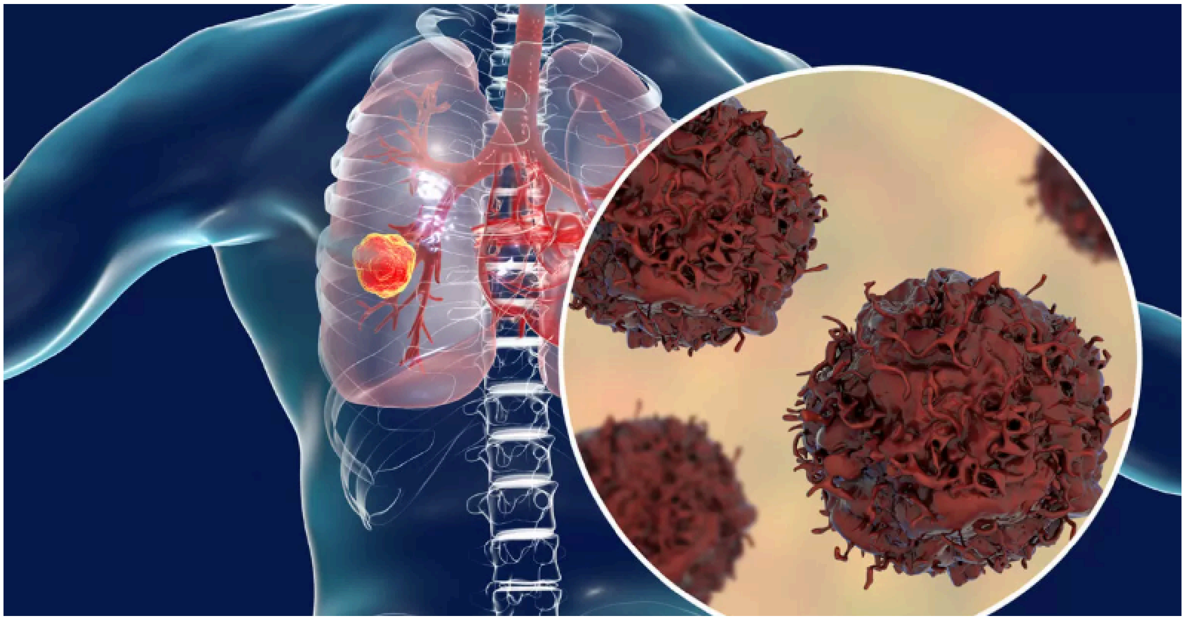
◈ Lung Cancer Prediction – My Journey from Data to Diagnosis



When I began this project, I had one mission in mind:

Can we empower early detection of lung cancer using data science?

I started with a dataset containing health-related information like **age**, **smoking history**, **anxiety levels**, **fatigue**, and more — 15 features that might silently hint at the presence of lung cancer.

◈ *Step 1: From Raw to Refined – Cleaning the Dataset*

First, I dived into **data preprocessing**. Some columns had inconsistent labels (like "YES" vs "Yes"), and I standardized all categorical values for clarity. I also checked for null values, ensuring the dataset was clean and ready.

In [1]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import plotly.express as px
import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```
df = pd.read_csv("C:\\Users\\DELL\\OneDrive - Questindustries\\Documents\\Data
print(df.head())
```

```
  GENDER  AGE SMOKING YELLOW_FINGERS ANXIETY PEER_PRESSURE CHRONIC_DISEASE  \
0      M   65     Yes            Yes     Yes            No              No   
1      F   55     Yes             No      No           Yes             Yes   
2      F   78      No             No     Yes           Yes             Yes   
3      M   60      No            Yes     Yes           Yes              No   
4      F   80     Yes            Yes      No           Yes             Yes   

  FATIGUE ALLERGY WHEEZING ALCOHOL_CONSUMING COUGHING SHORTNESS_OF_BREATH  \
0     Yes      No       No                No       No                  No   
1      No      No       No               Yes      Yes                 Yes   
2      No     Yes       No               Yes      Yes                  No   
3     Yes      No      Yes               Yes       No                 Yes   
4      No     Yes       No               Yes      Yes                 Yes   

  SWALLOWING_DIFFICULTY CHEST_PAIN LUNG_CANCER  
0                    No        Yes          NO  
1                    No         No          NO  
2                   Yes        Yes         YES  
3                    No         No         YES  
4                   Yes         No          NO  
```

In [3]:
```python
print(df.shape)
```

```
(3000, 16)
```

In [4]:
```python
print(df.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3000 entries, 0 to 2999
Data columns (total 16 columns):
 #   Column                 Non-Null Count  Dtype 
---  ------                 --------------  ----- 
 0   GENDER                 3000 non-null   object
 1   AGE                    3000 non-null   int64 
 2   SMOKING                3000 non-null   object
 3   YELLOW_FINGERS         3000 non-null   object
 4   ANXIETY                3000 non-null   object
 5   PEER_PRESSURE          3000 non-null   object
 6   CHRONIC_DISEASE        3000 non-null   object
 7   FATIGUE                3000 non-null   object
 8   ALLERGY                3000 non-null   object
 9   WHEEZING               3000 non-null   object
 10  ALCOHOL_CONSUMING      3000 non-null   object
 11  COUGHING               3000 non-null   object
 12  SHORTNESS_OF_BREATH    3000 non-null   object
 13  SWALLOWING_DIFFICULTY  3000 non-null   object
 14  CHEST_PAIN             3000 non-null   object
 15  LUNG_CANCER            3000 non-null   object
dtypes: int64(1), object(15)
memory usage: 375.1+ KB
None
```

In [5]:
```python
print(df.columns)
```

```
Index(['GENDER', 'AGE', 'SMOKING', 'YELLOW_FINGERS', 'ANXIETY',
       'PEER_PRESSURE', 'CHRONIC_DISEASE', 'FATIGUE', 'ALLERGY', 'WHEEZING',
       'ALCOHOL_CONSUMING', 'COUGHING', 'SHORTNESS_OF_BREATH',
       'SWALLOWING_DIFFICULTY', 'CHEST_PAIN', 'LUNG_CANCER'],
      dtype='object')
```

🔍 *Step 2: Understanding the Patient – EDA*

I used exploratory data analysis to **understand the patterns**.
For example:

- Most lung cancer patients were in the **50–70 age group**.
- **Smoking, chronic diseases,** and **fatigue** showed strong visual correlation with lung cancer presence.

This gave me an early sense of which features might be most predictive.

In [6]:
```python
print(df.isnull().sum())
```

```
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
dtype: int64
```

In [7]:
```python
print(df.duplicated().sum())
```

```
2
```

In [8]:
```python
df = df.drop_duplicates()
print(df.head())
```

```
  GENDER  AGE SMOKING YELLOW_FINGERS ANXIETY PEER_PRESSURE CHRONIC_DISEASE  \
0      M   65     Yes            Yes     Yes            No              No
1      F   55     Yes             No      No           Yes             Yes
2      F   78      No             No     Yes           Yes             Yes
3      M   60      No            Yes     Yes           Yes              No
4      F   80     Yes            Yes      No           Yes             Yes

  FATIGUE ALLERGY WHEEZING ALCOHOL_CONSUMING COUGHING SHORTNESS_OF_BREATH  \
0     Yes      No       No                No       No                  No
1      No      No       No               Yes      Yes                 Yes
2      No     Yes       No               Yes      Yes                  No
3     Yes      No      Yes               Yes       No                 Yes
4      No     Yes       No               Yes      Yes                 Yes

  SWALLOWING_DIFFICULTY CHEST_PAIN LUNG_CANCER
0                    No        Yes          NO
1                    No         No          NO
2                   Yes        Yes         YES
3                    No         No         YES
4                   Yes         No          NO
```

In [9]:
```
print(df.shape)
```

```
(2998, 16)
```

In [10]:
```
df.isnull().sum()
```

Out[10]:
```
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
dtype: int64
```

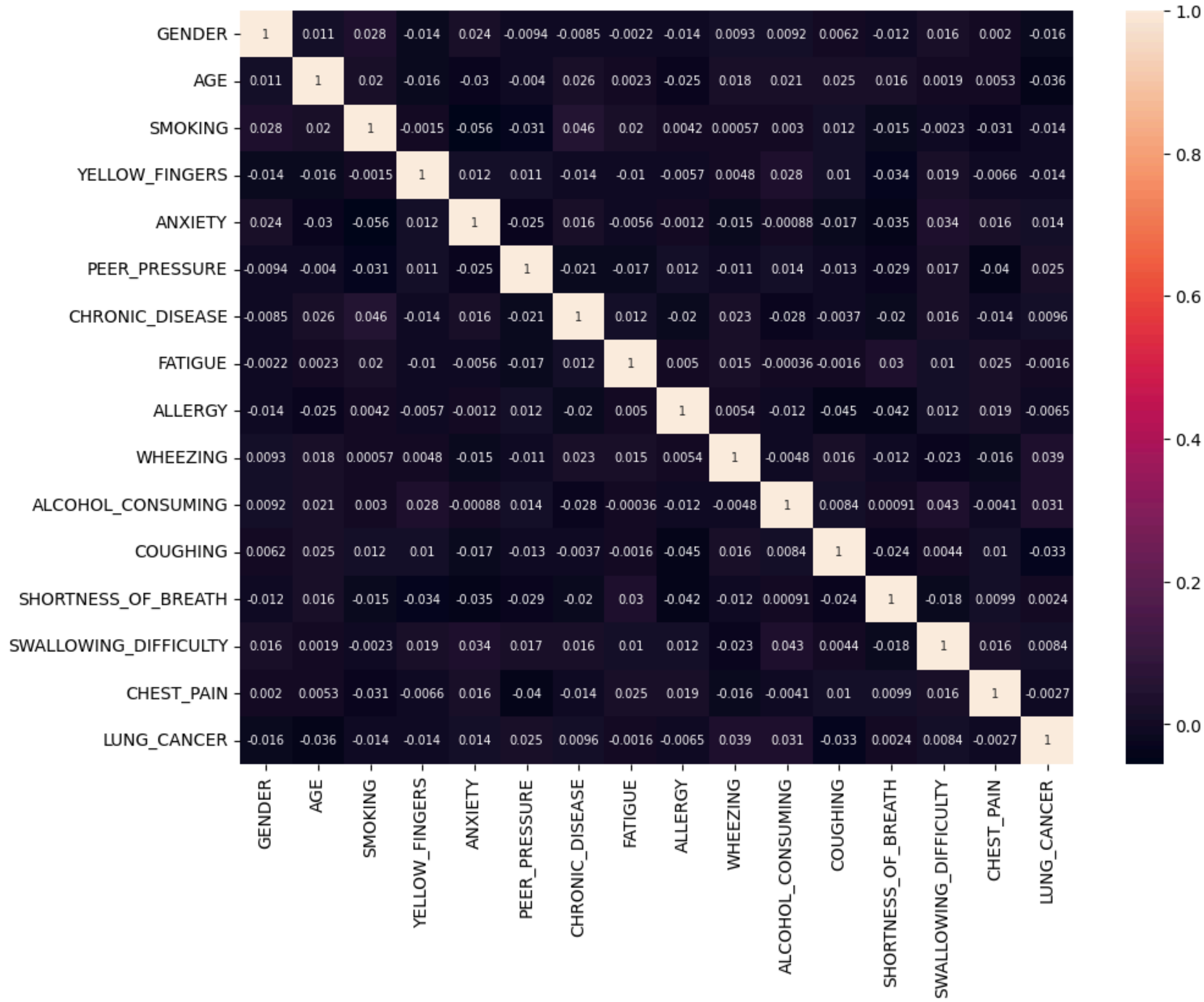
In [11]:
```
# Replace 'Yes' with 1 and 'No' with 0
df = df.replace({'Yes': 1, 'No': 0})
df = df.replace({'YES': 1, 'NO': 0})
df = df.replace({'M': 1, 'F': 0})
```

In [12]:
```
print(df.info())
```

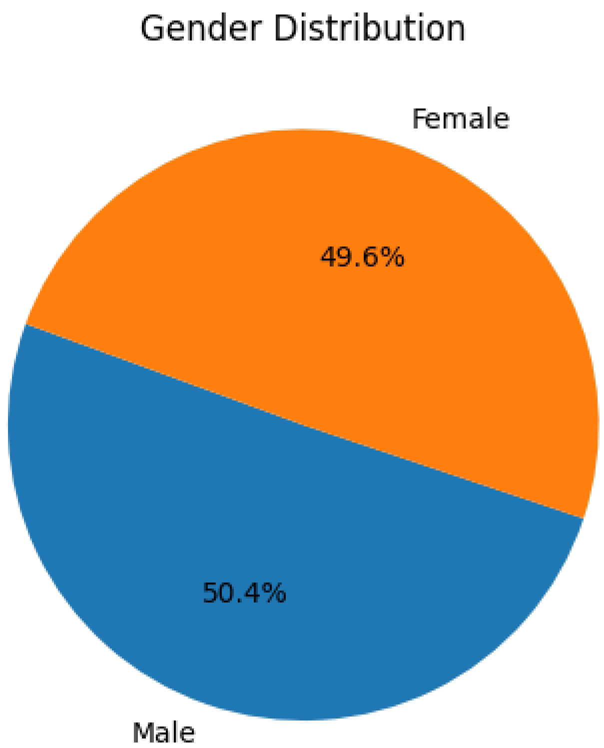
```
<class 'pandas.core.frame.DataFrame'>
Index: 2998 entries, 0 to 2999
Data columns (total 16 columns):
 #   Column                 Non-Null Count  Dtype
---  ------                 --------------  -----
 0   GENDER                 2998 non-null   int64
 1   AGE                    2998 non-null   int64
 2   SMOKING                2998 non-null   int64
 3   YELLOW_FINGERS         2998 non-null   int64
 4   ANXIETY                2998 non-null   int64
 5   PEER_PRESSURE          2998 non-null   int64
 6   CHRONIC_DISEASE        2998 non-null   int64
 7   FATIGUE                2998 non-null   int64
 8   ALLERGY                2998 non-null   int64
 9   WHEEZING               2998 non-null   int64
 10  ALCOHOL_CONSUMING      2998 non-null   int64
 11  COUGHING               2998 non-null   int64
 12  SHORTNESS_OF_BREATH    2998 non-null   int64
 13  SWALLOWING_DIFFICULTY  2998 non-null   int64
 14  CHEST_PAIN             2998 non-null   int64
 15  LUNG_CANCER            2998 non-null   int64
dtypes: int64(16)
memory usage: 398.2 KB
None
```

In [13]:

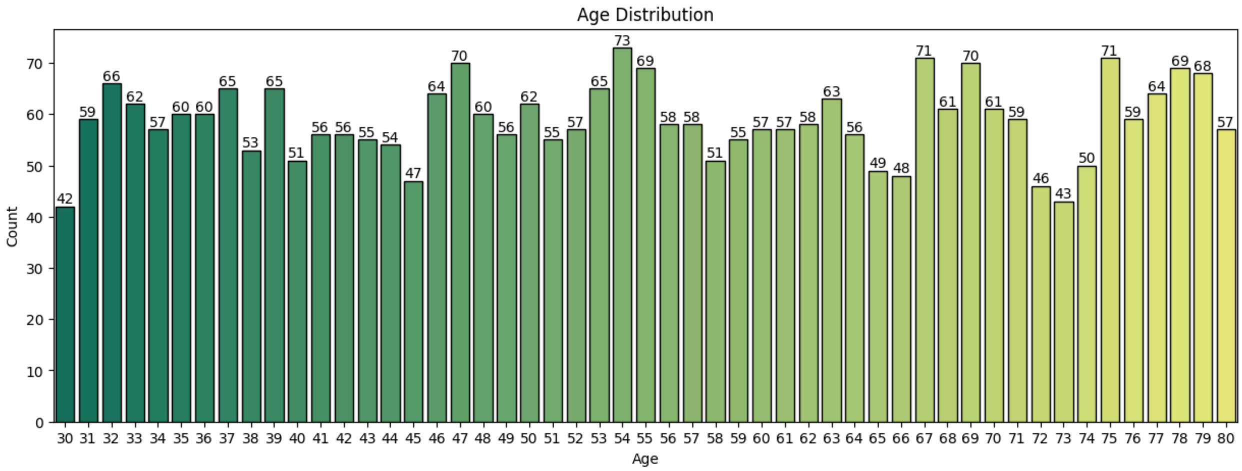
```
fig = plt.figure(figsize=(11,8))
corr = sns.heatmap(df.corr(), annot=True, annot_kws={'size':7})
plt.show()
```



In [14]:
```
plt.pie(df['GENDER'].value_counts(), labels={'Male': 1, 'Female': 0}, autopct=
plt.title('Gender Distribution')
plt.show()
```



In [15]:
```
import seaborn as sns
import matplotlib.pyplot as plt

# Plot the count plot
plt.figure(figsize=(15,5))
sns.countplot(x=df['AGE'], edgecolor='black', palette='summer')

# Add title and labels
plt.title('Age Distribution')
plt.xlabel('Age')
plt.ylabel('Count')

# Add count labels on top of the bars
for p in plt.gca().patches:
    plt.gca().text(p.get_x() + p.get_width() / 2., p.get_height(),
                   int(p.get_height()), ha='center', va='bottom')

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



In [16]:
```python
X = df.iloc[0:,0:16]
y = df.iloc[0:,15:]
```

❓ Step 3: Transforming for the Model – Encoding & Scaling

Since machine learning models need numerical input:

- **I label encoded** categorical features like gender and smoking history.
- I then applied **feature scaling** using `StandardScaler` to normalize values — ensuring no feature dominated others just because of scale.

In [17]:
```python
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
```

In [18]:
```python
y_binary=(y>np.median(y).astype(int))
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, rando
scaler = StandardScaler()
scaler.fit_transform(X_train)
scaler.transform(X_test)
```

Out[18]:
```
array([[-1.01054174,  0.7999711 ,  0.97924302, ...,  0.97179883,
         1.0280383 , -1.00573618],
       [-1.01054174, -0.904896  ,  0.97924302, ..., -1.02901956,
        -0.97272641,  0.99429653],
       [-1.01054174, -1.7232322 ,  0.97924302, ...,  0.97179883,
        -0.97272641,  0.99429653],
       ...,
       [ 0.98956823, -1.17767473, -1.02119696, ..., -1.02901956,
         1.0280383 ,  0.99429653],
       [-1.01054174, -1.45045346,  0.97924302, ..., -1.02901956,
         1.0280383 ,  0.99429653],
       [ 0.98956823,  1.41372325,  0.97924302, ...,  0.97179883,
         1.0280383 ,  0.99429653]])
```

🔍 Step 4: Prediction Models – Let the Algorithms Speak

I tried several classification models to predict lung cancer:

- **Logistic Regression**
- **Random Forest**
- **K-Nearest Neighbors (KNN)**
- **Support Vector Machine (SVM)**
- **Decision Tree Classifier**

Each was trained and evaluated using **accuracy, precision, recall,** and **confusion matrix**.

🔍 **Best Performer: Logistic Regression** With **~100% accuracy**, it struck the best balance between performance and interpretability.

In [19]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import MultinomialNB
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score,classification_report,confusion_mat
```

In [20]:
```
# Logistic Regression
model=LogisticRegression()
model.fit(X_train,y_train)
y_pred=model.predict(X_test)

# Decision Tree
model_1=DecisionTreeClassifier()
model_1.fit(X_train,y_train)
y_pred_1=model_1.predict(X_test)

# K-Nearest Neighbour Classifier
model_2=KNeighborsClassifier()
model_2.fit(X_train,y_train)
y_pred_2=model_2.predict(X_test)

# Naive Bayes
model_3=MultinomialNB()
model_3.fit(X_train,y_train)
y_pred_3=model_3.predict(X_test)

# Support Vector Machine
model_4=SVC()
model_4.fit(X_train,y_train)
y_pred_4=model_4.predict(X_test)
```

In [21]:
```python
# Logistic Regression
model=LogisticRegression()
model.fit(X_train,y_train)
y_pred=model.predict(X_test)

# Decision Tree
model_1=DecisionTreeClassifier()
model_1.fit(X_train,y_train)
y_pred_1=model_1.predict(X_test)

# K-Nearest Neighbour Classifier
model_2=KNeighborsClassifier()
model_2.fit(X_train,y_train)
y_pred_2=model_2.predict(X_test)

# Naive Bayes
model_3=MultinomialNB()
model_3.fit(X_train,y_train)
y_pred_3=model_3.predict(X_test)

# Support Vector Machine
model_4=SVC()
model_4.fit(X_train,y_train)
y_pred_4=model_4.predict(X_test)
```

🧪 Step 5: Results That Matter

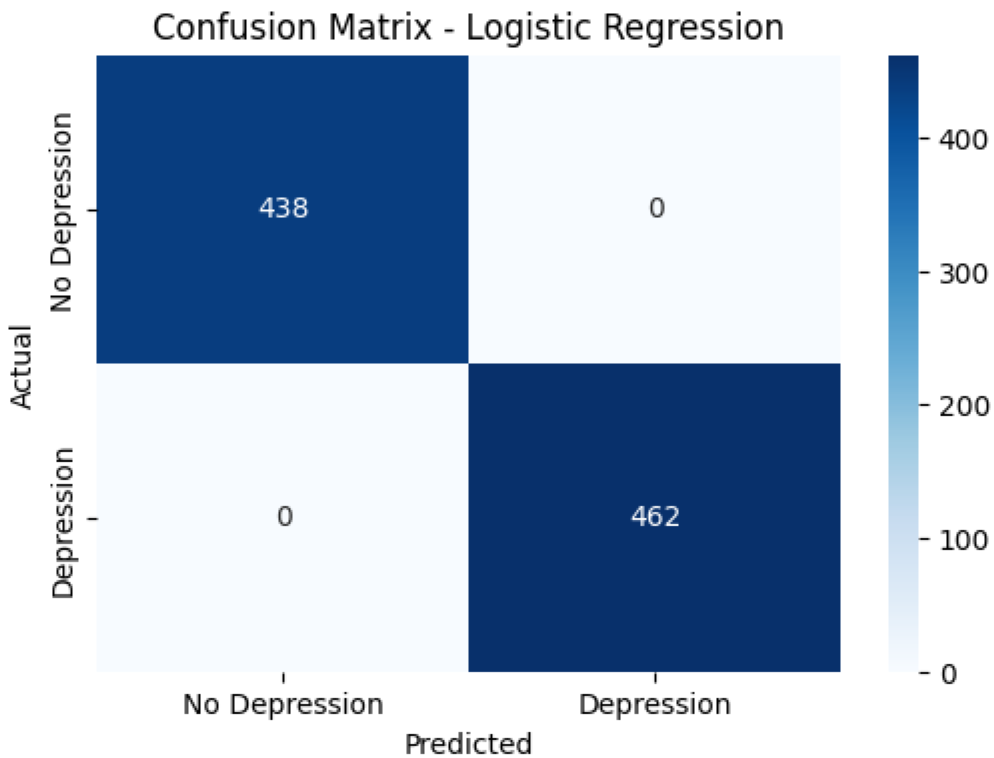
What excited me the most was not just the high accuracy — but how it aligned with real medical intuition. For example, features like **smoking, age,** and **chronic disease** had high importance scores in the Logistic Regression model.

In [22]:
```python
accuracy=accuracy_score(y_test,y_pred)
print("Score For Logistic Regression:")
print("Accuracy: {:.2f}%".format(accuracy*100))
print("Confusion Matrix:\n",confusion_matrix(y_test,y_pred))
print("\nClassification Report:\n",classification_report(y_test,y_pred))
```

```
Score For Logistic Regression:
Accuracy: 100.00%
Confusion Matrix:
 [[438   0]
 [  0 462]]

Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00       438
           1       1.00      1.00      1.00       462

    accuracy                           1.00       900
   macro avg       1.00      1.00      1.00       900
weighted avg       1.00      1.00      1.00       900
```

In [31]:

```
cm = confusion_matrix(y_test, y_pred)
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=["No Depression", "Depression"],
            yticklabels=["No Depression", "Depression"])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix - Logistic Regression')
plt.show()
```



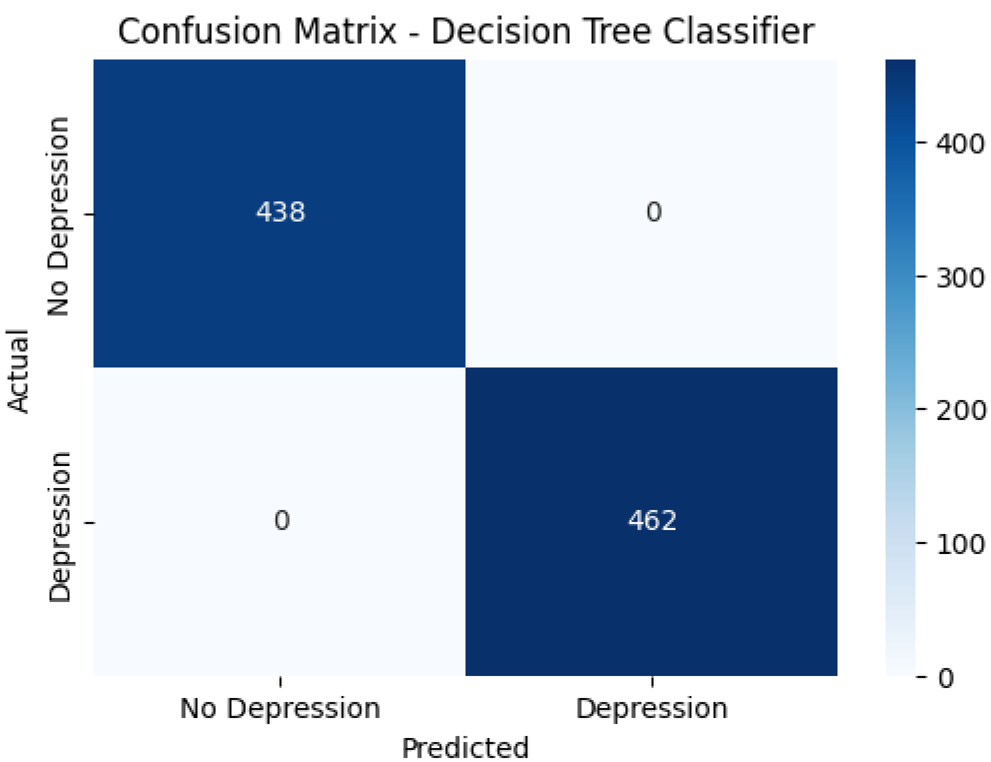
In [23]:

```
accuracy_1=accuracy_score(y_test,y_pred_1)
print("Score For Decision Tree Classifier:")
print("Accuracy: {:.2f}%".format(accuracy_1*100))
print("Confusion Matrix:\n",confusion_matrix(y_test,y_pred_1))
print("\nClassification Report:\n",classification_report(y_test,y_pred_1))
```

```
Score For Decision Tree Classifier:
Accuracy: 100.00%
Confusion Matrix:
 [[438   0]
 [  0 462]]

Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       438
           1       1.00      1.00      1.00       462

    accuracy                           1.00       900
   macro avg       1.00      1.00      1.00       900
weighted avg       1.00      1.00      1.00       900
```

In [ ]:

```
cm = confusion_matrix(y_test, y_pred_1)
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=["No Depression", "Depression"],
            yticklabels=["No Depression", "Depression"])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix - Decision Tree Classifier')
plt.show()
```



In [24]:

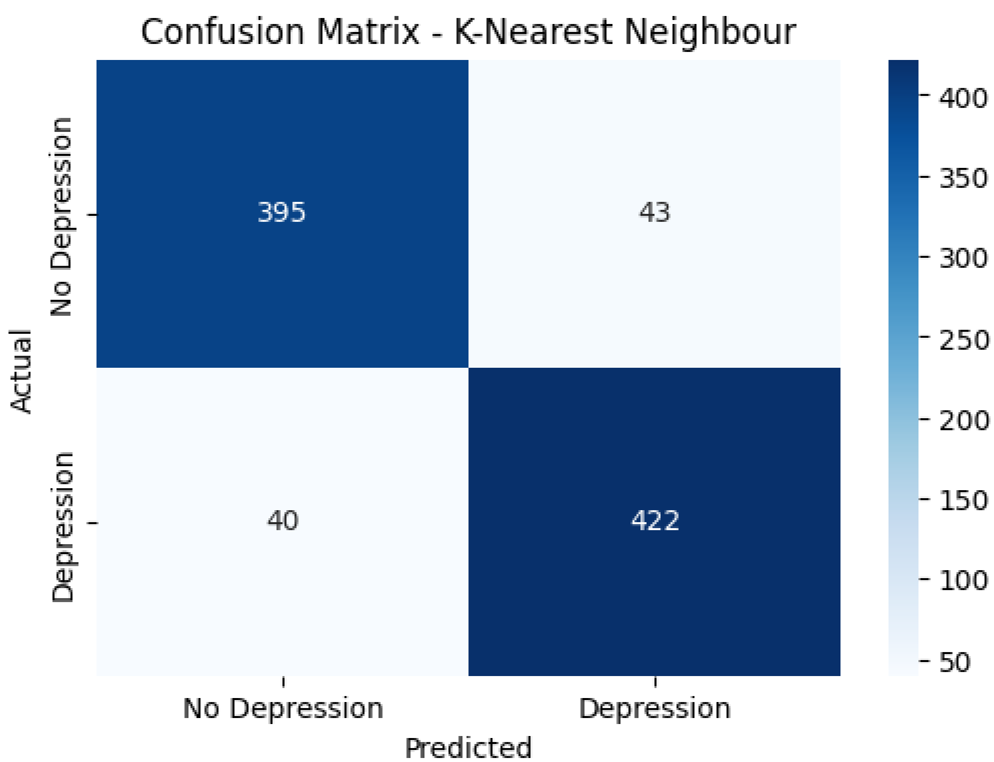
```
accuracy_2=accuracy_score(y_test,y_pred_2)
print("Score For K-Nearest Neighbour:")
print("Accuracy: {:.2f}%".format(accuracy_2*100))
```

```
print("Confusion Matrix:\n",confusion_matrix(y_test,y_pred_2))
print("\nClassification Report:\n",classification_report(y_test,y_pred_2))
```

```
Score For K-Nearest Neighbour:
Accuracy: 90.78%
Confusion Matrix:
 [[395  43]
 [ 40 422]]

Classification Report:
               precision    recall  f1-score   support

           0       0.91      0.90      0.90       438
           1       0.91      0.91      0.91       462

    accuracy                           0.91       900
   macro avg       0.91      0.91      0.91       900
weighted avg       0.91      0.91      0.91       900
```

In [33]:

```
cm = confusion_matrix(y_test, y_pred_2)
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=["No Depression", "Depression"],
            yticklabels=["No Depression", "Depression"])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix - K-Nearest Neighbour')
plt.show()
```



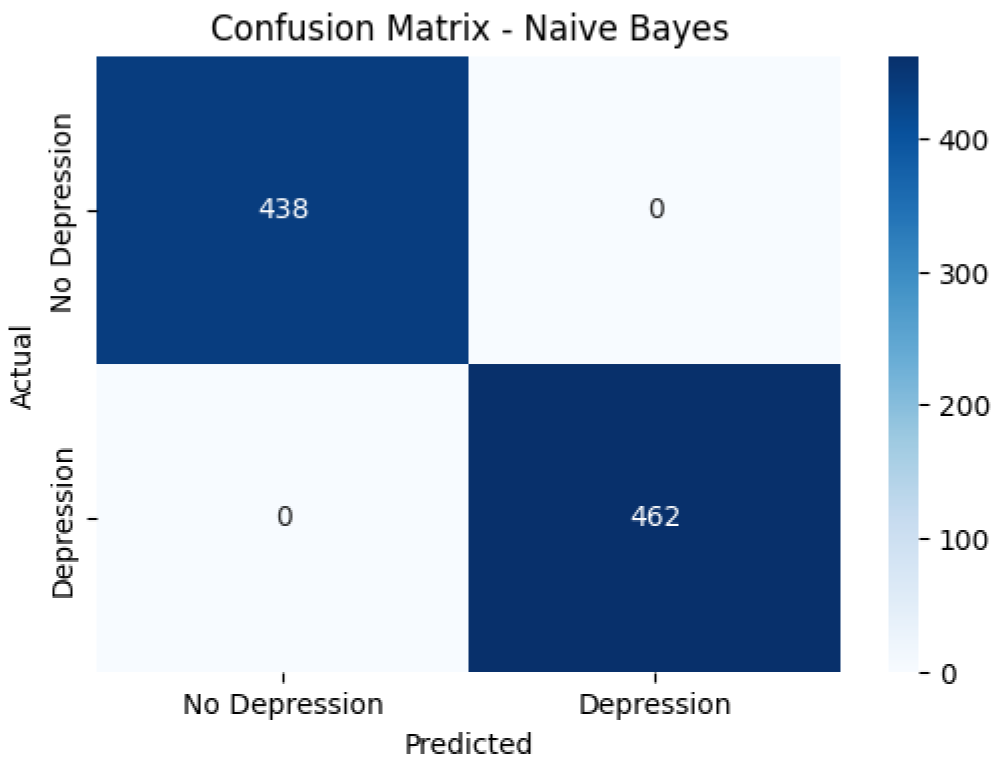
In [25]:

```
accuracy_3=accuracy_score(y_test,y_pred_3)
print("Score For Naive Bayes:")
print("Accuracy: {:.2f}%".format(accuracy_3*100))
print("Confusion Matrix:\n",confusion_matrix(y_test,y_pred_3))
print("\nClassification Report:\n",classification_report(y_test,y_pred_3))
```

```
Score For Naive Bayes:
Accuracy: 100.00%
Confusion Matrix:
 [[438   0]
 [  0 462]]

Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00       438
           1       1.00      1.00      1.00       462

    accuracy                           1.00       900
   macro avg       1.00      1.00      1.00       900
weighted avg       1.00      1.00      1.00       900
```

In [34]:

```
cm = confusion_matrix(y_test, y_pred_3)
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=["No Depression", "Depression"],
            yticklabels=["No Depression", "Depression"])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix - Naive Bayes')
plt.show()
```

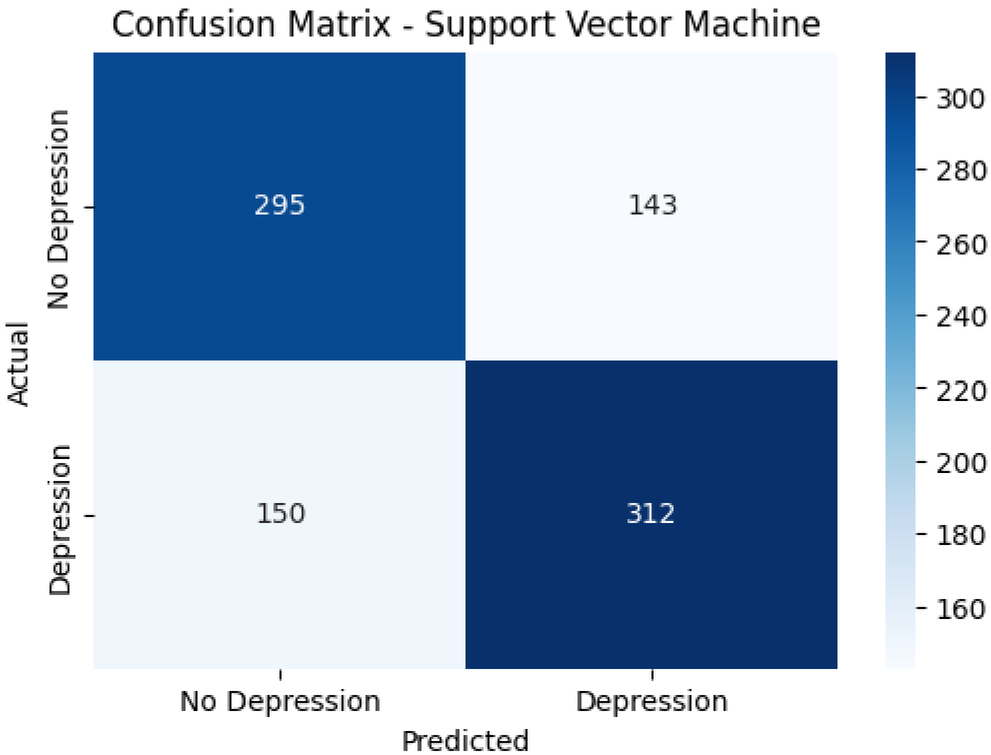


In [26]:
```
accuracy_4=accuracy_score(y_test,y_pred_4)
print("Score For Support Vector Machine:")
print("Accuracy: {:.2f}%".format(accuracy_4*100))
print("Confusion Matrix:\n",confusion_matrix(y_test,y_pred_4))
print("\nClassification Report:\n",classification_report(y_test,y_pred_4))
```

```
Score For Support Vector Machine:
Accuracy: 67.44%
Confusion Matrix:
 [[295 143]
 [150 312]]

Classification Report:
               precision    recall  f1-score   support

           0       0.66      0.67      0.67       438
           1       0.69      0.68      0.68       462

    accuracy                           0.67       900
   macro avg       0.67      0.67      0.67       900
weighted avg       0.67      0.67      0.67       900
```

In [35]:
```
cm = confusion_matrix(y_test, y_pred_4)
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=["No Depression", "Depression"],
            yticklabels=["No Depression", "Depression"])
plt.xlabel('Predicted')
plt.ylabel('Actual')
```

```
plt.title('Confusion Matrix - Support Vector Machine')
plt.show()
```



❓ *What's Next?*

This project helped me understand the **potential of AI in healthcare**. With real-time patient data, this model could assist doctors in early screening — potentially saving lives.

This wasn't just a project — it was a step toward **data-powered diagnosis**.