# **CLR204 Assessment 2** - COVID-19 Problem Analysis

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## Imports

```
import numpy as np # Numerical Python - used for arrays, linear algebra, fourier transform, matrices
import pandas as pd # Panel Data - used for data manipulation and analysis
import datetime as dt # Used for manipulating dates and times
import sklearn # Machine learning library
from scipy import stats # scipy is a scientific library dependant on numpy - stats is a statistic function sub-package
from sklearn import preprocessing # Common utility functions and transformer classes to change raw feature vectors
from sklearn.model_selection import GridSearchCV # Automates tuning of hyperparameters
from sklearn.ensemble import RandomForestClassifier # Meta Estimators
from sklearn.ensemble import AdaBoostClassifier
from sklearn.model_selection import train_test_split # Model validation simulator
from sklearn.metrics import recall_score as rs # Performance Metrics
from sklearn.metrics import precision_score as ps
from sklearn.metrics import fl_score as fs
from sklearn.metrics import log_loss # Lower log loss = better predictions, based off likelyhood function
encoder = preprocessing.LabelEncoder() # Transformer used to encode target values
```

# → Data Preprocessing

```
data = pd.read_csv('data.csv') # Retrieves data from data.csv
data = data.drop('id',axis=1) # Drops id column
data = data.fillna(np.nan,axis=0) # Fills NA/NAN values
data['location'] = encoder fit transform(data['location'] astyne(str)) # Label encoding
https://colab.research.google.com/drive/1ZnwzOctOy5QdWZzVt 061svsSPCs3027#scrollTo=ti3W5ccyDEzj&printMode=true
```

```
data['country'] = encoder.fit transform(data['country'].astype(str))
data['gender'] = encoder.fit transform(data['gender'].astype(str))
data['symptom1'] = encoder.fit transform(data['symptom1'].astype(str))
data['symptom2'] = encoder.fit transform(data['symptom2'].astype(str))
data['symptom3'] = encoder.fit transform(data['symptom3'].astype(str))
data['symptom4'] = encoder.fit transform(data['symptom4'].astype(str))
data['symptom5'] = encoder.fit transform(data['symptom5'].astype(str))
data['symptom6'] = encoder.fit transform(data['symptom6'].astype(str))
data['sym on'] = pd.to datetime(data['sym on']) # Convert sym-on to datetime object
data['hosp vis'] = pd.to datetime(data['hosp vis'])
data['sym on']= data['sym on'].map(dt.datetime.toordinal) # Datetime columns
data['hosp vis'] = data['hosp vis'].map(dt.datetime.toordinal)
data['diff sym hos']= data['hosp vis'] - data['sym on'] # New Feature
data = data.drop(['sym on', 'hosp vis'],axis=1) # Drops two indirectly used variables
print(data.dtypes)
     location
                      int64
                      int64
     country
     gender
                      int64
                    float64
     age
     vis wuhan
                      int64
     from wuhan
                    float64
     death
                      int64
                      int64
     recov
                      int64
     symptom1
                      int64
     symptom2
                      int64
     symptom3
                      int64
     symptom4
                      int64
     svmptom5
     symptom6
                      int64
     diff sym hos
                      int64
     dtype: object
```

The dataset used in this study has been compiled from various sources including the World Health Organization and John Hopkins University. Accessed from Kaggle as "Novel Corona Virus 2019 Dataset" and has been pre-processed further to meet the needs of the study - *COVID-19*Patient Health Prediction Using Boosted Random Forest Algorithm (Iwendi et al., 2019).

The feature of the data are presented below.

| Column     | Description  | Values (for categorical variables)           | Туре                    |
|------------|--|--|-------------------------|
| id         | Patient Id   | NA   | Numeric                 |
| location   | The location where the patient belongs to          | Multiple cities located throughout the world | String,<br>Categorical  |
| country    | Patient's native country                           | Multiple countries                           | String,<br>Categorical  |
| gender     | Patient's gender                                   | Male, Female                                 | String,<br>Categorical  |
| age        | Patient's age                                      | NA   | Numeric                 |
| sym_on     | The date patient started noticing the symptoms     | NA   | Date                    |
| hosp_vis   | Date when the patient visited the hospital         | NA   | Date                    |
| vis_wuhan  | Whether the patient visited Wuhan, China           | Yes (1), No (0)                              | Numeric,<br>Categorical |
| from_wuhan | Whether the patient<br>belonged to Wuhan,<br>China | Yes (1), No (0)                              | Numeric,<br>Categorical |
| death      | Whether the patient passed away due to             | Yes (1), No (0)                              | Numeric,<br>Categorical |

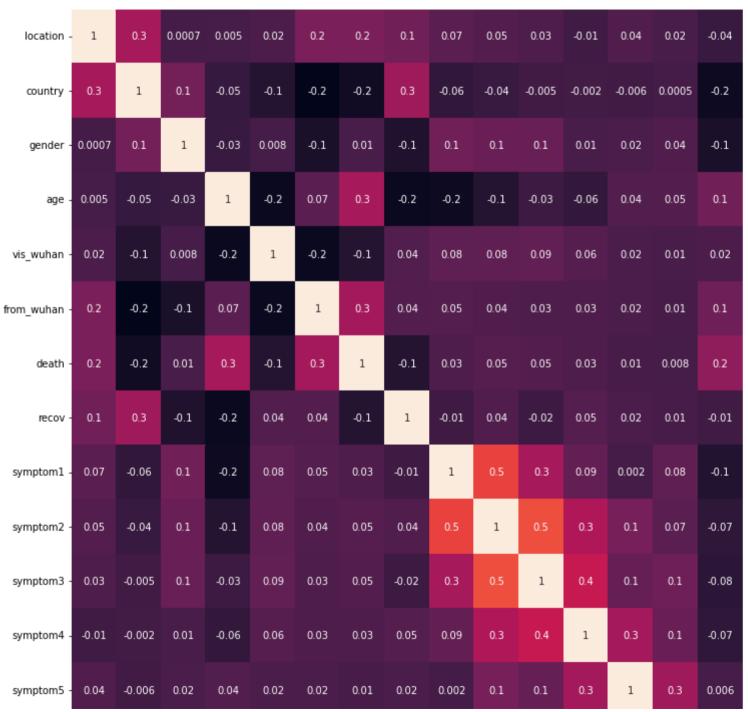
|   | COVID-19                         |  |                         |
|---|----------------------------------|--|-------------------------|
| Recov   | Whether the patient recovered    | Yes (1), No (0)                                    | Numeric,<br>Categorical |
| symptom1.<br>symptom2,<br>symptom3,<br>symptom4,<br>symptom5,<br>symptom6 | Symptoms noticed by the patients | Multiple<br>symptoms<br>noticed by the<br>patients | String,<br>Categorical  |

# Model Reproduction

## ▼ Visualisation

```
# Figure 2. Heat map of Correlation between data features
import seaborn as sb # Used for making statistical graphics
import matplotlib.pyplot as plt

fig, ax = plt.subplots(figsize=(15,15))  # Sample figsize in inches
dataplot=sb.heatmap(data.corr(),annot=True, fmt='.01g', ax=ax)
```



-1.0

- 0.8

- 0.6

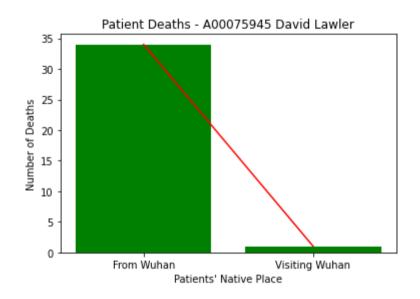
- 0.4

- 0.2

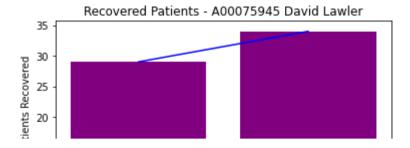
- 0.0

```
0.02 0.0005
                             0.04
                                   0.05
                                         0.01
                                               0.01
                                                           0.01
                                                                 0.08
                                                                       0.07
                                                                             0.1
                                                                                    0.1
                                                                                          0.3
                                                                                                     0.002
        symptom6
                                                     0.008
import matplotlib.pyplot as plt
def counter2(colname1,colname2): # for loop for 2 column logic
  colname1 = pd.Series(colname1)
  colname2 = pd.Series(colname2)
  count1 = 0
  for i in range(min([colname1.size,colname2.size])):
    if(colname1[i]==1 and colname2[i]==1):
      count1 = count1+1
  return count1
def counter1(colname): # for loop for 1 column logic
  colname1 = pd.Series(colname)
  count = 0
  for i in range(colname1.size):
    if(colname1[i]==1):
      count = count+1
  return count
fwuh = counter1(data['from wuhan'])
vwuh = counter1(data['vis wuhan'])
print(counter1(data['death'])) # Number of deaths
print(counter2(data['from wuhan'],data['death'])) # Number of deaths people from Wuhan
print(counter2(data['vis wuhan'],data['death'])) # Number of deaths people visiting Wuhan
     63
     34
     1
import matplotlib.pyplot as plt
```

```
plt.bar(['From Wuhan','Visiting Wuhan'],[counter2(data['death'],data['from_wuhan']),counter2(data['death'],data['vis_wuhan'])],color:
plt.title('Patient Deaths - A00075945 David Lawler')
plt.xlabel('Patients\' Native Place')
plt.ylabel('Number of Deaths')
plt.plot([counter2(data['death'],data['from_wuhan']),counter2(data['death'],data['vis_wuhan'])],color='red')
plt.show()
```



```
plt.bar(['From Wuhan','Visiting Wuhan'],[counter2(data['recov'],data['from_wuhan']),counter2(data['recov'],data['vis_wuhan'])],color=
plt.title('Recovered Patients - A00075945 David Lawler')
plt.xlabel('Patients\' Native Place')
plt.ylabel('Number of Patients Recovered')
plt.plot([counter2(data['recov'],data['from_wuhan']),counter2(data['recov'],data['vis_wuhan'])],color='blue')
plt.show()
```



## ▼ Training

```
≤ 5 †
```

tdata = pd.read\_csv('train.csv') # Reads train.csv
print(tdata.head())

|   | id  | 100     | cation | country g | gender  | age   | sy      | /m_on | hos   | p_vis   | vis_wuhan  | \    |
|---|-----|---------|--------|-----------|---------|-------|---------|-------|-------|---------|------------|------|
| 0 | 49  | Wuhan,  | Hubei  | China     | male    | 61.0  | 12/20/  | 2019  | 12/27 | /2019   | 0          |      |
| 1 | 50  | Wuhan,  | Hubei  | China     | male    | 69.0  | 12/30/  | 2019  | 1/3   | /2020   | 0          |      |
| 2 | 51  | Wuhan,  | Hubei  | China     | male    | 89.0  |         | NaN   |       | NaN     | 0          |      |
| 3 | 52  | Wuhan,  | Hubei  | China     | male    | 89.0  | 1/13/   | 2020  | 1/13  | /2020   | 0          |      |
| 4 | 53  | Wuhan,  | Hubei  | China     | male    | 66.0  | 1/10/   | 2020  | 1/16  | /2020   | 0          |      |
|   |     |         |        |           |         |       |         |       |       |         |            |      |
|   | fro | m_wuhan | death  | symptom1  | . sympt | om2 s | ymptom3 | symp  | tom4  | sympton | n5 sympton | n6   |
| Ω |     | 1       | 1      | NaN       | ı       | NaN   | NaN     |       | NaN   | NI-     | M M-       | - NI |

|   | _ | , |     | , , , | •   | , , , |     | , , |
|---|---|---|-----|-------|-----|-------|-----|-----|
| 0 | 1 | 1 | NaN | NaN   | NaN | NaN   | NaN | NaN |
| 1 | 1 | 1 | NaN | NaN   | NaN | NaN   | NaN | NaN |
| 2 | 1 | 1 | NaN | NaN   | NaN | NaN   | NaN | NaN |
| 3 | 1 | 1 | NaN | NaN   | NaN | NaN   | NaN | NaN |
| 4 | 1 | 1 | NaN | NaN   | NaN | NaN   | NaN | NaN |

```
tdata = pd.read_csv('train.csv') # Same preprocessing as with data.csv
tdata = tdata.drop('id',axis=1)
tdata = tdata.fillna(np.nan,axis=0)
tdata['age'] = tdata['age'].fillna(value=tdata['age'].mean())
tdata['location'] = encoder.fit_transform(tdata['location'].astype(str))
tdata['country'] = encoder.fit_transform(tdata['country'].astype(str))
tdata['gender'] = encoder.fit_transform(tdata['gender'].astype(str))
tdata['symptom1'] = encoder.fit_transform(tdata['symptom1'].astype(str))
```

```
tdata['symptom2'] = encoder.fit_transform(tdata['symptom2'].astype(str))
tdata['symptom3'] = encoder.fit_transform(tdata['symptom3'].astype(str))
tdata['symptom4'] = encoder.fit_transform(tdata['symptom4'].astype(str))
tdata['symptom5'] = encoder.fit_transform(tdata['symptom5'].astype(str))
tdata['symptom6'] = encoder.fit_transform(tdata['symptom6'].astype(str))

tdata['sym_on'] = pd.to_datetime(tdata['sym_on'])
tdata['hosp_vis'] = pd.to_datetime(tdata['hosp_vis'])
tdata['sym_on'] = tdata['sym_on'].map(dt.datetime.toordinal)
tdata['hosp_vis'] = tdata['hosp_vis'].map(dt.datetime.toordinal)
tdata['diff_sym_hos'] = tdata['hosp_vis'] - tdata['sym_on']

tdata = tdata.drop(['sym_on','hosp_vis'],axis=1)
print(tdata)
```

|     | location | country  | gender | age        | vis_wuhan  | from_wuhan | death \      |
|-----|----------|----------|--------|------------|------------|------------|--------------|
| 0   | 38       | 2        | 1      | 61.000000  | 0          | 1          | 1            |
| 1   | 38       | 2        | 1      | 69.000000  | 0          | 1          | 1            |
| 2   | 38       | 2        | 1      | 89.000000  | 0          | 1          | 1            |
| 3   | 38       | 2        | 1      | 89.000000  | 0          | 1          | 1            |
| 4   | 38       | 2        | 1      | 66.000000  | 0          | 1          | 1            |
|     | • • •    | • • •    |        | • • •      | • • •      |            | • • •        |
| 217 | 2        | 3        | 2      | 49.747537  | 0          | 0          | 0            |
| 218 | 22       | 6        | 2      | 49.747537  | 0          | 0          | 1            |
| 219 | 22       | 6        | 2      | 49.747537  | 0          | 0          | 1            |
| 220 | 22       | 6        | 2      | 49.747537  | 0          | 0          | 1            |
| 221 | 22       | 6        | 2      | 49.747537  | 0          | 0          | 1            |
|     |          |          |        |            |            |            |              |
|     | symptom1 | symptom2 | sympto | m3 symptom | 4 symptom5 | symptom6   | diff_sym_hos |
| 0   | 9        | 9        |        | 11         | 0 0        | 0          | 7            |
| 1   | 9        | 9        |        | 11         | 0 0        | 0          | 4            |
| 2   | 9        | 9        |        | 11         | 0 0        | 0          | 0            |
| 3   | 9        | 9        |        | 11         | 0 0        | 0          | 0            |
| 4   | 9        | 9        |        | 11         | 0 0        | 0          | 6            |
|     |          |          | •      |            |            |            | • • •        |
| 217 | 9        | 9        |        | 11         | 0 0        | 0          | 0            |
| 218 | 9        | 9        |        | 11         | 0 0        | 0          | 0            |

```
219
                                                                     0
                                                                                    0
                                  11
             9
                        9
220
                                  11
                                                          0
                                                                     0
                                                                                    0
             9
221
                        9
                                  11
                                                                     0
                                                                                    0
```

[222 rows x 14 columns]

```
print(tdata.isna().sum())
```

```
location
                0
country
                0
gender
age
vis wuhan
from wuhan
death
                0
symptom1
symptom2
                0
symptom3
symptom4
symptom5
symptom6
diff sym hos
dtype: int64
```

```
from sklearn.metrics import recall_score as rs # Importing metrics
from sklearn.metrics import precision_score as ps
from sklearn.metrics import f1_score as fs
from sklearn.metrics import balanced_accuracy_score as bas
from sklearn.metrics import confusion matrix as cm
```

## ▼ Logistic Regression

```
from sklearn.linear_model import LogisticRegression as lr
```

```
Y = tdata['death'].values.ravel() # Creates flattened array

X_train, X_test, Y_train, Y_test = train_test_split(X,Y,test_size=0.2,random_state=10) # split X and Y into training and testing sets classifier = lr(solver='lbfgs', max_iter=500 )
classifier.fit(X_train,np.array(Y_train).reshape(Y_train.shape[0],1).ravel())

LogisticRegression(max_iter=500)
```

### ▼ Evaluation of model

```
pred = np.array(classifier.predict(X_test)) # Evaluates test dataset using Logistic Regression
recall lr = rs(Y test,pred)
precision lr = ps(Y test,pred)
f1 lr = fs(Y test,pred)
ma lr = classifier.score(X_test,Y_test)
print('*** Evaluation metrics for test dataset ***\n')
print('Recall Score: ',recall lr)
print('Precision Score: ',precision lr)
print('F1 Score: ',f1 lr)
print('Accuracy: ',ma lr)
a = pd.DataFrame(Y test)
a['pred']= classifier.predict(X test)
print('\n\tTable 3\n')
print(a.head())
     *** Evaluation metrics for test dataset ***
     Recall Score: 0.72727272727273
     Precision Score: 0.6153846153846154
     F1 Score: 0.666666666666666667
     Accuracy: 0.8222222222222
```

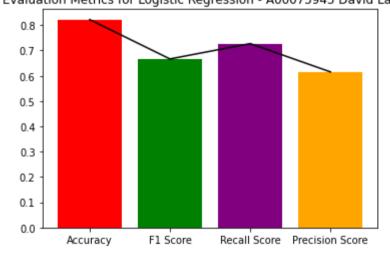
Table 3

|   | 0 | pred |
|---|---|------|
| 0 | 0 | 0    |
| 1 | 1 | 0    |
| 2 | 0 | 0    |
| 3 | 0 | 0    |
| 4 | 1 | 1    |

import matplotlib.pyplot as plt

```
plt.bar(['Accuracy','F1 Score','Recall Score','Precision Score'],[ma_lr,f1_lr,recall_lr,precision_lr],color=['red','green','purple',
plt.plot([ma_lr,f1_lr,recall_lr,precision_lr],color='black')
plt.title('Evaluation Metrics for Logistic Regression - A00075945 David Lawler')
```

Text(0.5, 1.0, 'Evaluation Metrics for Logistic Regression - A00075945 David Lawler') Evaluation Metrics for Logistic Regression - A00075945 David Lawler



print(pd.DataFrame({'Val':Y\_test,'Pred':classifier.predict(X\_test)}))

|   | Val | Pred |
|---|-----|------|
| 0 | 0   | 0    |
| 1 | 1   | 0    |
| 2 | 0   | 0    |

| 2                     | 0                     | a                                    |
|-----------------------|-----------------------|--------------------------------------|
| 3<br>1                | 0<br>1                | 0                                    |
| -                     | 1<br>0                | 1<br>0                               |
| 4<br>5<br>6<br>7<br>8 | 1                     | 0                                    |
| 7                     | 1<br>0                | 0                                    |
| ,<br>8                | 1                     | 1                                    |
| 9                     | 1<br>0<br>1<br>0<br>0 | a                                    |
| 10                    | 1                     | 0<br>1<br>0<br>0                     |
| 10<br>11              | a                     | a                                    |
| 12                    | 0                     | 0                                    |
| 13                    | 1                     | 1                                    |
| 14                    | 1<br>0<br>0<br>0      | 1<br>0                               |
| 15                    | 0                     | 0                                    |
| 16                    | 0                     | 0<br>0                               |
| 17                    | 1                     | 1                                    |
| 18                    | 0                     | 0                                    |
| 19                    | 0                     | 0                                    |
| 19<br>20<br>21<br>22  | 1<br>0<br>0<br>0<br>1 | 1<br>0<br>0<br>0<br>1<br>1<br>0<br>0 |
| 21                    | 1                     | 1                                    |
| 22                    | 0                     | 1                                    |
| 23<br>24<br>25        | 0                     | 0                                    |
| 24                    | 1<br>0<br>0           | 0                                    |
| 25                    | 0                     | 0                                    |
| 26                    | 0                     | 0                                    |
| 27                    | 0<br>0                | 0                                    |
| 28                    | 0                     | 0                                    |
| 29                    | 0<br>0<br>0           | 0<br>0<br>1<br>0                     |
| 30                    | 0                     | 0                                    |
| 31<br>32              | 0                     | 0                                    |
| 32                    | 0                     | 0                                    |
| 33                    | 0<br>0<br>0           | 0<br>0<br>1<br>0                     |
| 34<br>35              | 0                     | 7                                    |
| 36                    | 0                     | 1                                    |
| 37                    | 0                     | 0                                    |
| 38                    | 1                     | 1                                    |
| 39                    | 0                     | 0                                    |
| 40                    | 1                     | 1                                    |
| 41                    | 0                     | 0                                    |
| 42                    | 0                     | 0                                    |
| -                     |                       | -                                    |

```
43 0 1
44 0 6
```

### Decision Tree Classifier

```
from sklearn.tree import DecisionTreeClassifier as dtc # Decision Tree setup
classifier = dtc(max_depth=2)

X = tdata[['location','country','gender','age','vis_wuhan','from_wuhan','symptom1','symptom2','symptom3','symptom5','symptom9','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom2','symptom1','symptom1','symptom1','symptom2','symptom1','symptom1','symptom1','symptom2','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','symptom1','s
```

### ▼ Evaluation of the model

```
pred = np.array(classifier.predict(X_test))

recall_dtc = rs(Y_test,pred)
precision_dtc = ps(Y_test,pred)
f1_dtc = fs(Y_test,pred)
ma_dtc = classifier.score(X_test,Y_test)

print('*** Evaluation metrics for test dataset ***\n')
print('Recall Score: ',recall_dtc)
print('Precision Score: ',precision_dtc)
print('F1 Score: ',f1_dtc)
print('Accuracy: ',ma_dtc)
a = pd.DataFrame(Y_test)
```

Table 3

|     | death | pred |
|-----|-------|------|
| 184 | 0     | 0    |
| 170 | 1     | 0    |
| 142 | 0     | 0    |
| 182 | 0     | 0    |
| 49  | 1     | a    |

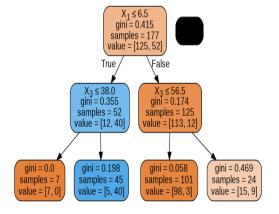
import matplotlib.pyplot as plt

```
plt.bar(['Accuracy','F1 Score','Recall Score','Precision Score'],[ma_dtc,f1_dtc,recall_dtc,precision_dtc],color=['red','green','purp']
plt.plot([ma_dtc,f1_dtc,recall_dtc,precision_dtc],color='black')
plt.title('Evaluation Metrics for Decision Tree - A00075945 David Lawler')
```

Text(0.5, 1.0, 'Evaluation Metrics for Decision Tree - A00075945 David Lawler')

Evaluation Metrics for Decision Tree - A00075945 David Lawler

▼ Visualizing the decision trees from random forest



### → SVM

```
from sklearn import svm # Support Vector Machine setup
classifier = svm.SVC()

X = tdata[['location','country','gender','age','vis_wuhan','from_wuhan','symptom1','symptom2','symptom3','symptom5','symptom5','symptom5','symptom1','symptom2','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom3','symptom5','symptom1','symptom2','symptom3','symptom3','symptom5','symptom1','symptom2','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3
```

### Evaluation of the model

```
pred = np.array(classifier.predict(X_test))

recall_svm = rs(Y_test,pred)
precision_svm = ps(Y_test,pred)
f1_svm = fs(Y_test,pred)
ma_svm = classifier.score(X_test,Y_test)

print('*** Evaluation metrics for test dataset ***\n')
print('Recall Score: ',recall_svm)
print('Precision Score: ',precision_svm)
print('F1 Score: ',f1_svm)
print('Accuracy: ',ma_svm)
a = pd.DataFrame(Y_test)
a['pred']= classifier.predict(X_test)
print('\n\tTable 3\n')
print(a.head())

*** Evaluation metrics for test dataset ***
```

https://colab.research.google.com/drive/1ZnwzOctOy5QdWZzVt 061svsSPCs3027#scrollTo=ti3W5ccyDEzj&printMode=true

Recall Score: 0.6363636363636364

Precision Score: 0.7

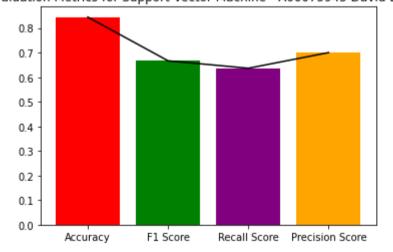
Table 3

|     | death | pred |
|-----|-------|------|
| 184 | 0     | 0    |
| 170 | 1     | 0    |
| 142 | 0     | 0    |
| 182 | 0     | 0    |
| 49  | 1     | 1    |

import matplotlib.pyplot as plt

plt.bar(['Accuracy','F1 Score','Recall Score','Precision Score'],[ma\_svm,f1\_svm,recall\_svm,precision\_svm],color=['red','green','purp]
plt.plot([ma\_svm,f1\_svm,recall\_svm,precision\_svm],color='black')
plt.title('Evaluation Metrics for Support Vector Machine - A00075945 David Lawler')

Text(0.5, 1.0, 'Evaluation Metrics for Support Vector Machine - A00075945 David Lawler') Evaluation Metrics for Support Vector Machine - A00075945 David Lawler



## → Gaussian Naive Bayes

```
from sklearn.naive_bayes import GaussianNB # GNB setup
classifier = GaussianNB()

X = tdata[['location','country','gender','age','vis_wuhan','from_wuhan','symptom1','symptom2','symptom3','symptom4','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom3','symptom5','symptom5','symptom1','symptom2','symptom2','symptom3','symptom5','symptom5','symptom6','symptom1','symptom1','symptom2','symptom3','symptom6','symptom5','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','symptom6','sympt
```

### Evaluation of the model

```
pred = np.array(classifier.predict(X_test))

recall_gnb = rs(Y_test,pred)
precision_gnb = ps(Y_test,pred)
f1_gnb = fs(Y_test,pred)
ma_gnb = classifier.score(X_test,Y_test)

print('*** Evaluation metrics for test dataset ***\n')
print('Recall Score: ',recall_gnb)
print('Precision Score: ',precision_gnb)
print('F1 Score: ',f1_gnb)
print('Accuracy: ',ma_gnb)
a = pd.DataFrame(Y_test)
a['pred']= classifier.predict(X_test)
print('\n\tTable 3\n')
```

```
print(a.head())
```

\*\*\* Evaluation metrics for test dataset \*\*\*

Recall Score: 0.72727272727273 Precision Score: 0.5333333333333333

F1 Score: 0.6153846153846153 Accuracy: 0.7777777777778

#### Table 3

|     | death | pred |
|-----|-------|------|
| 184 | 0     | 0    |
| 170 | 1     | 0    |
| 142 | 0     | 0    |
| 182 | 0     | 0    |
| 49  | 1     | 1    |

import matplotlib.pyplot as plt

```
plt.bar(['Accuracy','F1 Score','Recall Score','Precision Score'],[ma_gnb,f1_gnb,recall_gnb,precision_gnb],color=['red','green','purp:
plt.plot([ma_gnb,f1_gnb,recall_gnb,precision_gnb],color='black')
plt.title('Evaluation Metrics for Gaussian Naive Bayes - A00075945 David Lawler')
```

Text(0.5, 1.0, 'Evaluation Metrics for Gaussian Naive Bayes - A00075945 David Lawler')

### ▼ Boosted Random Forest

```
from sklearn.metrics import recall score as rs # BRF Setup
from sklearn.metrics import precision score as ps
from sklearn.metrics import f1 score as fs
from sklearn.metrics import balanced accuracy score as bas
from sklearn.metrics import confusion matrix as cm
from sklearn.ensemble import RandomForestClassifier
rf = RandomForestClassifierrf = RandomForestClassifier(bootstrap=True, ccp alpha=0.0, class weight=None,
                       criterion='gini', max depth=2, max features='auto',
                       max leaf nodes=None, max samples=None,
                       min impurity decrease=0.0,
                       min samples leaf=2, min samples split=2,
                       min weight fraction leaf=0.0, n estimators=100,
                       n jobs=None, oob score=False, random state=None,
                       verbose=0, warm start=False)
classifier = AdaBoostClassifier(rf)
X = tdata[['location','country','gender','age','vis wuhan','from wuhan','symptom1','symptom2','symptom3','symptom4','symptom5','symptom5',
Y = tdata['death'].values.ravel()
X_train, X_test, Y_train, Y_test = train_test_split(X,Y,test_size=0.2,random_state=0)
classifier.fit(X train,np.array(Y train).reshape(Y train.shape[0],1).ravel())
     AdaBoostClassifier(base estimator=RandomForestClassifier(max depth=2,
                                                              min samples leaf=2))
```

### Evaluation of the model

```
pred = np.array(classifier.predict(X test))
recall = rs(Y test,pred)
precision = ps(Y test,pred)
f1 = fs(Y test,pred)
ma = classifier.score(X test,Y test)
print('*** Evaluation metrics for test dataset ***\n')
print('Recall Score: ',recall)
print('Precision Score: ',precision)
print('F1 Score: ',f1)
print('Accuracy: ',ma)
a = pd.DataFrame(Y_test)
a['pred'] = classifier.predict(X test)
print('\n\tTable 3\n')
print(a.head())
     *** Evaluation metrics for test dataset ***
     Recall Score: 0.83333333333333334
     Precision Score: 1.0
     F1 Score: 0.9090909090909091
     Accuracy: 0.9555555555556
             Table 3
           pred
     1 0
     2 1
     4 0
```

## Comparison of Evaluation Metrics

```
import matplotlib.pyplot as plt # Evaluation of Evaluation Metrics
fig = plt.figure(figsize=(8,6))
plt.plot(['Logistic Regression','Decision Tree','Boosted Random Forest','SVM','Gaussian NB'],[f1_lr,f1_dtc,f1,f1_svm,f1_gnb],color='|
plt.plot(['Logistic Regression','Decision Tree','Boosted Random Forest','SVM','Gaussian NB'],[ma_lr,ma_dtc,ma,ma_svm,ma_gnb],color='|
plt.plot(['Logistic Regression','Decision Tree','Boosted Random Forest','SVM','Gaussian NB'],[precision_lr,precision_dtc,precision,precision]
plt.plot(['Logistic Regression','Decision Tree','Boosted Random Forest','SVM','Gaussian NB'],[recall_lr,recall_dtc,recall,recall_svm_plt.legend(('F1 Score','Accuracy','Precision','Recall'))
plt.title('Comparison of various models\' performance - A00075945 David Lawler')
```

### plt.show(fig)

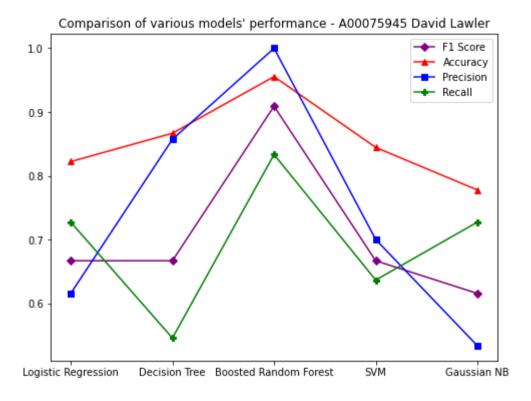
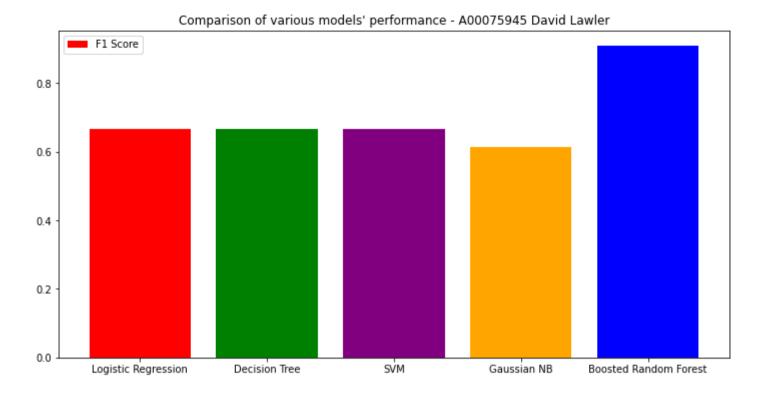


fig = plt.figure(figsize=(12,6)) # visualisation of evaluation of classifiers using f1
plt.bar(['Logistic Regression','Decision Tree','SVM','Gaussian NB','Boosted Random Forest'],[f1\_lr,f1\_dtc,f1\_svm,f1\_gnb,f1],color=['|
plt.legend(('F1 Score','Accuracy','Precision','Recall')) # Not sure why this won't print properly
plt.title('Comparison of various models\' performance - A00075945 David Lawler')

plt.show(fig)



## ▼ Takes 10 minutes - Meta Estimator

```
X1 = tdata[['location','country','gender','age','vis_wuhan','from_wuhan','symptom1','symptom2','symptom3','symptom4','symptom5','symptom1','symptom2','symptom3','symptom4','symptom5','symptom1','symptom2','symptom2','symptom3','symptom4','symptom5','symptom1','symptom2','symptom2','symptom3','symptom3','symptom4','symptom5','symptom1','symptom2','symptom2','symptom3','symptom3','symptom4','symptom5','symptom1','symptom2','symptom2','symptom3','symptom3','symptom5','symptom5','symptom1','symptom2','symptom3','symptom3','symptom3','symptom5','symptom1','symptom2','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3','symptom3'
```

min\_samples\_split = [1.0,2,6,7] # min number of samples to split an internal node

```
min samples leaf = [2,3,4,5] # min number of samples required to be at a leaf node
# parameter grid to explore
params grid = {'n estimators':n estimators, 'max depth':max depth, 'min samples split':min samples split, 'min samples leaf':min samples
gridder = GridSearchCV(estimator=classifier1,param grid=params grid,n jobs=-1,cv=5,verbose=5) # Finds best parameters
gridder.fit(X1,np.array(Y1).reshape(Y1.shape[0],1).ravel())
     Fitting 5 folds for each of 320 candidates, totalling 1600 fits
     GridSearchCV(cv=5, estimator=RandomForestClassifier(), n jobs=-1,
                  param grid={'max depth': [1, 2, 5, 6],
                              'min samples leaf': [2, 3, 4, 5],
                              'min samples split': [1.0, 2, 6, 7],
                              'n estimators': [100, 200, 300, 400, 500]},
                  verbose=5)
print(gridder.best estimator ) # prints best estimator
     RandomForestClassifier(max depth=6, min samples leaf=2, n estimators=300)
!ls # print files
     data.csv sample data test.xlsx train.csv
udata = pd.read excel('test.xlsx')
udata = udata.drop('id',axis=1)
print(udata.columns)
     Index(['location', 'country', 'gender', 'age', 'sym on', 'hosp vis',
            'vis wuhan', 'from wuhan', 'symptom1', 'symptom2', 'symptom3',
            'symptom4', 'symptom5', 'symptom6'],
           dtvpe='object')
udata = udata.fillna(np.nan,axis=0)
udata['age'] = udata['age'].fillna(value=udata['age'].mean())
```

```
udata['from wuhan'] = udata['from wuhan'].fillna(value=0)
udata['from wuhan'] = udata['from wuhan'].astype(int)
udata['location'] = encoder.fit transform(udata['location'].astype(str))
udata['country'] = encoder.fit transform(udata['country'].astype(str))
udata['gender'] = encoder.fit transform(udata['gender'].astype(str))
udata['symptom1'] = encoder.fit transform(udata['symptom1'].astype(str))
udata['symptom2'] = encoder.fit transform(udata['symptom2'].astype(str))
udata['symptom3'] = encoder.fit transform(udata['symptom3'].astype(str))
udata['symptom4'] = encoder.fit_transform(udata['symptom4'].astype(str))
udata['symptom5'] = encoder.fit transform(udata['symptom5'].astype(str))
udata['symptom6'] = encoder.fit transform(udata['symptom6'].astype(str))
print(udata['from wuhan'].mode())
     dtype: int64
udata['sym on'] = pd.to datetime(udata['sym on'])
udata['hosp vis'] = pd.to datetime(udata['hosp vis'])
udata['sym on'] = udata['sym on'].map(dt.datetime.toordinal)
udata['hosp vis'] = udata['hosp vis'].map(dt.datetime.toordinal)
udata['diff sym hos']= udata['hosp vis'] - udata['sym on']
print(udata['from wuhan'].unique())
     [0 1]
print(udata.dtypes)
     location
                       int64
     country
                       int64
     gender
                       int64
                     float64
     age
                       int64
     sym on
                       int64
     hosp vis
     vis wuhan
                       int64
```

```
from_wuhan
                       int64
                       int64
     symptom1
                       int64
     symptom2
                       int64
     symptom3
                       int64
     symptom4
                       int64
     symptom5
     symptom6
                       int64
     diff sym hos
                       int64
     dtype: object
udata = udata[['location','country','gender','age','vis_wuhan','from_wuhan','symptom1','symptom2','symptom3','symptom4','symptom5','s
udata['result'] = classifier.predict(udata)
print(udata['result'])
     0
            0
     1
            0
     2
            1
     3
            0
            1
     858
            1
     859
            0
     860
            0
     861
            0
     862
     Name: result, Length: 863, dtype: int64
```

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