

# lung cancer mortality

July 2, 2024

```
[1]: import pandas as pd
import matplotlib.pyplot as plt
df=pd.read_csv('lung_cancer_mortality_data_small.csv')
df
```

```
[1]:      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]

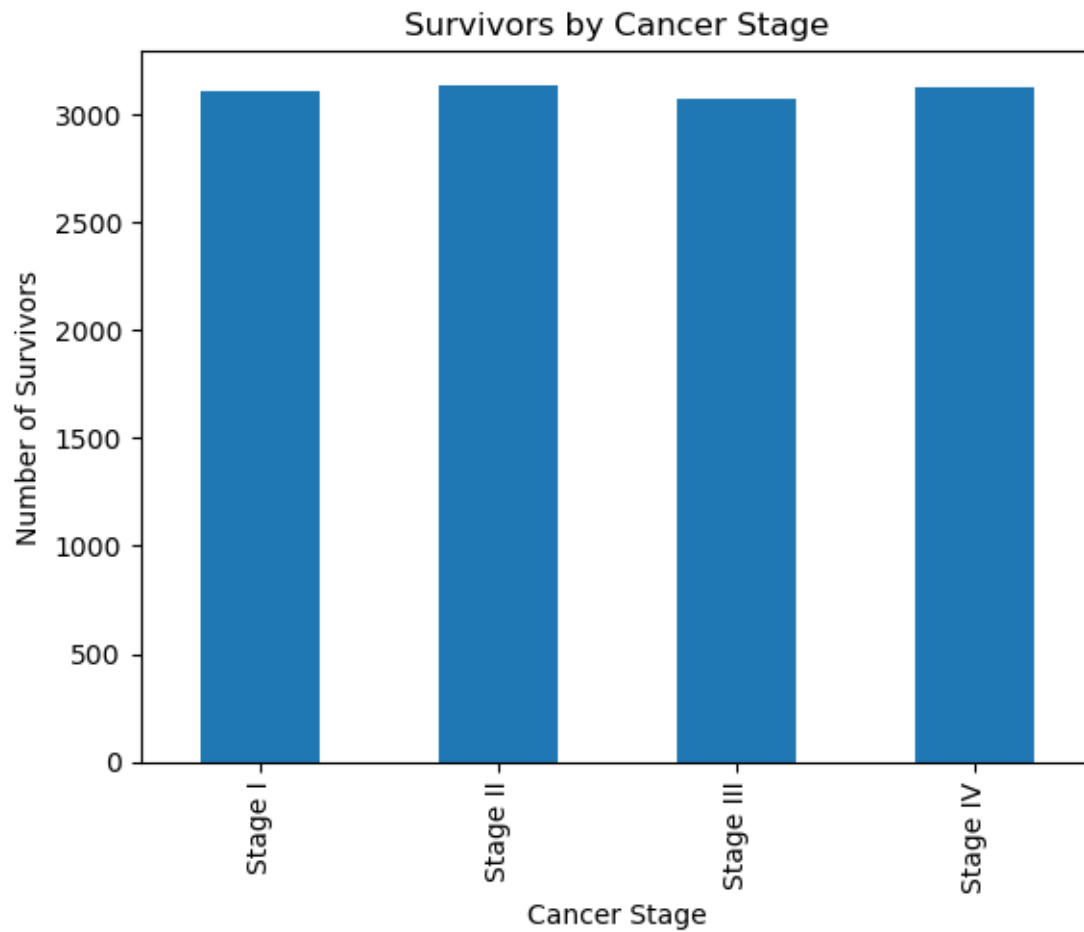
```
[2]: df[['age','bmi','cholesterol_level']].describe()
```

```
[2]:
```

	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

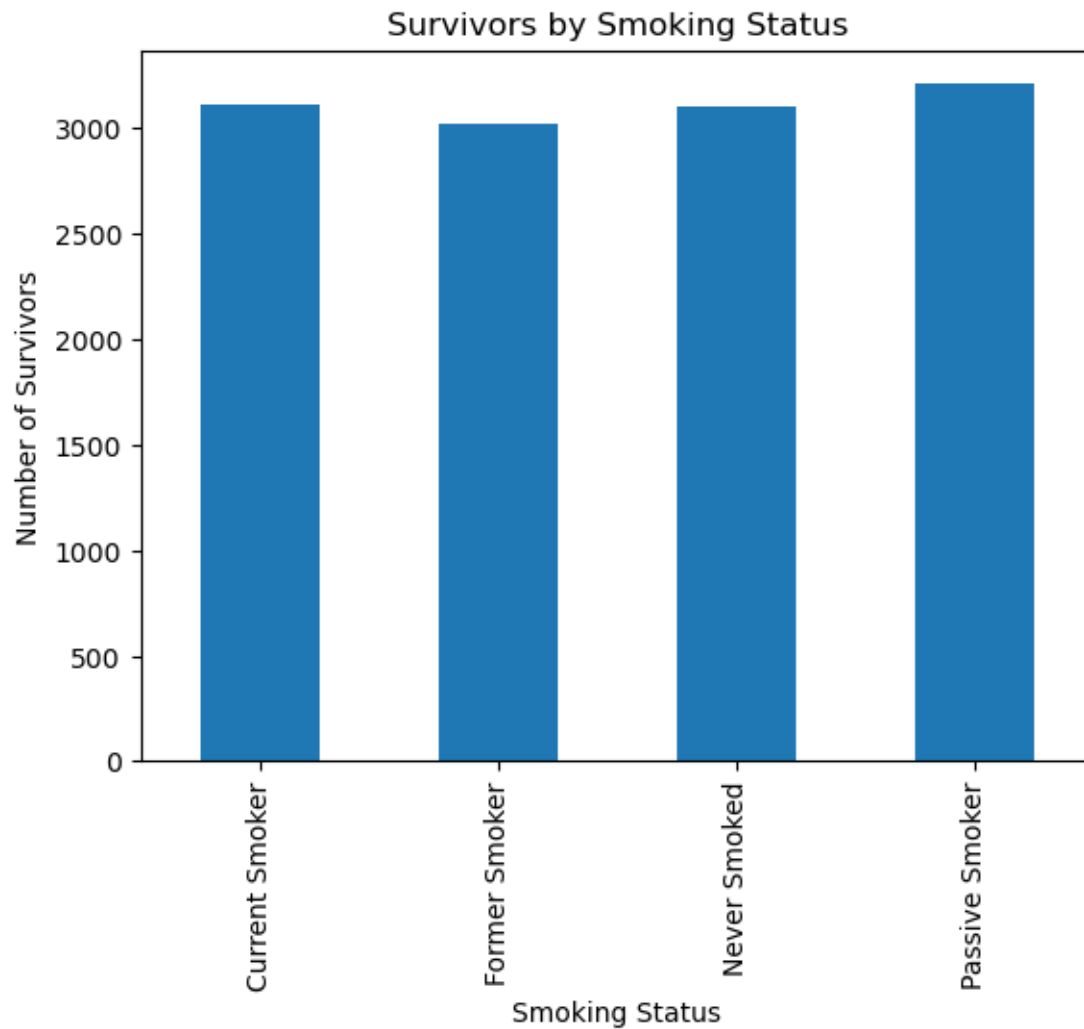
```
[3]: df.groupby('cancer_stage')['survived'].sum().plot(kind='bar',xlabel='Cancer_Stage',ylabel='Number of Survivors',title='Survivors by Cancer Stage')
```

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



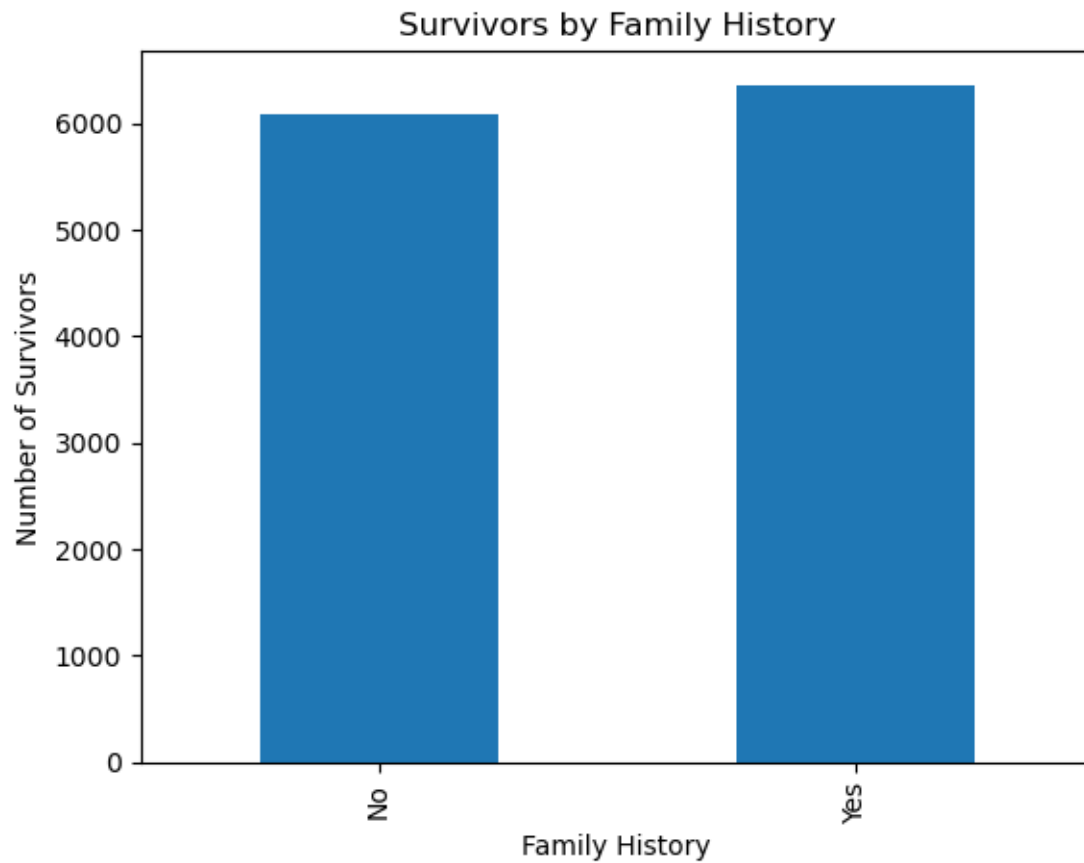
```
[4]: df.groupby('smoking_status')['survived'].sum().plot(kind='bar',xlabel='Smoking_
↳Status',ylabel='Number of Survivors',title='Survivors by Smoking Status')
```

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



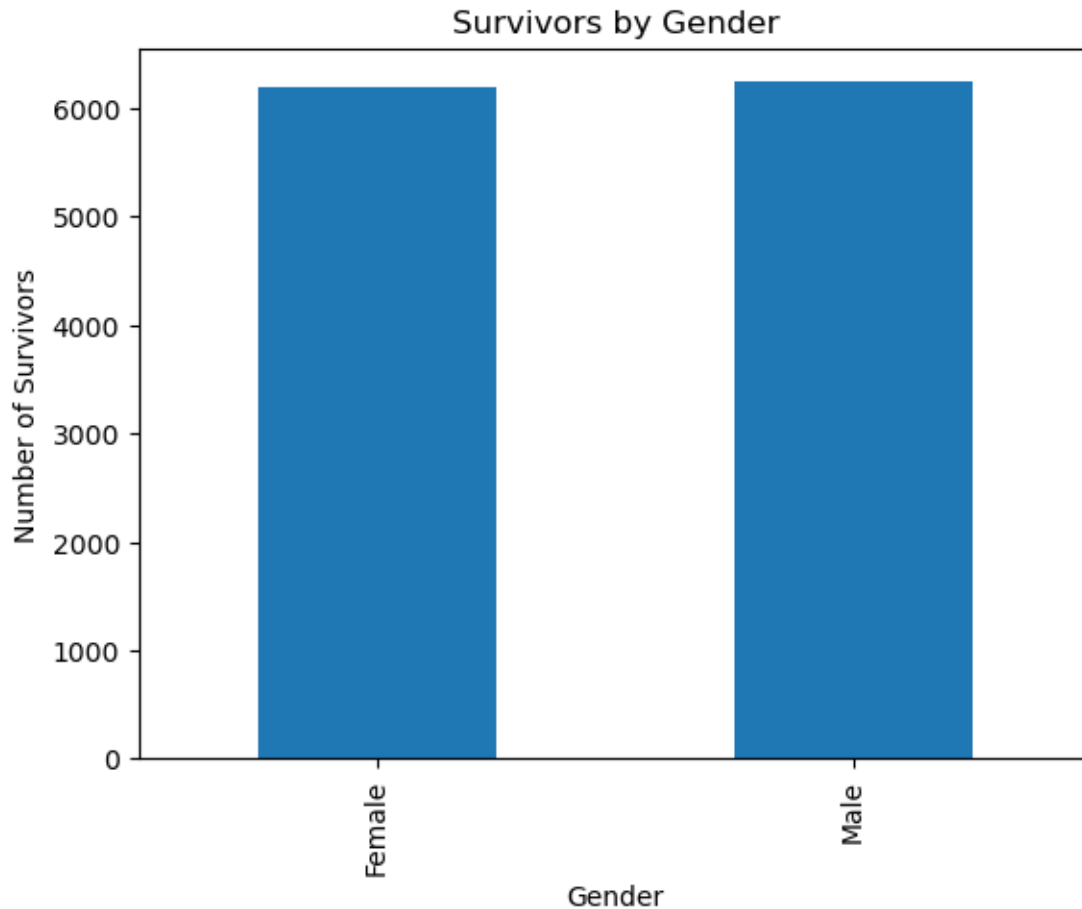
```
[5]: df.groupby('family_history')['survived'].sum().plot(kind='bar',xlabel='Family_
     ↪History',ylabel='Number of Survivors',title='Survivors by Family History')
```

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



```
[6]: df.groupby('gender')['survived'].sum().  
      ↪ plot(kind='bar',xlabel='Gender',ylabel='Number of_  
      ↪ Survivors',title='Survivors by Gender')
```

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



```
[7]: #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)
```

```
[7]:
```

	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

```
[8]: #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)
```

```
[8]:
```

	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

```
[9]: #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, precision_score, recall_score, confusion_matrix, classification_report

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', 'bmi', 'cholesterol_level', 'hypertension', 'asthma', 'cirrhosis', 'other_cancer']]
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)
logreg=LogisticRegression()
logreg.fit(x_train,y_train)
y_pred=logreg.predict(x_test)
#accuracy=overall correctness
accuracy=accuracy_score(y_test,y_pred)
#precision=ability to correctly predict positive class
precision=precision_score(y_test,y_pred)
#recall=quantifies ability to correctly predict positive class
recall=recall_score(y_test,y_pred)
#confmatrix=[TP FP][FN TN]
confmatrix=confusion_matrix(y_test,y_pred)
classreport=classification_report(y_test,y_pred)
print('Accuracy: ',accuracy)
print('Precision: ',precision)
print('Recall: ',recall)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)

```

Accuracy: 0.7757738095238095

Precision: 0.0

Recall: 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\639517\AppData\Local\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](https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression)

```
n_iter_i = _check_optimize_result(
```

C:\Users\639517\AppData\Local\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\639517\AppData\Local\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\639517\AppData\Local\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\639517\AppData\Local\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))
```

```
[10]: #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', 'bmi', 'cholesterol_level', 'hypertension', 'asthma', 'cirrhosis', 'other_cancer']]
x=df[['age', 'gender encoded', 'cancer stage encoded', 'family history',
    'smoking status',
    '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=overall correctness
accuracy=accuracy_score(y_test,y_pred)
#precision=ability to correctly predict positive class
precision=precision_score(y_test,y_pred)
#recall=quantifies ability to correctly predict positive class
recall=recall_score(y_test,y_pred)
#confmatrix=[TP FP][FN TN]
confmatrix=confusion_matrix(y_test,y_pred)
classreport=classification_report(y_test,y_pred)
print('Accuracy: ',accuracy)
```

```

print('Precision: ',precision)
print('Recall: ',recall)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)

```

```

Accuracy: 0.7695238095238095
Precision: 0.21311475409836064
Recall: 0.010353066100345103
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

```

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

```

```

[11]:

```

	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

```

[12]: #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','bmi','cholesterol_level','hypertension','asthma','cirrhosis','other_cancer']]

```

```

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=overall correctness
accuracy=accuracy_score(y_test,y_pred)
#precision=ability to correctly predict positive class
precision=precision_score(y_test,y_pred)
#recall=quantifies ability to correctly predict positive class
recall=recall_score(y_test,y_pred)
#confmatrix=[TP FP][FN TN]
confmatrix=confusion_matrix(y_test,y_pred)
classreport=classification_report(y_test,y_pred)
print('Accuracy: ',accuracy)
print('Precision: ',precision)
print('Recall: ',recall)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)

```

Accuracy: 0.7723809523809524

Precision: 0.23853211009174313

Recall: 0.006902044066896735

Confusion Matrix: [[12950 83]  
[ 3741 26]]

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	0.66	0.77	0.68	16800	

```

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

```

```

[13]:
      variables  importance
10  other_cancer  0.108651
9    cirrhosis   0.095026

```

2	cancer stage encoded	0.092776
1	gender encoded	0.092687
5	bmi	0.091114
6	cholesterol_level	0.088945
4	smoking status encoded	0.088729
3	family history encoded	0.087482
0	age	0.086039
8	asthma	0.084667
7	hypertension	0.083882

```
[14]: df['predicted']=xgb.predict(x)
#accuracy=overall correctness
accuracy=accuracy_score(df['survived'],df['predicted'])
#precision=ability to correctly predict positive class
precision=precision_score(df['survived'],df['predicted'])
#recall=quantifies ability to correctly predict positive class
recall=recall_score(df['survived'],df['predicted'])
#confmatrix=[TP FP][FN TN]
confmatrix=confusion_matrix(df['survived'],df['predicted'])
classreport=classification_report(df['survived'],df['predicted'])
print('Accuracy: ',accuracy)
print('Precision: ',precision)
print('Recall: ',recall)
print('Confusion Matrix: ',confmatrix)
print('Classification Report: ',classreport)
```

Accuracy: 0.786875

Precision: 0.862914862914863

Recall: 0.04807846920726805

Confusion Matrix: [[43467 95]  
[11840 598]]

Classification Report:			precision	recall	f1-score	support
0	0.79	1.00	0.88			43562
1	0.86	0.05	0.09			12438
accuracy			0.79			56000
macro avg			0.82	0.52	0.49	56000
weighted avg			0.80	0.79	0.70	56000