# Problem Statement: To Predict how likely individuals are to receive their H1N1 and Seasonal Flu Vaccines.

## Aim:

- To create and assess machine learning models that can precisely determine if individuals are likely to obtain the H1N1 and/or seasonal flu vaccines, utilizing demographic, behavioral, and health-related characteristics.

## Dataset Overview:

- training_set_features.csv

Rows: 26,707

Columns: 36

Contains demographic, behavioral, and health-related survey responses.

- test_set_features.csv

Rows: 26,708

Columns: 36

Same structure as training features, without the vaccination labels.

- training_set_labels.csv

Rows: 26,707

Columns: 3

Contains vaccination labels for H1N1 and seasonal flu.

- The dataset consists of survey responses gathered to comprehend the factors affecting the adoption of H1N1 and seasonal flu vaccinations. It contains three primary files: features for training, labels for training, and features for testing. The training dataset includes 26,707 entries and 36 attributes, encompassing a diverse array of demographic, behavioral, health-related, and attitudinal factors.

## Objective:

- Understand the dataset by performing exploratory data analysis (EDA) to identify patterns, distributions, and missing values.

- Handle missing data using appropriate imputation techniques, such as KNN imputation.

- Preprocess the data through encoding of categorical variables and normalization where required.

- Address class imbalance, particularly in the H1N1 vaccine target variable, using techniques like SMOTE.
- Build and compare multiple classification models, including:
- Logistic Regression
- Decision Tree
- Random Forest
- Gradient Boosting
- Support Vector Machine (SVM)
- Naive Bayes
- Evaluate model performance using appropriate metrics such as accuracy, precision, recall, F1-score, and AUC-ROC.
- Select the best-performing model for each vaccine type and interpret the results.
- Submit predictions to the competition platform (e.g., DrivenData) and analyze leaderboard performance.
- Draw conclusions and suggest recommendations based on findings, including public health insights or targeted outreach strategies.

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
```

In [2]:
```
import io
%cd "C:\Users\coolr\Dropbox\PC\Desktop\Project"
```

```
C:\Users\coolr\Dropbox\PC\Desktop\Project
```

In [3]:
```
vaccinetrain = pd.read_csv("training_set_features.csv")
vaccinetest = pd.read_csv("test_set_features.csv")
vaccinelabels = pd.read_csv("training_set_labels.csv")
```

In [4]:
```
print(vaccinetrain.shape)
print(vaccinetest.shape)
print(vaccinelabels.shape)
```

```
(26707, 36)
(26708, 36)
(26707, 3)
```

In [5]:
```
vaccinetrain.isnull().sum().sort_values(ascending=False)
```

```
Out[5]: employment_occupation          13470
        employment_industry            13330
        health_insurance               12274
        income_poverty                  4423
        doctor_recc_h1n1                2160
        doctor_recc_seasonal            2160
        rent_or_own                     2042
        employment_status               1463
        marital_status                  1408
        education                       1407
        chronic_med_condition            971
        child_under_6_months             820
        health_worker                    804
        opinion_seas_sick_from_vacc      537
        opinion_seas_risk                514
        opinion_seas_vacc_effective      462
        opinion_h1n1_sick_from_vacc      395
        opinion_h1n1_vacc_effective      391
        opinion_h1n1_risk                388
        household_children               249
        household_adults                 249
        behavioral_avoidance             208
        behavioral_touch_face            128
        h1n1_knowledge                   116
        h1n1_concern                      92
        behavioral_large_gatherings       87
        behavioral_outside_home           82
        behavioral_antiviral_meds         71
        behavioral_wash_hands             42
        behavioral_face_mask              19
        hhs_geo_region                     0
        census_msa                         0
        sex                                0
        race                               0
        age_group                          0
        respondent_id                      0
        dtype: int64
```

```
In [6]: vaccinetest.isnull().sum().sort_values(ascending=False)
```

Out[6]:
```
employment_occupation          13426
employment_industry            13275
health_insurance               12228
income_poverty                  4497
doctor_recc_h1n1                2160
doctor_recc_seasonal            2160
rent_or_own                     2036
employment_status               1471
marital_status                  1442
education                       1407
chronic_med_condition            932
child_under_6_months             813
health_worker                    789
opinion_seas_sick_from_vacc      521
opinion_seas_risk                499
opinion_seas_vacc_effective      452
opinion_h1n1_vacc_effective      398
opinion_h1n1_risk                380
opinion_h1n1_sick_from_vacc      375
household_children               225
household_adults                 225
behavioral_avoidance             213
behavioral_touch_face            128
h1n1_knowledge                   122
h1n1_concern                      85
behavioral_outside_home           82
behavioral_antiviral_meds         79
behavioral_large_gatherings       72
behavioral_wash_hands             40
behavioral_face_mask              19
hhs_geo_region                     0
census_msa                         0
sex                                0
race                               0
age_group                          0
respondent_id                      0
dtype: int64
```

## Columns:

In [7]:
```
vaccinetrain.columns

# To know the column names in the dataset
```

Out[7]:
```
Index(['respondent_id', 'h1n1_concern', 'h1n1_knowledge',
       'behavioral_antiviral_meds', 'behavioral_avoidance',
       'behavioral_face_mask', 'behavioral_wash_hands',
       'behavioral_large_gatherings', 'behavioral_outside_home',
       'behavioral_touch_face', 'doctor_recc_h1n1', 'doctor_recc_seasonal',
       'chronic_med_condition', 'child_under_6_months', 'health_worker',
       'health_insurance', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk',
       'opinion_h1n1_sick_from_vacc', 'opinion_seas_vacc_effective',
       'opinion_seas_risk', 'opinion_seas_sick_from_vacc', 'age_group',
       'education', 'race', 'sex', 'income_poverty', 'marital_status',
       'rent_or_own', 'employment_status', 'hhs_geo_region', 'census_msa',
       'household_adults', 'household_children', 'employment_industry',
       'employment_occupation'],
      dtype='object')
```

In [8]:
```
vaccinetest.columns

# To know the column names in the dataset
```

Out[8]:
```
Index(['respondent_id', 'h1n1_concern', 'h1n1_knowledge',
       'behavioral_antiviral_meds', 'behavioral_avoidance',
       'behavioral_face_mask', 'behavioral_wash_hands',
       'behavioral_large_gatherings', 'behavioral_outside_home',
       'behavioral_touch_face', 'doctor_recc_h1n1', 'doctor_recc_seasonal',
       'chronic_med_condition', 'child_under_6_months', 'health_worker',
       'health_insurance', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk',
       'opinion_h1n1_sick_from_vacc', 'opinion_seas_vacc_effective',
       'opinion_seas_risk', 'opinion_seas_sick_from_vacc', 'age_group',
       'education', 'race', 'sex', 'income_poverty', 'marital_status',
       'rent_or_own', 'employment_status', 'hhs_geo_region', 'census_msa',
       'household_adults', 'household_children', 'employment_industry',
       'employment_occupation'],
      dtype='object')
```

In [9]:
```
vaccinelabels.columns

# To know the column names in the dataset
```

Out[9]:
```
Index(['respondent_id', 'h1n1_vaccine', 'seasonal_vaccine'], dtype='object')
```

In [10]:
```
# Since there are missing values in both Train and Test Set Im combining both the D
combinedf = pd.concat([vaccinetrain,vaccinetest],axis=0) # Row Concatenation
```

In [11]:
```
# info() method shows some of the characteristics of the data such as Column Name,
#Dtype of the data, and Memory Usage.
combinedf.info()
# Many Variables have Null Values
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 53415 entries, 0 to 26707
Data columns (total 36 columns):
 #   Column                       Non-Null Count  Dtype  
---  ------                       --------------  -----  
 0   respondent_id                53415 non-null  int64  
 1   h1n1_concern                 53238 non-null  float64
 2   h1n1_knowledge               53177 non-null  float64
 3   behavioral_antiviral_meds    53265 non-null  float64
 4   behavioral_avoidance         52994 non-null  float64
 5   behavioral_face_mask         53377 non-null  float64
 6   behavioral_wash_hands        53333 non-null  float64
 7   behavioral_large_gatherings  53256 non-null  float64
 8   behavioral_outside_home      53251 non-null  float64
 9   behavioral_touch_face        53159 non-null  float64
 10  doctor_recc_h1n1             49095 non-null  float64
 11  doctor_recc_seasonal         49095 non-null  float64
 12  chronic_med_condition        51512 non-null  float64
 13  child_under_6_months         51782 non-null  float64
 14  health_worker                51822 non-null  float64
 15  health_insurance             28913 non-null  float64
 16  opinion_h1n1_vacc_effective  52626 non-null  float64
 17  opinion_h1n1_risk            52647 non-null  float64
 18  opinion_h1n1_sick_from_vacc  52645 non-null  float64
 19  opinion_seas_vacc_effective  52501 non-null  float64
 20  opinion_seas_risk            52402 non-null  float64
 21  opinion_seas_sick_from_vacc  52357 non-null  float64
 22  age_group                    53415 non-null  object 
 23  education                    50601 non-null  object 
 24  race                         53415 non-null  object 
 25  sex                          53415 non-null  object 
 26  income_poverty               44495 non-null  object 
 27  marital_status               50565 non-null  object 
 28  rent_or_own                  49337 non-null  object 
 29  employment_status            50481 non-null  object 
 30  hhs_geo_region               53415 non-null  object 
 31  census_msa                   53415 non-null  object 
 32  household_adults             52941 non-null  float64
 33  household_children           52941 non-null  float64
 34  employment_industry          26810 non-null  object 
 35  employment_occupation        26519 non-null  object 
dtypes: float64(23), int64(1), object(12)
memory usage: 15.1+ MB
```

## Missing Value Imputation: Strategy (KNN Imputer)

- KNN is a non parametric algorithm that uses distance like Euclidean to calculate distance between missing value and closest 5 neighbors(rows) and smallest distance value is imputed.
- Before applying KNN imputer labelencoding of data must be done

In [12]:
```
from sklearn.preprocessing import LabelEncoder
```

```
C:\Users\coolr\anaconda3\lib\site-packages\scipy\__init__.py:155: UserWarning: A N
umPy version >=1.18.5 and <1.26.0 is required for this version of SciPy (detected 
version 1.26.4
  warnings.warn(f"A NumPy version >={np_minversion} and <{np_maxversion}"
```

In [13]:
```
stringcols=combinedf.drop(['respondent_id'],axis=1)
```

In [14]:
```
stringcols=stringcols.astype(str).apply(lambda series:pd.Series(
LabelEncoder().fit_transform(series[series.notnull()]),index = series[series.notnul
```

In [15]:
```
from sklearn.impute import KNNImputer
```

In [16]:
```
imputer = KNNImputer()
```

In [17]:
```
stringcolsimp = imputer.fit_transform(stringcols)
```

In [18]:
```
stringcolsimp = pd.DataFrame(stringcolsimp,columns=stringcols.columns)
```

In [19]:
```
stringcolsimp.head()
```

Out[19]:

| | h1n1_concern | h1n1_knowledge | behavioral_antiviral_meds | behavioral_avoidance | behavioral_fac |
|---|---|---|---|---|---|
| **0** | 1.0 | 0.0 | 0.0 | 0.0 | |
| **1** | 3.0 | 2.0 | 0.0 | 1.0 | |
| **2** | 1.0 | 1.0 | 0.0 | 1.0 | |
| **3** | 1.0 | 1.0 | 0.0 | 1.0 | |
| **4** | 2.0 | 1.0 | 0.0 | 1.0 | |

5 rows × 35 columns

## Splitting back the data to Train data and Test data

In [20]:
```
vaccinetraindf = stringcolsimp.loc[0:26706]
```

In [21]:
```
vaccinetestdf = stringcolsimp.loc[26708:53415]
```

In [22]:
```
vaccinetraindf.shape
```

Out[22]:
```
(26707, 35)
```

In [23]:
```
vaccinetestdf.shape
```

Out[23]:
```
(26707, 35)
```

## Hypothesis Testing:

## a.) Seasonal Vaccine

In [24]:
```
from scipy.stats import chi2_contingency
```

In [25]:
```
# Null Hypothesis : There is Significance between seasonalvaccine and sex
pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.sex)
```

Out[25]:

| sex | 0.0 | 1.0 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 7970 | 6302 |
| **1** | 7888 | 4547 |

In [26]:
```
chi2_contingency(pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.sex))
# Since p value < 0.05 reject null
```

Out[26]:
```
(158.40462897107128,
 2.5248076319253385e-36,
 1,
 array([[8474.38409406, 5797.61590594],
        [7383.61590594, 5051.38409406]]))
```

In [27]:
```
# Null Hypothesis : There is Significance between seasonalvaccine and income_povert
pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.income_poverty)
```

Out[27]:

| income_poverty | 0.0 | 1.0 | 2.0 | 3.0 |
|---|---|---|---|---|
| **seasonal_vaccine** | | | | |
| **0** | 6686 | 3427 | 1719 | 2440 |
| **1** | 6091 | 3383 | 978 | 1983 |

In [28]:
```
chi2_contingency(pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.income_p
# Since p value < 0.05 reject null
```

Out[28]:
```
(153.17012658009583,
 5.455880245363045e-33,
 3,
 array([[6827.92316621, 3639.20769836, 1441.25450256, 2363.61463287],
        [5949.07683379, 3170.79230164, 1255.74549744, 2059.38536713]]))
```

In [29]:
```
# Null Hypothesis : There is Significance between seasonalvaccine and education
pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.education)
```

Out[29]:

| education | 0.0 | 1.0 | 2.0 | 3.0 | 4.0 |
|---|---|---|---|---|---|
| **seasonal_vaccine** | | | | | |
| **0** | 3199 | 1415 | 4933 | 3860 | 865 |
| **1** | 2598 | 948 | 5164 | 3183 | 542 |

In [30]:
```
chi2_contingency(pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.educatic
# Since p value < 0.05 reject null
```

Out[30]:
```
(173.57815735793127,
 1.7841137139002192e-36,
 4,
 array([[3097.86887333, 1262.76766391, 5395.7533231 , 3763.72097203,
          751.88916763],
        [2699.13112667, 1100.23233609, 4701.2466769 , 3279.27902797,
          655.11083237]]))
```

In [31]:
```
# Null Hypothesis : There is Significance between seasonalvaccine and doctor_recc_s
pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.doctor_recc_seasonal)
```

Out[31]:

| doctor_recc_seasonal | 0.0 | 1.0 | 2.0 |
|---|---|---|---|
| **seasonal_vaccine** | | | |
| **0** | 10756 | 2117 | 1399 |
| **1** | 5697 | 5977 | 761 |

In [32]:
```
chi2_contingency(pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.doctor_r
# Since p value < 0.05 reject null
```

Out[32]:
```
(3474.902794649153,
 0.0,
 2,
 array([[8792.3471749 , 4325.36668289, 1154.28614221],
        [7660.6528251 , 3768.63331711, 1005.71385779]]))
```

In [33]:
```
# Null Hypothesis : There is Significance between seasonalvaccine and behavioral_fa
pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.behavioral_face_mask)
```

Out[33]:

| behavioral_face_mask | 0.0 | 1.0 | 2.0 |
|---|---|---|---|
| **seasonal_vaccine** | | | |
| **0** | 13449 | 815 | 8 |
| **1** | 11398 | 1026 | 11 |

In [34]:
```
chi2_contingency(pd.crosstab(vaccinelabels.seasonal_vaccine,vaccinetraindf.behavior
# Since p value < 0.05 reject null
```

Out[34]:
```
(67.92302367431634,
 1.7811595018273916e-15,
 2,
 array([[1.32780314e+04, 9.83815180e+02, 1.01534429e+01],
        [1.15689686e+04, 8.57184820e+02, 8.84655708e+00]]))
```

## b.) H1N1_ Vaccine

In [35]:
```
# Null Hypothesis : There is no significance between h1n1vaccine and sex
pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.sex)
```

Out[35]:

| sex | 0.0 | 1.0 |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 12378 | 8655 |
| **1** | 3480 | 2194 |

In [36]:
```
chi2_contingency(pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.sex))
# Since p value < 0.05 reject null
```

Out[36]:
```
(11.309981152455997,
 0.0007709155489949327,
 1,
 array([[12488.90979893,  8544.09020107],
        [ 3369.09020107,  2304.90979893]]))
```

In [37]:
```
# Null Hypothesis : There is no significance between seasonalvaccine and income_pov
pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.income_poverty)
```

Out[37]:

| income_poverty | 0.0 | 1.0 | 2.0 | 3.0 |
|---|---|---|---|---|
| h1n1_vaccine | | | | |
| 0 | 10178 | 5087 | 2181 | 3587 |
| 1 | 2599 | 1723 | 516 | 836 |

In [38]:

```
chi2_contingency(pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.income_pover
# Since p value < 0.05 reject null
```

Out[38]:

```
(94.91226392182662,
 1.9282818704757377e-20,
 3,
 array([[10062.4795372 ,  5363.19054929,  2124.01246864,  3483.31744486],
        [ 2714.5204628 ,  1446.80945071,   572.98753136,   939.68255514]]))
```

In [39]:

```
# Null Hypothesis : There is no significance between h1n1_vaccine and education
pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.education)
```

Out[39]:

| education | 0.0 | 1.0 | 2.0 | 3.0 | 4.0 |
|---|---|---|---|---|---|
| h1n1_vaccine | | | | | |
| 0 | 4726 | 1968 | 7614 | 5579 | 1146 |
| 1 | 1071 | 395 | 2483 | 1464 | 261 |

In [40]:

```
chi2_contingency(pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.education))
# Since p value < 0.05 reject null
```

Out[40]:

```
(130.12342530584624,
 3.66443514946588e-27,
 4,
 array([[4565.40611076, 1860.97199236, 7951.85535627, 5546.68884562,
         1108.07769499],
        [1231.59388924,  502.02800764, 2145.14464373, 1496.31115438,
          298.92230501]]))
```

In [41]:

```
# Null Hypothesis : There is no significance between h1n1_vaccine and doctor_recc_s
pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.doctor_recc_seasonal)
```

Out[41]:

| doctor_recc_seasonal | 0.0 | 1.0 | 2.0 |
|---|---|---|---|
| h1n1_vaccine | | | |
| 0 | 13783 | 5275 | 1975 |
| 1 | 2670 | 2819 | 185 |

In [42]:

```
chi2_contingency(pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.doctor_recc_
# Since p value < 0.05 reject null
```

Out[42]:

```
(1347.6234370031846,
 2.329639991754564e-293,
 2,
 array([[12957.49986895,  6374.40004493,  1701.10008612],
        [ 3495.50013105,  1719.59995507,   458.89991388]]))
```

In [43]:

```
# Null Hypothesis : There is no significance between h1n1_vaccine and behavioral_fa
pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.behavioral_face_mask)
```

Out[43]:

| behavioral_face_mask | 0.0 | 1.0 | 2.0 |
|---|---|---|---|
| **h1n1_vaccine** | | | |
| **0** | 19765 | 1255 | 13 |
| **1** | 5082 | 586 | 6 |

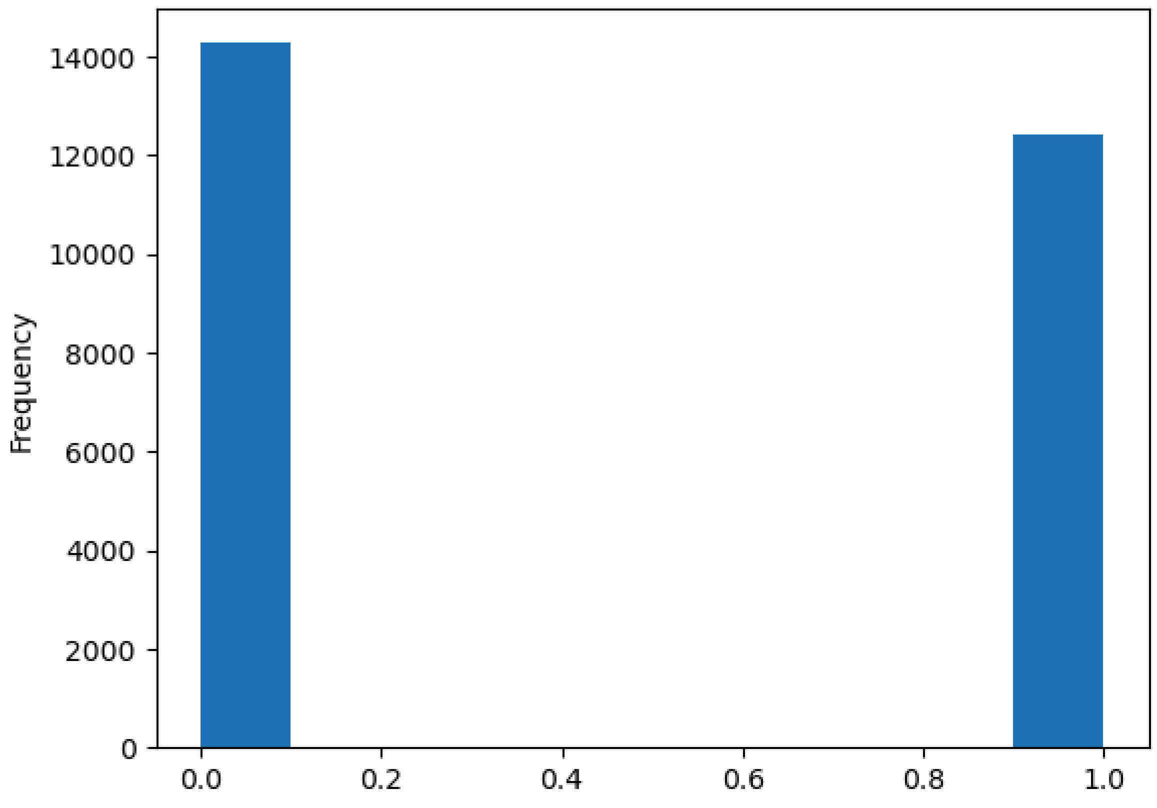
In [44]:
```
chi2_contingency(pd.crosstab(vaccinelabels.h1n1_vaccine,vaccinetraindf.behavioral_f
# Since p value < 0.05 reject null
```

Out[44]:
```
(133.81661811498145,
 8.751662937660443e-30,
 2,
 array([[1.95681638e+04, 1.44987280e+03, 1.49633804e+01],
        [5.27883619e+03, 3.91127195e+02, 4.03661961e+00]]))
```

In [45]:
```
y1  = vaccinelabels.h1n1_vaccine
y   = vaccinelabels.seasonal_vaccine
X   = vaccinetraindf
```

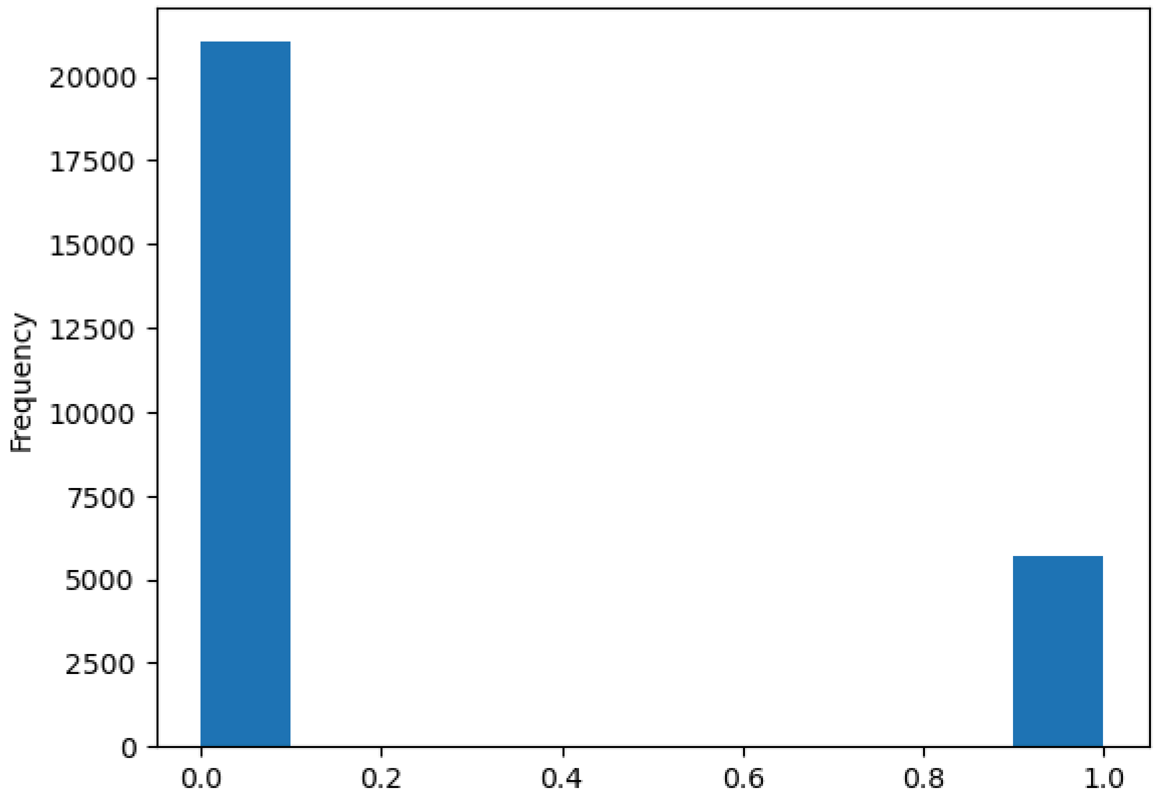
In [46]:
```
vaccinelabels.seasonal_vaccine.plot(kind='hist')
# Balanced Data
```

Out[46]:
```
<AxesSubplot: ylabel='Frequency'>
```



In [47]:
```
vaccinelabels.h1n1_vaccine.plot(kind='hist')
# Imbalance Data
```

Out[47]:
```
<AxesSubplot: ylabel='Frequency'>
```



# Methods

## Model Building and Idealogy :

- As there are two binary variables to target, Let's create a classification model for each variable separately.
- The variable seasonal vaccine is balanced, whereas the h1n1 vaccine variable is not.
- Let's use SMOTE to balance the h1n1 vaccine variable.

In [48]:
```
from sklearn.metrics import classification_report
from sklearn.model_selection import cross_val_score
from sklearn.metrics import plot_roc_curve
```

### Logistic Regression for Seasonal Vaccine

In [49]:
```
from sklearn.linear_model import LogisticRegression
```

In [50]:
```
logit = LogisticRegression(max_iter=300)
```

In [51]:
```
logitmodel= logit.fit(X,y)
```

In [52]:
```
logitmodel.score(X,y)
```

Out[52]:
```
0.7610738757629086
```

In [53]:
```
cross_val_score(logitmodel,X,y)
```

Out[53]:
```
array([0.75739423, 0.75870461, 0.76427635, 0.76652312, 0.75360419])
```

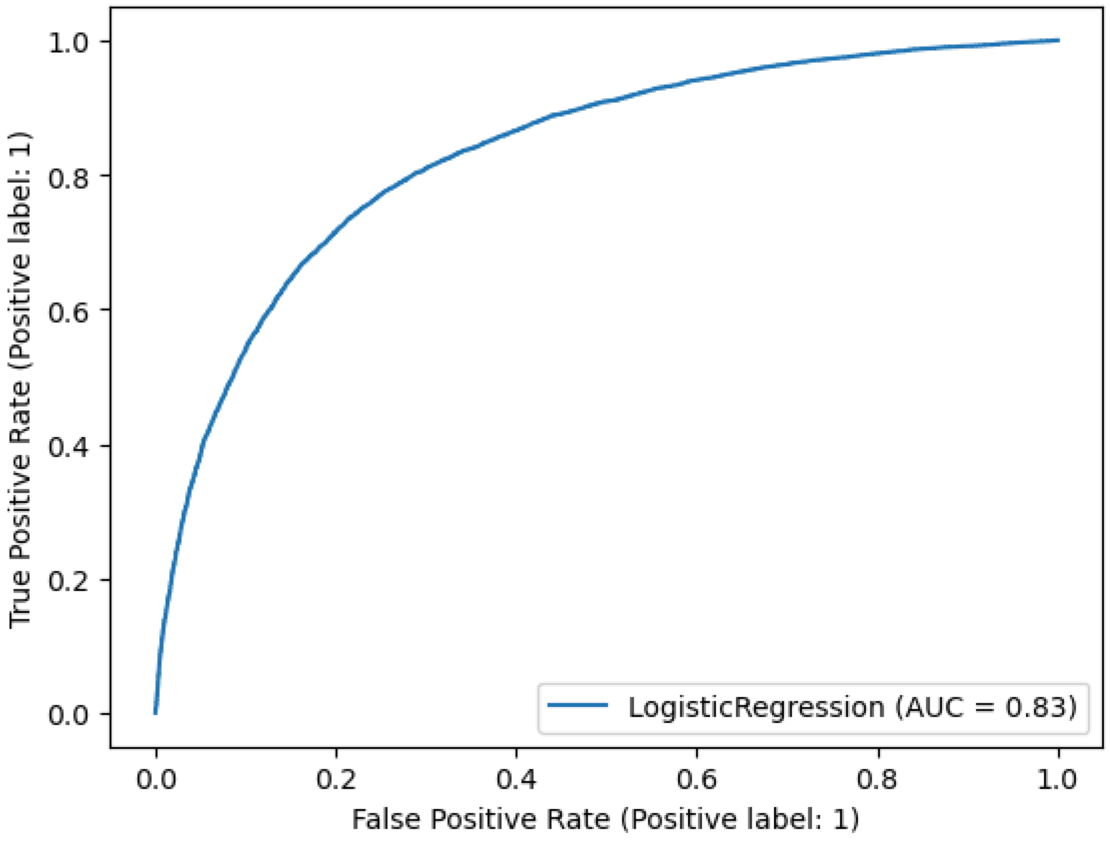
In [54]:
```
np.mean([0.75739423, 0.759079  , 0.76427635, 0.76671035, 0.75360419])
```
Out[54]:
```
0.760212824
```
In [55]:
```
logitpredict = logitmodel.predict(X)
```
In [56]:
```
logitpredict_test = logitmodel.predict_proba(vaccinetestdf)
```
In [57]:
```
pd.DataFrame(logitpredict_test).to_csv("seaslog.csv")
```
In [58]:
```
print(classification_report(y,logitpredict))
```
```
              precision    recall  f1-score   support

           0       0.77      0.79      0.78     14272
           1       0.75      0.73      0.74     12435

    accuracy                           0.76     26707
   macro avg       0.76      0.76      0.76     26707
weighted avg       0.76      0.76      0.76     26707
```
In [59]:
```
pd.crosstab(y,logitpredict)
```
Out[59]:

| col_0 | 0 | 1 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 11277 | 2995 |
| **1** | 3386 | 9049 |

In [60]:
```
plot_roc_curve(logitmodel,X,y)
```
```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```
Out[60]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19883229820>
```



## Decision Tree Classification for Seasonal Vaccine

```
In [61]: from sklearn.tree import DecisionTreeClassifier

In [62]: tree = DecisionTreeClassifier(max_depth=16)

In [63]: treemodel = tree.fit(X,y)

In [64]: treemodel.score(X,y)

Out[64]: 0.9402029430486389

In [65]: cross_val_score(treemodel,X,y)

Out[65]: array([0.69842756, 0.70254586, 0.70717094, 0.71241341, 0.69930725])

In [66]: np.mean([0.6963684 , 0.70647697, 0.70642202, 0.71241341, 0.69668601])

Out[66]: 0.7036733620000001

In [67]: treepredict = treemodel.predict(X)

In [68]: treepredict_test = treemodel.predict(vaccinetestdf)

In [69]: pd.DataFrame(treepredict_test).to_csv("seastree.csv")

In [70]: print(classification_report(y,treepredict))
```

```
              precision    recall  f1-score   support

           0       0.94      0.95      0.94     14272
           1       0.94      0.93      0.94     12435

    accuracy                           0.94     26707
   macro avg       0.94      0.94      0.94     26707
weighted avg       0.94      0.94      0.94     26707
```

In [71]:
```
pd.crosstab(y,treepredict)
```

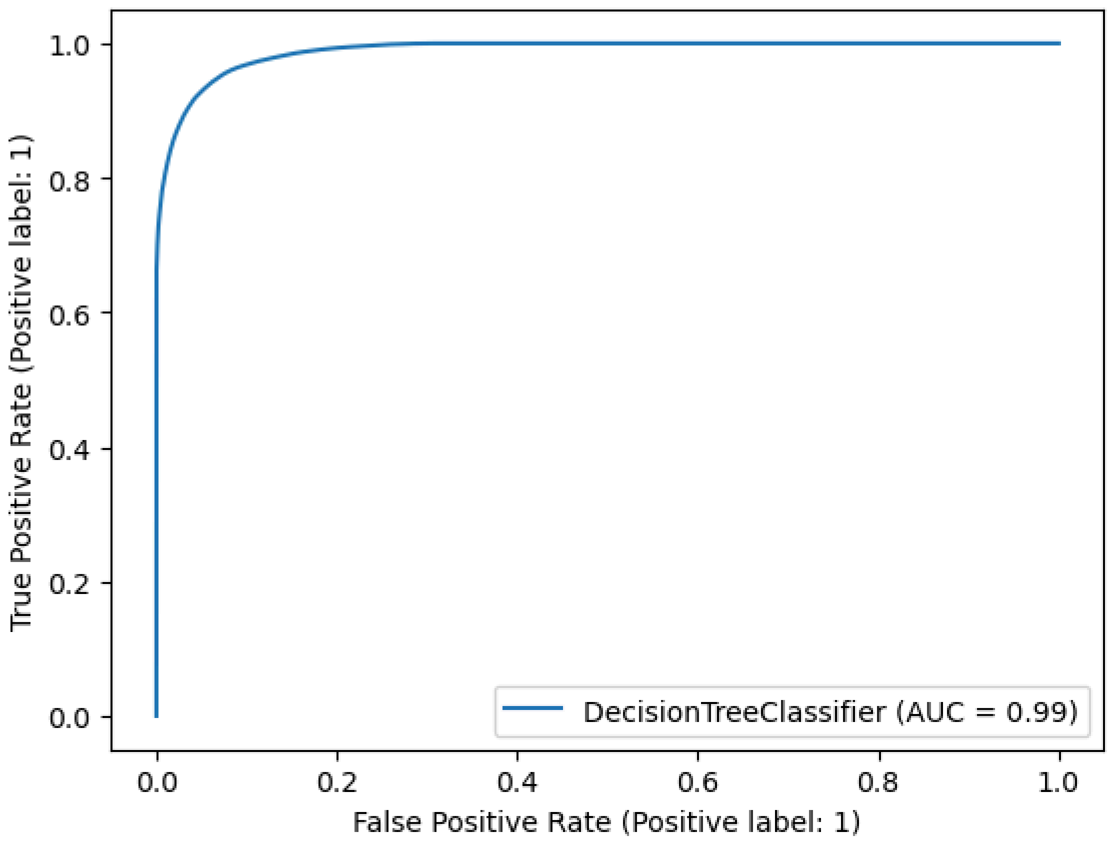
Out[71]:

| col_0 | 0 | 1 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 13508 | 764 |
| **1** | 833 | 11602 |

In [72]:
```
plot_roc_curve(treemodel,X,y)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[72]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x198833c7eb0>
```



## Random Forest Classification for Seasonal Vaccine

In [73]:
```
from sklearn.ensemble import RandomForestClassifier
```

```
In [74]: RF = RandomForestClassifier(n_estimators=3)
```

```
In [75]: RFmodel = RF.fit(X,y)
```

```
In [76]: RFmodel.score(X,y)
```

```
Out[76]: 0.9460441082862171
```

```
In [77]: cross_val_score(RFmodel,X,y)
```

```
Out[77]: array([0.71602396, 0.71246724, 0.72477064, 0.71934095, 0.70941771])
```

```
In [78]: np.mean([0.70497941, 0.70778735, 0.71316233, 0.72477064, 0.71035387])
```

```
Out[78]: 0.7122107200000001
```

```
In [79]: RFpredict = RFmodel.predict(X)
```

```
In [80]: RFpredict_test = RFmodel.predict_proba(vaccinetestdf)
```

```
In [81]: pd.DataFrame(RFpredict_test).to_csv('RFseas.csv')
```

```
In [82]: print(classification_report(y,RFpredict))
```

```
              precision    recall  f1-score   support

           0       0.95      0.95      0.95     14272
           1       0.94      0.94      0.94     12435

    accuracy                           0.95     26707
   macro avg       0.95      0.95      0.95     26707
weighted avg       0.95      0.95      0.95     26707
```

```
In [83]: pd.crosstab(y,RFpredict)
```

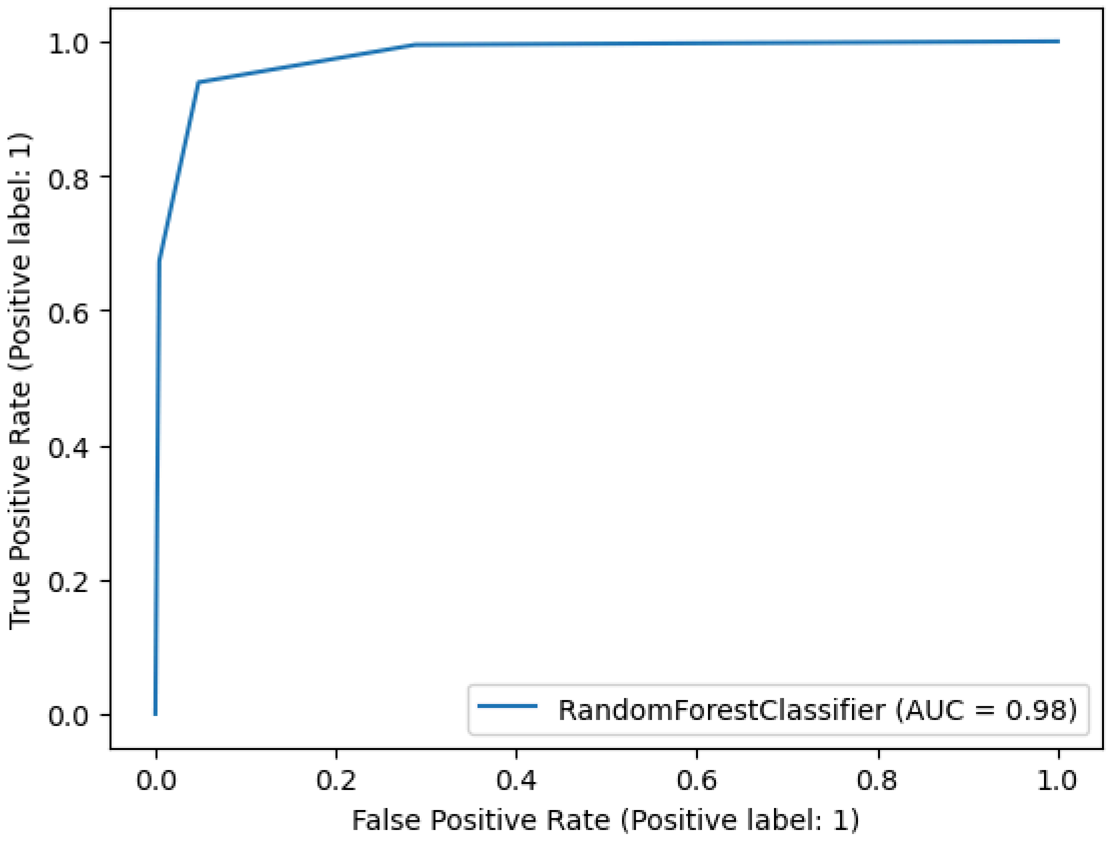
Out[83]:

| col_0 | 0 | 1 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 13589 | 683 |
| **1** | 758 | 11677 |

```
In [84]: plot_roc_curve(RFmodel,X,y)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

```
Out[84]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x198fda4dd60>
```



## Gradient Boosting Classification for Seasonal Vaccine

```
In [85]: from sklearn.ensemble import GradientBoostingClassifier
```

```
In [86]: gbm= GradientBoostingClassifier(n_estimators=4000)
```

```
In [87]: gbmmodel = gbm.fit(X,y)
```

```
In [88]: gbmmodel.score(X,y)

Out[88]: 0.8566667914778897
```

```
In [89]: cross_val_score(gbmmodel,X,y)

Out[89]: array([0.77031075, 0.77162112, 0.77588467, 0.78168882, 0.77813144])
```

```
In [90]: np.mean([0.77405466, 0.77461625, 0.77925482, 0.78674406, 0.78468452])

Out[90]: 0.7798708619999999
```

```
In [91]: gbmpredict = gbmmodel.predict(X)
```

```
In [92]: gbmpredict_test = gbmmodel.predict_proba(vaccinetestdf)
```

```
In [93]: pd.DataFrame(gbmpredict_test).to_csv('gbmseas.csv')
```

```
In [94]: print(classification_report(y,gbmpredict))
```

```
              precision    recall  f1-score   support

           0       0.86      0.87      0.87     14272
           1       0.85      0.84      0.84     12435

    accuracy                           0.86     26707
   macro avg       0.86      0.86      0.86     26707
weighted avg       0.86      0.86      0.86     26707
```

In [95]:
```
pd.crosstab(y,gbmpredict)
```

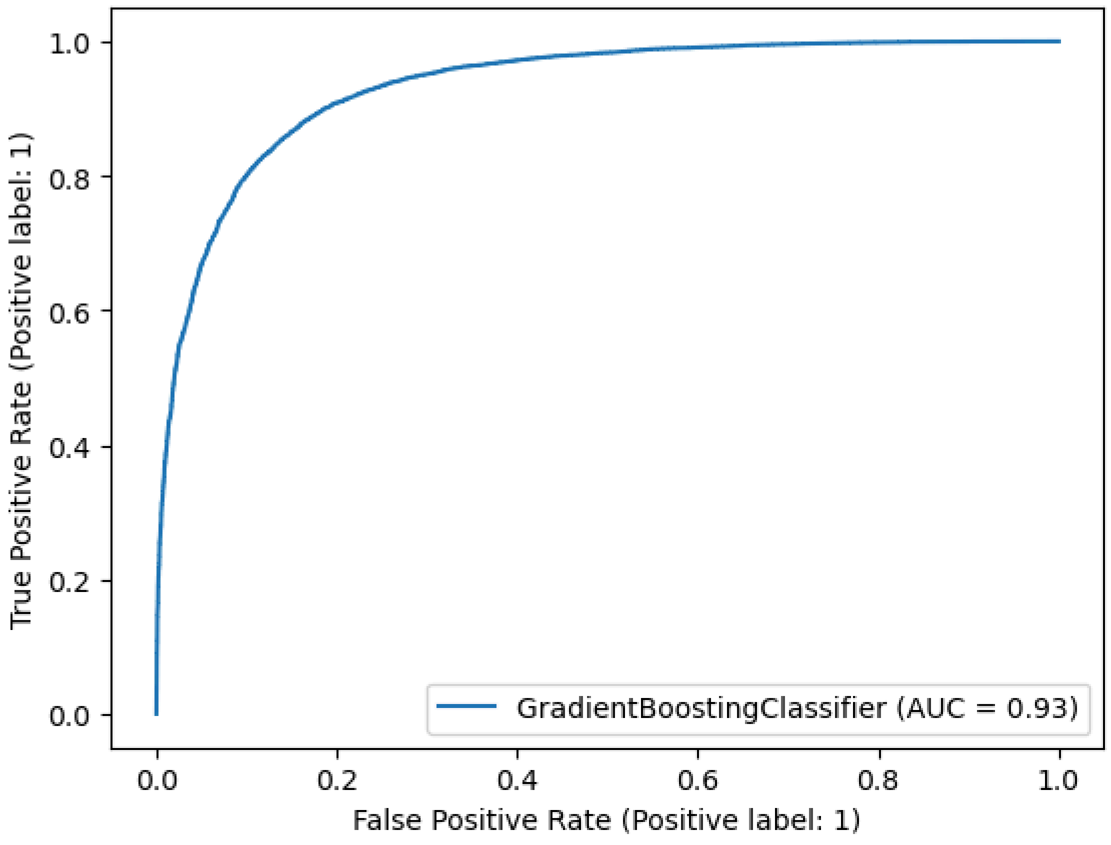
Out[95]:

| col_0 | 0 | 1 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 12460 | 1812 |
| **1** | 2016 | 10419 |

In [96]:
```
plot_roc_curve(gbmmodel,X,y)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[96]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x198eb60c160>
```



## Support Vector Machine Classification for Seasonal Vaccine

In [97]:
```
from sklearn.svm import SVC
```

```
In [98]:  svm = SVC()
```

```
In [99]:  svmmodel = svm.fit(X,y)
```

```
In [100…  svmmodel.score(X,y)

Out[100]: 0.7783352679072902
```

```
In [101…  cross_val_score(svmmodel,X,y)

Out[101]: array([0.76843879, 0.76506926, 0.77682082, 0.77625913, 0.77195282])
```

```
In [102…  np.mean([0.76843879, 0.76506926, 0.77682082, 0.77625913, 0.77195282])

Out[102]: 0.7717081640000001
```

```
In [103…  svmpredict_test = svmmodel.predict(X)
```

```
In [104…  pd.DataFrame(svmpredict_test).to_csv('svmseas.csv')
```

```
In [105…  print(classification_report(y,svmpredict_test))

              precision    recall  f1-score   support

           0       0.78      0.81      0.80     14272
           1       0.77      0.74      0.76     12435

    accuracy                           0.78     26707
   macro avg       0.78      0.78      0.78     26707
weighted avg       0.78      0.78      0.78     26707
```

```
In [106…  pd.crosstab(y,svmpredict_test)
```

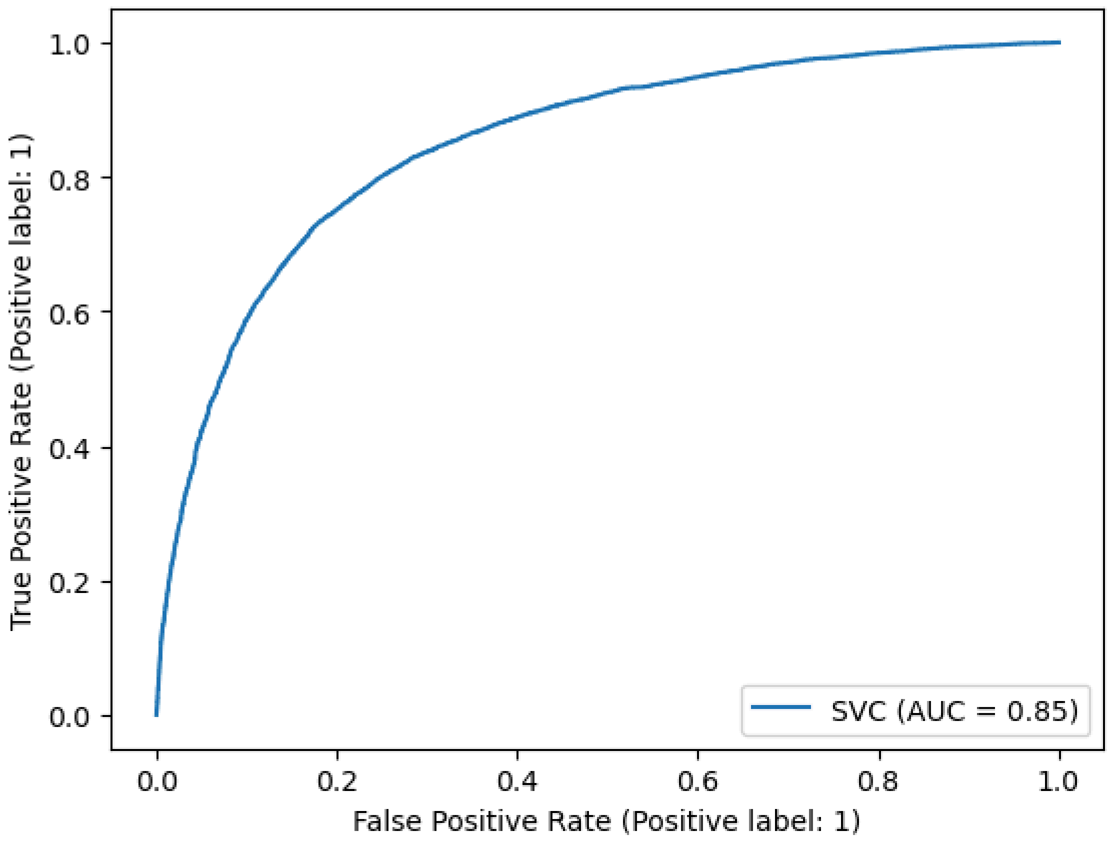
Out[106]:

| col_0 | 0 | 1 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 11580 | 2692 |
| **1** | 3228 | 9207 |

```
In [107…  plot_roc_curve(svmmodel,X,y)

C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)

Out[107]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19885d5ca30>
```



## Navie Bayes Classification for Seasonal Vaccine

In [108…
```
from sklearn.naive_bayes import BernoulliNB
```

In [109…
```
nb = BernoulliNB()
```

In [110…
```
nbmodel = nb.fit(X,y)
```

In [111…
```
nbmodel.score(X,y)
```

Out[111]:
```
0.6936383719624069
```

In [112…
```
cross_val_score(nbmodel,X,y)
```

Out[112]:
```
array([0.68045676, 0.70423063, 0.69106909, 0.69855832, 0.68938401])
```

In [113…
```
np.mean([0.68045676, 0.70423063, 0.69106909, 0.69855832, 0.68938401])
```

Out[113]:
```
0.692739762
```

In [114…
```
nbpredict = nbmodel.predict(X)
```

In [115…
```
nbpredict_test = nbmodel.predict_proba(vaccinetestdf)
```

In [116…
```
pd.DataFrame(nbpredict_test).to_csv('nbseas.csv')
```

In [117…
```
print(classification_report(y,nbpredict))
```

```
              precision    recall  f1-score   support

           0       0.72      0.69      0.71     14272
           1       0.66      0.70      0.68     12435

    accuracy                           0.69     26707
   macro avg       0.69      0.69      0.69     26707
weighted avg       0.69      0.69      0.69     26707
```

In [118…
```
pd.crosstab(y,nbpredict)
```

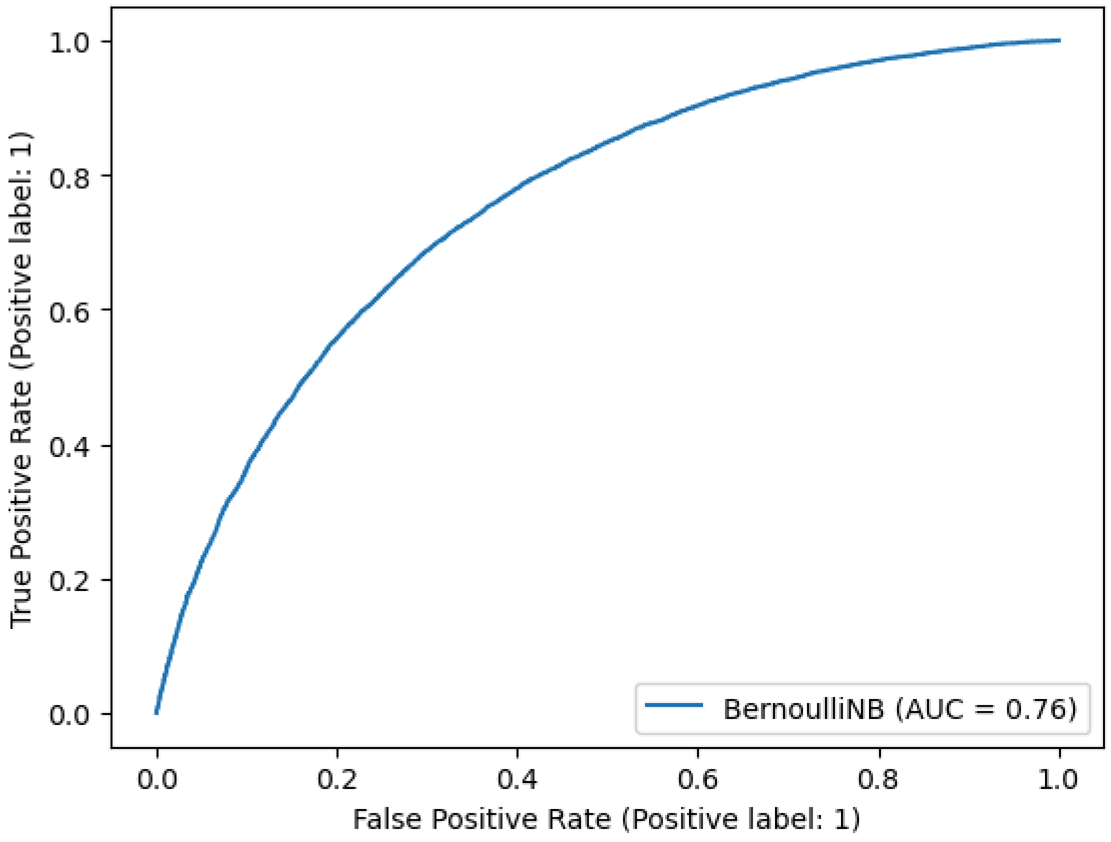
Out[118]:

| col_0 | 0 | 1 |
|---|---|---|
| **seasonal_vaccine** | | |
| **0** | 9878 | 4394 |
| **1** | 3788 | 8647 |

In [119…
```
plot_roc_curve(nbmodel,X,y)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[119]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19885e78a90>
```



## Balancing the Imbalance data using Smote

In [120…
```
from imblearn.over_sampling import SMOTE
```

In [121…
```
smote = SMOTE(random_state=60)
```

In [122…
```
X_smote,y_smote = smote.fit_resample(X,y1)
```

In [123…
```
print(pd.DataFrame(y1).value_counts())
print(pd.DataFrame(y_smote).value_counts())
```

```
h1n1_vaccine
0               21033
1                5674
dtype: int64
h1n1_vaccine
0               21033
1               21033
dtype: int64
```

## Logistic Regression for H1N1 Vaccine

In [124…
```
print(X_smote.shape)
print(y_smote.shape)
```

```
(42066, 35)
(42066,)
```

In [125…
```
logit2 = LogisticRegression(max_iter=400)
```

In [126…
```
logitmodel_smote = logit2.fit(X_smote,y_smote)
```

In [127…
```
logitmodel_smote.score(X_smote,y_smote)
```

Out[127]:
```
0.762943945228926
```

In [128…
```
cross_val_score(logitmodel_smote,X_smote,y_smote)
```

Out[128]:
```
array([0.75112907, 0.75680494, 0.76726495, 0.77011768, 0.76667063])
```

In [129…
```
np.mean([0.75124792, 0.75692381, 0.76714608, 0.77011768, 0.76678949])
```

Out[129]:
```
0.7624449959999999
```

In [130…
```
logitsmote_predict = logitmodel_smote.predict(X_smote)
```

In [131…
```
logitsmote_predict_test = logitmodel_smote.predict_proba(vaccinetestdf)
```

In [132…
```
pd.DataFrame(logitsmote_predict_test).to_csv('h1n1log.csv')
```

In [133…
```
print(classification_report(y_smote,logitsmote_predict))
```

```
              precision    recall  f1-score   support

           0       0.76      0.76      0.76     21033
           1       0.76      0.77      0.76     21033

    accuracy                           0.76     42066
   macro avg       0.76      0.76      0.76     42066
weighted avg       0.76      0.76      0.76     42066
```

In [134…

```
pd.crosstab(y_smote,logitsmote_predict)
```

Out[134]:

| col_0 | 0 | 1 |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 15990 | 5043 |
| **1** | 4929 | 16104 |

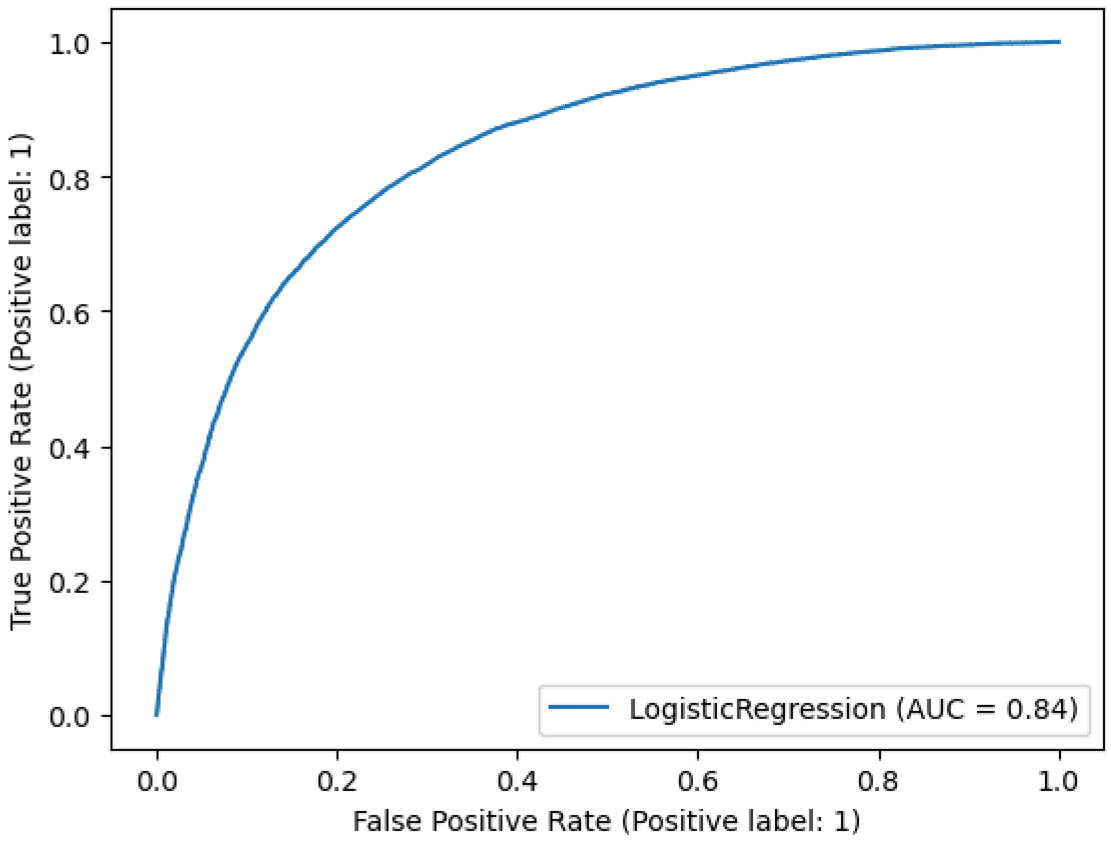
In [135…

```
plot_roc_curve(logitmodel_smote,X_smote,y_smote)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[135]:

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19885c69e80>
```



## Decision Tree Classification for H1N1 Vaccine :

In [136…

```
treesmote = DecisionTreeClassifier(max_depth=11)
```

In [137…

```
treemodel_smote = treesmote.fit(X_smote,y_smote)
```

In [138…

```
treemodel_smote.score(X_smote,y_smote)
```

Out[138]:

```
0.9075262682451386
```

In [139…

```
cross_val_score(treemodel_smote,X_smote,y_smote)
```

```
Out[139]: array([0.69562634, 0.85379769, 0.93022703, 0.93640794, 0.93153453])
```

```
In [140… np.mean([0.69550749, 0.85391656, 0.93010817, 0.9365268 , 0.93212885])
```

```
Out[140]: 0.8696375740000001
```

```
In [141… treepredict_smote = treemodel_smote.predict(X_smote)
```

```
In [142… treepredict_smote_test =treemodel_smote.predict_proba(vaccinetestdf)
```

```
In [143… pd.DataFrame(treepredict_smote_test).to_csv('h1n1tree.csv')
```

```
In [144… print(classification_report(y_smote,treepredict_smote))
```

```
              precision    recall  f1-score   support

           0       0.88      0.95      0.91     21033
           1       0.94      0.87      0.90     21033

    accuracy                           0.91     42066
   macro avg       0.91      0.91      0.91     42066
weighted avg       0.91      0.91      0.91     42066
```

```
In [145… pd.crosstab(y_smote,treepredict_smote)
```

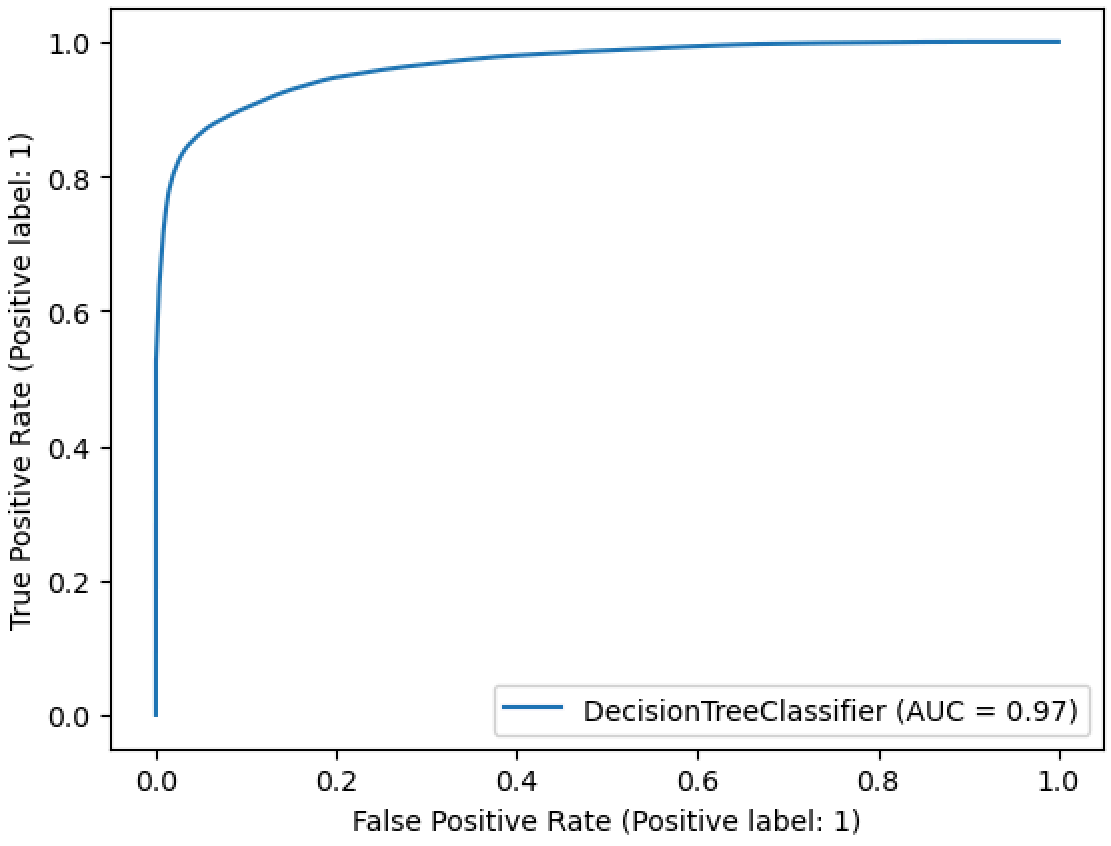
Out[145]:

| col_0 | 0 | 1 |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 19880 | 1153 |
| **1** | 2737 | 18296 |

```
In [146… plot_roc_curve(treemodel_smote,X_smote,y_smote)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

```
Out[146]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19885f37a60>
```



## Random Forest Classification for H1N1 Vaccine :

```
In [147…  RFsmote = RandomForestClassifier(n_estimators=7,max_depth=12)

In [148…  RFmodel_smote = RFsmote.fit(X_smote,y_smote)

In [149…  RFmodel_smote.score(X_smote,y_smote)

Out[149]: 0.9265440022821281

In [150…  cross_val_score(RFmodel_smote,X_smote,y_smote)

Out[150]: array([0.69681483, 0.88006656, 0.95245453, 0.95209794, 0.94449067])

In [151…  np.mean([0.6931305 , 0.87388565, 0.94591703, 0.95304885, 0.94413408])

Out[151]: 0.8820232220000002

In [152…  RFsmote_predict = RFmodel_smote.predict(X_smote)

In [153…  RFsmote_predict_test = RFmodel_smote.predict(vaccinetestdf)

In [154…  pd.DataFrame(RFsmote_predict_test).to_csv('h1h1RF.csv')

In [155…  print(classification_report(y_smote,RFsmote_predict))
```

```
              precision    recall  f1-score   support

           0       0.91      0.95      0.93     21033
           1       0.95      0.90      0.92     21033

    accuracy                           0.93     42066
   macro avg       0.93      0.93      0.93     42066
weighted avg       0.93      0.93      0.93     42066
```

In [156…

```
pd.crosstab(y_smote,RFsmote_predict)
```

Out[156]:

| col_0 | 0 | 1 |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 20021 | 1012 |
| **1** | 2078 | 18955 |

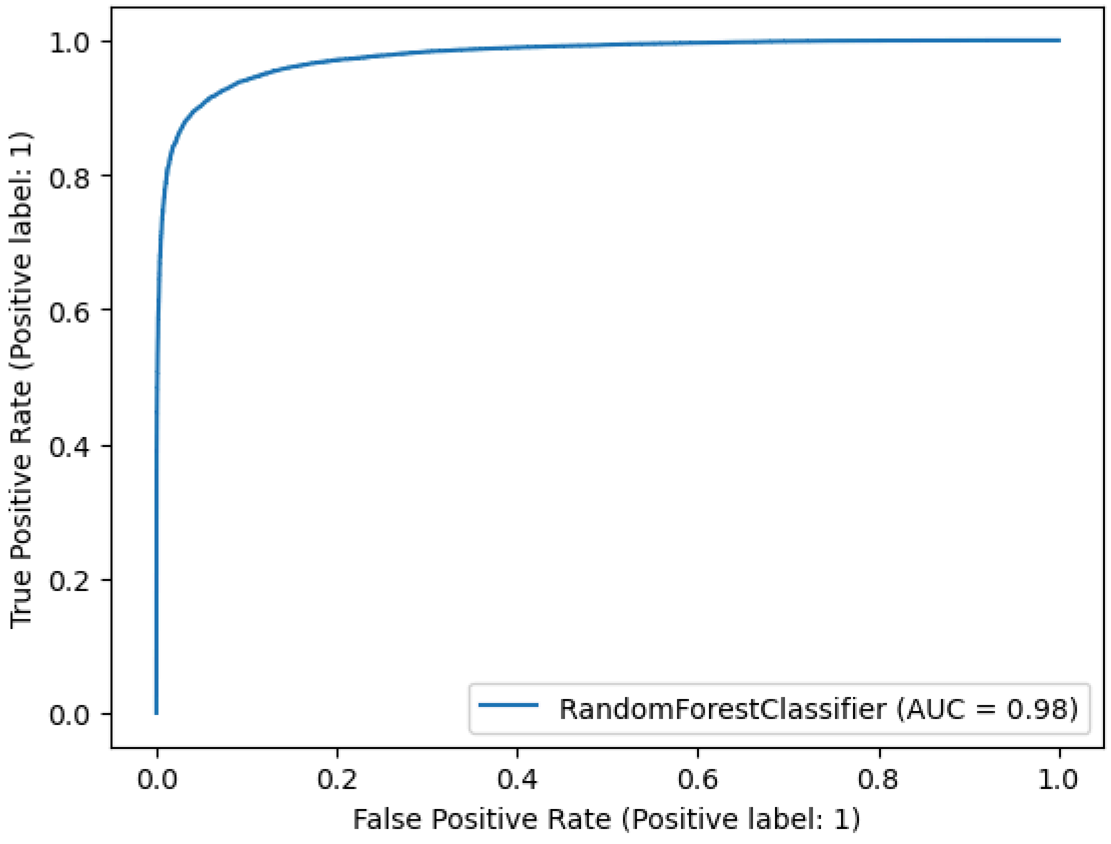
In [157…

```
plot_roc_curve(RFmodel_smote,X_smote,y_smote)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[157]:

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19885f82e50>
```



## Gradient Boosting Classification for H1N1 Vaccine :

In [158…

```
gbm_smote = GradientBoostingClassifier(n_estimators=700)
```

In [159…
```
gbmmodel_smote = gbm_smote.fit(X_smote,y_smote)
```

In [160…
```
gbmmodel_smote.score(X_smote,y_smote)
```

Out[160]:
```
0.9202443778823753
```

In [161…
```
cross_val_score(gbmmodel_smote,X_smote,y_smote)
```

Out[161]:
```
array([0.64879962, 0.88458338, 0.96576726, 0.96529181, 0.96208249])
```

In [162…
```
np.mean([0.64606608, 0.8851777 , 0.96612386, 0.9656484 , 0.9630334 ])
```

Out[162]:
```
0.885209888
```

In [163…
```
gbmpredict_smote = gbmmodel_smote.predict(X_smote)
```

In [164…
```
gbmpredict_smote_test = gbmmodel_smote.predict_proba(vaccinetestdf)
```

In [165…
```
pd.DataFrame(gbmpredict_smote_test).to_csv('h1n1gbm.csv')
```

In [166…
```
print(classification_report(y_smote,gbmpredict_smote))
```

```
              precision    recall  f1-score   support

           0       0.89      0.96      0.92     21033
           1       0.95      0.88      0.92     21033

    accuracy                           0.92     42066
   macro avg       0.92      0.92      0.92     42066
weighted avg       0.92      0.92      0.92     42066
```

In [167…
```
pd.crosstab(y_smote,gbmpredict_smote)
```

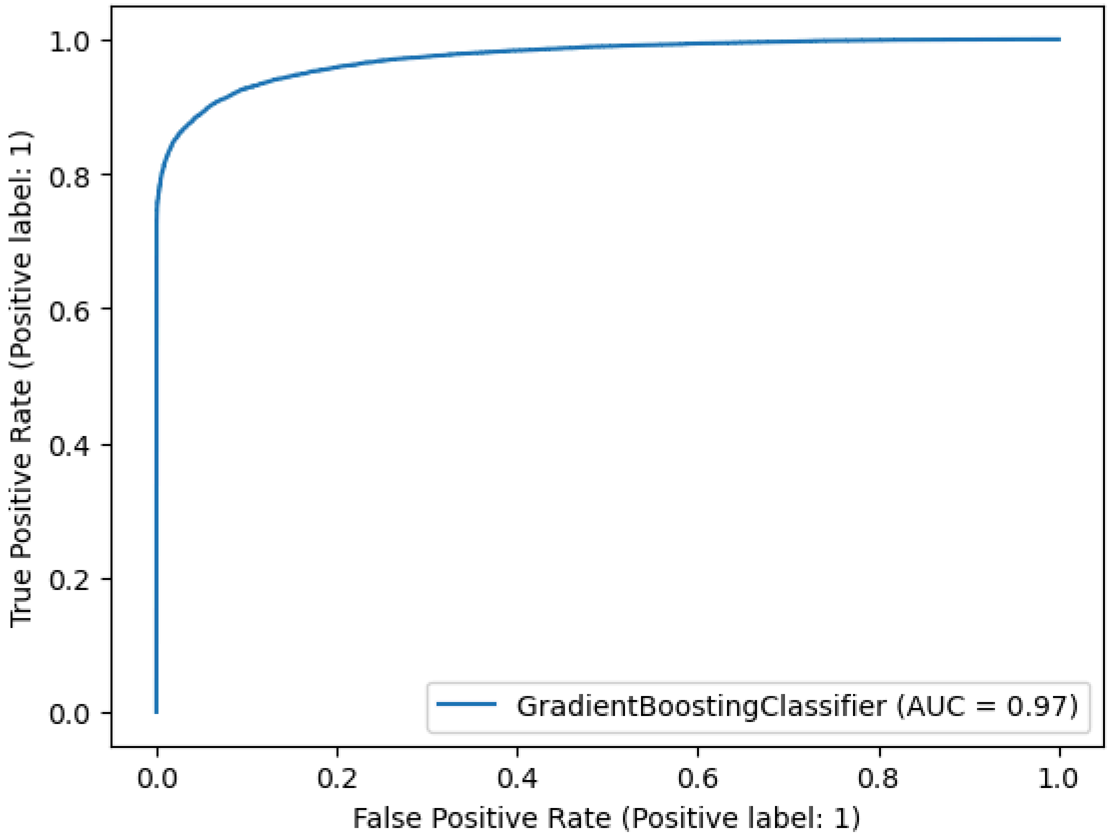
Out[167]:

| **col_0** | **0** | **1** |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 20099 | 934 |
| **1** | 2421 | 18612 |

In [168…
```
plot_roc_curve(gbmmodel_smote,X_smote,y_smote)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[168]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1988621aeb0>
```



## Support Vector Classification for H1N1 Vaccine :

```
In [169…  svmmodel_smote = svm.fit(X_smote,y_smote)
```

```
In [170…  svmmodel_smote.score(X_smote,y_smote)
Out[170]: 0.8064470118385394
```

```
In [171…  cross_val_score(svmmodel_smote,X_smote,y_smote)
Out[171]: array([0.75861659, 0.79044336, 0.81267087, 0.81564246, 0.80387496])
```

```
In [172…  np.mean([0.75861659, 0.79044336, 0.81267087, 0.81564246, 0.80387496])
Out[172]: 0.796249648
```

```
In [173…  svmsmote_predict = svmmodel_smote.predict(X_smote)
```

```
In [174…  svmsmote_predict_test = svmmodel_smote.predict(vaccinetestdf)
```

```
In [175…  pd.DataFrame(svmsmote_predict_test).to_csv('h1n1svm.csv')
```

```
In [176…  print(classification_report(y_smote,gbmpredict_smote))
```

```
              precision    recall  f1-score   support

           0       0.89      0.96      0.92     21033
           1       0.95      0.88      0.92     21033

    accuracy                           0.92     42066
   macro avg       0.92      0.92      0.92     42066
weighted avg       0.92      0.92      0.92     42066
```

In [177…
```
pd.crosstab(y_smote,gbmpredict_smote)
```

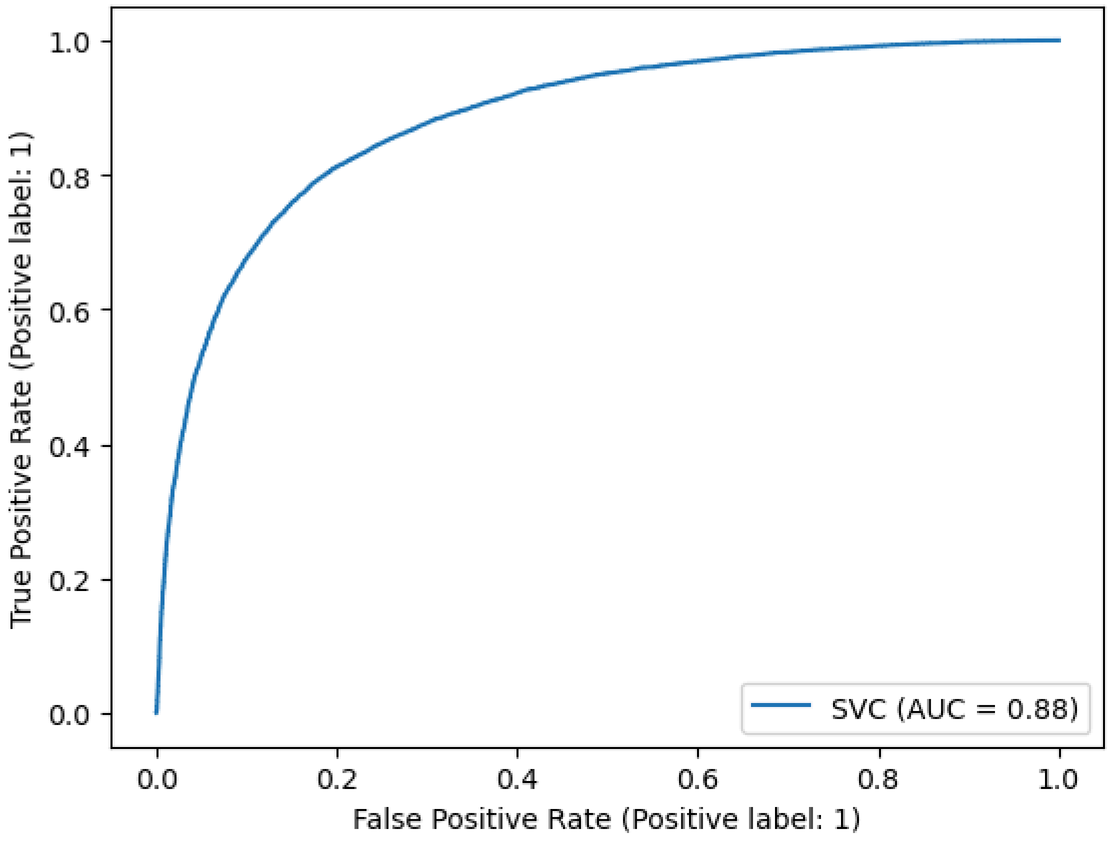
Out[177]:

| col_0 | 0 | 1 |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 20099 | 934 |
| **1** | 2421 | 18612 |

In [178…
```
plot_roc_curve(svmmodel_smote,X_smote,y_smote)
```

```
C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
```

Out[178]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x19886279310>
```



## Naive Bayes Classification for H1N1 Vaccine :

In [179…
```
nbmodel_smote = nb.fit(X_smote,y_smote)
```

```
In [180…  nbmodel_smote.score(X_smote,y_smote)

Out[180]: 0.7696001521418723
```

```
In [181…  cross_val_score(nbmodel_smote,X_smote,y_smote)

Out[181]: array([0.64606608, 0.75121835, 0.81397837, 0.81195768, 0.80744087])
```

```
In [182…  np.mean([0.64606608, 0.75121835, 0.81397837, 0.81195768, 0.80744087])

Out[182]: 0.76613227
```

```
In [183…  nbsmote_predict = nbmodel_smote.predict(X_smote)
```

```
In [184…  nbsmote_predict_test = nbmodel_smote.predict_proba(vaccinetestdf)
```

```
In [185…  pd.DataFrame(nbsmote_predict_test).to_csv('h1n1nb.csv')
```

```
In [186…  print(classification_report(y_smote,nbsmote_predict))

              precision    recall  f1-score   support

           0       0.78      0.75      0.76     21033
           1       0.76      0.79      0.77     21033

    accuracy                           0.77     42066
   macro avg       0.77      0.77      0.77     42066
weighted avg       0.77      0.77      0.77     42066
```

```
In [187…  pd.crosstab(y_smote,nbsmote_predict)
```

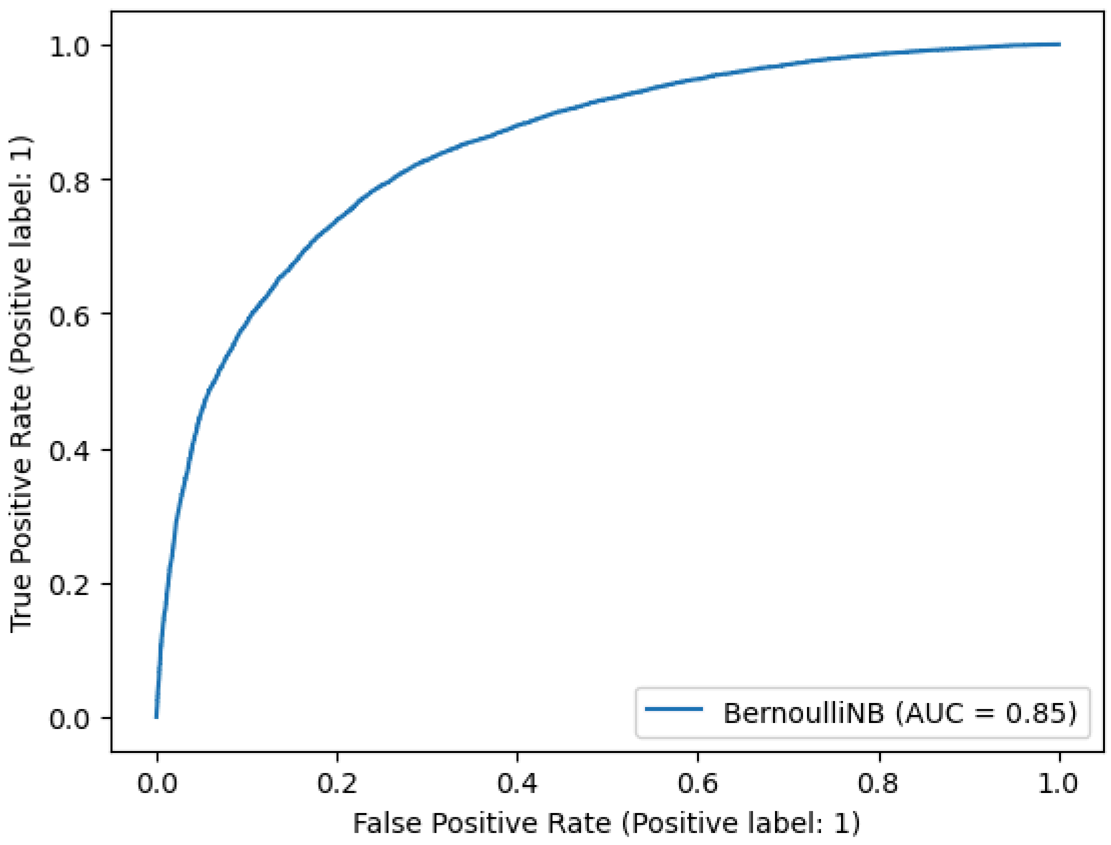
Out[187]:

| col_0 | 0 | 1 |
|---|---|---|
| **h1n1_vaccine** | | |
| **0** | 15716 | 5317 |
| **1** | 4375 | 16658 |

```
In [188…  from sklearn.metrics import RocCurveDisplay
```

```
In [189…  plot_roc_curve(nbmodel_smote,X_smote,y_smote)

C:\Users\coolr\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: Future
Warning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is
deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:
`sklearn.metric.RocCurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurv
eDisplay.from_estimator`.
  warnings.warn(msg, category=FutureWarning)
Out[189]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x198858f15b0>
```



## Results

## Performance Metric Report:

| Seasonal Vaccine | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Model** | **Cross Val Score** | **Accuracy** | | **Precesion** | **Recall** | **F1 Score** | **AUC** |
| **Logistic Regression** | 76.02 | 76.11 | 0 | 0.77 | 0.79 | 0.78 | 0.83 |
| | | | 1 | 0.75 | 0.73 | 0.74 | |
| **Decision Tree Classification** | 70.36 | 94.05 | 0 | 0.94 | 0.95 | 0.94 | 0.99 |
| | | | 1 | 0.94 | 0.93 | 0.94 | |
| **Random Forest Classification** | 71.22 | 94.6 | 0 | 0.95 | 0.95 | 0.95 | 0.98 |
| | | | 1 | 0.95 | 0.94 | 0.94 | |
| **Support Vector Classification** | 77.17 | 77.83 | 0 | 0.78 | 0.81 | 0.80 | 0.85 |
| | | | 1 | 0.77 | 0.74 | 0.76 | |
| **Naive Bayes** | 69.27 | 69.36 | 0 | 0.72 | 0.69 | 0.71 | 0.76 |
| | | | 1 | 0.66 | 0.7 | 0.68 | |
| **Gradient Boosting Classification** | 77.98 | 85.66 | 0 | 0.86 | 0.87 | 0.87 | 0.93 |
| | | | 1 | 0.85 | 0.84 | 0.84 | |

| H1N1 Vaccine | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Model** | **Cross Val Score** | **Accuracy** | | **Precesion** | **Recall** | **F1 Score** | **AUC** |
| **Logistic Regression** | 76.24 | 76.29 | 0 | 0.76 | 0.76 | 0.76 | 0.84 |
| | | | 1 | 0.76 | 0.77 | 0.76 | |
| **Decision Tree Classification** | 86.96 | 90.75 | 0 | 0.88 | 0.95 | 0.91 | 0.97 |
| | | | 1 | 0.94 | 0.87 | 0.90 | |
| **Random Forest Classification** | 88.20 | 92.42 | 0 | 0.90 | 0.95 | 0.93 | 0.98 |
| | | | 1 | 0.95 | 0.9 | 0.92 | |
| **Support Vector Classification** | 79.62 | 80.64 | 0 | 0.89 | 0.96 | 0.92 | 0.88 |
| | | | 1 | 0.95 | 0.88 | 0.92 | |
| **Naive Bayes** | 76.61 | 76.96 | 0 | 0.78 | 0.75 | 0.76 | 0.85 |
| | | | 1 | 0.76 | 0.79 | 0.77 | |
| **Gradient Boosting Classification** | 88.52 | 92.02 | 0 | 0.89 | 0.96 | 0.92 | 0.97 |
| | | | 1 | 0.95 | 0.88 | 0.92 | |

## Key Observation:

### Seasonal Vaccine prediction

- Gradient Boosting achieved the best balance of performance, with accuracy of 85.66% and AUC of 0.93.
- Random Forest and Decision Tree models also performed well, with very high recall and precision (AUCs of 0.98 and 0.99 respectively), though Decision Tree may be overfitting given its accuracy of 94.05% on a lower cross-validation score (70.36).
- Naive Bayes and Logistic Regression showed weaker generalization with lower accuracy and F1 scores.

### H1N1 Vaccine prediction

- Gradient Boosting again outperformed other models with accuracy of 92.02% and AUC of 0.97.
- Random Forest and Decision Tree closely followed, both showing high predictive power (AUC > 0.97).
- Support Vector Classification had strong recall (0.96 for class 0), which is valuable in public health applications where identifying individuals unlikely to take the vaccine is important.
- Naive Bayes and Logistic Regression underperformed compared to ensemble methods.

## Conclusion:

- For both vaccine types, Gradient Boosting Classification proved to be the most reliable and robust model. It achieved high scores across all evaluation metrics while balancing between precision and recall, making it highly suitable for public health prediction tasks. This model could help healthcare providers target outreach more effectively to individuals less likely to get vaccinated.

## References:

### Aim ref:

- https://www.drivendata.org/competitions/66/flu-shot-learning/

### Objective ref:

- https://www.cdc.gov/mmwr/volumes/68/rr/rr6803a1.htm

## Data set I took from this website:

- https://www.drivendata.org/competitions/66/flu-shot-learning/data/