lung cancer mortality

June 21, 2024

[2]:

```python
#Read in data
import pandas as pd
import matplotlib.pyplot as plt
df=pd.read_csv('lung_cancer_mortality_data_small.csv')
df
```

[2]:

```
          id   age  gender     country diagnosis_date cancer_stage  \
0          1  64.0    Male     Croatia     2016-04-05      Stage I
1          2  50.0  Female       Italy     2023-04-20    Stage III
2          3  65.0    Male    Slovakia     2023-04-05     Stage IV
3          4  51.0  Female      Greece     2016-02-05    Stage III
4          5  37.0  Female    Slovakia     2023-11-29    Stage III
…        …   …     …         …          …            …
55995  55996  49.0  Female     Germany     2014-11-15    Stage III
55996  55997  65.0    Male  Luxembourg     2016-03-13     Stage IV
55997  55998  60.0  Female      Latvia     2023-05-21     Stage II
55998  55999  63.0  Female    Bulgaria     2015-12-09    Stage III
55999  56000  55.0  Female      Latvia     2015-08-09      Stage I

      family_history  smoking_status   bmi  cholesterol_level  hypertension  \
0                Yes  Current Smoker  27.3                196             0
1                 No  Passive Smoker  22.4                234             1
2                 No   Former Smoker  20.2                210             0
3                Yes    Never Smoked  41.8                262             1
4                Yes  Passive Smoker  33.5                262             0
…              …             …   …                …            …
55995            Yes    Never Smoked  23.6                155             0
55996            Yes  Current Smoker  19.6                185             0
55997            Yes  Passive Smoker  33.5                261             0
55998             No   Former Smoker  24.0                221             0
55999            Yes  Passive Smoker  24.3                189             1

       asthma  cirrhosis  other_cancer treatment_type end_treatment_date  \
0           1          0             0      Radiation         2018-01-09
1           1          1             0   Chemotherapy         2023-11-28
2           0          0             0   Chemotherapy         2025-01-12
3           0          1             0        Surgery         2016-11-14
4           0          0             0   Chemotherapy         2025-03-10
```

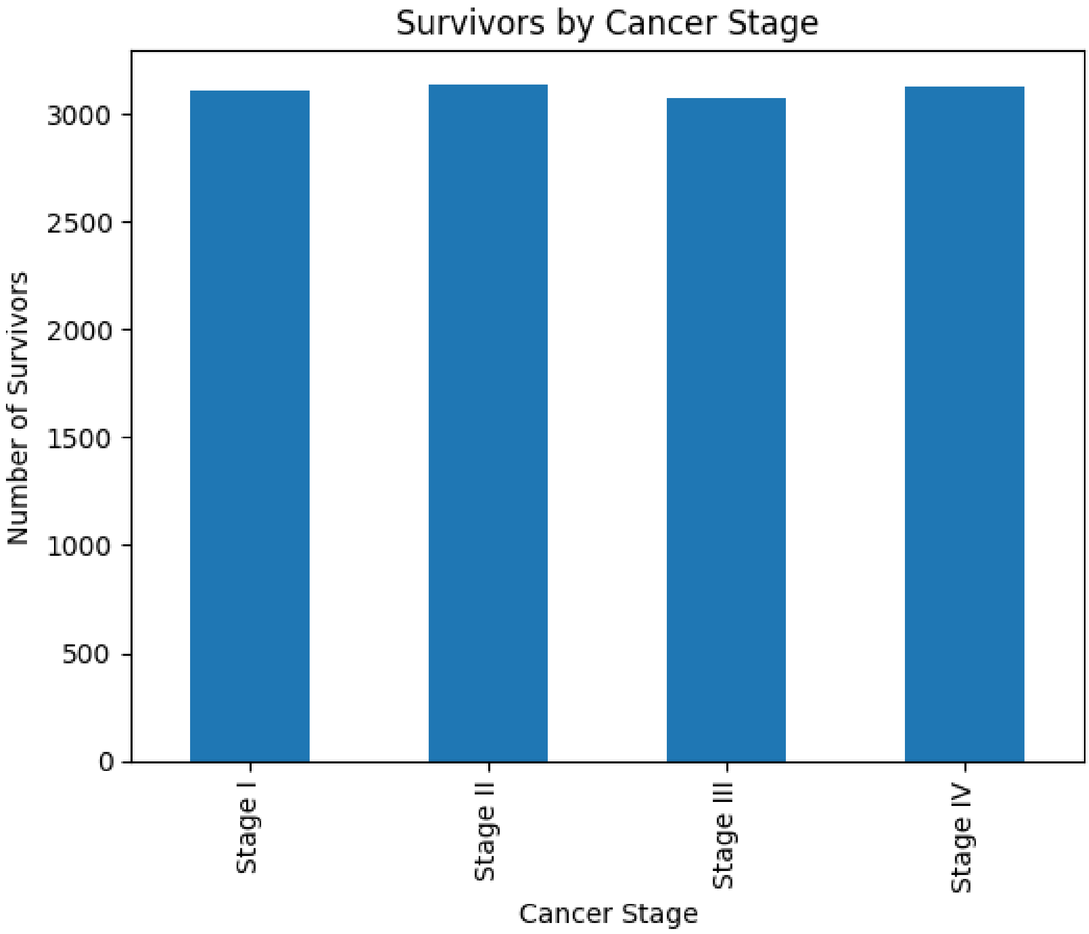
```
…        …        …          …          …                …
55995       0          0             0        Surgery       2016-02-13
55996       0          0             0       Combined       2017-11-11
55997       0          0             0      Radiation       2024-12-04
55998       0          0             0      Radiation       2017-05-10
55999       0          0             0      Radiation       2017-04-29

       survived
0             0
1             0
2             0
3             0
4             0
…           …
55995         0
55996         0
55997         1
55998         0
55999         0

[56000 rows x 17 columns]
```

[3]:
```
#Look at basic statistics for quantitative columns
df[['age','bmi','cholesterol_level']].describe()
```

[3]:
```
                age           bmi  cholesterol_level
count  56000.000000  56000.000000       56000.000000
mean      54.924929     30.576352         233.891286
std        9.995458      8.387948          43.470036
min       15.000000     16.000000         150.000000
25%       48.000000     23.300000         197.000000
50%       55.000000     30.600000         242.000000
75%       62.000000     37.900000         271.000000
max      101.000000     45.000000         300.000000
```

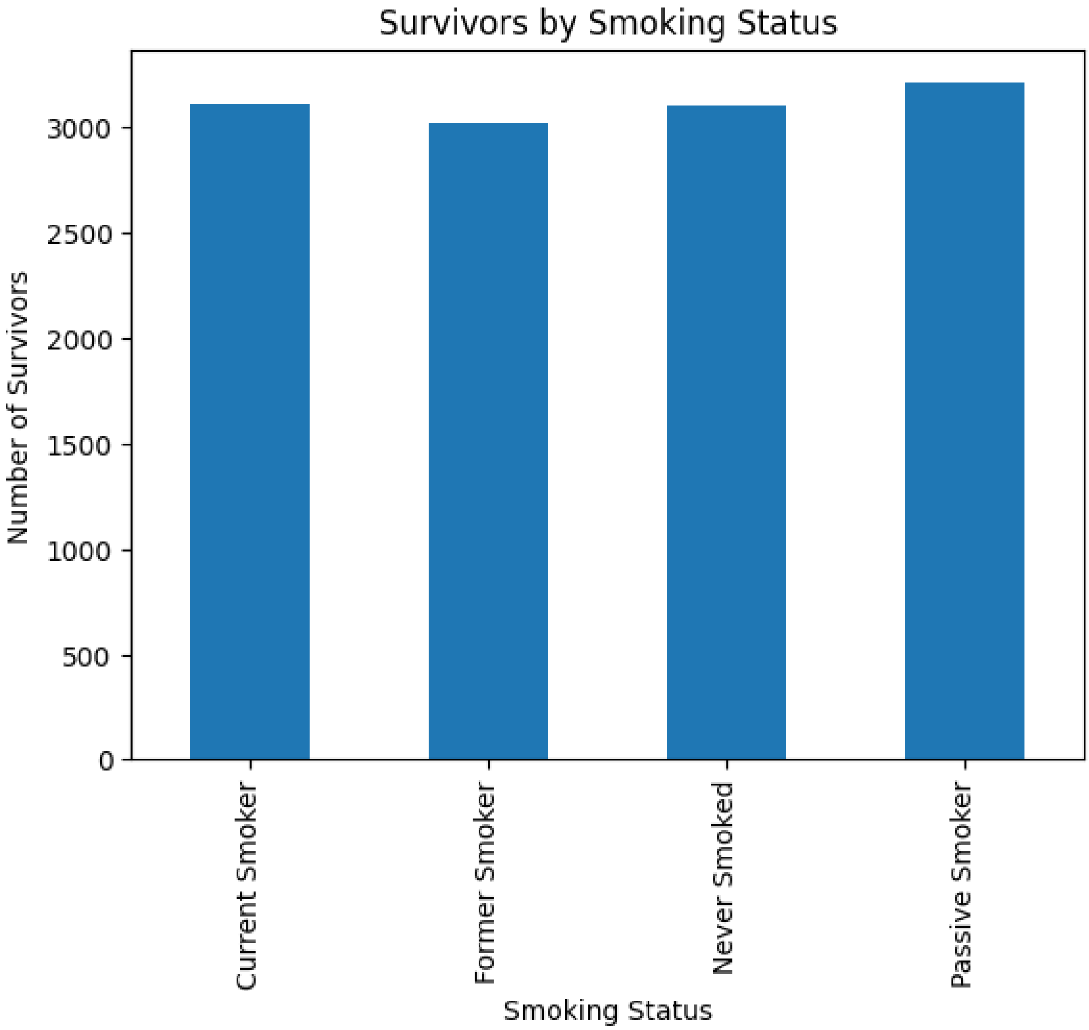
[4]:
```
#Number of survivors for each cancer stage
df.groupby('cancer_stage')['survived'].sum().plot(kind='bar',xlabel='Cancer␣
 ↪Stage',ylabel='Number of Survivors',title='Survivors by Cancer Stage')
```

[4]:
```
<Axes: title={'center': 'Survivors by Cancer Stage'}, xlabel='Cancer Stage',
ylabel='Number of Survivors'>
```



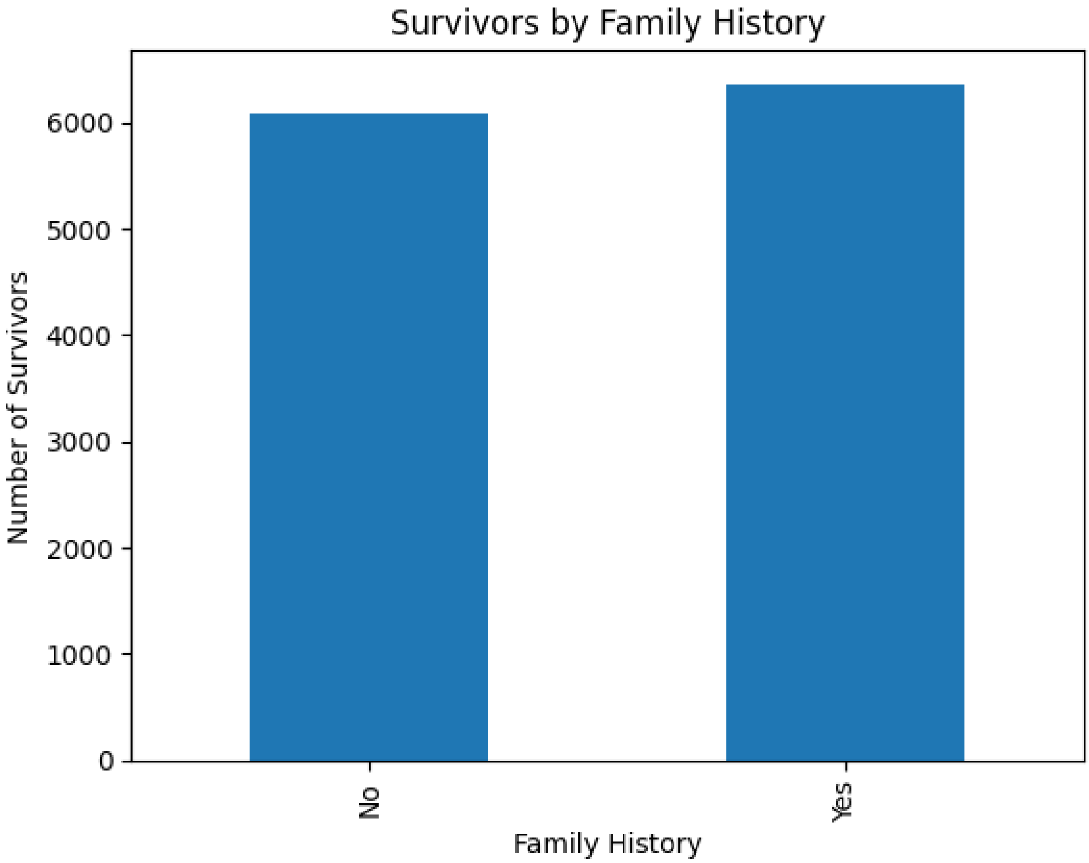
```
[5]: #Number of survivors for each smoking status
     df.groupby('smoking_status')['survived'].sum().plot(kind='bar',xlabel='Smoking␣
      ↪Status',ylabel='Number of Survivors',title='Survivors by Smoking Status')
```

```
[5]: <Axes: title={'center': 'Survivors by Smoking Status'}, xlabel='Smoking Status',
     ylabel='Number of Survivors'>
```



```
[6]: #Number of survivors by cancer family history
     df.groupby('family_history')['survived'].sum().plot(kind='bar',xlabel='Family␣
      ↪History',ylabel='Number of Survivors',title='Survivors by Family History')
```

```
[6]: <Axes: title={'center': 'Survivors by Family History'}, xlabel='Family History',
     ylabel='Number of Survivors'>
```

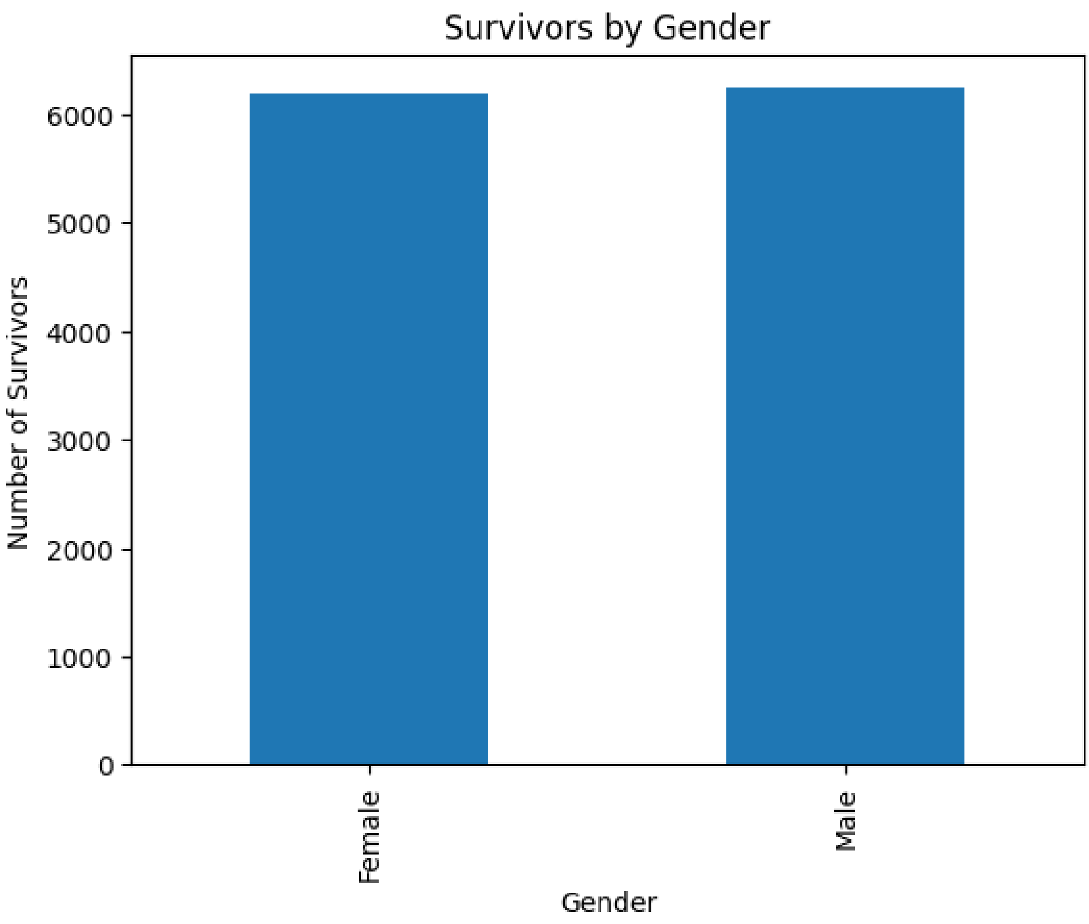


[7]:

```
#Number of survivors by gender
df.groupby('gender')['survived'].sum().
  ↪plot(kind='bar',xlabel='Gender',ylabel='Number of␣
  ↪Survivors',title='Survivors by Gender')
```

[7]:

```
<Axes: title={'center': 'Survivors by Gender'}, xlabel='Gender', ylabel='Number
of Survivors'>
```



[8]:
```
#Descending Survival Rate by Treatment Type
SRbytreatment=df.groupby('treatment_type')['survived'].
  ↪agg(total='count',survivors=lambda x:(x==1).sum())
SRbytreatment['survival rate']=SRbytreatment['survivors']/SRbytreatment['total']
SRbytreatment.sort_values('survival rate',ascending=False)
```

[8]:
```
                total  survivors  survival rate
treatment_type
Chemotherapy    14112       3189       0.225978
Combined        13899       3095       0.222678
Radiation       14074       3104       0.220549
Surgery         13915       3050       0.219188
```

[9]:
```
#Descending Survival Rate by Country
SRbycountry=df.groupby('country')['survived'].
  ↪agg(total='count',survivors=lambda x:(x==1).sum())
SRbycountry['survival rate']=SRbycountry['survivors']/SRbycountry['total']
SRbycountry.sort_values('survival rate',ascending=False)
```

[9]:

```
                 total  survivors  survival rate
country
Hungary           2113        506       0.239470
Netherlands       2047        484       0.236444
Sweden            1989        459       0.230769
Denmark           2115        488       0.230733
Portugal          2098        484       0.230696
Czech Republic    2115        487       0.230260
France            2023        463       0.228868
Belgium           2018        460       0.227948
Estonia           2015        458       0.227295
Slovenia          2031        458       0.225505
Latvia            2059        461       0.223895
Lithuania         2149        481       0.223825
Slovakia          2047        457       0.223254
Spain             2125        474       0.223059
Greece            2120        469       0.221226
Ireland           2083        457       0.219395
Croatia           2084        457       0.219290
Austria           2080        456       0.219231
Romania           2035        445       0.218673
Finland           2087        455       0.218016
Germany           2037        443       0.217477
Malta             2133        457       0.214252
Bulgaria          2115        452       0.213712
Luxembourg        2019        426       0.210996
Cyprus            2110        443       0.209953
Italy             2081        432       0.207593
Poland            2072        426       0.205598
```

[10]:

```
#Logistic Regression
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.metrics import␣
 ↪accuracy_score,confusion_matrix,classification_report,precision_score,r2_score
labelencoder=LabelEncoder()
df['gender encoded']=labelencoder.fit_transform(df['gender'])
df['cancer stage encoded']=labelencoder.fit_transform(df['cancer_stage'])
df['family history encoded']=labelencoder.fit_transform(df['family_history'])
df['smoking status encoded']=labelencoder.fit_transform(df['smoking_status'])
df['treatment type encoded']=labelencoder.fit_transform(df['treatment_type'])
x=df[['age','gender encoded','cancer stage encoded','family history␣
 ↪encoded','smoking status␣
 ↪encoded','bmi','cholesterol_level','hypertension','asthma','cirrhosis','other_cancer']]
y=df['survived']
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=.3,random_state=42)
```

```
log_reg=LogisticRegression()
log_reg.fit(x_train,y_train)
y_pred=log_reg.predict(x_test)
accuracy=accuracy_score(y_test,y_pred)
precision=precision_score(y_test,y_pred)
confmatrix=confusion_matrix(y_test,y_pred)
classreport=classification_report(y_test,y_pred)
rquared=r2_score(y_test,y_pred)
print('Accuracy: ',accuracy)
print('Precision: ',precision)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)
```

```
Accuracy:  0.7757738095238095
Precision:  0.0
Confusion Matrix:  [[13033     0]
 [ 3767     0]]
Classification Report:                precision    recall  f1-score   support

           0       0.78      1.00      0.87     13033
           1       0.00      0.00      0.00      3767

    accuracy                           0.78     16800
   macro avg       0.39      0.50      0.44     16800
weighted avg       0.60      0.78      0.68     16800


C:\Users\jakey\anaconda3\lib\site-
packages\sklearn\linear_model\_logistic.py:458: ConvergenceWarning: lbfgs failed
to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(
C:\Users\jakey\anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 due to no predicted samples. Use
`zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\jakey\anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning:
Precision and F-score are ill-defined and being set to 0.0 in labels with no
predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

```
C:\Users\jakey\anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning:
Precision and F-score are ill-defined and being set to 0.0 in labels with no
predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\jakey\anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:1344: UndefinedMetricWarning:
Precision and F-score are ill-defined and being set to 0.0 in labels with no
predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

[11]:
```python
#Random Forest Classifier: builds trees independently using random subset
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import␣
 ↪accuracy_score,confusion_matrix,classification_report,precision_score,r2_score
labelencoder=LabelEncoder()
df['gender encoded']=labelencoder.fit_transform(df['gender'])
df['cancer stage encoded']=labelencoder.fit_transform(df['cancer_stage'])
df['family history encoded']=labelencoder.fit_transform(df['family_history'])
df['smoking status encoded']=labelencoder.fit_transform(df['smoking_status'])
df['treatment type encoded']=labelencoder.fit_transform(df['treatment_type'])
x=df[['age','gender encoded','cancer stage encoded','family history␣
 ↪encoded','smoking status␣
 ↪encoded','bmi','cholesterol_level','hypertension','asthma','cirrhosis','other_cancer']]
y=df['survived']
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=.3,random_state=42)
rf=RandomForestClassifier(n_estimators=100,random_state=42)
rf.fit(x_train,y_train)
y_pred=rf.predict(x_test)
accuracy=accuracy_score(y_test,y_pred)
precision=precision_score(y_test,y_pred)
confmatrix=confusion_matrix(y_test,y_pred)
classreport=classification_report(y_test,y_pred)
rquared=r2_score(y_test,y_pred)
print('Accuracy: ',accuracy)
print('Precision: ',precision)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)
```

```
Accuracy:  0.7695238095238095
Precision:  0.21311475409836064
Confusion Matrix:  [[12889   144]
 [ 3728    39]]
Classification Report:                precision    recall  f1-score   support

           0       0.78      0.99      0.87     13033
           1       0.21      0.01      0.02      3767
```

```
    accuracy                           0.77     16800
   macro avg       0.49      0.50      0.44     16800
weighted avg       0.65      0.77      0.68     16800
```

[12]:

```
#Random Forest Factors' Importance
rfimportance=pd.DataFrame()
rfimportance['variables']=x.columns
rfimportance['importance']=rf.feature_importances_
rfimportance.sort_values(by='importance',ascending=False)
```

[12]:

```
                variables  importance
5                     bmi    0.287138
6       cholesterol_level    0.261529
0                     age    0.229232
2     cancer stage encoded    0.056331
4   smoking status encoded    0.054125
1          gender encoded    0.023882
8                  asthma    0.022923
9               cirrhosis    0.021598
7            hypertension    0.017211
3   family history encoded    0.013203
10           other_cancer    0.012828
```

[13]:

```
#Gradient Boost: builds trees sequentially, correcting errors of previous one
from xgboost import XGBClassifier
labelencoder=LabelEncoder()
df['gender encoded']=labelencoder.fit_transform(df['gender'])
df['cancer stage encoded']=labelencoder.fit_transform(df['cancer_stage'])
df['family history encoded']=labelencoder.fit_transform(df['family_history'])
df['smoking status encoded']=labelencoder.fit_transform(df['smoking_status'])
df['treatment type encoded']=labelencoder.fit_transform(df['treatment_type'])
x=df[['age','gender encoded','cancer stage encoded','family history␣
 ↪encoded','smoking status␣
 ↪encoded','bmi','cholesterol_level','hypertension','asthma','cirrhosis','other_cancer']]
y=df['survived']
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=.3,random_state=42)
xgb=XGBClassifier()
xgb.fit(x_train,y_train)
y_pred=xgb.predict(x_test)
accuracy=accuracy_score(y_test,y_pred)
precision=precision_score(y_test,y_pred)
confmatrix=confusion_matrix(y_test,y_pred)
classreport=classification_report(y_test,y_pred)
rquared=r2_score(y_test,y_pred)
print('Accuracy: ',accuracy)
print('Precision: ',precision)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)
```

```
Accuracy:  0.7724404761904762
Precision:  0.2358490566037736
Confusion Matrix:  [[12952    81]
 [ 3742    25]]
Classification Report:                precision    recall  f1-score   support

           0       0.78      0.99      0.87     13033
           1       0.24      0.01      0.01      3767

    accuracy                           0.77     16800
   macro avg       0.51      0.50      0.44     16800
weighted avg       0.65      0.77      0.68     16800
```

[14]:

```
#Gradient Boost Factors' Importance
xgbimportance=pd.DataFrame()
xgbimportance['variables']=x.columns
xgbimportance['importance']=xgb.feature_importances_
xgbimportance.sort_values(by='importance',ascending=False)
```

[14]:

```
                 variables  importance
10            other_cancer    0.109038
9                cirrhosis    0.097851
5                      bmi    0.094610
6        cholesterol_level    0.094005
4   smoking status encoded    0.091678
7             hypertension    0.088378
0                      age    0.087616
1           gender encoded    0.086794
3   family history encoded    0.084775
2     cancer stage encoded    0.084148
8                   asthma    0.081107
```