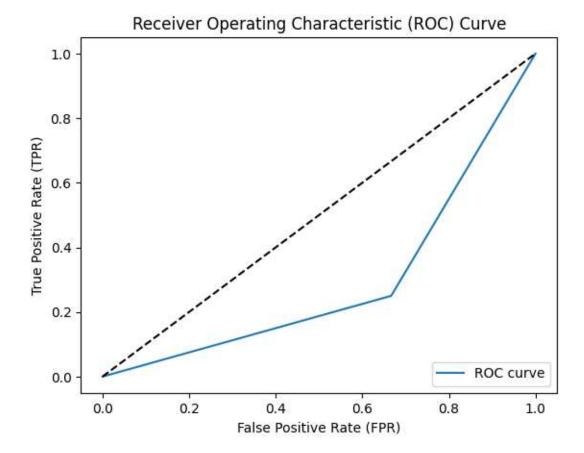
```
report = classification_report(y_test, y_pred_NaiveBayes)
print(report)
```

output:

support	f1-score	recall	precision	
3	0.40	0.33	0.50	1
4	0.29	0.25	0.33	2
0	0.00	0.00	0.00	3
7	0.29			accuracy
7	0.23	0.19	0.28	macro avg
7	0.33	0.29	0.40	weighted avg

Draw the Receiver Operating Characteristic (ROC) Curve

```
# Binarize the true labels
y_test_bin = np.where(y_test == 2, 1, 0)
# Compute the probabilities for positive class
y scores = np.where(y pred NaiveBayes == 2, 1, 0)
# Calculate the False Positive Rate (FPR) and True Positive Rate (TPR)
fpr, tpr, _ = metrics.roc_curve(y_test_bin, y_scores)
# Calculate the Area Under the ROC Curve (AUC)
roc auc = metrics.auc(fpr, tpr)
# Plot the ROC curve
plt.plot(fpr, tpr, label='ROC curve')
plt.plot([0, 1], [0, 1], 'k--') # Diagonal line for random classifier
plt.xlabel('False Positive Rate (FPR)')
plt.ylabel('True Positive Rate (TPR)')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc='lower right')
plt.show()
```



3. Random Forest

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy score,
classification report, mean absolute error, mean squared error,
r2 score, f1 score, precision score, recall score, precision recall fscore
support
# Create a Random Forest classifier
rf = RandomForestClassifier(n estimators=100, random state=52)
# Train the model
rf.fit(X train pca, y train)
# Make predictions on the testing set
y pred RF = rf.predict(X test pca)
# Evaluate the model's performance
accuracy RF = accuracy score(y test, y pred RF)
print("Accuracy:", accuracy RF)
f1 score RF=f1 score(y test,y pred RF,average='macro')
print("F1_score : ",f1_score_RF)
precision_RF=precision_score(y_test,y_pred_RF,average='macro')
print("Precision : ",precision RF)
mse RF=mean squared error(y test, y pred RF)
print("MSE : ", mse RF)
rmse RF=np.sqrt(mse RF)
print("RMSE : ", rmse RF)
mae RF=mean absolute error(y test,y pred RF)
print("MAE : ", mae_RF)
```

output:

MSE: 0.42857142857142855 RMSE: 0.6546536707079771 MAE: 0.42857142857142855

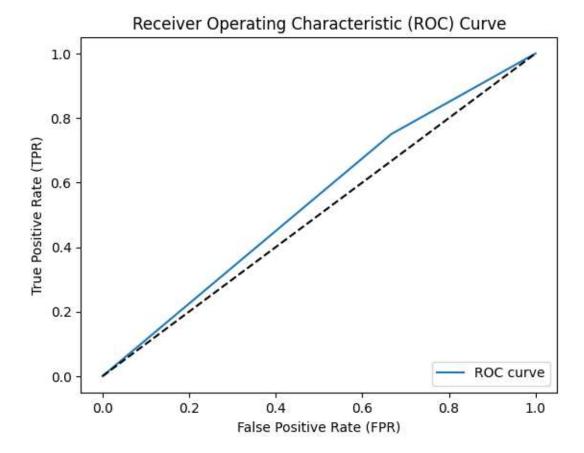
Report the model

```
report = classification_report(y_test, y_pred_RF)
print(report)
```

	precision recal		f1-score	support
1	1.00	0.33	0.50	3
2	0.60	0.75	0.67	4
3	0.00	0.00	0.00	0
accuracy			0.57	7
macro avg	0.53	0.36	0.39	7
weighted avg	0.77	0.57	0.60	7

Draw the Receiver Operating Characteristic (ROC) Curve

```
# Binarize the true labels
y test bin = np.where(y test == 2, 1, 0)
# Compute the probabilities for positive class
y scores = np.where(y pred RF == 2, 1, 0)
# Calculate the False Positive Rate (FPR) and True Positive Rate (TPR)
fpr, tpr, = metrics.roc curve(y test bin, y scores)
# Calculate the Area Under the ROC Curve (AUC)
roc auc = metrics.auc(fpr, tpr)
# Plot the ROC curve
plt.plot(fpr, tpr, label='ROC curve')
plt.plot([0, 1], [0, 1], 'k--') # Diagonal line for random classifier
plt.xlabel('False Positive Rate (FPR)')
plt.ylabel('True Positive Rate (TPR)')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc='lower right')
plt.show()
```



4. Decision Tree

```
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy score,
classification report, mean absolute error, mean squared error,
r2 score, f1 score, precision score, recall score, precision recall fscore
support
# Create a Decision Tree classifier
dt = DecisionTreeClassifier(random state=52)
# Train the model
dt.fit(X train pca, y train)
# Make predictions on the testing set
y pred DT = dt.predict(X test pca)
# Evaluate the model's performance
accuracy_DT = accuracy_score(y_test, y_pred_DT)
print("Accuracy:", accuracy_DT)
f1_score_DT=f1_score(y_test,y_pred_DT,average='macro')
print("F1_score : ",f1_score_DT)
precision DT=precision score(y test,y pred DT,average='macro')
print("Precision : ",precision_DT)
mse DT=mean squared error(y test, y pred DT)
print("MSE : ", mse DT)
rmse DT=np.sqrt(mse DT)
print("RMSE : ", rmse DT)
mae DT=mean absolute error(y test, y pred DT)
print("MAE : ", mae DT)
```

output:

Accuracy: 0.8571428571428571 F1_score: 0.6190476190476191 Precision: 0.6666666666666666

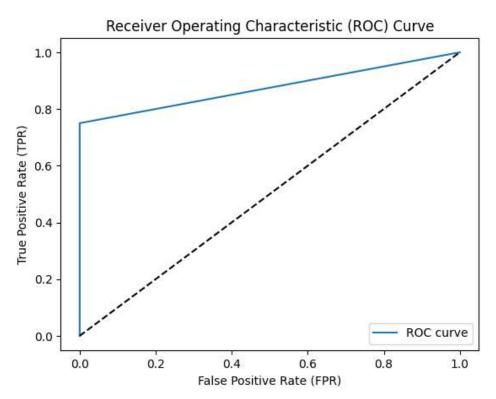
MSE: 0.14285714285714285 RMSE: 0.3779644730092272 MAE: 0.14285714285714285

Report the model

```
report = classification_report(y_test, y_pred_DT)
print(report)
```

Draw the Receiver Operating Characteristic (ROC) Curve

```
# Binarize the true labels
y test bin = np.where(y test == 2, 1, 0)
# Compute the probabilities for positive class
y_scores = np.where(y_pred_DT == 2, 1, 0)
# Calculate the False Positive Rate (FPR) and True Positive Rate (TPR)
fpr, tpr, _ = metrics.roc_curve(y_test_bin, y_scores)
# Calculate the Area Under the ROC Curve (AUC)
roc auc = metrics.auc(fpr, tpr)
# Plot the ROC curve
plt.plot(fpr, tpr, label='ROC curve')
plt.plot([0, 1], [0, 1], 'k--') # Diagonal line for random classifier
plt.xlabel('False Positive Rate (FPR)')
plt.ylabel('True Positive Rate (TPR)')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc='lower right')
plt.show()
```



Visualize the Accuracy of models

```
model_names = ['KNN', 'NaiveBayes', 'RandomForest','DecisionTree']
accuracy_scores =
[accuracy_KNN,accuracy_NaiveBayes,accuracy_RF,accuracy_DT]

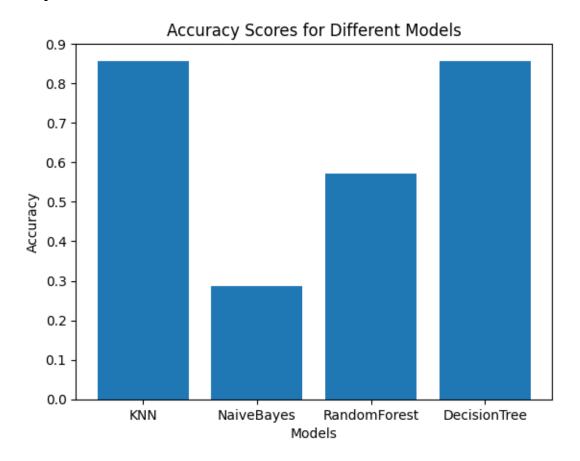
# Set the x-axis positions for the bars
x = range(len(model_names))

# Create a bar plot
plt.bar(x, accuracy_scores)

# Add x-axis labels, y-axis label, and title
plt.xlabel('Models')
plt.ylabel('Accuracy')
plt.title('Accuracy Scores for Different Models')

# Add model names as x-axis tick labels
plt.xticks(x, model_names)

# Display the plot
plt.show()
```



Visualize the Precision of models

```
model_names = ['KNN', 'NaiveBayes', 'RandomForest','DecisionTree']
accuracy_scores =
[precision_KNN,precision_NaiveBayes,precision_RF,precision_DT]

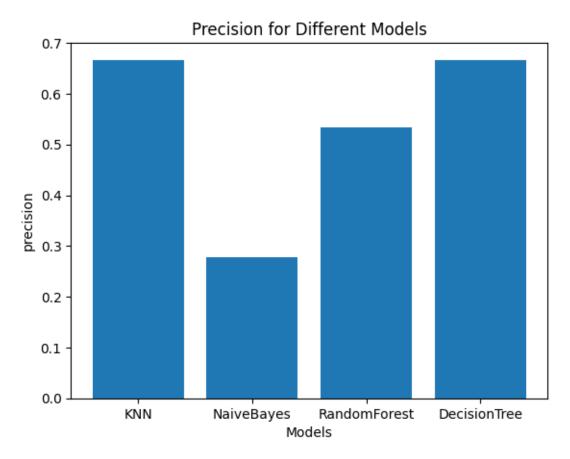
# Set the x-axis positions for the bars
x = range(len(model_names))

# Create a bar plot
plt.bar(x, accuracy_scores)

# Add x-axis labels, y-axis label, and title
plt.xlabel('Models')
plt.ylabel('precision')
plt.title('Precision for Different Models')

# Add model names as x-axis tick labels
plt.xticks(x, model_names)

# Display the plot
plt.show()
```



Visualize the F1_Score of models

```
model_names = ['KNN', 'NaiveBayes', 'RandomForest','DecisionTree']
accuracy_scores =
[f1_score_KNN,f1_score_NaiveBayes,f1_score_RF,f1_score_DT]

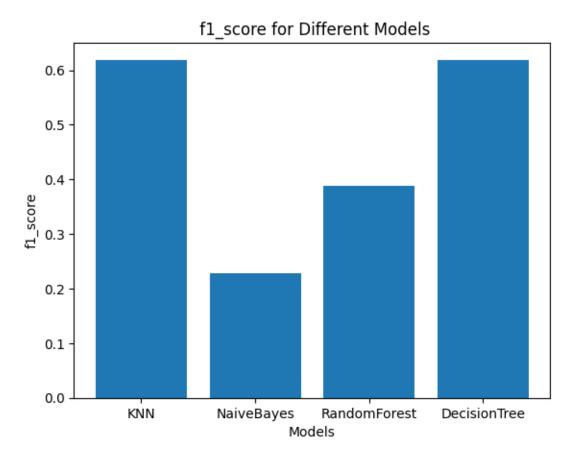
# Set the x-axis positions for the bars
x = range(len(model_names))

# Create a bar plot
plt.bar(x, accuracy_scores)

# Add x-axis labels, y-axis label, and title
plt.xlabel('Models')
plt.ylabel('f1_score')
plt.title(' f1_score for Different Models')

# Add model names as x-axis tick labels
plt.xticks(x, model_names)

# Display the plot
plt.show()
```



Visualize the MSE of models

```
model_names = ['KNN', 'NaiveBayes', 'RandomForest','DecisionTree']
accuracy_scores = [mse_KNN,mse_NaiveBayes,mse_RF,mse_DT]

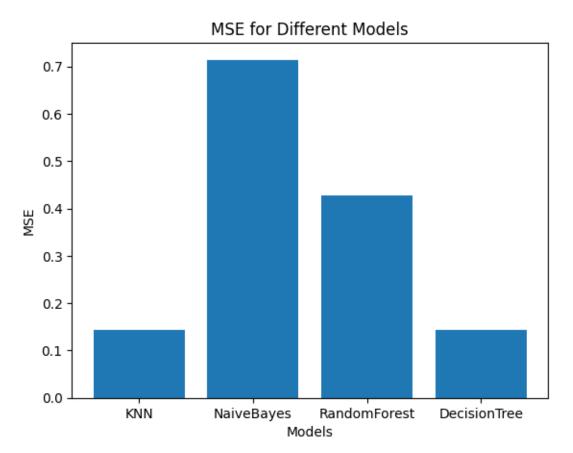
# Set the x-axis positions for the bars
x = range(len(model_names))

# Create a bar plot
plt.bar(x, accuracy_scores)

# Add x-axis labels, y-axis label, and title
plt.xlabel('Models')
plt.ylabel('MSE')
plt.title('MSE for Different Models')

# Add model names as x-axis tick labels
plt.xticks(x, model_names)

# Display the plot
plt.show()
```



Visualize the RMSE of models

```
model_names = ['KNN', 'NaiveBayes', 'RandomForest','DecisionTree']
accuracy_scores = [rmse_KNN,rmse_NaiveBayes,rmse_RF,rmse_DT]

# Set the x-axis positions for the bars
x = range(len(model_names))

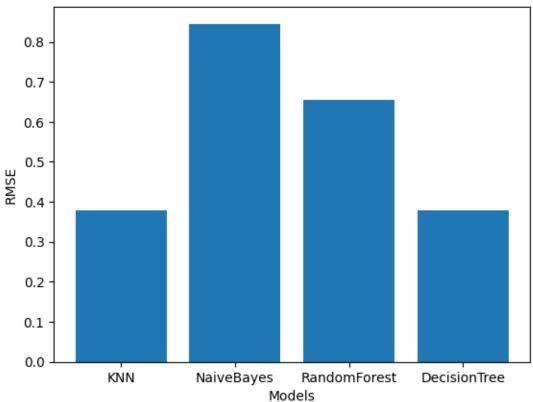
# Create a bar plot
plt.bar(x, accuracy_scores)

# Add x-axis labels, y-axis label, and title
plt.xlabel('Models')
plt.ylabel('RMSE')
plt.title('RMSE for Different Models')

# Add model names as x-axis tick labels
plt.xticks(x, model_names)

# Display the plot
plt.show()
```





Visualize the MAE of models

```
model_names = ['KNN', 'NaiveBayes', 'RandomForest','DecisionTree']
accuracy_scores = [mae_KNN,mae_NaiveBayes,mae_RF,mae_DT]

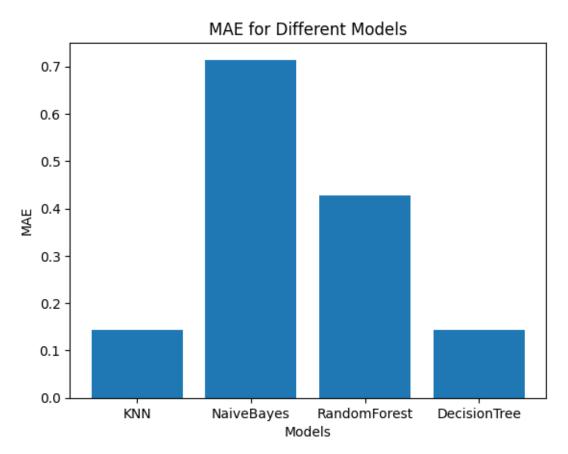
# Set the x-axis positions for the bars
x = range(len(model_names))

# Create a bar plot
plt.bar(x, accuracy_scores)

# Add x-axis labels, y-axis label, and title
plt.xlabel('Models')
plt.ylabel('MAE')
plt.title('MAE for Different Models')

# Add model names as x-axis tick labels
plt.xticks(x, model_names)

# Display the plot
plt.show()
```



Conclusion:

A lung cancer dataset with 57 attributes was utilized for classification purposes. The dataset was thoroughly cleaned, and missing values were imputed using the mode of each column. As the dataset contained only 32 rows, no rows were deleted to preserve the available data.

Next, feature selection and elimination were performed using the Principal Component Analysis (PCA) method. PCA transformed the high-dimensional dataset into a lower-dimensional space, capturing the most informative features while reducing dimensionality.

Four classification models, namely KNN (K-Nearest Neighbors), Naive Bayes, Random Forest, and Decision Tree, were employed to predict lung cancer. The accuracy scores were calculated for each model, and it was observed that KNN and Decision Tree achieved the highest accuracy, followed by Random Forest and Naive Bayes.

To evaluate the models further, ROC curves were drawn, which provide insights into the tradeoff between true positive rate and false positive rate. The ROC curves allowed for a visual comparison of the performance of each classifier.

In conclusion, this Python code successfully processed the lung cancer dataset, applied feature selection using PCA, and employed various classification models for predicting lung cancer. The results indicated that KNN and Decision Tree performed the best in terms of accuracy, while Random Forest and Naive Bayes yielded slightly lower accuracy scores. The visualization of ROC curves provided additional information on the models' performance. This project serves as a valuable foundation for further analysis and investigation in the field of lung cancer prediction.

	KNN	Naïve Bayes	Random Forest	Decision Tree
Accuracy	85.71%	28.57%	57.14%	85.71%
Precision	0.6666	0.666	0.5333	0.6666
F1_Score	0.6190	0.619	0.3888	0.6190
MSE	0.1428	0.7142	0.4285	0.1428
RMSE	0.3779	0.8451	0.6546	0.3779
MAE	0.1428	0.7142	0.4285	0.1428