Using Survey Data as a Predictor of Pandemic Vaccination
1 - EDA

Mark Patterson, March 2021

Introduction

My Capstone project utilizes a multi-method approach to answer the following analysis questions:
1. Can we use results of a public opinion survey to predict if people did or did not get an H1N1 vaccination? If so, how well can it predict?
2. What are the key factors that help predict if people did or did not get vaccinated?
3. Are there any other underlying patterns or groupings that can help us identify who did or did not get vaccinated?
4. And then linking this to the present… To improve chances of more people getting vaccinated, what questions about the COVID vaccine and vaccination need to be addre
the concerns and misperceptions?

Each question / part of the analysis is contained in a seperate notebook. This is Notebook 1 and covers initial data inspection, cleaning, and EDA.

Import Libraries and Load Data

In [1]:
```
# Import the relevant libraries
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns
import plotly.express as px

from sklearn.preprocessing import OrdinalEncoder
from sklearn.linear_model import LinearRegression
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.naive_bayes import MultinomialNB
from sklearn.model_selection import train_test_split
from sklearn.metrics import r2_score, explained_variance_score, confusion_matrix, accuracy_score, classification_report, log_loss
from math import sqrt

%matplotlib inline

# Increase column width to display df
pd.set_option('display.max_columns', None)
```

In [2]:
```
# Load the data - note that the Y variable was in a speerate CSV file.
raw_data_x = pd.read_csv('data/training_set_features.csv')
raw_data_y = pd.read_csv('data/training_set_labels.csv')

# print the shape
print("Raw_data_x:", raw_data_x.shape)
print("Raw_data_y:", raw_data_y.shape)
```

```
Raw_data_x: (26707, 36)
Raw_data_y: (26707, 3)
```

In [3]:
```
raw_data_y.head()
```

Out[3]:

	respondent_id	h1n1_vaccine	seasonal_vaccine
0	0	0	0
1	1	0	1
2	2	0	0
3	3	0	1
4	4	0	0

In [4]:
```
# Combine 2 original dataframes into one
raw_all = pd.merge(raw_data_x, raw_data_y, on="respondent_id", how="inner")
print(raw_all.shape)
raw_all.head()
```

```
(26707, 38)
```

Out[4]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	do
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	
2	2	1.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	
3	3	1.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	0.0	
4	4	2.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	1.0	

Initial Data Inspection and Understanding

In [5]:
```
# General Info on the Data
print("-----------------------------------------------")
print("Full, raw data set for Swine and Seasonal Vac Survey")
print("-----------------------------------------------")
print(raw_all.shape)
print("-----------------------------------------------")
print("Datatypes")
display(raw_all.info())
print("-----------------------------------------------")
print("Columns with null values")
display(raw_all.isnull().sum())
print("-----------------------------------------------")
print("-----------------------------------------------")
```

```
-----------------------------------------------
Full, raw data set for Swine and Seasonal Vac Survey
-----------------------------------------------
(26707, 38)
-----------------------------------------------
Datatypes
<class 'pandas.core.frame.DataFrame'>
Int64Index: 26707 entries, 0 to 26706
Data columns (total 38 columns):
respondent_id                  26707 non-null int64
h1n1_concern                   26615 non-null float64
h1n1_knowledge                 26591 non-null float64
behavioral_antiviral_meds      26636 non-null float64
behavioral_avoidance           26499 non-null float64
behavioral_face_mask           26688 non-null float64
behavioral_wash_hands          26665 non-null float64
behavioral_large_gatherings    26620 non-null float64
behavioral_outside_home        26625 non-null float64
behavioral_touch_face          26579 non-null float64
doctor_recc_h1n1               24547 non-null float64
doctor_recc_seasonal           24547 non-null float64
chronic_med_condition          25736 non-null float64
child_under_6_months           25887 non-null float64
health_worker                  25903 non-null float64
health_insurance               14433 non-null float64
opinion_h1n1_vacc_effective    26316 non-null float64
opinion_h1n1_risk              26319 non-null float64
opinion_h1n1_sick_from_vacc    26312 non-null float64
opinion_seas_vacc_effective    26245 non-null float64
opinion_seas_risk              26193 non-null float64
opinion_seas_sick_from_vacc    26170 non-null float64
age_group                      26707 non-null object
education                      25300 non-null object
race                           26707 non-null object
sex                            26707 non-null object
income_poverty                 22284 non-null object
marital_status                 25299 non-null object
rent_or_own                    24665 non-null object
employment_status              25244 non-null object
hhs_geo_region                 26707 non-null object
census_msa                     26707 non-null object
household_adults               26458 non-null float64
household_children             26458 non-null float64
employment_industry            13377 non-null object
employment_occupation          13237 non-null object
h1n1_vaccine                   26707 non-null int64
seasonal_vaccine               26707 non-null int64
dtypes: float64(23), int64(3), object(12)
memory usage: 7.9+ MB


None

-----------------------------------------------
Columns with null values

respondent_id                      0
h1n1_concern                      92
h1n1_knowledge                   116
behavioral_antiviral_meds         71
behavioral_avoidance             208
behavioral_face_mask              19
behavioral_wash_hands             42
behavioral_large_gatherings       87
behavioral_outside_home           82
behavioral_touch_face            128
doctor_recc_h1n1                2160
doctor_recc_seasonal            2160
chronic_med_condition            971
child_under_6_months             820
health_worker                    804
health_insurance               12274
opinion_h1n1_vacc_effective      391
opinion_h1n1_risk                388
opinion_h1n1_sick_from_vacc      395
opinion_seas_vacc_effective      462
opinion_seas_risk                514
opinion_seas_sick_from_vacc      537
age_group                          0
education                       1407
race                               0
sex                                0
income_poverty                  4423
marital_status                  1408
rent_or_own                     2042
employment_status               1463
hhs_geo_region                     0
census_msa                         0
household_adults                 249
household_children               249
employment_industry            13330
employment_occupation          13470
h1n1_vaccine                       0
seasonal_vaccine                   0
dtype: int64


-----------------------------------------------
-----------------------------------------------
```

Observations on the DataSet:

Quite a few features with missing values... some as high as 13,000 missing. This may necessitate dropping columns (employment and health_insurance); For some of the o
4,400 missing (income level).

In [6]:
```
# Examine classes within each feature (gain an understanding of data and look for oddities)
for column in raw_all:
    unique_values = raw_all[column].value_counts()
    nr_values = len(unique_values)
    if nr_values <= 14:
        print("values for {} is: {} -- {}".format(column, nr_values, unique_values))
    else:
        print("values for {} is: {}".format(column, nr_values))
```

```
Name: hhs_geo_region, dtype: int64
values for census_msa is: 3 -- MSA, Not Principle  City    11645
MSA, Principle City           7864
Non-MSA                       7198
Name: census_msa, dtype: int64
values for household_adults is: 4 -- 1.0    14474
0.0     8056
2.0     2803
3.0     1125
Name: household_adults, dtype: int64
values for household_children is: 4 -- 0.0    18672
1.0     3175
2.0     2864
3.0     1747
Name: household_children, dtype: int64
values for employment_industry is: 21
values for employment_occupation is: 23
values for h1n1_vaccine is: 2 -- 0    21033
1     5674
Name: h1n1_vaccine, dtype: int64
```

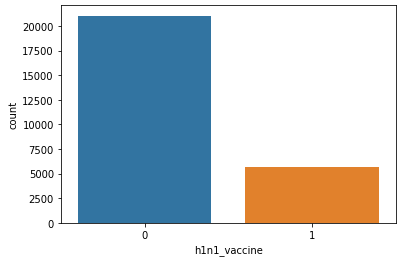
In [7]:
```
# Check for duplicated rows - apprears to be NO duplicates
duplicate = raw_all[raw_all.duplicated()]
duplicate.shape
```

Out[7]:
```
(0, 38)
```

In [8]:
```
# Check our class balance for our target variable - primarily interested in H1N1 and less so the seasonal.
print (raw_all['h1n1_vaccine'].value_counts())
sns.countplot(x = 'h1n1_vaccine', data = raw_all)
```

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

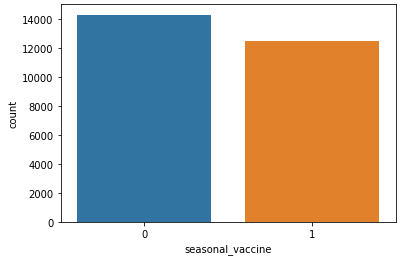
Out[8]:
```
<AxesSubplot:xlabel='h1n1_vaccine', ylabel='count'>
```



In [9]:
```
print (raw_all['seasonal_vaccine'].value_counts())
sns.countplot(x = 'seasonal_vaccine', data = raw_all)
```

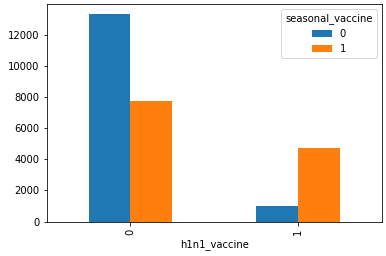
```
0    14272
1    12435
Name: seasonal_vaccine, dtype: int64
```

Out[9]:
```
<AxesSubplot:xlabel='seasonal_vaccine', ylabel='count'>
```



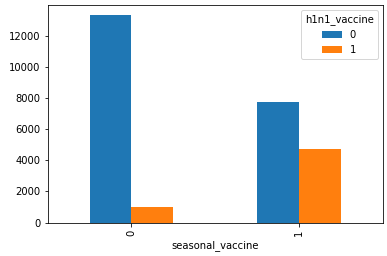
In [10]:
```
pd.crosstab(raw_all['h1n1_vaccine'],raw_all['seasonal_vaccine']).plot.bar()
```

Out[10]:
```
<AxesSubplot:xlabel='h1n1_vaccine'>
```



In [11]:
```
pd.crosstab(raw_all['seasonal_vaccine'],raw_all['h1n1_vaccine']).plot.bar()
```

Out[11]: <AxesSubplot:xlabel='seasonal_vaccine'>



Observations on the target variables

The incidence of having gotten the seasonal vacination is balanced No = 53% and Yes = 47% (12,435) The incidence for h1n1 vacination is quite unbalanced with No = 79% (5,674). May need to address this during modeling with SMOTE or other technique.

Looking at side by side plots above it is interesting that for the non h1n1 folk, about half of them DID get the seasonal vac. I wonder what role timing of the survey It is possible that some of these non-h1n1 vaccination folk may have been intending to get the vac but just hadnt yet?

Continued Data Understanding - Group, Describe, Visualize

First I will break the features into conceptual groups (8). Then I will examine frequencies feature of the classes both in tables and plots.

In [12]:
```
raw_all.columns
```

Out[12]:
```
Index(['respondent_id', 'h1n1_concern', 'h1n1_knowledge',
       'behavioral_antiviral_meds', 'behavioral_avoidance',
       'behavioral_face_mask', 'behavioral_wash_hands',
       'behavioral_large_gatherings', 'behavioral_outside_home',
       'behavioral_touch_face', 'doctor_recc_h1n1', 'doctor_recc_seasonal',
       'chronic_med_condition', 'child_under_6_months', 'health_worker',
       'health_insurance', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk',
       'opinion_h1n1_sick_from_vacc', 'opinion_seas_vacc_effective',
       'opinion_seas_risk', 'opinion_seas_sick_from_vacc', 'age_group',
       'education', 'race', 'sex', 'income_poverty', 'marital_status',
       'rent_or_own', 'employment_status', 'hhs_geo_region', 'census_msa',
       'household_adults', 'household_children', 'employment_industry',
       'employment_occupation', 'h1n1_vaccine', 'seasonal_vaccine'],
      dtype='object')
```

In [13]:
```
# Creating 7 lists of conceptually similar features.
pcols_1 = ['h1n1_concern', 'h1n1_knowledge', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk','opinion_h1n1_sick_from_vacc']
pcols_2 = ['opinion_seas_vacc_effective','opinion_seas_risk', 'opinion_seas_sick_from_vacc']
pcols_3 = ['doctor_recc_h1n1', 'doctor_recc_seasonal', 'chronic_med_condition', 'child_under_6_months', 'health_insurance']
pcols_4 = ['behavioral_antiviral_meds', 'behavioral_avoidance','behavioral_face_mask', 'behavioral_wash_hands','behavioral_large_gatherings', 'behavioral_outside_home
pcols_5 = ['sex', 'age_group', 'education', 'race', 'marital_status']
pcols_6 = ['employment_status', 'health_worker', 'income_poverty', 'rent_or_own', 'employment_occupation', 'employment_industry']
pcols_7 = ['hhs_geo_region', 'census_msa', 'household_adults', 'household_children']
```

Transform categorical text to numerical

Prior to ploting or creating summary tables, I will transform the remaining text values into numerical values. There are several options here. Based on some reading I I am going to use Decision Tree modeling, then it is suggested to NOT use one-hot encoding for this. Instead I will use OrdinalEncoder from sklearn to change the text a column to numerical values within the coulumn. This method still has a limitation of potential interpretation of ordered meaning between the values (which is approp of these features, but not all). A more manual alternative to this is to just assign the values myself through mapping via a dictionary of new numeric values.

In [145]:
```
raw_all.head()
```

Out[145]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	dc
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	
2	2	1.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	
3	3	1.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	0.0	
4	4	2.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	1.0	

In [14]:
```
raw_2 = raw_all
```

In [16]:
```
# Try the encoder on a couple of features.
encoder = OrdinalEncoder()
raw_2[['sex', 'race', 'age_group']] = encoder.fit_transform(raw_2[['sex', 'race', 'age_group']])
raw_2.head()
```

Out[16]:

ge_group	education	race	sex	income_poverty	marital_status	rent_or_own	employment_status	hhs_geo_region	census_msa	household_adults	household_children	employment_industry	employment_occupation	h1n1_vaccine
3.0	< 12 Years	3.0	0.0	Below Poverty	Not Married	Own	Not in Labor Force	oxchjgsf	Non-MSA	0.0	0.0	NaN	NaN	0
1.0	12 Years	3.0	1.0	Below Poverty	Not Married	Rent	Employed	bhuqouqj	MSA, Not Principle City	0.0	0.0	pxcmvdjn	xgwztkwe	0
0.0	College Graduate	3.0	1.0	<= $75,000, Above Poverty	Not Married	Own	Employed	qufhixun	MSA, Not Principle City	2.0	0.0	rucpziij	xtkaffoo	0
4.0	12 Years	3.0	0.0	Below Poverty	Not Married	Rent	Not in Labor Force	lrircsnp	MSA, Principle City	0.0	0.0	NaN	NaN	0
2.0	Some College	3.0	0.0	<= $75,000, Above Poverty	Married	Own	Employed	qufhixun	MSA, Not Principle City	1.0	0.0	wxleyezf	emcorrxb	0

In [19]:
```
raw_3 = raw_2
```

In [20]:
```
# Try the encoder on the rest of the non-Nan features.
encoder = OrdinalEncoder()
raw_3[['census_msa', 'hhs_geo_region']] = encoder.fit_transform(raw_3[['census_msa', 'hhs_geo_region']])
raw_3.head()
```

Out[20]:

ıe_group	education	race	sex	income_poverty	marital_status	rent_or_own	employment_status	hhs_geo_region	census_msa	household_adults	household_children	employment_industry	employment_occupation	h1n1_vaccine
3.0	< 12 Years	3.0	0.0	Below Poverty	Not Married	Own	Not in Labor Force	8.0	2.0	0.0	0.0	NaN	NaN	0
1.0	12 Years	3.0	1.0	Below Poverty	Not Married	Rent	Employed	1.0	0.0	0.0	0.0	pxcmvdjn	xgwztkwe	0
0.0	College Graduate	3.0	1.0	<= $75,000, Above Poverty	Not Married	Own	Employed	9.0	0.0	2.0	0.0	rucpziij	xtkaffoo	0
4.0	12 Years	3.0	0.0	Below Poverty	Not Married	Rent	Not in Labor Force	5.0	1.0	0.0	0.0	NaN	NaN	0
2.0	Some College	3.0	0.0	<= $75,000, Above Poverty	Married	Own	Employed	9.0	0.0	1.0	0.0	wxleyezf	emcorrxb	0

In [21]:
```
# Will use a manual map method for the remaining features ... change to numeric.
raw_3['marital_status'].value_counts()
```

Out[21]:
```
Married        13555
Not Married    11744
Name: marital_status, dtype: int64
```

In [22]:
```
marital = {'Not Married': 0,'Married': 1,}
raw_3['marital_status'] = raw_3['marital_status'].map(marital)
raw_3.head(2)
```

Out[22]:

ıe_group	education	race	sex	income_poverty	marital_status	rent_or_own	employment_status	hhs_geo_region	census_msa	household_adults	household_children	employment_industry	employment_occupation	h1n1_vaccine
3.0	< 12 Years	3.0	0.0	Below Poverty	0.0	Own	Not in Labor Force	8.0	2.0	0.0	0.0	NaN	NaN	0
1.0	12 Years	3.0	1.0	Below Poverty	0.0	Rent	Employed	1.0	0.0	0.0	0.0	pxcmvdjn	xgwztkwe	0

In [23]:
```
raw_3['rent_or_own'].value_counts()
```

Out[23]:
```
Own     18736
Rent     5929
Name: rent_or_own, dtype: int64
```

In [24]:
```
home = {'Rent': 0,'Own': 1}
raw_3['rent_or_own'] = raw_3['rent_or_own'].map(home)
raw_3.head(2)
```

Out[24]:

ı_seas_risk	opinion_seas_sick_from_vacc	age_group	education	race	sex	income_poverty	marital_status	rent_or_own	employment_status	hhs_geo_region	census_msa	household_adults	household_children	employment_indu
1.0	2.0	3.0	< 12 Years	3.0	0.0	Below Poverty	0.0	1.0	Not in Labor Force	8.0	2.0	0.0	0.0	
2.0	4.0	1.0	12 Years	3.0	1.0	Below Poverty	0.0	0.0	Employed	1.0	0.0	0.0	0.0	pxcm

In [25]:
```
raw_3['employment_status'].value_counts()
```

Out[25]:
```
Employed              13560
Not in Labor Force    10231
Unemployed             1453
Name: employment_status, dtype: int64
```

In [26]:
```
emp = {'Unemployed': 0,'Not in Labor Force': 1,'Employed': 2}
raw_3['employment_status'] = raw_3['employment_status'].map(emp)
raw_3.head(2)
```

Out[26]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	dc
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	

In [27]:
```
raw_3['education'].value_counts()
```

Out[27]:
```
College Graduate    10097
Some College         7043
12 Years             5797
< 12 Years           2363
Name: education, dtype: int64
```

In [28]:
```
edu = {'< 12 Years': 0,'12 Years': 1,'Some College': 2,'College Graduate': 3}
raw_3['education'] = raw_3['education'].map(edu)
raw_3.head(2)
```

Out[28]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	dc
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	

In [29]:
```
raw_3['income_poverty'].value_counts()
```

Out[29]:
```
<= $75,000, Above Poverty    12777
> $75,000                    6810
Below Poverty                2697
Name: income_poverty, dtype: int64
```

In [30]:
```
inc = {'Below Poverty': 0,'<= $75,000, Above Poverty': 1,'> $75,000': 2}
raw_3['income_poverty'] = raw_3['income_poverty'].map(inc)
raw_3.head(2)
```

Out[30]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	dc
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	

In [31]:
```
raw_3['employment_industry'].value_counts()
```

Out[31]:
```
fcxhlnwr    2468
wxleyezf    1804
ldnlellj    1231
pxcmvdjn    1037
atmlpfrs     926
arjwrbjb     871
xicduogh     851
mfikgejo     614
vjjrobsf     527
rucpziij     523
xgicxuve     511
saaquncn     338
cfqqtusy     325
nduyfdeo     286
mcubkhph     275
wlfvacwt     215
dotnnunm     201
haxffmxo     148
msuufmds     124
phxvnwax      89
qnlwzans      13
Name: employment_industry, dtype: int64
```

In [32]:
```
raw_3['employment_occupation'].value_counts()
```

Out[32]:
```
xtkaffoo    1778
mxkfnird    1509
emcorrxb    1270
cmhcxjea    1247
xgwztkwe    1082
hfxkjkmi     766
qxajmpny     548
xqwwgdyp     485
kldqjyjy     469
uqqtjvyb     452
tfqavkke     388
ukymxvdu     372
vlluhbov     354
oijqvulv     344
ccgxvspp     341
bxpfxfdn     331
haliazsg     296
rcertsgn     276
xzmlyyjv     248
dlvbwzss     227
hodpvpew     208
dcjcmpih     148
pvmttkik      98
Name: employment_occupation, dtype: int64
```

Describe the Data with basic counts and stats

Will cycle through the 7 lists of conceptually similar features and look at freq counts and descriptive stats.

In [70]:
```
# Examine frequency of classes within each feature - for h1n1 vaccine target values
print('1-Concern, knowledge and opinions')
print('_____________________________________________________')
for p in pcols_1:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-----------------------------------------------------------')
```

```
1-Concern, knowledge and opinions
_____________________________________________________
h1n1_vaccine  h1n1_concern
0             2.0             38.660114
              1.0             32.237439
              3.0             15.507945
              0.0             13.594503
1             2.0             43.708024
              1.0             24.690703
              3.0             23.700954
              0.0              7.900318
Name: h1n1_concern, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  h1n1_knowledge
0             1.0              57.046659
              2.0              32.709298
              0.0              10.244042
1             1.0              46.939137
              2.0              46.673744
              0.0               6.387120
Name: h1n1_knowledge, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  opinion_h1n1_vacc_effective
0             4.0                           46.442707
              5.0                           20.585964
              3.0                           20.388068
              2.0                            8.509509
              1.0                            4.073752
1             5.0                           51.822079
              4.0                           36.816720
              3.0                            8.913898
              2.0                            1.697035
              1.0                            0.750268
Name: opinion_h1n1_vacc_effective, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  opinion_h1n1_risk
0             2.0                  39.809946
              1.0                  35.791809
              4.0                  15.816893
              3.0                   4.452270
              5.0                   4.129082
1             4.0                  37.848962
              2.0                  29.813887
              5.0                  15.998568
              1.0                  12.866858
              3.0                   3.471725
Name: opinion_h1n1_risk, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  opinion_h1n1_sick_from_vacc
0             2.0                           36.430330
              1.0                           34.543173
              4.0                           20.773203
              5.0                            7.596892
              3.0                            0.656402
1             1.0                           32.916145
              2.0                           28.267477
              4.0                           27.641695
              5.0                           10.960129
              3.0                            0.214554
Name: opinion_h1n1_sick_from_vacc, dtype: float64
-----------------------------------------------------------
```

In [71]:
```
print('2-Seasonal opinions')
print('_____________________________________________________')
for p in pcols_2:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-----------------------------------------------------------')
```

```
2-Seasonal opinions
_____________________________________________________
h1n1_vaccine  opinion_seas_vacc_effective
0             4.0                           46.358225
              5.0                           33.378503
              2.0                            9.683976
              1.0                            5.478391
              3.0                            5.100905
1             5.0                           55.105697
              4.0                           36.725188
              2.0                            3.672519
              3.0                            2.902186
              1.0                            1.594411
Name: opinion_seas_vacc_effective, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  opinion_seas_risk
0             2.0                  36.569517
              1.0                  26.516658
              4.0                  25.677707
              5.0                   8.612579
              3.0                   2.623539
1             4.0                  41.905958
              2.0                  25.358938
              5.0                  21.213209
              1.0                   9.081120
              3.0                   2.440775
Name: opinion_seas_risk, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  opinion_seas_sick_from_vacc
0             1.0                           44.925707
              2.0                           30.023308
              4.0                           18.160629
              5.0                            6.472759
              3.0                            0.417597
1             1.0                           46.951220
              2.0                           26.004304
              4.0                           19.942611
              5.0                            6.958393
              3.0                            0.143472
Name: opinion_seas_sick_from_vacc, dtype: float64
-----------------------------------------------------------
```

In [72]:
```
print('3-Doctor and medical status')
print('_____________________________________________________________')
for p in pcols_3:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-------------------------------------------------------')
```

```
3-Doctor and medical status
_____________________________________________________________
h1n1_vaccine  doctor_recc_h1n1
0             0.0                86.729982
              1.0                13.270018
1             1.0                52.450355
              0.0                47.549645
Name: doctor_recc_h1n1, dtype: float64
-------------------------------------------------------
h1n1_vaccine  doctor_recc_seasonal
0             0.0                    72.321335
              1.0                    27.678665
1             1.0                    51.357260
              0.0                    48.642740
Name: doctor_recc_seasonal, dtype: float64
-------------------------------------------------------
h1n1_vaccine  chronic_med_condition
0             0.0                     73.908319
              1.0                     26.091681
1             0.0                     63.437728
              1.0                     36.562272
Name: chronic_med_condition, dtype: float64
-------------------------------------------------------
h1n1_vaccine  child_under_6_months
0             0.0                    92.701375
              1.0                     7.298625
1             0.0                    88.203365
              1.0                    11.796635
Name: child_under_6_months, dtype: float64
-------------------------------------------------------
h1n1_vaccine  health_insurance
0             1.0                85.408656
              0.0                14.591344
1             1.0                94.032634
              0.0                 5.967366
Name: health_insurance, dtype: float64
-------------------------------------------------------
```

In [73]:
```
print('4-Behaviors')
print('_____________________________________________________________')
for p in pcols_4:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-------------------------------------------------------')
```

```
4-Behaviors
_____________________________________________________________
h1n1_vaccine  behavioral_antiviral_meds
0             0.0                         95.569530
              1.0                          4.430470
1             0.0                         93.427812
              1.0                          6.572188
Name: behavioral_antiviral_meds, dtype: float64
-------------------------------------------------------
h1n1_vaccine  behavioral_avoidance
0             1.0                    71.454598
              0.0                    28.545402
1             1.0                    76.653076
              0.0                    23.346924
Name: behavioral_avoidance, dtype: float64
-------------------------------------------------------
h1n1_vaccine  behavioral_face_mask
0             0.0                    94.029496
              1.0                     5.970504
1             0.0                    89.661256
              1.0                    10.338744
Name: behavioral_face_mask, dtype: float64
-------------------------------------------------------
h1n1_vaccine  behavioral_wash_hands
0             1.0                     81.088675
              0.0                     18.911325
1             1.0                     88.018352
              0.0                     11.981648
Name: behavioral_wash_hands, dtype: float64
-------------------------------------------------------
h1n1_vaccine  behavioral_large_gatherings
0             0.0                           64.580153
              1.0                           35.419847
1             0.0                           62.491166
              1.0                           37.508834
Name: behavioral_large_gatherings, dtype: float64
-------------------------------------------------------
h1n1_vaccine  behavioral_outside_home
0             0.0                      66.803416
              1.0                      33.196584
1             0.0                      64.288237
              1.0                      35.711763
Name: behavioral_outside_home, dtype: float64
-------------------------------------------------------
h1n1_vaccine  behavioral_touch_face
0             1.0                    65.984801
              0.0                    34.015199
1             1.0                    74.169024
              0.0                    25.830976
Name: behavioral_touch_face, dtype: float64
-------------------------------------------------------
```

In [74]:
```
print('5-Main Demographics')
print('_____________________________________________________________')
for p in pcols_5:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-------------------------------------------------------')
```

```
5-Main Demographics
_____________________________________________________________
h1n1_vaccine  sex
0             0.0    58.850378
              1.0    41.149622
1             0.0    61.332393
              1.0    38.667607
Name: sex, dtype: float64
-------------------------------------------------------
h1n1_vaccine  age_group
0             4.0          25.160462
              0.0          20.082727
              2.0          20.054201
              3.0          20.025674
              1.0          14.676936
1             4.0          27.335213
              3.0          23.810363
              2.0          17.976736
              0.0          17.465633
              1.0          13.412055
Name: age_group, dtype: float64
-------------------------------------------------------
h1n1_vaccine  education
0             3.0          38.286318
              2.0          28.053502
              1.0          23.764268
              0.0           9.895912
1             3.0          45.871051
              2.0          27.046000
              1.0          19.785701
              0.0           7.297247
Name: education, dtype: float64
-------------------------------------------------------
h1n1_vaccine  race
0             3.0     78.814244
              0.0      8.572244
              1.0      6.608663
              2.0      6.004850
1             3.0     81.864646
              1.0      6.432852
              2.0      6.150864
              0.0      5.551639
Name: race, dtype: float64
-------------------------------------------------------
h1n1_vaccine  marital_status
0             1.0               52.245863
              0.0               47.754137
1             1.0               58.471761
              0.0               41.528239
Name: marital_status, dtype: float64
-------------------------------------------------------
```

In [75]:
```
print('6-Employment and Income')
print('_____________________________________________________________')
for p in pcols_6:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-------------------------------------------------------')
```

```
1             rcxnlnwr              33.827075
              wxleyezf              15.260076
              ldnlellj               7.302790
              arjwrbjb               7.165002
              pxcmvdjn               4.925939
              atmlpfrs               4.271443
              xicduogh               3.616948
              mfikgejo               3.444712
              haxffmxo               3.169135
              rucpziij               2.549087
              vjjrobsf               2.445746
              xqicxuve               2.445746
              saaquncn               1.997933
              nduyfdeo               1.687909
              cfqqtusy               1.619015
              mcubkhph               1.274544
              wlfvacwt               0.998967
              dotnnunm               0.757837
              msuufmds               0.620048
              phxvnwax               0.516707
```

In [76]:
```
print('7-Household numbers')
print('_____________________________________________________')
for p in pcols_7:
    print(raw_3.groupby('h1n1_vaccine')[p].value_counts(normalize=True)*100)
    print('-----------------------------------------------------')
```

```
7-Household numbers
_____________________________________________________
h1n1_vaccine  hhs_geo_region
0             6.0               16.749869
              3.0               12.394808
              9.0               11.467694
              4.0               10.892407
              8.0               10.454999
              1.0               10.031855
              7.0                8.206152
              5.0                7.802025
              0.0                7.564304
              2.0                4.435886
1             6.0               13.641170
              1.0               12.971449
              9.0               12.160733
              8.0               11.632006
              3.0               11.596757
              4.0                9.992950
              7.0                9.111738
              0.0                7.789919
              5.0                7.701798
              2.0                3.401480
Name: hhs_geo_region, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  census_msa
0             0.0           43.636191
              1.0           29.396662
              2.0           26.967147
1             0.0           43.479027
              1.0           29.626366
              2.0           26.894607
Name: census_msa, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  household_adults
0             1.0                53.829900
              0.0                31.076214
              2.0                10.757336
              3.0                 4.336551
1             1.0                57.941437
              0.0                28.127773
              2.0                 9.991127
              3.0                 3.939663
Name: household_adults, dtype: float64
-----------------------------------------------------------
h1n1_vaccine  household_children
0             0.0                  70.542189
              1.0                  12.010757
              2.0                  10.733324
              3.0                   6.713730
1             0.0                  70.683230
              1.0                  11.960958
              2.0                  11.162378
              3.0                   6.193434
Name: household_children, dtype: float64
-----------------------------------------------------------
```

Observations on the distribution of feature classes

This is a bit cumbersome to look through. I think a better approach will be a visual one with plotting of the frequencies grouped by the target classes (0,1). See bel

In [33]:
```
# Look at overall descriptive statistics
raw_3.describe()
```

Out[33]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face
count	26707.000000	26615.000000	26591.000000	26636.000000	26499.000000	26688.000000	26665.000000	26620.00000	26625.000000	26579.000000
mean	13353.000000	1.618486	1.262532	0.048844	0.725612	0.068982	0.825614	0.35864	0.337315	0.677264
std	7709.791156	0.910311	0.618149	0.215545	0.446214	0.253429	0.379448	0.47961	0.472802	0.467531
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.00000	0.000000	0.000000
25%	6676.500000	1.000000	1.000000	0.000000	0.000000	0.000000	1.000000	0.00000	0.000000	0.000000
50%	13353.000000	2.000000	1.000000	0.000000	1.000000	0.000000	1.000000	0.00000	0.000000	1.000000
75%	20029.500000	2.000000	2.000000	0.000000	1.000000	0.000000	1.000000	1.00000	1.000000	1.000000
max	26706.000000	3.000000	2.000000	1.000000	1.000000	1.000000	1.000000	1.00000	1.000000	1.000000

Plotting the proportion of target class (stacked bars) for each class of each variable

This is basically a visual method for looking at the frequencise that I attemped to do above. Will cycle through the sets of features to plot every variable.

In [146]:
```
# Take a look at one variable
counts = (raw_3[['h1n1_concern', 'h1n1_vaccine']]
              .groupby(['h1n1_concern', 'h1n1_vaccine'])
              .size()
              .unstack('h1n1_vaccine'))
counts
```

Out[146]:

h1n1_vaccine	0	1
h1n1_concern		
0.0	2849	447
1.0	6756	1397
2.0	8102	2473
3.0	3250	1341

In [147]:
```
# Change to proportion
h1n1_concern_counts = counts.sum(axis='columns')
h1n1_concern_counts
```

Out[147]:
```
h1n1_concern
0.0     3296
1.0     8153
2.0    10575
3.0     4591
dtype: int64
```

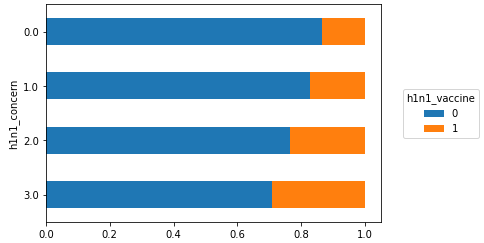
In [148]:
```
props = counts.div(h1n1_concern_counts, axis='index')
props
```

Out[148]:

h1n1_vaccine	0	1
h1n1_concern		
0.0	0.864381	0.135619
1.0	0.828652	0.171348
2.0	0.766147	0.233853
3.0	0.707907	0.292093

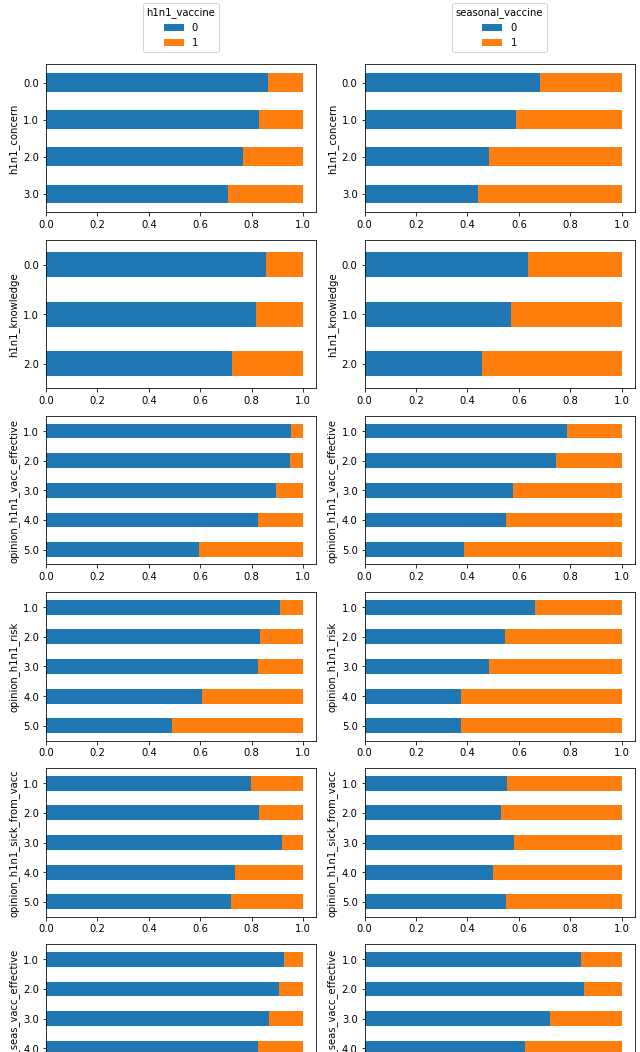
In [149]:
```
# Try using a stacked bar chart...
ax = props.plot.barh(stacked=True)
ax.invert_yaxis()
ax.legend(
    loc='center left',
    bbox_to_anchor=(1.05, 0.5),
    title='h1n1_vaccine')
```

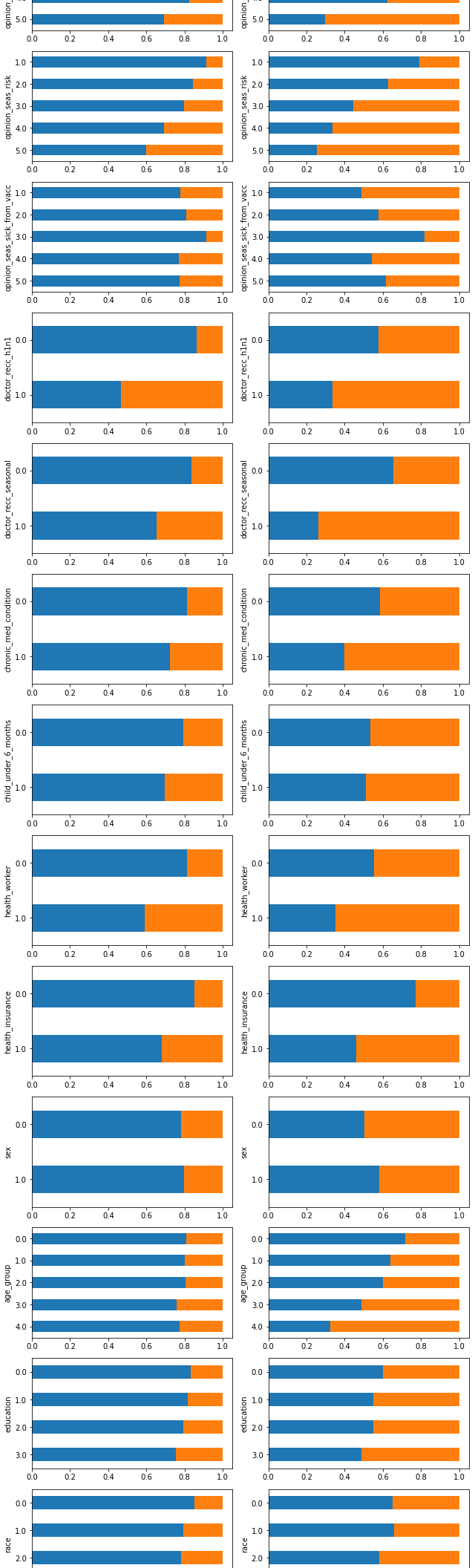
Out[149]:
```
<matplotlib.legend.Legend at 0x1a2b116a90>
```

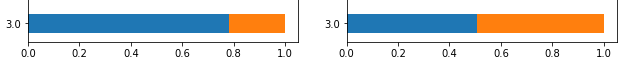


In [158]:
```
# Time to cycle throuh and Plot the first set of features.
cols_to_plot = [
    'h1n1_concern',
    'h1n1_knowledge',
    'opinion_h1n1_vacc_effective',
    'opinion_h1n1_risk',
    'opinion_h1n1_sick_from_vacc',
    'opinion_seas_vacc_effective',
    'opinion_seas_risk',
    'opinion_seas_sick_from_vacc',
    'doctor_recc_h1n1',
    'doctor_recc_seasonal',
    'chronic_med_condition',
    'child_under_6_months',
    'health_worker',
    'health_insurance',
    'sex',
    'age_group',
    'education',
    'race',
]

fig, ax = plt.subplots(
    len(cols_to_plot), 2, figsize=(9,len(cols_to_plot)*2.5)
)
for idx, col in enumerate(cols_to_plot):
    vaccination_rate_plot(
        col, 'h1n1_vaccine', raw_3, ax=ax[idx, 0]
    )
    vaccination_rate_plot(
        col, 'seasonal_vaccine', raw_3, ax=ax[idx, 1]
    )

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

```
/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:307: MatplotlibDeprecationWarning:

The rowNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().rowspan.start instead.

/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:307: MatplotlibDeprecationWarning:

The colNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().colspan.start instead.

/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:313: MatplotlibDeprecationWarning:

The rowNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().rowspan.start instead.

/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:313: MatplotlibDeprecationWarning:

The colNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().colspan.start instead.
```




opinion_seas_risk
opinion_seas_sick_from_vacc
doctor_recc_h1n1
doctor_recc_seasonal
chronic_med_condition
child_under_6_months
health_worker
health_insurance
sex
age_group
education
race

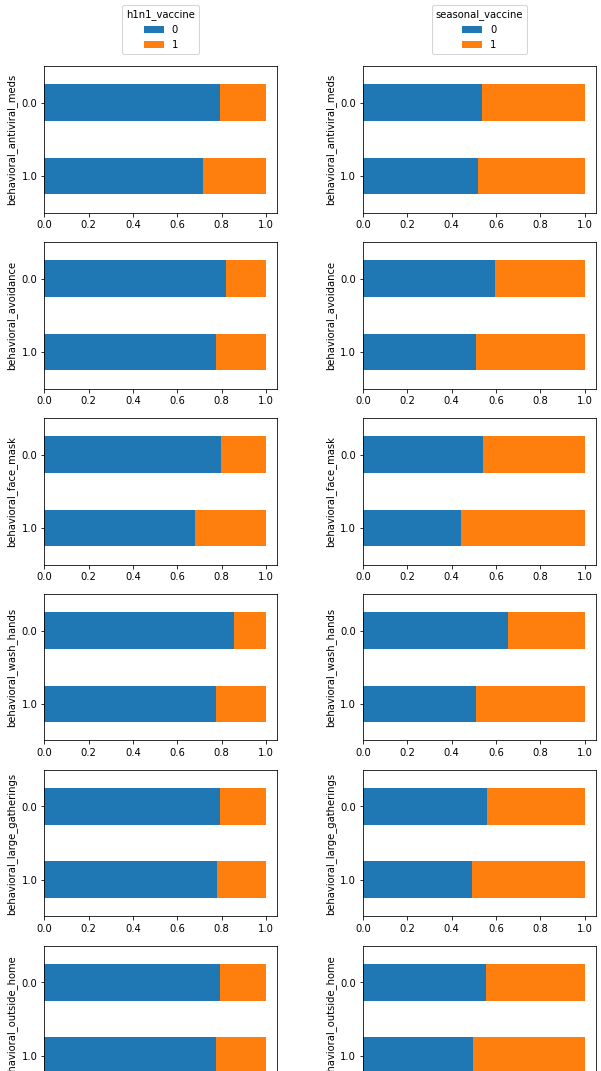


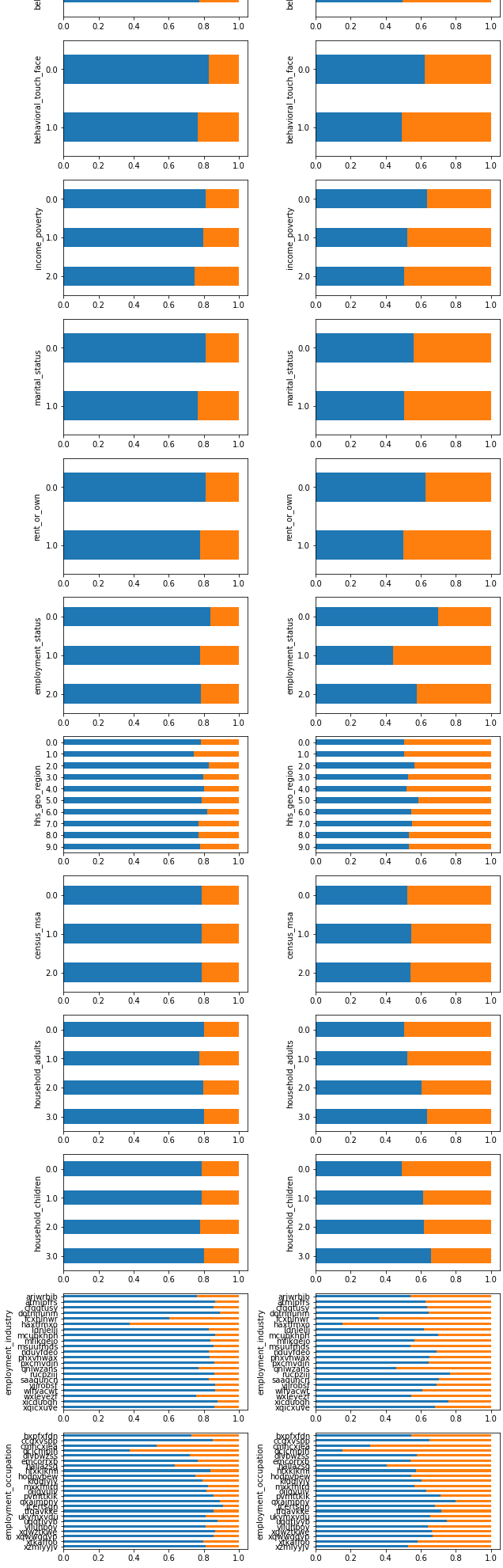
In [156]:
```
raw_3.columns
```

Out[156]:
```
Index(['respondent_id', 'h1n1_concern', 'h1n1_knowledge',
       'behavioral_antiviral_meds', 'behavioral_avoidance',
       'behavioral_face_mask', 'behavioral_wash_hands',
       'behavioral_large_gatherings', 'behavioral_outside_home',
       'behavioral_touch_face', 'doctor_recc_h1n1', 'doctor_recc_seasonal',
       'chronic_med_condition', 'child_under_6_months', 'health_worker',
       'health_insurance', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk',
       'opinion_h1n1_sick_from_vacc', 'opinion_seas_vacc_effective',
       'opinion_seas_risk', 'opinion_seas_sick_from_vacc', 'age_group',
       'education', 'race', 'sex', 'income_poverty', 'marital_status',
       'rent_or_own', 'employment_status', 'hhs_geo_region', 'census_msa',
       'household_adults', 'household_children', 'employment_industry',
       'employment_occupation', 'h1n1_vaccine', 'seasonal_vaccine'],
      dtype='object')
```

In [159]:
```
# Plot some MORE features - this is the second and final set.
cols_to_plot = [
    'behavioral_antiviral_meds',
    'behavioral_avoidance',
    'behavioral_face_mask',
    'behavioral_wash_hands',
    'behavioral_large_gatherings',
    'behavioral_outside_home',
    'behavioral_touch_face',
    'income_poverty',
    'marital_status',
    'rent_or_own',
    'employment_status',
    'hhs_geo_region',
    'census_msa',
    'household_adults',
    'household_children',
    'employment_industry',
    'employment_occupation'
]

fig, ax = plt.subplots(
    len(cols_to_plot), 2, figsize=(9,len(cols_to_plot)*2.5)
)
for idx, col in enumerate(cols_to_plot):
    vaccination_rate_plot(
        col, 'h1n1_vaccine', raw_3, ax=ax[idx, 0]
    )
    vaccination_rate_plot(
        col, 'seasonal_vaccine', raw_3, ax=ax[idx, 1]
    )

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

```
/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:307: MatplotlibDeprecationWarning:

The rowNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().rowspan.start instead.

/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:307: MatplotlibDeprecationWarning:

The colNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().colspan.start instead.

/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:313: MatplotlibDeprecationWarning:

The rowNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().rowspan.start instead.

/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/pandas/plotting/_matplotlib/tools.py:313: MatplotlibDeprecationWarning:

The colNum attribute was deprecated in Matplotlib 3.2 and will be removed two minor releases later. Use ax.get_subplotspec().colspan.start instead.
```





Observations on the class proportion plots for h1n1

NOTE: the proportion that got vaccinated (class 1) is in orange. The blue is the proportion that did not get vaccinated (class 0). The main differences we can see her
Opinion questions and the Doctor reccomend questions. There seem to be very little differences for the demographics (with the exection of employment occupation and in
geo location where differences are seen for just a few of the classes).

In [42]:
```
# Take a more detailed look at descriptive stats for each variable - grouped by target(s)
# Loop through the descriptive statistices for each feature - h1n1 vaccine
print('1-Concern, knowledge, opinions')
print('_____________________________________________________________')
for p in pcols_1:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('--------------------------------------------------------------------------------')
```

```
1-Concern, knowledge, opinions
_____________________________________________________________
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20957.0  1.560815  0.910159  0.0  1.0  2.0  2.0  3.0
1              5658.0  1.832096  0.878564  0.0  1.0  2.0  2.0  3.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20939.0  1.224653  0.615697  0.0  1.0  1.0  2.0  2.0
1              5652.0  1.402866  0.606937  0.0  1.0  1.0  2.0  2.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20718.0  3.709576  1.016101  1.0  3.0  4.0  4.0  5.0
1              5598.0  4.372633  0.777186  1.0  4.0  5.0  5.0  5.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20731.0  2.126815  1.179287  1.0  1.0  2.0  2.0  5.0
1              5588.0  3.142985  1.345780  1.0  2.0  4.0  4.0  5.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20719.0  2.304503  1.331919  1.0  1.0  2.0  4.0  5.0
1              5593.0  2.554622  1.454702  1.0  1.0  2.0  4.0  5.0
--------------------------------------------------------------------------------
```

In [43]:
```
print('2-Seasonal opinions')
print('_____________________________________________________________')
for p in pcols_2:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('--------------------------------------------------------------------------------')
```

```
2-Seasonal opinions
_____________________________________________________________
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20663.0  3.924745  1.122322  1.0  4.0  4.0  5.0  5.0
1              5582.0  4.400752  0.842616  1.0  4.0  5.0  5.0  5.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20621.0  2.533000  1.345229  1.0  1.0  2.0  4.0  5.0
1              5572.0  3.408112  1.310792  1.0  2.0  4.0  4.0  5.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20594.0  2.112314  1.322829  1.0  1.0  2.0  3.0  5.0
1              5576.0  2.139527  1.369590  1.0  1.0  2.0  4.0  5.0
--------------------------------------------------------------------------------
```

In [44]:
```
print('3-Doctor and medical status')
print('_____________________________________________________________')
for p in pcols_3:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('--------------------------------------------------------------------------------')
```

```
3-Doctor and medical status
_____________________________________________________________
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             19058.0  0.132700  0.339259  0.0  0.0  0.0  0.0  1.0
1              5489.0  0.524504  0.499445  0.0  0.0  1.0  1.0  1.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             19058.0  0.276787  0.447422  0.0  0.0  0.0  1.0  1.0
1              5489.0  0.513573  0.499861  0.0  0.0  1.0  1.0  1.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20244.0  0.260917  0.439145  0.0  0.0  0.0  1.0  1.0
1              5492.0  0.365623  0.481648  0.0  0.0  0.0  1.0  1.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             20360.0  0.072986  0.260120  0.0  0.0  0.0  0.0  1.0
1              5527.0  0.117966  0.322597  0.0  0.0  0.0  0.0  1.0
--------------------------------------------------------------------------------
                count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0             10143.0  0.854087  0.353037  0.0  1.0  1.0  1.0  1.0
1              4290.0  0.940326  0.236909  0.0  1.0  1.0  1.0  1.0
--------------------------------------------------------------------------------
```

In [45]:
```
print('4-Behaviors')
print('_____________________________________________________________')
for p in pcols_4:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
4-Behaviors
_____________________________________________________________
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20991.0  0.044305  0.205776  0.0  0.0  0.0  0.0  1.0
1             5645.0  0.065722  0.247817  0.0  0.0  0.0  0.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20858.0  0.714546  0.451641  0.0  0.0  1.0  1.0  1.0
1             5641.0  0.766531  0.423076  0.0  1.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            21020.0  0.059705  0.236945  0.0  0.0  0.0  0.0  1.0
1             5668.0  0.103387  0.304491  0.0  0.0  0.0  0.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20998.0  0.810887  0.391608  0.0  1.0  1.0  1.0  1.0
1             5667.0  0.880184  0.324775  0.0  1.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20960.0  0.354198  0.478281  0.0  0.0  0.0  1.0  1.0
1             5660.0  0.375088  0.484188  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20963.0  0.331966  0.470930  0.0  0.0  0.0  1.0  1.0
1             5662.0  0.357118  0.479192  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20923.0  0.659848  0.473771  0.0  0.0  1.0  1.0  1.0
1             5656.0  0.741690  0.437744  0.0  0.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
```

In [46]:
```
print('5-Main demographics')
print('_____________________________________________________________')
for p in pcols_5:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
5-Main demographics
_____________________________________________________________
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            21033.0  0.411496  0.492116  0.0  0.0  0.0  1.0  1.0
1             5674.0  0.386676  0.487031  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            21033.0  2.155042  1.460417  0.0  1.0  2.0  4.0  4.0
1             5674.0  2.301375  1.440068  0.0  1.0  3.0  4.0  4.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            19887.0  1.947302  1.006785  0.0  1.0  2.0  3.0  3.0
1             5413.0  2.114909  0.967174  0.0  1.0  2.0  3.0  3.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            21033.0  2.550611  0.945510  0.0  3.0  3.0  3.0  3.0
1             5674.0  2.643285  0.831473  0.0  3.0  3.0  3.0  3.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            19881.0  0.522459  0.499508  0.0  0.0  1.0  1.0  1.0
1             5418.0  0.584718  0.492816  0.0  0.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
```

In [47]:
```
print('6-Employment and income')
print('_____________________________________________________________')
for p in pcols_6:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
6-Employment and income
_____________________________________________________________
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            19841.0  1.474825  0.609885  0.0  1.0  2.0  2.0  2.0
1             5403.0  1.497131  0.581191  0.0  1.0  2.0  2.0  2.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20373.0  0.084033  0.277444  0.0  0.0  0.0  0.0  1.0
1             5530.0  0.214647  0.410615  0.0  0.0  0.0  0.0  1.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            17446.0  1.166571  0.623599  0.0  1.0  1.0  2.0  2.0
1             4838.0  1.249483  0.632958  0.0  1.0  1.0  2.0  2.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            19387.0  0.751896  0.431924  0.0  1.0  1.0  1.0  1.0
1             5278.0  0.787988  0.408772  0.0  1.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
              count unique       top  freq
h1n1_vaccine
0             10377     23  xtkaffoo  1416
1              2860     23  cmhcxjea   587
-------------------------------------------------------------------------------
              count unique       top  freq
h1n1_vaccine
0             10474     21  fcxhlnwr  1486
1              2903     21  fcxhlnwr   982
-------------------------------------------------------------------------------
```

In [48]:
```
print('7-Household numbers')
print('_____________________________________________________________')
for p in pcols_7:
    print(raw_3.groupby('h1n1_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
7-Household numbers
_____________________________________________________________
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            21033.0  4.834593  2.782922  0.0  3.0  5.0  7.0  9.0
1             5674.0  4.811773  2.890046  0.0  3.0  5.0  7.0  9.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            21033.0  0.833310  0.823578  0.0  0.0  1.0  2.0  2.0
1             5674.0  0.834156  0.822406  0.0  0.0  1.0  2.0  2.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20823.0  0.883542  0.760436  0.0  0.0  1.0  1.0  3.0
1             5635.0  0.897427  0.726876  0.0  0.0  1.0  1.0  3.0
-------------------------------------------------------------------------------
               count      mean       std  min  25%  50%  75%  max
h1n1_vaccine
0            20823.0  0.536186  0.930711  0.0  0.0  0.0  1.0  3.0
1             5635.0  0.528660  0.918794  0.0  0.0  0.0  1.0  3.0
-------------------------------------------------------------------------------
```

Observations on the comparative descriptive stats for h1n1

Beacuse the values are of a small range - in most cases 2 to 5, the quantiles are not very useful. I tried examining the means, but again this was not too easy. Howev
corroborated what was seen in the plots above. I noted differences in the means > 0.10, and the variables with differences in the mean larger than this were the opini
the doctor recommendation, and one of the behavioral questions. Only age group and education - in the demographic questions had mean differences above 0.10 (but not b

In [50]:
```
# Loop through the descriptive statistices for each feature - SEASONAL VACCINE (although this is less important)
print('1-Concern, knowledge, opinions')
print('_____________________________________________________________')
for p in pcols_1:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
1-Concern, knowledge, opinions
_____________________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14222.0  1.486922  0.922611  0.0  1.0  2.0  2.0  3.0
1                12393.0  1.769467  0.871893  0.0  1.0  2.0  2.0  3.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14212.0  1.193217  0.615942  0.0  1.0  1.0  2.0  2.0
1                12379.0  1.342112  0.611079  0.0  1.0  1.0  2.0  2.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14029.0  3.657281  1.056981  1.0  3.0  4.0  4.0  5.0
1                12287.0  4.071376  0.898223  1.0  4.0  4.0  5.0  5.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14031.0  2.081961  1.189337  1.0  1.0  2.0  2.0  5.0
1                12288.0  2.640137  1.326084  1.0  2.0  2.0  4.0  5.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14022.0  2.322707  1.363287  1.0  1.0  2.0  4.0  5.0
1                12290.0  2.397559  1.361130  1.0  1.0  2.0  4.0  5.0
-------------------------------------------------------------------------------
```

In [51]:
```
# Loop through the descriptive statistices for each feature - seasonal vaccine
print('2-Sesonal opinions')
print('_____________________________________________________________')
for p in pcols_2:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
2-Sesonal opinions
_____________________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13987.0  3.657897  1.164812  1.0  3.0  4.0  4.0  5.0
1                12258.0  4.445994  0.805401  1.0  4.0  5.0  5.0  5.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13959.0  2.213339  1.239794  1.0  1.0  2.0  3.0  5.0
1                12234.0  3.296305  1.314729  1.0  2.0  4.0  4.0  5.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13931.0  2.194961  1.348964  1.0  1.0  2.0  4.0  5.0
1                12239.0  2.030640  1.309060  1.0  1.0  2.0  2.0  5.0
-------------------------------------------------------------------------------
```

In [52]:
```
# Loop through the descriptive statistices for each feature - seasonal vaccine
print('3-Doctor and medical status')
print('_____________________________________________________')
for p in pcols_3:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
3-Doctor and medical status
_____________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                12873.0  0.141925  0.348987  0.0  0.0  0.0  0.0  1.0
1                11674.0  0.306750  0.461164  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                12873.0  0.164453  0.370700  0.0  0.0  0.0  0.0  1.0
1                11674.0  0.511992  0.499878  0.0  0.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13679.0  0.211273  0.408226  0.0  0.0  0.0  0.0  1.0
1                12057.0  0.364933  0.481431  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13767.0  0.079465  0.270474  0.0  0.0  0.0  0.0  1.0
1                12120.0  0.086139  0.280580  0.0  0.0  0.0  0.0  1.0
-------------------------------------------------------------------------------
                    count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                7204.0  0.814270  0.388916  0.0  1.0  1.0  1.0  1.0
1                7229.0  0.944944  0.228105  0.0  1.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
```

In [53]:
```
# Loop through the descriptive statistices for each feature - seasonal vaccine
print('4-Behaviors')
print('_____________________________________________________')
for p in pcols_4:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
4-Behaviors
_____________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14249.0  0.047582  0.212888  0.0  0.0  0.0  0.0  1.0
1                12387.0  0.050295  0.218561  0.0  0.0  0.0  0.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14164.0  0.693801  0.46093  0.0  0.0  1.0  1.0  1.0
1                12335.0  0.762140  0.42579  0.0  1.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14264.0  0.057137  0.232112  0.0  0.0  0.0  0.0  1.0
1                12424.0  0.082582  0.275261  0.0  0.0  0.0  0.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14248.0  0.785794  0.410284  0.0  1.0  1.0  1.0  1.0
1                12417.0  0.871305  0.334875  0.0  1.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14228.0  0.329983  0.470223  0.0  0.0  0.0  1.0  1.0
1                12392.0  0.391543  0.488115  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14230.0  0.313703  0.464014  0.0  0.0  0.0  1.0  1.0
1                12395.0  0.364421  0.481287  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14206.0  0.624806  0.484190  0.0  0.0  1.0  1.0  1.0
1                12373.0  0.737493  0.440014  0.0  0.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
```

In [54]:
```
# Loop through the descriptive statistices for each feature - seasonal vaccine
print('5-Main demographics')
print('_____________________________________________________')
for p in pcols_5:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('-------------------------------------------------------------------------------')
```

```
5-Main demographics
_____________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14272.0  0.441564  0.496591  0.0  0.0  0.0  1.0  1.0
1                12435.0  0.365661  0.481635  0.0  0.0  0.0  1.0  1.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14272.0  1.808716  1.413316  0.0  0.0  2.0  3.0  4.0
1                12435.0  2.619300  1.384842  0.0  2.0  3.0  4.0  4.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13407.0  1.918252  1.010994  0.0  1.0  2.0  3.0  3.0
1                11893.0  2.056336  0.984075  0.0  1.0  2.0  3.0  3.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14272.0  2.482623  0.995530  0.0  3.0  3.0  3.0  3.0
1                12435.0  2.670929  0.821118  0.0  3.0  3.0  3.0  3.0
-------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13412.0  0.511184  0.499894  0.0  0.0  1.0  1.0  1.0
1                11887.0  0.563557  0.495965  0.0  0.0  1.0  1.0  1.0
-------------------------------------------------------------------------------
```

In [55]:
```
# Loop through the descriptive statistices for each feature - seasonal vaccine
print('6-Employment and income')
print('_____________________________________________________')
for p in pcols_6:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('--------------------------------------------------------------------------------')
```

```
6-Employment and income
_____________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13376.0  1.510242  0.633672  0.0  1.0  2.0  2.0  2.0
1                11868.0  1.445062  0.566559  0.0  1.0  1.0  2.0  2.0
--------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13776.0  0.074260  0.262202  0.0  0.0  0.0  0.0  1.0
1                12127.0  0.154696  0.361630  0.0  0.0  0.0  0.0  1.0
--------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                11832.0  1.144354  0.643521  0.0  1.0  1.0  2.0  2.0
1                10452.0  1.230100  0.603597  0.0  1.0  1.0  2.0  2.0
--------------------------------------------------------------------------------
                   count     mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                13086.0  0.71481  0.451522  0.0  0.0  1.0  1.0  1.0
1                11579.0  0.81026  0.392112  0.0  1.0  1.0  1.0  1.0
--------------------------------------------------------------------------------
                  count unique       top  freq
seasonal_vaccine
0                  7650     23  xtkaffoo  1034
1                  5587     23  cmhcxjea   858
--------------------------------------------------------------------------------
                  count unique       top  freq
seasonal_vaccine
0                  7715     21  wxleyezf   985
1                  5662     21  fcxhlnwr  1575
--------------------------------------------------------------------------------
```

In [56]:
```
# Loop through the descriptive statistices for each feature - seasonal vaccine
print('7-Household numbers')
print('_____________________________________________________')
for p in pcols_7:
    print(raw_3.groupby('seasonal_vaccine')[p].describe())
    print('--------------------------------------------------------------------------------')
```

```
7-Household numbers
_____________________________________________________
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14272.0  4.878153  2.775398  0.0  3.0  5.0  7.0  9.0
1                12435.0  4.774186  2.839777  0.0  3.0  5.0  7.0  9.0
--------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14272.0  0.847534  0.822066  0.0  0.0  1.0  2.0  2.0
1                12435.0  0.817370  0.824481  0.0  0.0  1.0  2.0  2.0
--------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14087.0  0.932278  0.780158  0.0  0.0  1.0  1.0  3.0
1                12371.0  0.834371  0.718259  0.0  0.0  1.0  1.0  3.0
--------------------------------------------------------------------------------
                   count      mean       std  min  25%  50%  75%  max
seasonal_vaccine
0                14087.0  0.634273  0.985979  0.0  0.0  0.0  1.0  3.0
1                12371.0  0.421065  0.843429  0.0  0.0  0.0  0.0  3.0
--------------------------------------------------------------------------------
```

Observations on the comparative means for seasonal

As this is less important, skipping for now.

T-tests for each variable

We see that there are some differences in means, but are they significantly different? Will loop though T-Tests for each variable (using Welch's T-test). I found that did not like missing values, so used the data set after it had been imputed.

In [122]:
```
# Load the data
df1_imputed = pd.read_csv('data/df1imputed.csv')
df1_imputed.shape
```

Out[122]: (26707, 37)

In [123]:
```
df1_imputed.head()
```

Out[123]:

	Unnamed: 0	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	docto
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	
2	2	1.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	
3	3	1.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	0.0	
4	4	2.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	1.0	

In [124]:
```
h1_vacc_Y = df1_imputed[(df1_imputed['h1n1_vaccine'] == 1)]
h1_vacc_N = df1_imputed[(df1_imputed['h1n1_vaccine'] == 0)]
```

In [119]:
```
from scipy import stats
```

In [125]:
```
# Try one test first...
# Check for statistically different means; had tried with raw_3 but did not work - maybe not like the missing values?
stats.ttest_ind(h1_vacc_Y['opinion_h1n1_risk'], h1_vacc_N['opinion_h1n1_risk'], equal_var=False)
```

Out[125]: Ttest_indResult(statistic=51.67045369051645, pvalue=0.0)

In [128]:
```
# Loop through the T-test for each feature - by group of features - h1n1 (0,1)
print('1-H1N1 concern, knowledge and opinions')
print('_____________________________________________________')
for p in pcols_1:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
1-H1N1 concern, knowledge and opinions
_____________________________________________________
Ttest_indResult(statistic=20.510686913663324, pvalue=1.8596981908676164e-91)
-------------------------------------------------------------------------
Ttest_indResult(statistic=19.56410490012085, pvalue=1.6236291632798846e-83)
-------------------------------------------------------------------------
Ttest_indResult(statistic=53.09553619943674, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=51.67045369051645, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=11.729537749716494, pvalue=1.5815353523327127e-31)
-------------------------------------------------------------------------
```

In [129]:
```
print('2-Seasonal opinions')
print('_____________________________________________________')
for p in pcols_2:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
2-Seasonal opinions
_____________________________________________________
Ttest_indResult(statistic=35.21984765090239, pvalue=2.4069850414652085e-258)
-------------------------------------------------------------------------
Ttest_indResult(statistic=44.38540555296442, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=1.355953453780671, pvalue=0.17514904923807695)
-------------------------------------------------------------------------
```

In [130]:
```
print('3-Doctor and medical status')
print('_____________________________________________________')
for p in pcols_3:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
3-Doctor and medical status
_____________________________________________________
Ttest_indResult(statistic=55.234149886505556, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=32.50356870676048, pvalue=4.820383492899826e-218)
-------------------------------------------------------------------------
Ttest_indResult(statistic=14.944208612507946, pvalue=7.431157595802916e-50)
-------------------------------------------------------------------------
Ttest_indResult(statistic=9.674613092878907, pvalue=5.144858926991929e-22)
-------------------------------------------------------------------------
Ttest_indResult(statistic=17.744089993769776, pvalue=1.7826917129231177e-69)
-------------------------------------------------------------------------
```

In [131]:
```
print('4-Behaviors')
print('_____________________________________________________')
for p in pcols_4:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
4-Behaviors
_____________________________________________________
Ttest_indResult(statistic=6.001935291982516, pvalue=2.0357121771835943e-09)
-------------------------------------------------------------------------
Ttest_indResult(statistic=8.21325756203957, pvalue=2.435148211200556e-16)
-------------------------------------------------------------------------
Ttest_indResult(statistic=10.029519434985524, pvalue=1.5812416290564715e-23)
-------------------------------------------------------------------------
Ttest_indResult(statistic=13.611787397245248, pvalue=7.678192938010269e-42)
-------------------------------------------------------------------------
Ttest_indResult(statistic=2.847603227229391, pvalue=0.004415088522494424)
-------------------------------------------------------------------------
Ttest_indResult(statistic=3.482172901188056, pvalue=0.0004997645940054413)
-------------------------------------------------------------------------
Ttest_indResult(statistic=12.280168816640018, pvalue=2.101093399667916e-34)
-------------------------------------------------------------------------
```

In [132]:
```
print('5-Main demographics')
print('_____________________________________________________')
for p in pcols_5:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
5-Main demographics
_____________________________________________________
Ttest_indResult(statistic=-3.399100994792271, pvalue=0.0006789974280048363)
-------------------------------------------------------------------------
Ttest_indResult(statistic=6.77223070168082, pvalue=1.3469184654694845e-11)
-------------------------------------------------------------------------
Ttest_indResult(statistic=11.54814586283158, pvalue=1.2243980625194762e-30)
-------------------------------------------------------------------------
Ttest_indResult(statistic=7.228957922227945, pvalue=5.223532819123491e-13)
-------------------------------------------------------------------------
Ttest_indResult(statistic=8.149205441348807, pvalue=4.150866095460693e-16)
-------------------------------------------------------------------------
```

In [135]:
```
pcols_6 = ['employment_status', 'health_worker', 'income_poverty', 'rent_or_own', 'employment_industry']
```

In [136]:
```
print('6-Employment and income')
print('_____________________________________________________')
for p in pcols_6:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
6-Employment and income
_____________________________________________________
Ttest_indResult(statistic=2.3873789654572883, pvalue=0.016988860986239508)
-------------------------------------------------------------------------
Ttest_indResult(statistic=22.561790443788293, pvalue=6.307858068833229e-109)
-------------------------------------------------------------------------
Ttest_indResult(statistic=8.815132799670584, pvalue=1.4235812653389587e-18)
-------------------------------------------------------------------------
Ttest_indResult(statistic=5.772176775345721, pvalue=8.074945563152783e-09)
-------------------------------------------------------------------------
Ttest_indResult(statistic=-22.041654467274732, pvalue=8.484647447584251e-105)
-------------------------------------------------------------------------
```

In [134]:
```
print('7-Household numbers')
print('_____________________________________________________________')
for p in pcols_7:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
7-Household numbers
_____________________________________________________________
Ttest_indResult(statistic=-0.5319629611849604, pvalue=0.5947652027440007)
-------------------------------------------------------------------------
Ttest_indResult(statistic=0.06876337454170406, pvalue=0.9451795028677601)
-------------------------------------------------------------------------
Ttest_indResult(statistic=1.1961309633662738, pvalue=0.23167598896085778)
-------------------------------------------------------------------------
Ttest_indResult(statistic=-0.5485111399441805, pvalue=0.5833545129411885)
-------------------------------------------------------------------------
```

Observations on the h1n1 T-tests

Was suprised to see that almost all of the features had significantly different means. Th only 5 features did not have significanly differnct means - the opinion_seasonal_sick_from_vacc; and some demographics questions like number of household adults and children, and some of the location features.

Run T-test for the Seasonal values as well...

In [137]:
```
seasonal_vacc_Y = df1_imputed[(df1_imputed['seasonal_vaccine'] == 1)]
seasonal_vacc_N = df1_imputed[(df1_imputed['seasonal_vaccine'] == 0)]
```

In [138]:
```
# Loop through the T-test for each feature - by group of features - SEASONAL (0,1)
print('1-SEASONAL: H1N1 concern, knowledge and opinions')
print('_____________________________________________________________')
for p in pcols_1:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
1-SEASONAL: H1N1 concern, knowledge and opinions
_____________________________________________________________
Ttest_indResult(statistic=20.510686913663324, pvalue=1.8596981908676164e-91)
-------------------------------------------------------------------------
Ttest_indResult(statistic=19.56410490012085, pvalue=1.6236291632798846e-83)
-------------------------------------------------------------------------
Ttest_indResult(statistic=53.09553619943674, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=51.67045369051645, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=11.729537749716494, pvalue=1.5815353523327127e-31)
-------------------------------------------------------------------------
```

In [139]:
```
print('2-SEASONAL: Seasonal opinions')
print('_____________________________________________________________')
for p in pcols_2:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
2-SEASONAL: Seasonal opinions
_____________________________________________________________
Ttest_indResult(statistic=35.21984765090239, pvalue=2.4069850414652085e-258)
-------------------------------------------------------------------------
Ttest_indResult(statistic=44.38540555296442, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=1.355953453780671, pvalue=0.17514904923807695)
-------------------------------------------------------------------------
```

In [140]:
```
print('3-SEASONAL: Doctor and medical status')
print('_____________________________________________________________')
for p in pcols_3:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
3-SEASONAL: Doctor and medical status
_____________________________________________________________
Ttest_indResult(statistic=55.234149886505556, pvalue=0.0)
-------------------------------------------------------------------------
Ttest_indResult(statistic=32.50356870676048, pvalue=4.820383492899826e-218)
-------------------------------------------------------------------------
Ttest_indResult(statistic=14.944208612507946, pvalue=7.431157595802916e-50)
-------------------------------------------------------------------------
Ttest_indResult(statistic=9.674613092878907, pvalue=5.144858926991929e-22)
-------------------------------------------------------------------------
Ttest_indResult(statistic=17.744089993769776, pvalue=1.7826917129231177e-69)
-------------------------------------------------------------------------
```

In [141]:
```
print('4-SEASONAL: Behaviors')
print('_____________________________________________________________')
for p in pcols_4:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------')
```

```
4-SEASONAL: Behaviors
_____________________________________________________________
Ttest_indResult(statistic=6.001935291982516, pvalue=2.0357121771835943e-09)
-------------------------------------------------------------------------
Ttest_indResult(statistic=8.21325756203957, pvalue=2.435148211200556e-16)
-------------------------------------------------------------------------
Ttest_indResult(statistic=10.029519434985524, pvalue=1.5812416290564715e-23)
-------------------------------------------------------------------------
Ttest_indResult(statistic=13.611787397245248, pvalue=7.678192938010269e-42)
-------------------------------------------------------------------------
Ttest_indResult(statistic=2.847603227229391, pvalue=0.004415088522494424)
-------------------------------------------------------------------------
Ttest_indResult(statistic=3.482172901188056, pvalue=0.0004997645940054413)
-------------------------------------------------------------------------
Ttest_indResult(statistic=12.280168816640018, pvalue=2.101093399667916e-34)
-------------------------------------------------------------------------
```

In [142]:
```
print('5-SEASONAL: Main demographics')
print('_____________________________________________________________')
for p in pcols_5:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------------')
```

```
5-SEASONAL: Main demographics
_____________________________________________________________
Ttest_indResult(statistic=-3.399100994792271, pvalue=0.0006789974280048363)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=6.77223070168082, pvalue=1.3469184654694845e-11)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=11.54814586283158, pvalue=1.2243980625194762e-30)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=7.228957922227945, pvalue=5.223532819123491e-13)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=8.149205441348807, pvalue=4.150866095460693e-16)
-------------------------------------------------------------------------------
```

In [143]:
```
print('6-SEASONAL: Employment and income')
print('_____________________________________________________________')
for p in pcols_6:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------------')
```

```
6-SEASONAL: Employment and income
_____________________________________________________________
Ttest_indResult(statistic=2.3873789654572883, pvalue=0.016988860986239508)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=22.561790443788293, pvalue=6.307858068833229e-109)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=8.815132799670584, pvalue=1.4235812653389587e-18)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=5.772176775345721, pvalue=8.074945563152783e-09)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=-22.041654467274732, pvalue=8.484647447584251e-105)
-------------------------------------------------------------------------------
```

In [144]:
```
print('7-SEASONAL: Household numbers')
print('_____________________________________________________________')
for p in pcols_7:
    print(stats.ttest_ind(h1_vacc_Y[p], h1_vacc_N[p], equal_var=False))
    print('-------------------------------------------------------------------------------')
```

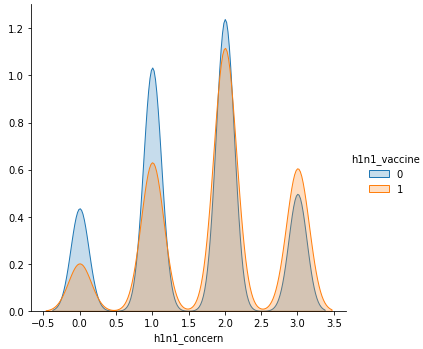
```
7-SEASONAL: Household numbers
_____________________________________________________________
Ttest_indResult(statistic=-0.5319629611849604, pvalue=0.5947652027440007)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=0.06876337454170406, pvalue=0.9451795028677601)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=1.1961309633662738, pvalue=0.23167598896085778)
-------------------------------------------------------------------------------
Ttest_indResult(statistic=-0.5485111399441805, pvalue=0.5833545129411885)
-------------------------------------------------------------------------------
```

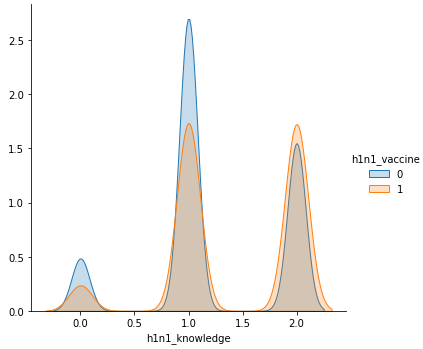
In [ ]:

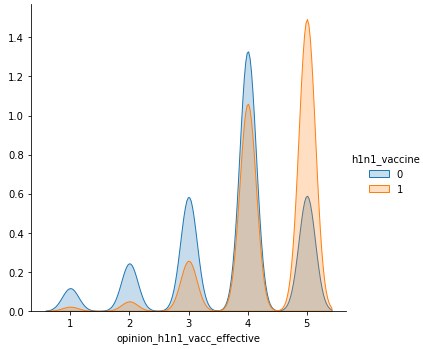
Distplots to visualize the comparative values for h1n1 vaccine status

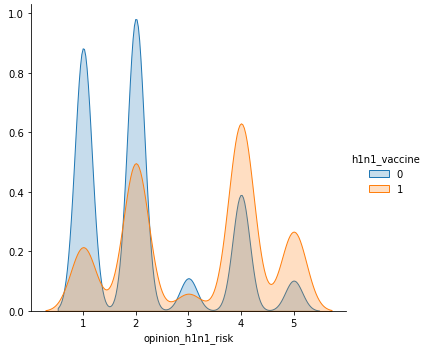
This is another method for trying to see differences between the target classes (0 = not vaccinated - in blue versus 1 = vaccinated - in orange) and the frequencies o
Again, I looped through all of the features by conceptual groups.

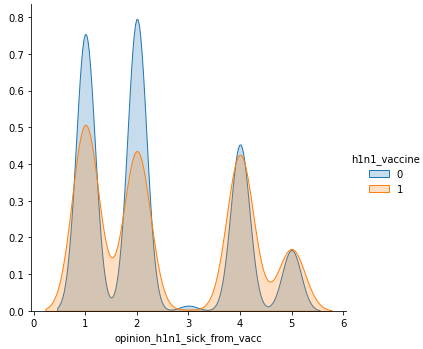
In [77]:
```
for p in pcols_1:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```



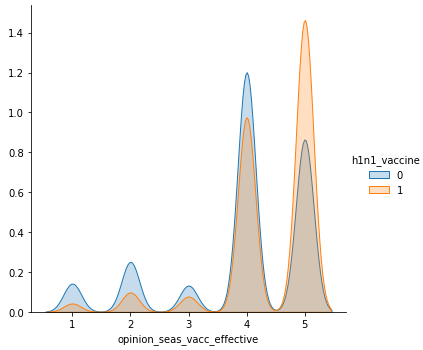


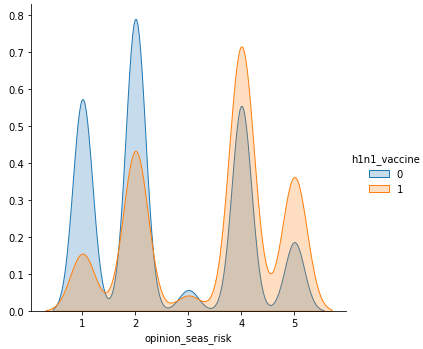


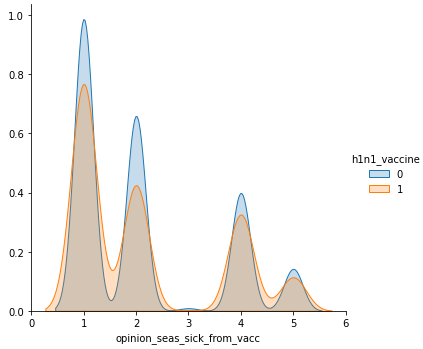




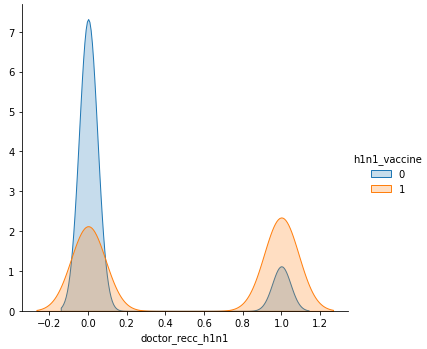
In [78]:
```
for p in pcols_2:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

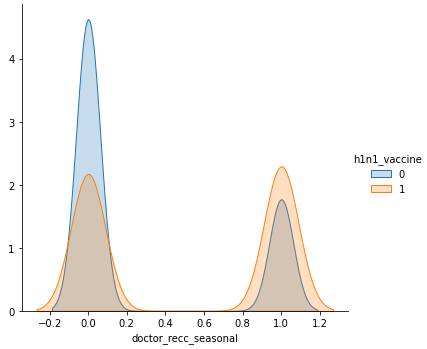


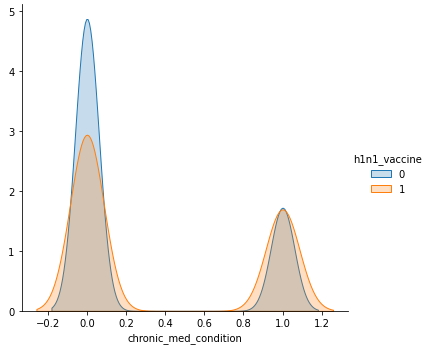


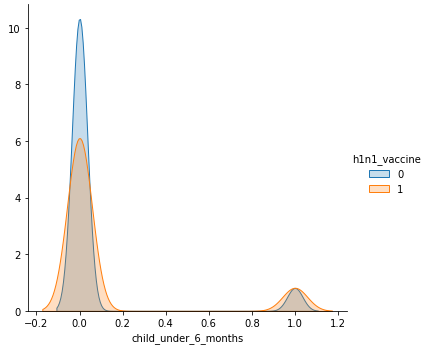


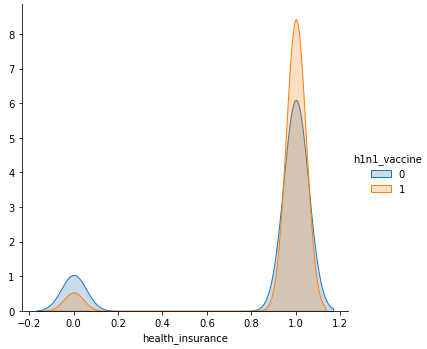
In [79]:
```
for p in pcols_3:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```



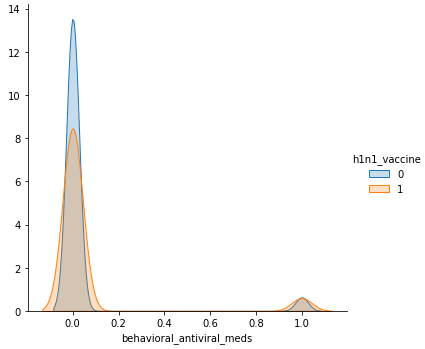


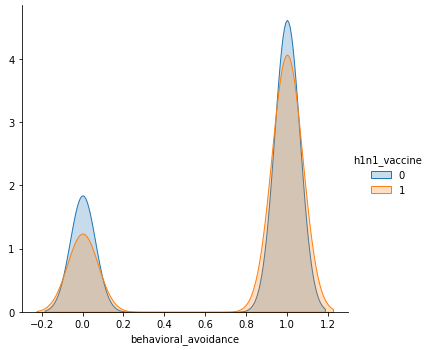


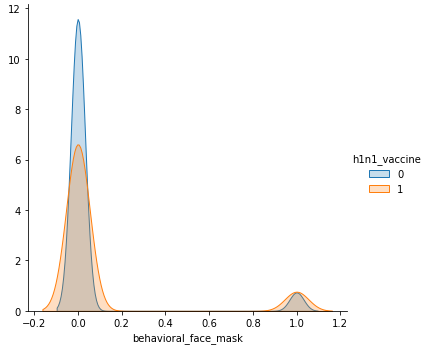


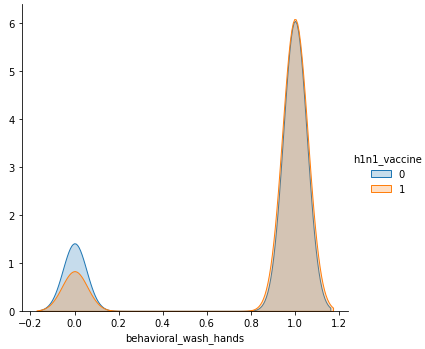


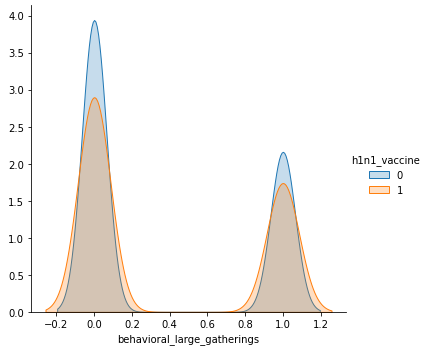
In [80]:
```
for p in pcols_4:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

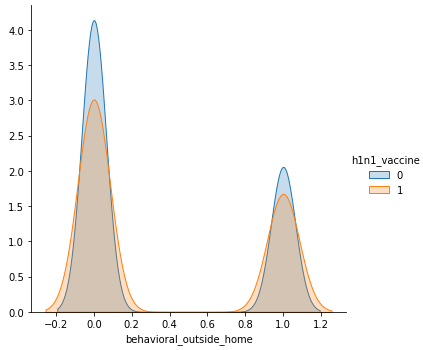


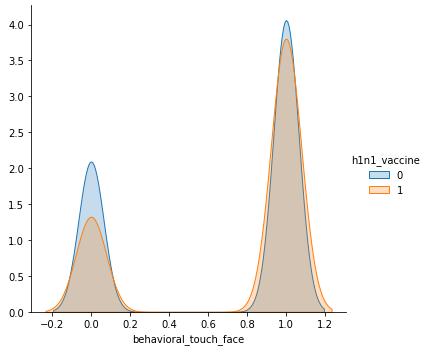




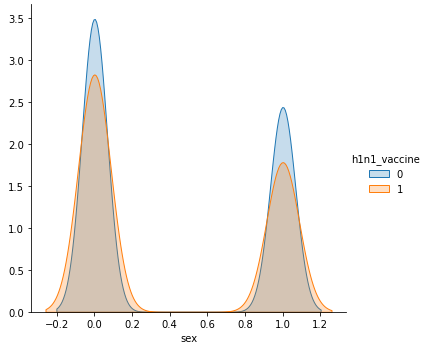


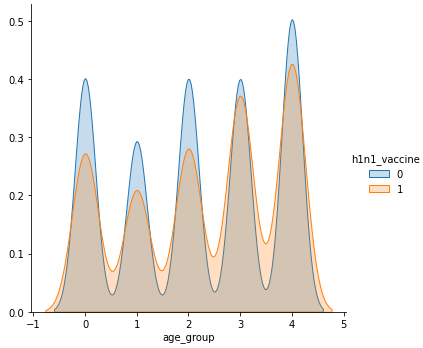

h1n1_vaccine
0
1
behavioral_large_gatherings

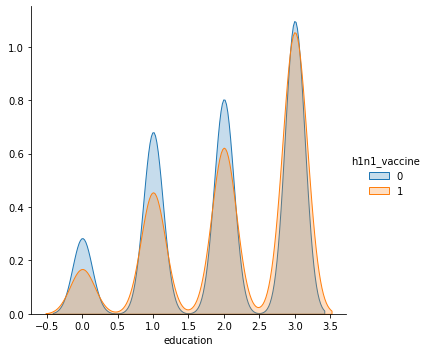

h1n1_vaccine
0
1
behavioral_outside_home

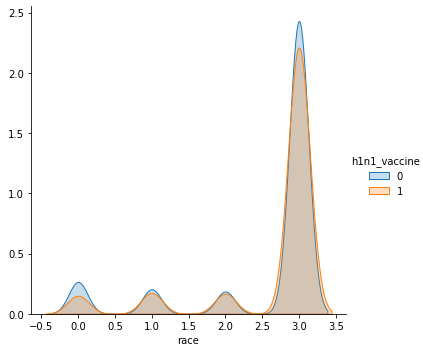

h1n1_vaccine
0
1
behavioral_touch_face

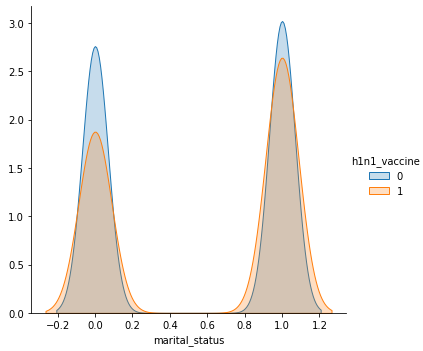
In [81]:
```
for p in pcols_5:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```





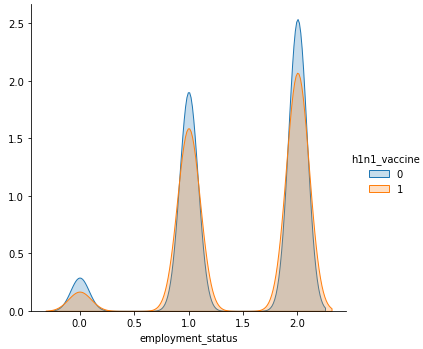


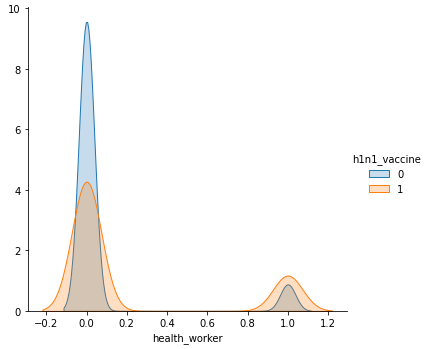


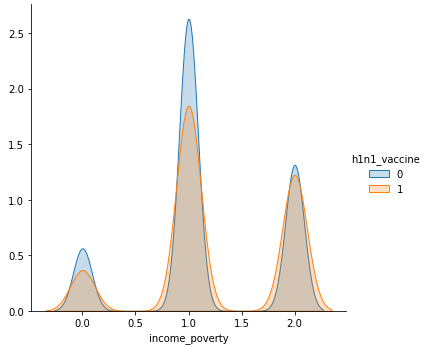


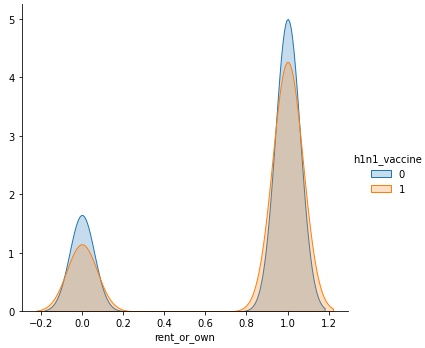
In [84]:
```
# Issues with the pcols_6 due to inclusion of text in 2 features so cut those out.
pcols_6b = ['employment_status', 'health_worker', 'income_poverty', 'rent_or_own']
```

In [85]:
```
for p in pcols_6b:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

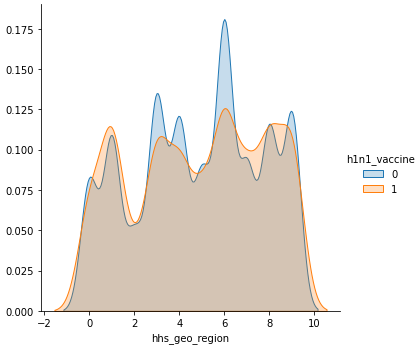


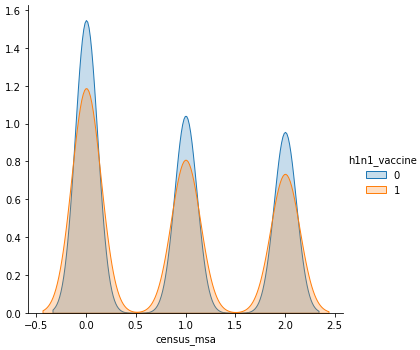


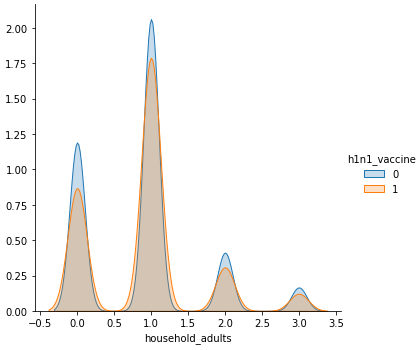


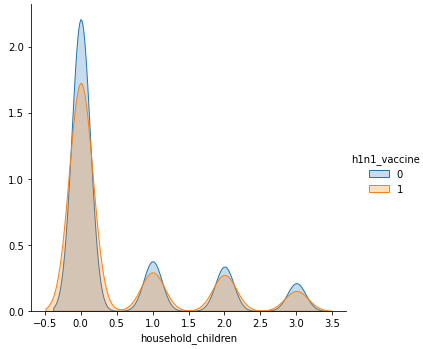


In [83]:
```
for p in pcols_7:
    (sns.FacetGrid(raw_3, hue='h1n1_vaccine',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```



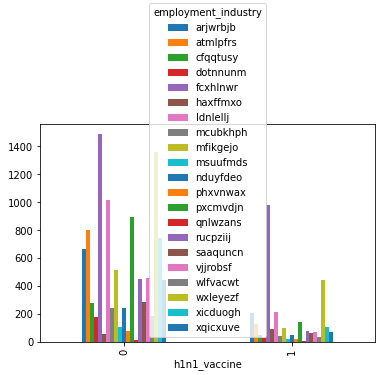






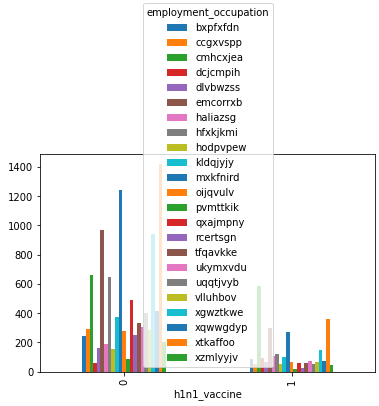
In [87]:
```
# Alternative plot for employment variables?
pd.crosstab(raw_3['h1n1_vaccine'],raw_3['employment_industry']).plot.bar()
```

Out[87]: <AxesSubplot:xlabel='h1n1_vaccine'>



In [88]:
```
pd.crosstab(raw_3['h1n1_vaccine'],raw_3['employment_occupation']).plot.bar()
```

Out[88]: <AxesSubplot:xlabel='h1n1_vaccine'>



Observations on the distribution plots

This corroborated what we saw in the earlier plots. The largest differences between or target classes appear for the opinion questions / features and a few of the hea
related variables. Overall, it is appearing that there is adequate variation between the target variable classes to get some meaningful classification modeling result

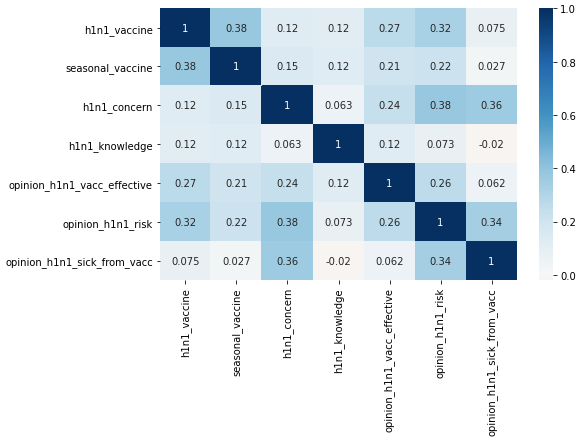
Look at correlations for each feature

Curious to see the level of correlation between each of the features.

In [ ]:
```
# Moving this listing of feature groups here for easy reference:
# Creating 7 lists of conceptually similar features.
pcols_1 = ['h1n1_concern', 'h1n1_knowledge', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk','opinion_h1n1_sick_from_vacc']
pcols_2 = ['opinion_seas_vacc_effective','opinion_seas_risk', 'opinion_seas_sick_from_vacc']
pcols_3 = ['doctor_recc_h1n1', 'doctor_recc_seasonal', 'chronic_med_condition', 'child_under_6_months', 'health_insurance']
pcols_4 = ['behavioral_antiviral_meds', 'behavioral_avoidance','behavioral_face_mask', 'behavioral_wash_hands','behavioral_large_gatherings', 'behavioral_outside_home
pcols_5 = ['sex', 'age_group', 'education', 'race', 'marital_status']
pcols_6 = ['employment_status', 'health_worker', 'income_poverty', 'rent_or_own', 'employment_occupation', 'employment_industry']
pcols_7 = ['hhs_geo_region', 'census_msa', 'household_adults', 'household_children']
```

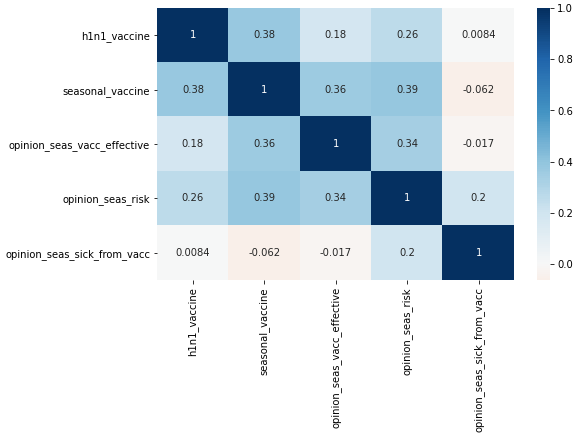
In [91]:
```
# Examine correlations via small groups / df - including the 2 target variables within each.
corr1 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'h1n1_concern', 'h1n1_knowledge', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk','opinion_h1n1_sick_from_vacc']
plt.figure(figsize=(8,5))
sns.heatmap(corr1, cmap='RdBu', annot=True, center=0)
```

Out[91]: <AxesSubplot:>



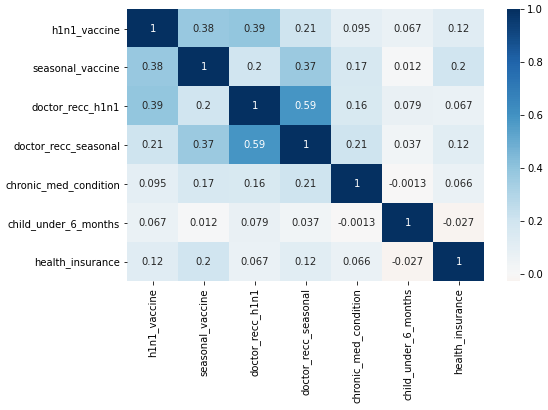
In [94]:
```
corr2 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'opinion_seas_vacc_effective','opinion_seas_risk', 'opinion_seas_sick_from_vacc']].corr()
plt.figure(figsize=(8,5))
sns.heatmap(corr2, cmap='RdBu', annot=True, center=0)
```

Out[94]: <AxesSubplot:>



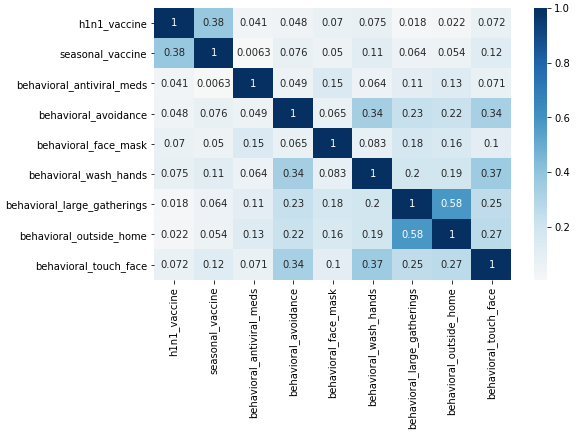
In [95]:
```
corr3 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'doctor_recc_h1n1', 'doctor_recc_seasonal', 'chronic_med_condition', 'child_under_6_months', 'health_insurance']].c
plt.figure(figsize=(8,5))
sns.heatmap(corr3, cmap='RdBu', annot=True, center=0)
```

Out[95]: <AxesSubplot:>



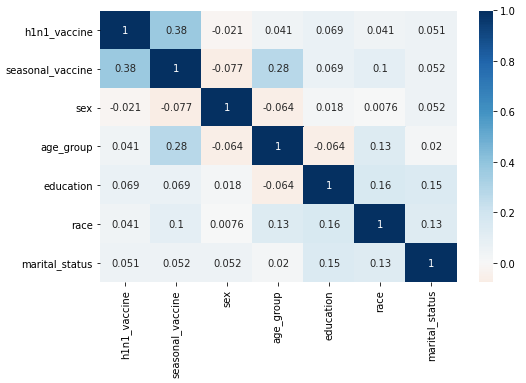
In [96]:
```
corr4 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'behavioral_antiviral_meds', 'behavioral_avoidance','behavioral_face_mask', 'behavioral_wash_hands','behavioral_lar
plt.figure(figsize=(8,5))
sns.heatmap(corr4, cmap='RdBu', annot=True, center=0)
```

Out[96]: <AxesSubplot:>



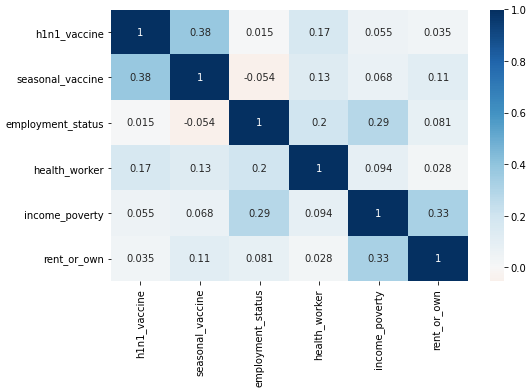
In [97]:
```
corr5 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'sex', 'age_group', 'education', 'race', 'marital_status']].corr()
plt.figure(figsize=(8,5))
sns.heatmap(corr5, cmap='RdBu', annot=True, center=0)
```

Out[97]: <AxesSubplot:>



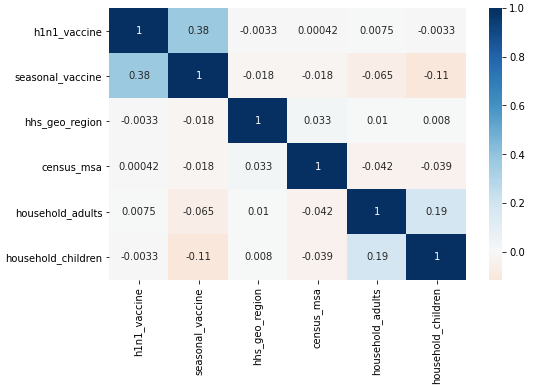
In [98]:
```
corr6 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'employment_status', 'health_worker', 'income_poverty', 'rent_or_own', 'employment_occupation', 'employment_industr
plt.figure(figsize=(8,5))
sns.heatmap(corr6, cmap='RdBu', annot=True, center=0)
```

Out[98]: <AxesSubplot:>

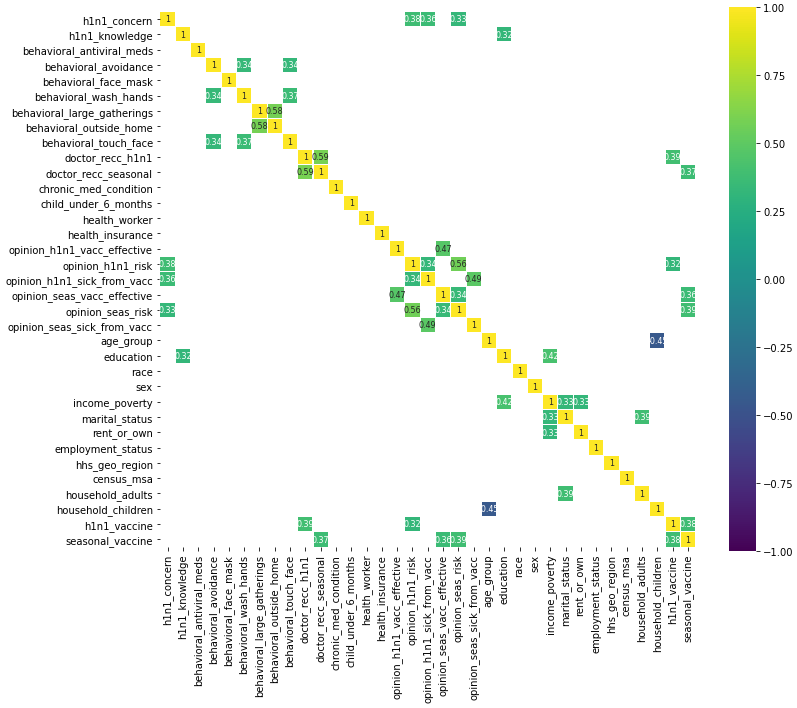


In [99]:
```
corr7 = raw_3[['h1n1_vaccine', 'seasonal_vaccine', 'hhs_geo_region', 'census_msa', 'household_adults', 'household_children']].corr()
plt.figure(figsize=(8,5))
sns.heatmap(corr7, cmap='RdBu', annot=True, center=0)
```

Out[99]: <AxesSubplot:>



In [117]:
```
# Try this alternative version of correlation grid where a correlation value can be set and only those above that are shown.
corr = raw_3.drop('respondent_id', axis=1).corr()
plt.figure(figsize=(12, 10))

sns.heatmap(corr[(corr >= 0.3) | (corr <= -0.4)],
            cmap='viridis', vmax=1.0, vmin=-1.0, linewidths=0.1,
            annot=True, annot_kws={"size": 8}, square=True);
```



Observations on the correlation matrices

Most of the correlation values were fairly low. Only 2 variables had a correlation with the target varialble greater than 0.30 and that was opinion_h1n1_risk (0.32) a
doctor_recc_h1n1 (0.39). And even looking at correlations with features other than the target, only 2 variables were above 0.50 = doctor_recc_h1n1 and doctor_recc_sea
and behavioral_large_gatherings and behavioral_outside_home (0.58). There were a hndful of others with correlation values in the 30 to 40 range.

Some data shaping...

Need to handle those last 2 features (employment-type)... will simplify it down to top 8-12 classes and then assign the rest to an "other" class.

In [100]:
```
raw_3.head()
```

Out[100]:

	respondent_id	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	dc
0	0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	
1	1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	
2	2	1.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	
3	3	1.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	0.0	
4	4	2.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0	1.0	

In [102]:
```
raw_3['employment_occupation'].value_counts(normalize=True)*100
```

Out[102]:
```
xtkaffoo    13.432047
mxkfnird    11.399864
emcorrxb     9.594319
cmhcxjea     9.420564
xgwztkwe     8.174058
hfxkjkmi     5.786810
qxajmpny     4.139911
xqwwgdyp     3.663972
kldqjyjy     3.543099
uqqtjvyb     3.414671
tfqavkke     2.931178
ukymxvdu     2.810304
vlluhbov     2.674322
oijqvulv     2.598776
ccgxvspp     2.576112
bxpfxfdn     2.500567
haliazsg     2.236156
rcertsgn     2.085065
xzmlyyjv     1.873536
dlvbwzss     1.714890
hodpvpew     1.571353
dcjcmpih     1.118078
pvmttkik     0.740349
Name: employment_occupation, dtype: float64
```

In [103]:
```
raw_3['employment_industry'].value_counts(normalize=True)*100
```

Out[103]:
```
fcxhlnwr    18.449578
wxleyezf    13.485834
ldnlellj     9.202362
pxcmvdjn     7.752112
atmlpfrs     6.922329
arjwrbjb     6.511176
xicduogh     6.361666
mfikgejo     4.589968
vjjrobsf     3.939598
rucpziij     3.909696
xqicxuve     3.819990
saaquncn     2.526725
cfqqtusy     2.429543
nduyfdeo     2.137998
mcubkhph     2.055767
wlfvacwt     1.607236
dotnnunm     1.502579
haxffmxo     1.106377
msuufmds     0.926964
phxvnwax     0.665321
qnlwzans     0.097182
Name: employment_industry, dtype: float64
```

In [104]:
```
#Get rid of 2 columns - decide to use employment industry and drop occupation
columns_to_cut = ['respondent_id','employment_occupation']
raw_4 = raw_3.drop(columns_to_cut, axis=1)
raw_4.shape
```

Out[104]:
```
(26707, 36)
```

In [105]:
```
# Reassign values to employment_industry as many of the tail end classes have few values
ind = {'fcxhlnwr': 0,'wxleyezf': 1,'ldnlellj': 2, 'pxcmvdjn': 3,'atmlpfrs': 4,'arjwrbjb': 5,'xicduogh': 6, 'mfikgejo': 7,'vjjrobsf': 8, 'rucpziij': 9,'xqicxuve': 10,
raw_4['employment_industry'] = raw_4['employment_industry'].map(ind)
raw_4.head(2)
```

Out[105]:

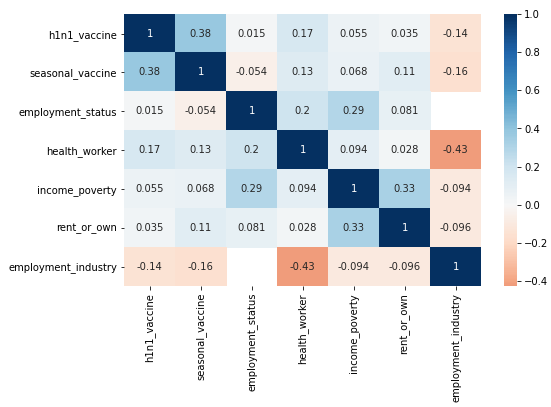
	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behavioral_large_gatherings	behavioral_outside_home	behavioral_touch_face	doctor_recc_h1n1
0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	0.0
1	3.0	2.0	0.0	1.0	0.0	1.0	0.0	1.0	1.0	0.0

In [107]:
```
# Run through the EDA pieces for employment_industry... as these were missing from above.
raw_4['employment_industry'].value_counts(normalize=True)*100
```

Out[107]:
```
0.0     18.449578
11.0    15.055693
1.0     13.485834
2.0      9.202362
3.0      7.752112
4.0      6.922329
5.0      6.511176
6.0      6.361666
7.0      4.589968
8.0      3.939598
9.0      3.909696
10.0     3.819990
Name: employment_industry, dtype: float64
```

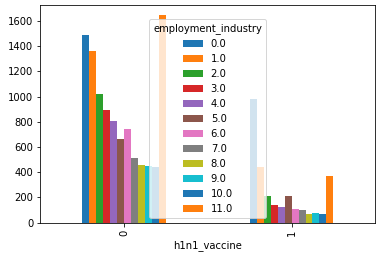
In [108]:
```
corr6 = raw_4[['h1n1_vaccine', 'seasonal_vaccine', 'employment_status', 'health_worker', 'income_poverty', 'rent_or_own', 'employment_industry']].corr()
plt.figure(figsize=(8,5))
sns.heatmap(corr6, cmap='RdBu', annot=True, center=0)
```

Out[108]:
```
<AxesSubplot:>
```



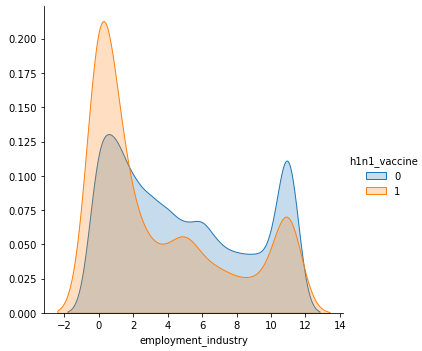
In [109]:
```
pd.crosstab(raw_4['h1n1_vaccine'],raw_4['employment_industry']).plot.bar()
```

Out[109]:
```
<AxesSubplot:xlabel='h1n1_vaccine'>
```



In [113]:
```
sns.FacetGrid(raw_4, hue='h1n1_vaccine',height=5).map(sns.kdeplot, 'employment_industry', shade=True).add_legend()
```

Out[113]:
```
<seaborn.axisgrid.FacetGrid at 0x1a2b73a400>
```



In [110]:
```
raw_4.groupby('h1n1_vaccine')['employment_industry'].describe()
```

Out[110]:

h1n1_vaccine	count	mean	std	min	25%	50%	75%	max
0	10474.0	4.854974	3.865996	0.0	1.0	4.0	8.0	11.0
1	2903.0	3.505339	3.945689	0.0	0.0	2.0	6.0	11.0

In [111]:
```
raw_4.groupby('seasonal_vaccine')['employment_industry'].describe()
```

Out[111]:

seasonal_vaccine	count	mean	std	min	25%	50%	75%	max
0	7715.0	5.085807	3.837022	0.0	2.0	4.0	9.0	11.0
1	5662.0	3.848463	3.926502	0.0	0.0	2.0	7.0	11.0

In [112]:
```
(raw_4.groupby('h1n1_vaccine')['employment_industry'].value_counts(normalize=True)*100)
```

Out[112]:
```
h1n1_vaccine  employment_industry
0             11.0                   15.696009
              0.0                    14.187512
              1.0                    12.994081
              2.0                     9.728852
              3.0                     8.535421
              4.0                     7.657056
              6.0                     7.122398
              5.0                     6.329960
              7.0                     4.907390
              8.0                     4.353638
              9.0                     4.286805
              10.0                    4.200878
1             0.0                    33.827075
              1.0                    15.260076
              11.0                   12.745436
              2.0                     7.302790
              5.0                     7.165002
              3.0                     4.925939
              4.0                     4.271443
              6.0                     3.616948
              7.0                     3.444712
              9.0                     2.549087
              8.0                     2.445746
              10.0                    2.445746
Name: employment_industry, dtype: float64
```

In [114]:
```
raw_5 = raw_4
```

In [115]:
```
# save raw_5 full df as csv file for later use - modeling
raw_5.to_csv(r'df_5.csv')
```

In [ ]:
```

```