PROJECT TITLE: *PREDICTING THE LIKELIHOOD OF INDIVIDUALS TAKING H1N1 FLU AND SEASONAL FLU VACCINES USING LOGISTIC REGRESSION MODEL AND DECISION TREE CLASSIFIER (ID3) MODELS*

BUSINESS UNDERSTANDING

Introduction

Vaccination is a key public health measure used to fight infectious diseases.It is a simple, safe, and effective way of protecting a person against harmful diseases, before they come into contact with them (WHO, 2024). Vaccines provide immunization for individuals, and enough immunization in a community can further reduce the spread of diseases through "herd immunity."

Project Overview

Mpox, just like covid 19 that affected the entire world in 2020, is a new viral infection which can spread between people, mainly through close contact, and occasionally from the environment to people via things and surfaces that have been touched by a person with mpox (WHO, 2024). It is an illness caused by the monkeypox virus. 3 cases of Mpox at the time of writing this have been reported in Kenya but the vaccines for the disease are still under development.

The data for this research on uptake of vaccines based on opinions, demoraphics and doctor's recommendation is from United States National 2009 H1N1 Flu Survey collected to monitor vaccination rates during the US Government Vaccination Campaign that began in October 2009. A phone survey was used to ask people whether they had received H1N1 and seasonal flu vaccines, in conjunction with information they shared about their lives, opinions, and behaviors.

Objectives

- **To predict whether people got H1N1 and Seasonal Flue Vaccines using infromation shared about their backgrounds, opinions and Health Behaviour.**
- **To determine the best performing model in predicting Vaccines**

DATA UNDERSTANDING

Here, the different sets of data as downloaded from the `DRIVENDATA` data repository are described:

Training Features:

- **These are the input variables that the model will use to predict the probability that people received H1N1 flu and seasonal flu vaccines. There are 35 feature columns in total, each a response to a survey question. These questions cover several different topics, such as whether people observed safe behavioral practices, their opinions about the diseases and the vaccines, and their demographics.**

Training Labels:

- **These are the labels corresponding to the observations in the training features. There are two target variables: h1n1_vaccine and seasonal_vaccine. Both are binary variables, with 1 indicating that a person received the respective flu vaccine and 0 indicating that a person did not receive the respective flu vaccine. This is a "multilabel" modeling task.**

Test Features:

- **These are the features for observations that will be used to generate the submission predictions after training a model.**

Submission Format:

- **This file serves as an example for how to format submission.**

DESCRIPTION OF FEATURES AND LABELS

FEATURES DATASET

The features dataset has 36 columns. The first column respondent_id is a unique and random identifier. The remaining 35 features are described below:

For all binary variables: 0 = No; 1 = Yes.

- **h1n1_concern** - Level of concern about the H1N1 flu. 0 = Not at all concerned; 1 = Not very concerned; 2 = Somewhat concerned; 3 = Very concerned.
- **h1n1_knowledge** - Level of knowledge about H1N1 flu. 0 = No knowledge; 1 = A little knowledge; 2 = A lot of knowledge.
- **behavioral_antiviral_meds** - Has taken antiviral medications. (binary)
- **behavioral_avoidance** - Has avoided close contact with others with flu-like symptoms. (binary)
- **behavioral_face_mask** - Has bought a face mask. (binary)
- **behavioral_wash_hands** - Has frequently washed hands or used hand sanitizer. (binary)
- **behavioral_large_gatherings** - Has reduced time at large gatherings. (binary)
- **behavioral_outside_home** - Has reduced contact with people outside of own household. (binary)
- **behavioral_touch_face**- Has avoided touching eyes, nose, or mouth. (binary)
- **doctor_recc_h1n1** - H1N1 flu vaccine was recommended by doctor. (binary)
- **doctor_recc_seasonal** - Seasonal flu vaccine was recommended by doctor. (binary)
- **chronic_med_condition** - Has any of the following chronic medical conditions: asthma or an other lung condition, diabetes, a heart condition, a kidney condition, sickle cell anemia or other anemia, a neurological or neuromuscular condition, a liver condition, or a weakened immune system caused by a chronic illness or by medicines taken for a chronic illness. (binary)
- **child_under_6_months** - Has regular close contact with a child under the age of six months. (binary)
- **health_worker**- Is a healthcare worker. (binary)
- **health_insurance**- Has health insurance. (binary)
- **opinion_h1n1_vacc_effective**- Respondent's opinion about H1N1 vaccine effectiveness. 1 = Not at all effective; 2 = Not very effective; 3 = Don't know; 4 = Somewhat effective; 5 = Very effective.
- **opinion_h1n1_risk** - Respondent's opinion about risk of getting sick with H1N1 flu without vaccine. 1 = Very Low; 2 = Somewhat low; 3 = Don't know; 4 = Somewhat high; 5 = Very high.
- **opinion_h1n1_sick_from_vacc** - Respondent's worry of getting sick from taking H1N1 vaccine. 1 = Not at all worried; 2 = Not very worried; 3 = Don't know; 4 = Somewhat worried; 5 = Very worried.
  opinion_seas_vacc_effective - Respondent's opinion about seasonal flu vaccine effectiveness. 1 = Not at all effective; 2 = Not very effective; 3 = Don't know; 4 = Somewhat effective; 5 = Very effective.
- **opinion_seas_risk** - Respondent's opinion about risk of getting sick with seasonal flu without vaccine. 1 = Very Low; 2 = Somewhat low; 3 = Don't know; 4 = Somewhat high; 5 = Very high.
- **opinion_seas_sick_from_vacc** - Respondent's worry of getting sick from taking seasonal flu vaccine. 1 = Not at all worried; 2 = Not very worried; 3 = Don't know; 4 = Somewhat worried; 5 = Very worried.
- **age_group** - Age group of respondent.
- **education** - Self-reported education level.
- **race**- Race of respondent.
- **sex**- Sex of respondent.
- **income_poverty** - Household annual income of respondent with respect to 2008 Census poverty thresholds.
- **marital_status** - Marital status of respondent.
- **rent_or_own** - Housing situation of respondent.
- **employment_status** - Employment status of respondent.
- **hhs_geo_region**- Respondent's residence using a 10-region geographic classification defined by the U.S. Dept. of Health and Human Services. Values are represented as short random character strings.
- **census_msa** - Respondent's residence within metropolitan statistical areas (MSA) as defined by the U.S. Census.
- **household_adults** - Number of other adults in household, top-coded to 3.
- **household_children** - Number of children in household, top-coded to 3.
- **employment_industry** - Type of industry respondent is employed in. Values are represented as short random character strings.
- **employment_occupation** - Type of occupation of respondent. Values are represented as short random character strings.

`Labels Dataset`

There are two target variables:

- **h1n1_vaccine** - Whether respondent received H1N1 flu vaccine.
- **seasonal_vaccine** - Whether respondent received seasonal flu vaccine.

Both are binary variables: 0 = No; 1 = Yes. Some respondents didn't get either vaccine, others got only one, and some got both. This is formulated as a multilabel (and not multiclass) problem.

Importing the libraries that will be used to load and explore the data

In [1]:

```
import pandas as pd
import numpy as np
```

Load and explore the features dataset

In [2]:

```
features_df = pd.read_csv("Data/training_set_features.csv", index_col = "respondent_id")
features_df.head()
```

Out[2]:

respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi
0	1.0	0.0	0.0	0.0	0.0	
1	3.0	2.0	0.0	1.0	0.0	
2	1.0	1.0	0.0	1.0	0.0	
3	1.0	1.0	0.0	1.0	0.0	
4	2.0	1.0	0.0	1.0	0.0	

5 rows × 35 columns

Check the shape of the features dataset

In [3]:

```
features_df.shape
```

Out[3]:

```
(26707, 35)
```

- The dataset has 26,707 observations and 35 features.
- Each row represents a person who took part in the survey as a respondent
- The columns are the values corresponding to the participants in the survey

checking the info of the features dataset

checking the info of the features dataset

In [4]:

```
features_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 26707 entries, 0 to 26706
Data columns (total 35 columns):
 #   Column                       Non-Null Count  Dtype  
---  ------                       --------------  -----  
 0   h1n1_concern                 26615 non-null  float64
 1   h1n1_knowledge               26591 non-null  float64
 2   behavioral_antiviral_meds    26636 non-null  float64
 3   behavioral_avoidance         26499 non-null  float64
 4   behavioral_face_mask         26688 non-null  float64
 5   behavioral_wash_hands        26665 non-null  float64
 6   behavioral_large_gatherings  26620 non-null  float64
 7   behavioral_outside_home      26625 non-null  float64
 8   behavioral_touch_face        26579 non-null  float64
 9   doctor_recc_h1n1             24547 non-null  float64
 10  doctor_recc_seasonal         24547 non-null  float64
 11  chronic_med_condition        25736 non-null  float64
 12  child_under_6_months         25887 non-null  float64
 13  health_worker                25903 non-null  float64
 14  health_insurance             14433 non-null  float64
 15  opinion_h1n1_vacc_effective  26316 non-null  float64
 16  opinion_h1n1_risk            26319 non-null  float64
 17  opinion_h1n1_sick_from_vacc  26312 non-null  float64
 18  opinion_seas_vacc_effective  26245 non-null  float64
 19  opinion_seas_risk            26193 non-null  float64
 20  opinion_seas_sick_from_vacc  26170 non-null  float64
 21  age_group                    26707 non-null  object 
 22  education                    25300 non-null  object 
 23  race                         26707 non-null  object 
 24  sex                          26707 non-null  object 
 25  income_poverty               22284 non-null  object 
 26  marital_status               25299 non-null  object 
 27  rent_or_own                  24665 non-null  object 
 28  employment_status            25244 non-null  object 
 29  hhs_geo_region               26707 non-null  object 
 30  census_msa                   26707 non-null  object 
 31  household_adults             26458 non-null  float64
 32  household_children           26458 non-null  float64
 33  employment_industry          13377 non-null  object 
 34  employment_occupation        13237 non-null  object 
dtypes: float64(23), object(12)
memory usage: 7.3+ MB
```

- **The dataset contains both object and float datatypes.**
- **The feautures of type float are 23 in number whereas the features of object data type are 12 in number**

Exporing the labels dataset

In [5]:

```
# load the data
labels_df = pd.read_csv("Data/training_set_labels.csv", index_col="respondent_id")
labels_df.head()
```

Out[5]:

respondent_id	h1n1_vaccine	seasonal_vaccine
0	0	0
1	0	1
2	0	0

	h1n1_vaccine	seasonal_vaccine
3	0	1
respondent_id		
4	0	0

check the shape of the labels dataset

In [6]:

```
labels_df.shape
```

Out[6]:

```
(26707, 2)
```

- The labels dataset has 26,707 observations just like the features dataset
- It dataset has two target variables.

EXPLORATORY DATA ANALYSIS

In [7]:

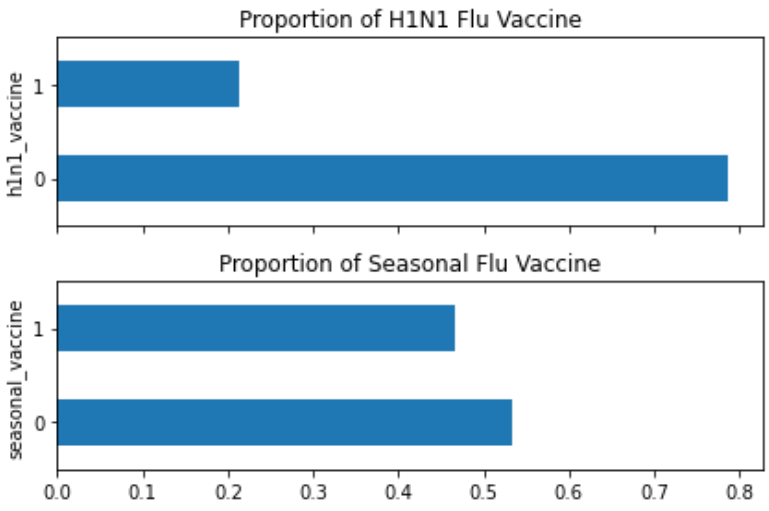
```
#import files for exploration
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
```

Exploring Labels (Target Variables)

The distribution of the target variables is explored here

In [8]:

```
fig, ax = plt.subplots(2, 1, sharex=True)

total_obs = labels_df.shape[0]

labels_df['h1n1_vaccine'].value_counts().div(total_obs).plot.barh(title="Proportion of H1
N1 Flu Vaccine", ax=ax[0])

ax[0].set_ylabel("h1n1_vaccine")

labels_df['seasonal_vaccine'].value_counts().div(total_obs).plot.barh(title="Proportion o
f Seasonal Flu Vaccine", ax=ax[1])

ax[1].set_ylabel("seasonal_vaccine")

fig.tight_layout()
```



- From the bar graph it is clear that almost 50% of the people received the seasonal flu vaccine but only about 20% of the people received the H1N1 flue Vaccine.
- The seasonal flu vaccine has balanced classes since both class 0 and class 1 have almost equal distribution.
- The H1N1 Flu Vaccine has imbalanced classes since class 0 is almost 80% whereas class 1 has only 20% distribution.

check how the vaccination status of participants is distributed between the two types of vaccines.

In [9]:

```
pd.crosstab(labels_df["h1n1_vaccine"], labels_df["seasonal_vaccine"], margins=True, normalize=True)
```

Out[9]:

seasonal_vaccine	0	1	All
h1n1_vaccine			
0	0.497810	0.289737	0.787546
1	0.036582	0.175871	0.212454
All	0.534392	0.465608	1.000000

- From the table it is clear that a large percentage of the population did not receive any vaccine (49.8%) represented as 0.497810 in the table
- Approximately 29% of the population received the seasonal vaccine repsented as 0.289737 in the table
- Only about 17.6% of the population received both vaccines (0.175871).
- About 3.7% (0.036582) received only the H1N1 vaccine but not the seasonal vaccine

Exploring Combined data set

Combining the features and labels dataframes

In [10]:

```
combined_df = features_df.join(labels_df)
combined_df.head()
```

Out[10]:

respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi
0	1.0	0.0	0.0	0.0	0.0	
1	3.0	2.0	0.0	1.0	0.0	
2	1.0	1.0	0.0	1.0	0.0	
3	1.0	1.0	0.0	1.0	0.0	
4	2.0	1.0	0.0	1.0	0.0	

5 rows × 37 columns

check the shape of the combined dataframe

In [11]:

```
combined_df.shape
```

Out[11]:

```
(26707, 37)
```

- **The combined df still has the same number of observations (26, 707) and 37 columns (35 features and 2 target variables)**

Types of variables

The dataset contains both categorical and numerical dataset.

Here the data is divided into numerical and categorical data.

Finding categorical data

In [12]:

```
categorical = [var for var in combined_df.columns if combined_df[var].dtype=='object']

print('There are {} categorical variables\n'.format(len(categorical)))

print('The categorical variables are :', categorical)
```

```
There are 12 categorical variables

The categorical variables are : ['age_group', 'education', 'race', 'sex', 'income_poverty
', 'marital_status', 'rent_or_own', 'employment_status', 'hhs_geo_region', 'census_msa',
'employment_industry', 'employment_occupation']
```

In [13]:

```
# view categorical variables
combined_df[categorical].head()
```

Out[13]:

respondent_id	age_group	education	race	sex	income_poverty	marital_status	rent_or_own	employment_status	hhs_g
0	55 - 64 Years	< 12 Years	White	Female	Below Poverty	Not Married	Own	Not in Labor Force	
1	35 - 44 Years	12 Years	White	Male	Below Poverty	Not Married	Rent	Employed	
2	18 - 34 Years	College Graduate	White	Male	<= $75,000, Above Poverty	Not Married	Own	Employed	
3	65+ Years	12 Years	White	Female	Below Poverty	Not Married	Rent	Not in Labor Force	
4	45 - 54 Years	Some College	White	Female	<= $75,000, Above Poverty	Married	Own	Employed	

Exploring Missing Values in Categorical Variables

Exploring missing values in categorical variables

In [14]:

```
combined_df[categorical].isnull().sum()
```

Out[14]:

```
age_group                   0
education                1407
race                        0
sex                         0
income_poverty           4423
marital_status           1408
rent_or_own              2042
employment_status        1463
hhs_geo_region              0
census_msa                  0
employment_industry     13330
employment_occupation   13470
dtype: int64
```

print categorical variables with missing values

In [15]:

```
cat_missing = [var for var in categorical if combined_df[var].isnull().sum()!=0]

print(combined_df[cat_missing].isnull().sum())
```

```
education                1407
income_poverty           4423
marital_status           1408
rent_or_own              2042
employment_status        1463
employment_industry     13330
employment_occupation   13470
dtype: int64
```

- **There are only 7 categorical variables in the dataset which contains missing values. These are** `education`, `income_poverty`, `marital_status`, `rent_or_own` `employment_status`, `employment_industry`, **and** `employment_occupation`.

Check the frequency distribution of categorical variables

In [16]:

```
# view frequency of categorical variables

for var in categorical:

    print(combined_df[var].value_counts())
```

```
65+ Years         6843
55 - 64 Years     5563
45 - 54 Years     5238
18 - 34 Years     5215
35 - 44 Years     3848
Name: age_group, dtype: int64
College Graduate    10097
Some College         7043
12 Years             5797
< 12 Years           2363
Name: education, dtype: int64
White                21222
Black                 2118
Hispanic              1755
Other or Multiple     1612
Name: race, dtype: int64
```

```
Female    15858
Male      10849
Name: sex, dtype: int64
<= $75,000, Above Poverty    12777
> $75,000                    6810
Below Poverty                2697
Name: income_poverty, dtype: int64
Married        13555
Not Married    11744
Name: marital_status, dtype: int64
Own     18736
Rent     5929
Name: rent_or_own, dtype: int64
Employed              13560
Not in Labor Force    10231
Unemployed             1453
Name: employment_status, dtype: int64
lzgpxyit    4297
fpwskwrf    3265
qufhixun    3102
oxchjgsf    2859
kbazzjca    2858
bhuqouqj    2846
mlyzmhmf    2243
lrircsnp    2078
atmpeygn    2033
dqpwygqj    1126
Name: hhs_geo_region, dtype: int64
MSA, Not Principle  City    11645
MSA, Principle City          7864
Non-MSA                      7198
Name: census_msa, dtype: int64
fcxhlnwr    2468
wxleyezf    1804
ldnlellj    1231
pxcmvdjn    1037
atmlpfrs     926
arjwrbjb     871
xicduogh     851
mfikgejo     614
vjjrobsf     527
rucpziij     523
xqicxuve     511
saaquncn     338
cfqqtusy     325
nduyfdeo     286
mcubkhph     275
wlfvacwt     215
dotnnunm     201
haxffmxo     148
msuufmds     124
phxvnwax      89
qnlwzans      13
Name: employment_industry, dtype: int64
xtkaffoo    1778
mxkfnird    1509
emcorrxb    1270
cmhcxjea    1247
xgwztkwe    1082
hfxkjkmi     766
qxajmpny     548
xqwwgdyp     485
kldqjyjy     469
uqqtjvyb     452
tfqavkke     388
ukymxvdu     372
vlluhbov     354
oijqvulv     344
ccgxvspp     341
bxpfxfdn     331
haliazsg     296
rcertsgn     276
```

```
xzmlyyjv     248
dlvbwzss     227
hodpvpew     208
dcjcmpih     148
pvmttkik      98
Name: employment_occupation, dtype: int64
```

checking Cardinality

Cardinality helps one to know the number of unique values contained in a particular variable

In [17]:

```
# check the number of variables in the categorical variables

for var in categorical:

    print(var, ' contains ', len(combined_df[var].unique()), ' labels')
```

```
age_group  contains  5  labels
education  contains  5  labels
race  contains  4  labels
sex  contains  2  labels
income_poverty  contains  4  labels
marital_status  contains  3  labels
rent_or_own  contains  3  labels
employment_status  contains  4  labels
hhs_geo_region  contains  10  labels
census_msa  contains  3  labels
employment_industry  contains  22  labels
employment_occupation  contains  24  labels
```

- **Apart from `employment_industry` and `employment_occupation` that contain 22 labels and 24 labels respectively, the rest of the variables contain less than 10 labels each.**
- **All these variables are relatively small therefore no preprocessing needed.**

Exploring Numerical Features

In [18]:

```
# check numerical features

numerical = [var for var in features_df.columns if features_df[var].dtype!='object']


print('There are {} numerical variables in the features dataset\n'.format(len(numerical))
)

print('The numerical variables are :', numerical)
```

```
There are 23 numerical variables in the features dataset

The numerical variables are : ['h1n1_concern', 'h1n1_knowledge', 'behavioral_antiviral_me
ds', '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_worke
r', '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', 'household_adults', 'household_children']
```

In [19]:

```
combined_df[numerical].head()
```

Out[19]:

	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi

respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi
respondent_id						
0	1.0	0.0	0.0	0.0	0.0	
1	3.0	2.0	0.0	1.0	0.0	
2	1.0	1.0	0.0	1.0	0.0	
3	1.0	1.0	0.0	1.0	0.0	
4	2.0	1.0	0.0	1.0	0.0	

5 rows × 23 columns

- There are 23 numerical features in total

Checking for Missing Values in the numerical variables

In [20]:

```
# Checking missing values
combined_df[numerical].isnull().sum()
```

Out[20]:

```
h1n1_concern                    92
h1n1_knowledge                 116
behavioral_antiviral_meds       71
behavioral_avoidance           208
behavioral_face_mask            19
behavioral_wash_hands           42
behavioral_large_gatherings     87
behavioral_outside_home         82
behavioral_touch_face          128
doctor_recc_h1n1              2160
doctor_recc_seasonal          2160
chronic_med_condition          971
child_under_6_months           820
health_worker                  804
health_insurance             12274
opinion_h1n1_vacc_effective    391
opinion_h1n1_risk              388
opinion_h1n1_sick_from_vacc    395
opinion_seas_vacc_effective    462
opinion_seas_risk              514
opinion_seas_sick_from_vacc    537
household_adults               249
household_children             249
dtype: int64
```

- All the 23 variables have missing values

Imputing numeric columns using median

In [21]:

```
# impute missing values with median
combined_df[numerical] = combined_df[numerical].apply(lambda x: x.fillna(x.median()))

# check whether there are still missing values.
combined_df[numerical].isnull().sum()
```

Out[21]:

```
h1n1_concern                  0
h1n1_knowledge                0
behavioral_antiviral_meds     0
behavioral_avoidance          0
```

```
behavioral_face_mask           0
behavioral_wash_hands          0
behavioral_large_gatherings    0
behavioral_outside_home        0
behavioral_touch_face          0
doctor_recc_h1n1               0
doctor_recc_seasonal           0
chronic_med_condition          0
child_under_6_months           0
health_worker                  0
health_insurance               0
opinion_h1n1_vacc_effective    0
opinion_h1n1_risk              0
opinion_h1n1_sick_from_vacc    0
opinion_seas_vacc_effective    0
opinion_seas_risk              0
opinion_seas_sick_from_vacc    0
household_adults               0
household_children             0
dtype: int64
```

- **The data no longer has any missing values after imputing**

Checking whether there is a relationship between h1n1_concern feature and h1n1_vaccine target variable

Here, only one of the two target variables is used.

In [22]:

```
# get the count of observations for each combination of those two variables.
counts = (combined_df[['h1n1_knowledge', 'h1n1_vaccine']]
              .groupby(['h1n1_knowledge', 'h1n1_vaccine'])
              .size()
              .unstack('h1n1_vaccine')
         )
counts
```

Out[22]:

h1n1_vaccine	0	1
h1n1_knowledge		
0.0	**2145**	**361**
1.0	**12039**	**2675**
2.0	**6849**	**2638**

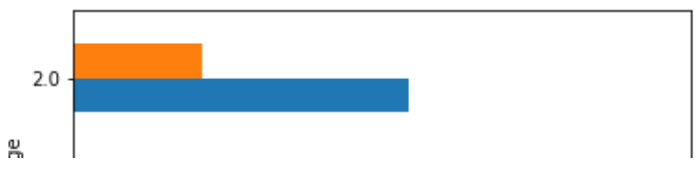
Use bar chart to compare the change in the two variables

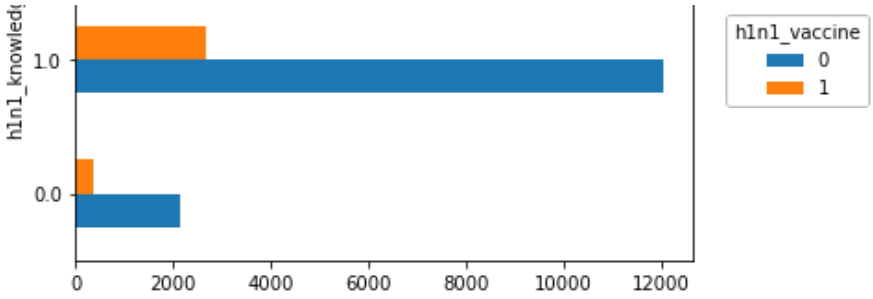
In [23]:

```
ax = counts.plot.barh()
ax.legend(
    loc='center right',
    bbox_to_anchor=(1.3, 0.5),
    title='h1n1_vaccine'
)
```

Out[23]:

```
<matplotlib.legend.Legend at 0x211a4f6d730>
```





- **From the bar chart, it's not easy to tell whether there a relation between levels of knowledge of h1n1 flu and likelihood of being vaccinated since the two classes are imbalanced. That is, about 80% were not vaccinated with H1N1_Vaccine whereas 20% get vaccinated.**

checking for rate of vaccination at each level

In [24]:

```
h1n1_knowledge_counts = counts.sum(axis='columns')
h1n1_knowledge_counts
```

Out[24]:

```
h1n1_knowledge
0.0     2506
1.0    14714
2.0     9487
dtype: int64
```

In [25]:

```
# checking probabilities of h1n1_concern levels
h1n1_knowledge_probs = counts.div(h1n1_knowledge_counts, axis='index')
h1n1_knowledge_probs
```

Out[25]:

h1n1_vaccine	0	1
h1n1_knowledge		
0.0	0.855946	0.144054
1.0	0.818200	0.181800
2.0	0.721935	0.278065

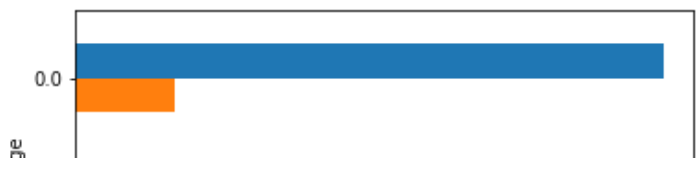
Bar chart for rate of vaccination for each level of h1n1_concern

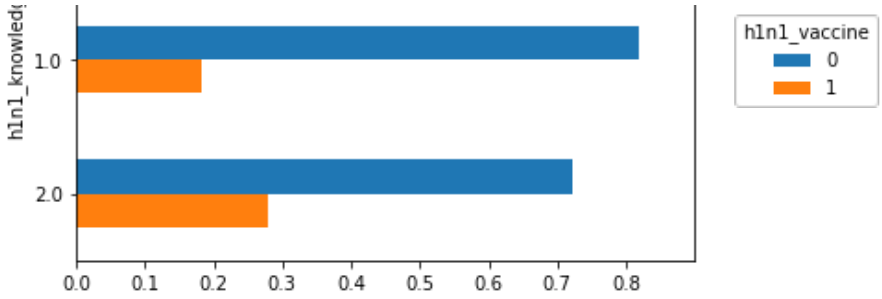
In [26]:

```
#
ax = h1n1_knowledge_probs.plot.barh()
ax.invert_yaxis()
ax.legend(
    loc='center left',
    bbox_to_anchor=(1.05, 0.5),
    title='h1n1_vaccine'
)
```

Out[26]:

```
<matplotlib.legend.Legend at 0x211a503c4c0>
```





- **From the bar chart it can clearly be seen that even though not many people get vaccinated with H1N1 flu vaccine, people are more likely to get vaccinated if they have more knowledge of flu vaccine.**
- **h1n1_knowledge can be used in modelling since there is a relationship between the level of knowledge and the number of people being vaccinated with h1n1_vaccine.**

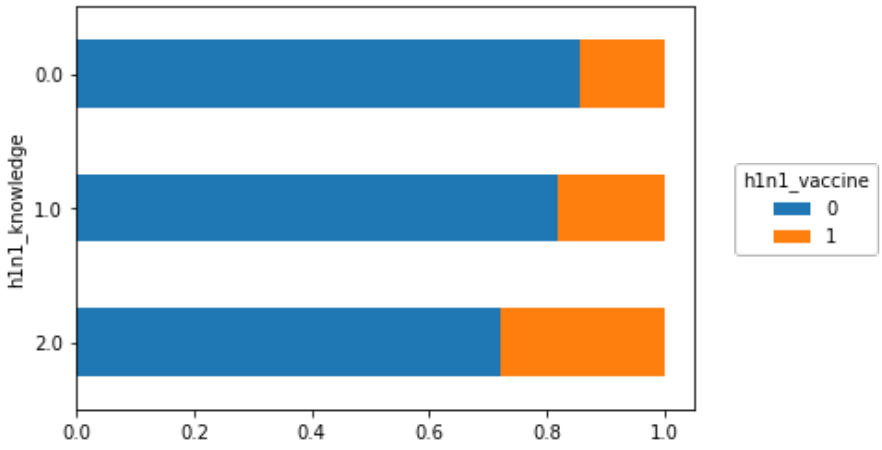
Using a stacked bar chart

In [27]:

```
ax = h1n1_knowledge_probs.plot.barh(stacked=True)
ax.invert_yaxis()
ax.legend(
    loc='center left',
    bbox_to_anchor=(1.05, 0.5),
    title='h1n1_vaccine'
)
```

Out[27]:

```
<matplotlib.legend.Legend at 0x211a2ea5880>
```



plot more variables

In [28]:

```
# creating a function to factor several variables
def vaccination_rate_plot(col, target, data, ax=None):
    counts = (combined_df[[target, col]]
                  .groupby([target, col])
                  .size()
                  .unstack(target)
              )
    group_counts = counts.sum(axis='columns')
    probabilities = counts.div(group_counts, axis='index')

    probabilities.plot(kind="barh", stacked=True, ax=ax)
    ax.invert_yaxis()
    ax.legend().remove()
```

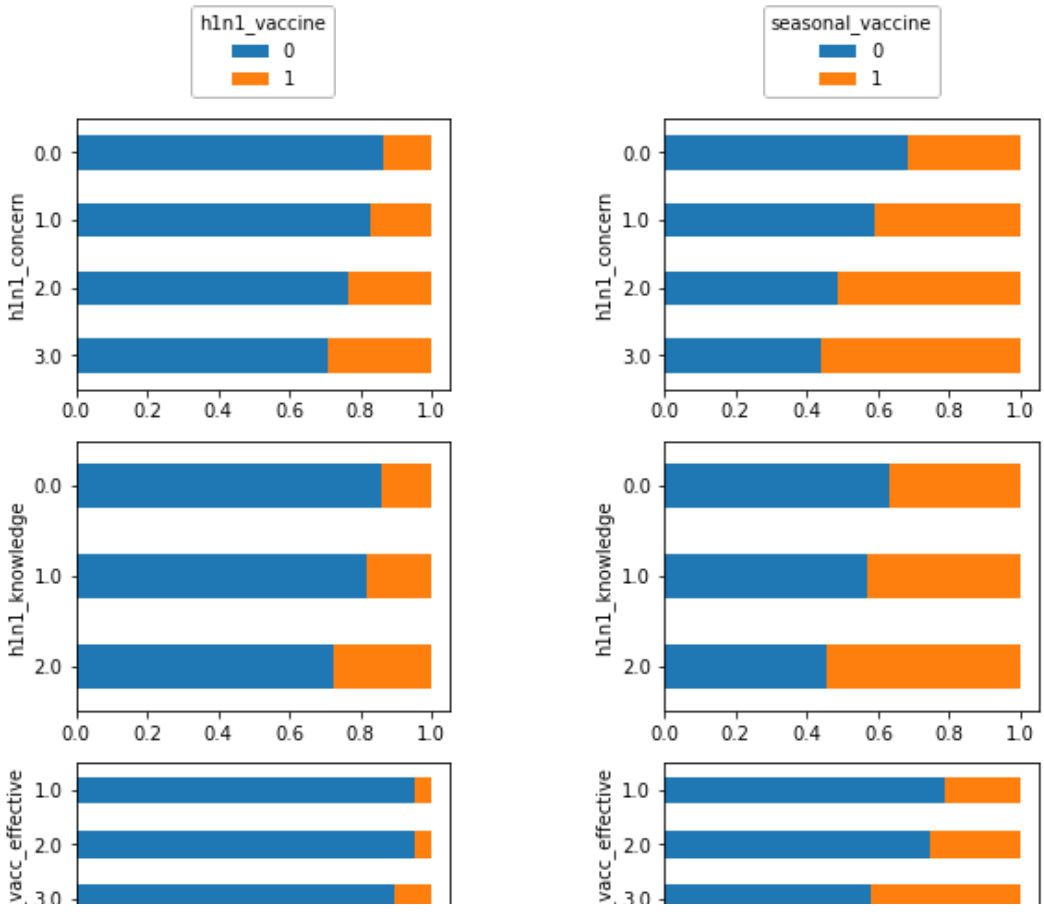
plotting selected columns against the target variables

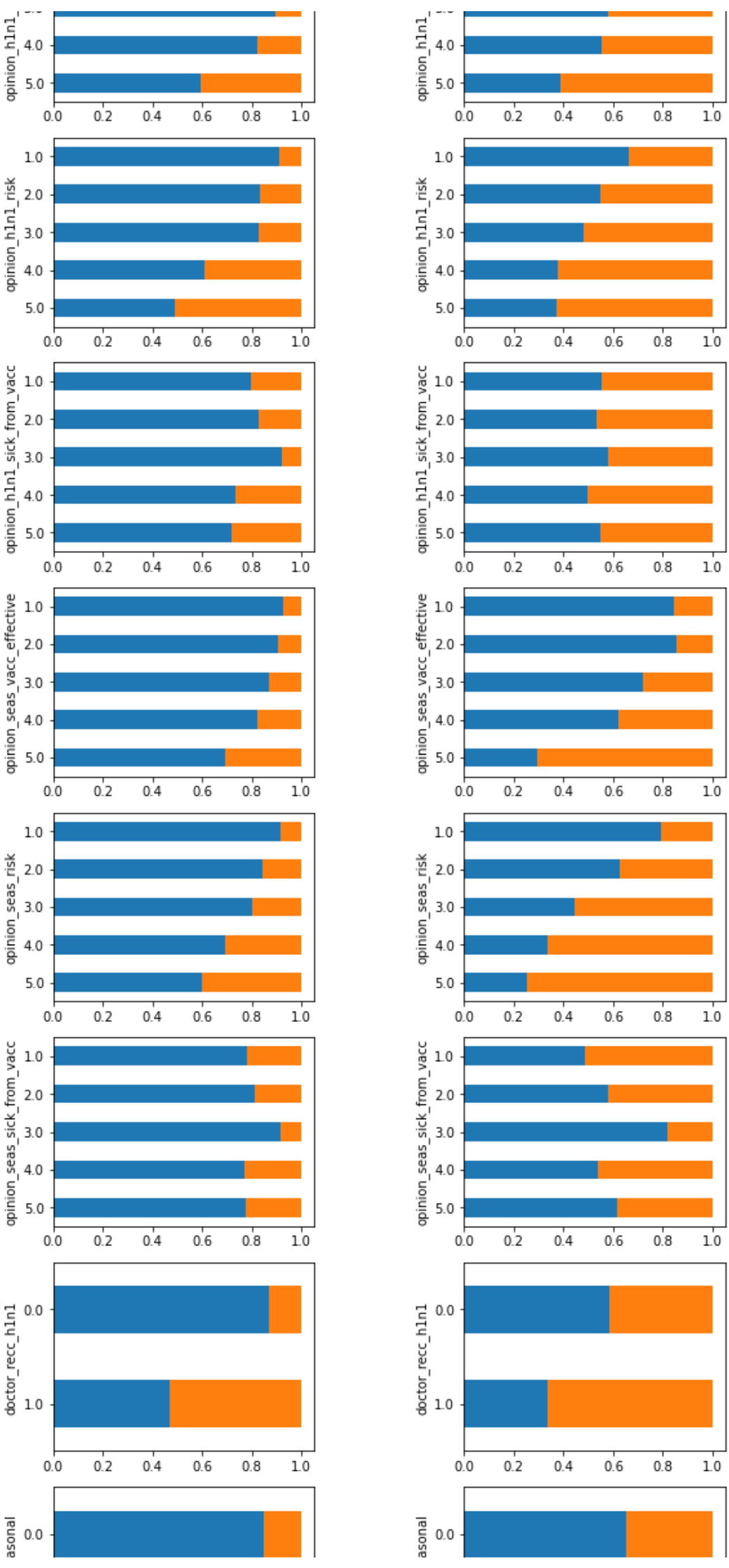
In [29]:

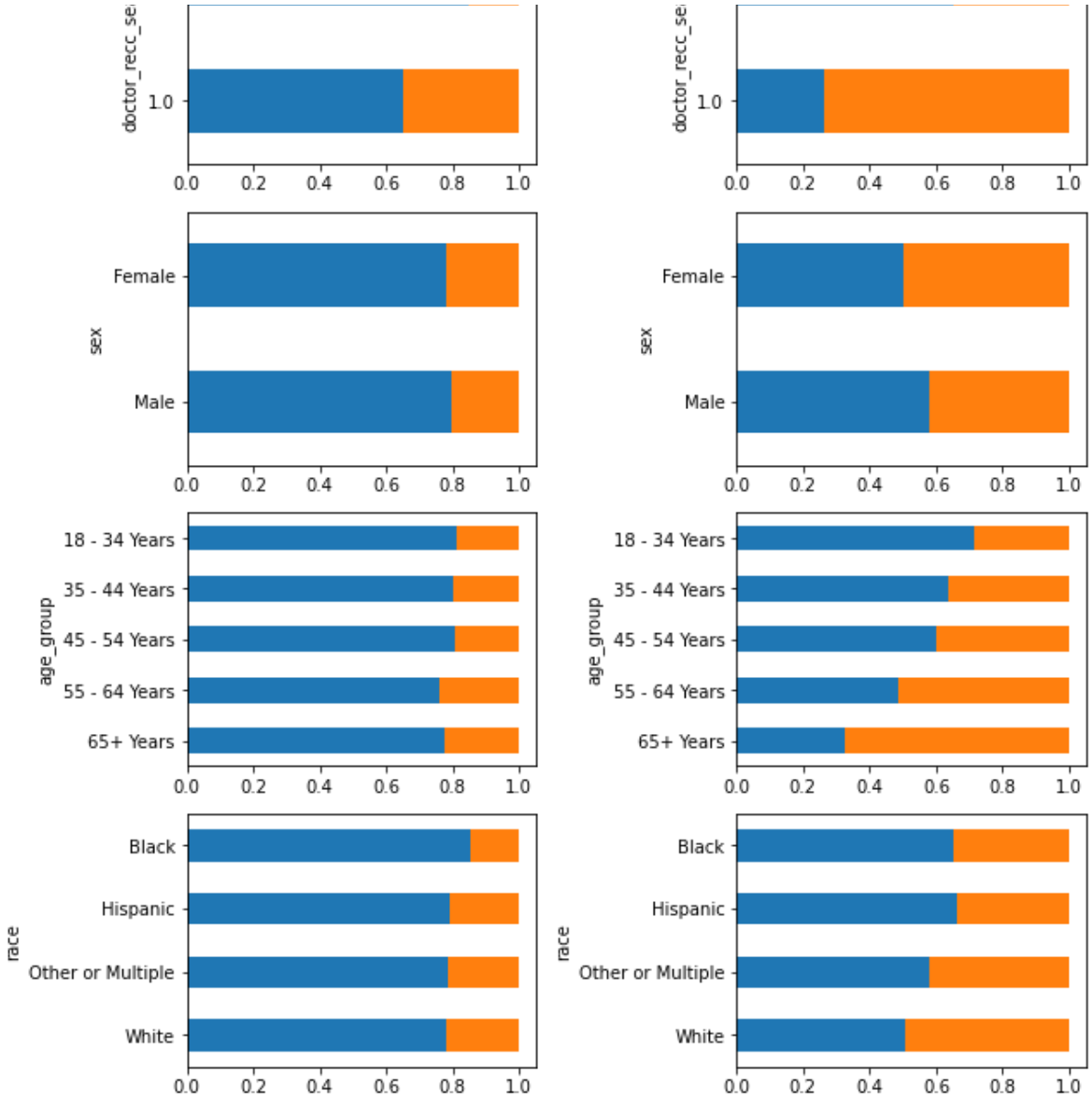
```
# code to select columns to plot
selected_columns =  [
    'h1n1_concern',
    'h1n1_knowledge',
    'opinion_h1n1_vacc_effective',
    'opinion_h1n1_risk',
    'opinion_h1n1_sick_from_vacc',
    'opinion_seas_vacc_effective',
    'opinion_seas_risk',
    'opinion_seas_sick_from_vacc',
    'doctor_recc_h1n1',
    'doctor_recc_seasonal',
    'sex',
    'age_group',
    'race',
]
```

In [30]:

```
# code to plot numeric variables against the target variables

fig, ax = plt.subplots(
    len(selected_columns), 2, figsize=(9,len(selected_columns)*2.5)
)
for idx, col in enumerate(selected_columns):
    vaccination_rate_plot(
        col, 'h1n1_vaccine', combined_df, ax=ax[idx, 0]
    )
    vaccination_rate_plot(
        col, 'seasonal_vaccine', combined_df, ax=ax[idx, 1]
    )

ax[0, 0].legend(
    loc='lower center', bbox_to_anchor=(0.5, 1.05), title='h1n1_vaccine'
)
ax[0, 1].legend(
    loc='lower center', bbox_to_anchor=(0.5, 1.05), title='seasonal_vaccine'
)
fig.tight_layout()
```




opinion_h1n1_
4.0
5.0
0.0 0.2 0.4 0.6 0.8 1.0
opinion_h1n1_risk
1.0
2.0
3.0
4.0
5.0
opinion_h1n1_sick_from_vacc
opinion_seas_vacc_effective
opinion_seas_risk
opinion_seas_sick_from_vacc
doctor_recc_h1n1
0.0
asonal



- **From the above, it is clear that concern, knowledge, opinion and doctor's recommendation of vaccines have a strong correlation with both the h1n1_vaccine and the seasonal_vaccine.**
- **age_group has a stong correlation with seasonal_vaccine whereby a large number of older people tend to accept the vaccine but doesn't show a strong correlation with the h1n1_vaccine.**
- **sex and race have high correlation with the seasonal_vaccine but does not show a strong correllation with the h1n1_vaccine.**

Model Development

Model 1: Building Logistic Regression Model

In [31]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.multioutput import MultiOutputClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import roc_curve, roc_auc_score
from sklearn.preprocessing import StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
```

Preprocessing

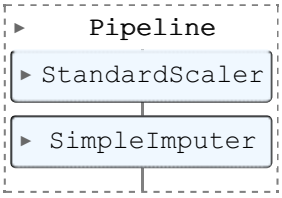
Instead of filling missing data separately then transforming the data using standard scaller, the two steps (scaling and imputing the data) will be combined together using pipeline to make work easier

Median will be used to fill missing values

In [32]:

```
# combine preprocessing into pipeline object on numeric data
numerical_preprocessing_steps = Pipeline([
    ('standard_scaler', StandardScaler()),
    ('simple_imputer', SimpleImputer(strategy='median'))
])

numerical_preprocessing_steps
```

Out[32]:

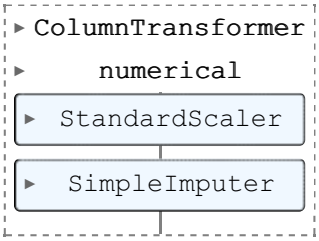


preprocess the data using column transformer

In [33]:

```
# creating preprocessor stage of final pipeline
preprocessor = ColumnTransformer(transformers=[("numerical", numerical_preprocessing_ste
ps, numerical)],
                                 remainder="drop"
                                 )
preprocessor
```

Out[33]:



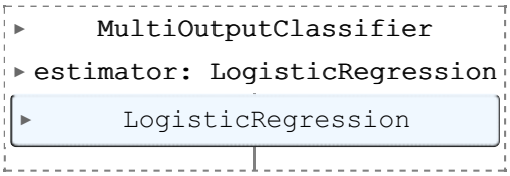
Estimator

Since the data has two different target variables, a Multioutput classifier will be used as an estimator

In [34]:

```
# code for estimator
estimators = MultiOutputClassifier(
    estimator=LogisticRegression(penalty="l2", C=1)
)

estimators
```

Out[34]:

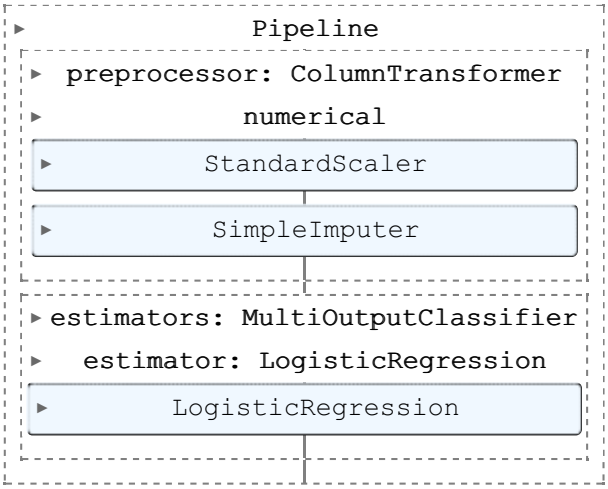


combining estimator and preprocessor to form a complete pipeline

In [35]:

```
model_1 = Pipeline([
    ("preprocessor", preprocessor),
    ("estimators", estimators),
])

model_1
```

Out[35]:



Model Training and Evaluation

The model will be trained and evaluated by splitting the train dataset into train and test.

Later the model will be evaluated using the separate test data that was provided as a separate file

In [36]:

```
X_train, X_train_test, y_train, y_train_test = train_test_split(
    features_df,
    labels_df,
    test_size=0.3,
    shuffle=True,
    stratify=labels_df, # enforce even splits
    random_state=42
)
```

Model training

In [37]:

```
# Train model
model_1.fit(X_train, y_train)

# Predict on evaluation set
y_preds = model_1.predict_proba(X_train_test)
y_preds
```

Out[37]:

```
[array([[0.95138922, 0.04861078],
        [0.854483  , 0.145517  ],
        [0.97502413, 0.02497587],
        ...,
        [0.70545918, 0.29454082],
        [0.41456829, 0.58543171],
        [0.93665301, 0.06334699]]),
 array([[0.93569526, 0.06430474],
        [0.69169398, 0.30830602],
        [0.98163324, 0.01836676],
        ...,
        [0.64042428, 0.35957572],
```

```
        [0.08724774, 0.91275226],
        [0.46803151, 0.53196849]])]
```

checking the shape of the

In [38]:

```
print("test_probas[0].shape", y_preds[0].shape)
print("test_probas[1].shape", y_preds[1].shape)
```

```
test_probas[0].shape (8013, 2)
test_probas[1].shape (8013, 2)
```

- **There are two arrays containing the (number of observations, 2) whereby the first one is for h1n1_vaccine whreas the second one is for the seasonal_vaccine which have the probabilities of 0 and 1 respectively**

In [39]:

```
# Display index 1 for each of the two arrays
y_prediction = pd.DataFrame(
    {
        "h1n1_vaccine": y_preds[0][:, 1],
        "seasonal_vaccine": y_preds[1][:, 1],
    },
    index = y_train_test.index
)
y_prediction.head()
```

Out[39]:

respondent_id	h1n1_vaccine	seasonal_vaccine
7572	0.048611	0.064305
3586	0.145517	0.308306
14114	0.024976	0.018367
2426	0.926849	0.951727
13147	0.087216	0.940136

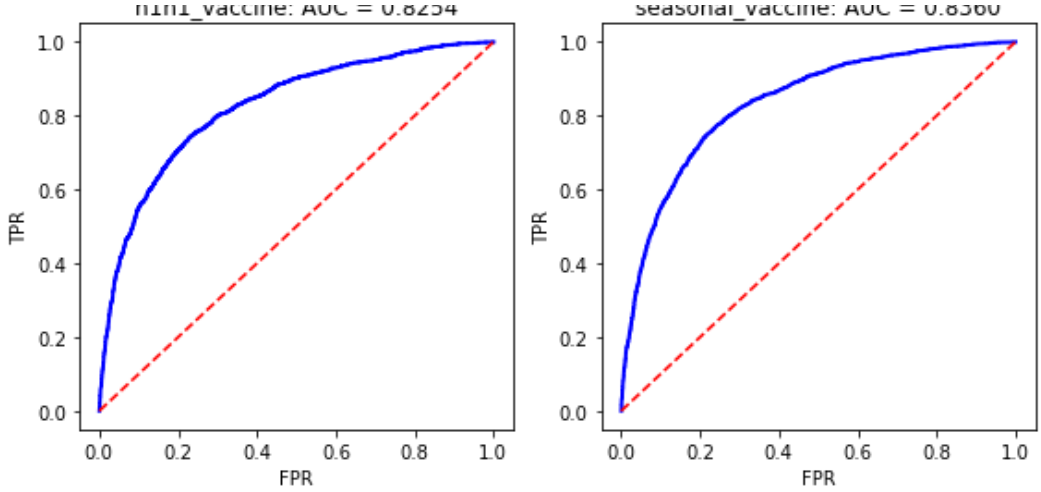
Plotting ROC Curves for Multilabel dataset

In [40]:

```
# Function to create ROC Curve.
def plot_roc(y_true, y_score, label_name, ax):
    fpr, tpr, thresholds = roc_curve(y_true, y_score)
    ax.plot(fpr, tpr, color = 'blue', lw=2)
    ax.plot([0, 1], [0, 1], color='red', linestyle='--')
    ax.set_ylabel('TPR')
    ax.set_xlabel('FPR')
    ax.set_title(f"{label_name}: AUC = {roc_auc_score(y_true, y_score):.4f}")
```

In [41]:

```
# Plotting ROC Curve

fig, ax = plt.subplots(1, 2, figsize=(8, 4))
plot_roc(y_train_test['h1n1_vaccine'], y_prediction['h1n1_vaccine'], 'h1n1_vaccine',ax=a
x[0])
plot_roc(y_train_test['seasonal_vaccine'], y_prediction['seasonal_vaccine'], 'seasonal_va
ccine',ax=ax[1])

fig.tight_layout()
```



- **Both models seem to be performing well since the AUC score on h1n1_vaccine is 0.8254 and the AUC score on seasonal_vaccine is 0.8360.**

In [42]:

```
# Average score for roc_auc
roc_auc_score(y_train_test, y_prediction)
```

Out[42]:

```
0.8307292673111957
```

- **The average performance of the model based on the two different target variables is 83%**

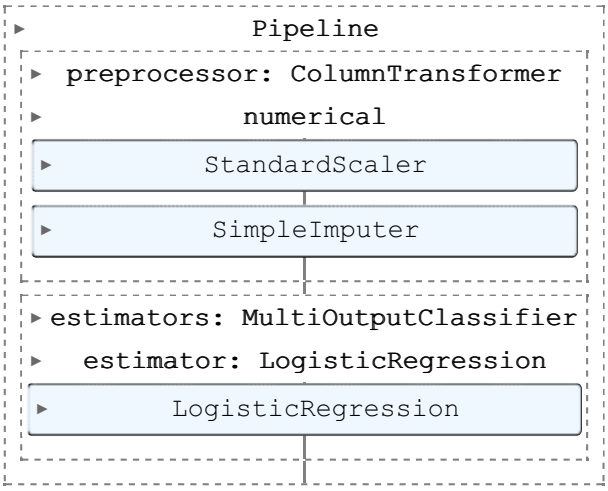
Generating and Testing Data Using The Test Set

Retrain the model on full dataset

In [43]:

```
model_1.fit(features_df, labels_df)
```

Out[43]:



In [44]:

```
# load the test set
test_features_df = pd.read_csv("Data/test_set_features.csv", index_col="respondent_id")
test_features_df.head()
```

Out[44]:

	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi

respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi
respondent_id						
26707	2.0	2.0	0.0	1.0	0.0	
26708	1.0	1.0	0.0	0.0	0.0	
26709	2.0	2.0	0.0	0.0	1.0	
26710	1.0	1.0	0.0	0.0	0.0	
26711	3.0	1.0	1.0	1.0	0.0	

5 rows × 35 columns

In [45]:

```
test_probabilities = model_1.predict_proba(test_features_df)
test_probabilities
```

Out[45]:

```
[array([[0.87280333, 0.12719667],
        [0.94475602, 0.05524398],
        [0.62906951, 0.37093049],
        ...,
        [0.80411015, 0.19588985],
        [0.9492446 , 0.0507554 ],
        [0.38421362, 0.61578638]]),
 array([[0.57359831, 0.42640169],
        [0.92876678, 0.07123322],
        [0.3626162 , 0.6373838 ],
        ...,
        [0.59872448, 0.40127552],
        [0.68003071, 0.31996929],
        [0.35787941, 0.64212059]])]
```

Comments on Logistic Regression

- **From the scores (83.14%) it is evident that based on the information that was shared about people's backgrounds, opinions and health behaviours, people took H1N1 and Seasonal Flue Vaccines.**
- **It therefore implies that a persons background, Opinion and Health Behaviour affect the uptake of a vaccine.**
- **The model performance is good but it is not perfect since it has an 83% performance out of the total 100%**

To test whether the a different model would perform better, a Decision Tree Classification Model (ID3) will be developed.

Model 2: Decision Tree Classifier Vanilla Model

Since the performance of the models are almost similar on H1N1 and Seasonal Flu Vaccine target variables, the Decision Tree Model will be developed using only one target variables.

A simple Decision Tree Model (Vanila Model) is built here

Importing Necessary Libraries

In [46]:

```
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import roc_curve, roc_auc_score, auc
from sklearn.preprocessing import OneHotEncoder
from sklearn import tree
```

Selecting Features and Target Variable

This model will use the columns that were previously selected based on domain knowledge and also one target variable instead of a multilabel problem which was done in the Logistic Regression.

The decision to use one target variable was arrived at after the first model proved to be performing almost similarly.

In [47]:

```
# Selecting Features
selected_cols_df = combined_df[selected_columns]
selected_cols_df.head()
```

Out[47]:

respondent_id	h1n1_concern	h1n1_knowledge	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc
0	1.0	0.0	3.0	1.0	2.0
1	3.0	2.0	5.0	4.0	4.0
2	1.0	1.0	3.0	1.0	1.0
3	1.0	1.0	3.0	3.0	5.0
4	2.0	1.0	3.0	3.0	2.0

Checking whether there are missing values in the selected columns

In [48]:

```
selected_cols_df.isna().sum()
```

Out[48]:

```
h1n1_concern                 0
h1n1_knowledge               0
opinion_h1n1_vacc_effective  0
opinion_h1n1_risk            0
opinion_h1n1_sick_from_vacc  0
opinion_seas_vacc_effective  0
opinion_seas_risk            0
opinion_seas_sick_from_vacc  0
doctor_recc_h1n1             0
doctor_recc_seasonal         0
sex                          0
age_group                    0
race                         0
dtype: int64
```

Comments

- **None of the selected colums have missing values.**
- **It is okay to proceed to feature selection since the data is clean**

In [49]:

```
# selected the features and the target variables
X = selected_cols_df
y = combined_df['seasonal_vaccine']
```

```
#spliting data into train and test
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3, random_state
= 42)
```

In [50]:

```
# check the data types of the data

X.dtypes
```

Out[50]:

```
h1n1_concern                   float64
h1n1_knowledge                 float64
opinion_h1n1_vacc_effective    float64
opinion_h1n1_risk              float64
opinion_h1n1_sick_from_vacc    float64
opinion_seas_vacc_effective    float64
opinion_seas_risk              float64
opinion_seas_sick_from_vacc    float64
doctor_recc_h1n1               float64
doctor_recc_seasonal           float64
sex                             object
age_group                       object
race                            object
dtype: object
```

- **The `sex`, `age_group` and `race` columns are categorical columns (object).**
- **The rest of the columns are numerical columns (float64).**

Encode categorical data as numbers

Since the data currently contains both categorical and numerical data, all the data need to be encoded as numbers. For this, the sklearn's `OneHotEncoder` from `preprocessing` will be used.

In [51]:

```
# One-hot encode the training data and show the resulting DataFrame with proper column na
mes
ohe = OneHotEncoder()

ohe.fit(X_train)
X_train_ohe = ohe.transform(X_train).toarray()

# show the result of the ohe
ohe_df = pd.DataFrame(X_train_ohe, columns=ohe.get_feature_names_out(X_train.columns))

ohe_df.head()
```

Out[51]:

	h1n1_concern_0.0	h1n1_concern_1.0	h1n1_concern_2.0	h1n1_concern_3.0	h1n1_knowledge_0.0	h1n1_knowledge_1.0	h1n1_
0	0.0	0.0	1.0	0.0	0.0	0.0	
1	0.0	0.0	1.0	0.0	0.0	1.0	
2	0.0	0.0	0.0	1.0	0.0	1.0	
3	0.0	1.0	0.0	0.0	0.0	0.0	
4	1.0	0.0	0.0	0.0	0.0	0.0	

5 rows × 52 columns

Train the decision tree

In [52]:

```
# Create the classifier, fit it on the training data and make predictions on the test set
model_2 = DecisionTreeClassifier(criterion='entropy', random_state=42)

model_2.fit(X_train_ohe, y_train)
```

Out[52]:

DecisionTreeClassifier(criterion='entropy', random_state=42)

Evaluate the predictive performance Using Probabilities

Evaluating the model using ROC_AUC Score

In [53]:

```
X_test_ohe = ohe.transform(X_test)

# Evaluate the model
y_probs = model_2.predict_proba(X_test_ohe)[:, 1]

# find the roc_auc score
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_probs)
roc_auc = auc(false_positive_rate, true_positive_rate)

print(f'roc_auc for test data: {roc_auc:.4f}')
```

```
roc_auc for test data: 0.6902
```

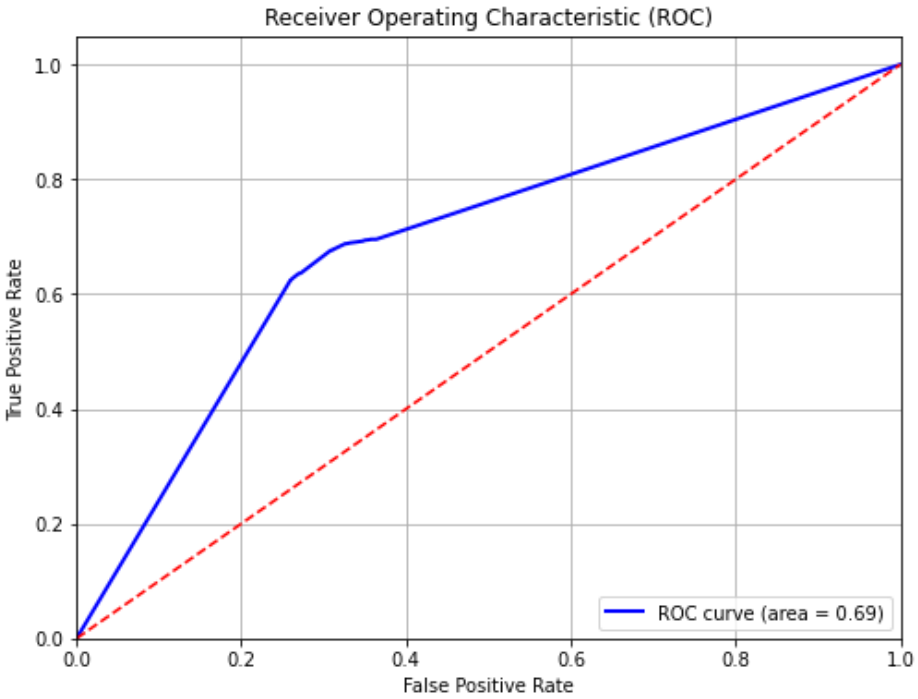
Creating a function for AUC_ROC Curve

In [54]:

```
def plot_roc_auc(model, X_test, y_test):
    # Get predicted probabilities for the positive class (usually the second column in bi
nary classification)
    y_preds = model.predict_proba(X_test)[:, 1]

    # Calculate the ROC curve
    false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_preds)

    # Calculate the AUC
    roc_auc = auc(false_positive_rate, true_positive_rate)

    # Plot the ROC curve
    plt.figure(figsize=(8, 6))
    plt.plot(false_positive_rate, true_positive_rate, color='blue', lw=2, label=f'ROC cu
rve (area = {roc_auc:.2f})')
    plt.plot([0, 1], [0, 1], color='red', linestyle='--')
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('Receiver Operating Characteristic (ROC)')
    plt.legend(loc='lower right')
    plt.grid(True)

    # Show the plot
    plt.show()

    # Return the AUC value
    return roc_auc
```

In [55]:

```
# Plot ROC AUC for model_2
auc_value = plot_roc_auc(model_2, X_test_ohe, y_test)
print(f'AUC for test data: {auc_value:.4f}')

y_train_probs = model_2.predict_proba(X_train_ohe)[:, 1]

# Calculate the ROC curve
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_train, y_train_probs)

# Calculate the AUC
roc_auc_train = auc(false_positive_rate, true_positive_rate)

print(f'roc_auc for training data: {roc_auc_train:.4f}')
```




```
AUC for test data: 0.6902
roc_auc for training data: 0.9962
```

Comments

- **The model performance using the decision tree is lower compaired to the performance of the Logistic Regression Model.**
- **The score roc_auc is 69% whereas the score in the Logistic Regression is 83%.**
- **This might be because the number of features selected in the Logistic Regression Model were higher compaired to the features selected for Decision Tree.**
- **The difference in score might also be caused by overfitting in the desion tree.**
- **The model performance on Training score is 99.62% indicating that the moodel is overfitted**
- **To solve the overfitting problem, tree prunning / hyperparameter tuning will be done in the next model**

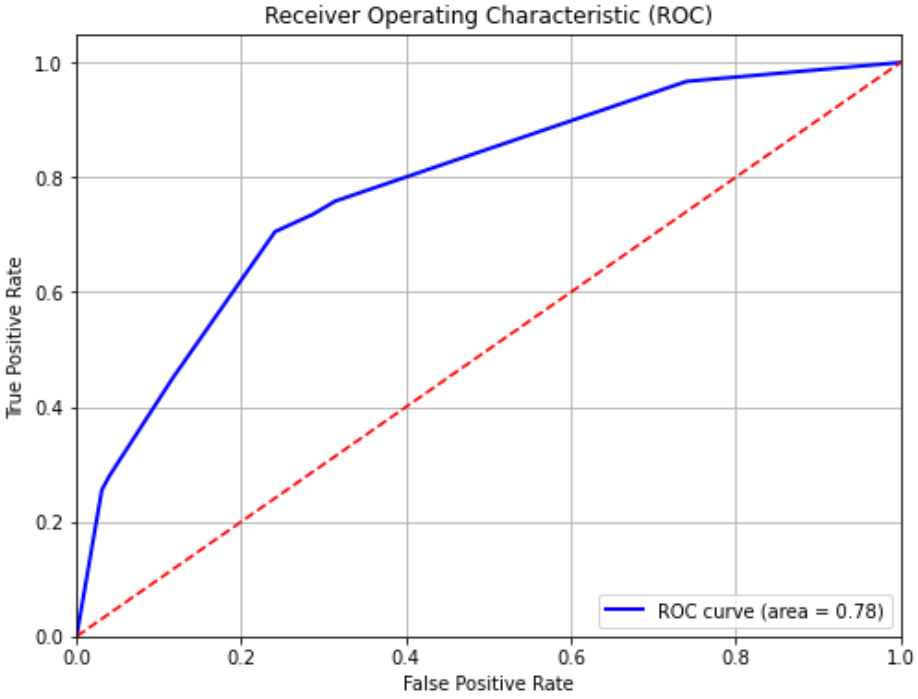
Model 3: Tree Prunning using Max_Depth

Similar Features that were used to develop the vanilla model are used here. The only difference is that the model is prunned to prevent overfitting

In [56]:

```
# Create the classifier, fit it on the training data and tune using max_depth=3
model_3 = DecisionTreeClassifier(criterion='entropy', max_depth=3, random_state=42)

#fit the model
model_3.fit(X_train_ohe, y_train)

# Evaluate the model
```

```
X_test_ohe = ohe.transform(X_test)

y_probs = model_3.predict_proba(X_test_ohe)[:, 1]

# find the roc_auc score
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_probs)
roc_auc = auc(false_positive_rate, true_positive_rate)


# Plot ROC AUC for model_4
auc_value = plot_roc_auc(model_3, X_test_ohe, y_test)

#print AUC value and the roc_AUC
print(f'AUC for test data: {auc_value:.4f}')
print(f'roc_auc: {roc_auc:.4f}')

y_train_probs = model_3.predict_proba(X_train_ohe)[:, 1]

# Calculate the ROC curve
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_train, y_train_probs)

# Calculate the AUC
roc_auc_train = auc(false_positive_rate, true_positive_rate)

print(f'roc_auc for training data: {roc_auc_train:.4f}')
```




```
AUC for test data: 0.7828
roc_auc: 0.7828
roc_auc for training data: 0.7856
```

Comments

- **The model has significantly improved (73% performance score) compaired to the Vanilla decision tree model (69% performance score) that was not prunned.**
- **The Logistic Regression Model that had two target variables still performs better (83% performance score) compaired to the two Decision Tree models.**
- **This might be attributed to the size of the Logistic Regression Model that had a higher number of Features compaired to the features selected for Decision Tree.**

Model 4: Prunned Decision Tree (ID3) with more Features Using 1 Target Variable

Here, all the numerical columns that were used to develop the Logistic Regression Model are used.

The categorical variables which had shown positive correllation with seasonal_vaccine are also used. These are

The categorical variables which had shown positive correlation with seasonal_vaccine are also used. These are `sex`, `age_group` and `race` columns.

In [57]:

```
# select numerical features
numeric_cols_df = combined_df[numerical]

# select categorical features from the selected columns
# the colums were previously selected during EDA and used in Model 2 & 3
categorical_cols = selected_cols_df.columns[selected_cols_df.dtypes == "object"]

# Data Frame for selected columns
selected_categorical_cols_df = combined_df[categorical_cols]

print(numeric_cols_df)
print(selected_categorical_cols_df)
```

```
               h1n1_concern  h1n1_knowledge  behavioral_antiviral_meds  \
respondent_id
0                       1.0             0.0                        0.0
1                       3.0             2.0                        0.0
2                       1.0             1.0                        0.0
3                       1.0             1.0                        0.0
4                       2.0             1.0                        0.0
...                     ...             ...                        ...
26702                   2.0             0.0                        0.0
26703                   1.0             2.0                        0.0
26704                   2.0             2.0                        0.0
26705                   1.0             1.0                        0.0
26706                   0.0             0.0                        0.0

               behavioral_avoidance  behavioral_face_mask  \
respondent_id
0                               0.0                   0.0
1                               1.0                   0.0
2                               1.0                   0.0
3                               1.0                   0.0
4                               1.0                   0.0
...                             ...                   ...
26702                           1.0                   0.0
26703                           1.0                   0.0
26704                           1.0                   1.0
26705                           0.0                   0.0
26706                           1.0                   0.0

               behavioral_wash_hands  behavioral_large_gatherings  \
respondent_id
0                                0.0                          0.0
1                                1.0                          0.0
2                                0.0                          0.0
3                                1.0                          1.0
4                                1.0                          1.0
...                              ...                          ...
26702                            0.0                          0.0
26703                            1.0                          0.0
26704                            1.0                          1.0
26705                            0.0                          0.0
26706                            0.0                          0.0

               behavioral_outside_home  behavioral_touch_face  \
respondent_id
0                                  1.0                    1.0
1                                  1.0                    1.0
2                                  0.0                    0.0
3                                  0.0                    0.0
4                                  0.0                    1.0
...                                ...                    ...
26702                              1.0                    0.0
26703                              0.0                    0.0
26704                              0.0                    1.0
26705                              0.0                    1.0
```

```
26706                            0.0                    0.0

               doctor_recc_h1n1  ...  health_worker  health_insurance  \
respondent_id                    ...
0                           0.0  ...            0.0               1.0
1                           0.0  ...            0.0               1.0
2                           0.0  ...            0.0               1.0
3                           0.0  ...            0.0               1.0
4                           0.0  ...            0.0               1.0
...                         ...  ...            ...               ...
26702                       0.0  ...            0.0               1.0
26703                       1.0  ...            1.0               1.0
26704                       0.0  ...            0.0               1.0
26705                       0.0  ...            0.0               0.0
26706                       0.0  ...            0.0               1.0

               opinion_h1n1_vacc_effective  opinion_h1n1_risk  \
respondent_id
0                                      3.0                1.0
1                                      5.0                4.0
2                                      3.0                1.0
3                                      3.0                3.0
4                                      3.0                3.0
...                                    ...                ...
26702                                  3.0                1.0
26703                                  4.0                2.0
26704                                  4.0                4.0
26705                                  3.0                1.0
26706                                  5.0                1.0

               opinion_h1n1_sick_from_vacc  opinion_seas_vacc_effective  \
respondent_id
0                                      2.0                          2.0
1                                      4.0                          4.0
2                                      1.0                          4.0
3                                      5.0                          5.0
4                                      2.0                          3.0
...                                    ...                          ...
26702                                  1.0                          5.0
26703                                  2.0                          5.0
26704                                  2.0                          5.0
26705                                  2.0                          2.0
26706                                  1.0                          5.0

               opinion_seas_risk  opinion_seas_sick_from_vacc  \
respondent_id
0                            1.0                          2.0
1                            2.0                          4.0
2                            1.0                          2.0
3                            4.0                          1.0
4                            1.0                          4.0
...                          ...                          ...
26702                        2.0                          2.0
26703                        1.0                          1.0
26704                        4.0                          2.0
26705                        1.0                          2.0
26706                        1.0                          1.0

               household_adults  household_children
respondent_id
0                           0.0                0.0
1                           0.0                0.0
2                           2.0                0.0
3                           0.0                0.0
4                           1.0                0.0
...                         ...                ...
26702                       0.0                0.0
26703                       1.0                0.0
26704                       0.0                0.0
26705                       1.0                0.0
26706                       1.0                0.0
```

```
[26707 rows x 23 columns]
                    sex      age_group      race
respondent_id
0                Female  55 - 64 Years     White
1                  Male  35 - 44 Years     White
2                  Male  18 - 34 Years     White
3                Female      65+ Years     White
4                Female  45 - 54 Years     White
...                 ...            ...       ...
26702            Female      65+ Years     White
26703              Male  18 - 34 Years     White
26704            Female  55 - 64 Years     White
26705            Female  18 - 34 Years  Hispanic
26706              Male      65+ Years     White

[26707 rows x 3 columns]
```

- **There are two different dataframes that need to be joined before using them to develop the fourth Model**

In [58]:

```
# combining the dataframe
large_df = numeric_cols_df.join(selected_categorical_cols_df)
large_df.head()
```

Out[58]:

respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavi
0	1.0	0.0	0.0	0.0	0.0	
1	3.0	2.0	0.0	1.0	0.0	
2	1.0	1.0	0.0	1.0	0.0	
3	1.0	1.0	0.0	1.0	0.0	
4	2.0	1.0	0.0	1.0	0.0	

5 rows × 26 columns

- **The new data frame consists of 26 different features and it has both numeric and categorical data (23 numeric and 3 categorical).**
- **The data need to be encoded using OneHotEncoder so as to convert all the features to numeric type.**

In [59]:

```
# selected the features and the target variables
X = large_df
y = combined_df['seasonal_vaccine']

#spliting data into train and test
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3, random_state
= 42)
```

Encoding the Data using OneHotEncoder

This will convert the entire dataset to numerical

In [60]:

```
# One-hot encode the training data and show the resulting DataFrame with proper column na
```

```
mes
ohe = OneHotEncoder()

ohe.fit(X_train)
X_train_ohe = ohe.transform(X_train).toarray()

#encode the test data
X_test_ohe = ohe.transform(X_test).toarray()

#show the result of the ohe on train dataset
ohe_df = pd.DataFrame(X_train_ohe, columns=ohe.get_feature_names_out(X_train.columns))

ohe_df.head()
```

Out[60]:

	h1n1_concern_0.0	h1n1_concern_1.0	h1n1_concern_2.0	h1n1_concern_3.0	h1n1_knowledge_0.0	h1n1_knowledge_1.0	h1n1_
0	0.0	0.0	1.0	0.0	0.0	0.0	
1	0.0	0.0	1.0	0.0	0.0	1.0	
2	0.0	0.0	0.0	1.0	0.0	1.0	
3	0.0	1.0	0.0	0.0	0.0	0.0	
4	1.0	0.0	0.0	0.0	0.0	0.0	

5 rows × 82 columns

Hyperparameter Tuning: Identify maximum tree depth

To create the best decision tree model, the optimal depth for the model had to be identified.

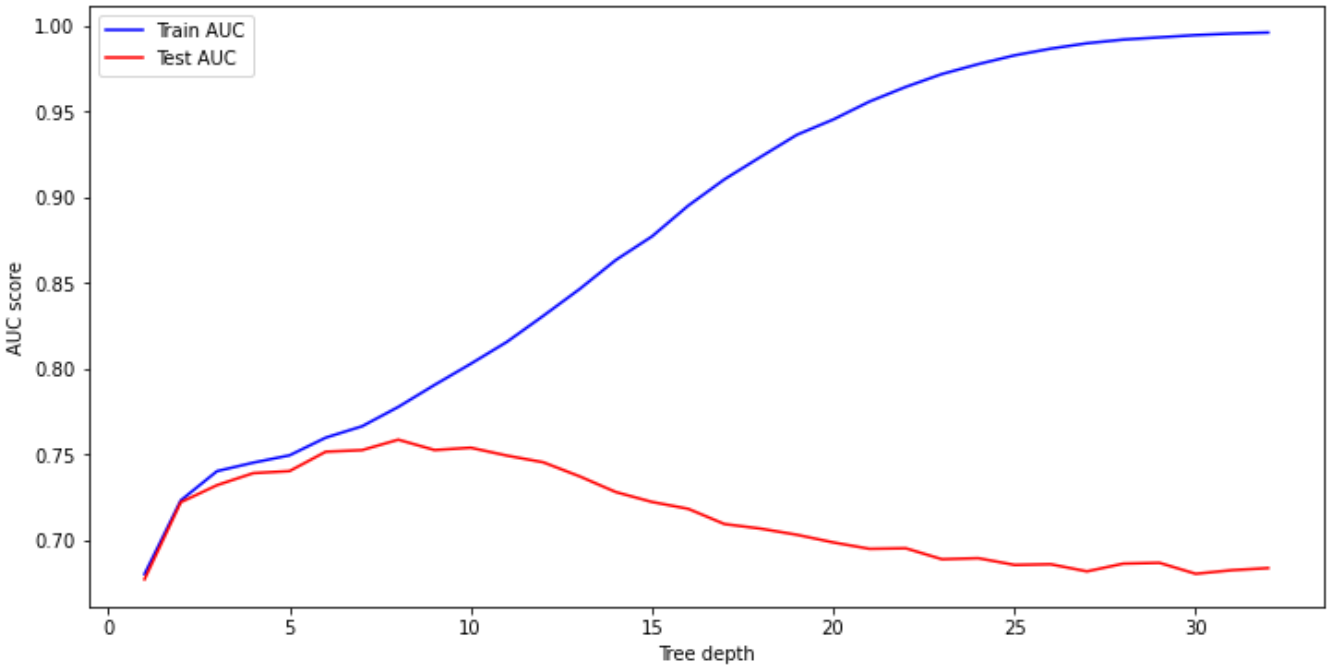
The graph showing the performance of a model as a function of the training process, AUC (Area Under the Curve), for both the training set (in blue) and the test set (in red) as the training progresses is created here.

The graph will show overfitting, undefitting and optimal values.

In [61]:

```
# Identify the optimal tree depth for given data
max_depths = list(range(1, 33))
train_results = []
test_results = []

for max_depth in max_depths:
    dt = DecisionTreeClassifier(criterion='entropy', max_depth=max_depth, random_state=4
2)
    dt.fit(X_train_ohe, y_train)
    train_pred = dt.predict(X_train_ohe)
    false_positive_rate, true_positive_rate, thresholds = roc_curve(y_train, train_pred)
    roc_auc = auc(false_positive_rate, true_positive_rate)

    # Add auc score to previous train results
    train_results.append(roc_auc)
    y_pred = dt.predict(X_test_ohe)
    false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred)
    roc_auc = auc(false_positive_rate, true_positive_rate)

    # Add auc score to previous test results
    test_results.append(roc_auc)

plt.figure(figsize=(12,6))
plt.plot(max_depths, train_results, 'b', label='Train AUC')
plt.plot(max_depths, test_results, 'r', label='Test AUC')
plt.ylabel('AUC score')
plt.xlabel('Tree depth')
plt.legend()
```

```
plt.show()
```



Comments on the Maximum Depth Graph

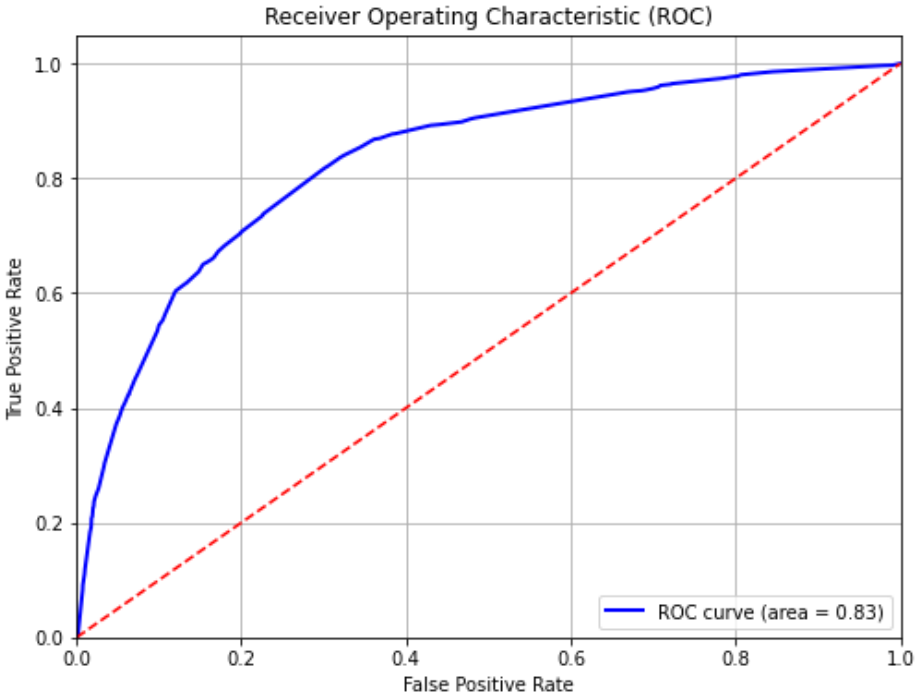
- **The AUC score on the training data (Blue Curve) increases continuously as the model is trained since the model is learning the patterns in the training data. The model improves at predicting the outcomes for the training set as it continues to learn the data.**
- **The AUC score on the test data (Red Curve) initially increases along with the training AUC, indicating that the model is generalizing well to unseen data at the start until it starts to decline the depth of about 7 even as the Train AUC continues to rise.**
- **The decline in the performance of the Test Data whereas the training data performance continues to increase indicate that the model has become overfitted.**
- **7 is therefore the optimal depth that will be used to tune the model**

Develop and Test the Model

In [62]:

```
# Create the ID3 classifier and prune the model using max_depth=8
model_4 = DecisionTreeClassifier(criterion='entropy', max_depth=7, random_state=42)

#fit the model
model_4.fit(X_train_ohe, y_train)

# Evaluate the model
y_probs = model_4.predict_proba(X_test_ohe)[:, 1]

# find the roc_auc score
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_probs)
roc_auc = auc(false_positive_rate, true_positive_rate)

# Plot ROC AUC for model_4
auc_value = plot_roc_auc(model_4, X_test_ohe, y_test)

# print ROC_AUC and AUC values
print(f'roc_auc for test data: {roc_auc:.4f}')
print(f'AUC for test data: {auc_value:.4f}')

y_train_probs = model_4.predict_proba(X_train_ohe)[:, 1]

# Calculate the ROC curve
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_train, y_train_probs)

# Calculate the AUC
```

```
roc_auc_train = auc(false_positive_rate, true_positive_rate)

print(f'roc_auc for training data: {roc_auc_train:.4f}')
```




```
roc_auc for test data: 0.8312
AUC for test data: 0.8312
roc_auc for training data: 0.8491
```

Comments on Model 4 Performance

- **The performance of the model has significantly improved (83% auc_roc score) compaired to the second and third models which were both decision tree models but had a performance of 69% and 78% respectively.**
- **This improvement in performance is attributed to the use of more features and the use of correct depth limit achieved through hyperparameter tuning.**
- **The model however, has thesame performance when compaired to the Logistic Regression model that had a performance score of 83% despite model four having more features than the Logistic Regression Model.**
- **To further improve the performance of the Decision Tree Classifier, other tree prunning methods like (minimum samples with leaf split, minimum leaf sample size, maximum leaf nodes, and maximum features) can be used instead of using miaximum depth alone.**

FINDINGS AND RECOMMENDATIONS

FINDINGS

1. **Logistic Regression Model has an average roc_auc score of 83.07% indicating that the model performs well in predicting H1N1 and Seasonal Flu Vaccines uptake**
2. **The Vanilla Decision Tree Model has an roc_auc score of 69% which is a poor performance compaired to the logistic regression model. This indicate that use of less variables without hypeperameter tuning results to poor model performance in Decision Trees.**
3. **The tuned decision tree using similar features as the Vanilla model had a n roc_auc score of 78% indicating that proper prunning of decision tree can lead to good performance of a model**
4. **The tuned decision tree that was developed using an optimal depth with more three more features (`sex`, `race` and `age_group`) compaired to the logistic regression that had only 23 features performed better than all the models (roc_auc of 83.12%). This indicate that with proper tuning and increasing the number features the model ca perform better in predicting vaccines**

Recommendations

1. **When performing hypeparameter tuning for the decision tree classifier, only the Maximum Depth was used.**

To improve the performance of the Decision Tree Classifier, other tree prunning methods like (minimum samples with leaf split, minimum leaf sample size, maximum leaf nodes, and maximum features) can be used instead of using miaximum depth alone.

2. **The decision tree classifier used only one target variable (seasonal_vaccine). Both outcomes can be included in the decision tree model to determine whether the model performance will improve.**