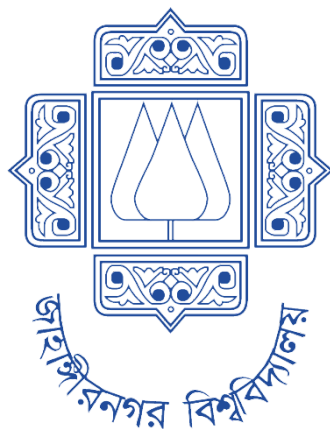


Institute of Information Technology (IIT)
Jahangirnagar University



Lab Report: 07

Submitted by:

Name: MD Zuleyenine Ibne Noman

Roll No: 2002

Lab Date: 4 September,2023

Submission Date: 28 August,2023

Dataset related information:

- filename : survey lung cancer.csv
- Link of dataset : <https://www.kaggle.com/code/kelvinfoo123/predicting-lung-cancer-with-knn/input> (<https://www.kaggle.com/code/kelvinfoo123/predicting-lung-cancer-with-knn/input>)
- following are the Dataset characterizations:
 - Total no. of attributes:16
 - No .of instances:284 Attribute information: 1. Gender: M(male), F(female) 2. Age: Age of the patient 3. Smoking: YES=2 , NO=1. 4. Yellow fingers: YES=2 , NO=1. 5. Anxiety: YES=2 , NO=1. 6. Peer_pressure: YES=2 , NO=1. 7. Chronic Disease: YES=2 , NO=1. 8. Fatigue: YES=2 , NO=1. 9. Allergy: YES=2 , NO=1. 10. Wheezing: YES=2 , NO=1. 11. Alcohol: YES=2 , NO=1. 12. Coughing: YES=2 , NO=1. 13. Shortness of Breath: YES=2 , NO=1. 14. Swallowing Difficulty: YES=2 , NO=1. 15. Chest pain: YES=2 , NO=1. 16. Lung Cancer: YES , NO.

All needed installations:

Import Libraries

```
In [7]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
```

Read the file /dataset

```
In [8]: cancer=pd.read_csv("survey lung cancer.csv")
```

In [9]: cancer

Out[9]:

	GENDER	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE
0	M	69	1	2	2	1	1
1	M	74	2	1	1	1	2
2	F	59	1	1	1	2	1
3	M	63	2	2	2	1	1
4	F	63	1	2	1	1	1
...
304	F	56	1	1	1	2	2
305	M	70	2	1	1	1	1
306	M	58	2	1	1	1	1
307	M	67	2	1	2	1	1
308	M	62	1	1	1	2	1

309 rows × 16 columns

Exploring the dataset

In [10]: cancer.head()

Out[10]:

	GENDER	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE	F
0	M	69	1	2	2	1	1	
1	M	74	2	1	1	1	2	
2	F	59	1	1	1	2	1	
3	M	63	2	2	2	1	1	
4	F	63	1	2	1	1	1	

In [11]: cancer.shape

Out[11]: (309, 16)

In [12]: cancer.info()

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 309 entries, 0 to 308
Data columns (total 16 columns):
#   Column                Non-Null Count  Dtype
---  -
0   GENDER                 309 non-null    object
1   AGE                    309 non-null    int64
2   SMOKING                309 non-null    int64
3   YELLOW_FINGERS         309 non-null    int64
4   ANXIETY                309 non-null    int64
5   PEER_PRESSURE          309 non-null    int64
6   CHRONIC DISEASE        309 non-null    int64
7   FATIGUE                309 non-null    int64
8   ALLERGY                309 non-null    int64
9   WHEEZING               309 non-null    int64
10  ALCOHOL CONSUMING      309 non-null    int64
11  COUGHING                309 non-null    int64
12  SHORTNESS OF BREATH    309 non-null    int64
13  SWALLOWING DIFFICULTY  309 non-null    int64
14  CHEST PAIN             309 non-null    int64
15  LUNG_CANCER            309 non-null    object
dtypes: int64(14), object(2)
memory usage: 38.8+ KB
```

In [13]: cancer.describe()

Out[13]:

	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE
count	309.000000	309.000000	309.000000	309.000000	309.000000	309.000000
mean	62.673139	1.563107	1.569579	1.498382	1.501618	1.504854
std	8.210301	0.496806	0.495938	0.500808	0.500808	0.500787
min	21.000000	1.000000	1.000000	1.000000	1.000000	1.000000
25%	57.000000	1.000000	1.000000	1.000000	1.000000	1.000000
50%	62.000000	2.000000	2.000000	1.000000	2.000000	2.000000
75%	69.000000	2.000000	2.000000	2.000000	2.000000	2.000000
max	87.000000	2.000000	2.000000	2.000000	2.000000	2.000000

Dataset preprocessing

!pip install sklearn !pip install scikit-learn

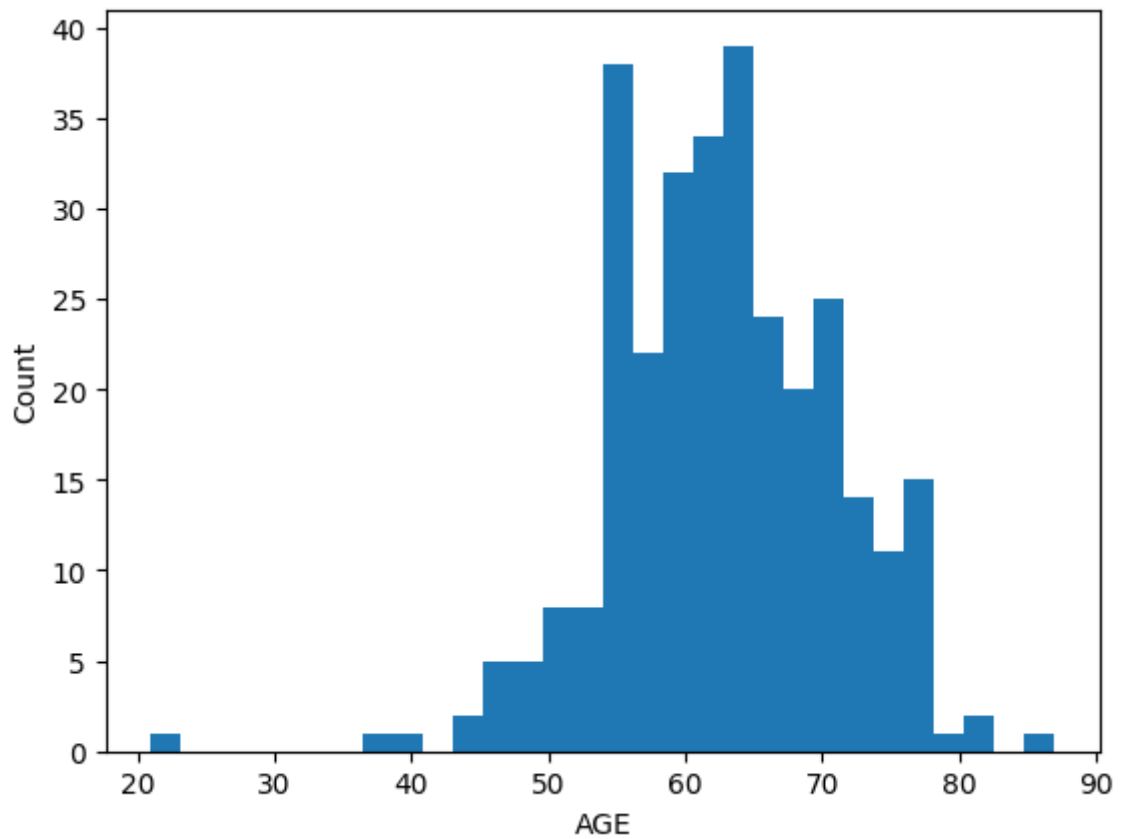
```
In [14]: from sklearn.preprocessing import LabelEncoder
lb=LabelEncoder()
cancer["LUNG_CANCER"]=lb.fit_transform(cancer["LUNG_CANCER"])
```

```
In [15]: cancer["GENDER"]=lb.fit_transform(cancer["GENDER"])
```

```
In [16]: cancer["LUNG_CANCER"].value_counts()
```

```
Out[16]: LUNG_CANCER  
1    270  
0     39  
Name: count, dtype: int64
```

```
In [17]: plt.hist(cancer["AGE"],bins=30)  
plt.xlabel("AGE")  
plt.ylabel("Count")  
plt.show()
```



```
In [18]: cancer=cancer[cancer.AGE>30]
```

```
In [19]: cancer_without_age = cancer.drop(["AGE"], axis = 1)
for i in cancer_without_age.columns:
    print(cancer_without_age[i].value_counts())
```

GENDER

1 162

0 146

Name: count, dtype: int64

SMOKING

2 173

1 135

Name: count, dtype: int64

YELLOW_FINGERS

2 176

1 132

Name: count, dtype: int64

ANXIETY

2 154

1 154

Name: count, dtype: int64

PEER_PRESSURE

2 155

1 153

Name: count, dtype: int64

CHRONIC DISEASE

2 155

1 153

Name: count, dtype: int64

FATIGUE

2 207

1 101

Name: count, dtype: int64

ALLERGY

2 171

1 137

Name: count, dtype: int64

WHEEZING

2 172

1 136

Name: count, dtype: int64

ALCOHOL CONSUMING

2 172

1 136

Name: count, dtype: int64

COUGHING

2 179

1 129

Name: count, dtype: int64

SHORTNESS OF BREATH

2 197

1 111

Name: count, dtype: int64

SWALLOWING DIFFICULTY

1 163

2 145

Name: count, dtype: int64

CHEST PAIN

2 172

```

1  136
Name: count, dtype: int64
LUNG_CANCER
1  270
0   38
Name: count, dtype: int64

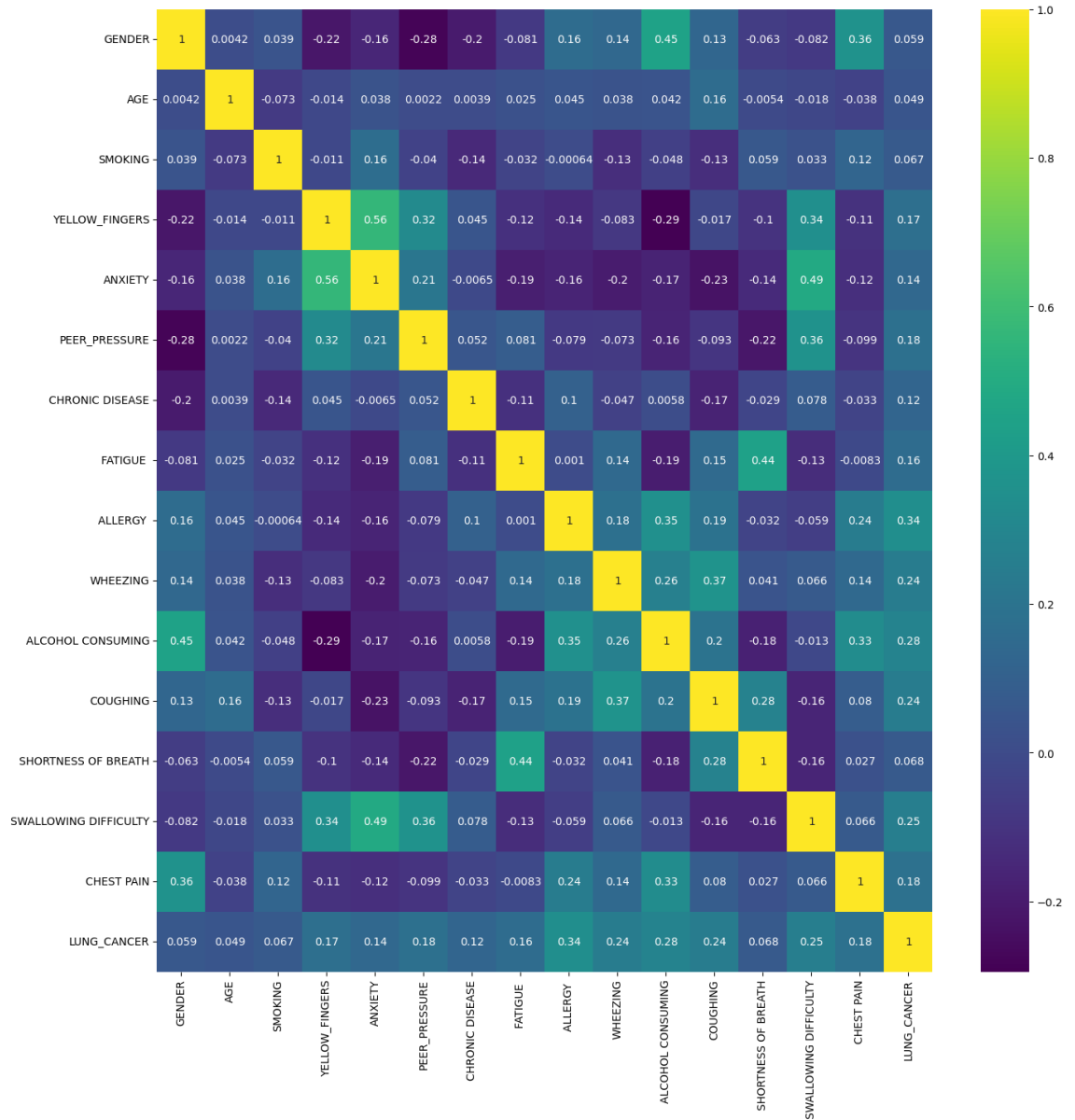
```

```

In [20]: plt.figure(figsize=(16,16))
sns.heatmap(cancer.corr(),annot=True,cmap="viridis")

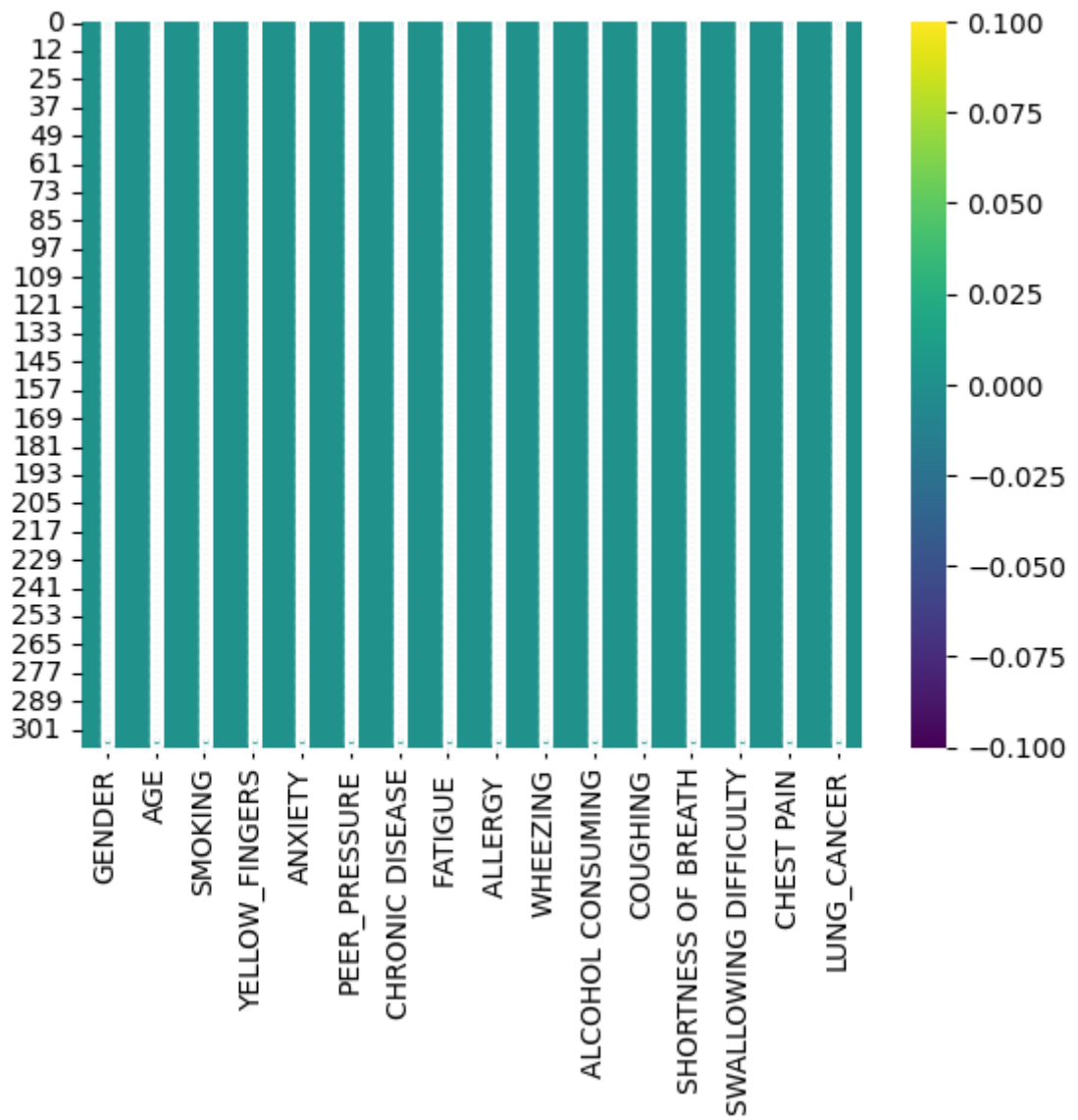
```

Out[20]: <AxesSubplot: >



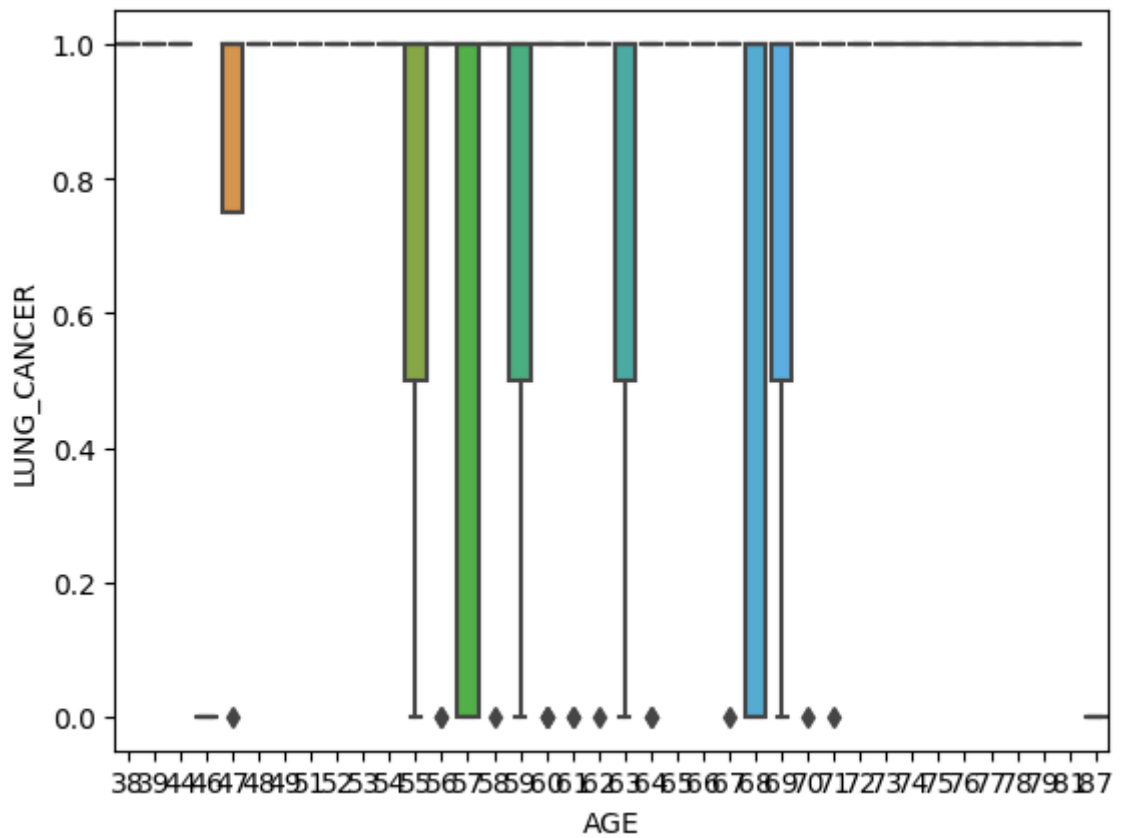

```
In [21]: sns.heatmap(cancer.isnull(),annot=True,cmap="viridis")
```

```
Out[21]: <AxesSubplot: >
```



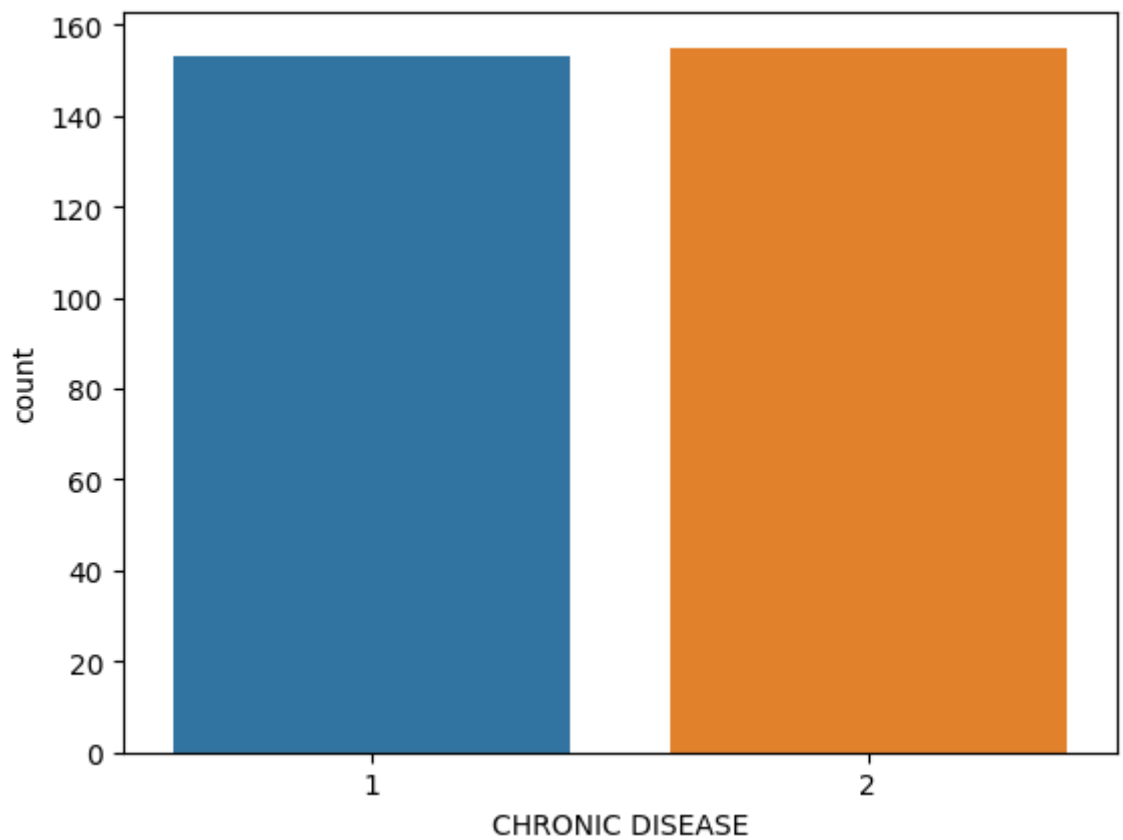
```
In [22]: sns.boxplot(x="AGE",y="LUNG_CANCER",data=cancer)
```

```
Out[22]: <AxesSubplot: xlabel='AGE', ylabel='LUNG_CANCER'>
```



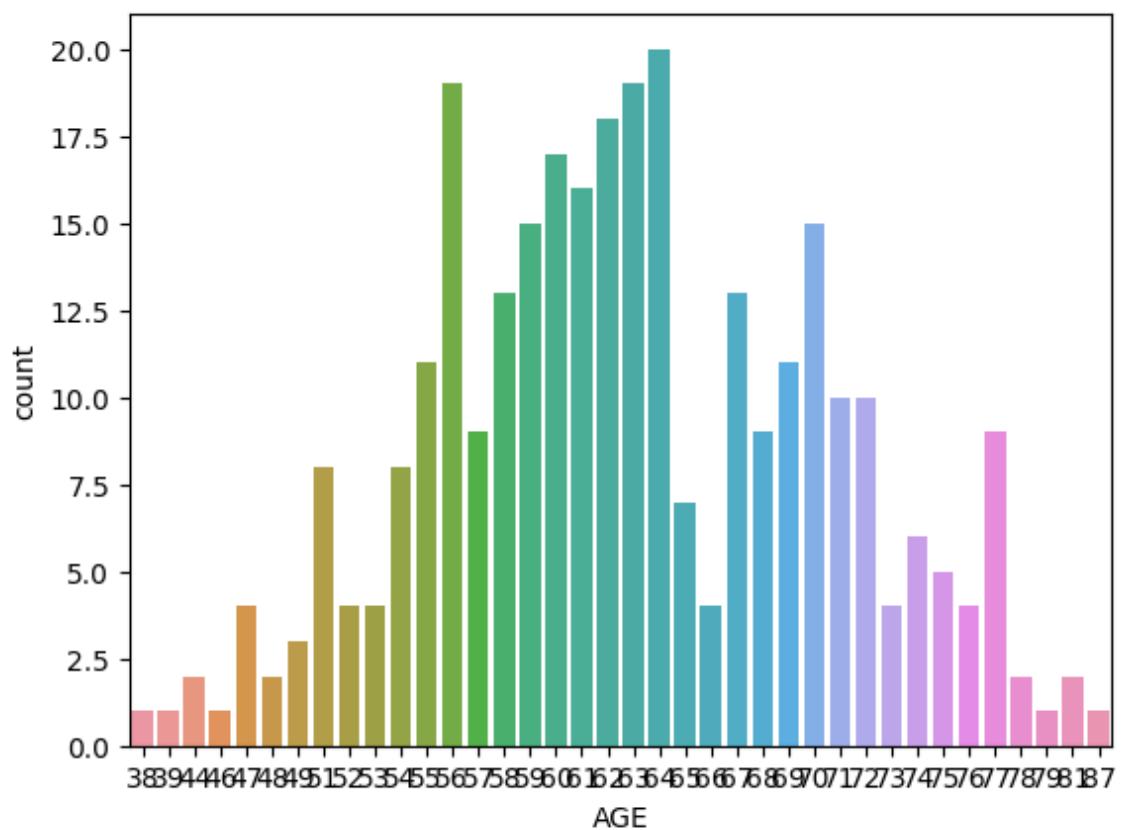
```
In [23]: sns.countplot(x="CHRONIC DISEASE",data=cancer)
```

```
Out[23]: <AxesSubplot: xlabel='CHRONIC DISEASE', ylabel='count'>
```



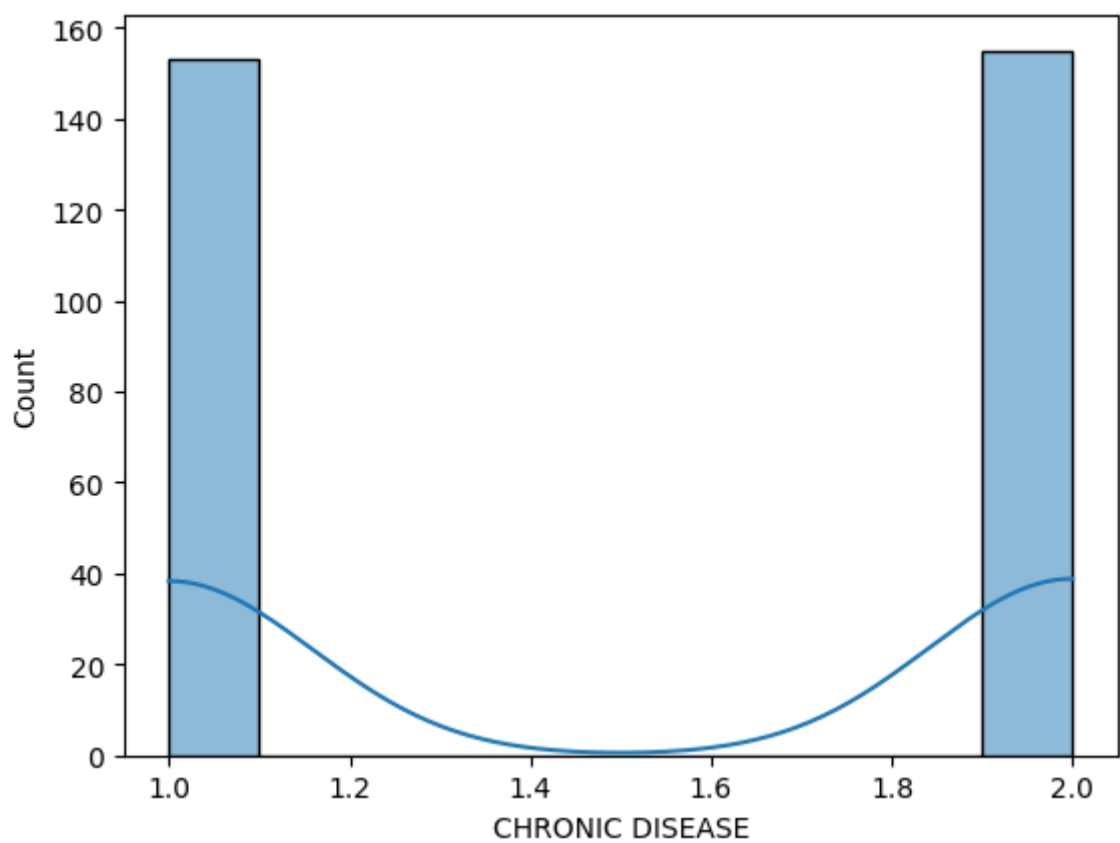
```
In [24]: sns.countplot(x="AGE",data=cancer)
```

```
Out[24]: <AxesSubplot: xlabel='AGE', ylabel='count'>
```



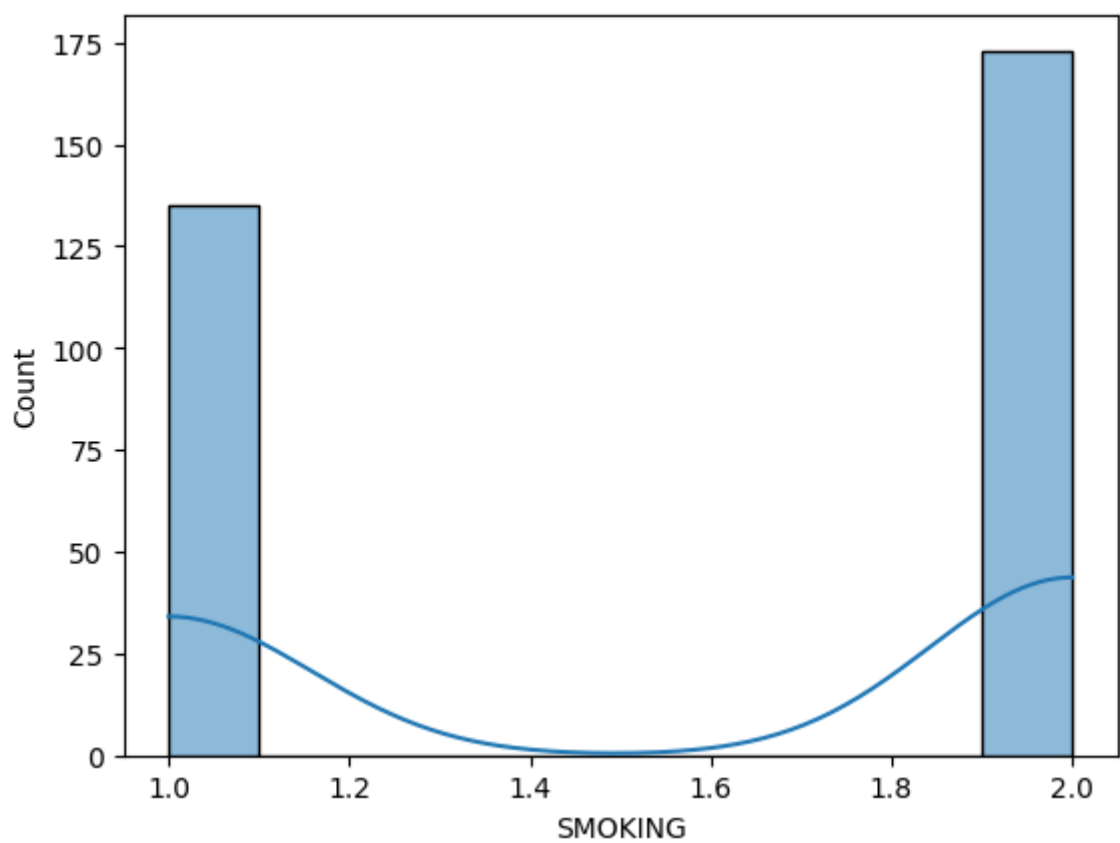
```
In [25]: sns.histplot(cancer["CHRONIC DISEASE"],bins=10,kde=True)
```

```
Out[25]: <AxesSubplot: xlabel='CHRONIC DISEASE', ylabel='Count'>
```



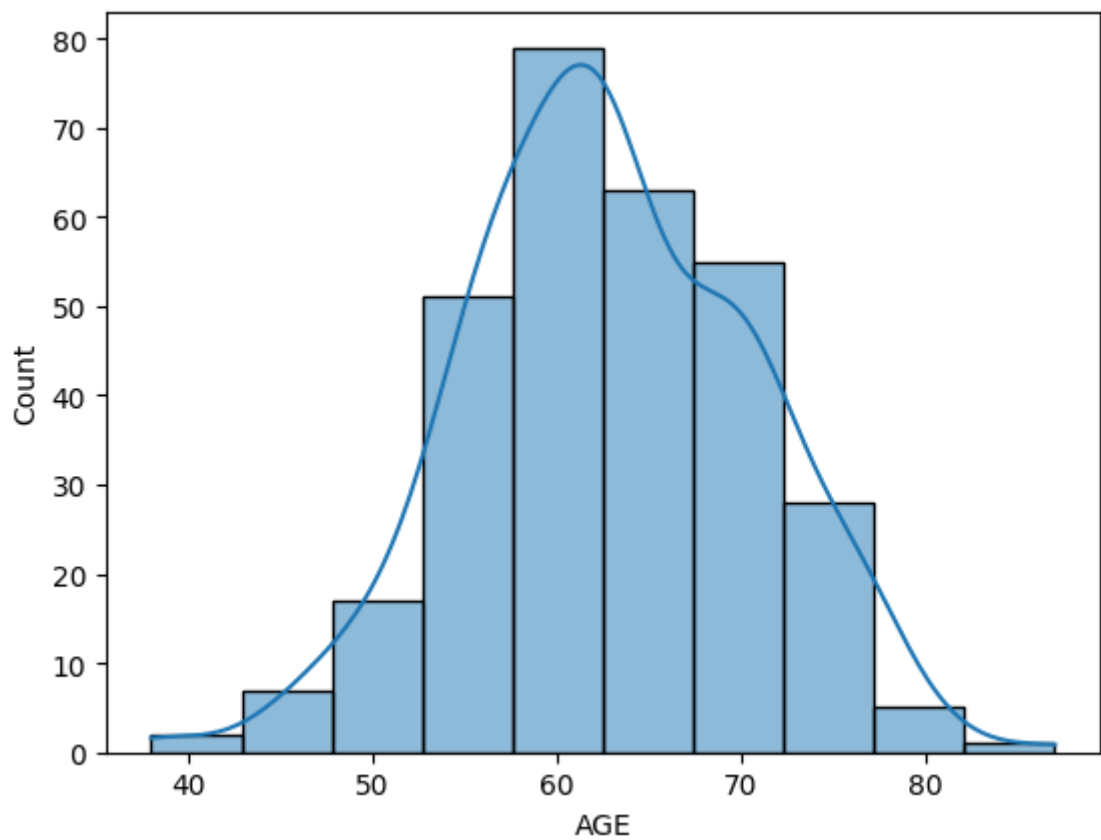
```
In [26]: sns.histplot(cancer["SMOKING"],bins=10,kde=True)
```

```
Out[26]: <AxesSubplot: xlabel='SMOKING', ylabel='Count'>
```

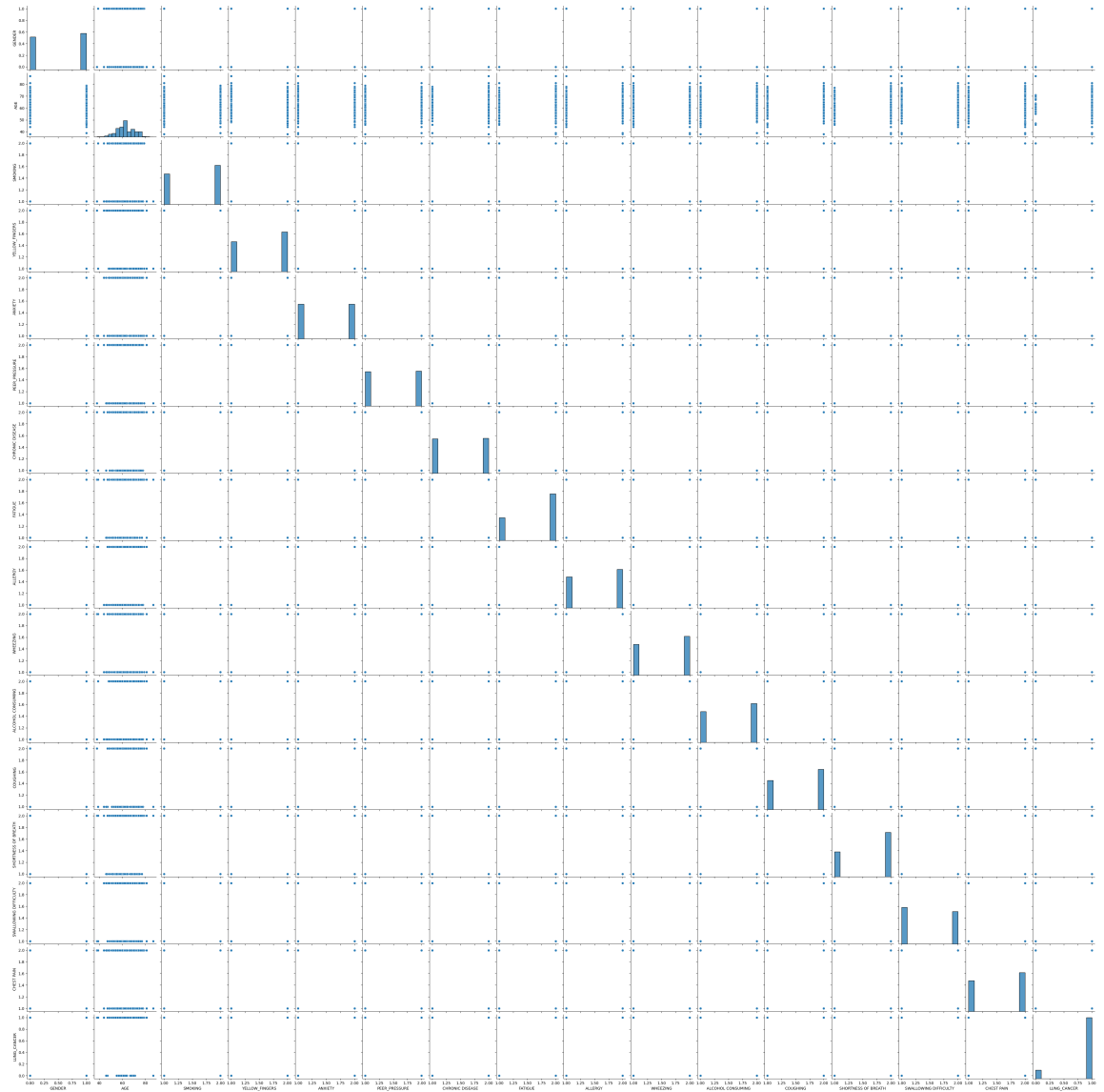


```
In [27]: sns.histplot(cancer["AGE"],bins=10,kde=True)
```

```
Out[27]: <AxesSubplot: xlabel='AGE', ylabel='Count'>
```



```
In [28]: sns.pairplot(cancer)
plt.show()
```



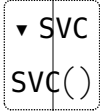
SVM model Training and Evaluation

```
In [29]: from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, precision_score, recall_score
from sklearn.metrics import confusion_matrix, classification_report
```

```
In [30]: x_train, x_test, y_train, y_test = train_test_split(cancer.drop('LUNG_',
```

```
In [31]: from sklearn.svm import SVC
model=SVC()
model.fit(x_train,y_train)
```

```
Out[31]:
```



```
In [32]: predictions=model.predict(x_test)
```

```
In [33]: print(confusion_matrix(y_test,predictions))
```

```
[[ 0 11]
 [ 0 82]]
```

```
In [34]: print(accuracy_score(y_test,predictions))
```

```
0.8817204301075269
```

```
In [35]: print(classification_report(y_test,predictions))
```

```

      precision    recall  f1-score   support

     0       0.00      0.00      0.00        11
     1       0.88      1.00      0.94        82
```

```

 accuracy                0.88      93
 macro avg              0.44      0.50      0.47      93
 weighted avg           0.78      0.88      0.83      93
```

```

/home/eyenine/.local/lib/python3.10/site-packages/sklearn/metrics/_
_classification.py:1469: UndefinedMetricWarning: Precision and F-score
are ill-defined and being set to 0.0 in labels with no predicted samples. U
se 'zero_division' parameter to control this behavior.
  warn_prf(average, modifier, msg_start, len(result))
/home/eyenine/.local/lib/python3.10/site-packages/sklearn/metrics/_
_classification.py:1469: UndefinedMetricWarning: Precision and F-score
are ill-defined and being set to 0.0 in labels with no predicted samples. U
se 'zero_division' parameter to control this behavior.
  warn_prf(average, modifier, msg_start, len(result))
/home/eyenine/.local/lib/python3.10/site-packages/sklearn/metrics/_
_classification.py:1469: UndefinedMetricWarning: Precision and F-score
are ill-defined and being set to 0.0 in labels with no predicted samples. U
se 'zero_division' parameter to control this behavior.
  warn_prf(average, modifier, msg_start, len(result))
```

```
In [36]: print(precision_score(y_test,predictions))
```

```
0.8817204301075269
```

```
In [37]: print(recall_score(y_test,predictions))
```

```
1.0
```



```
In [38]: print(f1_score(y_test, predictions))
```

```
0.937142857142857
```

```
In [39]: print(confusion_matrix(y_test, predictions))
```

```
[[ 0 11]
 [ 0 82]]
```

```
In [40]: import matplotlib.pyplot as plt
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

cm = confusion_matrix(y_test, predictions)

disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=["T", "F"])
disp.plot(cmap=plt.cm.Blues)
plt.title("Confusion Matrix")
plt.show()
```

