Project_4_Lung_cancer_detection

February 27, 2025

[1]:
```python
#load required library
import numpy as np, pandas as pd, matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import OneHotEncoder
import warnings
warnings.filterwarnings('ignore')
```

[2]:
```python
#load dataest
df = pd.read_csv('dataset_med.csv')
df.head()
```

[2]:
```
   id  age  gender      country diagnosis_date cancer_stage family_history  \
0   1   64    Male       Sweden     05 04 2016      Stage I            Yes
1   2   50  Female  Netherlands     20 04 2023    Stage III            Yes
2   3   65  Female      Hungary     05 04 2023    Stage III            Yes
3   4   51  Female      Belgium     05 02 2016      Stage I             No
4   5   37    Male   Luxembourg     29 11 2023      Stage I             No

   smoking_status   bmi  cholesterol_level  hypertension  asthma  cirrhosis  \
0  Passive Smoker  29.4                199             0       0          1
1  Passive Smoker  41.2                280             1       1          0
2   Former Smoker  44.0                268             1       1          0
3  Passive Smoker  43.0                241             1       1          0
4  Passive Smoker  19.7                178             0       0          0

   other_cancer treatment_type end_treatment_date  survived
0             0   Chemotherapy         10 09 2017         0
1             0        Surgery         17 06 2024         1
2             0       Combined         09 04 2024         0
3             0   Chemotherapy         23 04 2017         0
4             0       Combined         08 01 2025         0
```

[3]:
```python
#remove unused columns
df.drop(columns=['id', 'end_treatment_date', 'diagnosis_date'], inplace=True)
```

[4]:
```python
#check shape
df.shape
```

```
[4]: (890000, 14)
```

```
[5]: #check statistical report
     df.describe()
```

```
[5]:               age            bmi  cholesterol_level   hypertension  \
     count  890000.000000  890000.000000      890000.000000  890000.000000
     mean       55.007008      30.494172         233.633916       0.750024
     std         9.994485       8.368539          43.432278       0.432999
     min         4.000000      16.000000         150.000000       0.000000
     25%        48.000000      23.300000         196.000000       1.000000
     50%        55.000000      30.500000         242.000000       1.000000
     75%        62.000000      37.700000         271.000000       1.000000
     max       104.000000      45.000000         300.000000       1.000000

                  asthma      cirrhosis   other_cancer       survived
     count  890000.000000  890000.000000  890000.000000  890000.000000
     mean        0.469740       0.225956       0.088157       0.220229
     std         0.499084       0.418211       0.283524       0.414401
     min         0.000000       0.000000       0.000000       0.000000
     25%         0.000000       0.000000       0.000000       0.000000
     50%         0.000000       0.000000       0.000000       0.000000
     75%         1.000000       0.000000       0.000000       0.000000
     max         1.000000       1.000000       1.000000       1.000000
```

```
[6]: #check information about each column
     df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 890000 entries, 0 to 889999
Data columns (total 14 columns):
 #   Column             Non-Null Count   Dtype
---  ------             --------------   -----
 0   age                890000 non-null  int64
 1   gender             890000 non-null  object
 2   country            890000 non-null  object
 3   cancer_stage       890000 non-null  object
 4   family_history     890000 non-null  object
 5   smoking_status     890000 non-null  object
 6   bmi                890000 non-null  float64
 7   cholesterol_level  890000 non-null  int64
 8   hypertension       890000 non-null  int64
 9   asthma             890000 non-null  int64
 10  cirrhosis          890000 non-null  int64
 11  other_cancer       890000 non-null  int64
 12  treatment_type     890000 non-null  object
 13  survived           890000 non-null  int64
dtypes: float64(1), int64(7), object(6)
```

```
memory usage: 95.1+ MB
```

[7]:
```
#checking numerical column
df.select_dtypes(include=[int,float]).columns
```

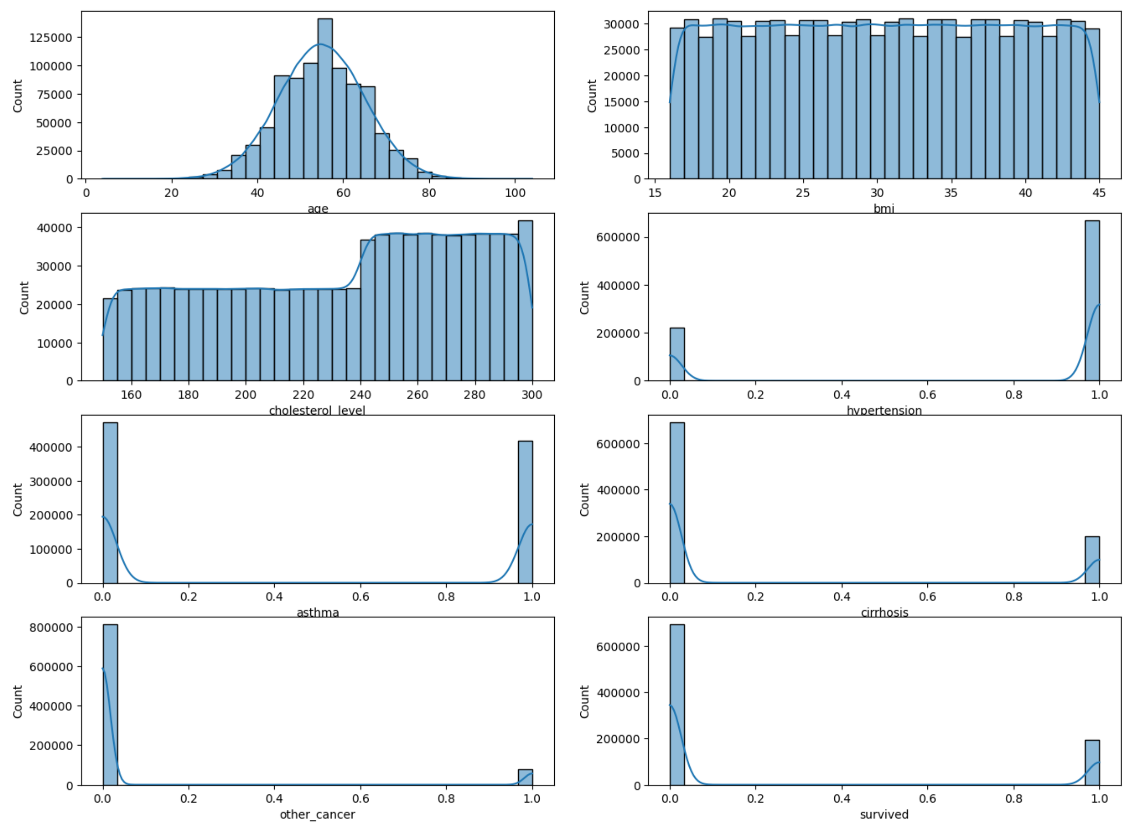
[7]:
```
Index(['age', 'bmi', 'cholesterol_level', 'hypertension', 'asthma',
       'cirrhosis', 'other_cancer', 'survived'],
      dtype='object')
```

[8]:
```
#checking categorical columns
df.select_dtypes(include=object).columns
```

[8]:
```
Index(['gender', 'country', 'cancer_stage', 'family_history', 'smoking_status',
       'treatment_type'],
      dtype='object')
```

[9]:
```
#find numerical column
num_col = ['age', 'bmi', 'cholesterol_level', 'hypertension', 'asthma',␣
 ↪'cirrhosis', 'other_cancer', 'survived']
```

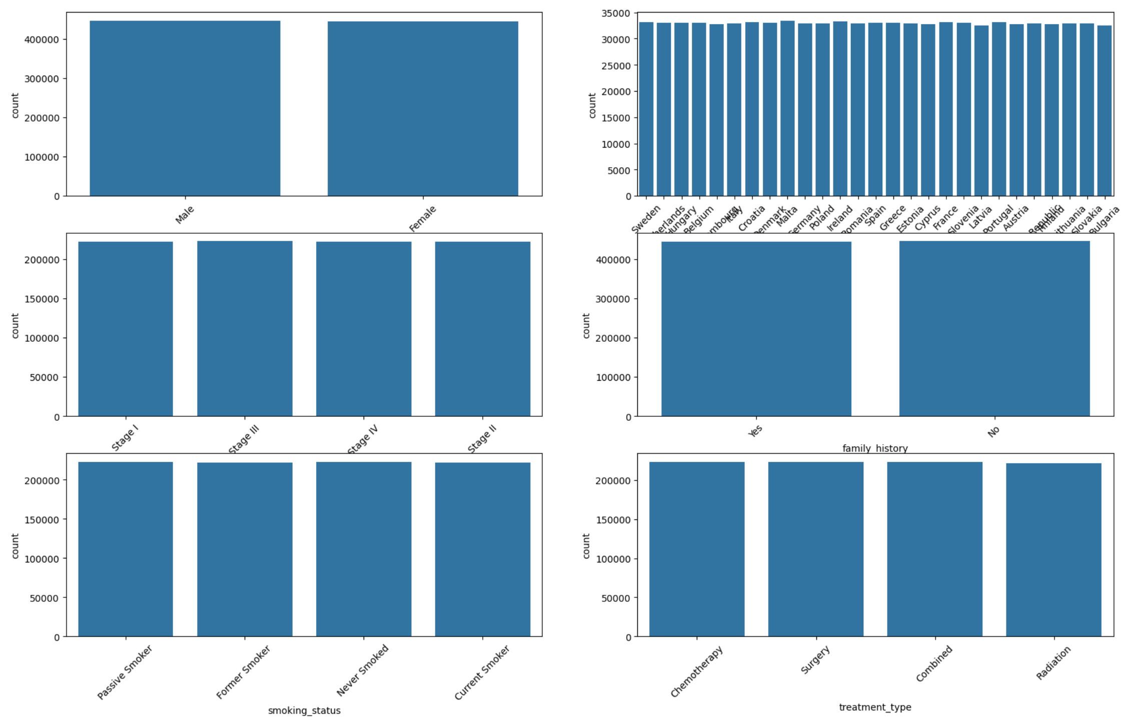
[10]:
```
#Data distribution
plt.figure(figsize=(16, 12))
for i, col in enumerate(num_col):
    plt.subplot(4,2,i+1)
    sns.histplot(df[col], bins=30, kde=True)
```



above all Numerical columns distribution is correct and range in thier scaled.

But Survived columns having Imbalanced.

```
[11]: #categorical columns distribution
col = ['gender', 'country', 'cancer_stage', 'family_history','smoking_status',␣
 ↪'treatment_type']
plt.figure(figsize=(20, 12))
for i, col in enumerate(col):
    plt.subplot(3,2,i+1)
    sns.countplot(x=df[col])
    plt.xticks(rotation=45)
```



```
[12]: #find categorical columns
      df.select_dtypes(include=object).columns
```

```
[12]: Index(['gender', 'country', 'cancer_stage', 'family_history', 'smoking_status',
             'treatment_type'],
            dtype='object')
```

```
[13]: #make list of categorical columns
      cat_col = ['gender', 'country', 'cancer_stage', 'family_history',␣
       ↪'smoking_status', 'treatment_type']
```

```
[14]: #load onehot_encoder and fit in categorical col
      onehot_encoder = OneHotEncoder(drop='first', sparse_output=False)
      onehot_encoder.fit(df[cat_col])

      #transform the onehotencoder to the dataset
      encoded_col = onehot_encoder.transform(df[cat_col])
      encoded_df = pd.DataFrame(encoded_col, columns=onehot_encoder.
       ↪get_feature_names_out(cat_col))
      df_encoded = pd.concat([df.drop(columns=cat_col), encoded_df], axis=1)
      df.shape
```

```
[14]: (890000, 14)
```

```
[15]: #check encoded df
      df_encoded.head()
```

```
[15]:    age   bmi  cholesterol_level  hypertension  asthma  cirrhosis  \
      0   64  29.4                199             0       0          1
      1   50  41.2                280             1       1          0
      2   65  44.0                268             1       1          0
      3   51  43.0                241             1       1          0
      4   37  19.7                178             0       0          0

         other_cancer  survived  gender_Male  country_Belgium  …  \
      0             0         0          1.0              0.0  …
      1             0         1          0.0              0.0  …
      2             0         0          0.0              0.0  …
      3             0         0          0.0              1.0  …
      4             0         0          1.0              0.0  …

         cancer_stage_Stage II  cancer_stage_Stage III  cancer_stage_Stage IV  \
      0                    0.0                     0.0                    0.0
      1                    0.0                     1.0                    0.0
      2                    0.0                     1.0                    0.0
      3                    0.0                     0.0                    0.0
      4                    0.0                     0.0                    0.0

         family_history_Yes  smoking_status_Former Smoker  \
      0                 1.0                           0.0
      1                 1.0                           0.0
      2                 1.0                           1.0
      3                 0.0                           0.0
      4                 0.0                           0.0

         smoking_status_Never Smoked  smoking_status_Passive Smoker  \
      0                          0.0                            1.0
      1                          0.0                            1.0
      2                          0.0                            0.0
      3                          0.0                            1.0
      4                          0.0                            1.0

         treatment_type_Combined  treatment_type_Radiation  treatment_type_Surgery
      0                      0.0                       0.0                     0.0
      1                      0.0                       0.0                     1.0
      2                      1.0                       0.0                     0.0
      3                      0.0                       0.0                     0.0
      4                      1.0                       0.0                     0.0

      [5 rows x 45 columns]
```

[16]:
```
#checking columns
df_encoded.columns
```

[16]:
```
Index(['age', 'bmi', 'cholesterol_level', 'hypertension', 'asthma',
       'cirrhosis', 'other_cancer', 'survived', 'gender_Male',
       'country_Belgium', 'country_Bulgaria', 'country_Croatia',
       'country_Cyprus', 'country_Czech Republic', 'country_Denmark',
       'country_Estonia', 'country_Finland', 'country_France',
       'country_Germany', 'country_Greece', 'country_Hungary',
       'country_Ireland', 'country_Italy', 'country_Latvia',
       'country_Lithuania', 'country_Luxembourg', 'country_Malta',
       'country_Netherlands', 'country_Poland', 'country_Portugal',
       'country_Romania', 'country_Slovakia', 'country_Slovenia',
       'country_Spain', 'country_Sweden', 'cancer_stage_Stage II',
       'cancer_stage_Stage III', 'cancer_stage_Stage IV', 'family_history_Yes',
       'smoking_status_Former Smoker', 'smoking_status_Never Smoked',
       'smoking_status_Passive Smoker', 'treatment_type_Combined',
       'treatment_type_Radiation', 'treatment_type_Surgery'],
      dtype='object')
```

[17]:
```
#split data in input and target variable
X = df_encoded.drop(columns=['survived'])
y = df_encoded['survived']

X.shape, y.shape
```

[17]:
```
((890000, 44), (890000,))
```

[18]:
```
#loading requeired library, randomforestclassfier and metrix.
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, confusion_matrix,␣
 ↪accuracy_score
```

[19]:
```
#split the input feature and target variable in to xtrain, ytrain, xtest and␣
 ↪y_test
xtrain, xtest, ytrain, ytest = train_test_split(X, y, random_state=42,␣
 ↪test_size=.2)
xtrain.shape, xtest.shape, ytrain.shape, ytest.shape
```

[19]:
```
((712000, 44), (178000, 44), (712000,), (178000,))
```

[20]:
```
#model creating using RF

rfc = RandomForestClassifier(random_state=42)
rfc.fit(xtrain, ytrain)
```

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

```
[21]: #predict the model
      rfc_pred = rfc.predict(xtest)

      #checking classification report and confusion metrix
      print(classification_report(ytest, rfc_pred))
      print(confusion_matrix(ytest, rfc_pred))
```

```
              precision    recall  f1-score   support

           0       0.78      1.00      0.87    138639
           1       0.23      0.00      0.01     39361

    accuracy                           0.78    178000
   macro avg       0.50      0.50      0.44    178000
weighted avg       0.66      0.78      0.68    178000

[[137981    658]
 [ 39169    192]]
```

above F1-score for 1 is highly biased that meeans imbalanced dataset. So, we will remove imbalanced

```
[22]: #load smote library for imbalanced data
      from imblearn.over_sampling import SMOTE
      sm = SMOTE()
```

```
[23]: #appling SMOTE
      X_resamble, y_resamble = sm.fit_resample(X, y)
```

```
[24]: #split dataset into train, test.
      xtrain, xtest, ytrain, ytest = train_test_split(X_resamble, y_resamble,␣
       ↪random_state=42, test_size=.2)
      xtrain.shape, xtest.shape, ytrain.shape, ytest.shape
```

```
[24]: ((1110393, 44), (277599, 44), (1110393,), (277599,))
```

```
[25]: #RF model using.
      rfc_imbalanced = RandomForestClassifier(random_state=42)
      #fitting the dataset.
      rfc_imbalanced.fit(xtrain, ytrain)
```

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

```
[26]: #predict the model
      rfc_imb_pred = rfc_imbalanced.predict(xtest)

      #checking the classification and confution metrix
```

```
print(classification_report(ytest, rfc_imb_pred))
print(confusion_matrix(ytest, rfc_imb_pred))
```

```
              precision    recall  f1-score   support

           0       0.78      0.97      0.87    138614
           1       0.97      0.73      0.83    138985

    accuracy                           0.85    277599
   macro avg       0.87      0.85      0.85    277599
weighted avg       0.87      0.85      0.85    277599

[[135074   3540]
 [ 38027 100958]]
```

[27]:
```
print(accuracy_score(ytest, rfc_imb_pred))
```

```
0.8502624288992395
```

our model has 85% accuracy.

[28]:
```
#now save our model.
import joblib

#saving model
joblib.dump(rfc_imbalanced, 'random_forest_model.pkl')

#save onehotencoder
joblib.dump(onehot_encoder, 'onehot_encoder.pkl')
```

[28]:
```
['onehot_encoder.pkl']
```

[29]:
```
rfc_imbalanced.feature_importances_
```

[29]:
```
array([0.10428272, 0.12043656, 0.11633123, 0.01323727, 0.01100567,
       0.01210045, 0.0094233 , 0.06336654, 0.0063427 , 0.00628626,
       0.00646505, 0.00609679, 0.00604109, 0.00626547, 0.00581283,
       0.00584679, 0.00741864, 0.00632842, 0.00645128, 0.00654287,
       0.00626022, 0.00654555, 0.0060309 , 0.00643853, 0.00615368,
       0.00616094, 0.00571796, 0.00586206, 0.00640378, 0.00598467,
       0.00647707, 0.00628602, 0.00600316, 0.00682076, 0.03497755,
       0.03494464, 0.03319997, 0.06320513, 0.03969594, 0.03628118,
       0.03503372, 0.03706084, 0.03588206, 0.03649175])
```

[30]:
```
rfc_imbalanced.feature_names_in_
```

[30]:
```
array(['age', 'bmi', 'cholesterol_level', 'hypertension', 'asthma',
       'cirrhosis', 'other_cancer', 'gender_Male', 'country_Belgium',
       'country_Bulgaria', 'country_Croatia', 'country_Cyprus',
       'country_Czech Republic', 'country_Denmark', 'country_Estonia',
       'country_Finland', 'country_France', 'country_Germany',
       'country_Greece', 'country_Hungary', 'country_Ireland',
       'country_Italy', 'country_Latvia', 'country_Lithuania',
       'country_Luxembourg', 'country_Malta', 'country_Netherlands',
       'country_Poland', 'country_Portugal', 'country_Romania',
       'country_Slovakia', 'country_Slovenia', 'country_Spain',
       'country_Sweden', 'cancer_stage_Stage II',
       'cancer_stage_Stage III', 'cancer_stage_Stage IV',
       'family_history_Yes', 'smoking_status_Former Smoker',
       'smoking_status_Never Smoked', 'smoking_status_Passive Smoker',
       'treatment_type_Combined', 'treatment_type_Radiation',
       'treatment_type_Surgery'], dtype=object)
```

```
[31]: #checing the columns
      df.columns
```

```
[31]: Index(['age', 'gender', 'country', 'cancer_stage', 'family_history',
             'smoking_status', 'bmi', 'cholesterol_level', 'hypertension', 'asthma',
             'cirrhosis', 'other_cancer', 'treatment_type', 'survived'],
            dtype='object')
```

```
[32]: #checking unique variable in each categorical columns
      for i in (df.select_dtypes(include=object)):
          print(f'df{[i]} : {df[i].unique()}')
```

```
df['gender'] : ['Male' 'Female']
df['country'] : ['Sweden' 'Netherlands' 'Hungary' 'Belgium' 'Luxembourg' 'Italy'
'Croatia'
 'Denmark' 'Malta' 'Germany' 'Poland' 'Ireland' 'Romania' 'Spain' 'Greece'
 'Estonia' 'Cyprus' 'France' 'Slovenia' 'Latvia' 'Portugal' 'Austria'
 'Czech Republic' 'Finland' 'Lithuania' 'Slovakia' 'Bulgaria']
df['cancer_stage'] : ['Stage I' 'Stage III' 'Stage IV' 'Stage II']
df['family_history'] : ['Yes' 'No']
df['smoking_status'] : ['Passive Smoker' 'Former Smoker' 'Never Smoked' 'Current
Smoker']
df['treatment_type'] : ['Chemotherapy' 'Surgery' 'Combined' 'Radiation']
```

1 Finish !

1.1 Deepak Kumar.

Thank you !