Predicting Uptake of Seasonal Flu Vaccine

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Introduction

Business Understanding

Problem Statement

Disease prevention is one key role of public health in addition to curative measures. Globally, vaccination is one of the public health departments' measures used to prevent infectious disease. This is because vaccines provide protection to individuals through immunity and the community at large through herd immunity. With this, little is known on how factors such as socioeconomic, behavioral, demographics, opinions on risks of illness and vaccines effectiveness and behavior towards mitigating tranmission influence the uptake of vaccines.

Understanding how these factors influence the uptake of the vaccines can help the policy makers formulates effective policies aimed at increase of the uptake of the vaccines. The manufacturers will also gain insight into the total number of the vaccines to manufacture incases of the pandemics.

General Objective

To understand which factors influence the uptake of the seasonal flu vaccine.

Specific Objectives

1. To determine how socioeconomic factors influence an individual's uptake of the seasonal flu vaccines.
2. To determine how behavioral factors influence an individual's uptake of the seasonal flu vaccines.
3. To determine how demographic background factors influence an individual's uptake of the seasonal flu vaccines.
4. To understand how an individual's knowledge, perception, and attitude towards seasonal flu vaccines influence the uptake of the vaccines.

Research Questions

1. How do socioeconomic factors influence an individual's uptake of the seasonal flu vaccines?
2. What is the impact of behavioral factors on an individual's uptake of the seasonal flu vaccines?
3. How do demographic background factors affect an individual's uptake of the seasonal flu vaccines?
4. How does an individual's knowledge, perception, and attitude towards seasonal flu vaccines influence the uptake of the vaccines?

Data Understanding

- The data is composed of approximately 26,000 instances of individual data and vaccine decision information.

Data Source

Data files were obtained from: DRIVENDATA(Source: CDC, NCRID and NCHS (2012), National 2009 H1N1 Flu Survey). This data was colleted over the phone between late 2009 and June 2010

The data labels are described in this link.

Data Science Cycle

The CRoss Industry Standard Process for Data Mining (CRISP-DM) was used for the analyzes of data. https://www.datascience-pm.com/crisp-dm-2/

```
#import libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from xgboost import XGBClassifier
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2
from sklearn.ensemble import ExtraTreesClassifier
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import confusion_matrix
from sklearn.dummy import DummyClassifier
from sklearn.metrics import confusion_matrix
from sklearn.preprocessing import OneHotEncoder
from sklearn.metrics import accuracy_score, recall_score, precision_score, f1_score
from sklearn.metrics import roc_curve, roc_auc_score
from sklearn.model_selection import GridSearchCV

import missingno as msno


#import datasets
train = pd.read_csv("training_set_features.csv")
target = pd.read_csv("training_set_labels.csv")
test = pd.read_csv("test_set_features.csv")

# Display the first few rows of each DataFrame to ensure data loading was successful
print("Training Data:")
print(train.head())

print("\nTarget Labels:")
print(target.head())

print("\nTest Data:")
print(test.head())
```

```
4         Own            Employed       lzgpxyit                  Non-MSA

   household_adults  household_children  employment_industry  \
0               1.0                 0.0             atmlpfrs
1               3.0                 0.0             atmlpfrs
2               1.0                 0.0             nduyfdeo
3               1.0                 0.0                  NaN
4               0.0                 1.0             fcxhlnwr

   employment_occupation
0               hfxkjkmi
1               xqwwgdyp
2               pvmttkik
3                    NaN
4               mxkfnird

[5 rows x 36 columns]
```

Some more data exploration

```
 #Examine Data Shape and Size
print("Train Shape:", train.shape)
print("Test Shape:", test.shape)
print("Target Shape:", target.shape)
```

```
Train Shape: (26707, 36)
Test Shape: (26708, 36)
Target Shape: (26707, 3)
```

The train feature dataset contains 26707 rows and 36 columns.

The test dataset contains 26708 rows and 36 columns

The target dataset contains 26707 rows and 3 columns

```
# Print column names and data types of the "train" DataFrame
print("\nTrain Data Columns:")
print(train.columns)
```

```
Train Data Columns:
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')
```

```
# Print column names and data types of the "test" DataFrame
print("\nTest Data Columns:")
print(test.columns)
```

```
Test Data Columns:
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')
```

```
# Print column names and data types of the "target" DataFrame
print("\nTarget Labels Columns:")
print(target.columns)
```

```
     Target Labels Columns:
     Index(['respondent_id', 'h1n1_vaccine', 'seasonal_vaccine'], dtype='object')
```

Drop information for HINI since our target feature is seasonal flu vaccines

- The columns are not directly relevant to the current analysis.

```
# Drop columns related to H1N1 flu from the "train" DataFrame
train.drop(columns=["h1n1_concern","h1n1_knowledge","doctor_recc_h1n1","opinion_h1n1_vacc_effective","opinion_h1n1_risk","opinion_h1n1_sick_f

# Drop columns related to H1N1 flu from the "test" DataFrame
test.drop(columns=["h1n1_concern","h1n1_knowledge","doctor_recc_h1n1","opinion_h1n1_vacc_effective","opinion_h1n1_risk","opinion_h1n1_sick_fr

# Drop columns related to H1N1 flu from the "test" DataFrame
target.drop(columns=["h1n1_vaccine"], axis=1, inplace=True)


# Check if the columns dropped
print("train Shape:", train.shape)
print("set Shape:", test.shape)
print("target Shape:", target.shape)
```

```
     train Shape: (26707, 30)
     set Shape: (26708, 30)
     target Shape: (26707, 2)
```

- Six columns were successfully dropped.

```
# Explore Data Structure

# train df
print("train Info:")
print(train.info())

#test df
print("\ntest Info:")
print(test.info())

# target df
print("\ntarget Info:")
print(target.info())
```

```
 17  education                  25301 non-null  object
 18  race                       26708 non-null  object
 19  sex                        26708 non-null  object
 20  income_poverty             22211 non-null  object
 21  marital_status             25266 non-null  object
 22  rent_or_own                24672 non-null  object
 23  employment_status          25237 non-null  object
 24  hhs_geo_region             26708 non-null  object
 25  census_msa                 26708 non-null  object
 26  household_adults           26483 non-null  float64
 27  household_children         26483 non-null  float64
 28  employment_industry        13433 non-null  object
 29  employment_occupation      13282 non-null  object
dtypes: float64(17), int64(1), object(12)
memory usage: 6.1+ MB
None

target Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26707 entries, 0 to 26706
Data columns (total 2 columns):
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   respondent_id     26707 non-null  int64
 1   seasonal_vaccine  26707 non-null  int64
dtypes: int64(2)
memory usage: 417.4 KB
None
```

- The training dataset contains float and object datatypes.
- The dataset shall remain as it is since it matches the test dataset data types.

```
# Explore train Summary Statistics
print("train Summary Statistics:")
print(train.describe())
```

```
count          26688.000000           26665.000000
mean               0.068982               0.825614
std                0.253429               0.379448
min                0.000000               0.000000
25%                0.000000               1.000000
50%                0.000000               1.000000
75%                0.000000               1.000000
max                1.000000               1.000000

       behavioral_large_gatherings  behavioral_outside_home  \
count                  26620.00000             26625.000000
mean                       0.35864                 0.337315
std                        0.47961                 0.472802
min                        0.00000                 0.000000
25%                        0.00000                 0.000000
50%                        0.00000                 0.000000
75%                        1.00000                 1.000000
max                        1.00000                 1.000000

       behavioral_touch_face  doctor_recc_seasonal  chronic_med_condition  \
count           26579.000000          24547.000000           25736.000000
mean                0.677264              0.329735               0.283261
std                 0.467531              0.470126               0.450591
min                 0.000000              0.000000               0.000000
25%                 0.000000              0.000000               0.000000
50%                 1.000000              0.000000               0.000000
75%                 1.000000              1.000000               1.000000
max                 1.000000              1.000000               1.000000

       child_under_6_months  health_worker  health_insurance  \
count          25887.000000   25903.000000       14433.00000
mean               0.082590       0.111918           0.87972
std                0.275266       0.315271           0.32530
min                0.000000       0.000000           0.00000
```

```
    75%                        5.000000           4.000000
    max                        5.000000           5.000000

           opinion_seas_sick_from_vacc  household_adults  household_children
    count                 26170.000000      26458.000000        26458.000000
    mean                      2.118112          0.886499            0.534583
    std                       1.332950          0.753422            0.928173
    min                       1.000000          0.000000            0.000000
    25%                       1.000000          0.000000            0.000000
    50%                       2.000000          1.000000            0.000000
    75%                       4.000000          1.000000            1.000000
    max                       5.000000          3.000000            3.000000
```

- From the summary statistics, **data does not have outliers** since the data contains the binary and categorical types of data.
- More on outliers will be checked during the EDA process.

Checking for duplicates

```
# Check duplicates
duplicates_train = train.duplicated()
duplicates_test = test.duplicated()
num_duplicates_train = duplicates_train.sum()
num_duplicates_test = duplicates_test.sum()

print("Duplicate Rows in Train Set:", num_duplicates_train)
print("Duplicate Rows in Test Set:", num_duplicates_test)
```

```
    Duplicate Rows in Train Set: 0
    Duplicate Rows in Test Set: 0
```

- There **are no duplicates** in the dataset.

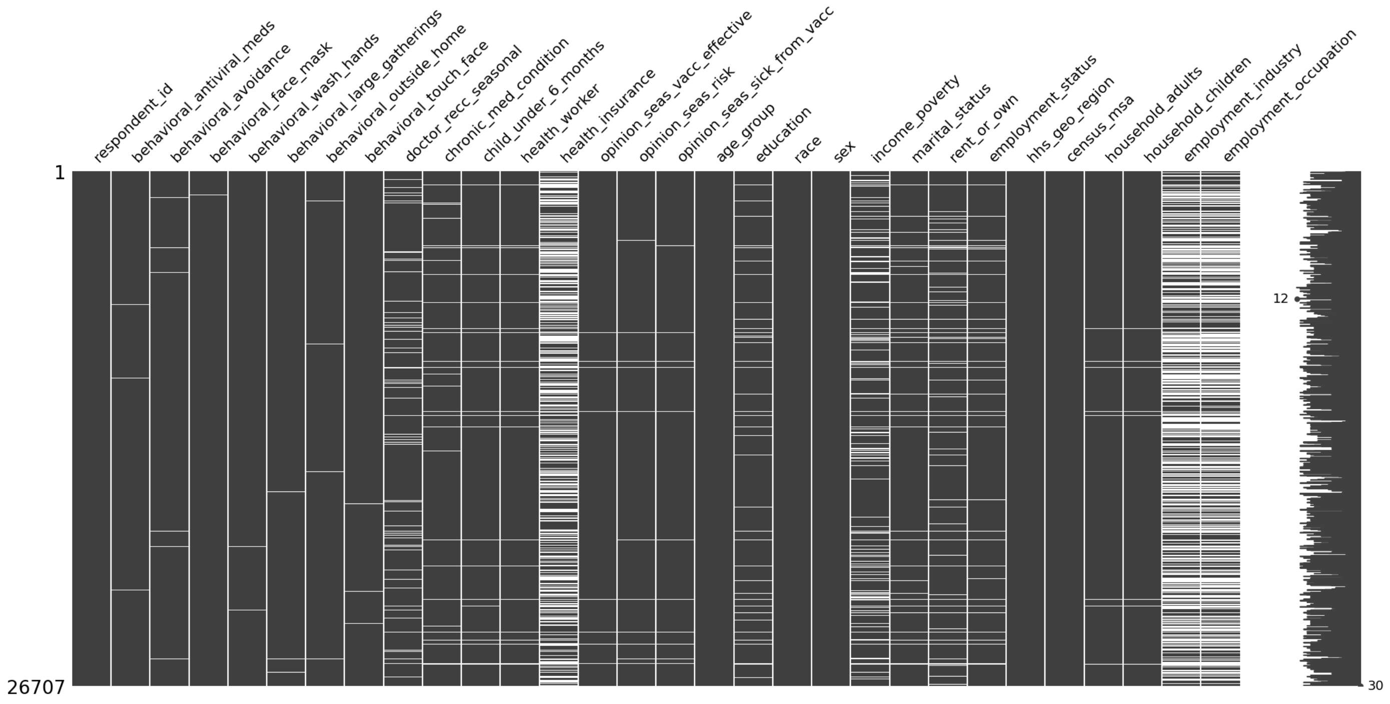
Checking for Missing Values

```
# check for the percentage of missing values
missing=(train.isnull().sum()/len(train))*100

# show columns with the highest missing percentages
missing = missing.sort_values(ascending=False)

print("Missing values:")
print(missing)
```

```
    Missing values:
    employment_occupation          50.436215
    employment_industry            49.912008
    health_insurance               45.957989
    income_poverty                 16.561201
    doctor_recc_seasonal            8.087767
    rent_or_own                     7.645936
    employment_status               5.477965
    marital_status                  5.272026
    education                       5.268282
    chronic_med_condition           3.635751
    child_under_6_months            3.070356
    health_worker                   3.010447
    opinion_seas_sick_from_vacc     2.010709
    opinion_seas_risk               1.924589
    opinion_seas_vacc_effective     1.729884
    household_children              0.932340
    household_adults                0.932340
    behavioral_avoidance            0.778822
    behavioral_touch_face           0.479275
    behavioral_large_gatherings     0.325757
    behavioral_outside_home         0.307036
    behavioral_antiviral_meds       0.265848
    behavioral_wash_hands           0.157262
    behavioral_face_mask            0.071142
    sex                             0.000000
    hhs_geo_region                  0.000000
    census_msa                      0.000000
    race                            0.000000
    age_group                       0.000000
    respondent_id                   0.000000
    dtype: float64
```

```
# Visualize missing values
msno.matrix(train)
```

```
<Axes: >
```



Observations

1. The employment_occupation, employment_industry, and health_insurance columns have the most missing values, with null values making up 50.4%, 49.9%, and 46.0% of the columns, respectively.
2. However, 10,231 of the null values for employment_occupation and employment_industry are basically "not applicable" rather than someone declining to answer because those are the respondents who answered "Not in Labor Force" for employment_status (see below).
3. See the same for an additional 1,453 observations representing all unemployed individuals. Again employment_occupation and employment_industry are better thought of as "not applicable" rather than someone declining to answer.

There are some clear patterns in missing values:

4. If respondent declined to answer whether their doctor recommended one type of vaccine, they usually declined to answer about whether their doctor recommended the other type.
5. Individuals also seemed to decline to answer whether they had a chronic medical condition, a child under 6 months, whether they were a health worker, all opinion questions, income, education, personal and home life questions.
6. These missing data patterns may indicate unique respondent categories. Treating missing values as a separate category can offer insights into non-provided features. Handling this significant portion of the dataset requires thoughtful data preprocessing and analysis.

1. Employment Columns

- For individuals marked as "Unemployed" in the `employment_status` column, the `employment_industry` is updated to "not employed".
- For individuals marked as "Not in Labor Force" in the `employment_status` column, the `employment_industry` is also updated to "not employed".
- For individuals marked as "Unemployed" in the `employment_status` column, the `employment_occupation` is updated to "not employed".
- For individuals marked as "Not in Labor Force" in the `employment_status` column, the `employment_occupation` is also updated to "not employed".

By labeling these cases as `not employed`, the missing values are now replaced with meaningful information, which can be utilized for further analysis without introducing any biased assumptions.

```
## if a person is unemployed, change their "employment_industry" to "not_employed"
train.loc[train["employment_status"] == "Unemployed", "employment_industry"] = "not employed"

## if a person is not in the labor force, change their "employment_industry" to "not_employed"
train.loc[train["employment_status"] == "Not in Labor Force", "employment_industry"] = "not employed"
```

```
## if a person is unemployed, change their "employment_industry" to "not_employed"
train.loc[train["employment_status"] == "Unemployed", "employment_occupation"] = "not employed"

## if a person is not in the labor force, change their "employment_industry" to "not_employed"
train.loc[train["employment_status"] == "Not in Labor Force", "employment_occupation"] = "not employed"
```

2. `health_insurance` Column

- Missing values in the "health_insurance" column are filled with 0, assuming that those with missing values likely do not have health insurance coverage, possibly due to financial constraints associated with a higher poverty index.

```
#Filling the missing values in health insurance with 0 assumptions is that there is correlation between the poverty index and health cover
train["health_insurance"].fillna(0, inplace=True)
```

```
# check again for the missing values
missing=(train.isnull().sum()/len(train))*100

missing = missing.sort_values(ascending=False)

print("Missing values:")
print(missing)
```

```
Missing values:
income_poverty                 16.561201
doctor_recc_seasonal            8.087767
rent_or_own                     7.645936
employment_occupation           6.687385
employment_industry             6.163178
employment_status               5.477965
marital_status                  5.272026
education                       5.268282
chronic_med_condition           3.635751
child_under_6_months            3.070356
health_worker                   3.010447
opinion_seas_sick_from_vacc     2.010709
opinion_seas_risk               1.924589
opinion_seas_vacc_effective     1.729884
household_children              0.932340
household_adults                0.932340
behavioral_avoidance            0.778822
behavioral_touch_face           0.479275
behavioral_large_gatherings     0.325757
behavioral_outside_home         0.307036
behavioral_antiviral_meds       0.265848
behavioral_wash_hands           0.157262
behavioral_face_mask            0.071142
census_msa                      0.000000
health_insurance                0.000000
hhs_geo_region                  0.000000
sex                             0.000000
race                            0.000000
age_group                       0.000000
respondent_id                   0.000000
dtype: float64
```

Calculating the frequency percentage of each unique value

- To help identify columns with a large number of unique values that might require special treatment during data preprocessing or feature engineering.

```
total_observations = len(train)

for col in train.columns:
    print(f"Column: {col}")
    freq_percentage = train[col].value_counts(dropna=False) / total_observations * 100
    print(freq_percentage)
    print()
```

```
Column: respondent_id
0        0.003744
17736    0.003744
17812    0.003744
17811    0.003744
17810    0.003744
           ...
8898     0.003744
8897     0.003744
8896     0.003744
8895     0.003744
26706    0.003744
Name: respondent_id, Length: 26707, dtype: float64

Column: behavioral_antiviral_meds
0.0    94.862770
1.0     4.871382
NaN     0.265848
Name: behavioral_antiviral_meds, dtype: float64

Column: behavioral_avoidance
1.0    71.996106
0.0    27.225072
NaN     0.778822
Name: behavioral_avoidance, dtype: float64

Column: behavioral_face_mask
0.0    93.035534
1.0     6.893324
NaN     0.071142
Name: behavioral_face_mask, dtype: float64

Column: behavioral_wash_hands
1.0    82.431572
0.0    17.411166
NaN     0.157262
Name: behavioral_wash_hands, dtype: float64

Column: behavioral_large_gatherings
0.0    63.927060
1.0    35.747182
NaN     0.325757
Name: behavioral_large_gatherings, dtype: float64

Column: behavioral_outside_home
0.0    66.065077
1.0    33.627888
NaN     0.307036
Name: behavioral_outside_home, dtype: float64

Column: behavioral_touch_face
1.0    67.401805
0.0    32.118920
NaN     0.479275
Name: behavioral_touch_face, dtype: float64

Column: doctor_recc_seasonal
0.0    61.605572
```

- Since the remaining missing values are categorical variables, we will fill using `Unknown` for the `education`, `marital_status`, `rent_or_own`, and `income_poverty` columns.
- This gives a clear label for the missing values and allows the values to be treated as a distinct category during data analysis and modeling.

```
# filling with unkwown for categorical isna values

# education
train["education"].fillna("Unknown", inplace=True)

# marital status
train["marital_status"].fillna("Unknown", inplace=True)

# rent
train["rent_or_own"].fillna("Unknown", inplace=True)

# income/poverty
train["income_poverty"].fillna("Unknown", inplace=True)
```

Filling with modal class for the missing values since the counts is insignificant

```
# fill all the categorical variable with the modal class
train_filled = train.fillna(train.mode().iloc[0])
missing2=train_filled.isnull().sum() # confirm if the data has been filled.

missing2
```

```
respondent_id                  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_seasonal           0
chronic_med_condition          0
child_under_6_months           0
health_worker                  0
health_insurance               0
opinion_seas_vacc_effective    0
opinion_seas_risk              0
opinion_seas_sick_from_vacc    0
age_group                      0
education                      0
race                           0
sex                            0
income_poverty                 0
marital_status                 0
rent_or_own                    0
employment_status              0
hhs_geo_region                 0
census_msa                     0
household_adults               0
household_children             0
employment_industry            0
employment_occupation          0
dtype: int64
```

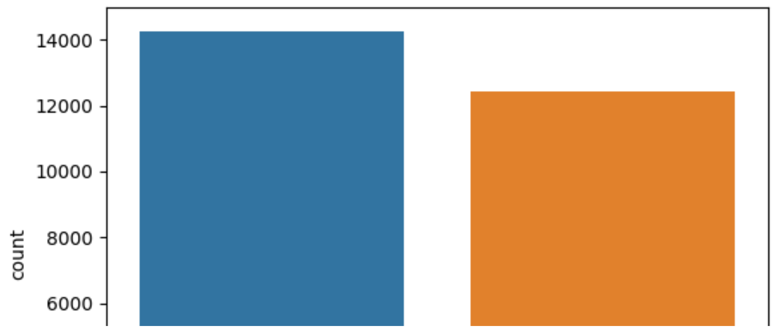
Exploratory Data Analysis

The Target Features

```
# Target variables dataset exploratory
target.head()
```

	respondent_id	seasonal_vaccine
0	0	0
1	1	1
2	2	0
3	3	1
4	4	0

```
# checking the distribution of the target variable

sns.countplot(data=target, x="seasonal_vaccine")
plt.savefig("images/seasonal_vaccine_count_plot.png")
```



Observations

- The number of respondents who had taken the seasonal flu vaccine is lower compared to those who had not taken it.

```
frequency = target["seasonal_vaccine"].value_counts()
frequency
```

```
    0    14272
    1    12435
    Name: seasonal_vaccine, dtype: int64
```

Class balance:

The counts of the two classes are not significantly different and are relatively close, we can consider dataset to be reasonably balanced.

More Preparation for Analysis

- First, a new DataFrame, `train_target`, is created from a merge of `train_filled` and `target` DataFrames to create a single DataFrame.
- The new DataFrame will contain all the information needed for univariate and multivariate analysis and for building machine learning models.

```
#Merge the two datasets
train_target = train_filled.merge(target, on="respondent_id")
```

- Next, the `respondent_id` column is made the the index of the DataFrame.

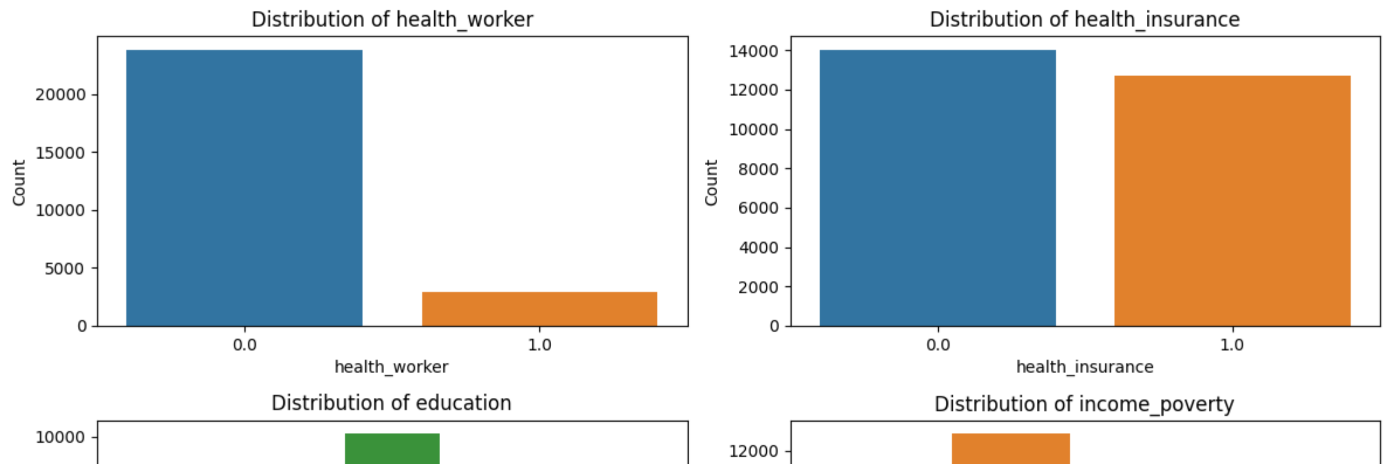
```
#make respondent id the index column
train_target.set_index("respondent_id", inplace=True)
train_target
```

	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gathering:
respondent_id					
0	0.0	0.0	0.0	0.0	0.(
1	0.0	1.0	0.0	1.0	0.(
2	0.0	1.0	0.0	0.0	0.(

Univariate Analysis

EDA Socioeconomic Features

```
# List of columns to create countplots for
columns_to_plot = ["health_worker", "health_insurance", "education",
                   "income_poverty", "rent_or_own", "employment_status"]

# Calculate the number of rows and columns for subplots dynamically
num_plots = len(columns_to_plot)
num_cols = 2
num_rows = (num_plots + num_cols - 1) // num_cols

# Create subplots
fig, axes = plt.subplots(num_rows, num_cols, figsize=(12, 10))

# Flatten the axes array for easier indexing
axes = axes.flatten()

# Loop through the columns and create individual countplots
for i, column in enumerate(columns_to_plot):
    if i >= num_rows * num_cols:  # Check if index exceeds total number of subplots
        fig.delaxes(axes[i])
    else:
        if column == "age_group":
            sns.countplot(data=train_target, x=column, order=train_target["age_group"].value_counts().index, ax=axes[i])
        else:
            sns.countplot(data=train_target, x=column, ax=axes[i])
        axes[i].set_xlabel(column)
        axes[i].set_ylabel("Count")
        axes[i].set_title(f"Distribution of {column}")

# Adjust the layout and spacing between subplots
plt.tight_layout()

# Save the image
plt.savefig("images/socio_econ.png")

# Show the subplots
plt.show()
```

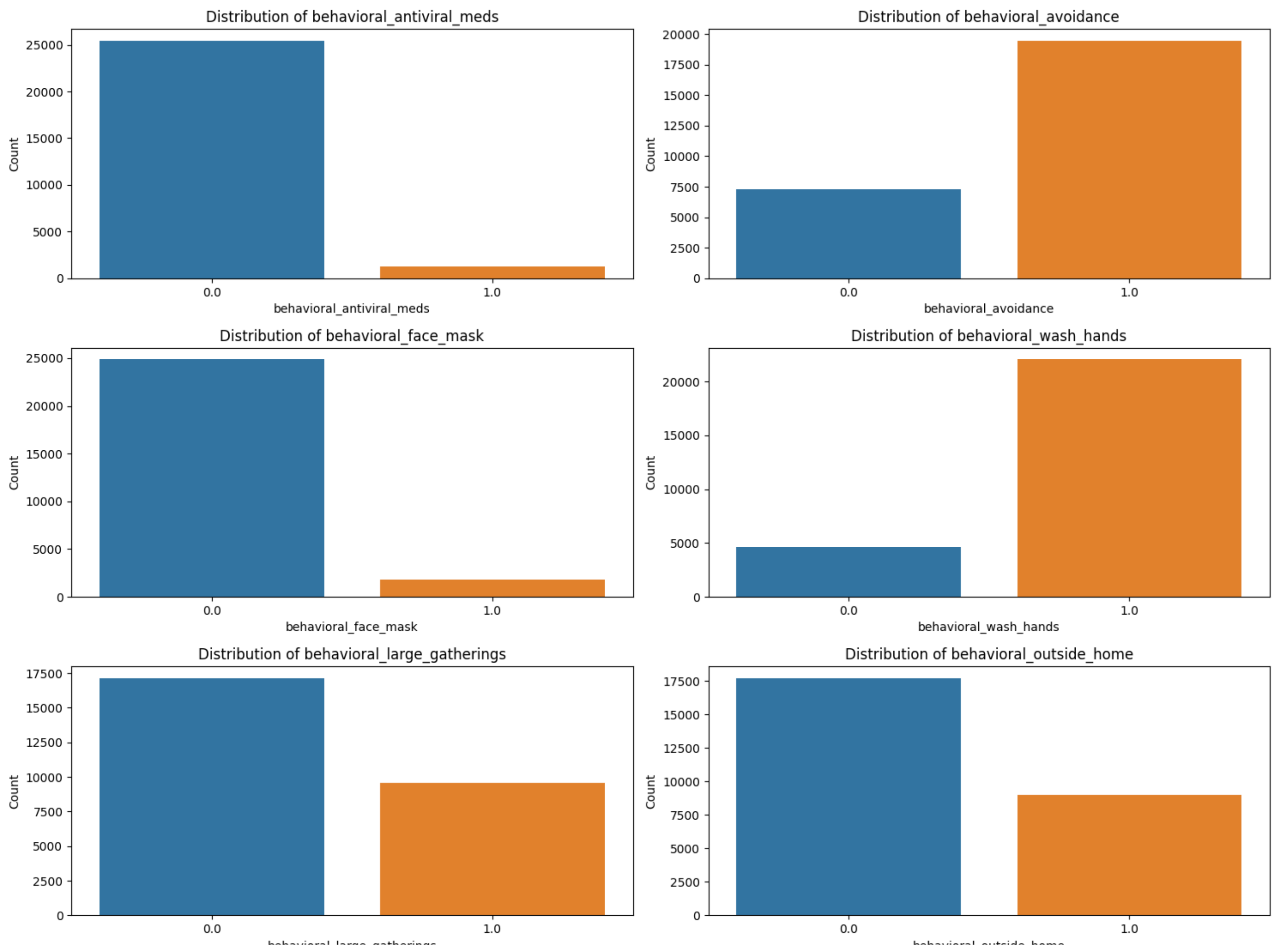


Observations

- The respondents were mostly made up of individuals in other professions other than health workers.
- The number of people with health insurance was almost similar to those who had no health insurance. However, those without were the majority. This is partly due to the assumption made earlier that the missing values were for those without insurance.
- A normal distribution in the education feature was observed with those who had a college education making up the majority.
- Most respondents had an annual household income of less than $75,000. A fair amount of respondents failed to disclose their income and were categorized as "Unknown".
- Majority of the respondents own the houses they live in.
- Majority were also employed at the time of the interview.

EDA for Behavioral Features

```
#EDA for behavioral factors
# List of columns to create countplots for
columns_to_plot = ["behavioral_antiviral_meds", "behavioral_avoidance", "behavioral_face_mask", "behavioral_wash_hands",
                   "behavioral_large_gatherings", "behavioral_outside_home", "behavioral_touch_face"]

# Define the number of rows and columns for subplots
num_rows = 4
num_cols = 2

# Create subplots
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 15))

# Flatten the axes array for easier indexing
axes = axes.flatten()

# Loop through the columns and create individual countplots
for i, column in enumerate(columns_to_plot):
    sns.countplot(data=train_target, x=column, ax=axes[i])
    axes[i].set_xlabel(column)
    axes[i].set_ylabel("Count")
    axes[i].set_title(f"Distribution of {column}")

# Adjust the layout and spacing between subplots
fig.delaxes(axes[-1])

# Adjust the layout and spacing between subplots
plt.tight_layout()

# save image
plt.savefig("images/behavior.png")

# Show the subplots
plt.show()
```

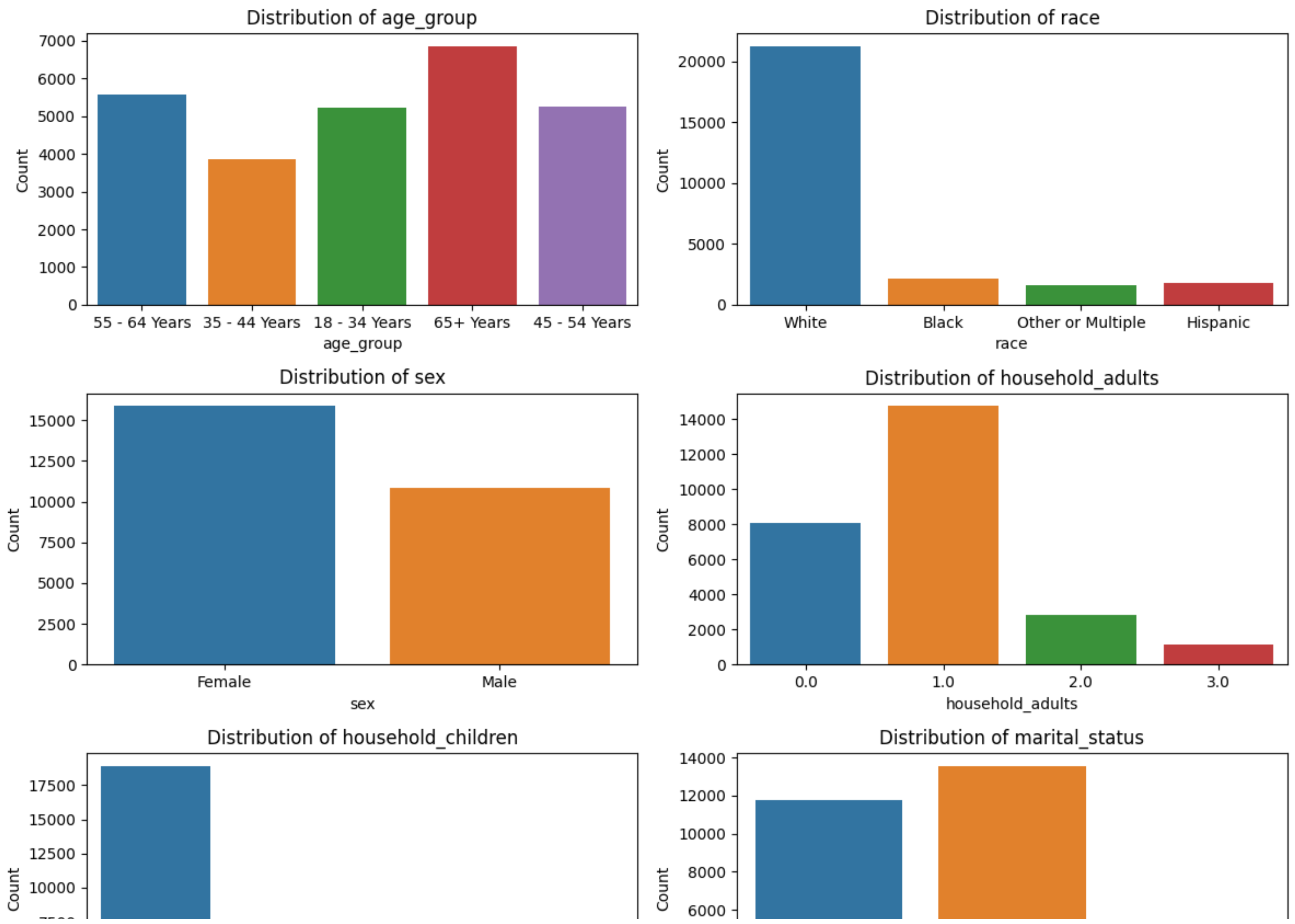


Observations

- Majority of the respondents appeared not to have taken any antiviral medication. The response might be subjective and would require further investigation on how the question was asked.
- Most of the respondents had also avoided close contact with people who had flu-like symptoms.Most were also in the practice of washing hands and using hand sanitizer.
- Majority had also not bought facemask. Similarly, most were avoiding touching their face, nose or mouth.
- There was no social-distancing among the respondents.

EDA for Demographic Features

```
# List of demographic columns to create countplots for
demographic_columns = ["age_group", "race", "sex", "household_adults", "household_children", "marital_status"]

# Calculate the number of rows and columns for subplots dynamically
num_plots = len(demographic_columns)
num_cols = 2
num_rows = (num_plots + num_cols - 1) // num_cols

# Create subplots
fig, axes = plt.subplots(num_rows, num_cols, figsize=(12, 10))

# Flatten the axes array for easier indexing
axes = axes.flatten()

# Loop through the columns and create individual countplots
for i, column in enumerate(demographic_columns):
    if i >= num_rows * num_cols:  # Check if index exceeds total number of subplots
        fig.delaxes(axes[i])
    else:
        sns.countplot(data=train_target, x=column, ax=axes[i])
        axes[i].set_xlabel(column)
        axes[i].set_ylabel("Count")
        axes[i].set_title(f"Distribution of {column}")

# Adjust the layout and spacing between subplots
plt.tight_layout()

# Save the image
plt.savefig("images/demographic.png")

# Show the subplots
plt.show()
```



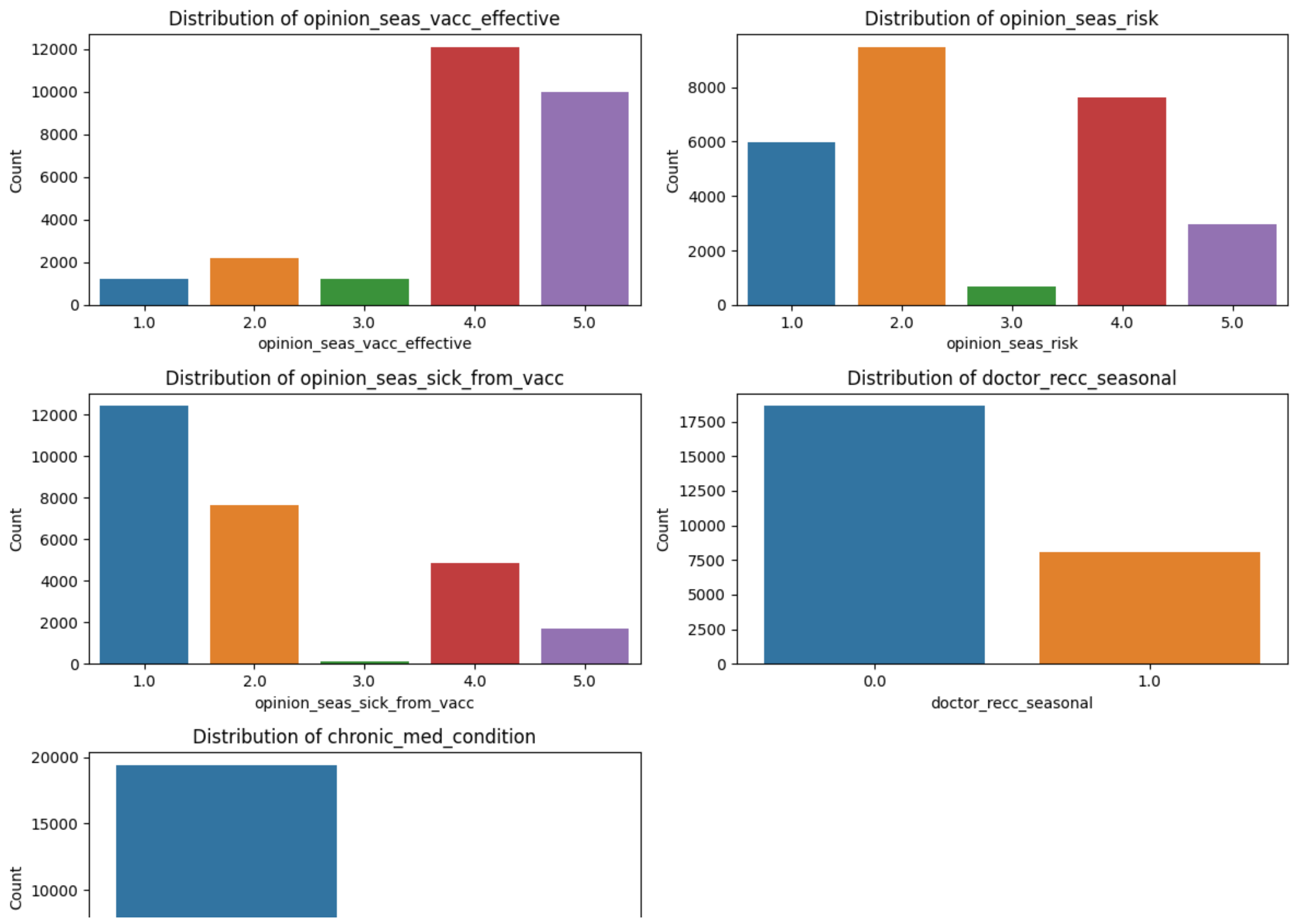
Observations

- The respondents" age groups were normally distributed with majority being 65 years and older. This is synonymous with developed countries. Most were also female and white.
- Majority of the households had at least two adults with no child(ren) at the time of the interview.
- The number of married and unmarried respondents was almost similar.
- Majority also lived outside the Metropolitan Statitistical Area (MSA) as defined by the US Census.

EDA for Knowledge, Attitudes and Beliefs Towards Vaccines

```
# List of columns to create countplots for
columns_to_plot = ["opinion_seas_vacc_effective", "opinion_seas_risk", "opinion_seas_sick_from_vacc",
                   "doctor_recc_seasonal","chronic_med_condition"]

# Define the number of rows and columns for subplots
num_rows = 3
num_cols = 2

# Create subplots
fig, axes = plt.subplots(num_rows, num_cols, figsize=(12, 10))
```

```
# Flatten the axes array for easier indexing
axes = axes.flatten()

# Loop through the columns and create individual countplots
for i, column in enumerate(columns_to_plot):
    sns.countplot(data=train_target, x=column, ax=axes[i])
    axes[i].set_xlabel(column)
    axes[i].set_ylabel("Count")
    axes[i].set_title(f"Distribution of {column}")

# Adjust the layout and spacing between subplots
fig.delaxes(axes[-1])


# Adjust the layout and spacing between subplots
plt.tight_layout()

# save image
plt.savefig("images/opinions.png")

# Show the subplots
plt.show()
```



Observations

- Majority believed that seasonal vaccines were effective and they were not worried about falling sick from taking the vaccine.
- However, a large number believed that the risk of contracting the flu without a vaccine was low.
- Majority of the respondents had not received any recommendations for the vaccine from their doctors.
- Most respondents did not have a chronic medical condition.

Bivariate Analysis

Socieconomic Features vs Seasonal Vaccine Uptake

```
# columns to plot
y = ["health_worker", "health_insurance", "education",
     "income_poverty", "rent_or_own", "employment_status"]

fig, axes = plt.subplots(nrows=3, ncols=2, figsize=(15, 12))

for i, variable in enumerate(y):
    row = i // 2
    col = i % 2
    ax = axes[row, col]
    sns.countplot(x=variable, hue="seasonal_vaccine", data=train_target, ax=ax)
    ax.set_title(f"Distribution of {variable} by Seasonal Vaccine Uptake")
    ax.set_xlabel(variable)
    ax.set_ylabel("Count")
    ax.legend(title="Seasonal Vaccine", labels=["No", "Yes"])

plt.tight_layout()

# save image
plt.savefig("images/socio-econ_binary.png")

# Show the subplots
plt.show()
```

Observations

- Majority of the health workers received vaccines as opposed to non-health workers where majority did not receive.
- Respondents with health insurance are likely to receive vaccines as compared to those without the insurance.
- Respondents with college level of education are more receptive of the vaccine.
- The poorer respondents in terms of annual income per household were less likely to receive the vaccine.
- More of those who lived in their own houses received the vaccine compared to those paying rent/with unknown housing conditions.
- The employed respondents were more likely to receive the vaccine compared to those not in any employment.

Behavioral Features vs Seasonal Vaccine Uptake

```
# columns to plot
y = ["behavioral_antiviral_meds", "behavioral_avoidance", "behavioral_face_mask",
     "behavioral_wash_hands", "behavioral_large_gatherings", "behavioral_outside_home"]

fig, axes = plt.subplots(nrows=3, ncols=2, figsize=(15, 15))

# Define custom color palette
custom_palette = ["#454545", "#FF6000"]

for i, variable in enumerate(y):
    row = i // 2
    col = i % 2
    ax = axes[row, col]
    sns.countplot(x=variable, hue="seasonal_vaccine", data=train_target, ax=ax, palette=custom_palette)
    ax.set_title(f"Distribution of {variable} and Seasonal Vaccine Uptake")
    ax.set_xlabel(variable)
    ax.set_ylabel("Count")
    ax.legend(title="Seasonal Vaccine", labels=["No", "Yes"])

plt.tight_layout()
plt.savefig("images/behavioral_binary.png")
plt.show()
```

Observations

- Generally, behavioral factors did not have much influence on whether the respondents took the vaccines.

- Whether the respondent was on antiviral medication, avoided contact with people showing flu symptoms even outside the home or washed hands/used santizers often and vice versa, the general outome was that less people ad received the vaccine.

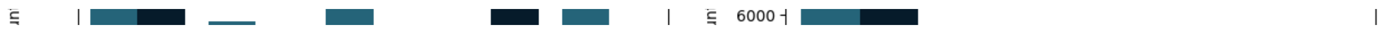
```
# columns to plot
y = ["age_group", "race", "sex", "household_adults", "household_children", "marital_status"]

fig, axes = plt.subplots(nrows=3, ncols=2, figsize=(15, 15))
custom_palette = ["#176B87", "#001C30"]
for i, variable in enumerate(y):
    row = i // 2
    col = i % 2
    ax = axes[row, col]
    sns.countplot(x=variable, hue="seasonal_vaccine", data=train_target, ax=ax,palette=custom_palette)
    ax.set_title(f"Distribution of {variable} by Seasonal Vaccine Uptake")
    ax.set_xlabel(variable)
    ax.set_ylabel("Count")
    ax.legend(title="Seasonal Vaccine", labels=["No", "Yes"])

# Adjust spacing between subplots
plt.subplots_adjust(hspace=0.4)

plt.savefig("images/demographic_binary.png")
plt.show()
```

Observations

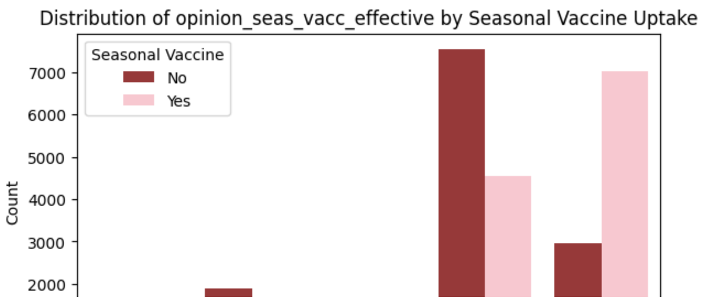
- The number of older people above 65 years of age were more likely to receive the vaccine compared to the younger population.

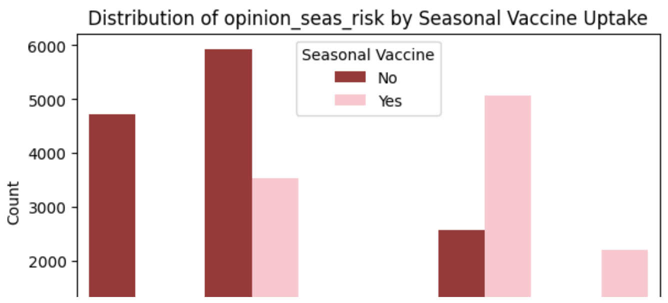
- More female and married respondents as well as people of White descent received the vaccine compared to others in their respective categories.
- Households with one adult and no children received the vaccine in more numbers than other respondents in the respective categories.

Knowledge, Attitudes and Beliefs Towards Vaccines vs Seasonal Vaccine Uptake



```
# columns to plot
y = ["opinion_seas_vacc_effective", "opinion_seas_risk", "opinion_seas_sick_from_vacc",
     "doctor_recc_seasonal", "chronic_med_condition"]

num_plots = len(y)
num_cols = 2
num_rows = (num_plots + num_cols - 1) // num_cols

fig, axes = plt.subplots(nrows=num_rows, ncols=num_cols, figsize=(15, 15))
custom_palette = ["brown", "pink"]

for i, variable in enumerate(y):
    if i >= num_plots:
        break

    row = i // num_cols
    col = i % num_cols

    ax = axes[row, col]
    sns.countplot(x=variable, hue="seasonal_vaccine", data=train_target, ax=ax, palette=custom_palette)
    ax.set_title(f"Distribution of {variable} by Seasonal Vaccine Uptake")
    ax.set_xlabel(variable)
    ax.set_ylabel("Count")
    ax.legend(title="Seasonal Vaccine", labels=["No", "Yes"])

# Adjust spacing between subplots
plt.subplots_adjust(hspace=0.4)

# Remove any extra blank subplot
if num_plots < num_cols * num_rows:
    fig.delaxes(axes.flatten()[num_plots])

plt.savefig("images/opinion_binary.png")
plt.show()
```





Observations

- The majority of respondents who received the vaccine hold the opinion that it is effective.
- A general observation is that the lower the opinion towards the vaccine factor, the lower the vaccine uptake. A respondent was less likely to receive the vaccine if they:
  - did not believe that there is a risk of getting sick with seasonal flu without vaccine;
  - was not worried of getting sick from taking seasonal flu vaccine;
  - did not get a doctor's recommendation to take the vaccine, and;
  - had no chronic medical condition.

Feature Engineering

Data Encoding

First, the data types are displayed once again to determine the affected features.

```
train_target.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 26707 entries, 0 to 26706
Data columns (total 30 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   behavioral_antiviral_meds    26707 non-null  float64
 1   behavioral_avoidance         26707 non-null  float64
 2   behavioral_face_mask         26707 non-null  float64
 3   behavioral_wash_hands        26707 non-null  float64
 4   behavioral_large_gatherings  26707 non-null  float64
 5   behavioral_outside_home      26707 non-null  float64
 6   behavioral_touch_face        26707 non-null  float64
 7   doctor_recc_seasonal         26707 non-null  float64
 8   chronic_med_condition        26707 non-null  float64
 9   child_under_6_months         26707 non-null  float64
 10  health_worker                26707 non-null  float64
 11  health_insurance             26707 non-null  float64
 12  opinion_seas_vacc_effective  26707 non-null  float64
 13  opinion_seas_risk            26707 non-null  float64
 14  opinion_seas_sick_from_vacc  26707 non-null  float64
 15  age_group                    26707 non-null  object
 16  education                    26707 non-null  object
 17  race                         26707 non-null  object
 18  sex                          26707 non-null  object
 19  income_poverty               26707 non-null  object
 20  marital_status               26707 non-null  object
 21  rent_or_own                  26707 non-null  object
 22  employment_status            26707 non-null  object
 23  hhs_geo_region               26707 non-null  object
 24  census_msa                   26707 non-null  object
 25  household_adults             26707 non-null  float64
 26  household_children           26707 non-null  float64
 27  employment_industry          26707 non-null  object
 28  employment_occupation        26707 non-null  object
 29  seasonal_vaccine             26707 non-null  int64
dtypes: float64(17), int64(1), object(12)
memory usage: 6.3+ MB
```

One-Hot Encoding

Columns - "age_group", "education", "race", "sex", "marital_status", "rent_or_own", "employment_status", "census_msa", and "income_poverty."

```
from sklearn.preprocessing import OneHotEncoder
encoded_df = train_target[["age_group", "education", "race", "sex", "marital_status", "rent_or_own", "employment_status",
                           "census_msa", "income_poverty"]]
#using one-encoding to create dummy column
ohe = OneHotEncoder()
data_enc1= ohe.fit_transform(encoded_df)

#converting the finding into dataframe
data_enc1.todense()

#getting feature names
ohe.get_feature_names_out()

# geting feature names in a dataframe
data_encoded = pd.DataFrame(data_enc1.todense(), columns=ohe.get_feature_names_out())
data_encoded.head()
```

	age_group_18 - 34 Years	age_group_35 - 44 Years	age_group_45 - 54 Years	age_group_55 - 64 Years	age_group_65+ Years	education_12 Years	education_< 12 Years	education_College Graduate	education_Some College
0	0.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0
1	0.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0
2	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0
3	0.0	0.0	0.0	0.0	1.0	1.0	0.0	0.0	0.0
4	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	1.0

5 rows × 32 columns

- A copy of the DataFrame was made to avoid overwritng the main dataset during data manipulation.

```
train_target_copy = train_target.copy()
train_target_copy.head()
```

respondent_id	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gathering
0	0.0	0.0	0.0	0.0	0.
1	0.0	1.0	0.0	1.0	0.
2	0.0	1.0	0.0	0.0	0.
3	0.0	1.0	0.0	1.0	1.
4	0.0	1.0	0.0	1.0	1.

5 rows × 30 columns

```
columns_to_drop = ["age_group", "education", "race", "sex", "marital_status", "rent_or_own", "employment_status",
                   "census_msa", "income_poverty", "hhs_geo_region", "employment_industry", "employment_occupation"]
train_target_copy.drop(columns_to_drop, axis=1, inplace=True)
train_target_copy.head()
```

	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gathering
respondent_id					
0	0.0	0.0	0.0	0.0	0.
1	0.0	1.0	0.0	1.0	0.
2	0.0	1.0	0.0	0.0	0.
3	0.0	1.0	0.0	1.0	1.
4	0.0	1.0	0.0	1.0	1.

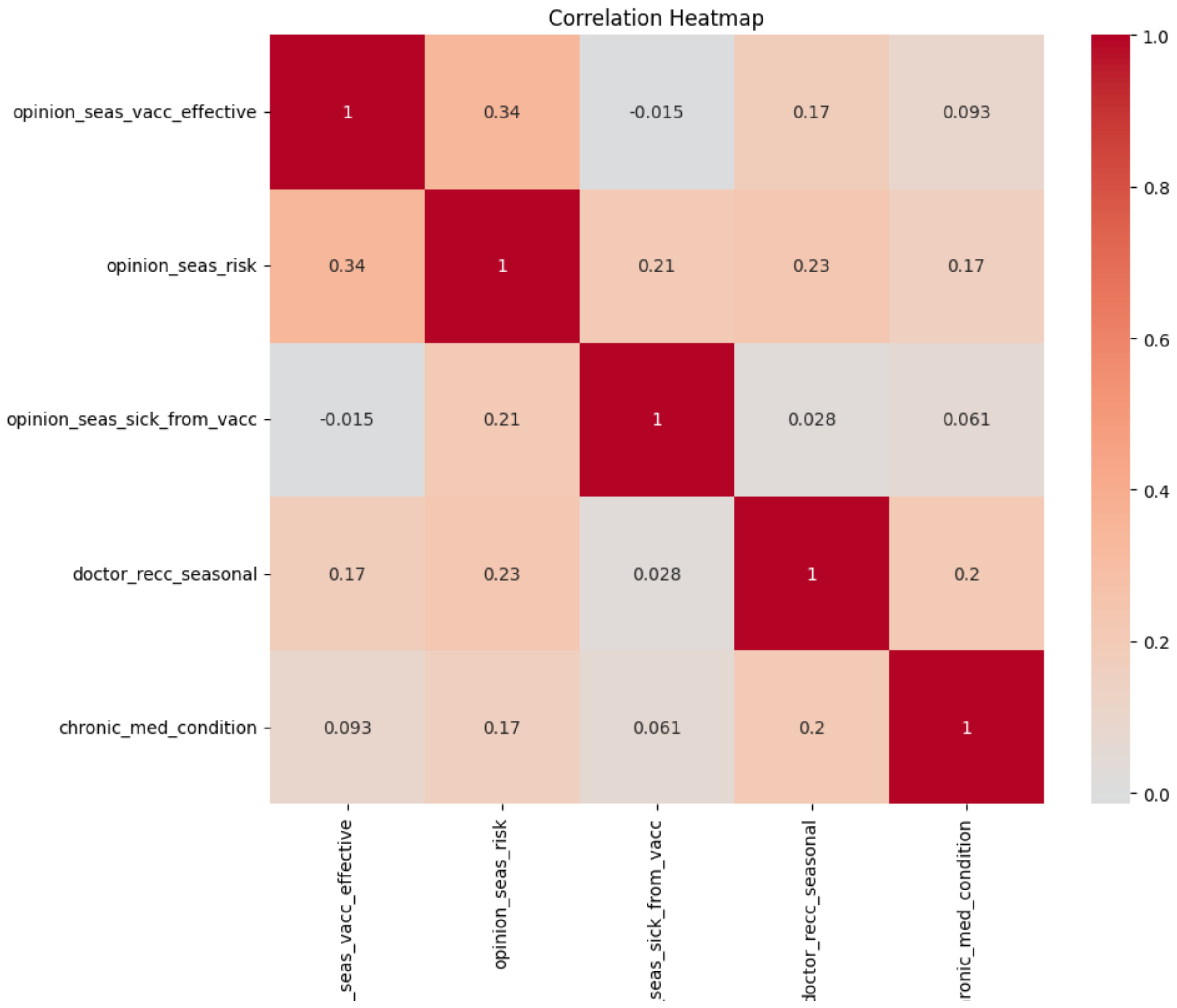
- The merged `train_target_float` DataFrame has a combination of numerical columns from `train_target_copy` and the **one-hot encoded binary columns** from `data_encoded`.
- This merged DataFrame has all the features are represented in numerical format.

```
train_target_float = pd.merge(train_target_copy, data_encoded, left_index=True, right_index=True)
train_target_float.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 26707 entries, 0 to 26706
Data columns (total 50 columns):
 #   Column                                  Non-Null Count  Dtype  
---  ------                                  --------------  -----  
 0   behavioral_antiviral_meds               26707 non-null  float64
 1   behavioral_avoidance                    26707 non-null  float64
 2   behavioral_face_mask                    26707 non-null  float64
 3   behavioral_wash_hands                   26707 non-null  float64
 4   behavioral_large_gatherings             26707 non-null  float64
 5   behavioral_outside_home                 26707 non-null  float64
 6   behavioral_touch_face                   26707 non-null  float64
 7   doctor_recc_seasonal                    26707 non-null  float64
 8   chronic_med_condition                   26707 non-null  float64
 9   child_under_6_months                    26707 non-null  float64
 10  health_worker                           26707 non-null  float64
 11  health_insurance                        26707 non-null  float64
 12  opinion_seas_vacc_effective             26707 non-null  float64
 13  opinion_seas_risk                       26707 non-null  float64
 14  opinion_seas_sick_from_vacc             26707 non-null  float64
 15  household_adults                        26707 non-null  float64
 16  household_children                      26707 non-null  float64
 17  seasonal_vaccine                        26707 non-null  int64  
 18  age_group_18 - 34 Years                 26707 non-null  float64
 19  age_group_35 - 44 Years                 26707 non-null  float64
 20  age_group_45 - 54 Years                 26707 non-null  float64
 21  age_group_55 - 64 Years                 26707 non-null  float64
 22  age_group_65+ Years                     26707 non-null  float64
 23  education_12 Years                      26707 non-null  float64
 24  education_< 12 Years                    26707 non-null  float64
 25  education_College Graduate              26707 non-null  float64
 26  education_Some College                  26707 non-null  float64
 27  education_Unknown                       26707 non-null  float64
 28  race_Black                              26707 non-null  float64
 29  race_Hispanic                           26707 non-null  float64
 30  race_Other or Multiple                  26707 non-null  float64
 31  race_White                              26707 non-null  float64
 32  sex_Female                              26707 non-null  float64
 33  sex_Male                                26707 non-null  float64
 34  marital_status_Married                  26707 non-null  float64
 35  marital_status_Not Married              26707 non-null  float64
 36  marital_status_Unknown                  26707 non-null  float64
 37  rent_or_own_Own                         26707 non-null  float64
 38  rent_or_own_Rent                        26707 non-null  float64
 39  rent_or_own_Unknown                     26707 non-null  float64
 40  employment_status_Employed              26707 non-null  float64
 41  employment_status_Not in Labor Force    26707 non-null  float64
 42  employment_status_Unemployed            26707 non-null  float64
 43  census_msa_MSA, Not Principle  City     26707 non-null  float64
 44  census_msa_MSA, Principle City          26707 non-null  float64
 45  census_msa_Non-MSA                      26707 non-null  float64
 46  income_poverty_<= $75,000, Above Poverty  26707 non-null  float64
 47  income_poverty_> $75,000                26707 non-null  float64
 48  income_poverty_Below Poverty            26707 non-null  float64
 49  income_poverty_Unknown                  26707 non-null  float64
dtypes: float64(49), int64(1)
memory usage: 11.4 MB
```

Multivariate Analysis using Correlation

```
# Set the data for corr
corr = train_target_float.corr()['seasonal_vaccine'].sort_values(ascending = False)
corr = corr[(corr > 0.1)] # correlation greater than 0.1
columns = corr.index.tolist()

# df with only the selected columns
corr_df = train_target_float[columns_to_plot]

# plot heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(corr_df.corr(), annot=True, cmap='coolwarm', center=0)
plt.title("Correlation Heatmap")
plt.savefig("images/corr_map.png")

plt.show()
```



Modelling

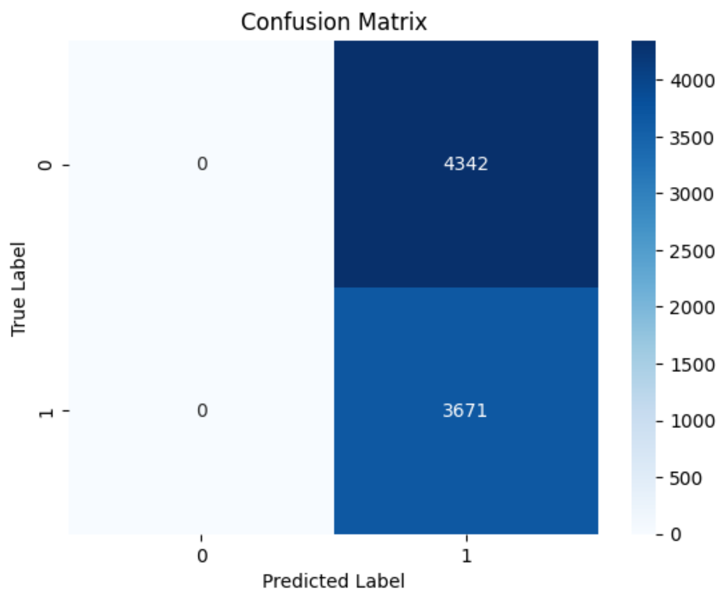
Baseline model

Baseline Metrics

Before conducting any modeling on the data, a "dummy" model that always predicts the positive class is first used.

- "negative" is defined as a 0 (not received vaccine) and "positive" as a 1 (received thye vaccine).
- Focus is on the test data, since this is will be used to evaluate the actual model as well.

```
# split data into train and test, claze size=0.3
X = train_target_float.drop(columns=["seasonal_vaccine"], axis=1)
y = train_target_float["seasonal_vaccine"]

# Perform train test split
X_train, X_test, y_train, y_test = train_test_split(X, y, random_state=42,test_size=0.3)

# Scale data
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

# Training the dummy classifier
dummy_classifier = DummyClassifier(strategy="constant", constant=1)
dummy_classifier.fit(X_train_scaled, y_train)

# Make predictions
y_pred = dummy_classifier.predict(X_test_scaled)

# Create confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Plot confusion matrix
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues")
plt.xlabel("Predicted Label")
plt.ylabel("True Label")
plt.title("Confusion Matrix")

plt.savefig("images/baseline_cm.png")
plt.show()
```



```
# Evaluation of the baseline model

#Accuracy=TP+TN/TP+TN+FP+FN
TP=3671
TN=0
FP=4342
FN=0
baseline_accuracy=(TP+TN)/(TP+FP+TN+FN)
print("Baseline Accuracy: " ,baseline_accuracy)

#precision TP/TP+FP
baseline_precision=(TP/(TP+FP))
print("Baseline Precision: " ,baseline_precision)

baseline_recall=(TP/(TP+FN))
```

```
print("Baseline Recall: " ,baseline_recall)

baseline_F1score=(2*baseline_precision* baseline_recall)/(baseline_precision+baseline_recall)
print("Baseline F1score: " ,baseline_F1score)
```

```
     Baseline Accuracy:  0.4581305378759516
     Baseline Precision:  0.4581305378759516
     Baseline Recall:  1.0
     Baseline F1score:  0.6283806915439919
```

Baseline Model Observations

1. **Baseline Accuracy** is approximately 45.81%, it means that the dummy classifier, correctly predicts around 45.81% of instances in the test data.
2. **Baseline Precision** is also 45.81%. It is equal to the accuracy since the dummy classifier always predicts the positive class.
3. **Baseline Recall** is 100%. Since the dummy classifier always predicts the positive class, it correctly identifies all the actual positive instances.
4. **Baseline F1-score** is approximately 62.84%. A higher F1-score would indicate a better balance between precision and recall.

These metrics will be used to reference the performance of subsequent models, hoping that they will outperform the baseline model.

1. Logistic Regression

```
# fit the model in logistic regression

# Instantiate the model
model1 = LogisticRegression(random_state=42)

# Fit the model on the scaled data
model1.fit(X_train_scaled, y_train)

# Make predictions on the training data
y_train_pred1 = model1.predict(X_train_scaled)

# Create confusion matrix
cm = confusion_matrix(y_train, y_train_pred1)

# Plot confusion matrix
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues")
plt.xlabel("Predicted Label")
plt.ylabel("True Label")
plt.title("Confusion Matrix (Training Set)")

plt.savefig("images/logistic_cm.png")

plt.show()
```

```
# cross validate the model using 3 kfolds
from sklearn.model_selection import cross_val_score
cv_scores = cross_val_score(model1, X_train_scaled, y_train, cv=3)
print("Cross-Validation Scores:", cv_scores)

average_cv_score = cv_scores.mean()
print("Average Cross-Validation Score:", average_cv_score * 100) # in percentage
```

```
    Cross-Validation Scores: [0.76813222 0.77210721 0.77820575]
    Average Cross-Validation Score: 77.28150573893545
```

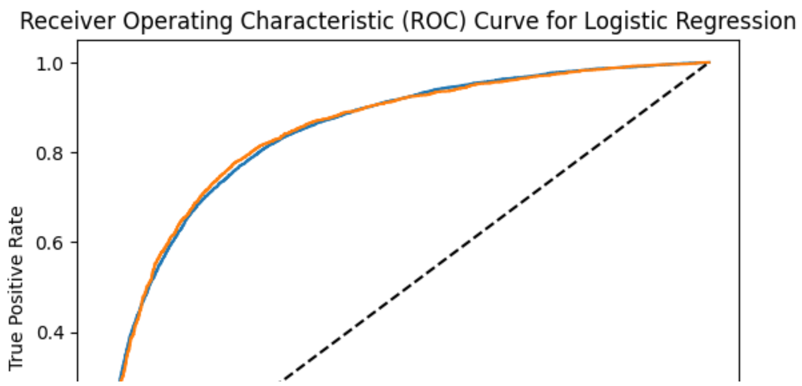
- The scores indicate that the model is approximately 77.28% accurate in its performance.

```
#evaluation of model
y_pred = model1.predict(X_test_scaled)
model1_accuracy = accuracy_score(y_test, y_pred)
model1_recall = recall_score(y_test, y_pred)
model1_precision = precision_score(y_test, y_pred)
model1_f1 = f1_score(y_test, y_pred)

print(f"""
Accuracy Fitted Model 1: {model1_accuracy:1.3f}
Recall Fitted Model 1: {model1_recall:1.3f}
Precision Fitted Model 1: {model1_precision:1.3f}
F1 Score Fitted Model 1: {model1_f1:1.3f}
""")
```

```
    Accuracy Fitted Model 1: 0.782
    Recall Fitted Model 1: 0.739
    Precision Fitted Model 1: 0.774
    F1 Score Fitted Model 1: 0.756
```

```
# calcluate ROC

# Obtain the predicted probabilities for the positive class
y_test_prob = model1.predict_proba(X_test_scaled)[:, 1]
y_train_prob = model1.predict_proba(X_train_scaled)[:, 1]

# Calculate the false positive rate (fpr), true positive rate (tpr), and thresholds
train_fpr_l, train_tpr_l, thresholds = roc_curve(y_train, y_train_prob)
test_fpr_l, test_tpr_l, thresholds = roc_curve(y_test, y_test_prob)

# Calculate the AUC score
auc_score_model1_train = roc_auc_score(y_train, y_train_prob)
auc_score_model1_test = roc_auc_score(y_test, y_test_prob)

print("Train AUC Score", auc_score_model1_train)
print("Test AUC Score", auc_score_model1_test)

# Plot the ROC curve
plt.plot(train_fpr_l, train_tpr_l, label="Train ROC Curve (AUC = {:.4f})".format(auc_score_model1_train))
plt.plot(test_fpr_l, test_tpr_l, label="Test ROC Curve (AUC = {:.4f})".format(auc_score_model1_test))
plt.plot([0, 1], [0, 1], "k--", label="Random Guess")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver Operating Characteristic (ROC) Curve for Logistic Regression")
plt.legend(loc="lower right")

plt.savefig("images/logistic_roc_curve.png")

plt.show()
```

```
Train AUC Score 0.8503931732533946
Test AUC Score 0.8522644587822867
```



Logistic Regression Observations

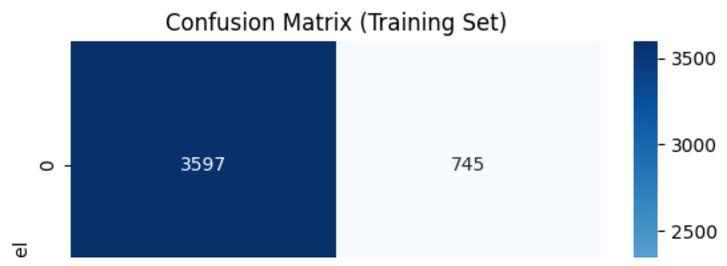
- An **accuracy** of 0.782 means that the model is correctly predicting the seasonal vaccine outcome for around 78% of the samples in the test data.
- A **recall** of 0.739 indicates that the model is able to correctly identify around 74% of the positive instances (those who received the flu vaccine) in the test data.
- A **precision** of 0.774 implies that around 77% of the instances predicted as positive by the model are actually true positives.
- The **F1 score** combines both precision and recall into a single metric. With an F1 score of 0.756, it suggests a balanced performance between precision and recall. These metrics are a good indication that the logistic regression model is providing reasonably accurate predictions on the uptake of the seasonal flu vaccine.

The **ROC curve** above shows a AUC score of 0.8523 on the test set, revealing that the model is quite good on distinguishing between those who received the seasonal flu vaccine or not (positives and negatives).

- The score is close to 1, meaning that the predictive power of the model can be trusted.

Model 2 - Decision Trees

```
# Test set predictions
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import classification_report

# instantiate
model2 = DecisionTreeClassifier(criterion="gini", max_depth=5)

# fit the model on train data
model2.fit(X_train_scaled, y_train)

y_pred2 = model2.predict(X_test_scaled)

# Plot confusion matrix
cm = confusion_matrix(y_test, y_pred2)

sns.heatmap(cm, annot=True, fmt="d", cmap="Blues")
plt.xlabel("Predicted Label")
plt.ylabel("True Label")
plt.title("Confusion Matrix (Training Set)")

plt.savefig("images/decision_trees_cm.png")
```

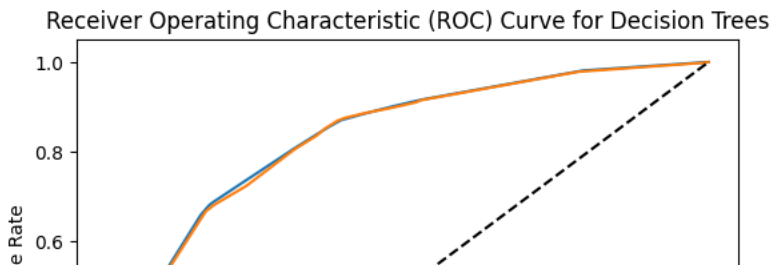


```
#evaluation of model
y_pred = model2.predict(X_test_scaled)
model2_accuracy = accuracy_score(y_test, y_pred)
model2_recall = recall_score(y_test, y_pred)
model2_precision = precision_score(y_test, y_pred)
model2_f1 = f1_score(y_test, y_pred)

print(f"""
Accuracy Fitted Model: {model2_accuracy:1.3f}
Recall Fitted Model: {model2_recall:1.3f}
Precision Fitted Model: {model2_precision:1.3f}
F1 Score Fitted Model: {model2_f1:1.3f}
""")
```

```
    Accuracy Fitted Model: 0.758
    Recall Fitted Model: 0.675
    Precision Fitted Model: 0.769
    F1 Score Fitted Model: 0.719
```

```
# ROC and AUC
# calcluate ROC

# Obtain the predicted probabilities for the positive class
y_test_pred = model2.predict_proba(X_test_scaled)[:, 1]
y_train_pred = model2.predict_proba(X_train_scaled)[:, 1]

# Calculate the false positive rate (fpr), true positive rate (tpr), and thresholds
training_fpr_d, training_tpr_d, _  = roc_curve(y_train, y_train_pred)
test_fpr_d, test_tpr_d, _  = roc_curve(y_test, y_test_pred)

# Calculate the AUC score
auc_score_model2_test = roc_auc_score(y_test, y_test_pred)
auc_score_model2_train = roc_auc_score(y_train, y_train_pred)

print("Train AUC Score", auc_score_model2_train)
print("Test AUC Score", auc_score_model2_test)

# Plot the ROC curve
plt.plot(training_fpr_d, training_tpr_d, label="Train ROC Curve (AUC = {:.4f})".format(auc_score_model2_train))
plt.plot(test_fpr_d, test_tpr_d, label="Test ROC Curve (AUC = {:.4f})".format(auc_score_model2_test))
plt.plot([0, 1], [0, 1], "k--", label="Random Guess")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver Operating Characteristic (ROC) Curve for Decision Trees")
plt.legend(loc="lower right")

plt.savefig("images/decision_trees_roc_curve.png")

plt.show()
```

```
Train AUC Score 0.8308051327342516
Test AUC Score 0.8264301813572109
```



Decision Trees Observations

- **Accuracy**: overall, accuracy stands at approximately 0.76, indicating that around 76% of samples are correctly predicted.
- **Recall** shows that about 67.5% of those who received the vaccine were identified.
- **Precision** indicates the model got 76.9% in prediciting vaccine recipients as actual recipients.
- **F1-Score**of 71.9% represents precision and recall in a balanced way.

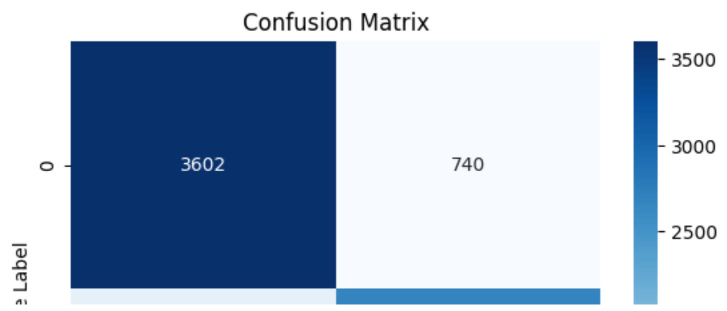
As per the **ROC curve**, this model has AUC of 0.8264, which is slightly lower than the Logistic Regression model. It is still a commendable performance of predicting positives as positives and negatives as negatives.

Model 3 - Random Forest

```
# Perform feature engineering or transformation

from sklearn.model_selection import GridSearchCV
from sklearn.ensemble import RandomForestClassifier

# instantiate
model3 = RandomForestClassifier(random_state=42)

# Perform hyperparameter tuning using grid search
param_grid = {"n_estimators": [100, 200, 300], "max_depth": [None, 5, 10]}
grid_search = GridSearchCV(model3, param_grid, cv=5)
grid_search.fit(X_train_scaled, y_train)
best_model3 = grid_search.best_estimator_

# Fit the best model on the scaled data
best_model3.fit(X_train_scaled, y_train)
```

```
▾                          RandomForestClassifier
RandomForestClassifier(max_depth=10, n_estimators=200, random_state=42)
```

```
y_pred3 = best_model3.predict(X_test_scaled)

# Create confusion matrix
cm = confusion_matrix(y_test, y_pred3)

# Plot confusion matrix
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues")
plt.xlabel("Predicted Label")
plt.ylabel("True Label")
plt.title("Confusion Matrix")

plt.savefig("images/random_forest_cm.png")
plt.show()
```

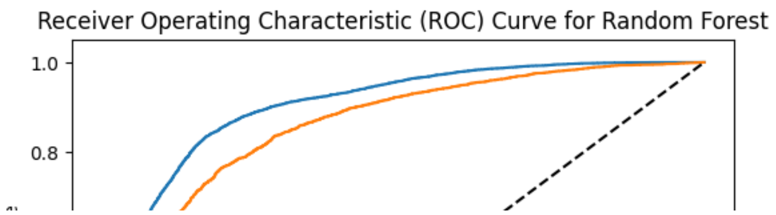


```
#evaluation of model
y_pred = best_model3.predict(X_test_scaled)
model3_accuracy = accuracy_score(y_test, y_pred)
model3_recall = recall_score(y_test, y_pred)
model3_precision = precision_score(y_test, y_pred)
model3_f1 = f1_score(y_test, y_pred)

print(f"""
Accuracy Fitted Model: {model3_accuracy:1.3f}
Recall Fitted Model: {model3_recall:1.3f}
Precision Fitted Model: {model3_precision:1.3f}
F1 Score Fitted Model: {model3_f1:1.3f}
""")
```

```
    Accuracy Fitted Model: 0.784
    Recall Fitted Model: 0.729
    Precision Fitted Model: 0.783
    F1 Score Fitted Model: 0.755
```

```
# Predict on training and test sets
training_preds3 = best_model3.predict_proba(X_train_scaled)[:, 1]
test_preds3 = best_model3.predict_proba(X_test_scaled)[:, 1]

# Calculate false positive rate (fpr), true positive rate (tpr), and thresholds for ROC curve
training_fpr_r, training_tpr_r, _ = roc_curve(y_train, training_preds3)
test_fpr_r, test_tpr_r, _ = roc_curve(y_test, test_preds3)

# Calculate the AUC score
training_auc_model3 = roc_auc_score(y_train, training_preds3)
test_auc_model3 = roc_auc_score(y_test, test_preds3)
print("Train AUC Score: {:.4f}". format(training_auc_model3))
print("Test AUC Score: {:.4f}".format(test_auc_model3))

# Plot the ROC curve
plt.plot(training_fpr_r, training_tpr_r, label="Train ROC Curve (AUC = {:.4f})".format(training_auc_model3))
plt.plot(test_fpr_r, test_tpr_r, label="Test ROC Curve (AUC = {:.4f})".format(test_auc_model3))
plt.plot([0, 1], [0, 1], "k--", label="Random Guess")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver Operating Characteristic (ROC) Curve for Random Forest")
plt.legend(loc="lower right")

plt.savefig("images/random_forest_roc_curve.png")

plt.show()
```

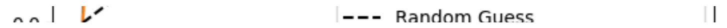
```
Train AUC Score: 0.9040
Test AUC Score: 0.8539
```



Random Forest Observations

- **Accuracy**: the model correctly predicted vaccine uptake with a score of 78.4%.
- **Recall**: 72.9% of actual vaccine recipients were correctly identified.
- **Precision**: 78.3% of those predicted to have taken the vaccine actually took the vaccine.
- **F1-Score**: at 75.5%, it is a good balance between precision and recall.

This model's **ROC curve** shows AUC of 0.8539, the highest so far. The model is more effective in predicting the seasonal vaccine uptake based on the provided features.It is able to differentiate between vaccine recipients and non-recipients effectively.



4. XGBoost Algorithm

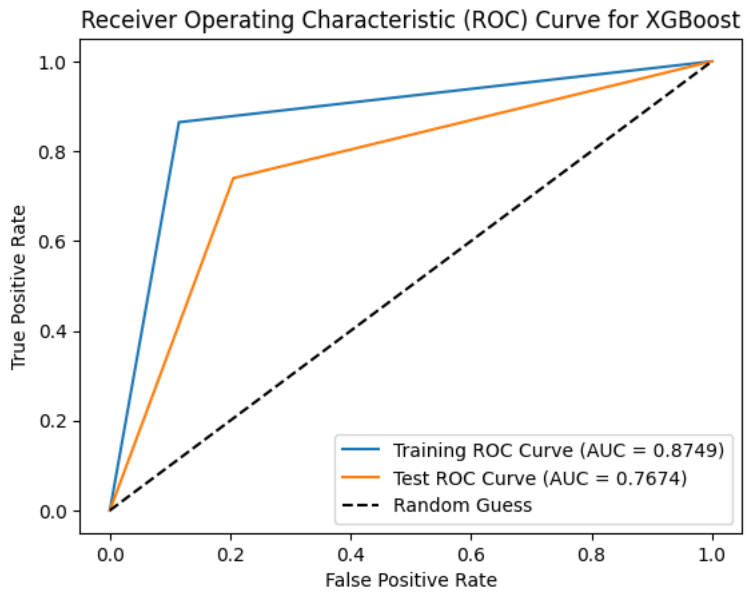
```
# import library
from xgboost import XGBClassifier

# Instantiate XGBClassifier
model4 = XGBClassifier()

# Fit XGBClassifier
model4.fit(X_train_scaled, y_train)

# Predict on training and test sets
training_preds = model4.predict_proba(X_train_scaled)[:, 1]
test_preds = model4.predict_proba(X_test_scaled)[:, 1]


# Predict on training and test sets
training_preds = model4.predict(X_train_scaled)
test_preds = model4.predict(X_test_scaled)

# Accuracy of training and test sets
training_accuracy = accuracy_score(y_train, training_preds)
test_accuracy = accuracy_score(y_test, test_preds)

print("Training Accuracy: {:.4}".format(training_accuracy))
print("Validation accuracy: {:.4}".format(test_accuracy))
print()

# evaluation
# Calculating precision, recall, and F1-score for the validation set
model4_precision = precision_score(y_test, test_preds)
model4_recall = recall_score(y_test, test_preds)
model4_f1 = f1_score(y_test, test_preds)

print("Precision: {:.4f}".format(model4_precision))
print("Recall: {:.4f}".format(model4_recall))
print("F1-Score: {:.4f}".format(model4_f1))
```

```
Training Accuracy: 0.8755
Validation accuracy: 0.7697

Precision: 0.7532
Recall: 0.7399
F1-Score: 0.7465
```

```
# Calculate false positive rate (fpr), true positive rate (tpr), and thresholds for ROC curve
training_fpr_x, training_tpr_x, _ = roc_curve(y_train, training_preds)
test_fpr_x, test_tpr_x, _ = roc_curve(y_test, test_preds)

# Calculate AUC scores for training and test sets
training_auc_model4 = roc_auc_score(y_train, training_preds)
test_auc_model4 = roc_auc_score(y_test, test_preds)
```

```
# Print AUC Score
print("Train AUC Score: {:.4f}". format(training_auc_model4))
print("Test AUC Score: {:.4f}".format(test_auc_model4))

# Plot the ROC curve
plt.plot(training_fpr_x, training_tpr_x, label="Training ROC Curve (AUC = {:.4f})".format(training_auc_model4))
plt.plot(test_fpr_x, test_tpr_x, label="Test ROC Curve (AUC = {:.4f})".format(test_auc_model4))
plt.plot([0, 1], [0, 1], "k--", label="Random Guess")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver Operating Characteristic (ROC) Curve for XGBoost")
plt.legend(loc="lower right")

plt.savefig("images/xgboost_roc_curve.png")
plt.show()
```

```
    Train AUC Score: 0.8749
    Test AUC Score: 0.7674
```



XGBoost Algorithm Observations

- This model has performed better than Logistic Regression and Decision Trees. It is highly likely that the algorithm has lived up to its performance characteristics of capturing complex patterns in data to provide high and improved accuracy. The results are as follows:
    - **Training Accuracy** of 87.55% suggests that this model was able to classify approcximately 87.55% of the samples in the training data.
    - **Validation Accuracy** of 76.97% suggests that this model was able to classify approcximately 76.97% of the samples in the test data.
    - **Recall**: 73.99% of actual vaccine recipients (actual positives) were correctly identified.
    - **Precision**: at 75.32%, the model correcty identified vaccine recipients as true positives.
    - **F1-Score**: at 74.65%, it is a good balance between precision and recall.

Analysis of the **ROC curve** reveals that the model was the least powerful in prediciting the test data. An AUC of 0.7674 on the test data, while still high, is the least among the four models.

Model Evaluation Summary

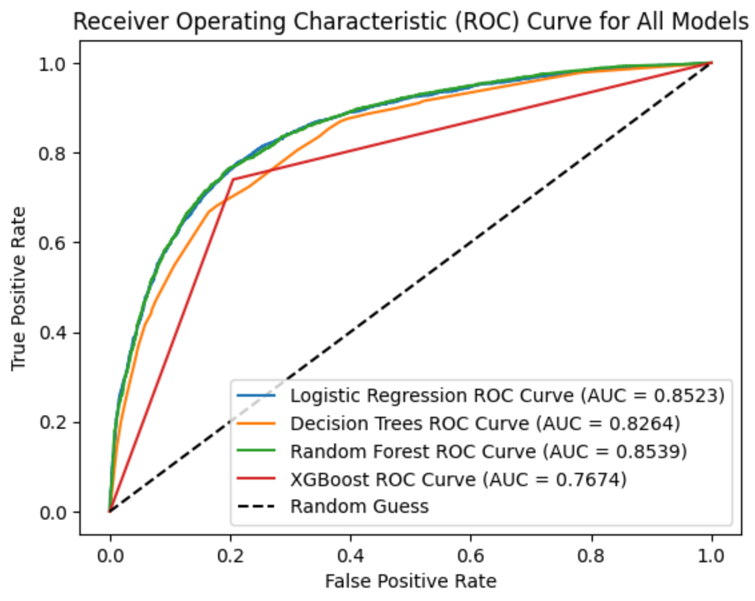
```
# create the summary df and define columns
scores = pd.DataFrame(np.array([
        ['Logistic Regression', 78.2, 73.9, 77.4, 85.0, 85.2],
        ['Decision Tree', 75.8, 67.5, 76.9, 83.1, 82.6],
        ['Random Forest', 78.4, 72.9, 78.3, 90.4, 85.4],
        ['XGBoost', 77.0, 74.0, 75.3, 87.5, 76.7]
]))
scores.columns = ["Model", "Accuracy", "Recall", "Precision", "Training AUC Score", "Test AUC Score"]
scores
```

	Model	Accuracy	Recall	Precision	Training AUC Score	Test AUC Score
0	Logistic Regression	78.2	73.9	77.4	85.0	85.2
1	Decision Tree	75.8	67.5	76.9	83.1	82.6
2	Random Forest	78.4	72.9	78.3	90.4	85.4
3	XGBoost	77.0	74.0	75.3	87.5	76.7

- The **Random Forest Model** (best_model3) has demonstrated commendable performance in predicting the uptake of the seasonal flu vaccine. It has strong evaluation metrics and an ROC curve with strong discriminatory power.

Final ROC Curve (all combined for test data)

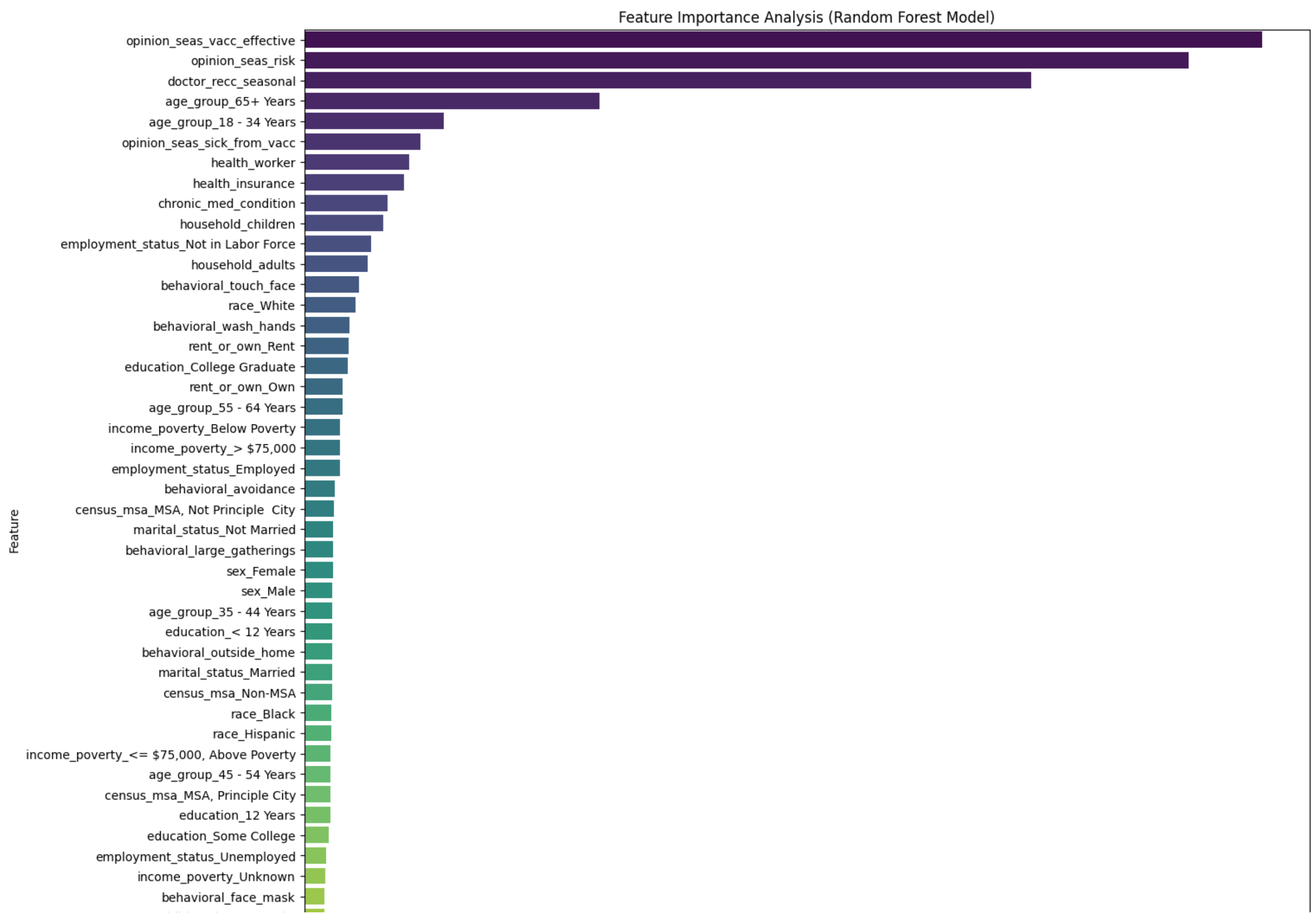
```
plt.plot(test_fpr_l, test_tpr_l, label="Logistic Regression ROC Curve (AUC = {:.4f})".format(auc_score_model1_test))
plt.plot(test_fpr_d, test_tpr_d, label="Decision Trees ROC Curve (AUC = {:.4f})".format(auc_score_model2_test))
plt.plot(test_fpr_r, test_tpr_r, label="Random Forest ROC Curve (AUC = {:.4f})".format(test_auc_model3))
plt.plot(test_fpr_x, test_tpr_x, label="XGBoost ROC Curve (AUC = {:.4f})".format(test_auc_model4))

plt.plot([0, 1], [0, 1], "k--", label="Random Guess")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("Receiver Operating Characteristic (ROC) Curve for All Models")
plt.legend(loc="lower right")

plt.savefig("images/all_roc_curve.png")
plt.show()
```



Feature Importance Analysis

- This step will help to further understand the most important features when predicting seasonal flu vaccine uptake.

```
# Get feature importances from the Random Forest model (Model 3)
importance_scores = best_model3.feature_importances_

# DataFrame with feature names and importance scores
feature_importance_df = pd.DataFrame({"Feature": X_train.columns, "Importance": importance_scores})

# Sort the features by importance in descending order
feature_importance_df = feature_importance_df.sort_values(by="Importance", ascending=False)

# Plotting feature importance
plt.figure(figsize=(15, 15))
sns.barplot(x="Importance", y="Feature", data=feature_importance_df, palette="viridis")
plt.xlabel("Importance")
plt.ylabel("Feature")
plt.title("Feature Importance Analysis (Random Forest Model)")
plt.savefig("images/random_forest_feature_importance.png")
plt.show()
```



```
# Set a threshold for feature importance
threshold = 0.05

# Select the features with importance scores above the threshold
selected_features = feature_importance_df.loc[feature_importance_df["Importance"] > threshold, "Feature"]
selected_features
```

```
12    opinion_seas_vacc_effective
13              opinion_seas_risk
7            doctor_recc_seasonal
21             age_group_65+ Years
Name: Feature, dtype: object
```

Feature Importance Observations

The following were the top features influencing the uptake of the seasonal vaccine in order of importance:

1. **`opinion_seas_vacc_effective`**

- As the most influential feature, a respondent's opinion on whether the seasonal flu vaccine was effective mattered a lot.
- This feature is under objective 4

2. **`opinion_seas_risk`**

- An individual's opinion about risk of getting sick with seasonal flu without the vaccine was the second most important feature in determining the indivuals uptake of the vaccine.
- This feature is under objective 4.

3. **`doctor_recc_seasonal`**

- This is the third most influential feature. It suggests that a doctor recommending the seasonal flu vaccine had a significant influence on vaccine uptake.
- This feature is under objective 4.

4. `age_group_65+ Years`

- Older respondents (65 and above) seemed to prioritize vaccination as the feature played a big role in the decision on vaccine uptake. Other concerns such as health may have influenced respondents in this age group.
- This is a demographic feature.

These are the features that play the most significant role in predicting how likely an individual is to get the seasonal flu vaccine out of all available features.

Conclusion

The Data

- The data required a lot of exploration and engineering. Some important features had missing values that would have made the data biased. Other features showed a bias, such as the race feature that was heavily tilted towards the white race.

The Models

- The models' performance was almost similar. However, with each iteration, the scores and accuracies changed. **Random Forest** emerged the best with an AUC score of 0.8539 on the test data.
- The process of choosing and optimizing model hyperparameters was time consuming.
- A better balance on the data may give more promising results.

In summary:

- The role of healthcare professionals can never be downplayed as evidenced by the fact that a doctor's recommendation to get the flu vaccine played a big role.
- Public perception is also important. How people view and feel about vaccines is a big influence on vaccine uptake.
- Age is also a factor. Older people tended to get the seasonal flue vaccine more than younger people.

Recommendations

1. Embrace personalized outreach as a campaign tool so as to target individuals and mould their perception towards immunization.
2. Public campaigns should be geared towards bringing onboard more younger people as it seems that they are less likely to get the seasonal flu vaccines.
3. The public health sector should continue encouraging doctors to recommend suitable vaccines to their clients. This modelling and analysis process has shown that people are highly likely to listen to their doctor's advice.

For further improvements:

1. Conduct more feature engineering to get more insight on features influencing uptake of the vaccine.
2. Using more recent data to create predictions, especially after the recent Covid-19 pandemic, may provide better outlooks on the results.