main

June 11, 2025

```
[6]: import os
     import pandas as pd

     df = pd.read_csv("/home/ajay/Documents/sleeping_dog_don/Lung_cancer_detection/
       ↪dataset_med.csv")
     df.head()
     print(df.columns.tolist())
```

```
['id', 'age', 'gender', 'country', 'diagnosis_date', 'cancer_stage',
'family_history', 'smoking_status', 'bmi', 'cholesterol_level', 'hypertension',
'asthma', 'cirrhosis', 'other_cancer', 'treatment_type', 'end_treatment_date',
'survived']
```

```
[7]: if 'id' in df.columns:
         df.drop('id', axis=1, inplace=True)

     if "diagnosis_date" in df.columns and 'end_treatment_date' in df.columns :
         df["diagnosis_date"]= pd.to_datetime(df['diagnosis_date'])
         df['end_treatment_date']= pd.to_datetime(df['end_treatment_date'])

         #CReating New Column since we need exact no of days survived

         df["treatment_duration"] = (df['end_treatment_date']-df["diagnosis_date"]).
       ↪dt.days

         df.drop(['diagnosis_date','end_treatment_date'],axis=1,inplace=True)

         df.fillna(df.mode().iloc[0],inplace=True)

     df.head()
```

```
[7]:    age  gender      country cancer_stage family_history  smoking_status  \
     0  64.0    Male       Sweden      Stage I            Yes  Passive Smoker
     1  50.0  Female  Netherlands    Stage III            Yes  Passive Smoker
     2  65.0  Female      Hungary    Stage III            Yes   Former Smoker
     3  51.0  Female      Belgium      Stage I             No  Passive Smoker
     4  37.0    Male   Luxembourg      Stage I             No  Passive Smoker
```

```
    bmi  cholesterol_level  hypertension  asthma  cirrhosis  other_cancer  \
0  29.4                199             0       0          1             0
1  41.2                280             1       1          0             0
2  44.0                268             1       1          0             0
3  43.0                241             1       1          0             0
4  19.7                178             0       0          0             0

  treatment_type  survived  treatment_duration
0   Chemotherapy         0                 523
1        Surgery         1                 424
2       Combined         0                 370
3   Chemotherapy         0                 443
4       Combined         0                 406
```

[8]:
```
from sklearn.preprocessing import LabelEncoder , StandardScaler

categorical_columns =␣
  ↪['gender','country','cancer_stage','family_history','smoking_status','hypertension',
                                   ␣
  ↪'asthma','cirrhosis','other_cancer','treatment_type','survived']

lencoder = LabelEncoder()

for columns in categorical_columns :
    df[columns] = lencoder.fit_transform(df[columns])

df.head()
```

[8]:
```
    age  gender  country  cancer_stage  family_history  smoking_status   bmi  \
0  64.0       1       26             0               1               3  29.4
1  50.0       0       19             2               1               3  41.2
2  65.0       0       12             2               1               1  44.0
3  51.0       0        1             0               0               3  43.0
4  37.0       1       17             0               0               3  19.7

   cholesterol_level  hypertension  asthma  cirrhosis  other_cancer  \
0                199             0       0          1             0
1                280             1       1          0             0
2                268             1       1          0             0
3                241             1       1          0             0
4                178             0       0          0             0

   treatment_type  survived  treatment_duration
0               0         0                 523
1               3         1                 424
2               1         0                 370
3               0         0                 443
```

```
4                1          0                 406
```

[9]:
```
sscaler = StandardScaler()

numerical_columns = ['age','bmi','cholesterol_level','treatment_duration']

df[numerical_columns] = sscaler.fit_transform(df[numerical_columns])

df.head()
```

[9]:
```
        age  gender  country  cancer_stage  family_history  smoking_status  \
0  0.899796       1       26             0               1               3
1 -0.500977       0       19             2               1               3
2  0.999851       0       12             2               1               1
3 -0.400922       0        1             0               0               3
4 -1.801696       1       17             0               0               3

        bmi  cholesterol_level  hypertension  asthma  cirrhosis  other_cancer  \
0 -0.130748          -0.797424             0       0          1             0
1  1.279296           1.067550             1       1          0             0
2  1.613882           0.791257             1       1          0             0
3  1.494387           0.169599             1       1          0             0
4 -1.289852          -1.280936             0       0          0             0

   treatment_type  survived  treatment_duration
0               0         0            0.465906
1               3         1           -0.244658
2               1         0           -0.632238
3               0         0           -0.108287
4               1         0           -0.373851
```

[12]:
```
from sklearn.model_selection import train_test_split
X = df.drop('survived',axis=1)
y = df['survived']
"""
X_train ,X_test , y_train , y_test = train_test_split(X , y , test_size= 0.2 ,␣
↪random_state= 42 )
"""

from imblearn.over_sampling import SMOTE

smote = SMOTE(random_state=42)



X_resampled, y_resampled = smote.fit_resample(X, y)
```

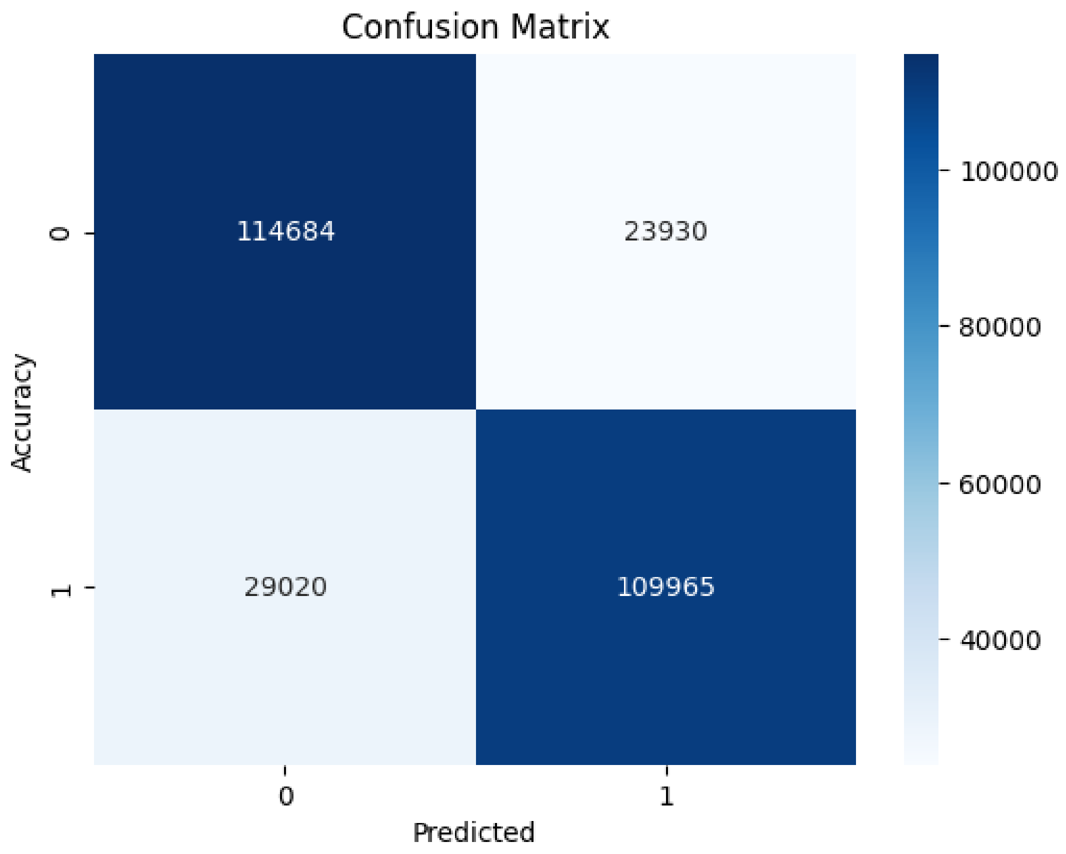
```
X_train, X_test, y_train, y_test = train_test_split(X_resampled,␣
 ↪y_resampled,test_size=0.2 , random_state=42)
```

```
[13]: from sklearn.ensemble import RandomForestClassifier

model = RandomForestClassifier(class_weight=None,random_state=42)
model.fit(X_train,y_train)
```

```
[13]: RandomForestClassifier(random_state=42)
```

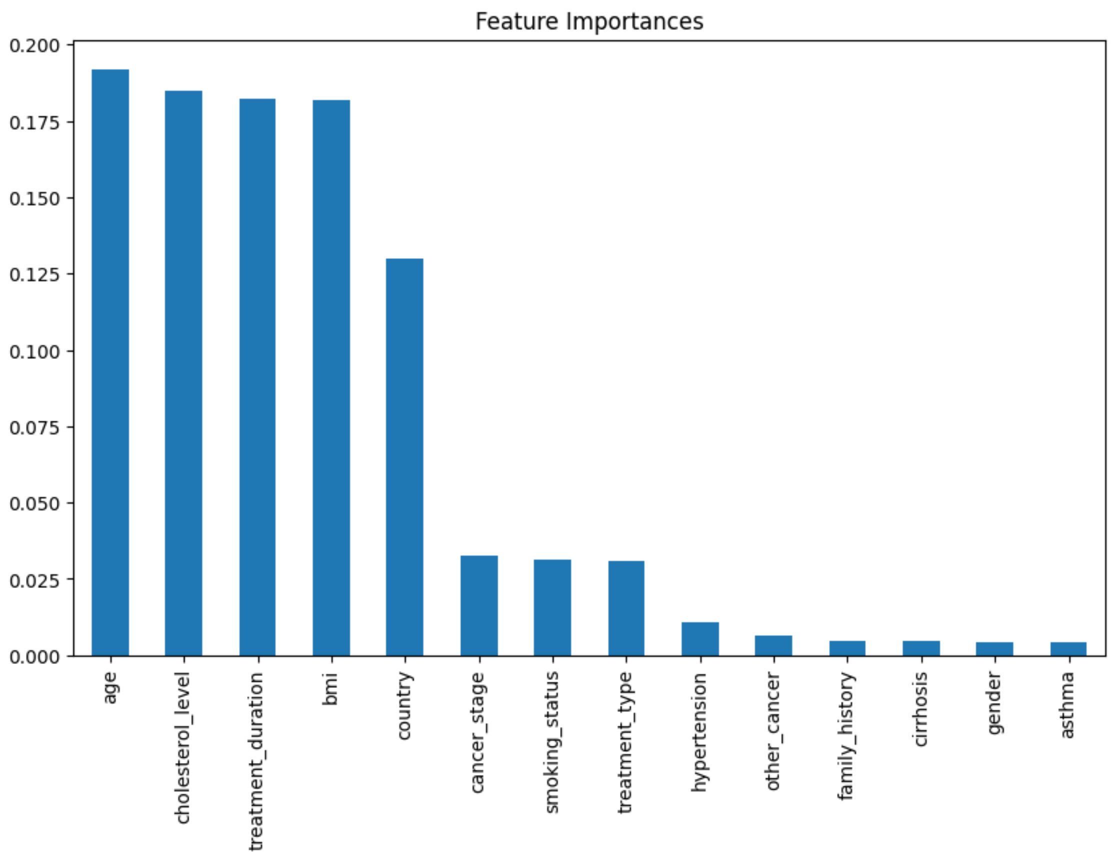
```
[14]: from sklearn.metrics import confusion_matrix, classification_report,␣
 ↪accuracy_score, roc_auc_score

y_pred = model.predict(X_test)
y_prob = model.predict_proba(X_test)[:,1]

print(f"Accuracy : {accuracy_score(y_test,y_pred)}")
print(f"\n Classification Repoort \n : {classification_report(y_test,y_pred)}")
print(f"ROC-AUC SCORE : {roc_auc_score(y_test,y_prob)}")

import seaborn as sns

sns.heatmap(confusion_matrix(y_test , y_pred),annot = True ,fmt = 'd', cmap =␣
 ↪'Blues')

import matplotlib.pyplot as plt

plt.title("Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Accuracy")
plt.show()

print(df['survived'].value_counts())
```

```
Accuracy : 0.80925723795835

 Classification Repoort
 :               precision    recall  f1-score   support

           0       0.80      0.83      0.81    138614
           1       0.82      0.79      0.81    138985

    accuracy                           0.81    277599
   macro avg       0.81      0.81      0.81    277599
weighted avg       0.81      0.81      0.81    277599

ROC-AUC SCORE : 0.8811956814847721
```



```
survived
0    693996
1    196004
Name: count, dtype: int64
```

[15]:
```
importances = pd.Series(model.feature_importances_, index=X.columns)
importances.sort_values(ascending=False).plot(kind='bar', figsize=(10,6))
plt.title("Feature Importances")
plt.show()
```


Feature Importances
0.200
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
age
cholesterol_level
treatment_duration
bmi
country
cancer_stage
smoking_status
treatment_type
hypertension
other_cancer
family_history
cirrhosis
gender
asthma