CSE3040 Exploratory Data Analysis

J Component - Project Report

Review III

Health Status Prediction

By

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Integrated M.Tech CSE Business Analytics

Submitted to

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Vellore Institute of Technology
(Deemed to be University under section 3 of UGC Act, 1956)

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School of Computing Science and Engineering

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WINTER SEM 23-24

Worklet details

Programme	M.Tech with Business Analytics	
Course Name / Code	CSE3040	
Slot	F1+TF1	
Faculty Name	Dr.A.Bhuvaneswari	
Digital Assignment	Review 3	
Team Members Name | Reg. No	22MIA1123	Abishek.N
	22MIA1150	Ramanan.G
	22MIA1113	Dhanush.P

Team Members(s) Contributions – Tentatively planned for implementation:

Worklet Tasks	*Contributor's Names*
Dataset Collection	Dhanush.P
Preprocessing	Ramanan.G
Architecture/ Model/ Flow diagram	Abishek.N
Model building (suitable algorithm)	Abishek.N, Dhanush.P
Results – Tables, Graphs	Ramanan.G
Technical Report writing	Abishek.N, Ramanan.G
Presentation preparation	Dhanush.P

ABSTRACT

Smoking is acknowledged as the primary risk factor for lung cancer, which continues to be a serious public health concern. But a significant fraction of lung cancer diagnoses occurs in people who have never smoked, suggesting the existence of other risk factors. The goal of this study is to create an integrated prediction model for assessing the risk of lung cancer that takes into account symptoms associated with both smoking and non-smoking factors.

The study draws upon a comprehensive dataset comprising clinical records of lung cancer patients, encompassing demographic information, smoking history, non-smoking related symptoms, diagnostic tests, and treatment outcomes. Of particular emphasis are symptoms like chronic cough, hemoptysis, dyspnea, chest pain, and weight loss, while accounting for other non-smoking factors such as environmental exposures and genetic predisposition.

The prediction model is built using sophisticated machine learning approaches, which include feature selection, model training, and evaluation. Numerous algorithms are investigated to maximize the incorporation of smoking and non-smoking associated symptoms into the model, including logistic regression, decision trees, random forests, and gradient boosting.

Validation of the predictive model is conducted using independent datasets to assess its accuracy, sensitivity, specificity, and generalizability across diverse populations. Additionally, the clinical utility of the model is evaluated through retrospective analysis and comparison with existing risk assessment tools.

The results of this study have the potential to improve lung cancer prevention and early detection methods. The prediction approach enables healthcare practitioners to target interventions and deliver tailored risk assessments by identifying patients at heightened risk based on a combination of smoking and non-smoking related symptoms. In the end, this strategy might result in improved patient outcomes and lower mortality rates from lung cancer.

Moreover, the development of an integrative predictive model has broader implications for public health interventions and resource allocation. By identifying modifiable risk factors and high-risk populations, policymakers and healthcare stakeholders can implement targeted prevention programs and allocate resources more efficiently to reduce the burden of lung cancer on individuals and healthcare systems.

In conclusion, this project contributes to advancing our understanding of lung cancer risk factors and developing effective predictive tools for risk assessment. By integrating smoking and non-smoking related symptoms into the predictive model, we aim to improve early detection, personalize interventions, and ultimately reduce the impact of lung cancer on public health.

Table of Contents:

1. Introduction and Problem Background:

Lung cancer remains one of the most prevalent and lethal forms of cancer worldwide, posing significant challenges to public health systems and medical practitioners. Early detection and prediction of lung cancer are crucial for improving patient outcomes and reducing mortality rates. In recent years, the integration of machine learning techniques with medical data has shown promising results in predicting cancer risk, including lung cancer.

Challenges Faced:

1. Data Quality: Ensuring the dataset is comprehensive, accurate, and representative of diverse populations to build a robust predictive model.

2. Feature Selection: Determining which features are most relevant and impactful in predicting lung cancer risk among a wide array of potential variables.

3. Imbalanced Data: Addressing potential class imbalances in the dataset, as lung cancer cases may be significantly outnumbered by non-cancer cases.

4. Ethical Considerations: Ensuring patient privacy and confidentiality while handling sensitive medical data, adhering to ethical guidelines and regulations.

5. Model Interpretability: Ensuring the developed predictive model is interpretable and transparent, enabling medical professionals to understand and trust its recommendations.

2. Literature review:

Lung cancer remains a formidable public health challenge, with smoking widely acknowledged as the primary risk factor. However, a notable fraction of lung cancer cases occurs in non-smokers, underscoring the importance of exploring additional risk factors. Common symptoms associated with lung cancer, such as chronic cough, hemoptysis, and weight loss, warrant comprehensive risk assessment strategies that consider both smoking and non-smoking related factors.

Recent advancements in predictive modeling have facilitated the integration of diverse risk factors into comprehensive risk assessment tools for lung cancer. Machine learning algorithms, including logistic regression and decision trees, have demonstrated efficacy in developing predictive models that incorporate smoking history, environmental exposures, and genetic predisposition. Validation studies have shown promising results, emphasizing the potential of these models for accurate risk assessment and early detection.

Our project seeks to address the gap in existing lung cancer risk assessment tools by developing an integrated prediction model that accounts for both smoking and non-smoking related symptoms. Leveraging a comprehensive dataset comprising clinical records of lung cancer patients, our primary objective is to identify key risk factors and construct a robust predictive model using advanced machine learning techniques. By improving early detection and personalized risk assessment, our project aims to enhance patient outcomes and reduce mortality rates from lung cancer.

To achieve our objectives, we will employ a systematic approach involving data preprocessing, feature selection, model training, and validation. Our methodology includes exploring various machine learning algorithms such as logistic regression, random forests, and gradient boosting to maximize the incorporation of smoking and non-smoking related symptoms into the predictive model. Validation of the model will be conducted using independent datasets to assess its accuracy, sensitivity, specificity, and generalizability across diverse populations.

In conclusion, our project represents a significant step towards improving lung cancer risk assessment and early detection methods. By integrating smoking and non-smoking related symptoms into a comprehensive predictive model, we aim to provide healthcare practitioners with a valuable tool for identifying high-risk individuals and delivering personalized risk assessments. Continued research and development in this area are crucial for addressing the challenges associated with lung cancer prevention and management and ultimately reducing the burden of this disease on individuals and healthcare systems.

3. Problem Statement & Objectives:

The primary focus of this research is to develop a predictive model for lung cancer utilizing a dataset comprising various parameters such as age, gender, lifestyle factors (like alcohol use, smoking habits), environmental exposures (such as air pollution, dust allergy), and medical history (like chronic lung diseases). The goal is to leverage these features to predict the likelihood of an individual developing lung cancer.

Objectives:

1. Develop a machine learning model capable of accurately predicting lung cancer risk based on the provided dataset.

2. Identify the most significant factors contributing to lung cancer for chain-smokers, occasional smokers and non-smokers.

3. Evaluate the performance of the developed model through appropriate metrics such as accuracy, precision, recall, and F1-score.

4. Provide insights and recommendations for preventive measures and early intervention strategies based on the predictive model's findings.

4. Dataset and Database Specific Tools Description:

Dataset comprises lung cancer prediction data including symptoms, diagnostic outcomes, age, gender, and smoking history. (source: Kaggle.com)

Support Vector Machines (SVM) and Gradient Boosting Machines (GBM):

Employing SVM or GBM for predictive modeling due to their effectiveness in handling non-linear relationships and high-dimensional data.

Data Visualization Tool: PowerBI:

Leveraging PowerBI for interactive data visualization and business intelligence, facilitating exploration of patterns and insights within the lung cancer prediction dataset.

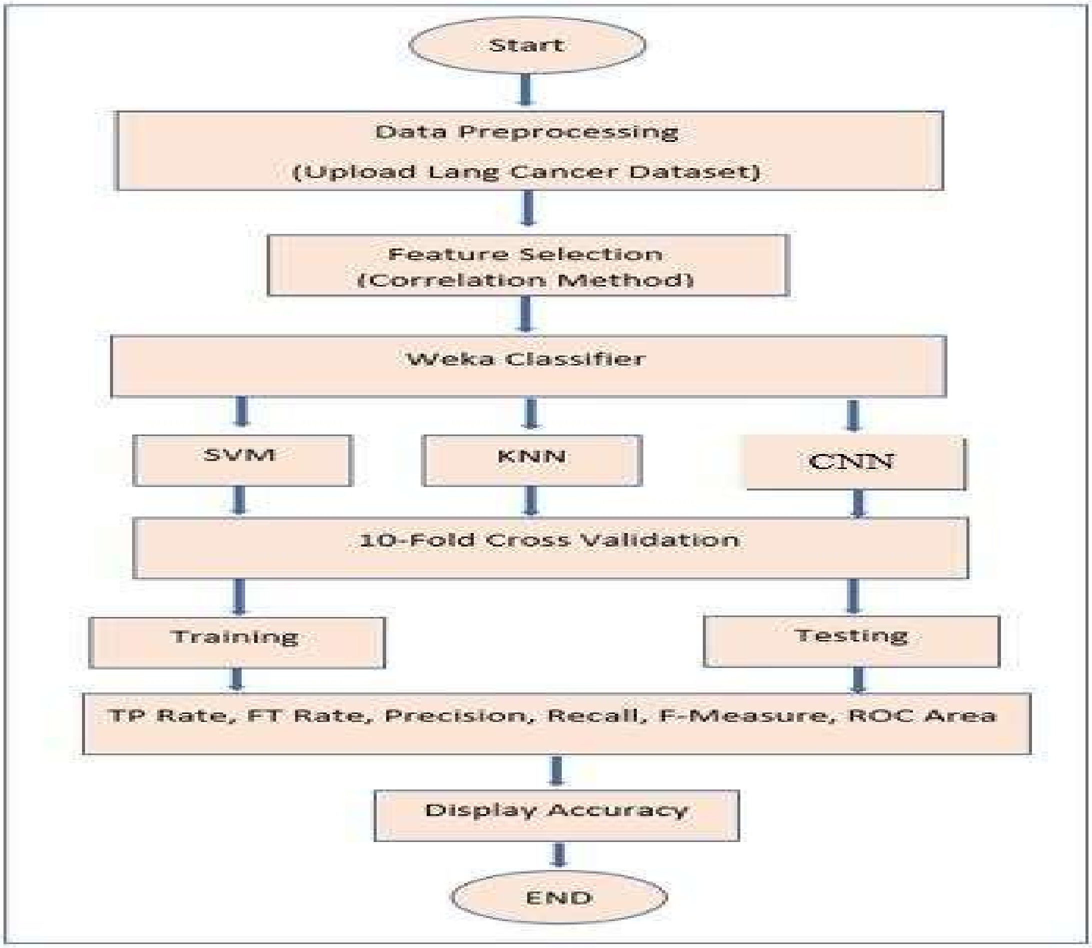
Data Manipulation and Analysis Tool: Jupyter Notebook:

Utilizing Jupyter Notebook for seamless data manipulation and analysis, integrating with libraries such as Pandas, NumPy, and scikit-learn to preprocess, analyze, and visualize data efficiently.

5. Hardware Description Used to Implement the Project:

- Lenovo ThinkPad - Intel(R) Core(TM) i5-10210U CPU @ 1.60GHz 2.10 GHz, RAM- 8.00 GB, ROM-512 GB
- Hp Pavillion - Ryzen 5000 Series, RTX GeForce 3050, RAM-16GB, ROM- 512 GB
- Lenovo IdeaPad Slim 3 - i3 11th gen, RAM-8 GB, ROM- 512 GB

6. System Architecture or Block Diagram of the Project:



7. Module Description and Implementation:

Data Preprocessing Module:

Description: This module focuses on preparing the dataset for analysis by handling missing values, removing duplicates, and performing feature engineering.

Functionality: It includes tasks such as dropping duplicate rows, filling missing values, and converting categorical variables to numerical format if necessary.

Implementation: Utilizes pandas functions for data manipulation, such as drop_duplicates(), fillna(), and replace(). It may also involve data scaling or normalization using techniques like StandardScaler.

Descriptive Statistics Module:

Description: This module calculates summary statistics and explores the distribution of variables in the dataset.

Functionality: It provides insights into the central tendency, dispersion, and shape of data distributions using measures like mean, median, standard deviation, and visualizations like histograms and box plots.

Implementation: Employs pandas' describe() function for summary statistics and matplotlib or seaborn for visualization of distributions.

Feature Selection Module:

Description: This module identifies the most relevant features that contribute to predicting lung cancer severity.

Functionality: It utilizes statistical methods or machine learning algorithms to rank features based on their importance or significance.

Implementation: Utilizes feature selection techniques such as ANOVA F-value, correlation analysis, or recursive feature elimination (RFE) from scikit-learn.

Outlier Detection Module:

Description: This module identifies and handles outliers in the dataset that may affect the analysis results.

Functionality: It detects outliers using statistical methods like the interquartile range (IQR) or Z-score and may choose to remove, replace, or impute outlier values.

Implementation: Employs pandas functions for outlier detection and manipulation, such as calculating quartiles and applying threshold conditions.

Correlation Analysis Module:

Description: This module examines the relationships between variables in the dataset to identify patterns and dependencies.

Functionality: It computes correlation coefficients between pairs of variables and visualizes correlation matrices to assess the strength and direction of relationships.

Implementation: Utilizes pandas' corr() function for correlation computation and seaborn or matplotlib for heatmap visualization.

Clustering Analysis Module:

Description: This module applies clustering algorithms to identify natural groupings or patterns in the dataset.

Functionality: It partitions data points into clusters based on similarity measures and visualizes cluster assignments.

Implementation: Utilizes algorithms like K-means clustering from scikit-learn and matplotlib for cluster visualization.

Conclusion and Insights Module:

Description: This module summarizes the findings and insights derived from the exploratory data analysis process.

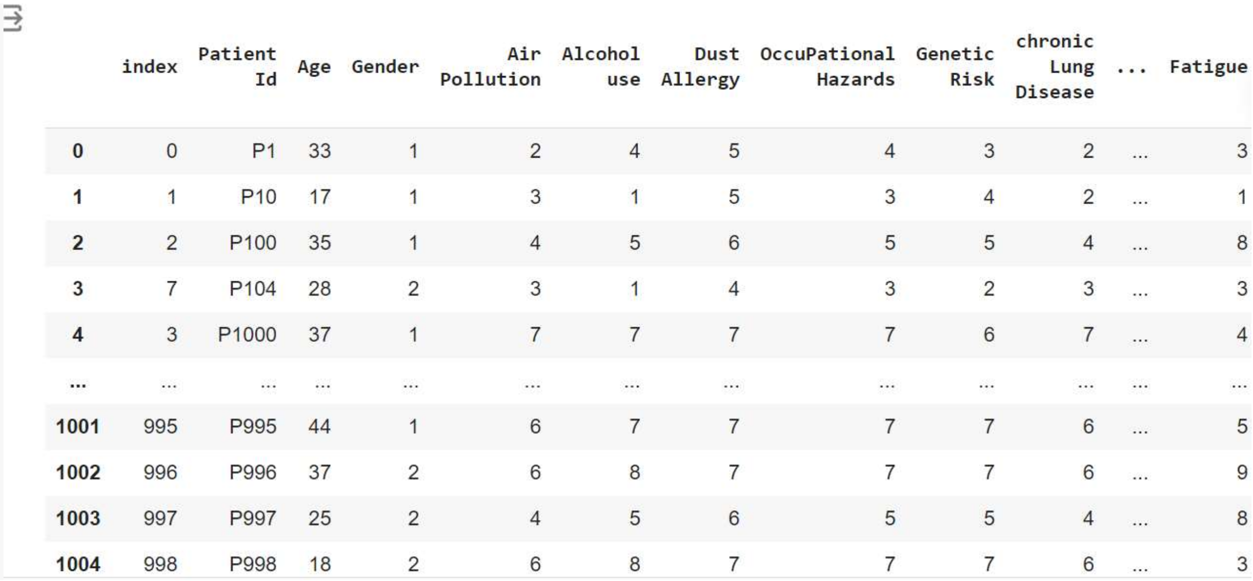
Functionality: It presents key observations, trends, and potential implications for predicting lung cancer severity based on the analyzed features.

Provides a concise summary of the EDA results and may include actionable recommendations for further analysis or model development.

8. Result Analysis:

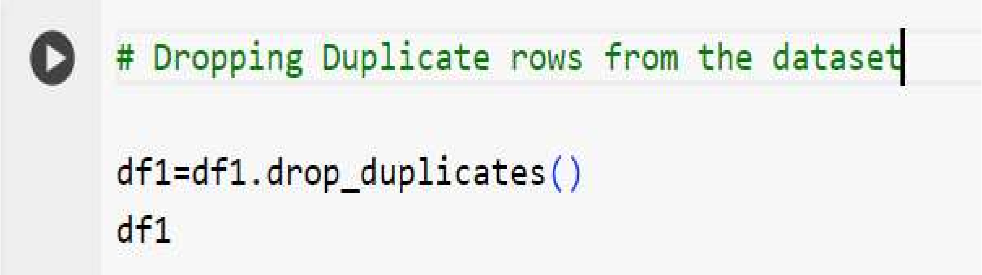
Importing Dataset:

```
import pandas as pd

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

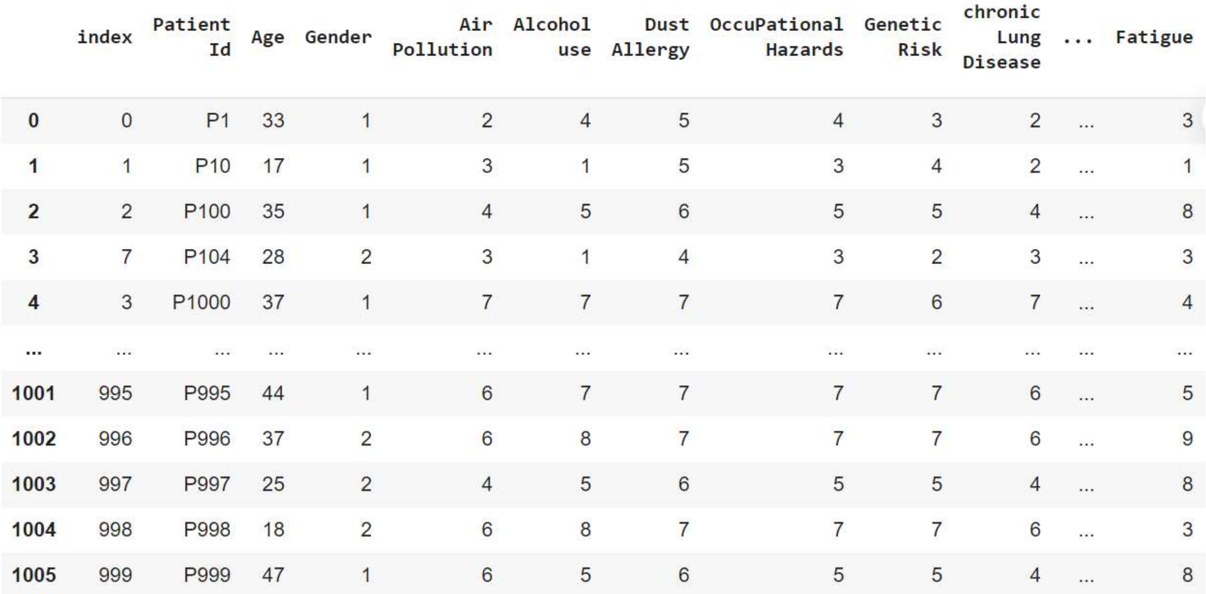


	index	Patient Id	Age	Gender	Air Pollution	Alcohol use	Dust Allergy	OccuPational Hazards	Genetic Risk	chronic Lung Disease	...	Fatigue
0	0	P1	33	1	2	4	5	4	3	2	...	3
1	1	P10	17	1	3	1	5	3	4	2	...	1
2	2	P100	35	1	4	5	6	5	5	4	...	8
3	7	P104	28	2	3	1	4	3	2	3	...	3
4	3	P1000	37	1	7	7	7	7	6	7	...	4
...	...	...	...	...	...	...	...	...	...	...	...	...
1001	995	P995	44	1	6	7	7	7	7	6	...	5
1002	996	P996	37	2	6	8	7	7	7	6	...	9
1003	997	P997	25	2	4	5	6	5	5	4	...	8
1004	998	P998	18	2	6	8	7	7	7	6	...	3

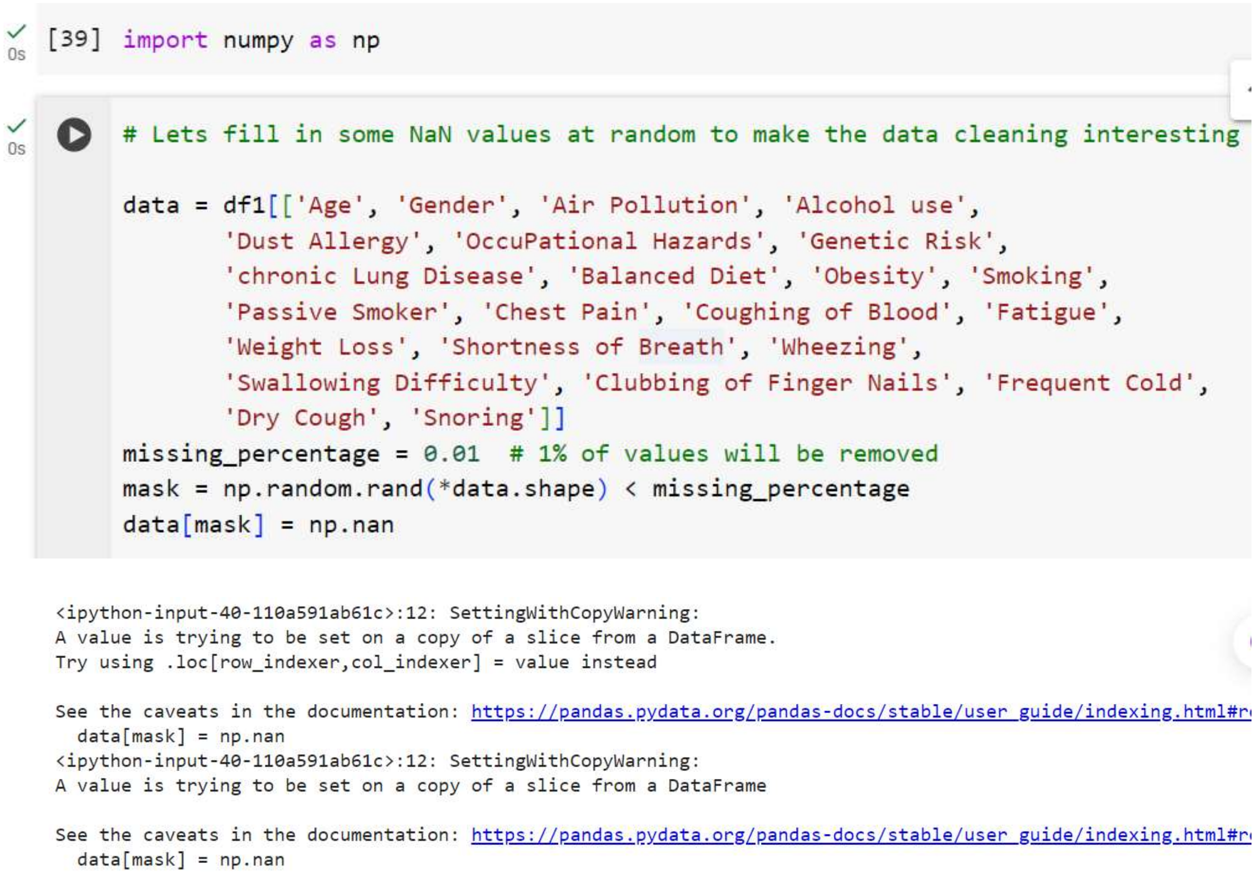
Data Pre-Processing:



```
# Dropping Duplicate rows from the dataset

df1=df1.drop_duplicates()
df1
```



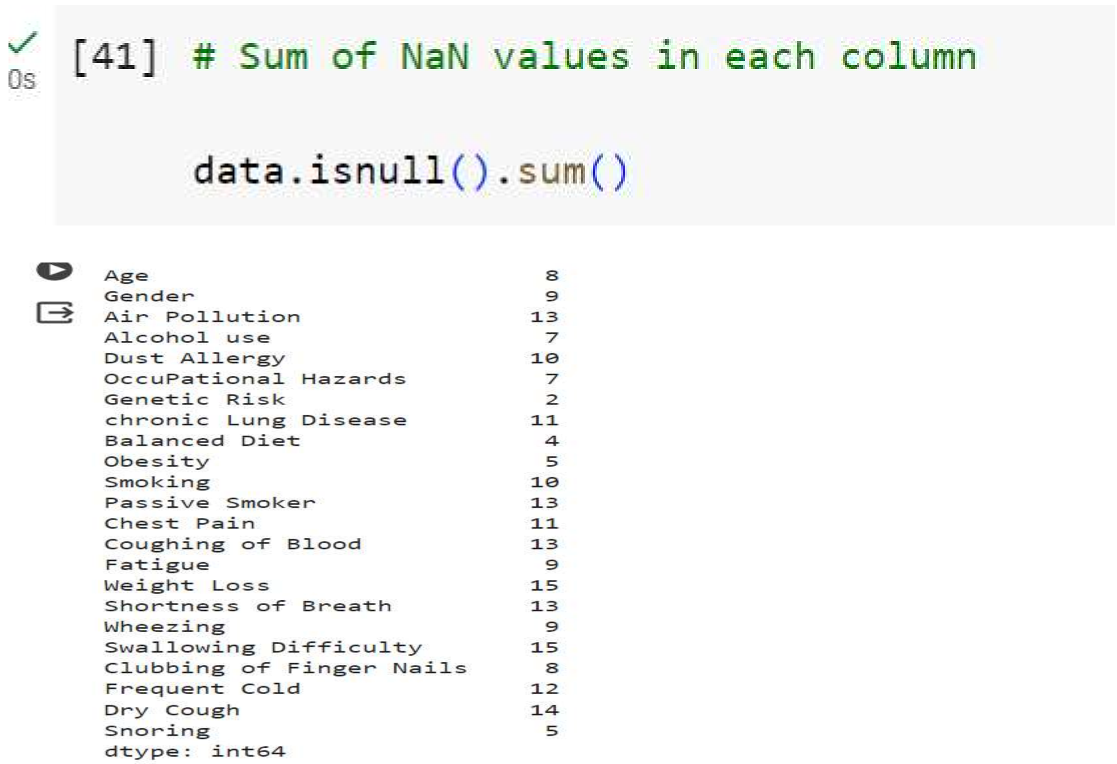
	index	Patient Id	Age	Gender	Air Pollution	Alcohol use	Dust Allergy	OccuPational Hazards	Genetic Risk	chronic Lung Disease	...	Fatigue
0	0	P1	33	1	2	4	5	4	3	2	...	3
1	1	P10	17	1	3	1	5	3	4	2	...	1
2	2	P100	35	1	4	5	6	5	5	4	...	8
3	7	P104	28	2	3	1	4	3	2	3	...	3
4	3	P1000	37	1	7	7	7	7	6	7	...	4
...	...	...	...	...	...	...	...	...	...	...	...	...
1001	995	P995	44	1	6	7	7	7	7	6	...	5
1002	996	P996	37	2	6	8	7	7	7	6	...	9
1003	997	P997	25	2	4	5	6	5	5	4	...	8
1004	998	P998	18	2	6	8	7	7	7	6	...	3
1005	999	P999	47	1	6	5	6	5	5	4	...	8



```
[39] import numpy as np
```

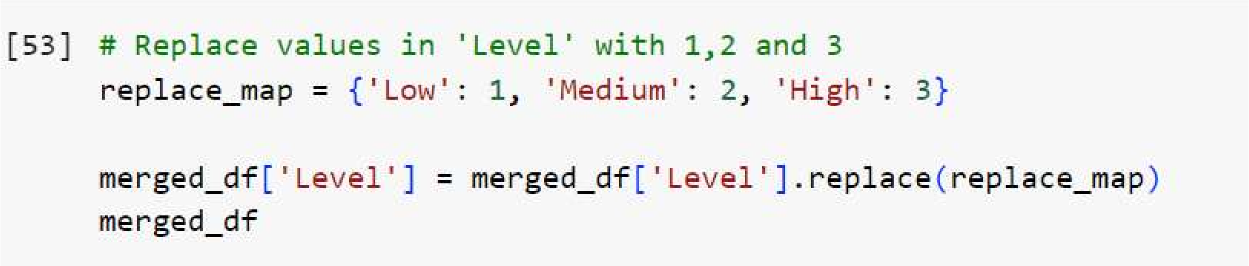
```
# Lets fill in some NaN values at random to make the data cleaning interesting

data = df1[['Age', 'Gender', 'Air Pollution', 'Alcohol use',
       'Dust Allergy', 'OccuPational Hazards', 'Genetic Risk',
       'chronic Lung Disease', 'Balanced Diet', 'Obesity', 'Smoking',
       'Passive Smoker', 'Chest Pain', 'Coughing of Blood', 'Fatigue',
       'Weight Loss', 'Shortness of Breath', 'Wheezing',
       'Swallowing Difficulty', 'Clubbing of Finger Nails', 'Frequent Cold',
       'Dry Cough', 'Snoring']]
missing_percentage = 0.01  # 1% of values will be removed
mask = np.random.rand(*data.shape) < missing_percentage
data[mask] = np.nan
```

```
<ipython-input-40-110a591ab61c>:12: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#r
  data[mask] = np.nan
<ipython-input-40-110a591ab61c>:12: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#r
  data[mask] = np.nan
```

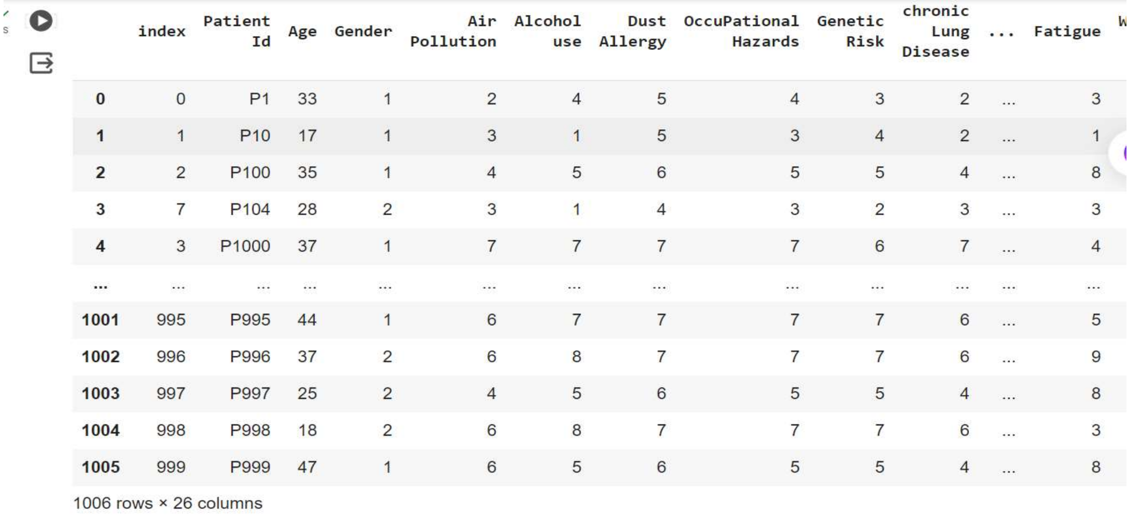


```
[41] # Sum of NaN values in each column

     data.isnull().sum()
```

```
Age                          8
Gender                       9
Air Pollution               13
Alcohol use                  7
Dust Allergy                10
OccuPational Hazards         7
Genetic Risk                 2
chronic Lung Disease        11
Balanced Diet                4
Obesity                      5
Smoking                     10
Passive Smoker              13
Chest Pain                  11
Coughing of Blood           13
Fatigue                      9
Weight Loss                 15
Shortness of Breath         13
Wheezing                     9
Swallowing Difficulty       15
Clubbing of Finger Nails     8
Frequent Cold               12
Dry Cough                   14
Snoring                      5
dtype: int64
```



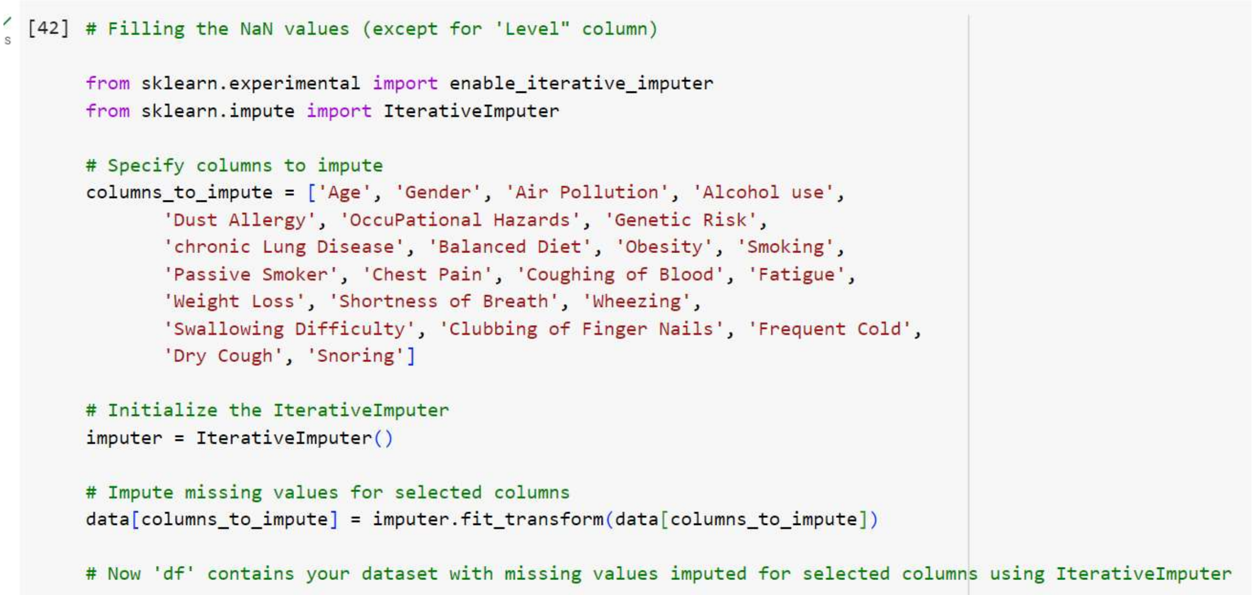
```
[53] # Replace values in 'Level' with 1,2 and 3
     replace_map = {'Low': 1, 'Medium': 2, 'High': 3}

     merged_df['Level'] = merged_df['Level'].replace(replace_map)
     merged_df
```



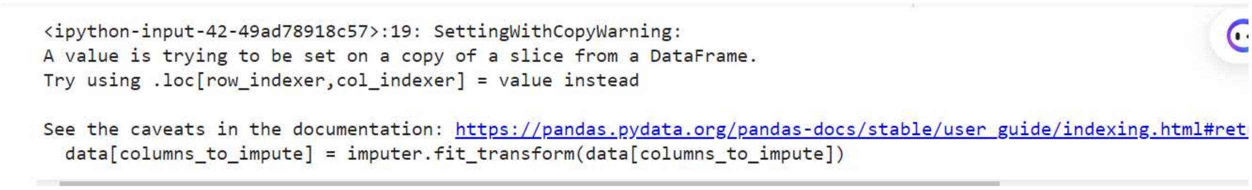
	index	Patient Id	Age	Gender	Air Pollution	Alcohol use	Dust Allergy	OccuPational Hazards	Genetic Risk	chronic Lung Disease	...	Fatigue
0	0	P1	33	1	2	4	5	4	3	2	...	3
1	1	P10	17	1	3	1	5	3	4	2	...	1
2	2	P100	35	1	4	5	6	5	5	4	...	8
3	7	P104	28	2	3	1	4	3	2	3	...	3
4	3	P1000	37	1	7	7	7	7	6	7	...	4
...	...	...	...	...	...	...	...	...	...	...	...	...
1001	995	P995	44	1	6	7	7	7	7	6	...	5
1002	996	P996	37	2	6	8	7	7	7	6	...	9
1003	997	P997	25	2	4	5	6	5	5	4	...	8
1004	998	P998	18	2	6	8	7	7	7	6	...	3
1005	999	P999	47	1	6	5	6	5	5	4	...	8

1006 rows × 26 columns

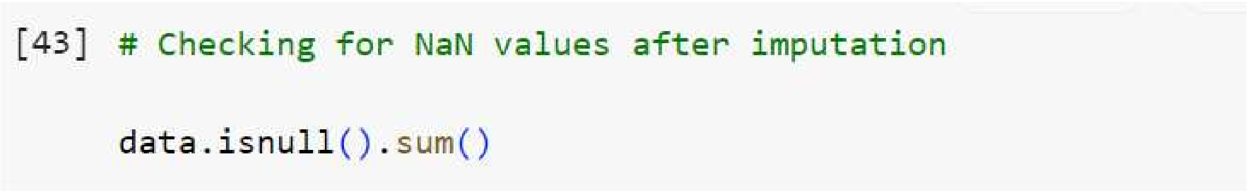
Imputation of NaN values:



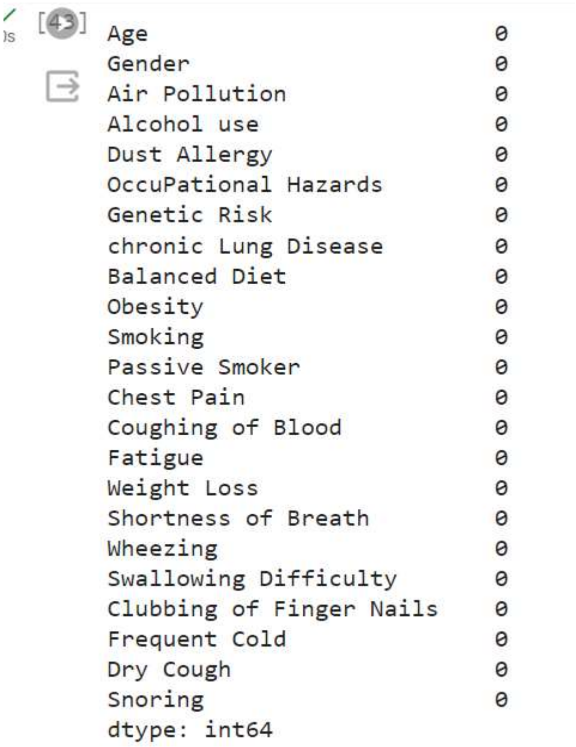
```
[42] # Filling the NaN values (except for 'Level" column)

     from sklearn.experimental import enable_iterative_imputer
     from sklearn.impute import IterativeImputer

     # Specify columns to impute
     columns_to_impute = ['Age', 'Gender', 'Air Pollution', 'Alcohol use',
            'Dust Allergy', 'OccuPational Hazards', 'Genetic Risk',
            'chronic Lung Disease', 'Balanced Diet', 'Obesity', 'Smoking',
            'Passive Smoker', 'Chest Pain', 'Coughing of Blood', 'Fatigue',
            'Weight Loss', 'Shortness of Breath', 'Wheezing',
            'Swallowing Difficulty', 'Clubbing of Finger Nails', 'Frequent Cold',
            'Dry Cough', 'Snoring']

     # Initialize the IterativeImputer
     imputer = IterativeImputer()

     # Impute missing values for selected columns
     data[columns_to_impute] = imputer.fit_transform(data[columns_to_impute])

     # Now 'df' contains your dataset with missing values imputed for selected columns using IterativeImputer
```



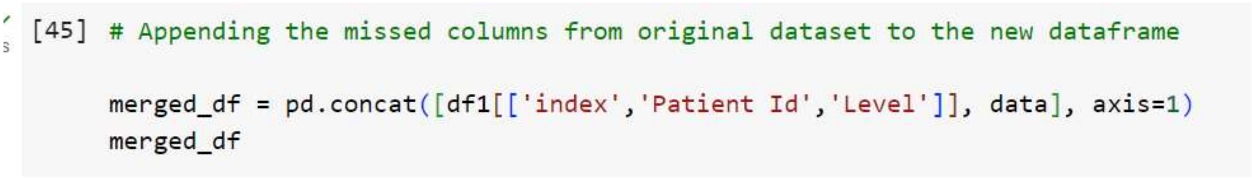
```
<ipython-input-42-49ad78918c57>:19: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ret
  data[columns_to_impute] = imputer.fit_transform(data[columns_to_impute])
```



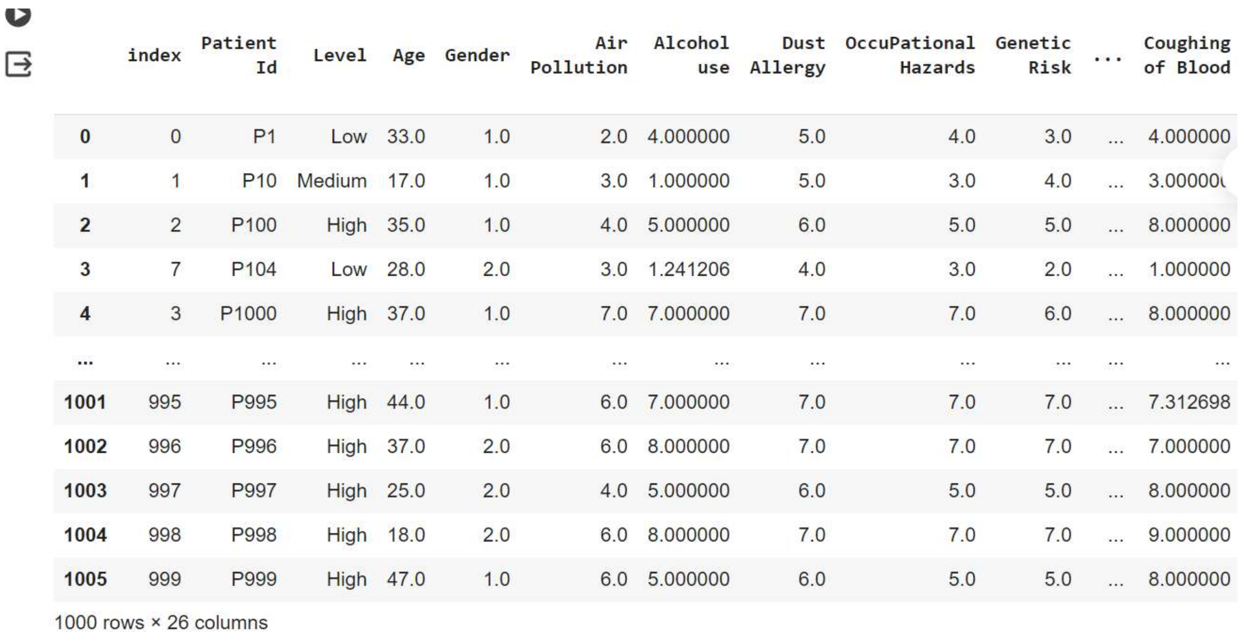
```
[43] # Checking for NaN values after imputation

     data.isnull().sum()
```



```
[43] Age                          0
     Gender                       0
     Air Pollution                0
     Alcohol use                  0
     Dust Allergy                 0
     OccuPational Hazards         0
     Genetic Risk                 0
     chronic Lung Disease         0
     Balanced Diet                0
     Obesity                      0
     Smoking                      0
     Passive Smoker               0
     Chest Pain                   0
     Coughing of Blood            0
     Fatigue                      0
     Weight Loss                  0
     Shortness of Breath          0
     Wheezing                     0
     Swallowing Difficulty        0
     Clubbing of Finger Nails     0
     Frequent Cold                0
     Dry Cough                    0
     Snoring                      0
     dtype: int64
```



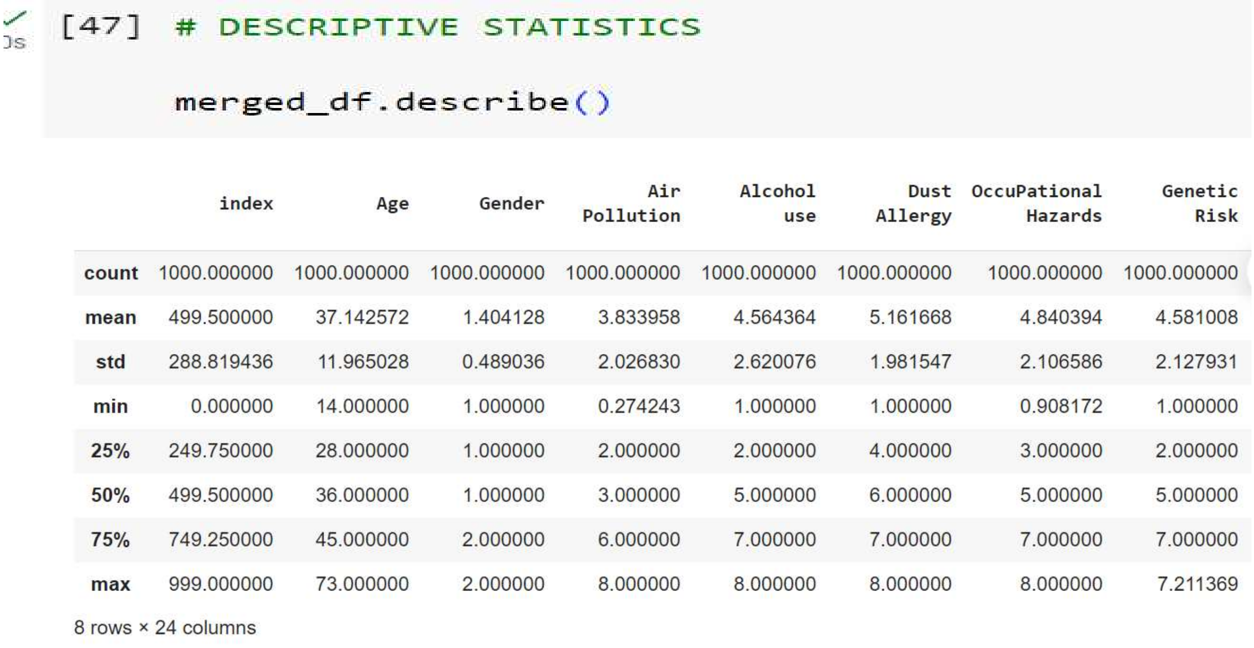
```
[45] # Appending the missed columns from original dataset to the new dataframe

     merged_df = pd.concat([df1[['index','Patient Id','Level']], data], axis=1)
     merged_df
```



	index	Patient Id	Level	Age	Gender	Air Pollution	Alcohol use	Dust Allergy	OccuPational Hazards	Genetic Risk	...	Coughing of Blood
0	0	P1	Low	33.0	1.0	2.0	4.000000	5.0	4.0	3.0	...	4.000000
1	1	P10	Medium	17.0	1.0	3.0	1.000000	5.0	3.0	4.0	...	3.00000
2	2	P100	High	35.0	1.0	4.0	5.000000	6.0	5.0	5.0	...	8.000000
3	7	P104	Low	28.0	2.0	3.0	1.241206	4.0	3.0	2.0	...	1.000000
4	3	P1000	High	37.0	1.0	7.0	7.000000	7.0	7.0	6.0	...	8.000000
...	...	...	...	...	...	...	...	...	...	...	...	...
1001	995	P995	High	44.0	1.0	6.0	7.000000	7.0	7.0	7.0	...	7.312698
1002	996	P996	High	37.0	2.0	6.0	8.000000	7.0	7.0	7.0	...	7.000000
1003	997	P997	High	25.0	2.0	4.0	5.000000	6.0	5.0	5.0	...	8.000000
1004	998	P998	High	18.0	2.0	6.0	8.000000	7.0	7.0	7.0	...	9.000000
1005	999	P999	High	47.0	1.0	6.0	5.000000	6.0	5.0	5.0	...	8.000000

1000 rows × 26 columns

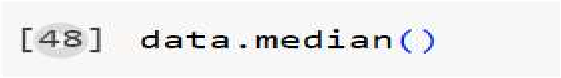
Descriptive Analysis: (Central Analysis):



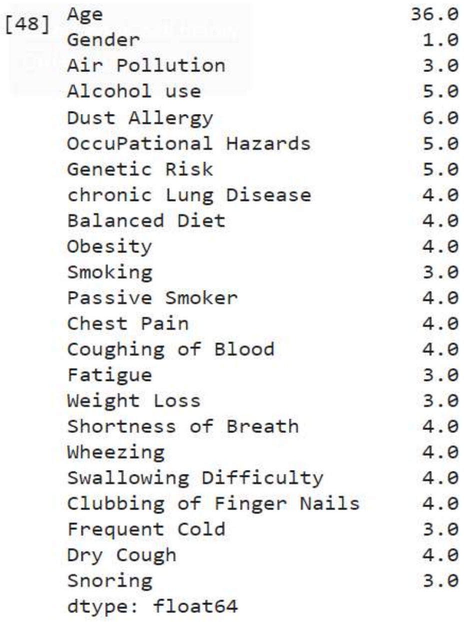
```
[47]  # DESCRIPTIVE STATISTICS

      merged_df.describe()
```

	index	Age	Gender	Air Pollution	Alcohol use	Dust Allergy	OccuPational Hazards	Genetic Risk
count	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000
mean	499.500000	37.142572	1.404128	3.833958	4.564364	5.161668	4.840394	4.581008
std	288.819436	11.965028	0.489036	2.026830	2.620076	1.981547	2.106586	2.127931
min	0.000000	14.000000	1.000000	0.274243	1.000000	1.000000	0.908172	1.000000
25%	249.750000	28.000000	1.000000	2.000000	2.000000	4.000000	3.000000	2.000000
50%	499.500000	36.000000	1.000000	3.000000	5.000000	6.000000	5.000000	5.000000
75%	749.250000	45.000000	2.000000	6.000000	7.000000	7.000000	7.000000	7.000000
max	999.000000	73.000000	2.000000	8.000000	8.000000	8.000000	8.000000	7.211369

8 rows × 24 columns

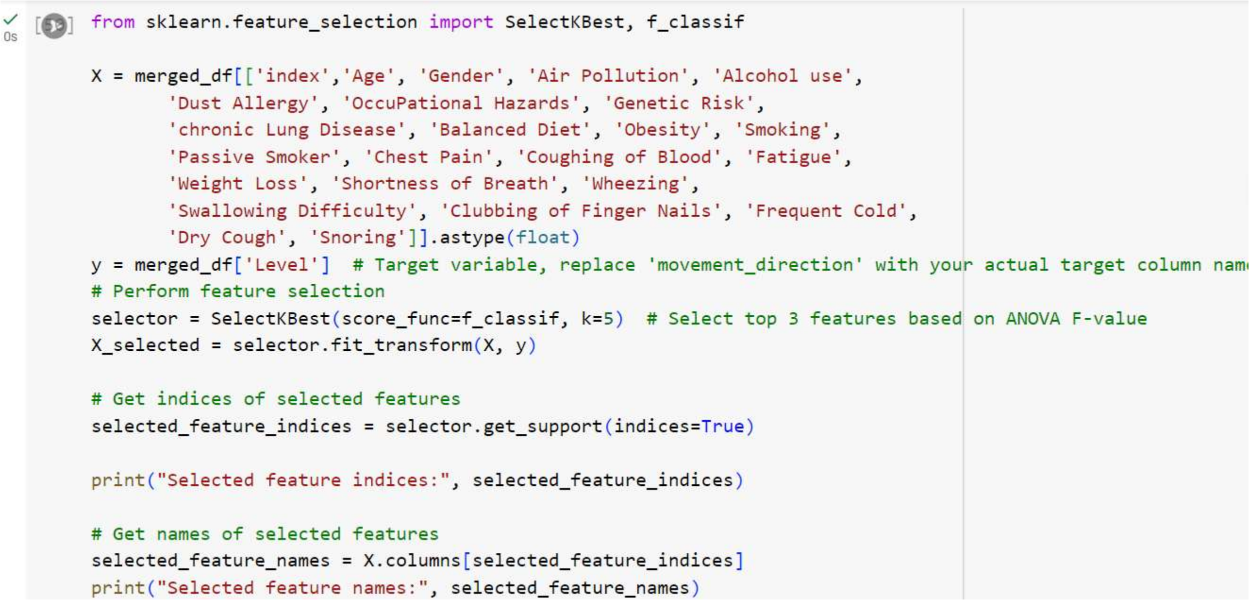


```
[48]  data.median()
```

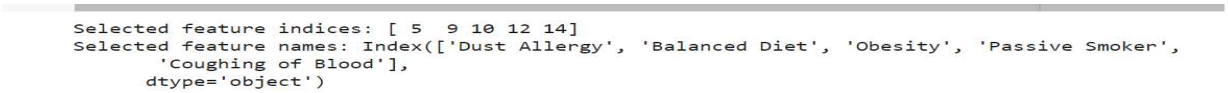


```
[48] Age                          36.0
     Gender                        1.0
     Air Pollution                 3.0
     Alcohol use                   5.0
     Dust Allergy                  6.0
     OccuPational Hazards          5.0
     Genetic Risk                  5.0
     chronic Lung Disease          4.0
     Balanced Diet                 4.0
     Obesity                       4.0
     Smoking                       3.0
     Passive Smoker                4.0
     Chest Pain                    4.0
     Coughing of Blood             4.0
     Fatigue                       3.0
     Weight Loss                   3.0
     Shortness of Breath           4.0
     Wheezing                      4.0
     Swallowing Difficulty         4.0
     Clubbing of Finger Nails      4.0
     Frequent Cold                 3.0
     Dry Cough                     4.0
     Snoring                       3.0
     dtype: float64
```

Feature Selection: (ANOVA F-VALUE based):

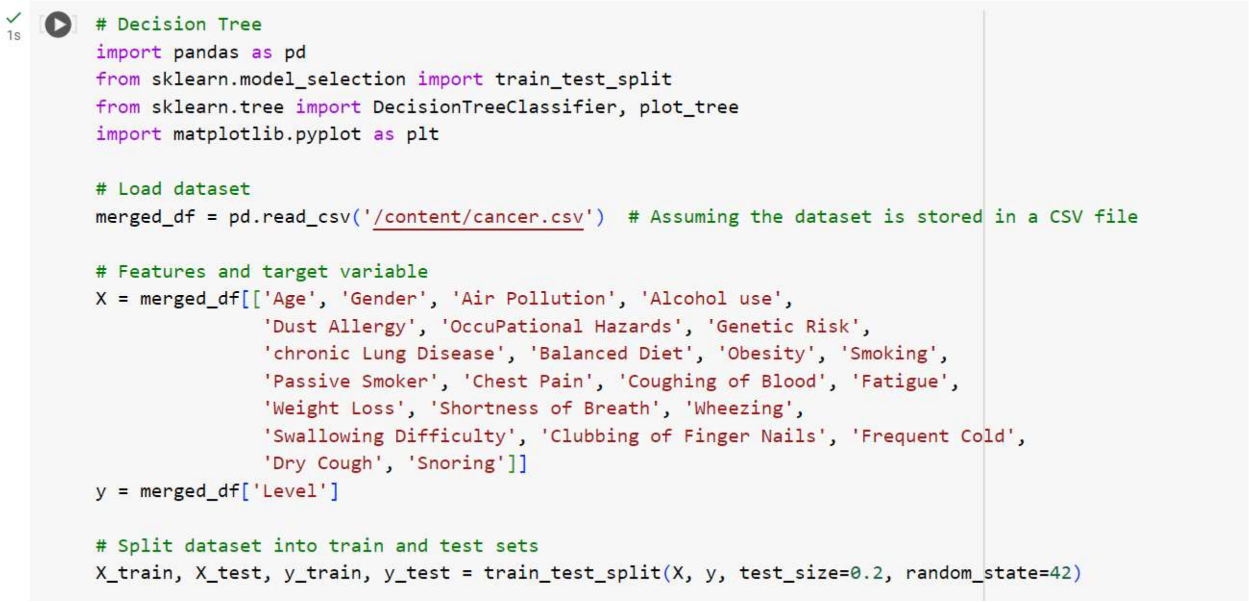


```
from sklearn.feature_selection import SelectKBest, f_classif

X = merged_df[['index','Age', 'Gender', 'Air Pollution', 'Alcohol use',
       'Dust Allergy', 'OccuPational Hazards', 'Genetic Risk',
       'chronic Lung Disease', 'Balanced Diet', 'Obesity', 'Smoking',
       'Passive Smoker', 'Chest Pain', 'Coughing of Blood', 'Fatigue',
       'Weight Loss', 'Shortness of Breath', 'Wheezing',
       'Swallowing Difficulty', 'Clubbing of Finger Nails', 'Frequent Cold',
       'Dry Cough', 'Snoring']].astype(float)
y = merged_df['Level']  # Target variable, replace 'movement_direction' with your actual target column nam
# Perform feature selection
selector = SelectKBest(score_func=f_classif, k=5)  # Select top 3 features based on ANOVA F-value
X_selected = selector.fit_transform(X, y)

# Get indices of selected features
selected_feature_indices = selector.get_support(indices=True)

print("Selected feature indices:", selected_feature_indices)

# Get names of selected features
selected_feature_names = X.columns[selected_feature_indices]
print("Selected feature names:", selected_feature_names)
```

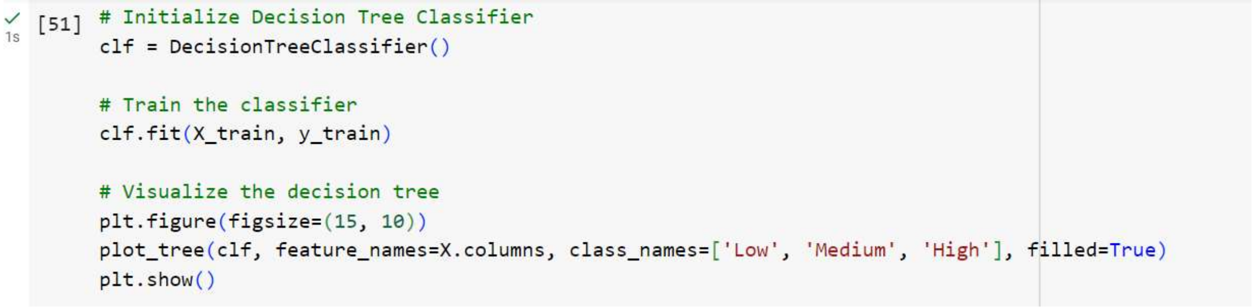


```
Selected feature indices: [ 5  9 10 12 14]
Selected feature names: Index(['Dust Allergy', 'Balanced Diet', 'Obesity', 'Passive Smoker',
       'Coughing of Blood'],
      dtype='object')
```

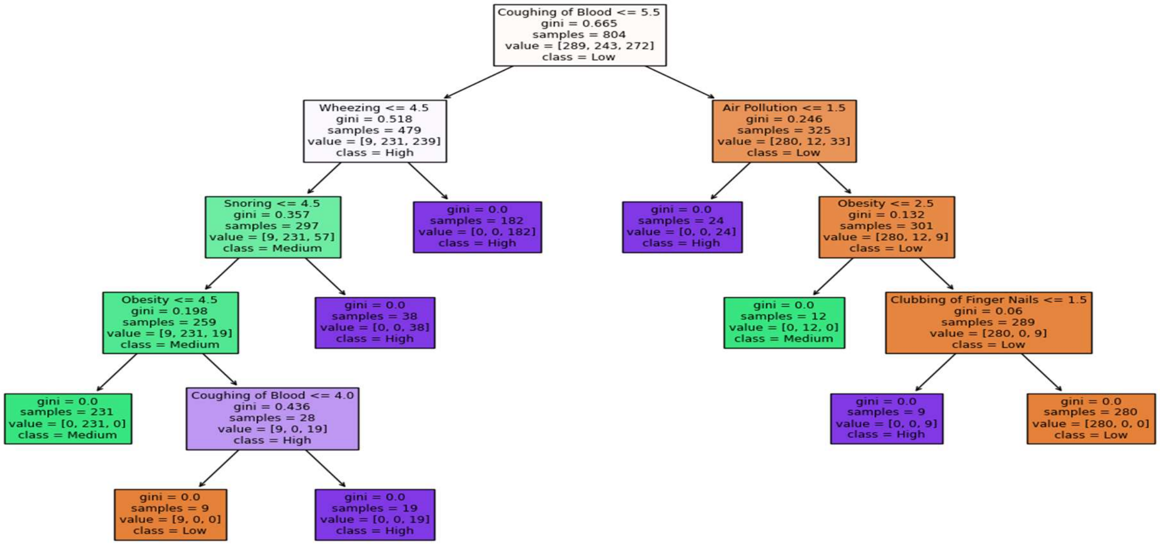
Prediction Analysis:



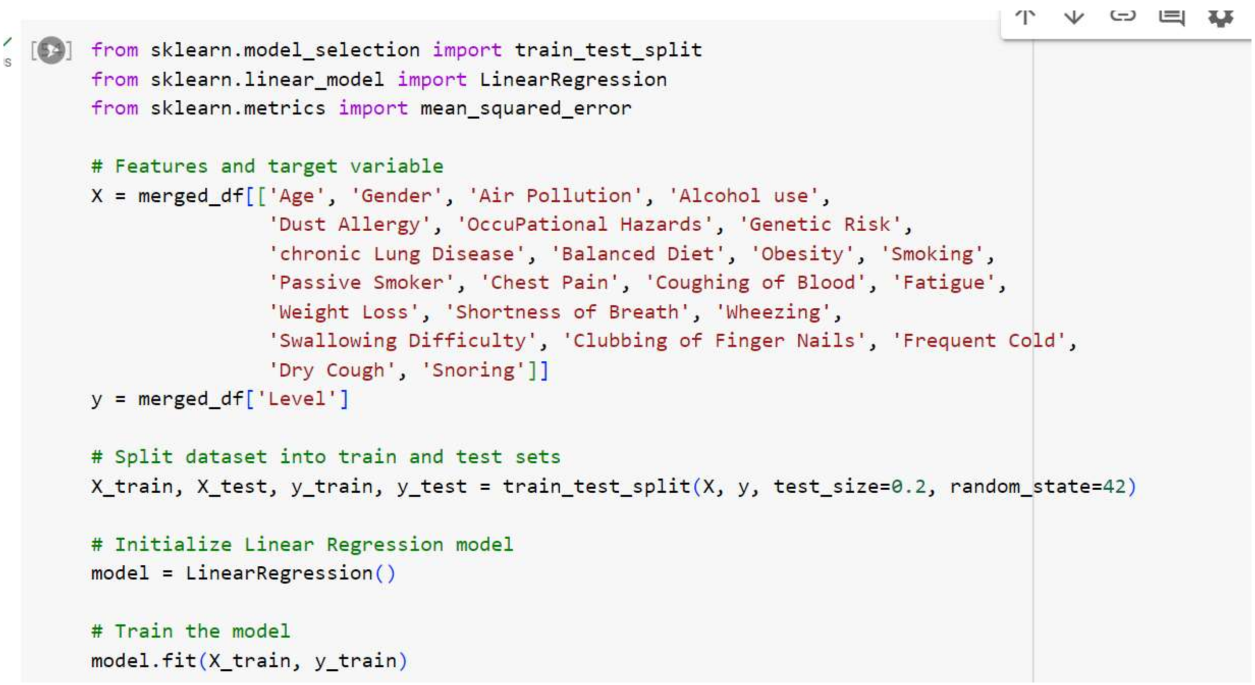
```
# Decision Tree
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier, plot_tree
import matplotlib.pyplot as plt

# Load dataset
merged_df = pd.read_csv('/content/cancer.csv')  # Assuming the dataset is stored in a CSV file

# Features and target variable
X = merged_df[['Age', 'Gender', 'Air Pollution', 'Alcohol use',
               'Dust Allergy', 'OccuPational Hazards', 'Genetic Risk',
               'chronic Lung Disease', 'Balanced Diet', 'Obesity', 'Smoking',
               'Passive Smoker', 'Chest Pain', 'Coughing of Blood', 'Fatigue',
               'Weight Loss', 'Shortness of Breath', 'Wheezing',
               'Swallowing Difficulty', 'Clubbing of Finger Nails', 'Frequent Cold',
               'Dry Cough', 'Snoring']]
y = merged_df['Level']

# Split dataset into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```



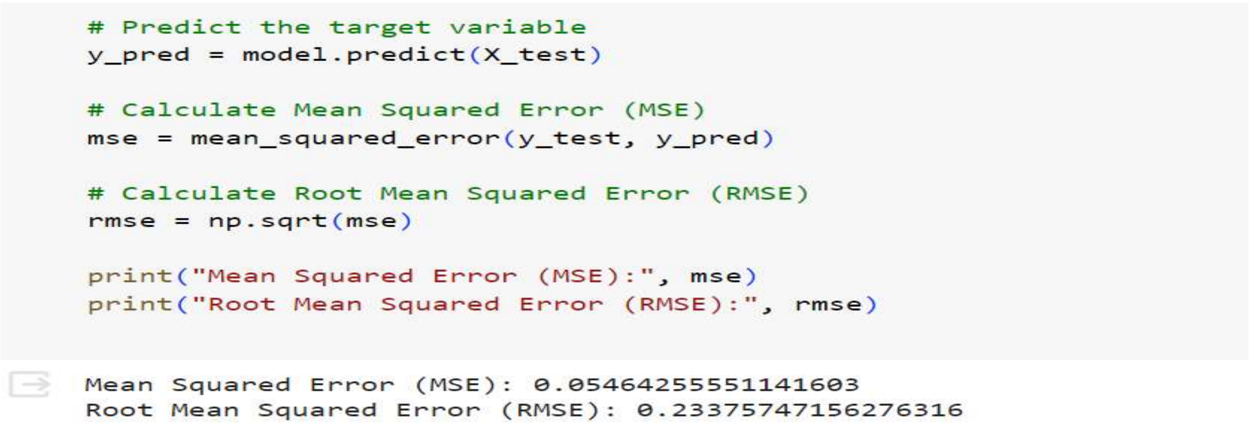
```
# Initialize Decision Tree Classifier
clf = DecisionTreeClassifier()

# Train the classifier
clf.fit(X_train, y_train)

# Visualize the decision tree
plt.figure(figsize=(15, 10))
plot_tree(clf, feature_names=X.columns, class_names=['Low', 'Medium', 'High'], filled=True)
plt.show()
```



Accuracy for Predictive Model Using Linear Regression:



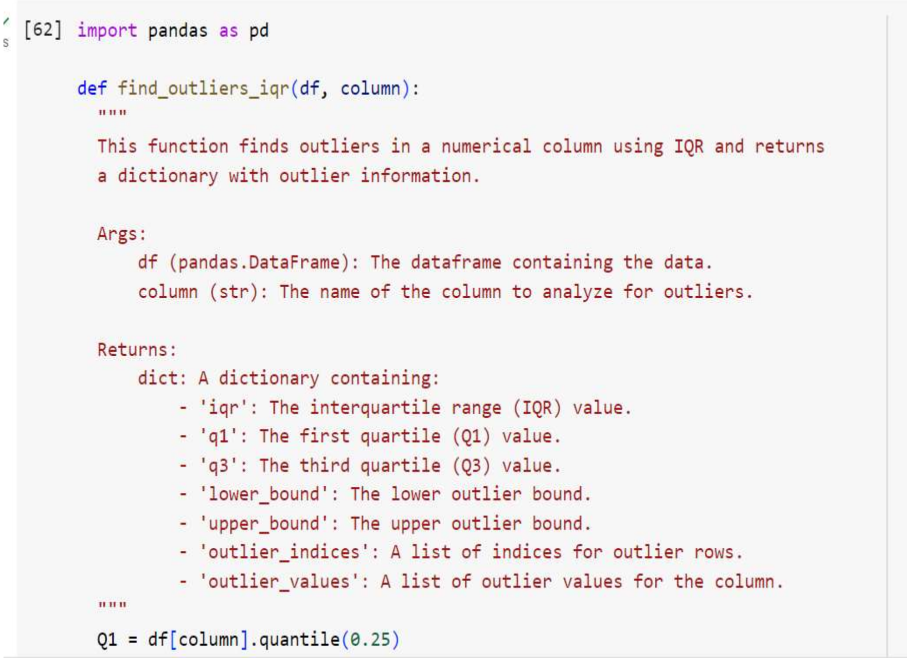
```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error

# Features and target variable
X = merged_df[['Age', 'Gender', 'Air Pollution', 'Alcohol use',
               'Dust Allergy', 'OccuPational Hazards', 'Genetic Risk',
               'chronic Lung Disease', 'Balanced Diet', 'Obesity', 'Smoking',
               'Passive Smoker', 'Chest Pain', 'Coughing of Blood', 'Fatigue',
               'Weight Loss', 'Shortness of Breath', 'Wheezing',
               'Swallowing Difficulty', 'Clubbing of Finger Nails', 'Frequent Cold',
               'Dry Cough', 'Snoring']]
y = merged_df['Level']

# Split dataset into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Initialize Linear Regression model
model = LinearRegression()

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



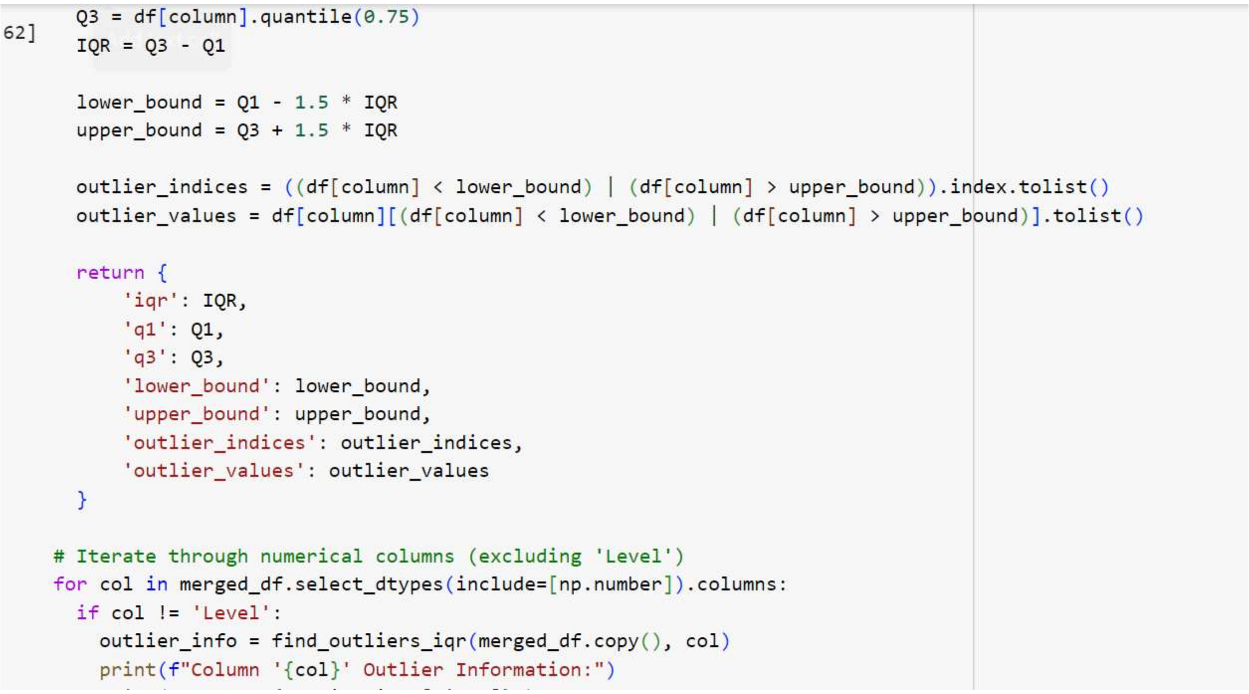
```
# Predict the target variable
y_pred = model.predict(X_test)

# Calculate Mean Squared Error (MSE)
mse = mean_squared_error(y_test, y_pred)

# Calculate Root Mean Squared Error (RMSE)
rmse = np.sqrt(mse)

print("Mean Squared Error (MSE):", mse)
print("Root Mean Squared Error (RMSE):", rmse)
```

```
Mean Squared Error (MSE): 0.05464255551141603
Root Mean Squared Error (RMSE): 0.23375747156276316
```

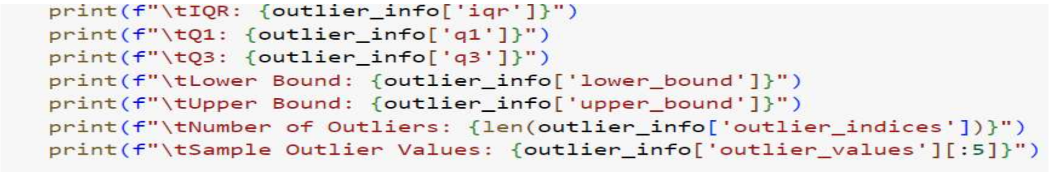
Outlier Detection:



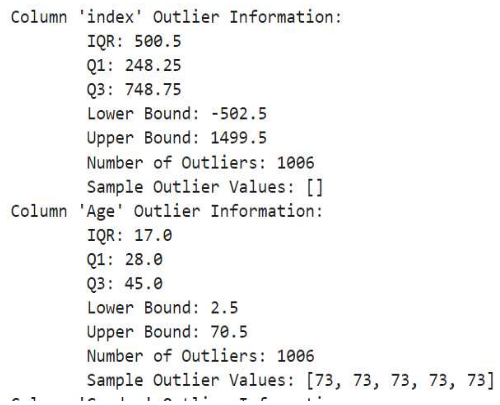
```
[62] import pandas as pd

     def find_outliers_iqr(df, column):
       """
       This function finds outliers in a numerical column using IQR and returns
       a dictionary with outlier information.

       Args:
           df (pandas.DataFrame): The dataframe containing the data.
           column (str): The name of the column to analyze for outliers.

       Returns:
           dict: A dictionary containing:
               - 'iqr': The interquartile range (IQR) value.
               - 'q1': The first quartile (Q1) value.
               - 'q3': The third quartile (Q3) value.
               - 'lower_bound': The lower outlier bound.
               - 'upper_bound': The upper outlier bound.
               - 'outlier_indices': A list of indices for outlier rows.
               - 'outlier_values': A list of outlier values for the column.
       """
       Q1 = df[column].quantile(0.25)
```



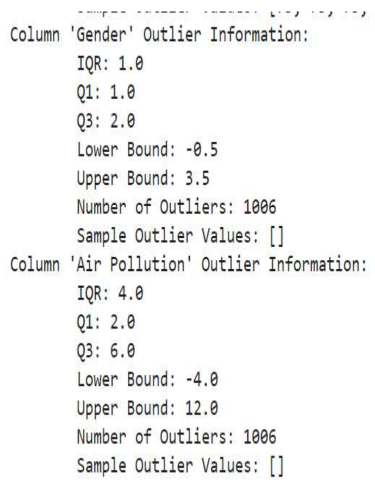
```
62]    Q3 = df[column].quantile(0.75)
       IQR = Q3 - Q1

       lower_bound = Q1 - 1.5 * IQR
       upper_bound = Q3 + 1.5 * IQR

       outlier_indices = ((df[column] < lower_bound) | (df[column] > upper_bound)).index.tolist()
       outlier_values = df[column][(df[column] < lower_bound) | (df[column] > upper_bound)].tolist()

       return {
           'iqr': IQR,
           'q1': Q1,
           'q3': Q3,
           'lower_bound': lower_bound,
           'upper_bound': upper_bound,
           'outlier_indices': outlier_indices,
           'outlier_values': outlier_values
       }

     # Iterate through numerical columns (excluding 'Level')
     for col in merged_df.select_dtypes(include=[np.number]).columns:
       if col != 'Level':
         outlier_info = find_outliers_iqr(merged_df.copy(), col)
         print(f"Column '{col}' Outlier Information:")
```



```
         print(f"\tIQR: {outlier_info['iqr']}")
         print(f"\tQ1: {outlier_info['q1']}")
         print(f"\tQ3: {outlier_info['q3']}")
         print(f"\tLower Bound: {outlier_info['lower_bound']}")
         print(f"\tUpper Bound: {outlier_info['upper_bound']}")
         print(f"\tNumber of Outliers: {len(outlier_info['outlier_indices'])}")
         print(f"\tSample Outlier Values: {outlier_info['outlier_values'][:5]}")
```

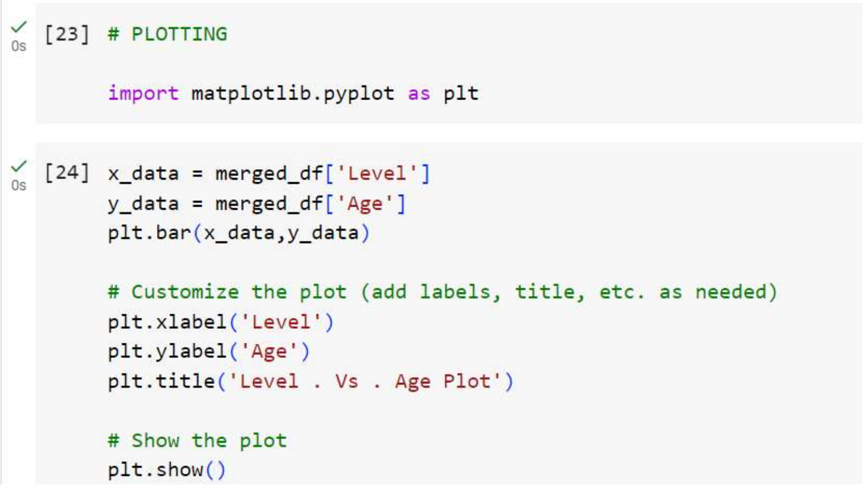


```
Column 'index' Outlier Information:
        IQR: 500.5
        Q1: 248.25
        Q3: 748.75
        Lower Bound: -502.5
        Upper Bound: 1499.5
        Number of Outliers: 1006
        Sample Outlier Values: []
Column 'Age' Outlier Information:
        IQR: 17.0
        Q1: 28.0
        Q3: 45.0
        Lower Bound: 2.5
        Upper Bound: 70.5
        Number of Outliers: 1006
        Sample Outlier Values: [73, 73, 73, 73, 73]
```



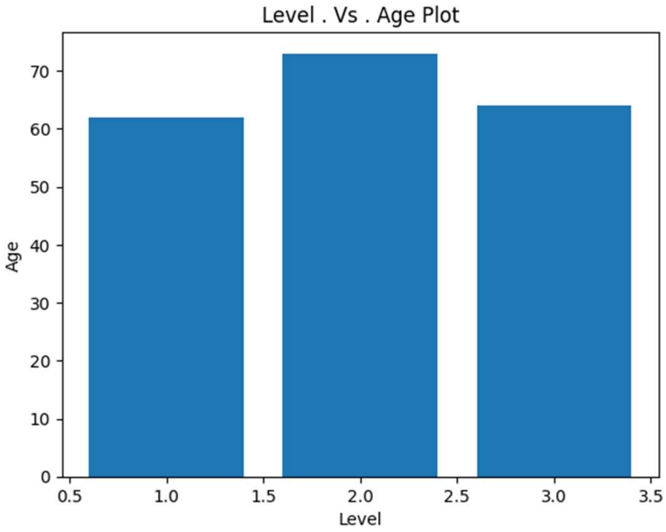
```
Column 'Gender' Outlier Information:
        IQR: 1.0
        Q1: 1.0
        Q3: 2.0
        Lower Bound: -0.5
        Upper Bound: 3.5
        Number of Outliers: 1006
        Sample Outlier Values: []
Column 'Air Pollution' Outlier Information:
        IQR: 4.0
        Q1: 2.0
        Q3: 6.0
        Lower Bound: -4.0
        Upper Bound: 12.0
        Number of Outliers: 1006
        Sample Outlier Values: []
```

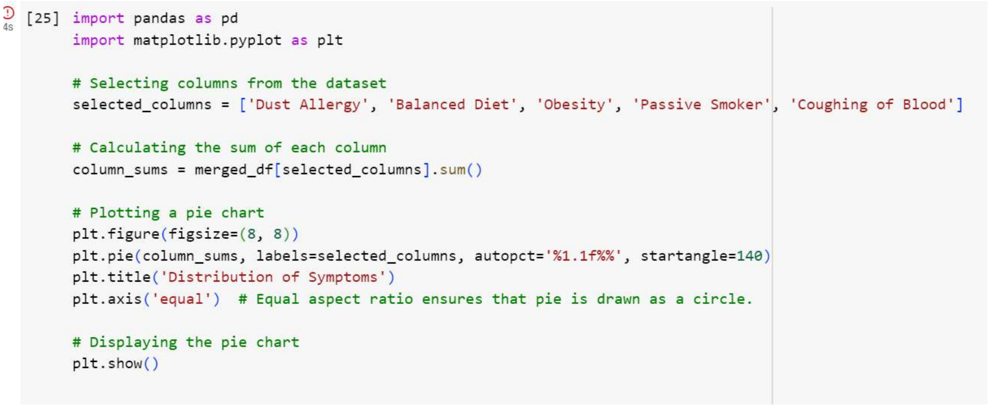
Plotting:



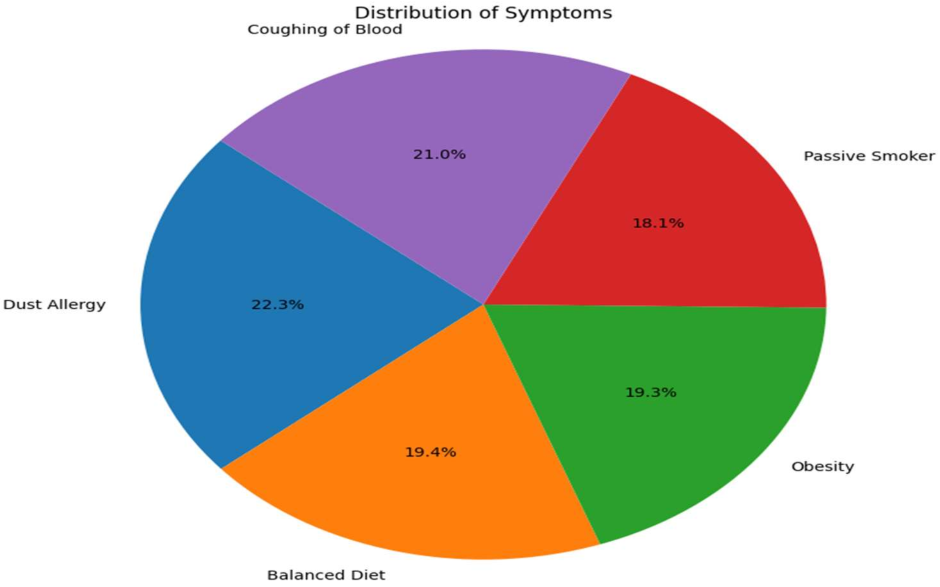
```
[23] # PLOTTING

     import matplotlib.pyplot as plt
```

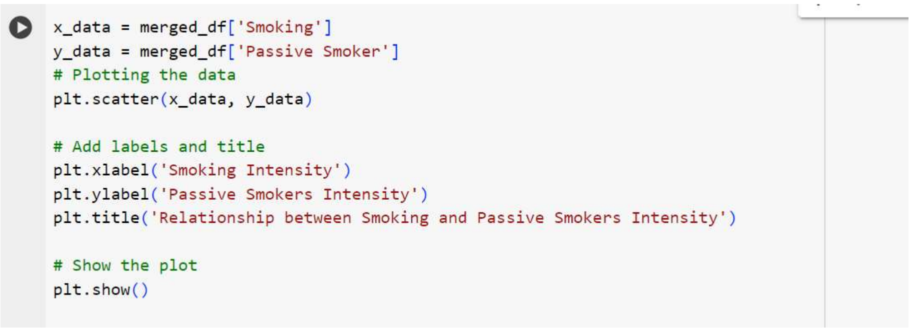
```
[24] x_data = merged_df['Level']
     y_data = merged_df['Age']
     plt.bar(x_data,y_data)

     # Customize the plot (add labels, title, etc. as needed)
     plt.xlabel('Level')
     plt.ylabel('Age')
     plt.title('Level . Vs . Age Plot')

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



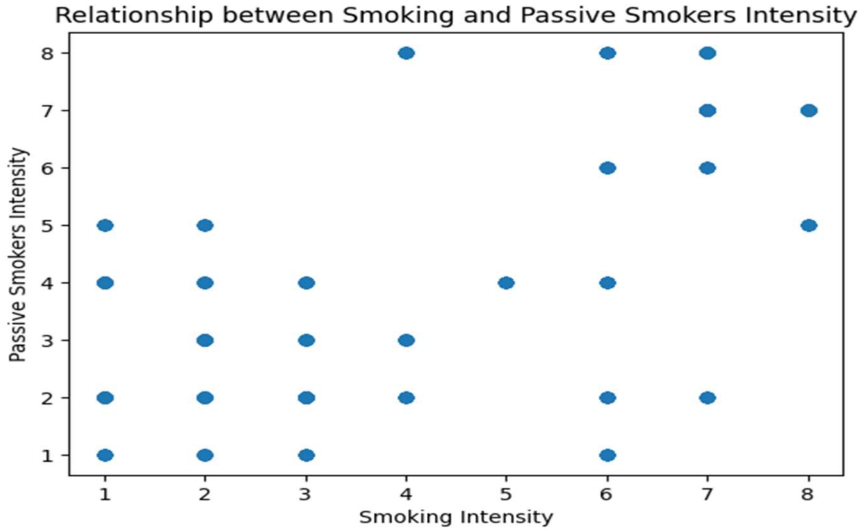


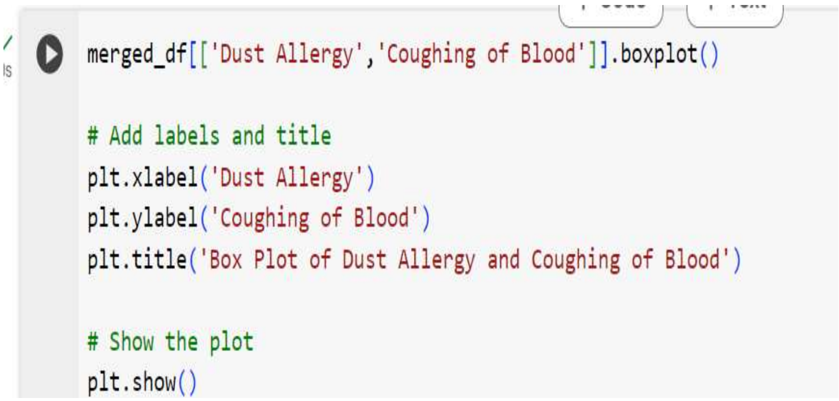
```
import pandas as pd
import matplotlib.pyplot as plt

# Selecting columns from the dataset
selected_columns = ['Dust Allergy', 'Balanced Diet', 'Obesity', 'Passive Smoker', 'Coughing of Blood']

# Calculating the sum of each column
column_sums = merged_df[selected_columns].sum()

# Plotting a pie chart
plt.figure(figsize=(8, 8))
plt.pie(column_sums, labels=selected_columns, autopct='%1.1f%%', startangle=140)
plt.title('Distribution of Symptoms')
plt.axis('equal')  # Equal aspect ratio ensures that pie is drawn as a circle.

# Displaying the pie chart
plt.show()
```



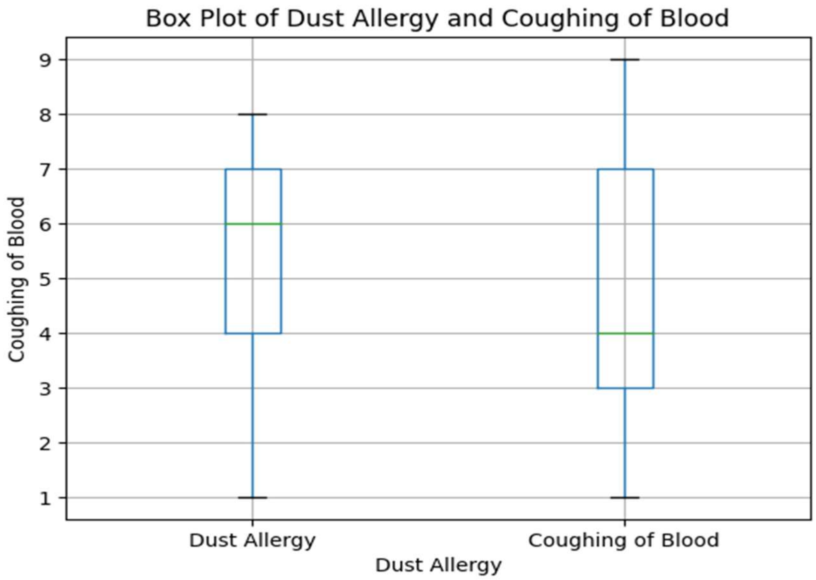


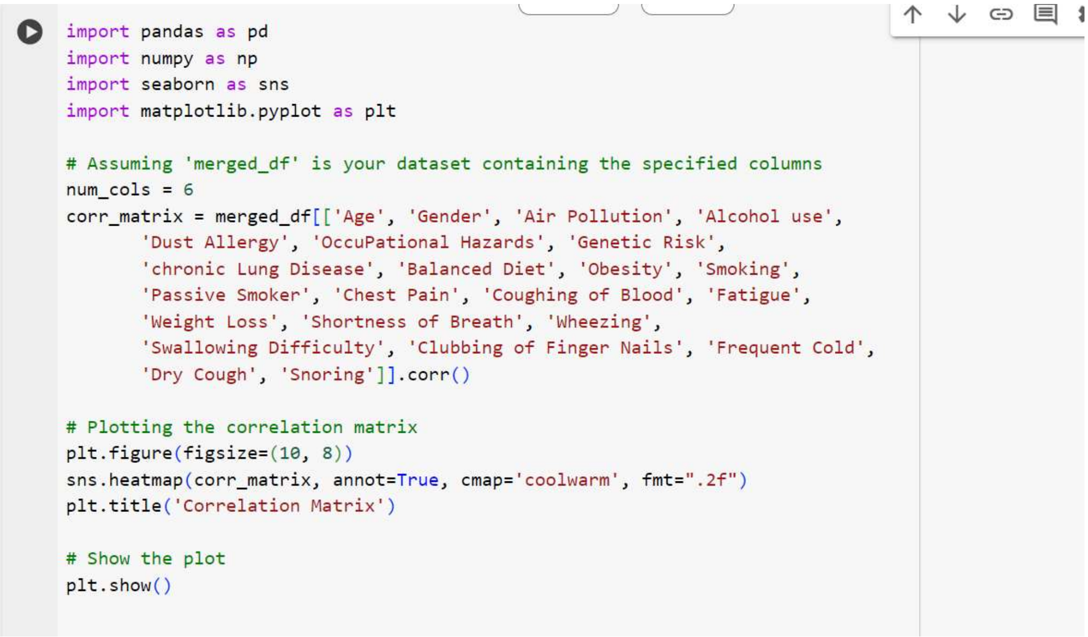
```
x_data = merged_df['Smoking']
y_data = merged_df['Passive Smoker']
# Plotting the data
plt.scatter(x_data, y_data)

# Add labels and title
plt.xlabel('Smoking Intensity')
plt.ylabel('Passive Smokers Intensity')
plt.title('Relationship between Smoking and Passive Smokers Intensity')

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



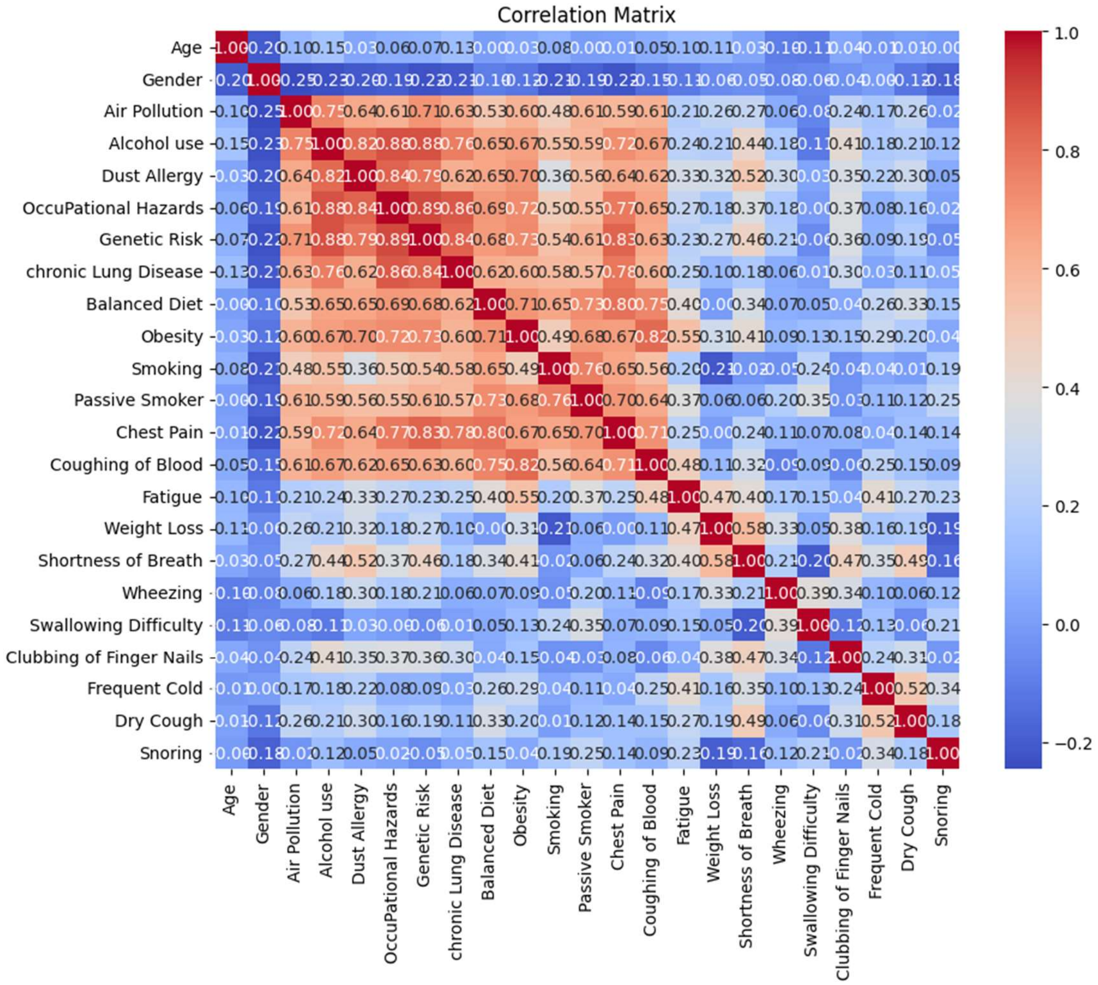


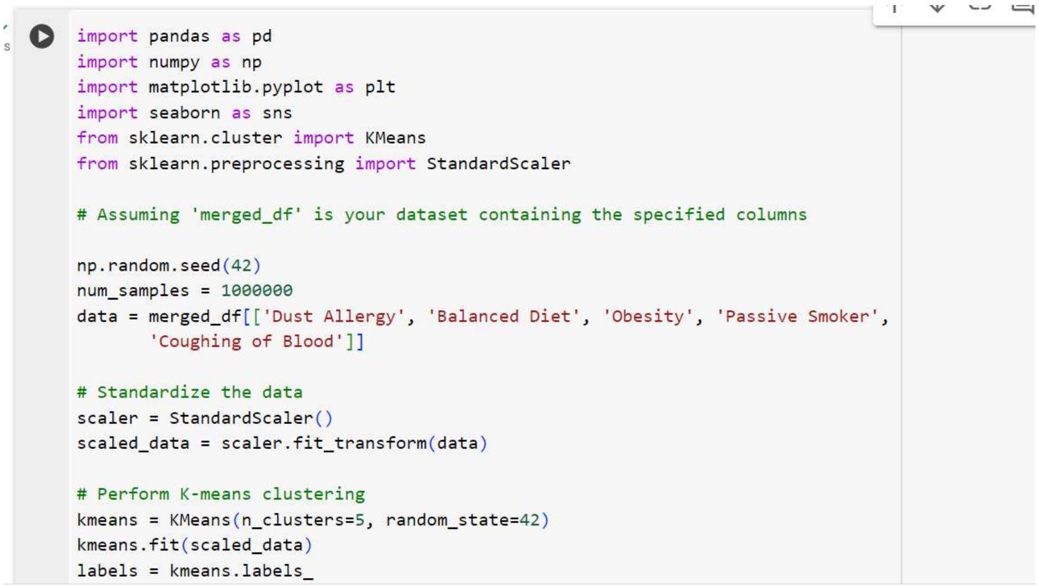
```
merged_df[['Dust Allergy','Coughing of Blood']].boxplot()

# Add labels and title
plt.xlabel('Dust Allergy')
plt.ylabel('Coughing of Blood')
plt.title('Box Plot of Dust Allergy and Coughing of Blood')

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



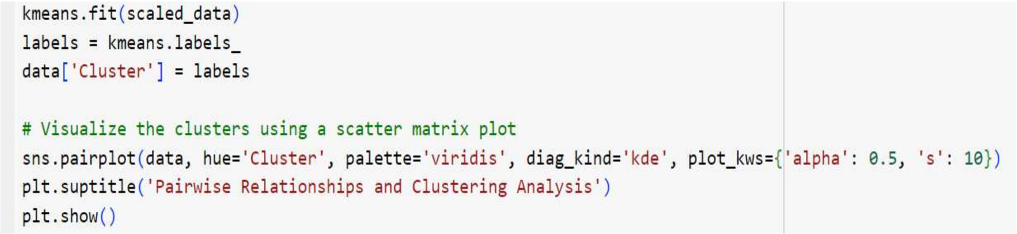


```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt

# Assuming 'merged_df' is your dataset containing the specified columns
num_cols = 6
corr_matrix = merged_df[['Age', 'Gender', 'Air Pollution', 'Alcohol use',
       'Dust Allergy', 'OccuPational Hazards', 'Genetic Risk',
       'chronic Lung Disease', 'Balanced Diet', 'Obesity', 'Smoking',
       'Passive Smoker', 'Chest Pain', 'Coughing of Blood', 'Fatigue',
       'Weight Loss', 'Shortness of Breath', 'Wheezing',
       'Swallowing Difficulty', 'Clubbing of Finger Nails', 'Frequent Cold',
       'Dry Cough', 'Snoring']].corr()

# Plotting the correlation matrix
plt.figure(figsize=(10, 8))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', fmt=".2f")
plt.title('Correlation Matrix')

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

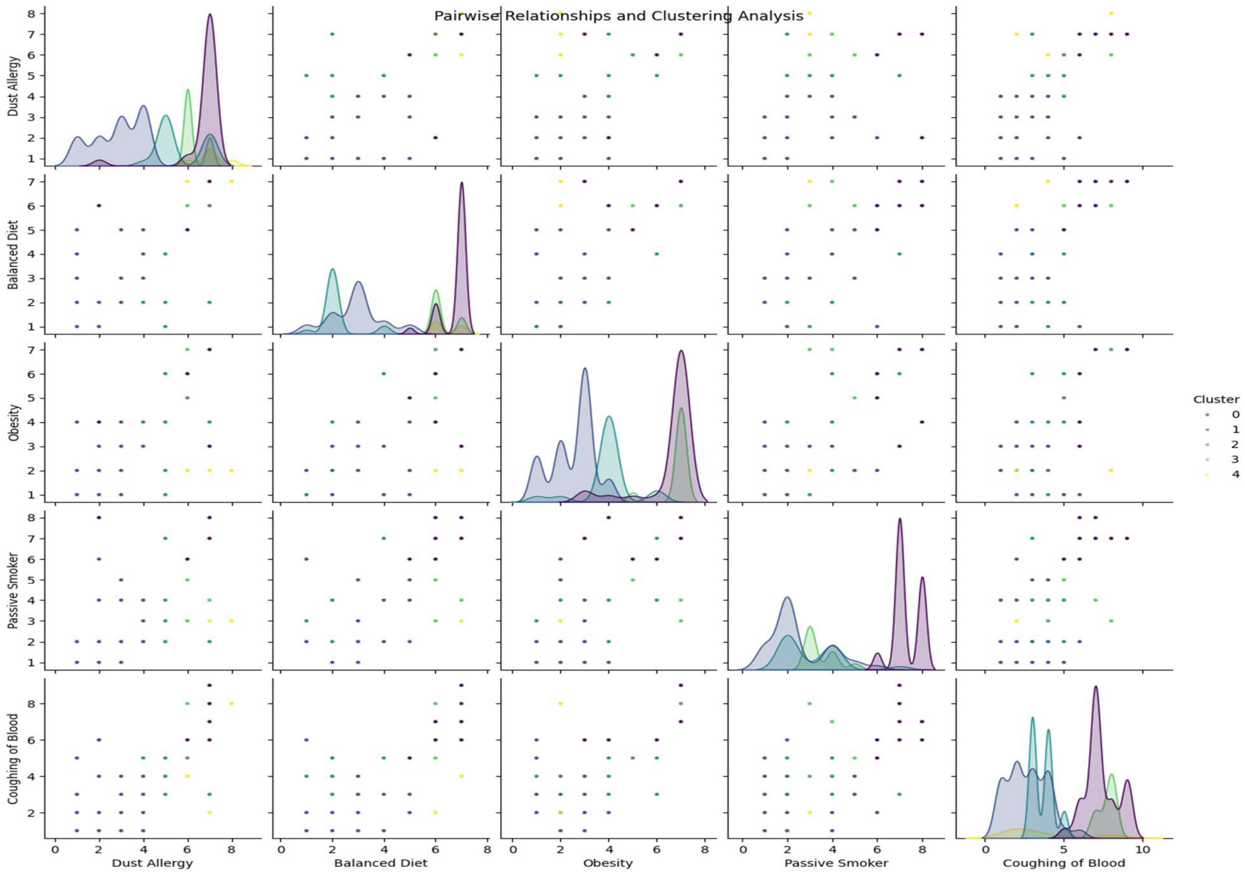




```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.cluster import KMeans
from sklearn.preprocessing import StandardScaler

# Assuming 'merged_df' is your dataset containing the specified columns

np.random.seed(42)
num_samples = 1000000
data = merged_df[['Dust Allergy', 'Balanced Diet', 'Obesity', 'Passive Smoker',
       'Coughing of Blood']]

# Standardize the data
scaler = StandardScaler()
scaled_data = scaler.fit_transform(data)

# Perform K-means clustering
kmeans = KMeans(n_clusters=5, random_state=42)
kmeans.fit(scaled_data)
labels = kmeans.labels_
```



```
kmeans.fit(scaled_data)
labels = kmeans.labels_
data['Cluster'] = labels

# Visualize the clusters using a scatter matrix plot
sns.pairplot(data, hue='Cluster', palette='viridis', diag_kind='kde', plot_kws={'alpha': 0.5, 's': 10})
plt.suptitle('Pairwise Relationships and Clustering Analysis')
plt.show()
```



9. **Conclusion and Future Enhancements:**

Conclusion:

In this study, we developed a predictive model for lung cancer risk by integrating smoking and non-smoking related symptoms. Using machine learning techniques and a diverse clinical dataset, we identified key risk factors and improved risk assessment accuracy.

Our findings highlight the significance of both smoking and non-smoking related symptoms in lung cancer risk prediction. The validation of our model across diverse populations demonstrates its potential utility in clinical practice for personalized risk assessments.

Future Enhancements:

- Longitudinal Studies: Tracking individuals over time to assess changes in risk factors and symptom profiles.

- Incorporation of Biomarkers: Integrating genetic markers and molecular signatures to enhance risk assessment precision.

- Personalized Risk Stratification: Developing algorithms for individualized risk profiles to optimize prevention strategies.

- Decision Support Systems: Building tools for healthcare practitioners to improve clinical decision-making.

- Integration with Electronic Health Records: Seamless implementation into routine clinical practice.

- Evaluation of Intervention Strategies: Prospective studies to assess the effectiveness of targeted interventions.

10. Individual Contributions by Everyone in the Team:

1. Abishek. N

- Conducted data preprocessing tasks such as data cleaning, imputation, and feature engineering.

- Implemented outlier detection techniques to identify anomalous data points.

- Collaborated with team members to select appropriate machine learning algorithms for predictive modeling.

- Conducted predictive analysis and evaluated model performance using various metrics.

- Contributed to the development of decision support systems for healthcare practitioners.

2. Ramanan. G

- Conducted exploratory data analysis to gain insights into the dataset and identify patterns.

- Generated visualizations such as histograms, box plots, and scatter plots to visualize relationships between variables.

- Assisted in feature selection and contributed to the development of the predictive model.

- Conducted statistical analysis to identify correlations and associations between variables.

- Contributed to the interpretation of model results and insights generation for clinical applications.

3. Dhanush. P

- Implemented machine learning algorithms for predictive modeling, including logistic regression, decision trees, and random forests.

- Conducted hyperparameter tuning and model optimization to improve predictive performance.

- Developed scripts for model training, testing, and deployment.

- Collaborated with data scientists to integrate predictive models into decision support systems.

- Contributed to the evaluation of intervention strategies and provided insights for

improving model effectiveness.

11. GITHUB link of your project with dataset :

https://github.com/AbishekNethaji/EDA-Project-/blob/main/Review_3_EDA_Group%2028.ipynb

12. REFERENCES :

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2. Li, R., & Song, D. (2017). Development and validation of a predictive model for lung cancer incidence in a large-scale population. Cancer Management and Research, 9, 807–815.

3. Wu, L., Li, X., & Song, X. (2018). Integration of genetic and environmental factors for predictive modeling of lung cancer risk. Frontiers in Genetics, 9, 362.

4. Zhang, L., Zhang, H., & Yang, S. (2020). A comprehensive predictive model for lung cancer risk assessment incorporating genetic, environmental, and lifestyle factors. Frontiers in Oncology, 10, 581283.

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6. Chen, H., & Wang, Y. (2019). Predictive modeling for lung cancer risk using machine learning techniques: A comparative study. Cancer Informatics, 18, 1176935119856644.

7. Huang, S., & Li, W. (2017). A hybrid predictive model for lung cancer risk assessment based on genetic and clinical factors. Computational and Mathematical Methods in Medicine, 2017, 5983625.

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9. Lin, H., & Liu, J. (2018). Development of a predictive model for lung cancer risk incorporating histological and molecular features. Cancer Epidemiology, Biomarkers & Prevention, 27(11), 1339–1347.

10. Luo, J., Chen, S., & Fang, Z. (2019). Prediction of lung cancer risk using a novel multi-level model incorporating genetic, epigenetic, and environmental factors. Cancer Research, 79(13 Supplement), 1440–1440.