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

GENDER : M [Male] , F [Female]

AGE : Age of patients

SMOKING : 2 [Yes] , 1 [No]

YELLOW_FINGERS : 2 [Yes] , 1 [No]

ANXIETY :2 [Yes] , 1 [No] PEER_PRESSURE : 2 [Yes] , 1 [No]

CHRONIC DISEASE : 2 [Yes] , 1 [No]

FATIGUE : 2 [Yes] , 1 [No]

ALLERGY : 2 [Yes] , 1 [No]

WHEEZING : 2 [Yes] , 1 [No]

ALCOHOL CONSUMING : 2 [Yes] , 1 [No]

COUGHING : 2 [Yes] , 1 [No]

SHORTNESS OF BREATH : 2 [Yes] , 1 [No]

SWALLOWING DIFFICULTY : 2 [Yes] , 1 [No]

CHEST PAIN : 2 [Yes] , 1 [No]

LUNG_CANCER : YES [Positive] , NO [Negative]

```
data = pd.read_csv("survey lung cancer.csv")
```

```
print(f"Shape of The Dataset : {data.shape}")
print(f"\nGlimpse of The Dataset :")
data.head()
```

```
Shape of The Dataset : (309, 16)

Glimpse of The Dataset :
```

	GENDER	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE	FATIGUE	ALLERGY	WHEEZING	ALCOHOL CONSUMING	COUGHING	SHORTNESS OF BREATH	SWA DIF
0	M	69	1	2	2	1	1	2	1	2	2	2	2	
1	M	74	2	1	1	1	2	2	2	1	1	1	2	
2	F	59	1	1	1	2	1	2	1	2	1	2	2	
3	M	63	2	2	2	1	1	1	1	1	2	1	1	

```
print(f"Informations About The Dataset :\n")
print(data.info())
```

```
Informations About The Dataset :

<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
None
```

```
print(f"Summary of This Dataset :")
data.describe()
```

```
Summary of This Dataset :
```

	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE	F
count	309.000000	309.000000	309.000000	309.000000	309.000000	309.000000	309.
mean	62.673139	1.563107	1.569579	1.498382	1.501618	1.504854	1.
std	8.210301	0.496806	0.495938	0.500808	0.500808	0.500787	0.
min	21.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.
25%	57.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.
50%	62.000000	2.000000	2.000000	1.000000	2.000000	2.000000	2.
75%	69.000000	2.000000	2.000000	2.000000	2.000000	2.000000	2.

```
data.describe(include=object)
```

	GENDER	LUNG_CANCER
count	309	309
unique	2	2
top	M	YES
freq	162	270

```
data.isna().sum().to_frame()
```

	0
GENDER	0
AGE	0
SMOKING	0
YELLOW_FINGERS	0
ANXIETY	0
PEER_PRESSURE	0
CHRONIC DISEASE	0
FATIGUE	0
ALLERGY	0
WHEEZING	0
ALCOHOL CONSUMING	0
COUGHING	0
SHORTNESS OF BREATH	0
SWALLOWING DIFFICULTY	0
CHEST PAIN	0
LUNG_CANCER	0

Here, we can see there is no null value exists in this dataset. Let's check if there exists any duplicate entry in this dataset. If exists then we will remove them from the dataset. After that we will initialize the visualization style and custom pallete for visualization.

```
dup = data[data.duplicated()].shape[0]
print(f"There are {dup} duplicate entries among {data.shape[0]} entries in this dataset.")

data.drop_duplicates(keep='first',inplace=True)
print(f"\nAfter removing duplicate entries there are {data.shape[0]} entries in this dataset.")
```

```
There are 33 duplicate entries among 309 entries in this dataset.

After removing duplicate entries there are 276 entries in this dataset.
```

```
data_temp = data.copy()
data_temp["GENDER"] = data_temp["GENDER"].replace({"M" : "Male" , "F" : "Female"})

for column in data_temp.columns:
    data_temp[column] = data_temp[column].replace({2: "Yes" , 1 : "No"})

data_temp.head()
```

	GENDER	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE	FATIGUE	ALLERGY	WHEEZING	ALCOHOL CONSUMING	COUGHING	SHORTNESS OF BREATH	SWA DIF
0	Male	69	No	Yes	Yes	No	No	Yes	No	Yes	Yes	Yes	Yes	
1	Male	74	Yes	No	No	No	Yes	Yes	Yes	No	No	No	Yes	
2	Female	59	No	No	No	Yes	No	Yes	No	Yes	No	Yes	Yes	
3	Male	63	Yes	Yes	Yes	No	No	No	No	No	Yes	No	No	

Custom Palette For Visualization

```
sns.set_style("whitegrid")
sns.set_context("poster",font_scale = .7)

palette = ["#1d7874","#679289","#f4c095","#ee2e31","#ffb563","#918450","#f85e00","#a41623","#9a031e","#d6d6d6","#ffee32","#ffd100","#333533",

# sns.palplot(sns.color_palette(palette))
# plt.show()
```

Positive Lung Cancer Cases

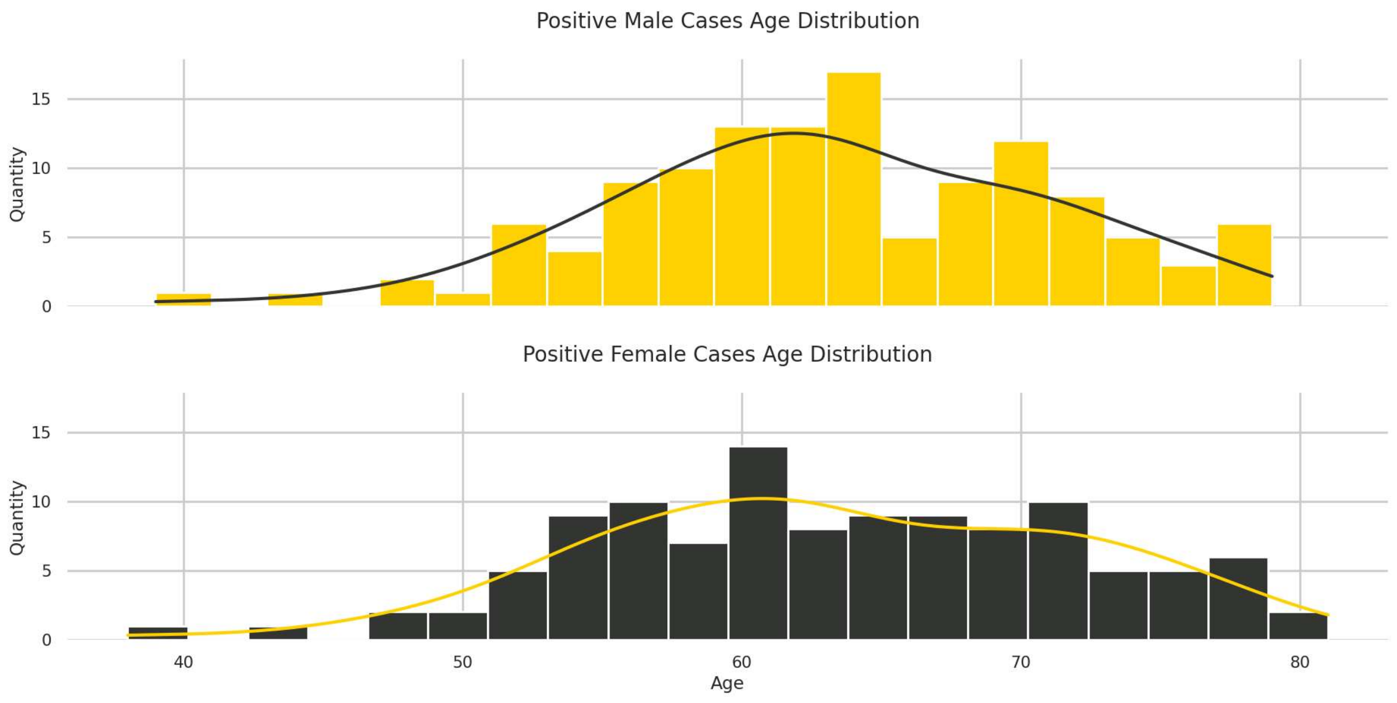
Let's create a new dataframe containing only positive cases data.

```
data_temp_pos = data_temp[data_temp["LUNG_CANCER"] == "YES"]
data_temp_pos.head()
```

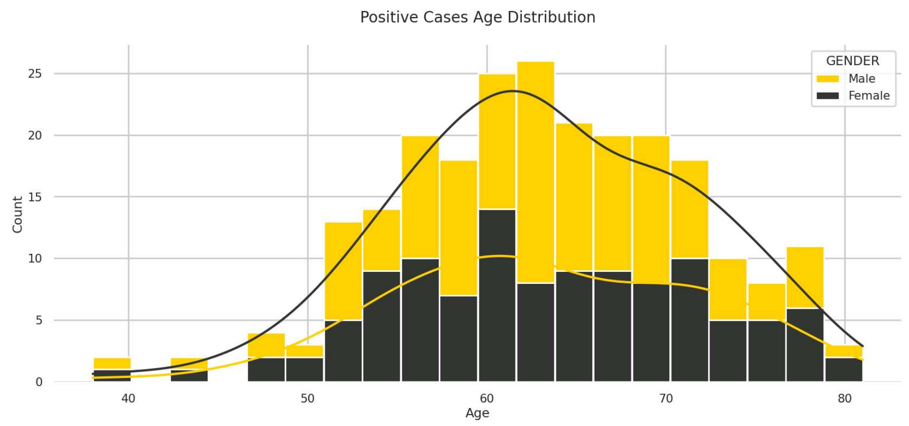
	GENDER	AGE	SMOKING	YELLOW_FINGERS	ANXIETY	PEER_PRESSURE	CHRONIC DISEASE	FATIGUE	ALLER
0	Male	69	No	Yes	Yes	No	No	Yes	N
1	Male	74	Yes	No	No	No	Yes	Yes	Y
5	Female	75	No	Yes	No	No	Yes	Yes	Y
6	Male	52	Yes	No	No	No	No	Yes	N

Positive Cases' Age Distribution

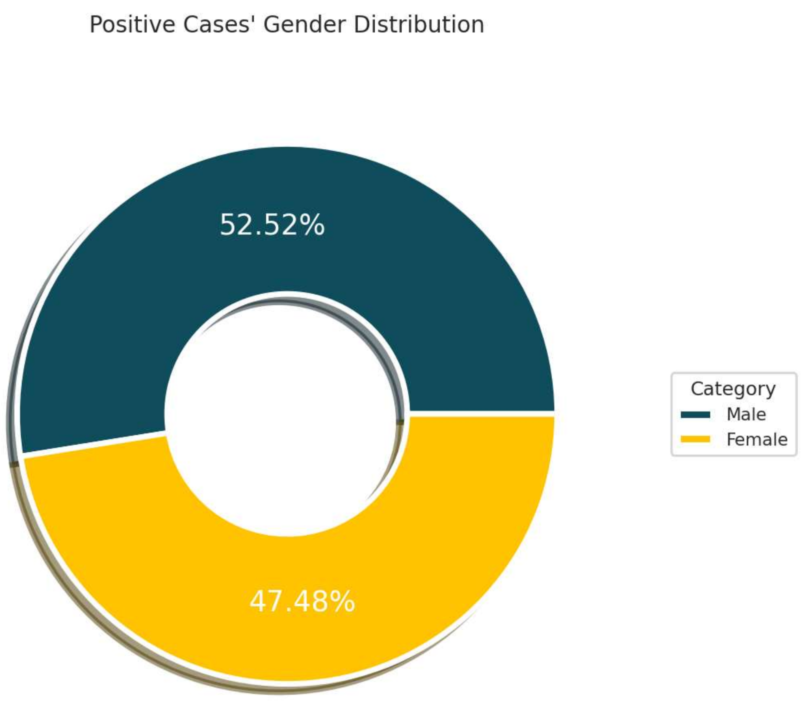
```
_, axs = plt.subplots(2,1,figsize=(20,10),sharex=True,sharey=True)
plt.tight_layout(pad=4.0)

sns.histplot(data_temp_pos[data_temp_pos["GENDER"]=="Male"]["AGE"],color=palette[11],kde=True,ax=axs[0],bins=20,alpha=1,fill=True)
axs[0].lines[0].set_color(palette[12])
axs[0].set_title("\nPositive Male Cases Age Distribution\n",fontsize=20)
axs[0].set_xlabel("Age")
axs[0].set_ylabel("Quantity")

sns.histplot(data_temp_pos[data_temp_pos["GENDER"]=="Female"]["AGE"],color=palette[12],kde=True,ax=axs[1],bins=20,alpha=1,fill=True)
axs[1].lines[0].set_color(palette[11])
axs[1].set_title("\nPositive Female Cases Age Distribution\n",fontsize=20)
axs[1].set_xlabel("Age")
axs[1].set_ylabel("Quantity")

sns.despine(left=True, bottom=True)
plt.show()
```



```
plt.subplots(figsize=(20, 8))
p = sns.histplot(data=data_temp_pos,x="AGE",hue="GENDER",multiple="stack",palette=palette[11:13],kde=True,shrink=.99,bins=20,alpha=1,fill=Tr
p.axes.lines[0].set_color(palette[11])
p.axes.lines[1].set_color(palette[12])
p.axes.set_title("\nPositive Cases Age Distribution\n",fontsize=20)
plt.ylabel("Count")
plt.xlabel("Age")

sns.despine(left=True, bottom=True)
plt.show()
```

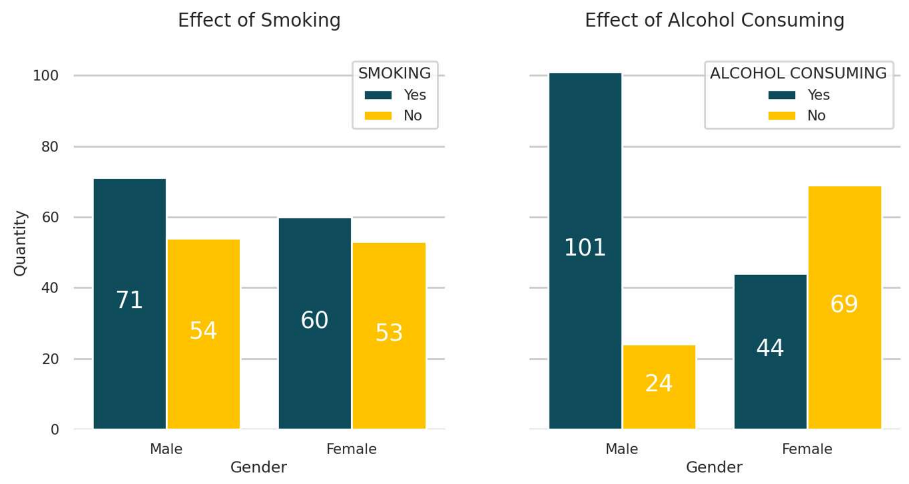


```
plt.subplots(figsize=(12, 12))

labels = "Male","Female"
size = 0.5

wedges, texts, autotexts = plt.pie([len(data_temp_pos[data_temp_pos["GENDER"]=="Male"]["GENDER"]),
                                    len(data_temp_pos[data_temp_pos["GENDER"]=="Female"]["GENDER"])],
                                    explode = (0,0),
                                    textprops=dict(size= 25, color= "white"),
                                    autopct="%.2f%%",
                                    pctdistance = 0.7,
                                    radius=.9,
                                    colors = ["#0f4c5c","#FFC300"],
                                    shadow = True,
                                    wedgeprops=dict(width = size, edgecolor = "white",
                                    linewidth = 5),
                                    startangle = 0)

plt.legend(wedges, labels, title="Category",loc="center left",bbox_to_anchor=(1, 0, 0.5, 1))
plt.title("\nPositive Cases' Gender Distribution",fontsize=20)
plt.show()
```



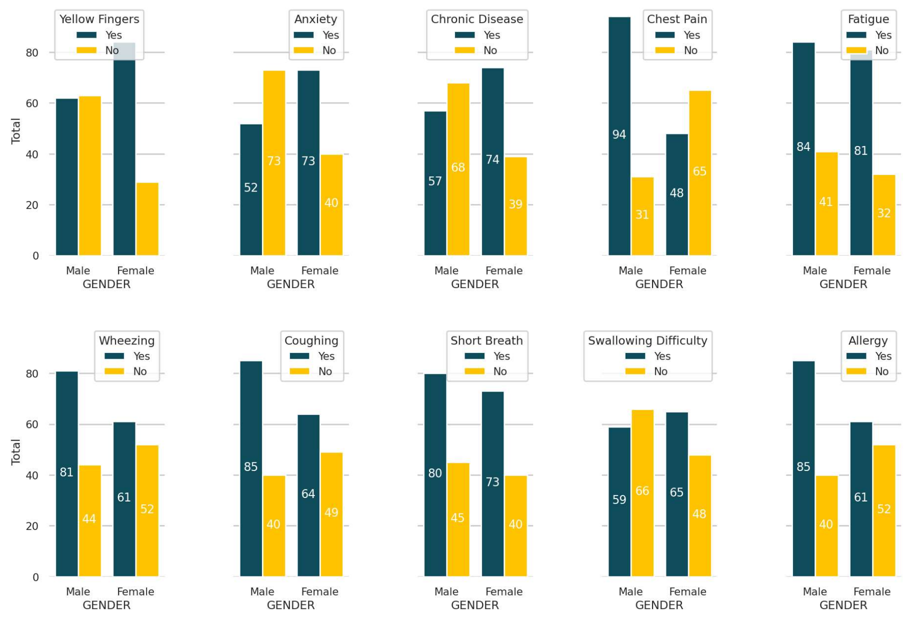
Gender-wise Positive Cases' Reasons

```
_, axs = plt.subplots(1,2,figsize=(15,8),sharex=True,sharey=True)
plt.tight_layout(pad=4.0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="SMOKING",hue_order=["Yes","No"],ax=axs[0],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[0].set_title("\nEffect of Smoking\n",fontsize=20)
axs[0].set_xlabel("Gender")
axs[0].set_ylabel("Quantity")
for container in axs[0].containers:
    axs[0].bar_label(container,label_type="center",padding=2,size=25,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="ALCOHOL CONSUMING",hue_order=["Yes","No"],ax=axs[1],palette=["#0f4c5c","#FFC300"],saturatic
axs[1].set_title("\nEffect of Alcohol Consuming\n",fontsize=20)
axs[1].set_xlabel("Gender")
axs[1].set_ylabel("Quantity")
for container in axs[1].containers:
    axs[1].bar_label(container,label_type="center",padding=2,size=25,color="white",rotation=0)

sns.despine(left=True, bottom=True)
plt.show()
```



Gender-wise Positive Cases' Symptoms

```
_, axs = plt.subplots(2,5,figsize=(20,14),sharex=False,sharey=True)
plt.tight_layout(pad=4.0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="YELLOW_FINGERS",hue_order=["Yes","No"],ax=axs[0,0],palette=["#0f4c5c","#FFC300"],saturatior
axs[0,0].set_ylabel("Total")
axs[0,0].legend(title="Yellow Fingers",loc="upper left")


sns.countplot(data=data_temp_pos,x="GENDER",hue="ANXIETY",hue_order=["Yes","No"],ax=axs[0,1],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[0,1].set_ylabel("Total")
axs[0,1].legend(title="Anxiety",loc="upper right")
for container in axs[0,1].containers:
    axs[0,1].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="CHRONIC DISEASE",hue_order=["Yes","No"],ax=axs[0,2],palette=["#0f4c5c","#FFC300"],saturatic
axs[0,2].set_ylabel("Total")
axs[0,2].legend(title="Chronic Disease",loc="upper right")
for container in axs[0,2].containers:
    axs[0,2].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="CHEST PAIN",hue_order=["Yes","No"],ax=axs[0,3],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[0,3].set_ylabel("Total")
axs[0,3].legend(title="Chest Pain",loc="upper right")
for container in axs[0,3].containers:
    axs[0,3].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="FATIGUE ",hue_order=["Yes","No"],ax=axs[0,4],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[0,4].set_ylabel("Total")
axs[0,4].legend(title="Fatigue",loc="upper right")
for container in axs[0,4].containers:
    axs[0,4].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="WHEEZING",hue_order=["Yes","No"],ax=axs[1,0],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[1,0].set_ylabel("Total")
axs[1,0].legend(title="Wheezing",loc="upper right")
for container in axs[1,0].containers:
    axs[1,0].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="COUGHING",hue_order=["Yes","No"],ax=axs[1,1],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[1,1].set_ylabel("Total")
axs[1,1].legend(title="Coughing",loc="upper right")
for container in axs[1,1].containers:
    axs[1,1].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="SHORTNESS OF BREATH",hue_order=["Yes","No"],ax=axs[1,2],palette=["#0f4c5c","#FFC300"],satur
axs[1,2].set_ylabel("Total")
axs[1,2].legend(title="Short Breath",loc="upper right")
for container in axs[1,2].containers:
    axs[1,2].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="SWALLOWING DIFFICULTY",hue_order=["Yes","No"],ax=axs[1,3],palette=["#0f4c5c","#FFC300"],sat
axs[1,3].set_ylabel("Total")
axs[1,3].legend(title="Swallowing Difficulty",loc="upper right")
for container in axs[1,3].containers:
    axs[1,3].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.countplot(data=data_temp_pos,x="GENDER",hue="ALLERGY ",hue_order=["Yes","No"],ax=axs[1,4],palette=["#0f4c5c","#FFC300"],saturation=1)
axs[1,4].set_ylabel("Total")
axs[1,4].legend(title="Allergy",loc="upper right")
for container in axs[1,4].containers:
    axs[1,4].bar_label(container,label_type="center",padding=2,size=17,color="white",rotation=0)

sns.despine(left=True, bottom=True)
plt.show()
```



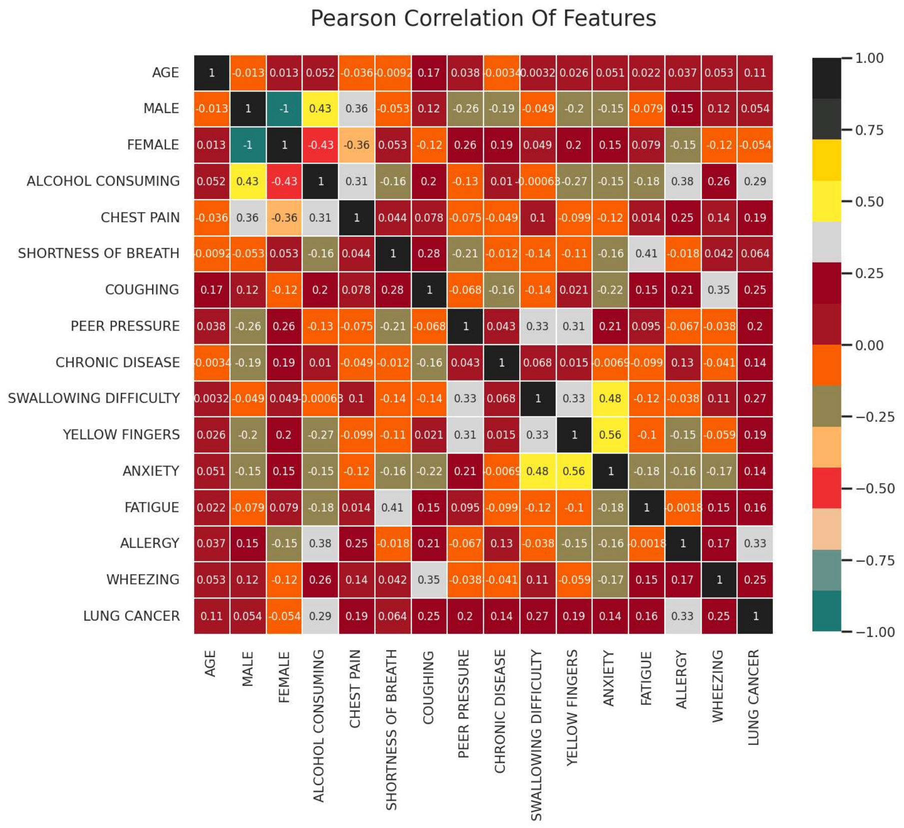
Correlation Heatmap

Converting the target feature "LUNG_CANCER" from Categorical to Numerical data type by using Label Encoder. And converting the "GENDER" column from Categorical to Numerical data type by using "One Hot Encoder" for avoiding unexpected gender bias.

```
from sklearn.preprocessing import LabelEncoder
LabelEncoder = LabelEncoder()

data["GENDER"] = data["GENDER"].replace({"M" : "Male" , "F" : "Female"})
data["LUNG_CANCER"] = LabelEncoder.fit_transform(data["LUNG_CANCER"])

data = pd.get_dummies(data, columns= ["GENDER"])
data.rename(columns={"GENDER_Male" : "MALE", "GENDER_Female" : "FEMALE", "YELLOW_FINGERS" : "YELLOW FINGERS", "PEER_PRESSURE" : "PEER PRESSU
data = data[["AGE","MALE","FEMALE","ALCOHOL CONSUMING","CHEST PAIN","SHORTNESS OF BREATH","COUGHING","PEER PRESSURE","CHRONIC DISEASE","SWAL
data.head()
```

	AGE	MALE	FEMALE	ALCOHOL CONSUMING	CHEST PAIN	SHORTNESS OF BREATH	COUGHING	PEER PRESSURE	CHRONIC DISEASE	SWALLOWI DIFFICUL
0	69	1	0	2	2	2	2	1	1	
1	74	1	0	1	2	2	1	1	2	
2	59	0	1	1	2	2	2	2	1	
3	63	1	0	2	2	1	1	1	1	

```
plt.subplots(figsize =(16, 12))

p=sns.heatmap(data.corr(), cmap = palette, square=True, cbar_kws=dict(shrink =.99),
            annot=True, vmin=-1, vmax=1, linewidths=0.1,linecolor='white',annot_kws=dict(fontsize =12))
p.axes.set_title("Pearson Correlation Of Features\n", fontsize=25)
plt.xticks(rotation=90)
plt.show()
```



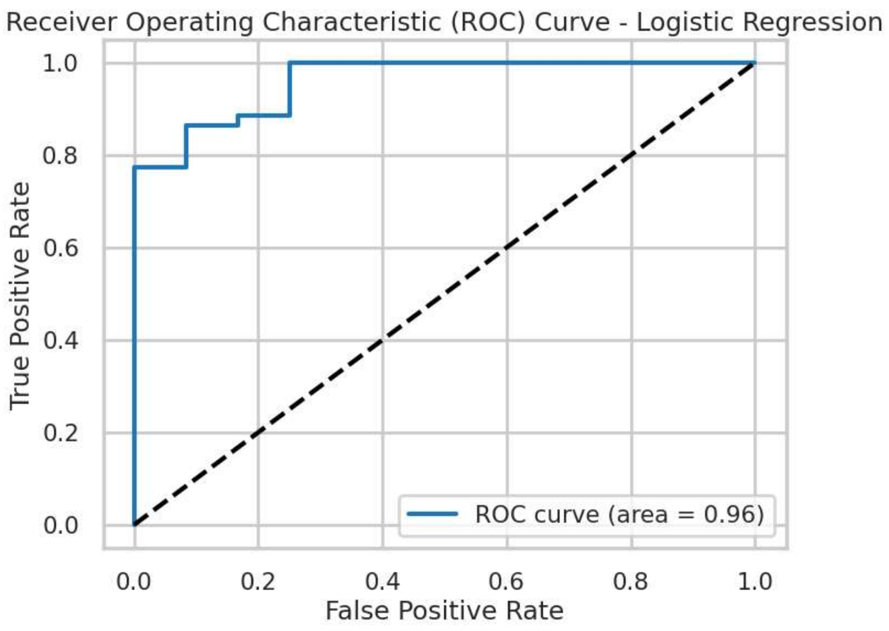
Preprocessing For Classification

```
x = data.drop("LUNG CANCER", axis = 1)
y = data["LUNG CANCER"]

from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split

scaler = StandardScaler()
x = scaler.fit_transform(x)
x_train, x_test, y_train, y_test = train_test_split(x,y, test_size=0.2, random_state=42)

print(f"Shape of training data : {x_train.shape}, {y_train.shape}")
print(f"Shape of testing data : {x_test.shape}, {y_test.shape}")
```

```
     Shape of training data : (220, 15), (220,)
     Shape of testing data : (56, 15), (56,)
```

Logistic Regression Model

```
from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt

lr = LogisticRegression()
lr.fit(x_train, y_train)

# Make predictions
lr_pred = lr.predict(x_test)

# Calculate predicted probabilities for the positive class
lr_pred_prob = lr.predict_proba(x_test)[:, 1]

# Calculate ROC curve
fpr, tpr, thresholds = roc_curve(y_test, lr_pred_prob)

# Plot ROC curve
plt.figure(figsize=(8, 6))
plt.plot(fpr, tpr, label=f'ROC curve (area = {auc(fpr, tpr):.2f})')
plt.plot([0, 1], [0, 1], 'k--')  # Random guess line
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve - Logistic Regression')
plt.legend()
plt.show()


lr_conf = confusion_matrix(y_test, lr_pred)
lr_report = classification_report(y_test, lr_pred)
lr_acc = round(accuracy_score(y_test, lr_pred) * 100, ndigits=2)

print(f"Confusion Matrix : \n\n{lr_conf}")
print(f"\nClassification Report : \n\n{lr_report}")
print(f"\nThe Accuracy of Logistic Regression is {lr_acc} %")
```



```
Confusion Matrix :

[[ 5  7]
 [ 0 44]]

Classification Report :

              precision    recall  f1-score   support

           0       1.00      0.42      0.59        12
           1       0.86      1.00      0.93        44

    accuracy                           0.88        56
   macro avg       0.93      0.71      0.76        56
weighted avg       0.89      0.88      0.85        56


The Accuracy of Logistic Regression is 87.5 %
```

Gaussian Naive Bayes Model

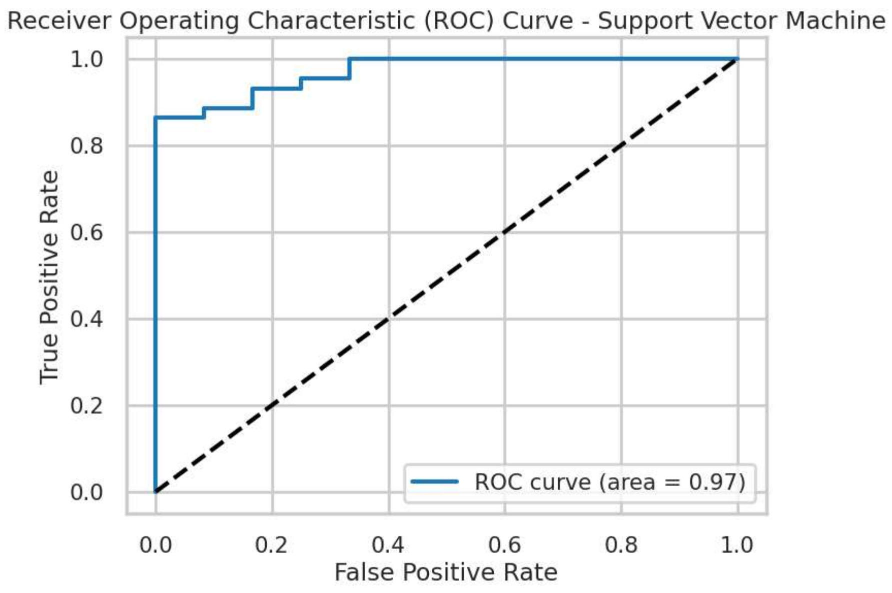
```
from sklearn.naive_bayes import GaussianNB

gnb = GaussianNB()
gnb.fit(x_train, y_train)
gnb_pred = gnb.predict(x_test)
gnb_conf = confusion_matrix(y_test, gnb_pred)
gnb_report = classification_report(y_test, gnb_pred)
gnb_acc = round(accuracy_score(y_test, gnb_pred)*100, ndigits = 2)
print(f"Confusion Matrix : \n\n{gnb_conf}")
print(f"\nClassification Report : \n\n{gnb_report}")
print(f"\nThe Accuracy of Gaussian Naive Bayes is {gnb_acc} %")
```

```
Confusion Matrix :

[[ 8  4]
 [ 1 43]]

Classification Report :

              precision    recall  f1-score   support

           0       0.89      0.67      0.76        12
           1       0.91      0.98      0.95        44

    accuracy                           0.91        56
```

```
   macro avg       0.90      0.82      0.85        56
weighted avg       0.91      0.91      0.91        56


The Accuracy of Gaussian Naive Bayes is 91.07 %
```

Support Vector Machine Model

```
from sklearn.svm import SVC
from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt

svm = SVC(C=100, gamma=0.002)
svm.fit(x_train, y_train)

# Make predictions
svm_pred = svm.predict(x_test)

# Calculate predicted probabilities for the positive class
svm_pred_prob = svm.decision_function(x_test)  # For SVC, use decision_function instead of predict_proba

# Calculate ROC curve
fpr_svm, tpr_svm, thresholds_svm = roc_curve(y_test, svm_pred_prob)

# Plot ROC curve
plt.figure(figsize=(8, 6))
plt.plot(fpr_svm, tpr_svm, label=f'ROC curve (area = {auc(fpr_svm, tpr_svm):.2f})')
plt.plot([0, 1], [0, 1], 'k--')  # Random guess line
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve - Support Vector Machine')
plt.legend()
plt.show()

# Continue with the rest of your code
svm_conf = confusion_matrix(y_test, svm_pred)
svm_report = classification_report(y_test, svm_pred)
svm_acc = round(accuracy_score(y_test, svm_pred) * 100, ndigits=2)

print(f"Confusion Matrix : \n\n{svm_conf}")
print(f"\nClassification Report : \n\n{svm_report}")
print(f"\nThe Accuracy of Support Vector Machine is {svm_acc} %")
```



```
Confusion Matrix :

[[ 4  8]
 [ 0 44]]

Classification Report :

              precision    recall  f1-score   support

           0       1.00      0.33      0.50        12
           1       0.85      1.00      0.92        44

    accuracy                           0.86        56
   macro avg       0.92      0.67      0.71        56
weighted avg       0.88      0.86      0.83        56


The Accuracy of Support Vector Machine is 85.71 %
```

Random Forest Model

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt

rfg = RandomForestClassifier(n_estimators=100, random_state=42)
rfg.fit(x_train, y_train)

# Make predictions
rfg_pred = rfg.predict(x_test)

# Calculate predicted probabilities for the positive class
rfg_pred_prob = rfg.predict_proba(x_test)[:, 1]

# Calculate ROC curve
fpr_rfg, tpr_rfg, thresholds_rfg = roc_curve(y_test, rfg_pred_prob)

# Plot ROC curve
plt.figure(figsize=(8, 6))
plt.plot(fpr_rfg, tpr_rfg, label=f'ROC curve (area = {auc(fpr_rfg, tpr_rfg):.2f})')
plt.plot([0, 1], [0, 1], 'k--')  # Random guess line
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve - Random Forest Classifier')
plt.legend()
plt.show()

# Continue with the rest of your code
rfg_conf = confusion_matrix(y_test, rfg_pred)
rfg_report = classification_report(y_test, rfg_pred)
rfg_acc = round(accuracy_score(y_test, rfg_pred) * 100, ndigits=2)

print(f"Confusion Matrix : \n\n{rfg_conf}")
print(f"\nClassification Report : \n\n{rfg_report}")
print(f"\nThe Accuracy of Random Forest Classifier is {rfg_acc} %")
```

Gradient Boosting Model

```
from xgboost import XGBClassifier

xgb = XGBClassifier(use_label_encoder = False)
xgb.fit(x_train, y_train)
xgb_pred = xgb.predict(x_test)
xgb_conf = confusion_matrix(y_test, xgb_pred)
xgb_report = classification_report(y_test, xgb_pred)
xgb_acc = round(accuracy_score(y_test, xgb_pred)*100, ndigits = 2)
print(f"Confusion Matrix : \n\n{xgb_conf}")
print(f"\nClassification Report : \n\n{xgb_report}")
print(f"\nThe Accuracy of Extreme Gradient Boosting Classifier is {xgb_acc} %")
```

```
    Confusion Matrix :

    [[ 6  6]
     [ 0 44]]

    Classification Report :

                  precision    recall  f1-score   support

               0       1.00      0.50      0.67        12
               1       0.88      1.00      0.94        44

        accuracy                           0.89        56
       macro avg       0.94      0.75      0.80        56
    weighted avg       0.91      0.89      0.88        56


    The Accuracy of Extreme Gradient Boosting Classifier is 89.29 %
```

Neural Network Architecture

```
import tensorflow as tf
from tensorflow.keras import Sequential
from tensorflow.keras import regularizers
from tensorflow.keras.optimizers import Adam

regularization_parameter = 0.003

neural_model = Sequential([tf.keras.layers.Dense(units=32, input_dim=(x_train.shape[-1]), activation="relu", kernel_regularizer = regularize
                    tf.keras.layers.Dense(units=64, activation="relu", kernel_regularizer = regularizers.l1(regularization_parameter)),
                    tf.keras.layers.Dense(units=128, activation="relu", kernel_regularizer = regularizers.l1(regularization_parameter)),
                    tf.keras.layers.Dropout(0.3),
                    tf.keras.layers.Dense(units=16,activation="relu", kernel_regularizer = regularizers.l1(regularization_parameter)),
                    tf.keras.layers.Dense(units=1, activation="sigmoid")
                    ])

print(neural_model.summary())
```

```
    Model: "sequential"
    _________________________________________________________________
     Layer (type)                Output Shape              Param #
    =================================================================
     dense (Dense)               (None, 32)                512

     dense_1 (Dense)             (None, 64)                2112

     dense_2 (Dense)             (None, 128)               8320
```