

# Phase 3 Vaccination status prediction

- Student name: Kevin Spring
- Student pace: Flex
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- Instructor name: Morgan Jones
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## Summary

- Moderna is developing a dual seasonal flu and COVID-19 vaccination.
- Moderna needs to understand what features lead to vaccination or unvaccination and to predict individuals who will be vaccinated or not.
- Machine learning algorithms such as decision trees, random forests, and gradient boosting (XGBoost) can solve this problem.
- Specificity is the best metric as it measures the ability of the model to correctly identify not getting a vaccine.
- Model 5 using XGBoost is the best model and has a specificity score of 81.7%.
- The most important features according to model 5 are access to healthcare, opinion on vaccine effectiveness, opinion on risk of infection, and age group.
- This prediction tool is limited to people with access to healthcare.

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## Introduction

Moderna, Inc. is a biotechnology company based in Cambridge, Massachusetts focused on RNA therapeutics such as mRNA vaccines. Their use of RNA technology speeds up design and production as compared to traditional vaccines. Moderna's only current commercial product is Spikevax, a vaccine for SARS-CoV-2, the causative agent of COVID-19. With the success of Spikevax, Moderna has been developing other RNA-based vaccines for diseases such as influenza, HIV, and various cancers. Moderna currently has 44 vaccines and treatments in their production pipeline, of which 22 are in clinical trials. One of these vaccines in Phase 3 trials is a single-shot SARS-CoV-2 and influenza vaccine, called mRNA-1073, to prevent severe reactions and hospitalization to the seasonal influenza virus and COVID-19.

## Influenza

Influenza (the flu) is an infectious disease caused by influenza viruses. Symptoms may include a runny nose, sore throat, muscle pain, headache, coughing, and fatigue. Symptoms begin one to four days after exposure and may last for two to eight days. Influenza can lead to complications such as pneumonia, acute respiratory distress syndrome, meningitis, and encephalitis. The virus is spread through droplet transmission when they are produced by coughing and sneezing and directly inhaled or picked up through intermediate objects.

In high-risk groups like those with asthma or cardiovascular illness, an influenza virus infection can be fatal. The Centers for Disease Control and Prevention (CDC), estimates that 35 million people in the United States had symptoms of influenza in 2020 that lead to 17 million medical office visits and 380,000 hospitalizations [1](#). It was the cause of death for 18,000 to 80,000 people in the United States between 2019-2020.



The best ways to prevent infection of influenza is to wash hands regularly when in public, avoid touching your mouth, eyes, and get a seasonal flu vaccination. The CDC recommends everyone 6 months of age or older to get an annual influenza vaccine [2](#).

The current seasonal flu vaccine can be categorized by how it is produced, egg-based, cell-based, or recombinant. The most common way is using an egg-based manufacturing process. Production begins when the WHO Global Influenza Surveillance and Response System provides vaccine manufacturers candidate vaccine viruses. These viruses are then grown in fertilized eggs, the fluid from the egg extracted, the virus inactivated, and then the inactivated virus purified. The process continues with testing and FDA

approval. The cell-based production is similar except that instead of fertilized eggs, the virus is grown in cultured mammalian cells. The recombinant method uses cultured recombinant cells to produce the proteins of the virus and packaging those proteins into a different, inactivated virion [3](#).

When the inactivated virus is injected into a patient, the patient's immune system recognizes these proteins as foreign and creates an immune response. Other specialized immune cells of the patients body (memory B cells) may then produce an adaptive immune response to protect the patient from natural infection of the virus.

The process of developing and testing a new influenza vaccine takes 12 to 18 months. The influenza virus quickly mutates and during this time a strain of influenza may have evolved that would not be included in the seasonal flu vaccine. This leads to the seasonal vaccine having low efficacy. The flu vaccine has been shown to reduce the risk of having severe illness by 40 - 60% [4](#).



## COVID-19

COVID-19 is an infectious respiratory disease caused by SARS-CoV-2 virus. Symptoms include fever, headache, sore throat, loss of smell, fatigue, and breathing difficulties. A severe illness may lead to pneumonia, hypoxia, or respiratory failure. The virus is transmitted through the respiratory system when contaminated droplets and airborne particles that contain the virus are inhaled [5](#).

The first reported case of COVID-19 was in December of 2019 at Wuhan, China. Since then SARS-CoV-2 has become a pandemic with over one million deaths in the United States. The CDC recommends everyone 6 months of age or older to get vaccinated against COVID-19[6](#).

COVID-19 vaccines approved for use in the United States include those manufactured by Pfizer-BioNTech, Moderna, Novavax, and Johnson & Johnson. Pfizer-BioNTech and Moderna are both RNA-based vaccinations and have a 95% efficacy. Novavax and Johnson & Johnson have non-RNA based vaccines and have a efficacy of 90% and 67% efficacy, respectively [7](#).

## mRNA Vaccines

The goal of vaccinations is to teach a person's immune system how to recognize a virus or other pathogen so a natural infection does not lead to serious illness. Viruses are noncellular biological entities made up of proteins, genetic material (DNA or RNA), and sometimes lipids. When a person is infected with a virus, the person's immune system detects the pathogen's foreign proteins in its cells and proceeds to fight the infection. A person's immune system will then use the proteins from the virus to train other cells to recognize this virus on a subsequent infection. This is what creates adaptive immunity [8](#)

Conventional vaccines make use of inactivating or attenuating the pathogen. This may involve using the entire virus or only some proteins that make up the virus. This requires that the virus be grown in media such as eggs or cultured cells. This take a lot of time and prolongs the ability to get a vaccine out to the public when a new virus emerges or an endemic virus evolves.

RNA-based vaccines use a different approach. The instructions to create the viral protein is found in RNA. RNA is how all cells in the body make proteins. Instead of growing the virus in eggs or cultured cells, inactivating them, and then injecting the vaccine into the patient, the patient becomes the manufacturing process. The patient's cells take in the mRNA in the vaccine and makes some of the viral proteins. These proteins would be identified as being foreign to the body by immune cells and then the adaptive immune response would take over.

Moderna's mRNA vaccine technology shows 90+% effectiveness against symptoms while the traditional seasonal influenza vaccine is 40-60% effective. If mRNA-1073 is granted FDA approval, this combined vaccine is expected to supplant the current seasonal influenza vaccine as it is more convient to get a single vaccine than multiple ones.

## Business Problem

While a vaccine may be very effective, it is only going to help if a patient is willing to take the vaccine. In this regard, Moderna needs knowledge of how people's backgrounds, opinions, and health behaviors are related to their personal vaccination patterns. With this understanding, Moderna can design targeted information and create a prediction platform on their vaccines and get susceptible populations vaccinated.

Specifically, Moderna needs:

- To know what variables are most relevant in predicting if someone chooses or does not choose to be vaccinated
- A prediction tool to predict if a person will not receive the vaccine.

## Business Solution

I will use machine learning algorithms on a structured dataset that has information about vaccination status. I need to use machine learning to be able to identify the important variables that are associated with vaccination status and to predict the outcome whether a person is vaccinated or unvaccinated with new data.

## Stakeholders

- Moderna, Inc. executives
- Moderna, Inc. pharmaceutical representatives

## Data

### Data Source

Between 2009 and 2010, the [2009 National Health Flu Survey \(NHFS\)](#) was conducted by the CDC. This phone survey asked respondents whether they had received the H1N1 influenza and seasonal influenza vaccines and additional questions covering their demographic background, opinions on risks of illness, opinion of vaccine effectiveness, and behaviors towards mitigating transmission. This was in reaction to a novel influenza virus, H1N1 or 'swine flu', beginning to circulate in the United States. A vaccine for H1N1 was developed and available to the public by the end of 2009. This vaccine was separate from the traditional influenza vaccine because H1N1 emerged too late to be included in the trivalent seasonal influenza vaccine for 2009.

## Suitability of Data

While this data is over ten years old and targets only part of the potential vaccine cocktail Moderna, Inc. will include in their combined Flu-COVID vaccine, this dataset is suitable to build a predictive model in line with Moderna's needs. Moderna Inc. wants to have a predictive model to identify individuals that will be vaccinated against influenza and COVID-19 in a combined vaccine. The last time there was a serious novel respiratory virus pandemic like COVID-19 was in 2009 during the H1N1 pandemic. This time period accurately reflects our current period of having a regular seasonal flu vaccine and a separate novel respiratory virus circulating. After 2009, H1N1 was included in the seasonal influenza vaccine and the population only had to have a single influenza vaccination.

```
In [1]: # Import the data
import pandas as pd
data_features = pd.read_csv('data/training_set_features.csv') # predictors
data_target = pd.read_csv('data/training_set_labels.csv') # target
data = pd.concat([data_features, data_target], axis=1) # combine target and predictor data
```

## Data Exploration

```
In [2]: # Shape of data features
print(f'Size of dataset')
print(f'Number of Observations: {data.shape[0]}')
print(f'Number of variables: {data.shape[1]}')
data.info()
```

```
Size of dataset
Number of Observations: 26707
Number of variables: 39
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26707 entries, 0 to 26706
Data columns (total 39 columns):
 #   Column           Non-Null Count  Dtype  
 --- 
 0   respondent_id    26707 non-null   int64  
 1   h1n1_concern     26615 non-null   float64
 2   h1n1_knowledge   26591 non-null   float64
 3   behavioral_antiviral_meds 26636 non-null   float64
 4   behavioral_avoidance 26499 non-null   float64
 5   behavioral_face_mask 26688 non-null   float64
 6   behavioral_wash_hands 26665 non-null   float64
 7   behavioral_large_gatherings 26620 non-null   float64
 8   behavioral_outside_home 26625 non-null   float64
 9   behavioral_touch_face 26579 non-null   float64
 10  doctor_recc_h1n1  24547 non-null   float64
 11  doctor_recc_seasonal 24547 non-null   float64
 12  chronic_med_condition 25736 non-null   float64
 13  child_under_6_months 25887 non-null   float64
 14  health_worker    25903 non-null   float64
 15  health_insurance 14433 non-null   float64
 16  opinion_h1n1_vacc_effective 26316 non-null   float64
 17  opinion_h1n1_risk  26319 non-null   float64
 18  opinion_h1n1_sick_from_vacc 26312 non-null   float64
 19  opinion_seas_vacc_effective 26245 non-null   float64
 20  opinion_seas_risk  26193 non-null   float64
 21  opinion_seas_sick_from_vacc 26170 non-null   float64
 22  age_group        26707 non-null   object  
 23  education         25300 non-null   object  
 24  race              26707 non-null   object  
 25  sex               26707 non-null   object  
 26  income_poverty   22284 non-null   object  
 27  marital_status   25299 non-null   object  
 28  rent_or_own      24665 non-null   object  
 29  employment_status 25244 non-null   object  
 30  hhs_geo_region   26707 non-null   object  
 31  census_msa       26707 non-null   object  
 32  household_adults 26458 non-null   float64
 33  household_children 26458 non-null   float64
 34  employment_industry 13377 non-null   object  
 35  employment_occupation 13237 non-null   object  
 36  respondent_id    26707 non-null   int64  
 37  h1n1_vaccine     26707 non-null   int64  
 38  seasonal_vaccine 26707 non-null   int64  
dtypes: float64(23), int64(4), object(12)
memory usage: 7.9+ MB
```

## Variable Information

Variable	Data Type	Description	Values
h1n1_concern	Ordinal	Level of concern about H1N1 flu	0 = Not at all concerned, 1 = Not very concerned, 2 = Somewhat concerned, 3 = Very concerned,
h1n1_knowledge	Ordinal	Level of knowledge about H1N1 flu	0 = No knowledge, 1 = A little knowledge, 2 = A lot of knowledge,
behavioral_antiviral_meds	Binary	Has taken antiviral medication	0 = No, 1 = Yes
behavioral_avoidance	Binary	Has avoided close contact with others with flu-like symptoms	0 = No, 1 = Yes
behavioral_face_mask	Binary	Has bought a face mask	0 = No, 1 = Yes
behavioral_large_gatherings	Binary	Has reduced time at large gatherings	0 = No, 1 = Yes

Variable	Data Type	Description	Values
behavioral_outside_home	Binary	Has reduced contact with people outside of own household	0 = No, 1 = Yes
behavioral_touch_face	Binary	Has avoided touching eyes, nose, or mouth	0 = No, 1 = Yes
doctor_recc_h1n1	Binary	H1N1 flu vaccine was recommended by doctor	0 = No, 1 = Yes
doctor_recc_seasonal	Binary	Seasonal flu vaccine was recommended by doctor	0 = No, 1 = Yes
chronic_med_condition	Binary	Has chronic medical condition	0 = No, 1 = Yes
children_under_6_months	Binary	Has regular close contact with a child under the age of six months	0 = No, 1 = Yes
health_worker	Binary	Is a healthcare worker	0 = No, 1 = Yes
health_insurance	Binary	Has health insurance	0 = No, 1 = Yes
opinion_h1n1_risk	Ordinal	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_vacc_effective	Ordinal	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_sick_from_vacc	Ordinal	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_risk	Ordinal	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_vacc_effective	Ordinal	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_sick_from_vacc	Ordinal	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	Ordinal	Age group of respondent	65+ Years, 55 - 64 Years, 45 - 54 Years, 35 - 44 Years, 18 - 34 Years
education	Ordinal	Self-reported education level	College graduate, Some college, 12 years, < 12 Years
sex	Nominal	Sex of respondent	Male or Female
race	Nominal	Race of respondent	White, Black, Hispanic, Other or Multiple
income_poverty	Ordinal	Household annual income of respondent with respect to 2008 Census poverty thresholds	> \$75,000, <= \$75,000 Above poverty, Below poverty
marital_status	Nominal	Marital status of respondent	Married or Not Married
rent_or_own	Nominal	Housing situation of respondent	Rent or Own
employment_status	Nominal	Employment status of respondent	Employed, Unemployed, Not in labor force
hhs_geo_region	Nominal	Respondent's residence using a 10-region geographic coded classification	Coded random strings
census_msa	Nominal	Respondent's residence within metropolitan statistical areas	MSA not principle city, MSA principle city, Non-MSA
household_adults	Discrete	Number of other adults in household, top-coded to 3	0, 1, 2, 3
household_children	Discrete	Number of children in household, top-coded to 3	0, 1, 2, 3
employment_industry	Nominal	Type of industry respondent is employed	Coded random strings
employment_occupation	Nominal	Type of occupation of respondent	Coded random strings
seasonal_vaccine	Binary	Respondent's report of getting the seasonal influenza vaccination	0, 1
h1n1_vaccine	Binary	Respondent's report of getting the H1N1 influenza vaccination	0, 1

In [3]: `data.describe(include='all').T`

Out[3]:

	count	unique	top	freq	mean	std	min	25%	50%	75%	max
<b>respondent_id</b>	26707.0	NaN		NaN	NaN	13353.0	7709.791156	0.0	6676.5	13353.0	20029.5
<b>h1n1_concern</b>	26615.0	NaN		NaN	NaN	1.618486	0.910311	0.0	1.0	2.0	2.0
<b>h1n1_knowledge</b>	26591.0	NaN		NaN	NaN	1.262532	0.618149	0.0	1.0	1.0	2.0
<b>behavioral_antiviral_meds</b>	26636.0	NaN		NaN	NaN	0.048844	0.215545	0.0	0.0	0.0	1.0
<b>behavioral_avoidance</b>	26499.0	NaN		NaN	NaN	0.725612	0.446214	0.0	0.0	1.0	1.0
<b>behavioral_face_mask</b>	26688.0	NaN		NaN	NaN	0.068982	0.253429	0.0	0.0	0.0	1.0
<b>behavioral_wash_hands</b>	26665.0	NaN		NaN	NaN	0.825614	0.379448	0.0	1.0	1.0	1.0
<b>behavioral_large_gatherings</b>	26620.0	NaN		NaN	NaN	0.35864	0.47961	0.0	0.0	0.0	1.0
<b>behavioral_outside_home</b>	26625.0	NaN		NaN	NaN	0.337315	0.472802	0.0	0.0	0.0	1.0
<b>behavioral_touch_face</b>	26579.0	NaN		NaN	NaN	0.677264	0.467531	0.0	0.0	1.0	1.0
<b>doctor_recc_h1n1</b>	24547.0	NaN		NaN	NaN	0.220312	0.414466	0.0	0.0	0.0	1.0
<b>doctor_recc_seasonal</b>	24547.0	NaN		NaN	NaN	0.329735	0.470126	0.0	0.0	0.0	1.0
<b>chronic_med_condition</b>	25736.0	NaN		NaN	NaN	0.283261	0.450591	0.0	0.0	0.0	1.0
<b>child_under_6_months</b>	25887.0	NaN		NaN	NaN	0.08259	0.275266	0.0	0.0	0.0	1.0
<b>health_worker</b>	25903.0	NaN		NaN	NaN	0.111918	0.315271	0.0	0.0	0.0	1.0
<b>health_insurance</b>	14433.0	NaN		NaN	NaN	0.87972	0.3253	0.0	1.0	1.0	1.0
<b>opinion_h1n1_vacc_effective</b>	26316.0	NaN		NaN	NaN	3.850623	1.007436	1.0	3.0	4.0	5.0
<b>opinion_h1n1_risk</b>	26319.0	NaN		NaN	NaN	2.342566	1.285539	1.0	1.0	2.0	4.0
<b>opinion_h1n1_sick_from_vacc</b>	26312.0	NaN		NaN	NaN	2.35767	1.362766	1.0	1.0	2.0	4.0
<b>opinion_seas_vacc_effective</b>	26245.0	NaN		NaN	NaN	4.025986	1.086565	1.0	4.0	4.0	5.0
<b>opinion_seas_risk</b>	26193.0	NaN		NaN	NaN	2.719162	1.385055	1.0	2.0	2.0	5.0
<b>opinion_seas_sick_from_vacc</b>	26170.0	NaN		NaN	NaN	2.118112	1.33295	1.0	1.0	2.0	4.0
<b>age_group</b>	26707	5	65+ Years	6843	NaN		NaN	NaN	NaN	NaN	NaN
<b>education</b>	25300	4	College Graduate	10097	NaN		NaN	NaN	NaN	NaN	NaN
<b>race</b>	26707	4	White	21222	NaN		NaN	NaN	NaN	NaN	NaN
<b>sex</b>	26707	2	Female	15858	NaN		NaN	NaN	NaN	NaN	NaN
<b>income_poverty</b>	22284	3	<= \$75,000, Above Poverty	12777	NaN		NaN	NaN	NaN	NaN	NaN
<b>marital_status</b>	25299	2	Married	13555	NaN		NaN	NaN	NaN	NaN	NaN
<b>rent_or_own</b>	24665	2	Own	18736	NaN		NaN	NaN	NaN	NaN	NaN
<b>employment_status</b>	25244	3	Employed	13560	NaN		NaN	NaN	NaN	NaN	NaN
<b>hhs_geo_region</b>	26707	10	Izgpxyit	4297	NaN		NaN	NaN	NaN	NaN	NaN
<b>census_msa</b>	26707	3	MSA, Not Principle City	11645	NaN		NaN	NaN	NaN	NaN	NaN
<b>household_adults</b>	26458.0	NaN		NaN	NaN	0.886499	0.753422	0.0	0.0	1.0	3.0
<b>household_children</b>	26458.0	NaN		NaN	NaN	0.534583	0.928173	0.0	0.0	0.0	1.0
<b>employment_industry</b>	13377	21	fcxhlnwr	2468	NaN		NaN	NaN	NaN	NaN	NaN
<b>employment_occupation</b>	13237	23	xtkaffoo	1778	NaN		NaN	NaN	NaN	NaN	NaN
<b>respondent_id</b>	26707.0	NaN		NaN	NaN	13353.0	7709.791156	0.0	6676.5	13353.0	20029.5
<b>h1n1_vaccine</b>	26707.0	NaN		NaN	NaN	0.212454	0.409052	0.0	0.0	0.0	1.0
<b>seasonal_vaccine</b>	26707.0	NaN		NaN	NaN	0.465608	0.498825	0.0	0.0	0.0	1.0

## Data Scrubbing

### Strategy

1. Identify imbalance of target variables
2. Identify duplicated data
3. Identify missing data with NA or placeholders
4. Variable selection
5. Encode variables

### 1. Identify unbalanced target variable

```
In [5]: # Proportion of unvaccinated
vacc_no = 1 - data[['seasonal_vaccine', 'h1n1_vaccine']].sum()/len(data)
# Proportion of vaccinated
vacc = data[['seasonal_vaccine', 'h1n1_vaccine']].sum()/len(data)

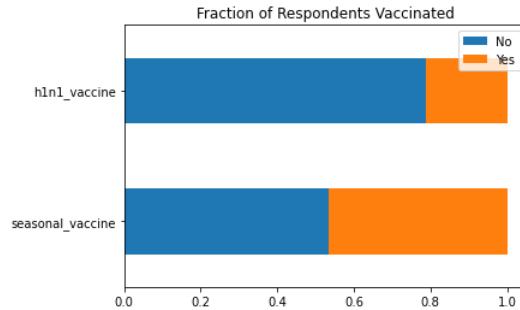
# Make 2-way table
df1 = pd.DataFrame([vacc_no, vacc], index=['No', 'Yes']).T
df1
```

	No	Yes
seasonal_vaccine	0.534392	0.465608
h1n1_vaccine	0.787546	0.212454

```
In [6]: import matplotlib.pyplot as plt
%matplotlib inline

# barplot of 2-way table
df1.plot(kind='barh', stacked=True, title='Fraction of Respondents Vaccinated')
plt.legend(loc='upper right')

<matplotlib.legend.Legend at 0x1f3bd877ac0>
```



### Imbalance Discussion

In regards to the `seasonal_vaccine` target, this variable is balanced with the possible responses, 'No' (0) and 'Yes' (1) both being about 50% in the data.

As shown in the description of the data, the `h1n1_vaccine` variable is not balanced. This is identified with a mean of about 0.2. My prediction only needs to target one possible vaccination thus I will not be using `h1n1_vaccine` variable as a target.

## 2. Identify duplicated data

```
In [7]: # Duplicates

## After merging the datasets the column respondent_id is duplicated.
## Delete both columns because they are unnecessary
data.drop(['respondent_id'], axis=1, inplace=True)

# Look at the rest of the data for duplicates
duplicates_len = data.duplicated().sum()
print(f"Results:\nThere are {duplicates_len} duplicated records.")

Results:
There are 0 duplicated records.
```

### Duplicated Data Discussion

According to my results there is no duplicated data in this dataset.

## 3. Identify missing data

```
In [8]: # null values
print(f'''There is {data.shape[0]} records and
{data.shape[1]} variable in the dataset.
''')

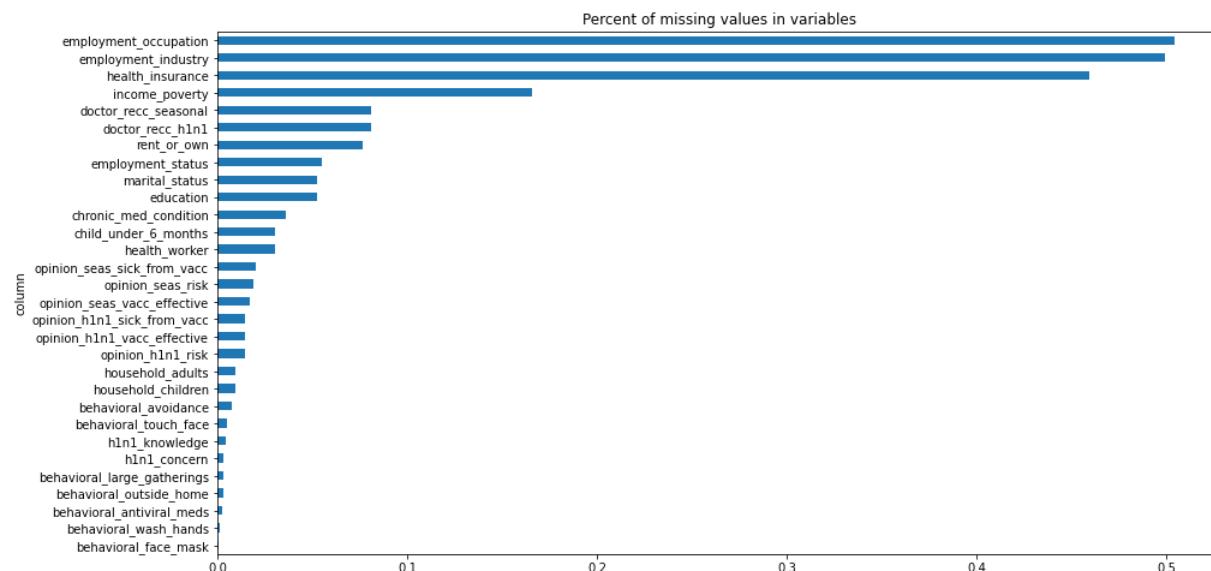
fraction_na = data.isna().sum()/len(data)

print(f'Fraction of Missing values\n-----\n{fraction_na.sort_values(ascending=False)}')
```

```
There is 26707 records and  
37 variable in the dataset.
```

```
Fraction of Missing values  
-----  
employment_occupation      0.504362  
employment_industry        0.499120  
health_insurance           0.459580  
income_poverty              0.165612  
doctor_recc_h1n1            0.080878  
doctor_recc_seasonal        0.080878  
rent_or_own                 0.076459  
employment_status           0.054780  
marital_status               0.052720  
education                   0.052683  
chronic_med_condition       0.036358  
child_under_6_months         0.030704  
health_worker                0.030104  
opinion_seas_sick_from_vacc 0.020107  
opinion_seas_risk            0.019246  
opinion_seas_vacc_effective 0.017299  
opinion_h1n1_sick_from_vacc 0.014790  
opinion_h1n1_vacc_effective 0.014640  
opinion_h1n1_risk             0.014528  
household_adults            0.009323  
household_children           0.009323  
behavioral_avoidance        0.007788  
behavioral_touch_face        0.004793  
h1n1_knowledge               0.004343  
h1n1_concern                 0.003445  
behavioral_large_gatherings 0.003258  
behavioral_outside_home      0.003070  
behavioral_antiviral_meds    0.002658  
behavioral_wash_hands         0.001573  
behavioral_face_mask          0.000711  
sex                          0.000000  
race                         0.000000  
age_group                    0.000000  
hhs_geo_region                0.000000  
census_msa                   0.000000  
h1n1_vaccine                  0.000000  
seasonal_vaccine                0.000000  
dtype: float64
```

```
In [9]: import pylab  
import matplotlib.pyplot as plt  
  
def plot_missing_values(df):  
    # Attribute: https://marloz.github.io/projects/skLearn/pipeline/missing/preprocessing/2020/03/20/skLearn-pipelines-missing-values.html  
    """ For each column with missing values plot proportion that is missing."""  
    dataset = [(col, df[col].isnull().sum() / len(df))  
               for col in df.columns if df[col].isnull().sum() > 0]  
    col_names = ['column', 'percent_missing']  
    missing_df = pd.DataFrame(dataset, columns=col_names).sort_values('percent_missing')  
    pylab.rcParams['figure.figsize'] = (15, 8)  
    missing_df.plot(kind='barh', x='column', y='percent_missing')  
    plt.title('Percent of missing values in variables')  
    plt.gca().get_legend().remove()  
  
plot_missing_values(data)
```



## Placeholders for missing data

```
In [10]: # Any placeholders?  
# Look for top occurring values  
print('2009 National Influenza Survey\n')
```

```
for col in data.columns:  
    print(col, '\n', data[col].value_counts(normalize = True).head(10), '\n')
```

2009 National Influenza Survey

```
h1n1_concern
2.0    0.397332
1.0    0.306331
3.0    0.172497
0.0    0.123840
Name: h1n1_concern, dtype: float64

h1n1_knowledge
1.0    0.548983
2.0    0.356775
0.0    0.094242
Name: h1n1_knowledge, dtype: float64

behavioral_antiviral_meds
0.0    0.951156
1.0    0.048844
Name: behavioral_antiviral_meds, dtype: float64

behavioral_avoidance
1.0    0.725612
0.0    0.274388
Name: behavioral_avoidance, dtype: float64

behavioral_face_mask
0.0    0.931018
1.0    0.068982
Name: behavioral_face_mask, dtype: float64

behavioral_wash_hands
1.0    0.825614
0.0    0.174386
Name: behavioral_wash_hands, dtype: float64

behavioral_large_gatherings
0.0    0.64136
1.0    0.35864
Name: behavioral_large_gatherings, dtype: float64

behavioral_outside_home
0.0    0.662685
1.0    0.337315
Name: behavioral_outside_home, dtype: float64

behavioral_touch_face
1.0    0.677264
0.0    0.322736
Name: behavioral_touch_face, dtype: float64

doctor_recc_h1n1
0.0    0.779688
1.0    0.220312
Name: doctor_recc_h1n1, dtype: float64

doctor_recc_seasonal
0.0    0.670265
1.0    0.329735
Name: doctor_recc_seasonal, dtype: float64

chronic_med_condition
0.0    0.716739
1.0    0.283261
Name: chronic_med_condition, dtype: float64

child_under_6_months
0.0    0.91741
1.0    0.08259
Name: child_under_6_months, dtype: float64

health_worker
0.0    0.888082
1.0    0.111918
Name: health_worker, dtype: float64

health_insurance
1.0    0.87972
0.0    0.12028
Name: health_insurance, dtype: float64

opinion_h1n1_vacc_effective
4.0    0.443950
5.0    0.272306
3.0    0.179473
2.0    0.070603
1.0    0.033668
Name: opinion_h1n1_vacc_effective, dtype: float64

opinion_h1n1_risk
2.0    0.376876
1.0    0.309244
4.0    0.204947
5.0    0.066492
3.0    0.042441
Name: opinion_h1n1_risk, dtype: float64

opinion_h1n1_sick_from_vacc
2.0    0.346952
1.0    0.341973
4.0    0.222332
```

```
5.0    0.083118
3.0    0.005625
Name: opinion_h1n1_sick_from_vacc, dtype: float64

opinion_seas_vacc_effective
4.0    0.443094
5.0    0.379996
2.0    0.084054
1.0    0.046523
3.0    0.046333
Name: opinion_seas_vacc_effective, dtype: float64

opinion_seas_risk
2.0    0.341847
4.0    0.291299
1.0    0.228076
5.0    0.112931
3.0    0.025847
Name: opinion_seas_risk, dtype: float64

opinion_seas_sick_from_vacc
1.0    0.453573
2.0    0.291670
4.0    0.185403
5.0    0.065762
3.0    0.003592
Name: opinion_seas_sick_from_vacc, dtype: float64

age_group
65+ Years      0.256225
55 - 64 Years   0.208297
45 - 54 Years   0.196128
18 - 34 Years   0.195267
35 - 44 Years   0.144082
Name: age_group, dtype: float64

education
College Graduate  0.399091
Some College       0.278379
12 Years           0.229130
< 12 Years         0.093399
Name: education, dtype: float64

race
White            0.794623
Black             0.079305
Hispanic          0.065713
Other or Multiple 0.060359
Name: race, dtype: float64

sex
Female           0.593777
Male              0.406223
Name: sex, dtype: float64

income_poverty
<= $75,000, Above Poverty  0.573371
> $75,000           0.305600
Below Poverty      0.121029
Name: income_poverty, dtype: float64

marital_status
Married           0.535792
Not Married        0.464208
Name: marital_status, dtype: float64

rent_or_own
Own               0.759619
Rent              0.240381
Name: rent_or_own, dtype: float64

employment_status
Employed          0.537157
Not in Labor Force 0.405284
Unemployed         0.057558
Name: employment_status, dtype: float64

hhs_geo_region
lzgpxyit      0.160894
fpwskwrf      0.122253
qufhixun      0.116149
oxchjgsf      0.107051
kbazzjca      0.107013
bhuguouqj     0.106564
mlyznmhf      0.083985
lrircsnp      0.077807
atmpneygn     0.076122
dppwygqj      0.042161
Name: hhs_geo_region, dtype: float64

census_msa
MSA, Not Principle City  0.436028
MSA, Principle City      0.294455
Non-MSA                 0.269517
Name: census_msa, dtype: float64

household_adults
1.0    0.547056
0.0    0.304483
2.0    0.105941
```

```

3.0    0.042520
Name: household_adults, dtype: float64

household_children
0.0    0.705722
1.0    0.120002
2.0    0.108247
3.0    0.066029
Name: household_children, dtype: float64

employment_industry
fcxhlwr    0.184496
wxleyezf   0.134858
ldnllelj   0.092024
pxcmvdjn   0.077521
atmlpfrs   0.069223
arjwrbjb   0.065112
xicduogh   0.063617
mfikgejo   0.045900
vjjrobsf   0.039396
rucpziij   0.039097
Name: employment_industry, dtype: float64

employment_occupation
xtkaffoo   0.134320
mxkfnird   0.113999
emcorrrxb  0.095943
cmhcxjea   0.094206
xgwztkwe   0.081741
hfkjkmi    0.057868
qxajmpny   0.041399
xqwgdydyp  0.036640
klldqjyjy  0.035431
uqqtjvyb   0.034147
Name: employment_occupation, dtype: float64

h1n1_vaccine
0    0.787546
1    0.212454
Name: h1n1_vaccine, dtype: float64

seasonal_vaccine
0    0.534392
1    0.465608
Name: seasonal_vaccine, dtype: float64

```

```
In [11]: # Number of observations with at least 1 missing value
print(f'No. of rows with at least 1 missing value: {len(data.loc[data.isna().any(axis=1)])}')
```

No. of rows with at least 1 missing value: 20270

```
In [12]: # Number of observations with all variables missing
print(f'No. of rows with all missing values: {len(data.loc[data.isna().all(axis=1)])}')
```

No. of rows with all missing values: 0

## Discussion

- Large proportion of missing data for `health_insurance`, `employment_industry`, and `employment_occupation`
- No missing data in `age_group`, `race`, `sex`, `hhs_geo_region`, and `census_msa`
- In `race`, hispanic is an option while on the U.S. Census it is listed as an ethnicity.
- There is an equal number of NA in `household_adults` and `household_children`
- There is an equal number of NA in `doctor_recc_h1n1` and `doctor_recc_seasonal`
- `census_msa`: msa means metropolitan statistical area.
  - MSA = urban
  - MSA, Not Principle city = suburban
  - Non-MSA = rural
- `hhs_geo_region` is in code and won't be meaningful
- `employment_history` is coded and won't be meaningful
- `employment_occupation` is coded and won't be meaningful

## Correcting Missing Data

The [original documentation](#) for the survey indicates the respondent can refuse to answer a question so the missing data may be due to error, refusal, or mistakes. There is a large amount of missing data in `health_insurance`, `income_poverty`, `employment_industry`, and `employment_occupation` which may be due to refusal to answer a question out of privacy concerns by the respondent. The variables `age_group`, `race`, `sex`, `hhs_geo_region`, and `census_msa` have no missing data, while the remaining variables have a minor amount of missing data. I hypothesize that the variables with large proportion of missing data are due to refusal or ignorance. For this reason, I will keep missing data during encoding of the variables and create new variables (`*variable_is_na`) to indicate that this respondent has missing information for that variable.

## 4. Variable Selection

As shown previously, the variable `h1n1_vaccine` is the respondent's answer to the question if they got the single H1N1 vaccination. This variable is very imbalanced and would not be a good predictor for Moderna's current business problem of whether a person would receive a vaccination. Moderna wants to be able to predict if a person would get a combined seasonal influenza and SARS-CoV-2 vaccination and it would be more logical to use the `seasonal_vaccine` as a target instead of `h1n1_vaccine`.

```
In [13]: print('Probability of receiving a seasonal flu or H1N1 vaccine')
pd.crosstab(index=data['seasonal_vaccine'], columns=data['h1n1_vaccine'], normalize=True)
```

Probability of receiving a seasonal flu or H1N1 vaccine

```
Out[13]: h1n1_vaccine      0      1
           seasonal_vaccine
0  0.497810  0.036582
1  0.289737  0.175871
```

The data also shows that it is more common for people that received the H1N1 vaccine to also have received the seasonal flu vaccine. Almost half (50%) of respondents are not vaccinated against the seasonal flu and H1N1. Only 3.6% of respondents claim they received only the H1N1 vaccine and not the seasonal influenza vaccine, but 17.5% of respondents claim they received both the seasonal and H1N1 vaccine. Almost 30% of respondents claim they only received the seasonal influenza vaccination and not the H1N1 vaccine.

Because of the high correlation with receiving the H1N1 vaccine and receiving the seasonal vaccine, the high imbalance in the variable, and no real-world need for this question in the future, this variable will be removed from the analysis.

The variables `hhs_geo_region`, `employment_industry`, and `employment_occupation` are all coded so to keep the respondent's privacy. Since will not offer any beneficial information, they will be removed from the dataset.

### Other H1N1 information

Variables associated with H1N1, such as `H1N1_concern` will be kept and act as a substitute for an emerging respiratory virus such as we are experiencing with COVID-19. While this is not exactly data on SARS-CoV-2, both are highly contagious, new respiratory viruses.

### Variable Analysis

```
In [14]: # Feature/Variable data exploration
features = data.columns[1:-4] # select all variables in the data except the targets and respondent_id
target='seasonal_vaccine'
# https://drivendata.co/blog/predict-flu-vaccine-data-benchmark/
# set number of columns
ncols = 2

# calculate number of rows
nrows = len(features) // ncols + (len(features) % ncols > 0)

fig, axes = plt.subplots(nrows, ncols, figsize=(15, 50))
#fig.subplots_adjust(hspace=1.0, wspace=0.2)

# unpack the axes subplots
axe = axes.ravel()

# Assign the plot to each subplot in the axe
for idx, feature in enumerate(features):

    # Calculate the counts
    counts = (data[[target, feature]]
              .groupby([target, feature])
              .size()
              .unstack(target))
    group_counts = counts.sum(axis='columns')
    props = counts.div(group_counts, axis='index')
    props.plot(kind="barh", stacked=True, ax=axe[idx])

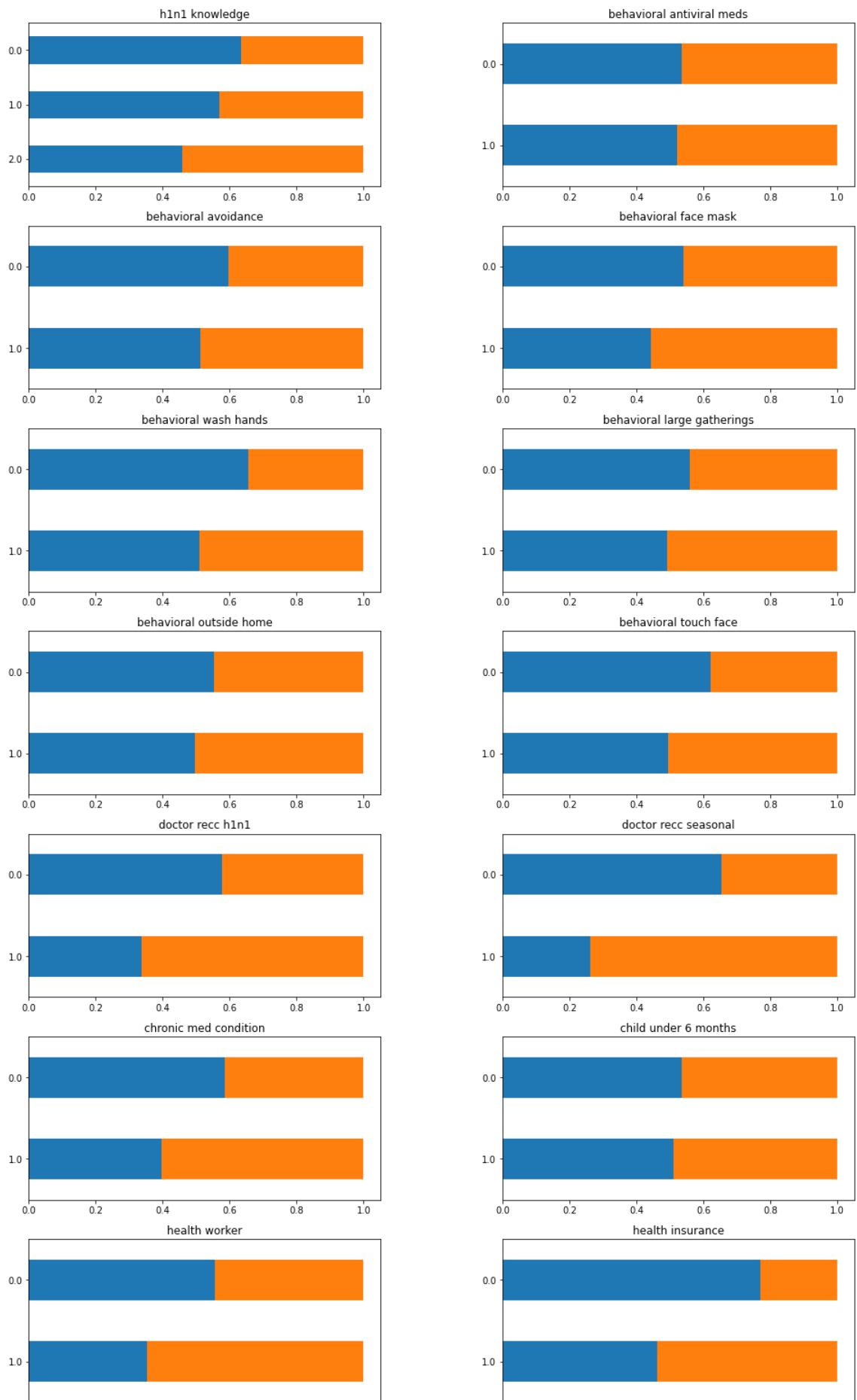
    # Chart formatting
    axe[idx].set_title(feature.replace('_', ' '))
    axe[idx].invert_yaxis()
    axe[idx].legend().remove()
    axe[idx].set_ylabel("")
    axe[idx].set_xlabel("")

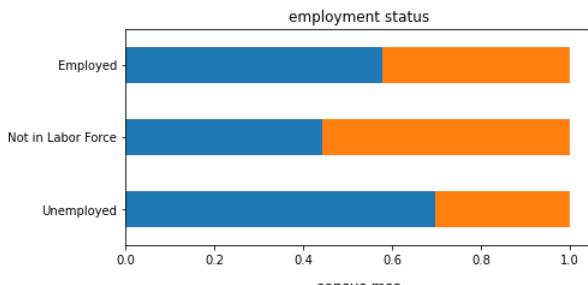
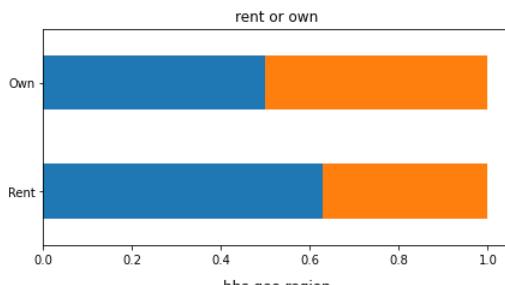
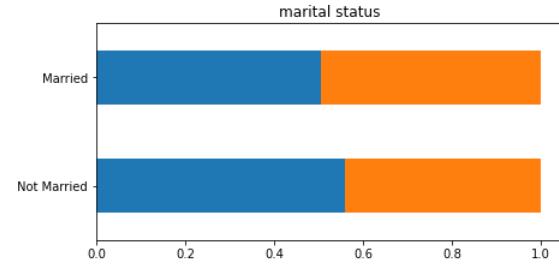
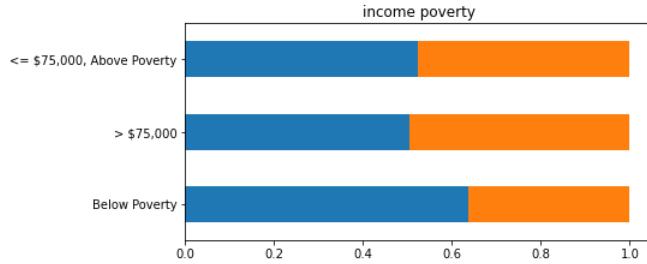
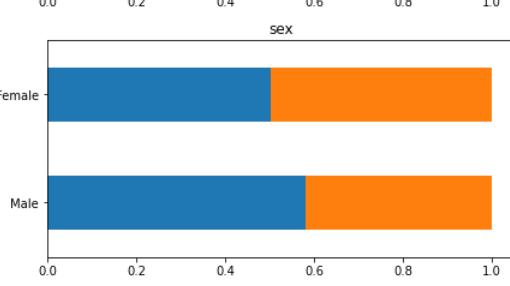
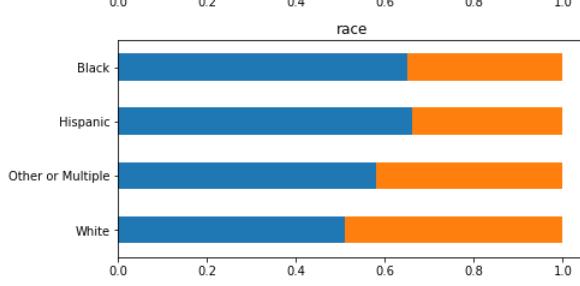
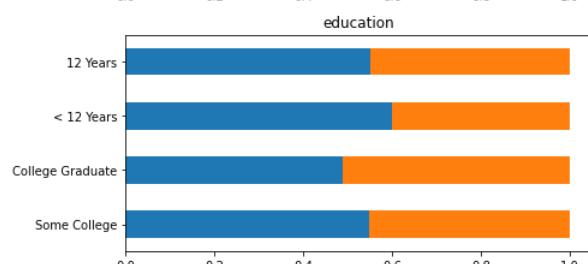
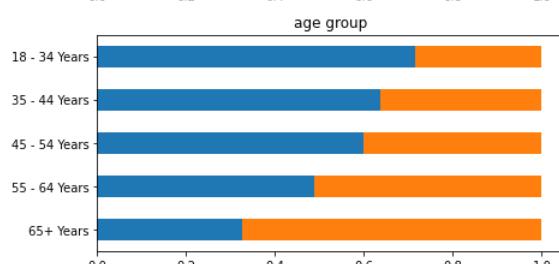
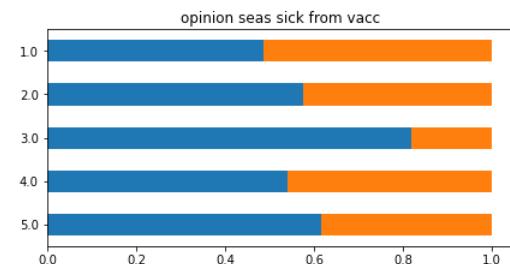
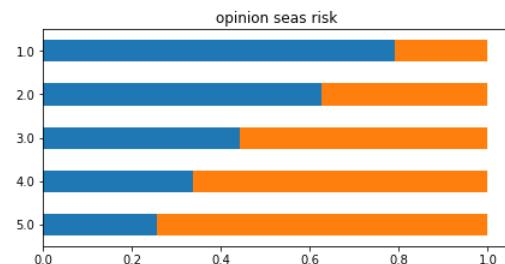
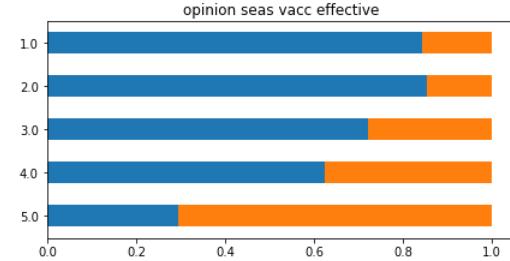
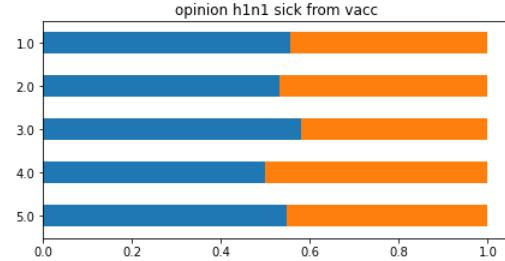
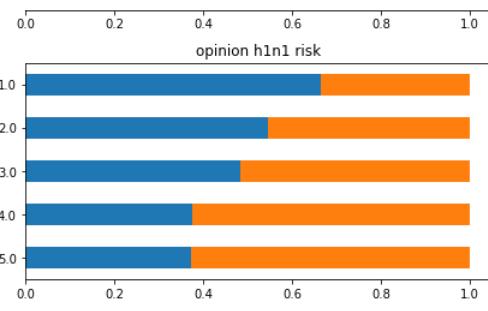
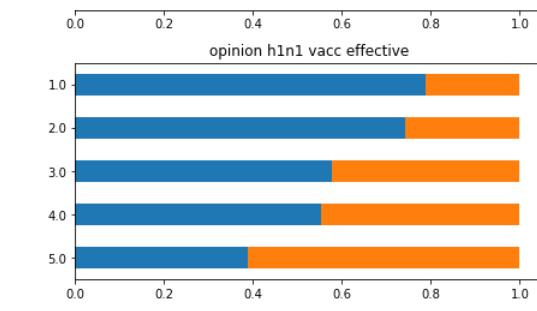
fig.tight_layout()
fig.suptitle('Proportion of Vaccine use by Variable', fontsize=18, y=1.02)
fig.legend(['No Vaccine', 'Vaccine'], loc='upper right', bbox_to_anchor=(1, 1.02), title='Seasonal Vaccine')
```

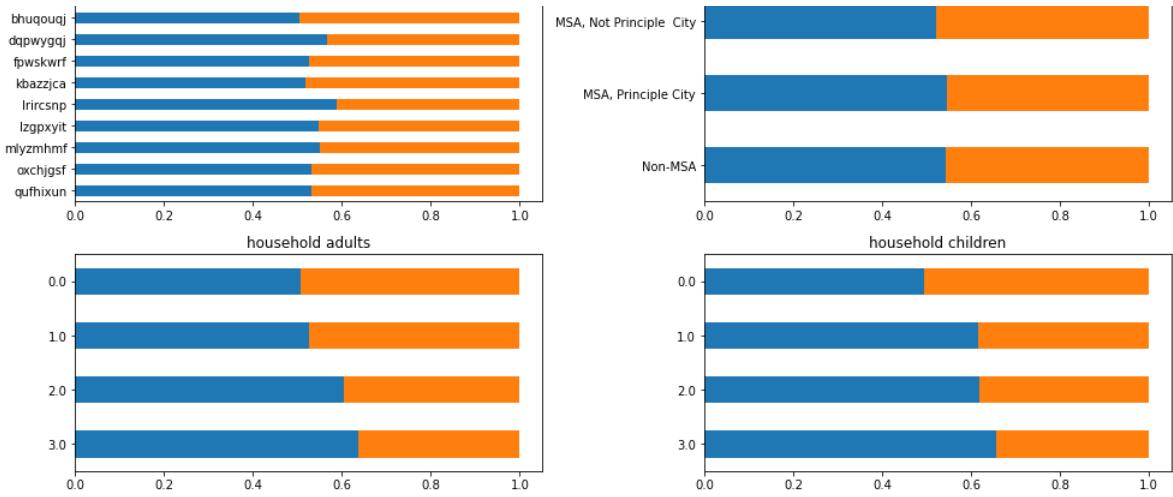
```
Out[14]: <matplotlib.legend.Legend at 0x1f3c0bfddc0>
```

### Proportion of Vaccine use by Variable

Seasonal Vaccine  
— No vaccine  
— Vaccine







### Graph Interpretation

Many of the variables have a positive relationship between them and whether the respondents are vaccinated or unvaccinated. Some of these variables include `opinion_seas_vacc_effective`, `opinion_seas_risk`, `age_group`, `health_insurance`, `doctor_recc_seasonal`, `doctor_recc_h1n1`. The importance of these variables will be determined with the machine learning models.

### Variable Selection Discussion

The following variables will be removed from the dataset and not used to build the prediction model:

Variable	Reason Removed
<code>respondent_id</code>	Each observation has a specific code
<code>h1n1_vaccine</code>	Not realistic for our needs, highly correlated with <code>seasonal_vaccine</code> , and only need to predict one vaccination status
<code>hhs_geo_region</code>	Coded and not interpretable
<code>employment_industry</code>	Coded and not interpretable
<code>employment_occupation</code>	Coded and not interpretable

```
In [15]: # Remove unnecessary or redundant variables
#data_features.drop(['respondent_id'], axis=1, inplace=True)
data.drop(['h1n1_vaccine', 'hhs_geo_region', 'employment_industry', 'employment_occupation'],
          axis=1,
          inplace=True)
```

```
In [16]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26707 entries, 0 to 26706
Data columns (total 33 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      25983 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  census_msa          26707 non-null   object  
 30  household_adults    26458 non-null   float64
 31  household_children   26458 non-null   float64
 32  seasonal_vaccine     26707 non-null   int64 

dtypes: float64(23), int64(1), object(9)
memory usage: 6.7+ MB
```

## 5. Encode variables

All variables will be One-Hot-Encoded (OHE) and missing values will be given their own category. Some variables are ordinal but that extra information is unnecessary for the models I will be using.

```
In [17]: from sklearn.model_selection import train_test_split

y = data['seasonal_vaccine'] # target
X = data.drop('seasonal_vaccine', axis=1) # features

# Train-test split
SEED = 42 # seed to set random_state for all models
X_train, X_test, y_train, y_test = train_test_split(X,
                                                    y,
                                                    test_size=0.25,
                                                    random_state=SEED)
```

```
In [18]: # import OneHotEncoder
from sklearn.preprocessing import OneHotEncoder

# Initialize
ohe = OneHotEncoder()
# fit encoder on X data
ohe.fit(X_train) # includes is_na group
X_train_ohe = ohe.transform(X_train).toarray()

# Dataframe to visualize
X_train_ohe_df = pd.DataFrame(X_train_ohe, columns=ohe.get_feature_names(X_train.columns))
```

# Modeling

## Model 1: Decision Tree

A decision tree is a machine learning algorithm that builds a tree-based classification model with a collection of if-else statements. It was chosen for this analysis because it is a powerful classification tool, solves classification problems, and is easy to interpret. This model used the default values and the splitting criterion was Gini-index. This base model will use the training data to build a decision tree to predict if a person is vaccinated or unvaccinated against the seasonal influenza vaccine.

```
In [19]: # Decision Tree
# Modeling
# Base model: Decision Tree
from sklearn import tree
from sklearn import metrics
from sklearn.model_selection import cross_validate
from sklearn.metrics import make_scorer, recall_score, precision_score

dt_clf = tree.DecisionTreeClassifier()

# Make specificity scorer
# https://stackoverflow.com/questions/64538838/using-cross-validation-for-calculating-specificity
# Specificity is the recall of the negative class
specificity = make_scorer(recall_score, pos_label=0)
npv = make_scorer(precision_score, pos_label=0)

# Make scoring method
# https://stackoverflow.com/a/35886445/1144724

scoring = {'accuracy': 'accuracy',
           'precision': 'precision',
           'recall': 'recall',
           'f1': 'f1',
           'specificity': specificity,
           'NPV': npv}

dt_clf_cv = cross_validate(dt_clf,
                           X_train_ohe_df,
                           y_train,
                           scoring = scoring,
                           cv=5)

# Output Cross-validated metrics
print('Cross Validated Training Scores')
for key in dt_clf_cv:
    if key != 'fit_time' and key != 'score_time':
        print(f'Decision Tree {key}: {dt_clf_cv[key].mean():.2%}')
```

```
Cross Validated Training Scores
Decision Tree test_accuracy: 67.79%
Decision Tree test_precision: 65.37%
Decision Tree test_recall: 66.64%
Decision Tree test_f1: 65.99%
Decision Tree test_specificity: 68.81%
Decision Tree test_NPV: 70.02%
```

## Model 1 Evaluation

Model 1 has accuracy, precision, recall, f1-score, and specificity in the upper 60% range. This is low for a prediction model and may be able to be increased by tuning the hyperparameters of the decision tree and using other machine learning algorithms such as Random Forests and Gradient Boosting (XGBoost). The next models will implement these and the metrics will be reported in Model Evaluation.

## Model 2: Tuned Decision Tree

Model 1 can be improved by searching for the best hyperparameters to tune the decision tree to avoid over and underfitting. Two different algorithms will be used. The first is `sklearn.RandomizedSearchCV` which will randomly search over a set of specified hyperparameters. Then `GridSearchCV` is used to find tune the best hyperparameters found by `RandomizedSearchCV`.

The hyperparameters that will be tuned include

- `criterion`: The function to measure the quality of a split. Supported criteria are "gini" for the Gini impurity and "log\_loss" and "entropy" both for the Shannon information gain
- `splitter`: The strategy used to choose the split at each node. Supported strategies are "best" to choose the best split and "random" to choose the best random split.
- `max_depth`: The maximum depth of the tree. If None, then nodes are expanded until all leaves are pure or until all leaves contain less than `min_samples_split` samples.
- `min_samples_split`: The minimum number of samples required to split an internal node.
- `min_samples_leaf`: The minimum number of samples required to be at a leaf node. A split point at any depth will only be considered if it leaves at least `min_samples_leaf` training samples in each of the left and right branches.
- `max_features`: The number of features to consider when looking for the best split.

```
In [20]: # Model 2: Tune DecisionTree using RandomizedSearchCV and GridSearchCV

# Start by using RandomizedSearchCV to narrow down the range for each
## hyperparameter

from sklearn.model_selection import RandomizedSearchCV

# Create the random grid
max_depth = [int(x) for x in range(0, 55, 5)]
max_depth.append(None)
dt_param_grid = {'criterion': ['gini', 'entropy', 'log-loss'],
                 'splitter': ['best', 'random'],
                 # Number of features to consider at every split
                 'max_features': ['auto', 'sqrt', 'log2'],
                 # Maximum number of levels in tree
                 'max_depth': max_depth,
                 # Minimum number of samples required to split a node
                 'min_samples_split': [int(x) for x in range(2, 22, 2)],
                 # Minimum number of samples required at each Leaf node
                 'min_samples_leaf': [int(x) for x in range(5, 50, 5)]}

# Base model to tune
dt = tree.DecisionTreeClassifier(random_state=SEED)

# Random search of parameters, using 5 fold cross validation,
dt_random = RandomizedSearchCV(estimator = dt,
                                 param_distributions = dt_param_grid,
                                 n_iter = 1000,
                                 cv = 5,
                                 verbose=1,
                                 random_state=SEED,
                                 n_jobs = -1) # use all available cores

# Fit the random search model
dt_random.fit(X_train_ohe_df, y_train)
```

Fitting 5 folds for each of 1000 candidates, totalling 5000 fits

D:\ProgramData\Anaconda3\lib\site-packages\sklearn\model\_selection\\_search.py:922: UserWarning: One or more of the test scores are non-finite: [0.70589116  
0.71912132 0.70863704 nan nan 0.71003495  
0.71817274 nan 0.73325012 0.71712431 nan 0.73290065  
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    nan 0.70903645      nan
warnings.warn('

```

```

Out[20]: RandomizedSearchCV(cv=5, estimator=DecisionTreeClassifier(random_state=42),
   n_iter=1000, n_jobs=-1,
   param_distributions={'criterion': ['gini', 'entropy',
                                      'log-loss'],
                        'max_depth': [0, 5, 10, 15, 20, 25, 30,
                                      35, 40, 45, 50, None],
                        'max_features': ['auto', 'sqrt',
                                         'log2'],
                        'min_samples_leaf': [5, 10, 15, 20, 25,
                                         30, 35, 40, 45],
                        'min_samples_split': [2, 4, 6, 8, 10,
                                         12, 14, 16, 18,
                                         20],
                        'splitter': ['best', 'random']},
   random_state=42, verbose=1)

```

```
In [21]: # Best parameters in the Random Search grid
dt_random.best_params_
```

```
Out[21]: {'splitter': 'best',
   'min_samples_split': 6,
   'min_samples_leaf': 25,
   'max_features': 'auto',
   'max_depth': 15,
   'criterion': 'gini'}
```

```
In [22]: # Use best parameters from RandomSearchCV and put in Grid Search to fine tune
# the hyperparameters
```

```
from sklearn.model_selection import GridSearchCV
```

```
# Make a new parameter grid based on the best parameters from the RandomSearchCV
dt_param_grid = {
    'splitter':[dt_random.best_params_['splitter']],
    'criterion':[dt_random.best_params_['criterion']],
    'max_features':[dt_random.best_params_['max_features']],
    'max_depth':[int(x) for x in range((dt_random.best_params_['max_depth']-5),
                                         (dt_random.best_params_['max_depth']+5),
                                         1)],
    'min_samples_split':[int(x) for x in range((dt_random.best_params_['min_samples_split']-5),
                                                (dt_random.best_params_['min_samples_split']+5),
                                                1)],
    'min_samples_leaf':[int(x) for x in range(dt_random.best_params_['min_samples_leaf']-5,
                                                dt_random.best_params_['min_samples_leaf']+5,
                                                1)]}
}

# Initialize GridSearchCV
dt_grid = GridSearchCV(dt,
                       param_grid=dt_param_grid,
                       cv=3,
                       return_train_score=False,
                       n_jobs = -1,
                       verbose=1)

# Fit data using GridSearchCV object
dt_grid.fit(X_train_ohe_df, y_train)
```

Fitting 3 folds for each of 1000 candidates, totalling 3000 fits

D:\ProgramData\Anaconda3\lib\site-packages\sklearn\model\_selection\\_search.py:922: UserWarning: One or more of the test scores are non-finite: [an 0.72371406 0.72371406 0.72371406 0.72371406 0.72371406  
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```
Out[22]: GridSearchCV(cv=3, estimator=DecisionTreeClassifier(random_state=42), n_jobs=-1,
param_grid={'criterion': ['gini'],
            'max_depth': [10, 11, 12, 13, 14, 15, 16, 17, 18, 19],
            'max_features': ['auto'],
            'min_samples_leaf': [20, 21, 22, 23, 24, 25, 26, 27,
                                 28, 29],
            'min_samples_split': [1, 2, 3, 4, 5, 6, 7, 8, 9, 10],
            'splitter': ['best']},
verbose=1)
```

```
In [23]: # Best parameters according to GridSearchCV  
dt_grid.best_params_
```

```
Out[23]: {'criterion': 'gini',
          'max_depth': 15,
          'max_features': 'auto',
          'min_samples_leaf': 28,
          'min_samples_split': 2,
          'splitter': 'best'}
```

```
In [24]: # Extracting the importances from Model 2
importances_sk = dt_grid.best_estimator_.fit(X_train_ohe, y_train).feature_importances_

# Create a dataframe with the feature importance by sklearn
feature_importance_sk = {}
for i, feature in enumerate(X_train_ohe_df.columns):
    feature_importance_sk[feature] = round(importances_sk[i], 3)

# Display table in order of importance
print('Feature Importance According to Model 2')
display(pd.DataFrame(feature_importance_sk.items(),
```

```
columns=['Feature',
        'Importance']).sort_values('Importance', ascending=False).head(15)
```

Feature Importance According to Model 2

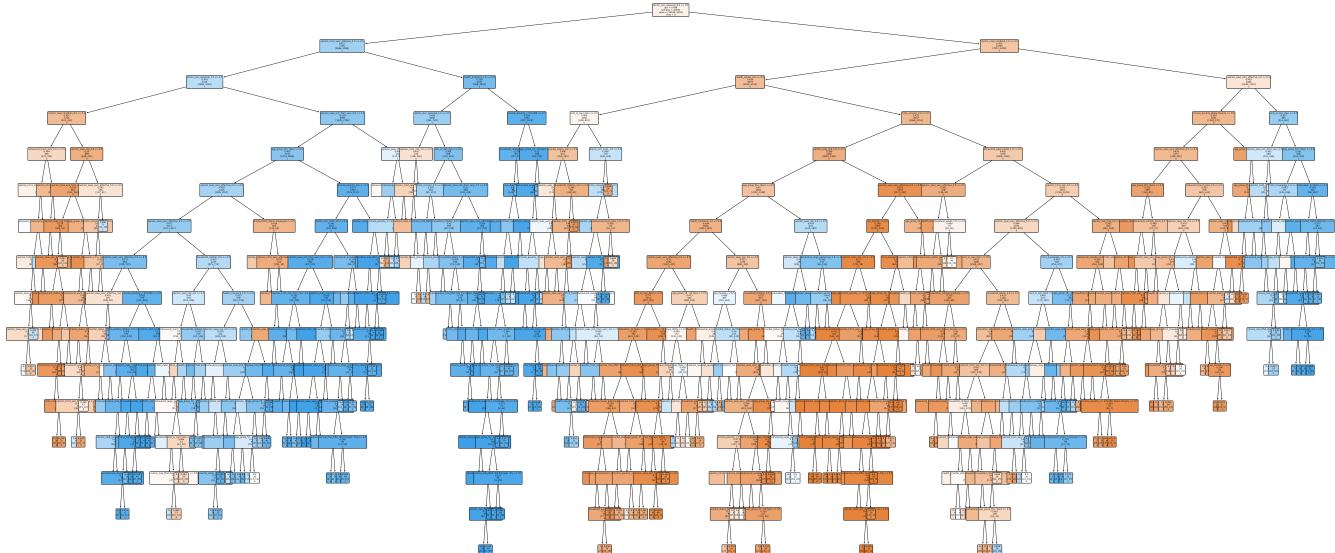
	Feature	Importance
33	doctor_recc_seasonal_0.0	0.275
70	opinion_seas_vacc_effective_5.0	0.135
34	doctor_recc_seasonal_1.0	0.103
88	age_group_65+ Years	0.067
72	opinion_seas_risk_1.0	0.049
52	opinion_h1n1_vacc_effective_5.0	0.029
75	opinion_seas_risk_4.0	0.026
73	opinion_seas_risk_2.0	0.023
46	health_insurance_1.0	0.022
42	health_worker_0.0	0.021
107	rent_or_own_Own	0.019
67	opinion_seas_vacc_effective_2.0	0.019
37	chronic_med_condition_1.0	0.017
69	opinion_seas_vacc_effective_4.0	0.015
84	age_group_18 - 34 Years	0.015

In [25]: # Decision Tree Plot

```
import numpy as np

fig, axes = plt.subplots(nrows=1, ncols=1, figsize=(55,25), dpi=600)
tree.plot_tree(dt_grid.best_estimator_.fit(X_train_ohe_df, y_train), # choose best params
               feature_names = X_train_ohe_df.columns,
               class_names=np.unique(y_train).astype('str'),
               filled = True,
               rounded=True,
               fontsize=5,
               impurity='False',
               label='root')

plt.savefig('images/decision_tree_plot.pdf')
plt.savefig('images/decision_tree_plot.png')
plt.show()
plt.close()
```



## Model 3: Random Forest

A decision tree will maximize the information gain at every branch. This may lead to overfitting.

Random Forest is a machine learning algorithm that uses a bagging technique. This bagging technique uses various decision trees on subsets of the dataset. So instead of relying on one decision tree, the model from the Random Forest algorithm predicts the final output based on the majority vote of all the decision trees in the forest. This leads to a reduction of overfitting.

The hyperparameters used were the best hyperparameters found during the search in model 2.

In [143]: # Instantiate and fit a Random Forest Classifier

```
from sklearn.ensemble import RandomForestClassifier
```

```
# Start with hyperparameters from Decision Tree Grid Search Best Parameters
```

```
forest = RandomForestClassifier(random_state=SEED,
```

```

        criterion=dt_grid.best_params_['criterion'],
        max_depth=dt_grid.best_params_['max_depth'],
        max_features=dt_grid.best_params_['max_features'],
        min_samples_leaf=dt_grid.best_params_['min_samples_leaf'],
        min_samples_split=dt_grid.best_params_['min_samples_split'])

forest.fit(X_train_ohe_df, y_train)
RandomForestClassifier(max_depth=15, min_samples_leaf=28, random_state=42)

```

Out[143]:

## Model 4: Tuned Random Forest

Random Forest classifiers can also be tuned using hyperparameters similarly to decision trees. Due to computational limits only RandomSearchGrid will be used to find the best hyperparameters that limit under and overfitting.

The hyperparameters optimized include:

- criterion: The function to measure the quality of a split.
- n\_estimators: The number of trees in the forest
- max\_depth: The maximum depth of the tree. If None, then nodes are expanded until all leaves are pure or until all leaves contain less than min\_samples\_split samples.
- max\_features: The number of features to consider when looking for the best split.
- min\_samples\_split: The minimum number of samples required to split an internal node.
- min\_samples\_leaf: The minimum number of samples required to be at a leaf node.
- bootstrap: Whether bootstrap samples are used when building trees.

```

In [153]: # Random Forest Hyperparameter Tuning

from sklearn.model_selection import RandomizedSearchCV

# Create the random grid parameters
max_depth = [int(x) for x in range(0, 55, 5)]
max_depth.append(None)

random_grid_rf = {
    'criterion': ['gini', 'entropy'],
    # Number of trees in the forest
    'n_estimators': [100, 500, 1000],
    # Number of features to consider when looking for the best split
    'max_features': ['auto', 'sqrt', 'log2', None],
    # Maximum number of levels in tree
    'max_depth': max_depth,
    # Minimum number of samples required to split a node
    'min_samples_split': [int(x) for x in range(2, 22, 2)],
    # Minimum number of samples required at each Leaf node
    'min_samples_leaf': [int(x) for x in range(5, 50, 5)],
    # If bootstrapped samples are used to build trees
    'bootstrap': [True, False]}

# Use the random grid to search for best hyperparameters
# First create the base model to tune
rf = RandomForestClassifier(random_state=SEED, n_jobs=-1)

# Random search of parameters, using 3 fold cross validation,
# search across 100 different combinations, and use all available cores
rf_random = RandomizedSearchCV(estimator = rf,
                                param_distributions = random_grid_rf,
                                n_iter = 50,
                                cv = 3,
                                scoring = specificity, # Reuse from model 1
                                random_state=SEED,
                                n_jobs = -1, # all available cores
                                verbose=1)

# Fit the random search model
rf_random.fit(X_train_ohe_df, y_train)

```

Fitting 3 folds for each of 50 candidates, totalling 150 fits

```

Out[153]: RandomizedSearchCV(cv=3,
                           estimator=RandomForestClassifier(n_jobs=-1, random_state=42),
                           n_iter=50, n_jobs=-1,
                           param_distributions={'bootstrap': [True, False],
                                                'criterion': ['gini', 'entropy'],
                                                'max_depth': [0, 5, 10, 15, 20, 25, 30,
                                                              35, 40, 45, 50, None],
                                                'max_features': ['auto', 'sqrt', 'log2',
                                                                None],
                                                'min_samples_leaf': [5, 10, 15, 20, 25,
                                                                     30, 35, 40, 45],
                                                'min_samples_split': [2, 4, 6, 8, 10,
                                                                     12, 14, 16, 18,
                                                                     20],
                                                'n_estimators': [100, 500, 1000]},
                           random_state=42,
                           scoring=make_scoring(recall_score, pos_label=0), verbose=1)

```

```

In [154]: # Extracting the importances from Model 4
importances_sk = rf_random.best_estimator_.feature_importances_

# Create a dataframe with the feature importance by sklearn
feature_importance_sk = {}
for i, feature in enumerate(X_train_ohe_df.columns):
    feature_importance_sk[feature] = round(importances_sk[i], 3)

# Display table in order of importance
print('Feature Importance According to Model 4')
forest_importance_df = pd.DataFrame(feature_importance_sk.items())

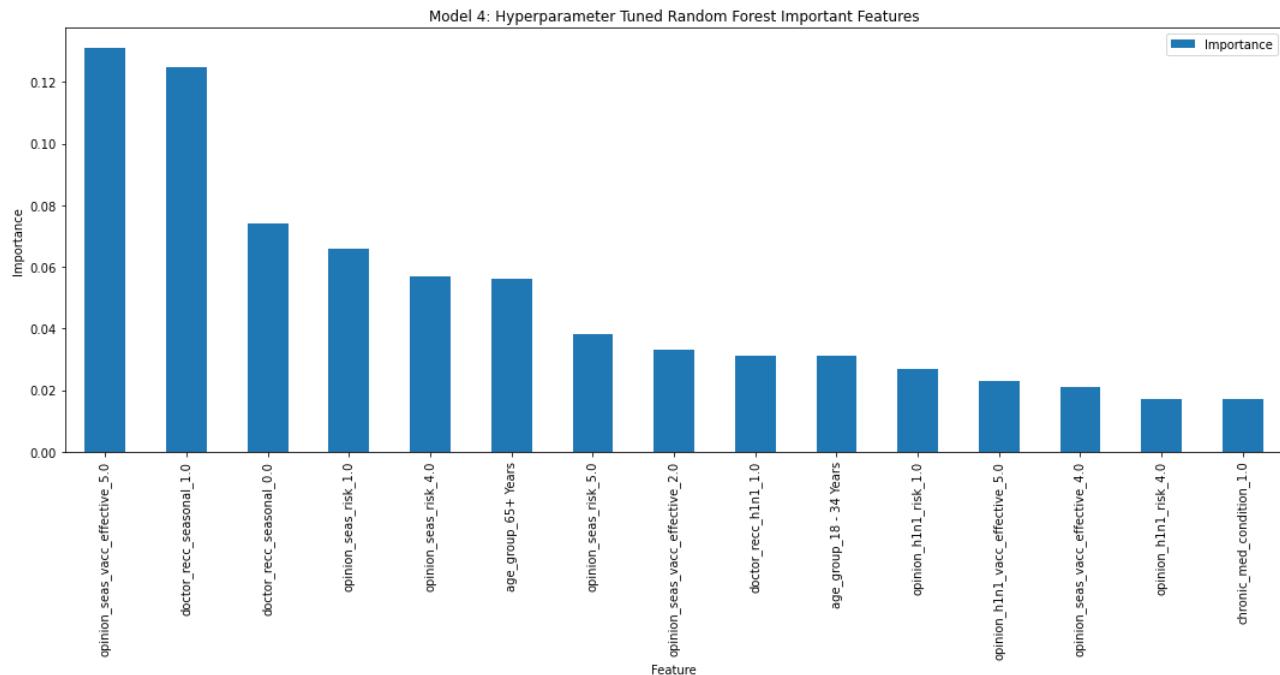
```

```
columns=['Feature',
        'Importance']).sort_values('Importance', ascending=False).head(15)
display(forest_importance_df)
```

Feature Importance According to Model 4

	Feature	Importance
70	opinion_seas_vacc_effective_5.0	0.131
34	doctor_recc_seasonal_1.0	0.125
33	doctor_recc_seasonal_0.0	0.074
72	opinion_seas_risk_1.0	0.066
75	opinion_seas_risk_4.0	0.057
88	age_group_65+ Years	0.056
76	opinion_seas_risk_5.0	0.038
67	opinion_seas_vacc_effective_2.0	0.033
31	doctor_recc_h1n1_1.0	0.031
84	age_group_18 - 34 Years	0.031
54	opinion_h1n1_risk_1.0	0.027
52	opinion_h1n1_vacc_effective_5.0	0.023
69	opinion_seas_vacc_effective_4.0	0.021
57	opinion_h1n1_risk_4.0	0.017
37	chronic_med_condition_1.0	0.017

```
In [155]: fig, ax = plt.subplots()
forest_importance_df.plot.bar(x='Feature', y='Importance', ax=ax)
ax.set_title("Model 4: Hyperparameter Tuned Random Forest Important Features")
ax.set_ylabel("Importance")
fig.tight_layout()
```



## Model 5: XGBoost

The final algorithm used is Gradient Boosting (XGBoost) trees. This algorithm uses an ensemble of weak decision trees as it builds the trees. It uses gradient descent to minimize the loss function. With this information it concentrates on where the model went wrong and creates new learners and continuously improves. XGBoost has been found to outperform Random Forests in many instances [9](#).

The hyperparameters optimized are:

- `base_score` : The initial prediction score of all instances.
- `learning_rate` : Step size shrinkage used in update to prevents overfitting. After each boosting step, we can directly get the weights of new features.
- `max_depth` : Maximum depth of a tree. Increasing this value will make the model more complex and more likely to overfit. 0 indicates no limit on depth
- `min_child_weight` : Minimum sum of instance weight (hessian) needed in a child.
- `subsample` : Subsample ratio of the training instances. Setting it to 0.5 means that XGBoost would randomly sample half of the training data prior to growing trees. and this will prevent overfitting.
- `n_estimators` : The number of trees (or rounds) in an XGBoost model.

```
In [156]: # XGBoost Model
from xgboost import XGBClassifier
```

```

# XGBoost requires all classification categories be integers that count up from 0.
# Which is met

# Make parameter grid
param_grid = {
    'base_score': [0.25, 0.5, 0.75, 1],
    'learning_rate': [0.01, 0.1, 0.5, 1],
    'max_depth': [1, 10, 100],
    'min_child_weight': [1, 2],
    'subsample': [0.5, 0.75, 1],
    'n_estimators': [10, 100, 1000],
}

# Grid Search of XGBoost classifier
xgb_clf = XGBClassifier(use_label_encoder=False,
                        random_state=SEED)
## ALL my variables are one-hot encoded so they have 0 and 1 as their only values
## so I do not need to transform the data.

xgb_random = RandomizedSearchCV(xgb_clf,
                                 param_grid,
                                 scoring=specificity, # use from model 1
                                 cv=3,
                                 n_jobs=-1,
                                 verbose=1)

# Must input .values because of the following error:
## feature_names must be string, and may not contain [, ] or < so use .values
xgb_random.fit(X_train_ohe_df.values, y_train.values)

Fitting 3 folds for each of 10 candidates, totalling 30 fits
[15:13:27] WARNING: C:\Windows\Temp\abs_557yfx63ll\croots\recipe\xgboost-split_1659548953302\work\src\learner.cc:1115: Starting in XGBoost 1.3.0, the default evaluation metric used with the objective 'binary:logistic' was changed from 'error' to 'logloss'. Explicitly set eval_metric if you'd like to restore the old behavior.
RandomizedSearchCV(cv=3,
                    estimator=XGBClassifier(base_score=None, booster=None,
                                            colsample_bylevel=None,
                                            colsample_bynode=None,
                                            colsample_bytree=None,
                                            enable_categorical=False, gamma=None,
                                            gpu_id=None, importance_type=None,
                                            interaction_constraints=None,
                                            learning_rate=None,
                                            max_delta_step=None, max_depth=None,
                                            min_child_weight=None, missing=nan,
                                            monotone_constraints...
                                            subsample=None, tree_method=None,
                                            use_label_encoder=False,
                                            validate_parameters=None,
                                            verbosity=None),
                    n_jobs=-1,
                    param_distributions={'base_score': [0.25, 0.5, 0.75, 1],
                                         'learning_rate': [0.01, 0.1, 0.5, 1],
                                         'max_depth': [1, 10, 100],
                                         'min_child_weight': [1, 2],
                                         'n_estimators': [10, 100, 1000],
                                         'subsample': [0.5, 0.75, 1]},
                    scoring=make_scorer(recall_score, pos_label=0), verbose=1)

In [157... best_parameters = xgb_random.best_params_
print('Randomized Search found the following optimal parameters: ')
for param_name in sorted(best_parameters.keys()):
    print('%s: %r' % (param_name, best_parameters[param_name]))

Randomized Search found the following optimal parameters:
base_score: 0.25
learning_rate: 0.1
max_depth: 1
min_child_weight: 1
n_estimators: 1000
subsample: 1

In [158... # Extracting the importances from Model 5
importances_sk = xgb_random.best_estimator_.feature_importances_

# Create a dataframe with the feature importance by sklearn
xgboost_importance_sk = {}
for i, feature in enumerate(X_train_ohe_df.columns):
    xgboost_importance_sk[feature] = round(importances_sk[i], 3)

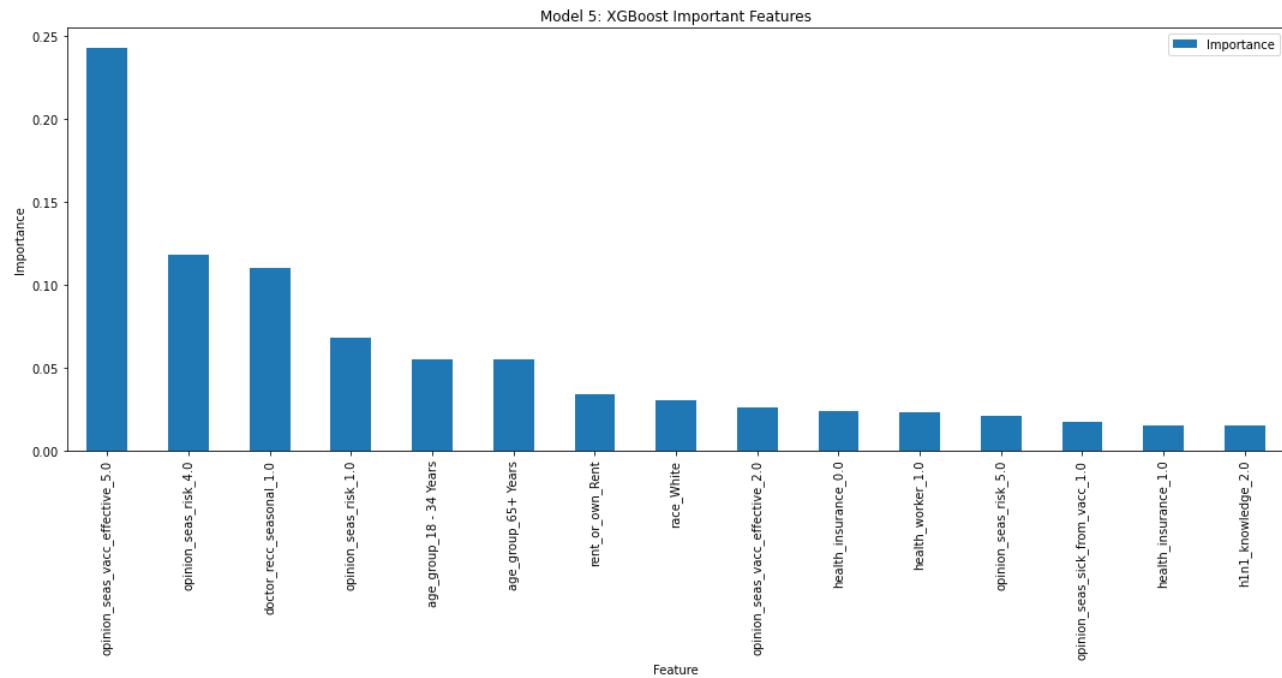
# Display table in order of importance
print('Feature Importance According to Model 5')
xgboost_importance_df = pd.DataFrame(xgboost_importance_sk.items(),
                                      columns=['Feature',
                                                'Importance']).sort_values('Importance', ascending=False).head(15)
display(xgboost_importance_df)

```

Feature Importance According to Model 5

	Feature	Importance
70	opinion_seas_vacc_effective_5.0	0.243
75	opinion_seas_risk_4.0	0.118
34	doctor_recc_seasonal_1.0	0.110
72	opinion_seas_risk_1.0	0.068
84	age_group_18 - 34 Years	0.055
88	age_group_65+ Years	0.055
108	rent_or_own_Rent	0.034
97	race_White	0.030
67	opinion_seas_vacc_effective_2.0	0.026
45	health_insurance_0.0	0.024
43	health_worker_1.0	0.023
76	opinion_seas_risk_5.0	0.021
78	opinion_seas_sick_from_vacc_1.0	0.017
46	health_insurance_1.0	0.015
7	h1n1_knowledge_2.0	0.015

```
In [159]: fig, ax = plt.subplots()
xgboost_importance_df.plot.bar(x='Feature', y='Importance', ax=ax)
ax.set_title("Model 5: XGBoost Important Features")
ax.set_ylabel("Importance")
fig.tight_layout()
```



```
In [160]: # Pickle these models so don't have to run models again
import joblib
import pickle

#Model 1
with open('pickled_models/decision_tree_model.pkl', 'wb') as f:
    joblib.dump(dt_clf, f)

#Model 2
with open('pickled_models/decision_tree_grid.pkl', 'wb') as f:
    joblib.dump(dt_grid, f)

#Model 3
with open('pickled_models/random_forest.pkl', 'wb') as f:
    joblib.dump(forest, f)

# Model 4
with open('pickled_models/random_forest_grid.pkl', 'wb') as f:
    joblib.dump(rf_random, f)

# Model 5
with open('pickled_models/xgboost.pkl', 'wb') as f:
    joblib.dump(xgb_random, f)
```

## Model Evaluation

Moderna wants to be able to predict who will and will not get the vaccine. With this information Moderna can organize resources to enable more people to be vaccinated. For example, a person may be predicted to not get the vaccine. This person can be given literature or informed by a healthcare representative on the harms of the virus and the efficacy of the vaccine. A person that is predicted to get the vaccine can be followed up with a reminder to get the vaccine.

In our situation, false positives are more harmful than false negatives thus we want to limit false positives. This is because falsely predicting that someone will not get the vaccine when in fact they will (false negative) is less harmful than if the model predicts that someone will get the vaccine but in fact they will not (false positive). People falsely predicted to get the vaccine (false positive) would not be put into the proper treatment of encouraging them to get vaccinated.

In this regard the most important metrics are those that minimize false positives, which include, specificity, sensitivity, F1-score, and negative predictive value (NPV).

## Specificity

$$\text{specificity} = \frac{TN}{(TN + FP)}$$

Also called the True Negative Rate (TNR), specificity quantifies of how well a test can identify true negatives. The specificity score would be what percent of those negative vaccination outcomes did the model predict correctly.

We want to limit false positive in our situation because that outcome can have more harmful effects on the patient. The sensitivity metric is penalized with more false positives and is the most important metric in our situation. A false positive denotes respondents that indicated they did not get a vaccination but were incorrectly given the positive assignment by the model.

## Precision

Also known as the Positive Predictive Value (PPV), precision is the ratio of the positives that are correctly identified by the model over total positive records. Precision measures the proportion of positively predicted labels that are actually correct.

$$\text{precision} = \frac{TP}{(TP + FP)}$$

Precision answers the question, out of all the respondents the model predicted were vaccinated, how many times did the respondent actually have the vaccine?

Precision is sensitive to false positive values and the lower the number of false positives, the higher the precision score.

## Negative Predictive Value

The negative predictive value (NPV) is the probability that subjects that are predicted to be negative actually do not get the vaccine.

$$NPV = \frac{TN}{(TN + FN)}$$

In our situation NPV calculates the proportion of subjects predicted as not getting vaccinated when in truth they will not be vaccinated. This answers the question, in cases where our model predicts a subject as being unvaccinated, how likely would they not get vaccinated?

## Recall

Also known as sensitivity and the True Positive Rate (TPR), recall represents the model's ability to correctly predict the positives out of actual positives.

$$\text{sensitivity} = \frac{TP}{(TP + FN)}$$

Sensitivity answers the question, out of all the respondents that actually got the vaccine, what percentage of them did our model correctly predict as having the vaccine? The sensitivity score would be what percent of those positive vaccination outcomes did the model predict correctly.

A high recall/sensitivity score indicates that the model is good at identifying positive examples. This is important for our situation but we also want to do this while still having low false positive results.

## F1-score

The F1 score is a harmonic average of precision and recall/sensitivity. It is often used for binary classification models. It measures the ability of the model to predict positive cases and is accurate with the cases it does predict.

$$F1 = 2 * \frac{\text{precision} * \text{recall}}{(\text{precision} + \text{recall})}$$

The F1-score takes both precision and recall into account. The higher the precision and recall, the higher the F1-score.

```
In [161]: # Make a list of all the model classifier objects
classifiers = {'M2: Hyperparameter Tuned Decision Tree': dt_grid,
               'M3: Random Forest': forest,
               'M4: Hyperparameter Tuned Random Forest': rf_random,
               'M5: Hyperparameter Tuned XGBoost': xgb_random
              }
```

 Example Confusion Matrix

```
In [162]: # Plot Confusion Matrix of Training Data
from sklearn.metrics import plot_confusion_matrix

# Confusion matrix plot helper function
def confusion_matrix_models_plot(model_name_dict, features, target, training=True, save_plot = False):
```

```

...
Plot confusion matrix for your models
...
fig, axes = plt.subplots(nrows=len(model_name_dict)//2, ncols=len(model_name_dict)//2, figsize=(15,10))

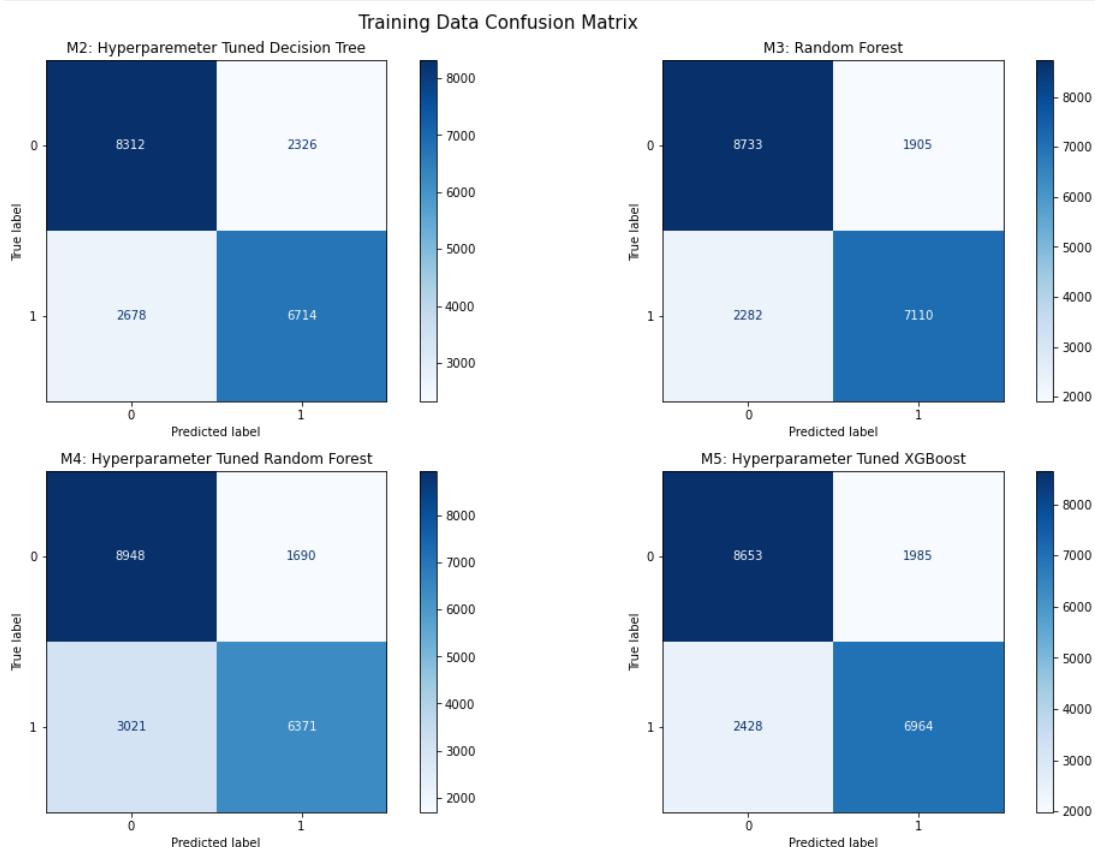
# set fixture title
if training:
    title = 'Training Data Confusion Matrix'
else:
    title = 'Testing Data Confusion Matrix'

fig.suptitle(title, fontsize=15)

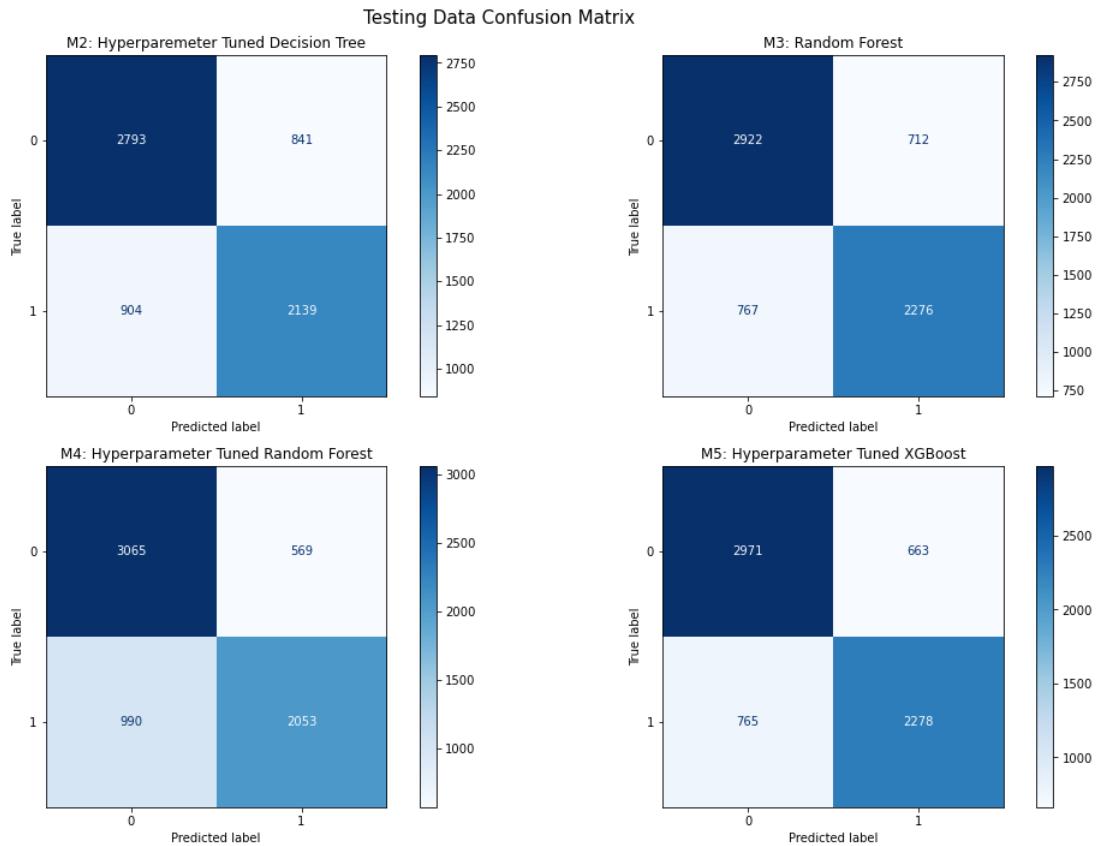
# Loop through models and generate a confusion_matrix
for cls, ax in zip(model_name_dict, axes.flatten()):
    plot_confusion_matrix(model_name_dict[cls],
                          features,
                          target,
                          ax=ax,
                          cmap='Blues',
                          display_labels=None)
    ax.title.set_text(cls)
plt.tight_layout()
plt.show()

```

In [163]: # Training Data Confusion Matrix for each classifier model  
`#X_train_ohe_df = pd.DataFrame(X_train_ohe, columns=ohe.get_feature_names(X_train.columns))  
confusion_matrix_models_plot(classifiers, X_train_ohe_df, y_train, True, False)`



In [192]: # Testing Data For each classifier model  
`# One-Hot encode testing features  
X_test_ohe = ohe.transform(X_test).toarray()  
# Dataframe to visualize  
X_test_ohe_df = pd.DataFrame(X_test_ohe, columns=ohe.get_feature_names(X_test.columns))  
# Wrapper plot function  
confusion_matrix_models_plot(classifiers, X_test_ohe_df, y_test, False, False)`



```
In [165]: # Performance metric score helper function
def metric_measurements(model, features, target):
    from sklearn import metrics

    predict = model.predict(features) # make predictions from features
    tn, fp, fn, tp = metrics.confusion_matrix(target, predict).ravel()

    report = {} # initialize dictionary

    metric_report = metrics.classification_report(target, predict, output_dict=True)
    # Accuracy
    report['accuracy'] = metric_report['accuracy']
    # Precision
    report['precision'] = metric_report['1']['precision']
    # Recall or Sensitivity
    report['recall'] = metric_report['1']['recall']
    # F1 score
    report['f1_score'] = metric_report['1']['f1-score']
    # Specificity or recall of negative case
    report['specificity'] = metric_report['0']['recall'] # tn/(tn+fp)
    # Negative Predictive Value
    report['NPV'] = tn/(tn+fn)

    return report
```

```
In [166]: # Helper function builds a dataframe for models and their performance metrics
def metric_df(model_dict, X, y):
    # get help from https://stackoverflow.com/questions/28669482/appending-pandas-dataframes-generated-in-a-for-loop
    results = []

    for key in model_dict:
        report = metric_measurements(model_dict[key], X, y)
        df_temp = pd.DataFrame.from_records(report, index=[key])
        results.append(df_temp)

    results = pd.concat(results)

    return results
```

```
In [167]: # Display model performance metrics using the helper functions
metrics_train_df = metric_df(classifiers, X_train_ohe_df, y_train)
metrics_test_df = metric_df(classifiers, X_test_ohe_df, y_test)

fig, axes = plt.subplots(2,1, figsize=(12,12))
metrics_train_df.plot(kind='barh', ax=axes[0])
metrics_test_df.plot(kind='barh', ax=axes[1])
axes[0].set_xlim(left=0, right=1)
axes[0].title.set_text('Training Metrics')
axes[1].set_xlim(left=0, right=1)
axes[1].title.set_text('Testing Metrics')
print('-----Training Data Model Metrics-----')
display(metrics_train_df)
print('-----Testing Data Model Metrics-----')
display(metrics_test_df)
```

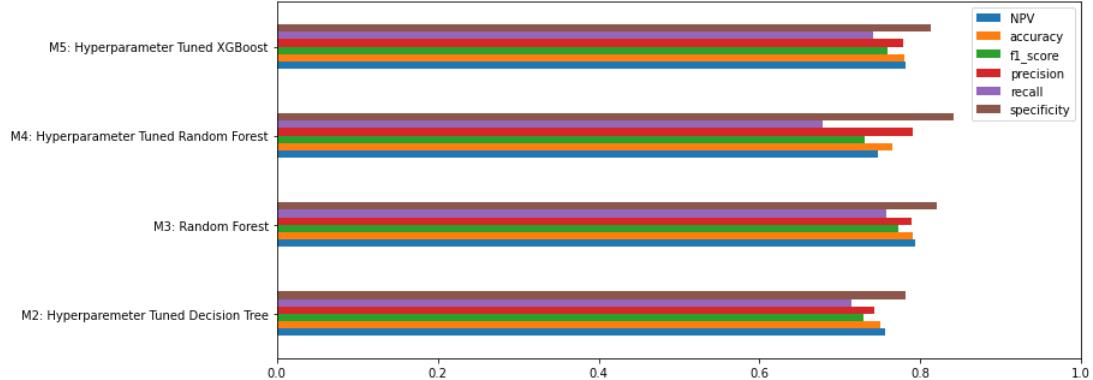
-----Training Data Model Metrics-----

	NPV	accuracy	f1_score	precision	recall	specificity
M2: Hyperparameter Tuned Decision Tree	0.756324	0.750175	0.728516	0.742699	0.714864	0.781350
M3: Random Forest	0.792828	0.790964	0.772532	0.788686	0.757027	0.820925
M4: Hyperparameter Tuned Random Forest	0.747598	0.764803	0.730075	0.790349	0.678343	0.841136
M5: Hyperparameter Tuned XGBoost	0.780886	0.779680	0.759392	0.778188	0.741482	0.813405

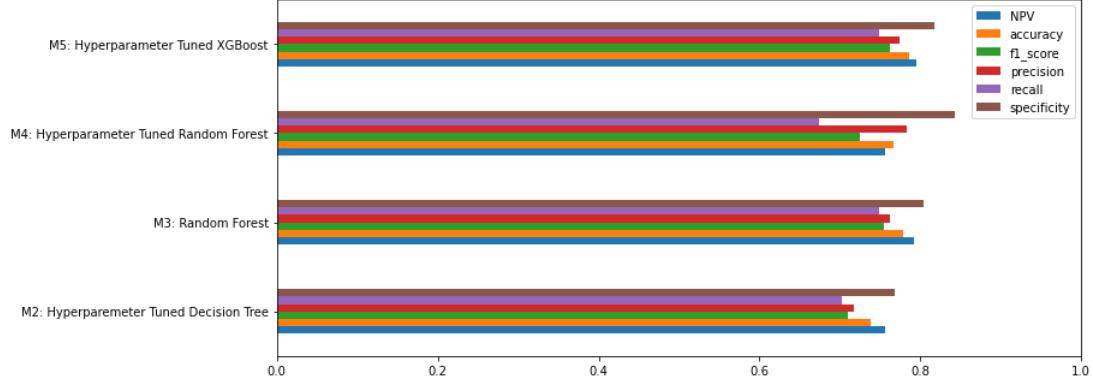
-----Testing Data Model Metrics-----

	NPV	accuracy	f1_score	precision	recall	specificity
M2: Hyperparameter Tuned Decision Tree	0.755477	0.738655	0.710277	0.717785	0.702925	0.768575
M3: Random Forest	0.792085	0.778493	0.754767	0.761714	0.747946	0.804073
M4: Hyperparameter Tuned Random Forest	0.755857	0.766512	0.724801	0.782990	0.674663	0.843423
M5: Hyperparameter Tuned XGBoost	0.795236	0.786131	0.761364	0.774566	0.748603	0.817556

Training Metrics



Testing Metrics



## Model Performance

Model 2 had improvement over model 1 in all reported metrics: accuracy, precision, recall, F1-score, specificity, and NPV. Running the data through a baseline random forest model as in model 3 also increased the metric scores reported as compared with models 1 and 2.

Model 4 had the highest specificity score of all the models but the recall score was worse than model 2, 3, and 5 and is comparable to the baseline model 1. Model 4 had the highest precision score but this is close to model 5's precision score. Model 4 had a lower NPV, accuracy, and F1-score as compared to models 3 and 5.

In my opinion, model 5 is the best model found in this analysis. Model 5's specificity of 81.7% means that model 5 has an 81.7% chance of predicting someone that does not get the vaccine when they will not actually get it. Model 5 also has an accuracy of 78.6%, precision of 77.4%, and recall of 74.9%. This is compared to the next best model, model 4, with a specificity of 84.3%, accuracy of 76.7%, precision of 78.3%, and recall of 67.5%. A F1-score is the harmonic mean of precision and recall. It measures the ability of the model to predict positive cases and is accurate with the cases it does predict. Model 5 has an F1-score of 76.1%, which is the highest of all the models.

In our situation, it is more important to minimize false positives because these are patients that the model would predict to be vaccinated when in actuality they would not. These people would then not get the treatment of being counseled by a healthcare practitioner about the benefits of being vaccinated. While model 4 does have a slightly higher specificity score, this comes at a cost of a much lower recall score.

In a real-world setting it is meaningful to predict whether a specific person will actually get vaccinated based on the model's prediction of being vaccinated or unvaccinated. For example, a healthcare provider that uses this model to predict if their patient will or will not be vaccinated may ask, 'Given the model predicts a negative vaccination status, what is the probability that this patient will not get vaccinated?' This can be measured using the negative predictive value (NPV). NPV for model 5 is 79.5%. This means 79.5% of respondents that were predicted to not have been vaccinated would truly not have been vaccinated.

NPV is dependent on pre-test probability. In our situation, this is the probability of the presence of the vaccination state before prediction. For our training and testing data, this probability is about half for vaccinated and unvaccinated, but this proportion could change depending on the population that the model is used in.

All models had variables indicated as the most important. These can be organized into the following categories.

- Opinion of vaccine effectiveness
- Opinion of risk of infection
- Access to healthcare
- Age group

```
In [168]: print('M5: XGBoost Variable Importance')
display(xgboost_importance_df)
```

M5: XGBoost Variable Importance

	Feature	Importance
70	opinion_seas_vacc_effective_5.0	0.243
75	opinion_seas_risk_4.0	0.118
34	doctor_recc_seasonal_1.0	0.110
72	opinion_seas_risk_1.0	0.068
84	age_group_18 - 34 Years	0.055
88	age_group_65+ Years	0.055
108	rent_or_own_Rent	0.034
97	race_White	0.030
67	opinion_seas_vacc_effective_2.0	0.026
45	health_insurance_0.0	0.024
43	health_worker_1.0	0.023
76	opinion_seas_risk_5.0	0.021
78	opinion_seas_sick_from_vacc_1.0	0.017
46	health_insurance_1.0	0.015
7	h1n1_knowledge_2.0	0.015

## Prediction Tool Prototype

This prediction tool gives real time prediction for healthcare workers. A survey can be given to each patient at a clinic or healthcare outreach program. From the patient survey a prediction can be made on if that patient will get a vaccination or not. Patients that are predicted to get a vaccination can be offered one right then if the facilities allow it. Patients that are predicted but want to get vaccinated at another time can be scheduled and/or reminded about the vaccination.

Patients predicted to not get the vaccination would be given additional information about the risk of the seasonal flu and COVID-19, the low risk of vaccination, and the effectivenss of the vaccination in preventing serious illness.

```
In [169]: # Randomly select individuals from the testing data

def vaccine_prediction(model, ohe, features, actual):
    ...
    This function takes in a model and Pandas series object and returns
    an estimated price range for the house to be listed.

    Input:
    model = Best model
    ohe = one hot encoder model
    data: Pandas Series with variables needed for the model

    Output:
    Prediction of 1 or 0
    ...
    # Did the patient actually get vaccinated?
    pred_index = features.index[0] # get index of new data
    print(f'Index: {pred_index}')
    outcome_results = actual.loc[pred_index]

    if outcome_results == 1:
        outcome = 'Vaccinated (1)'
    else:
        outcome = 'NOT Vaccinated (0)'

    # Encode the new data
    data_new = ohe.transform(features)

    predict_results = model.predict(data_new)[0]

    if predict_results == 1:
        predict = 'Vaccinated (1)'
    else:
        predict = 'NOT Vaccinated (0)'

    print('Information about patient')
    print('-----')
    print(f'Prediction: {predict}')
    print('-----')
    print(f'Truth: {outcome}')
    print('-----')
    print(features.loc[pred_index].squeeze())
    return outcome_results, predict_results
```

```
In [170]: # Prediction Tool example using randomly select data from testing
vaccine_prediction(xgb_random, ohe, X_test.sample(), y_test)

Index: 8714
Information about patient
-----
Prediction: NOT Vaccinated (0)
-----
Truth: NOT Vaccinated (0)
-----
h1n1_concern           1.0
h1n1_knowledge          1.0
behavioral_antiviral_meds 0.0
behavioral_avoidance     1.0
behavioral_face_mask     0.0
behavioral_wash_hands    0.0
behavioral_large_gatherings 1.0
behavioral_outside_home   1.0
behavioral_touch_face    0.0
doctor_recc_h1n1         0.0
doctor_recc_seasonal     0.0
chronic_med_condition    0.0
child_under_6_months     0.0
health_worker            0.0
health_insurance          1.0
opinion_h1n1_vacc_effective 5.0
opinion_h1n1_risk         1.0
opinion_h1n1_sick_from_vacc 2.0
opinion_seas_vacc_effective 5.0
opinion_seas_risk          1.0
opinion_seas_sick_from_vacc 2.0
age_group                18 - 34 Years
education               < 12 Years
race                     White
sex                      Male
income_poverty            NaN
marital_status            Not Married
rent_or_own               Own
employment_status          Unemployed
census_msa                 Non-MSA
household_adults          3.0
household_children         0.0
Name: 8714, dtype: object
```

Out[170]:

## Conclusions and Recommendations

Moderna, Inc. is developing a single-shot seasonal Flu and COVID-19 vaccination. Moderna needs to understand what variables influence a person to be vaccinated or unvaccinated and to predict if a patient will be vaccinated or unvaccinated. Implementing this prediction in a healthcare facility will get more people vaccinated against the seasonal Flu and COVID-19 and reduce the harmful effects of these diseases. In this situation, it is more harmful for the model to predict false positive. This is when the model predicts someone will get a vaccine when in fact they will not. Those that are predicted as such will not be given further information on the risks of infection or the effectiveness of the vaccine because they are predicted to be vaccinated. For this reason I used metrics that would penalize predictions that are false positives.

We want to minimize false positives because this is more harmful to patients as they will not get vaccinated even though they are predicted to be vaccinated. These patients will not get the counseling from their healthcare provider and only given the option to be vaccinated at their visit. While model 4 does have a higher specificity score and thus lower false positive rate, model 5 is the better model to use for vaccination prediction.

Healthcare workers' time are very valuable as they are in short supply. Using model 5 in a population of 1000 patients, 181 patients would be predicted to get vaccinated when in fact they would not. This is in comparison to model 4 which we would expect to have only 157 patients predicted as false positives. The recall score helps us identify the false negative rate. False negative predictions are people that are predicted to not get the vaccine when in fact they will. These patients would be further counseled by their healthcare provider on the effectiveness of the vaccine or the risk of getting the seasonal Flu and COVID-19 even though they do not need this counseling. If we estimate that it will take 5 additional minutes for a healthcare provider to further counsel a predicted unvaccinated patient, this be an 370 minutes per 1000 patients of wasted time. Scaling this to millions of patients would be unproductive.

The best model in this analysis is model 5 using XGBoost. The model does have limitations as it will only be used in a healthcare setting but this setting is the best place to use this model as it will get more people vaccinated. The model may be improved by getting more accurate data with less missing values as found in the training data. These missing values may include respondents refusing to answer a question and this is realistic in a real-world setting. For example, people that refuse to answer if a doctor gave a recommendation for the seasonal flu vaccination because they are embarrassed they do not have health insurance. These people may be more likely to not get a vaccination because they do not have access to healthcare. In a real world setting the respondent could be encouraged to answer every question but they may still refuse or give inaccurate answers. In my opinion, it is better to have missing data that denotes a refusal to answer the question rather than incorrect information.

Using the variable importance from this model can help us build proper information materials to provide to people that are hesitant in getting vaccinated. They will be given information that show the effectiveness of the vaccine, the risks of infection with COVID or the seasonal flu, and the convenience of only having a single vaccine for both of these viruses.

These different groups, predicted vaccinated and predicted unvaccinated can be determined in a healthcare facility. Patients are given a survey before visiting a healthcare provider in which the provider's clinic can predict if this is a person that is predicted to be vaccinated or unvaccinated. Those predicted to be unvaccinated would be given the information produced from the feature importance and concerns discussed with their healthcare provider.

## Summary

- Moderna is developing a dual seasonal flu and covid-19 vaccination.
- Moderna needs to understand what features lead to vaccination or unvaccination and to predict individuals who will be vaccinated or not.
- Machine learning algorithms such as decision trees, random forests, and gradient boosting (XGBoost) can solve this problem.
- Specificity is the best metric as it measures the ability of the model to correctly identify not getting a vaccine.

- Model 5 using XGBoost is the best model and has a specificity score of 81.7%.
- The most important features according to model 5 are access to healthcare, opinion on vaccine effectiveness, opinion on risk of infection, and age group.
- This prediction tool is limited to people with access to healthcare.

## Actionable Recommendation

- Moderna's pharmaceutical representatives and healthcare partners will use the prediction tool to predict if a patient will be vaccinated or not.
- Patients would be given a survey before consultation with their healthcare provider and the answers inputted into the prediction tool.
  - Patients predicted to be vaccinated would be given the option to be vaccinated and followed up about their vaccination status
  - Patients predicted to be unvaccinated would be given additional information by their healthcare provider.
    - Patients 55 years or older would be given information based on the risk of infection and disease.
    - Patients younger than 55 years old would be given information about the effectiveness of vaccination.
    - Both groups of patients would have a follow-up call to determine their vaccination status.

## References

### Ref 1

[\(CDC: Disease Burden of Flu\)](#)

### Ref 2

[\(CDC: Influenza a Summary for Physicians\)](#)

### Ref 3

[How Influenza \(Flu\) Vaccines Are Made](#)

### Ref 4

[mRNA vaccines - a new era in vaccinology](#)

### Ref 5

[CDC: Symptoms of COVID-19](#)

### Ref 6

[CDC: Stay Up to Date with COVID-19 Vaccines Including Boosters](#)

### Ref 7

[\(Yale Medicine: Comparing COVID-19 Vaccines\)](#)

### Ref 8

[\(Harvard: Why are mRNA Vaccines So Exciting\)](#)

### Ref 9

[XGBoost Documentation](#)

## Appendix

## Plots for Stakeholder Presentation

```
In [131]: # Function: Crosstabulation Stacked Proportion Plot of 2 variables
def stacked_prop_plot(df, features, axis_order = [None], title=None, save=False):
    ...
    df = the pandas dataframe holding your data
    features = The two categorical features
    axis_order = The order you want the feature groups to be displayed
    title = title of the plot
    save = if you want to save the file as pdf, named as the title
    ...

    # Import dependencies
    import warnings
    warnings.filterwarnings('ignore')
    import numpy as np
    import matplotlib.pyplot as plt

    # arrange data
    data = df[features]
    data.fillna('No Response', inplace=True)

    # Make and display crosstab
    crosstab_df = pd.crosstab(index=data[features[0]],
                               columns=data[features[1]],
                               normalize='index')

    # Arrange crosstab_df column order to move No Response to front
```

```

col_order = [e for e in crosstab_df.columns]
col_order = col_order[-1:]+col_order[:-1]
crosstab_df = crosstab_df[col_order]

# Rearrange the crosstab index if specified
if axis_order is None:
    axis_order = [e for e in crosstab_df.index]
    display(crosstab_df.loc[axis_order])
else:
    display(crosstab_df.loc[(axis_order)])
    axis_order.reverse()

# Plot
crosstab_df.loc[axis_order].plot(kind='barh', stacked=True, colormap='winter', figsize=(16,12))

# Figure settings
plt.title(title, fontdict={'fontsize':35})
legend_title = features[1].replace('_', ' ').title() # Legend title
# plt.legend(loc="Lower Left", ncol = len(ax.lines))
plt.legend(loc=(.25, -.25), ncol = len(col_order), title=legend_title, fontsize=15) # display legend

# X and y axis labels and size
plt.xlabel("Proportion of by respondent's {features[0].replace('_', ' ') group", fontsize=20)
plt.ylabel(f"{{features[0].replace('_', ' ').title()}", fontsize=20)
plt.gca().set_xticklabels([f'{x:.0%}' for x in plt.gca().get_xticks()], fontsize=20) # axis as %
plt.gca().set_yticklabels(plt.gca().get_yticklabels(), fontsize=20) # axis as %

# Fonts
plt.rcParams["font.family"] = "sans-serif"
# plt.rcParams["font.style"] = "normal"
plt.tight_layout() # Layout

# Save File as title of the graph
if save:
    plt.savefig('images/' + title.replace(' ', '_') + '.pdf')

```

In [132]:

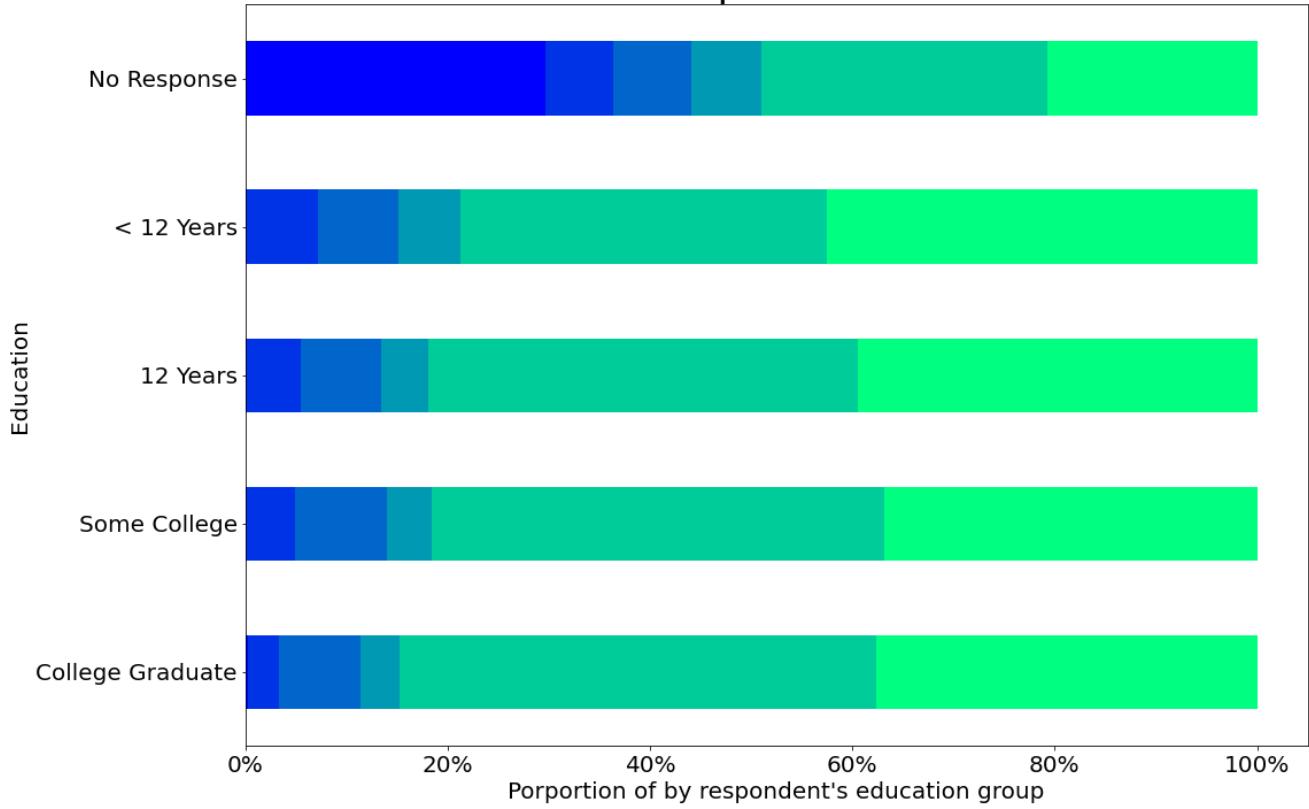
```

# Education Level and opinion on vaccine effectiveness
features = ['education', 'opinion_seas_vacc_effective']
axis_order = ['No Response', '< 12 Years', '12 Years', 'Some College', 'College Graduate']
stacked_prop_plot(data,
                  features,
                  title='Education Level and Opinion Vaccine Effectiveness',
                  axis_order = axis_order,
                  save=True)

```

opinion_seas_vacc_effective	No Response	1.0	2.0	3.0	4.0	5.0
education						
No Response	0.296375	0.067520	0.076759	0.069652	0.282871	0.206823
< 12 Years	0.001270	0.071096	0.079137	0.060939	0.362675	0.424884
12 Years	0.001553	0.053131	0.080041	0.046231	0.424357	0.394687
Some College	0.001420	0.047565	0.091012	0.044583	0.447111	0.368309
College Graduate	0.002278	0.031197	0.079826	0.038823	0.471922	0.375953

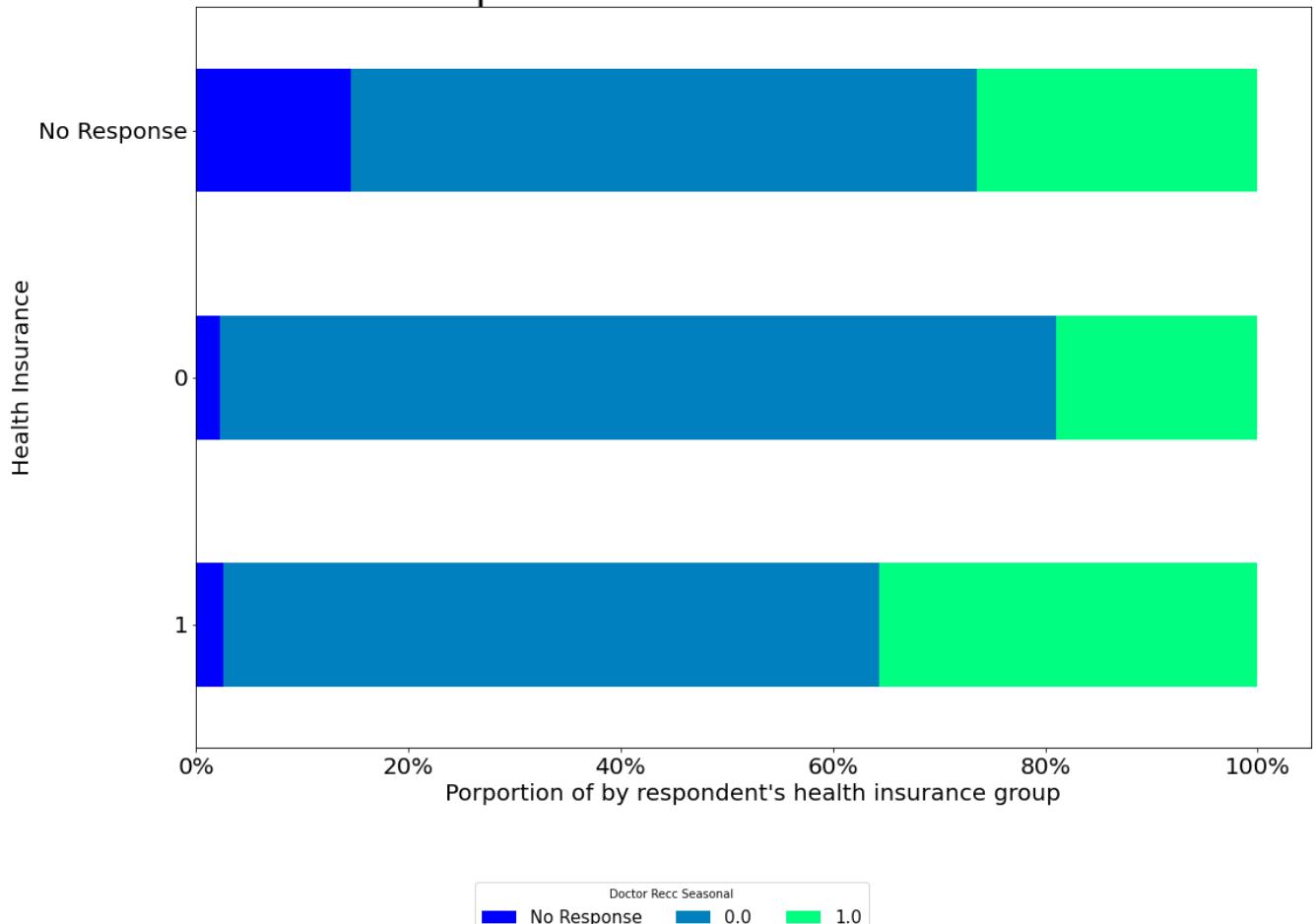
## Education Level and Opinion Vaccine Effectiveness



```
In [133]: # Respondent's Healthcare access
features = ['health_insurance', 'doctor_recc_seasonal']
axis_order = ['No Response', 0, 1]
stacked_prop_plot(data,
                  features,
                  axis_order,
                  title="Respondent's access to healthcare",
                  save=True)
```

doctor_recc_seasonal	No Response	0.0	1.0
health_insurance			
No Response	0.146326	0.589539	0.264136
0	0.022465	0.787442	0.190092
1	0.025597	0.618256	0.356147

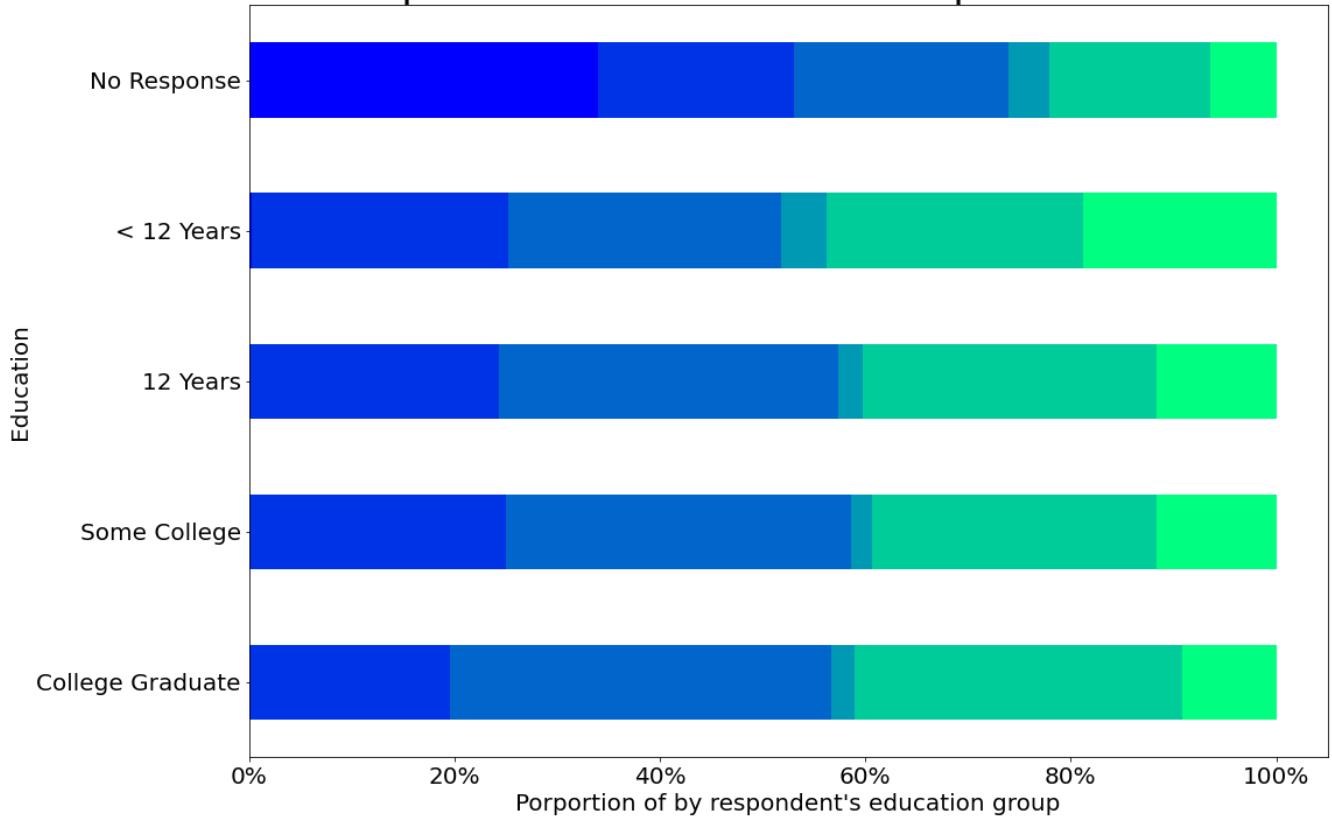
## Respondent's access to healthcare



```
In [134]: # Respondent's education and Opinion Flu Risk
features = ['education', 'opinion_seas_risk']
axis_order = ['No Response', '< 12 Years', '12 Years', 'Some College', 'College Graduate']
stacked_prop_plot(data,
                  features,
                  axis_order,
                  title="Respondent's education and Opinion Flu Risk",
                  save=True)
```

opinion_seas_risk	No Response	1.0	2.0	3.0	4.0	5.0
education						
No Response	0.339730	0.191187	0.208244	0.040512	0.156361	0.063966
< 12 Years	0.002116	0.250529	0.264917	0.044435	0.250106	0.187897
12 Years	0.001380	0.241849	0.330171	0.024495	0.285492	0.116612
Some College	0.000852	0.248900	0.336788	0.020446	0.276303	0.116712
College Graduate	0.001684	0.193919	0.371298	0.022680	0.318709	0.091710

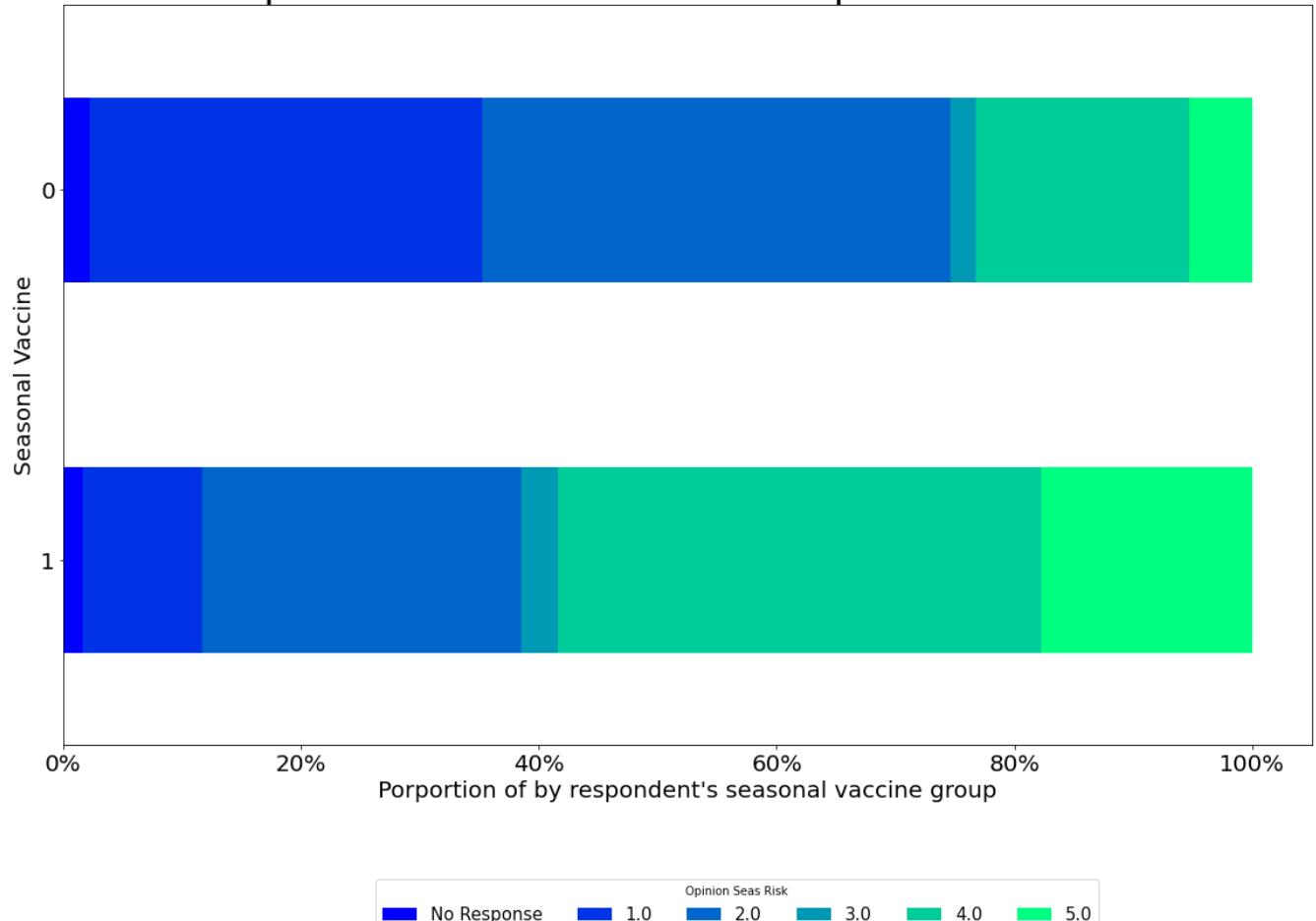
## Respondent's education and Opinion Flu Risk



```
In [135]: # Proportion of Vaccinated with Opinion of Flu Risk
features = ['seasonal_vaccine', 'opinion_seas_risk']
axis_order = [0, 1]
stacked_prop_plot(data,
                   features,
                   axis_order,
                   title="Proportion of Vaccinated with Opinion of Flu Risk",
                   save=True)
```

	No Response	1.0	2.0	3.0	4.0	5.0
seasonal_vaccine						
0	0.021931	0.330928	0.393288	0.021020	0.179933	0.052901
1	0.016164	0.100603	0.268677	0.030318	0.407077	0.177161

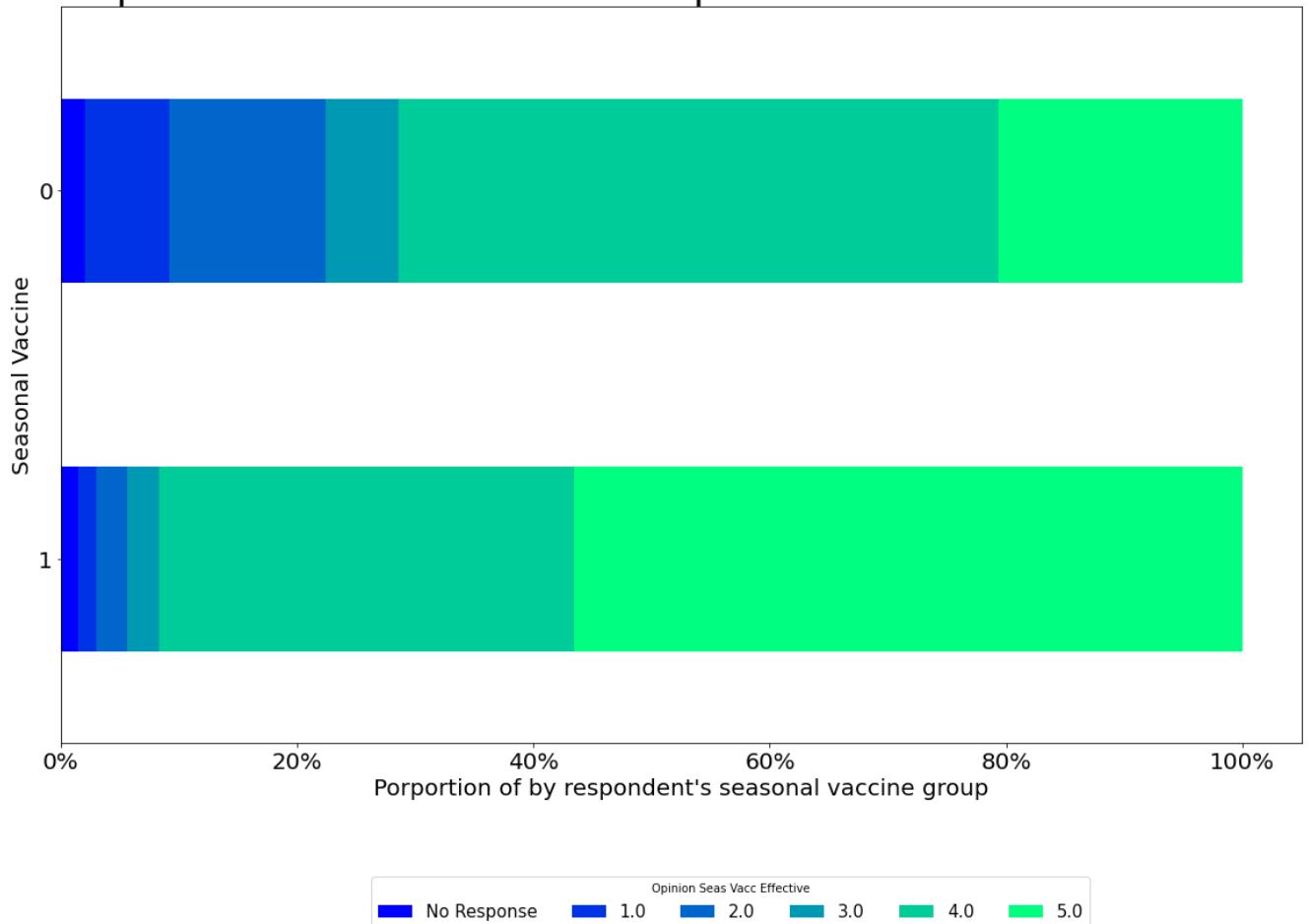
## Proportion of Vaccinated with Opinion of Flu Risk



```
In [136]: # Proportion of Vaccination with Opinion of Vaccine Effectiveness
features = ['seasonal_vaccine', 'opinion_seas_vacc_effective']
axis_order = [0, 1]
stacked_prop_plot(data,
                  features,
                  axis_order,
                  title="Proportion of Vaccination with Opinion of Vaccine Effectiveness",
                  save=True)
```

opinion_seas_vacc_effective	No Response	1.0	2.0	3.0	4.0	5.0
seasonal_vaccine						
0	0.019969	0.072029	0.132077	0.061379	0.508198	0.206348
1	0.014234	0.015521	0.025814	0.027342	0.351910	0.565179

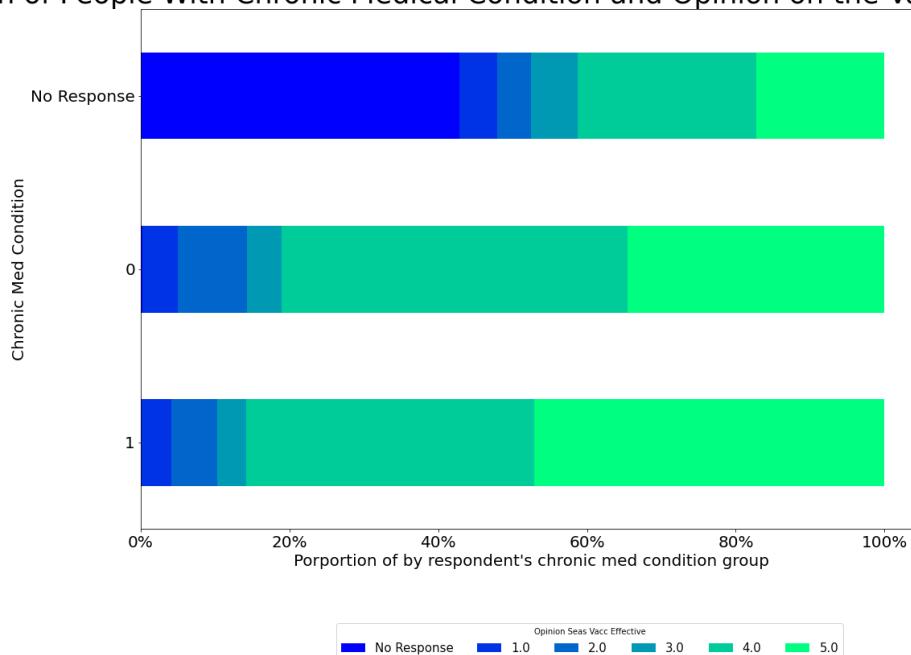
## Proportion of Vaccination with Opinion of Vaccine Effectiveness



```
In [137]: # Proportion of People with a chronic medical condition and their opinion on the vaccine effectiveness
features = ['chronic_med_condition', 'opinion_seas_vacc_effective']
axis_order = ['No Response', 0, 1]
stacked_prop_plot(data,
                   features,
                   axis_order,
                   title="Proportion of People With Chronic Medical Condition and Opinion on the Vaccine Effectiveness",
                   save=True)
```

opinion_seas_vacc_effective	No Response	1.0	2.0	3.0	4.0	5.0
chronic_med_condition						
No Response	0.428424	0.050463	0.045314	0.062822	0.240989	0.171988
0	0.001952	0.047924	0.092595	0.047382	0.464654	0.345495
1	0.001372	0.039506	0.062277	0.038546	0.387380	0.470919

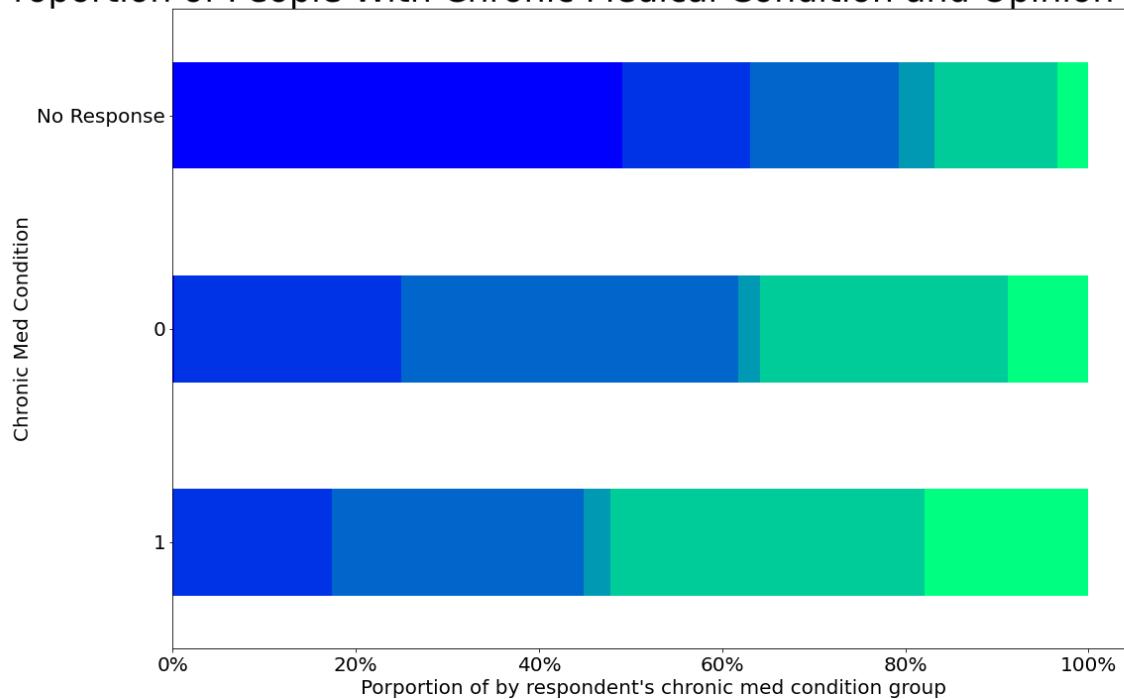
## Proportion of People With Chronic Medical Condition and Opinion on the Vaccine Effectiveness



```
In [138]: # Proportion of People with a chronic medical condition and their opinion on flu risk
features = ['chronic_med_condition', 'opinion_seas_risk']
axis_order = ['No Response', 0, 1]
stacked_prop_plot(data,
                   features,
                   axis_order,
                   title="Proportion of People With Chronic Medical Condition and Opinion on Flu Risk",
                   save=True)
```

opinion_seas_risk	No Response	1.0	2.0	3.0	4.0	5.0	
chronic_med_condition	No Response	0.491246	0.139032	0.162719	0.039135	0.133883	0.033986
0	0.001518	0.248130	0.368318	0.022986	0.271333	0.087715	
1	0.001235	0.173114	0.274623	0.029492	0.342250	0.179287	

## Proportion of People With Chronic Medical Condition and Opinion on Flu Risk



```
In [139]: # Vaccination status and recommendation from their doctor
```

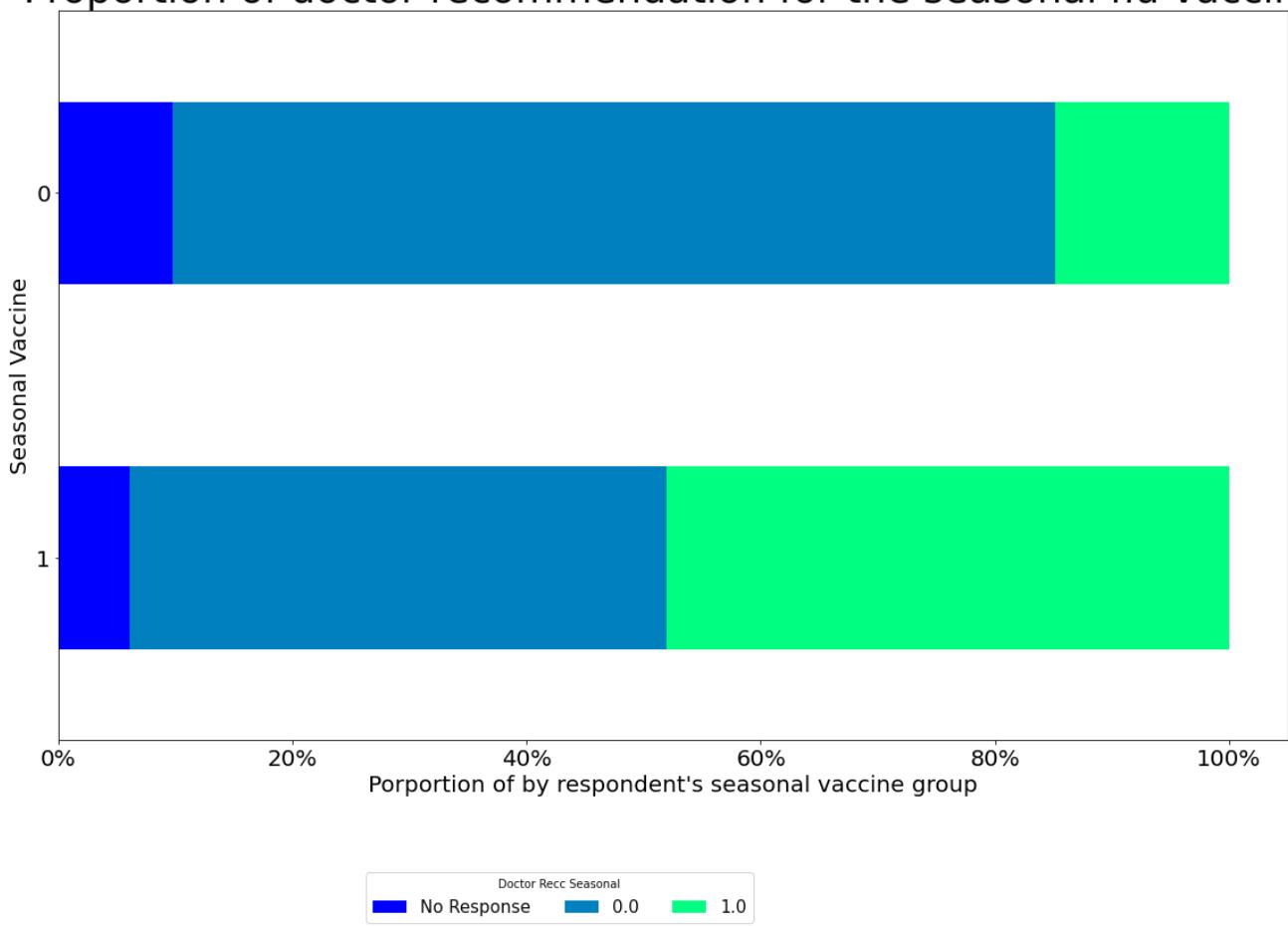
```

features = ['seasonal_vaccine', 'doctor_recc_seasonal']
axis_order = [0, 1]
stacked_prop_plot(data,
                  features,
                  axis_order,
                  title="Proportion of doctor recommendation for the seasonal flu vaccine",
                  save=True)

```

doctor_recc_seasonal	No Response	0.0	1.0
seasonal_vaccine			
0	0.098024	0.753643	0.148332
1	0.061198	0.458142	0.480659

Proportion of doctor recommendation for the seasonal flu vaccine



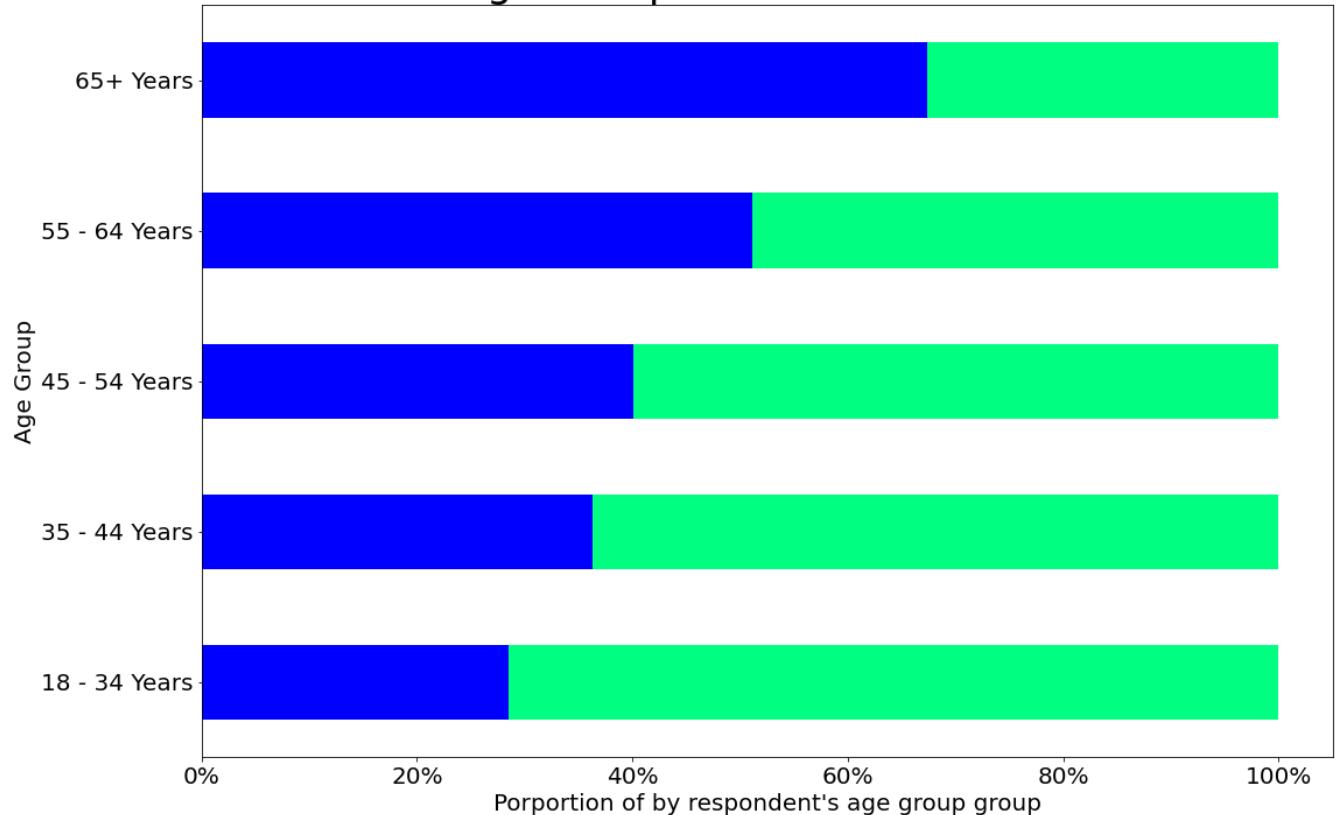
```

In [140]: # Vaccination status and recommendation from their doctor
features = ['age_group', 'seasonal_vaccine']
axis_order = ['65+ Years',
             '55 - 64 Years',
             '45 - 54 Years',
             '35 - 44 Years',
             '18 - 34 Years']
stacked_prop_plot(data,
                  features,
                  axis_order,
                  title="Age Group and Vaccine Status",
                  save=True)

```

seasonal_vaccine	1	0
age_group		
65+ Years	0.673681	0.326319
55 - 64 Years	0.511235	0.488765
45 - 54 Years	0.401298	0.598702
35 - 44 Years	0.362526	0.637474
18 - 34 Years	0.284564	0.715436

## Age Group and Vaccine Status



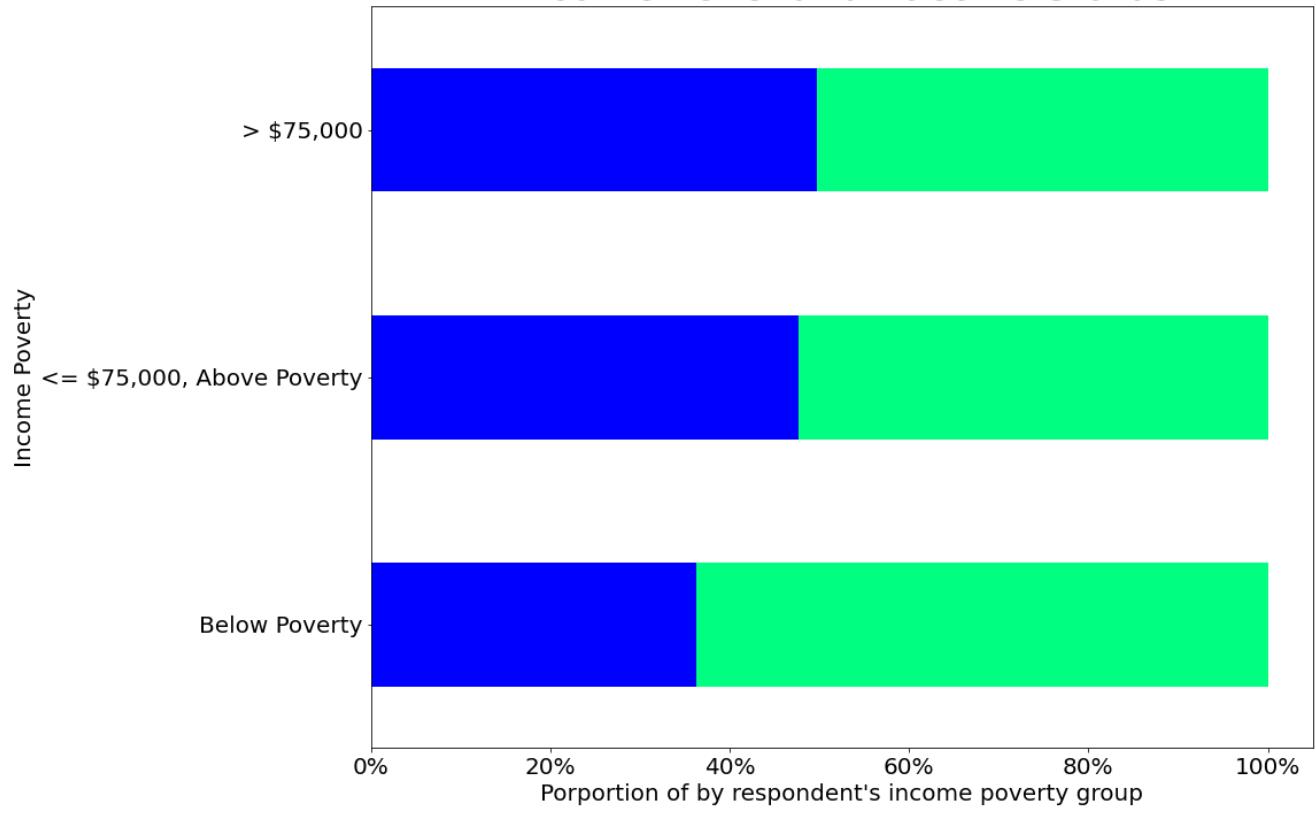
```
In [141]: axis_order = [e for e in data['income_poverty'].value_counts().index]
axis_order
```

```
Out[141]: ['<= $75,000, Above Poverty', '> $75,000', 'Below Poverty']
```

```
In [142]: # Vaccination status and income level
features = ['income_poverty', 'seasonal_vaccine']
axis_order = ['> $75,000',
             '<= $75,000, Above Poverty',
             'Below Poverty']
stacked_prop_plot(data,
                   features,
                   axis_order,
                   title="Income Level and Vaccine Status",
                   save=True)
```

	1	0
seasonal_vaccine	1	0
income_poverty		
> \$75,000	0.496769	0.503231
<= \$75,000, Above Poverty	0.476716	0.523284
Below Poverty	0.362625	0.637375

## Income Level and Vaccine Status



In [ ]: