Vaccine Project

Business Understanding

The client is a leader in the field of health care. The client has resources at their disposal that can be used to encourage non-vaccinated persons to become vaccinated. It would be beneficial to the client to know what groups of persons are less likely to be vaccinated in order to make the best use of the client's resources. Therefore, it would be helpful for the client to have a model that could predict which persons are less likely to be vaccinated based on various known factors, related to the person's background, views and behaviors, and also it would be helpful to know more generally which of these factors leads a group to be less or more likely to be vaccinated. This model and knowledge would facilitate efforts to reach persons individually and as groups in order to efficiently encourage vaccination.

Data Understanding

The data comes from the National 2009 H1N1 Flu Survey conducted by the United States after the outbreak of the virus in 2009. The survey covers various topics included one's background, views and behaviors. The survey also covers whether one has been vaccinated against the H1N1 virus, which will be the target variable for this project. More specifically, the potential predictor variables include socio-economic related factors, views about vaccines, and health-related behaviors and statuses (e.g., health insurance and doctor recommendation.) Given that H1N1 can be categorized as a risky virus, the data, though H1N1 specific, can be thought of as analagous to any risky virus such that insights from the data will be applicable to future viral outbreaks.

About half the features are categorical in nature as opposed to numerical. (Of the float and integer type features, about half are binary/categorical.) The columns with most missing data have about 10,000 of 27,000 missing. About 21% of respondents received the H1N1 vaccine.

Features with signficant correlation to the target variable are doctor reccomendation, opinion of virus risk, and opinion of vaccine effective.

See the data (./data).

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

In [2]:
```
dataX = pd.read_csv('./data/training_set_features.csv')
datay = pd.read_csv('./data/training_set_labels.csv')
dataX.head()
```

Out[2]:

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

5 rows × 36 columns

In [3]:
```
datay.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]:
```
ata = pd.concat([datay, dataX], axis = 1) #Combining the feature and label data into one dataframe to faciliate preparation:
```

Drop unneeded columns including those specific to the seasonal flu.

In [5]:
```
eas_vacc_effective', 'opinion_seas_risk', 'opinion_seas_sick_from_vacc', 'doctor_recc_seasonal', 'seasonal_vaccine'], axis=1)
```

In [6]:
```
data.head()
```

Out[6]:

	h1n1_vaccine	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behaviora
0	0	1.0	0.0	0.0	0.0	0.0	0.0	
1	0	3.0	2.0	0.0	1.0	0.0	1.0	
2	0	1.0	1.0	0.0	1.0	0.0	0.0	
3	0	1.0	1.0	0.0	1.0	0.0	1.0	
4	0	2.0	1.0	0.0	1.0	0.0	1.0	

5 rows × 32 columns

In [7]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26707 entries, 0 to 26706
Data columns (total 32 columns):
 #   Column                       Non-Null Count  Dtype  
---  ------                       --------------  -----  
 0   h1n1_vaccine                 26707 non-null  int64  
 1   h1n1_concern                 26615 non-null  float64
 2   h1n1_knowledge               26591 non-null  float64
 3   behavioral_antiviral_meds    26636 non-null  float64
 4   behavioral_avoidance         26499 non-null  float64
 5   behavioral_face_mask         26688 non-null  float64
 6   behavioral_wash_hands        26665 non-null  float64
 7   behavioral_large_gatherings  26620 non-null  float64
 8   behavioral_outside_home      26625 non-null  float64
 9   behavioral_touch_face        26579 non-null  float64
 10  doctor_recc_h1n1             24547 non-null  float64
 11  chronic_med_condition        25736 non-null  float64
 12  child_under_6_months         25887 non-null  float64
 13  health_worker                25903 non-null  float64
 14  health_insurance             14433 non-null  float64
 15  opinion_h1n1_vacc_effective  26316 non-null  float64
 16  opinion_h1n1_risk            26319 non-null  float64
 17  opinion_h1n1_sick_from_vacc  26312 non-null  float64
 18  age_group                    26707 non-null  object 
 19  education                    25300 non-null  object 
 20  race                         26707 non-null  object 
 21  sex                          26707 non-null  object 
 22  income_poverty               22284 non-null  object 
 23  marital_status               25299 non-null  object 
 24  rent_or_own                  24665 non-null  object 
 25  employment_status            25244 non-null  object 
 26  hhs_geo_region               26707 non-null  object 
 27  census_msa                   26707 non-null  object 
 28  household_adults             26458 non-null  float64
 29  household_children           26458 non-null  float64
 30  employment_industry          13377 non-null  object 
 31  employment_occupation        13237 non-null  object 
dtypes: float64(19), int64(1), object(12)
memory usage: 6.5+ MB
```

In [8]:
```
data.describe()
```

Out[8]:

	h1n1_vaccine	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	beha
count	26707.000000	26615.000000	26591.000000	26636.000000	26499.000000	26688.000000	26665.000000	
mean	0.212454	1.618486	1.262532	0.048844	0.725612	0.068982	0.825614	
std	0.409052	0.910311	0.618149	0.215545	0.446214	0.253429	0.379448	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	0.000000	1.000000	1.000000	0.000000	0.000000	0.000000	1.000000	
50%	0.000000	2.000000	1.000000	0.000000	1.000000	0.000000	1.000000	
75%	0.000000	2.000000	2.000000	0.000000	1.000000	0.000000	1.000000	
max	1.000000	3.000000	2.000000	1.000000	1.000000	1.000000	1.000000	

In [9]:
```
data.iloc[:,8:17].describe()
```

Out[9]:

	behavioral_outside_home	behavioral_touch_face	doctor_recc_h1n1	chronic_med_condition	child_under_6_months	health_worker	health_insurance
count	26625.000000	26579.000000	24547.000000	25736.000000	25887.000000	25903.000000	14433.00000
mean	0.337315	0.677264	0.220312	0.283261	0.082590	0.111918	0.87972
std	0.472802	0.467531	0.414466	0.450591	0.275266	0.315271	0.32530
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.00000
25%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.00000
50%	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	1.00000
75%	1.000000	1.000000	0.000000	1.000000	0.000000	0.000000	1.00000
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.00000

Of the float and integer type features, about half are binary/categorical. The columns with most missing data have about 10,000 of 27,000 missing. About 21% of respondents received the H1N1 vaccine.

Some of the columns are not self-explanatory: census_msa, hhs_geo_region.

In [10]:
```
data.census_msa.value_counts()
```

Out[10]:
```
MSA, Not Principle  City    11645
MSA, Principle City          7864
Non-MSA                      7198
Name: census_msa, dtype: int64
```

Metropolitan Statistical Area, it seems that these designation roughly mean: {MSA, Not Principle City: suburban; MSA, Principle City: urban; Non-MSA: rural }

hhs_geo_region, employment_industry, and employment_occupation are coded as random strings. Thus without decoding, they will provide little information.

In [11]:
```
data.hhs_geo_region.value_counts()
```

Out[11]:
```
lzgpxyit    4297
fpwskwrf    3265
qufhixun    3102
oxchjgsf    2859
kbazzjca    2858
bhuqouqj    2846
mlyzmhmf    2243
lrircsnp    2078
atmpeygn    2033
dqpwygqj    1126
Name: hhs_geo_region, dtype: int64
```

In [12]:
```
data.employment_industry.value_counts()
```

Out[12]:
```
fcxhlnwr    2468
wxleyezf    1804
ldnlellj    1231
pxcmvdjn    1037
atmlpfrs     926
arjwrbjb     871
xicduogh     851
mfikgejo     614
vjjrobsf     527
rucpziij     523
xqicxuve     511
saaquncn     338
cfqqtusy     325
nduyfdeo     286
mcubkhph     275
wlfvacwt     215
dotnnunm     201
haxffmxo     148
msuufmds     124
phxvnwax      89
qnlwzans      13
Name: employment_industry, dtype: int64
```

In [13]:
```
data.employment_occupation.value_counts()
```

Out[13]:
```
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
```

In [14]:
```
data.education.value_counts()
```

Out[14]:
```
College Graduate    10097
Some College         7043
12 Years             5797
< 12 Years           2363
Name: education, dtype: int64
```

In [15]:
```
data.sex.value_counts()
```

Out[15]:
```
Female    15858
Male      10849
Name: sex, dtype: int64
```

In [16]:
```
data.race.value_counts()
```

Out[16]:
```
White                21222
Black                 2118
Hispanic              1755
Other or Multiple     1612
Name: race, dtype: int64
```

In [17]:
```
data.age_group.value_counts()
```

Out[17]:
```
65+ Years        6843
55 - 64 Years    5563
45 - 54 Years    5238
18 - 34 Years    5215
35 - 44 Years    3848
Name: age_group, dtype: int64
```

In [18]:
```
data.income_poverty.value_counts()
```

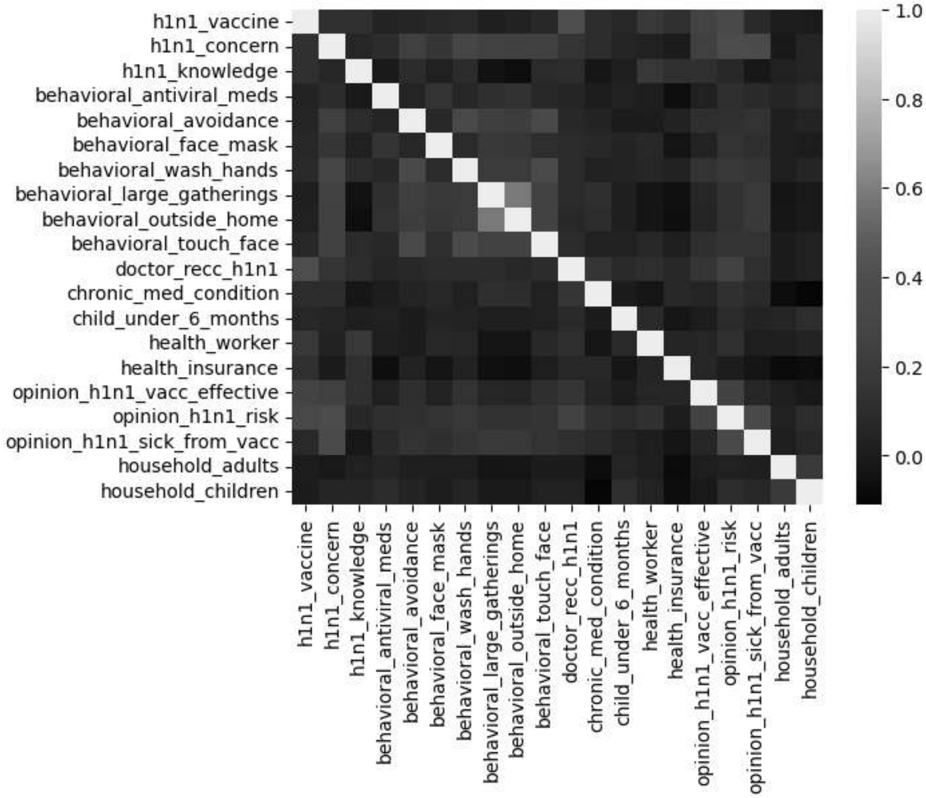
Out[18]:
```
<= $75,000, Above Poverty    12777
> $75,000                     6810
Below Poverty                 2697
Name: income_poverty, dtype: int64
```

Above, the survey seems to be fairly cross-sectional in terms of various background factors.

Check correlations with target variable and for multicollinearity.

In [19]:
```
sns.heatmap(data.corr())
```

Out[19]: <AxesSubplot:>




```
The potential predictor variables don't appear highly correlated amonst each other.  Significant correlations appear to be:
Doctor reccomendation, opinion of virus risk, opinion of vaccine effective.
```

```
Create dummy variables for each categorical variable so correlations/other calculations can be made.
```

In [20]:
```
datawd = pd.get_dummies(data)
```

In [ ]:
```

```

In [21]:
```
datawd.head()
```

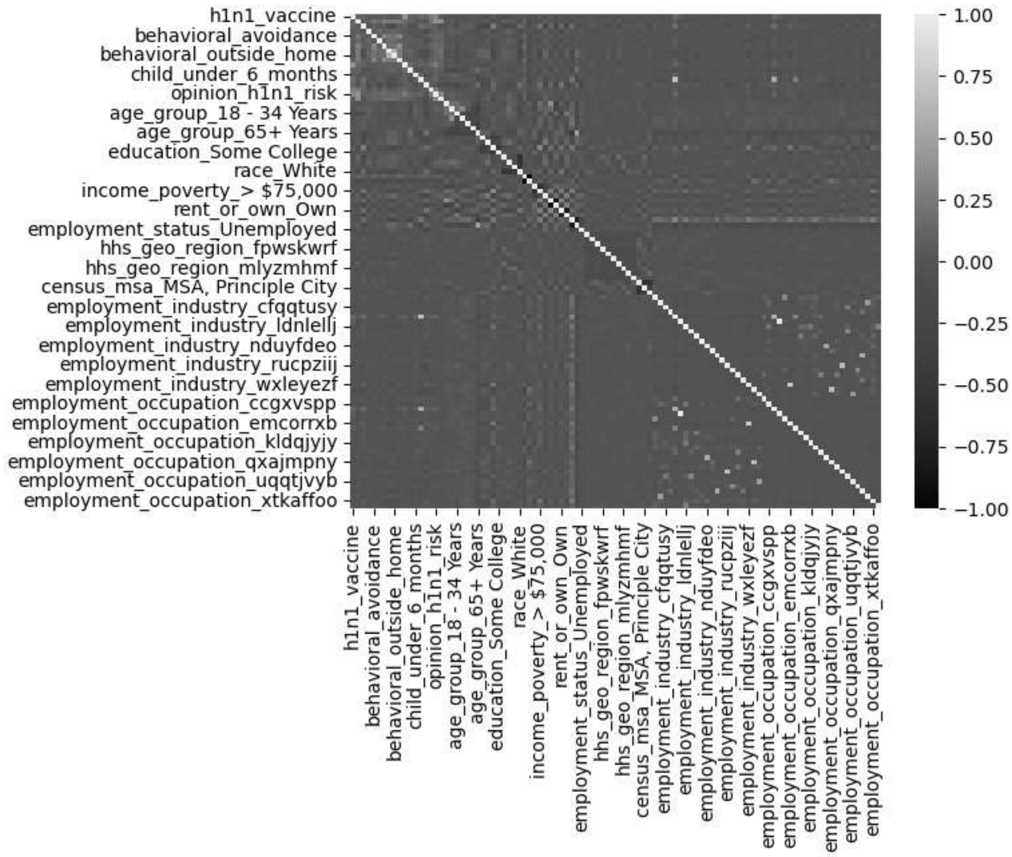
Out[21]:

	h1n1_vaccine	h1n1_concern	h1n1_knowledge	behavioral_antiviral_meds	behavioral_avoidance	behavioral_face_mask	behavioral_wash_hands	behaviora
0	0	1.0	0.0	0.0	0.0	0.0	0.0	
1	0	3.0	2.0	0.0	1.0	0.0	1.0	
2	0	1.0	1.0	0.0	1.0	0.0	0.0	
3	0	1.0	1.0	0.0	1.0	0.0	1.0	
4	0	2.0	1.0	0.0	1.0	0.0	1.0	

5 rows × 102 columns

In [22]:
```
sns.heatmap(datawd.corr())
```

Out[22]: <AxesSubplot:>



Above, most dummy variables don't seem highly correlated to target.

```
Find all correlations over .25:
```

In [23]:
```
datawdcor = datawd.corr()
```

In [24]:
```
corrs=[]

for i in range(len(datawdcor)):#iter over rows
    for j in range(len(datawdcor)):#iter over cols
        if abs((datawdcor[datawdcor.columns[i]][datawdcor.columns[j]])>.25) & (datawdcor[datawdcor.columns[i]][datawdcor.colu
            tup = datawdcor[datawdcor.columns[i]][datawdcor.columns[j]],datawdcor.columns[i], datawdcor.columns[j]
            corrs.append(tup)
corrs
```

Out[24]:
```
[(0.39389048123870213, 'h1n1_vaccine', 'doctor_recc_h1n1'),
 (0.26934700167297715, 'h1n1_vaccine', 'opinion_h1n1_vacc_effective'),
 (0.32326466034778245, 'h1n1_vaccine', 'opinion_h1n1_risk'),
 (0.2935651485017993, 'h1n1_concern', 'behavioral_wash_hands'),
 (0.2550310154400835, 'h1n1_concern', 'behavioral_large_gatherings'),
 (0.3770328126230567, 'h1n1_concern', 'opinion_h1n1_risk'),
 (0.3600697383652842, 'h1n1_concern', 'opinion_h1n1_sick_from_vacc'),
 (0.26208698574014516, 'h1n1_knowledge', 'education_College Graduate'),
 (0.3381295192965343, 'behavioral_avoidance', 'behavioral_wash_hands'),
 (0.3353354496707589, 'behavioral_avoidance', 'behavioral_touch_face'),
 (0.2935651485017993, 'behavioral_wash_hands', 'h1n1_concern'),
 (0.3381295192965343, 'behavioral_wash_hands', 'behavioral_avoidance'),
 (0.36506407130000645, 'behavioral_wash_hands', 'behavioral_touch_face'),
 (0.2550310154400835, 'behavioral_large_gatherings', 'h1n1_concern'),
 (0.5840845791409999,
  'behavioral_large_gatherings',
  'behavioral_outside_home'),
 (0.2536834927481906, 'behavioral_large_gatherings', 'behavioral_touch_face'),
 (0.5840845791409999,
```

In [25]:
```python
#Convert list of tuples to DF.
corrlist =[]
var1 =[]
var2 =[]
for i in corrs:
    corrlist.append(i[0])
    var1.append(i[1])
    var2.append(i[2])
corrdf = pd.DataFrame([corrlist,var1, var2]).transpose()
```

Find signficant correlations with target variable.

In [26]:
```python
corrdf.loc[(corrdf[1]=='h1n1_vaccine')|(corrdf[2]=='h1n1_vaccine')]
```

Out[26]:

	0	1	2
0	0.39389	h1n1_vaccine	doctor_recc_h1n1
1	0.269347	h1n1_vaccine	opinion_h1n1_vacc_effective
2	0.323265	h1n1_vaccine	opinion_h1n1_risk
22	0.39389	doctor_recc_h1n1	h1n1_vaccine
27	0.269347	opinion_h1n1_vacc_effective	h1n1_vaccine
29	0.323265	opinion_h1n1_risk	h1n1_vaccine

Significant correlations are: Doctor reccomendation, opinion of virus risk, opinion of vaccine effective.

Check these potential predictors correlations amongst each other

In [27]:
```python
corrdf.tail(30)
```

Out[27]:

	0	1	2
66	0.254746	employment_industry_ldnlellj	employment_occupation_kldqjyjy
67	0.29149	employment_industry_ldnlellj	employment_occupation_xzmlyyjv
68	0.313859	employment_industry_mcubkhph	employment_occupation_ukymxvdu
69	0.547199	employment_industry_nduyfdeo	employment_occupation_pvmttkik
70	0.57704	employment_industry_pxcmvdjn	employment_occupation_xgwztkwe
71	0.676177	employment_industry_rucpziij	employment_occupation_tfqavkke
72	0.352989	employment_industry_saaquncn	employment_occupation_vlluhbov
73	0.270303	employment_industry_vjjrobsf	employment_occupation_oijqvulv
74	0.265018	employment_industry_wxleyezf	employment_status_Employed
75	0.765692	employment_industry_wxleyezf	employment_occupation_emcorrxb
76	0.68051	employment_industry_xicduogh	employment_occupation_qxajmpny
77	0.460559	employment_industry_xqicxuve	employment_occupation_uqqtjvyb
78	0.566283	employment_occupation_cmhcxjea	health_worker
79	0.598581	employment_occupation_cmhcxjea	employment_industry_fcxhlnwr
80	0.343521	employment_occupation_dlvbwzss	employment_industry_arjwrbjb
81	0.765692	employment_occupation_emcorrxb	employment_industry_wxleyezf
82	0.263106	employment_occupation_haliazsg	health_worker
83	0.304601	employment_occupation_haliazsg	employment_industry_fcxhlnwr
84	0.254746	employment_occupation_kldqjyjy	employment_industry_ldnlellj
85	0.270303	employment_occupation_oijqvulv	employment_industry_vjjrobsf
86	0.547199	employment_occupation_pvmttkik	employment_industry_nduyfdeo
87	0.68051	employment_occupation_qxajmpny	employment_industry_xicduogh
88	0.676177	employment_occupation_tfqavkke	employment_industry_rucpziij
89	0.313859	employment_occupation_ukymxvdu	employment_industry_mcubkhph
90	0.460559	employment_occupation_uqqtjvyb	employment_industry_xqicxuve
91	0.352989	employment_occupation_vlluhbov	employment_industry_saaquncn
92	0.57704	employment_occupation_xgwztkwe	employment_industry_pxcmvdjn
93	0.473896	employment_occupation_xqwwgdyp	employment_industry_atmlpfrs
94	0.262964	employment_occupation_xtkaffoo	employment_status_Employed
95	0.29149	employment_occupation_xzmlyyjv	employment_industry_ldnlellj

The potential predictor variables are not highly correlated amonst each other.

Data preparation

Separate predictor variables and target variables from unused data, drop rows with missing values and then split both into train and test sets.

In [28]:
```
from sklearn.model_selection import train_test_split
```

In [29]:
```

dataPT= datawd.loc[:,['doctor_recc_h1n1', 'opinion_h1n1_risk', 'opinion_h1n1_vacc_effective', 'h1n1_vaccine']]
```

In [30]:
```
dataPT.describe()
```

Out[30]:

	doctor_recc_h1n1	opinion_h1n1_risk	opinion_h1n1_vacc_effective	h1n1_vaccine
count	24547.000000	26319.000000	26316.000000	26707.000000
mean	0.220312	2.342566	3.850623	0.212454
std	0.414466	1.285539	1.007436	0.409052
min	0.000000	1.000000	1.000000	0.000000
25%	0.000000	1.000000	3.000000	0.000000
50%	0.000000	2.000000	4.000000	0.000000
75%	0.000000	4.000000	5.000000	0.000000
max	1.000000	5.000000	5.000000	1.000000

In [32]:
```
dataPT = dataPT.dropna(axis=0)
```

In [33]:
```
dataPT.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 24246 entries, 0 to 26706
Data columns (total 4 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   doctor_recc_h1n1             24246 non-null  float64
 1   opinion_h1n1_risk            24246 non-null  float64
 2   opinion_h1n1_vacc_effective  24246 non-null  float64
 3   h1n1_vaccine                 24246 non-null  int64
dtypes: float64(3), int64(1)
memory usage: 947.1 KB
```

In [34]:
```
y = dataPT['h1n1_vaccine']
X= dataPT.drop('h1n1_vaccine',axis=1)
```

In [35]:
```
np.shape(y), np.shape(X)
```

Out[35]: ((24246,), (24246, 3))

In [36]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y)
```

In [37]:
```
np.shape(X_test), np.shape(y_train)
```

Out[37]: ((6062, 3), (18184,))

Data Modeling

In the data modeling section, I start from a baseline logistic regression using three features and the response variable (whether the person has received the H1N1 vaccine). From there, I explore non-parametric models, starting with a fairly simple decision tree model. Based on the the results from this model, a more complex tree model is fitted and evaluated to achieve better results.

In [38]:
```
from sklearn.linear_model import LogisticRegression
```

In [39]:
```
reg = LogisticRegression(C=1e5, solver = "liblinear")
```

In [40]:
```
reg.fit(X_train, y_train)
```

Out[40]: LogisticRegression(C=100000.0, solver='liblinear')

Check accuracies below:

In [41]:
```
reg.score(X_train, y_train)
```
Out[41]:
```
0.8197866256049274
```

In [42]:
```
reg.score(X_test, y_test)
```
Out[42]:
```
0.81326294952161
```

In [43]:
```
reg.decision_function(X_test)
```
Out[43]:
```
array([-2.46924764, -1.20906706, -1.40036619, ..., -2.27794851,
       -0.56024581, -2.46924764])
```

In [44]:
```
reg.coef_
```
Out[44]:
```
array([[1.64255822, 0.42006019, 0.64882125]])
```

Doctor recommendation appears to be the most important feature

In [45]:
```
from sklearn.metrics import confusion_matrix
```

In [46]:
```
y_test_preds = reg.predict(X_test)
cm = confusion_matrix(y_test, y_test_preds)
```

In [47]:
```
cm
```
Out[47]:
```
array([[4415,  252],
       [ 880,  515]], dtype=int64)
```

The number of false positives, 259, seems material but low, given the roughly 27,000 predicitions.

Non-parametric model : Decision Tree

In [48]:
```
from sklearn.tree import DecisionTreeClassifier
```

In [49]:
```
tree = DecisionTreeClassifier(criterion = 'entropy', max_depth = 5)
```

In [50]:
```
tree = tree.fit(X_train, y_train)
```

In [51]:
```
tree.score(X_train, y_train)
```
Out[51]:
```
0.8199516058073031
```

In [52]:
```
tree.score(X_test, y_test)
```
Out[52]:
```
0.8150775321676015
```

Accuracy scores are very similar for test and train set (also to logistic regression). Since there does not appear to be any overfitting, it may make sense to build a more complex tree to try to pick up on more patterns in the training set.

In [53]:
```
y_tepreds_t = tree.predict(X_test)
cm_t =  confusion_matrix(y_test, y_tepreds_t)
cm_t
```
Out[53]:
```
array([[4398,  269],
       [ 852,  543]], dtype=int64)
```

Final model (tree and tuned)

Since there does not appear to be any overfitting, and possible underfitting, a more complex tree is used to produce better results.

In [54]:
```
tree_big = DecisionTreeClassifier(criterion = 'entropy', max_depth = 10) # The maximum depth of the tree is increased from 5
```

In [55]:
```
tree_big =  tree_big.fit(X_train, y_train)
```

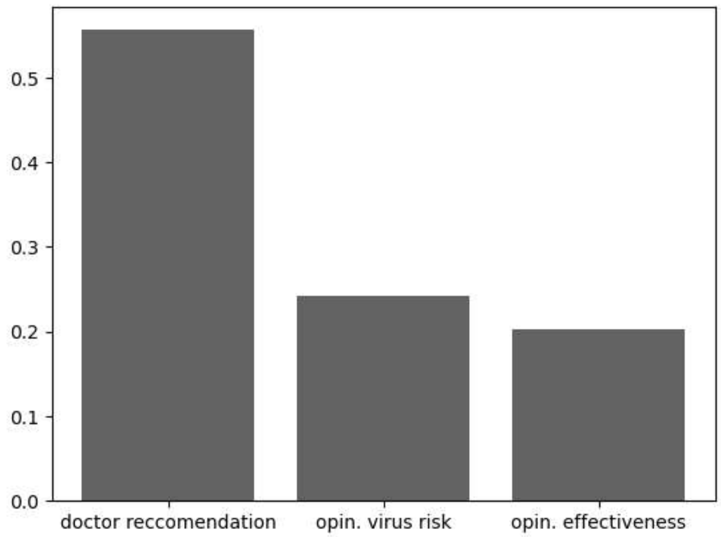
In [56]:
```
tree_big.score(X_train, y_train)
```
Out[56]:
```
0.8202265728112627
```

In [57]:
```
tree_big.score(X_test, y_test)
```
Out[57]:
```
0.8155724183437809
```

The accuracy scores in this more complex tree are highly similar to the initial tree, however the training and test scores have slightly improved and converged. This suggests that we now have a marginally improved model.

In [58]:
```
tree_big.feature_importances_
```
Out[58]:
```
array([0.55442769, 0.24312792, 0.20244439])
```

In [59]:
```
plt.bar(['doctor reccomendation', 'opin. virus risk', 'opin. effectiveness'], [0.55599157, 0.24206617, 0.20194226])
```
Out[59]:
```
<BarContainer object of 3 artists>
```



Doctor recommendation appears to be the most important feature

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In [60]:
```
from sklearn.metrics import ConfusionMatrixDisplay
```

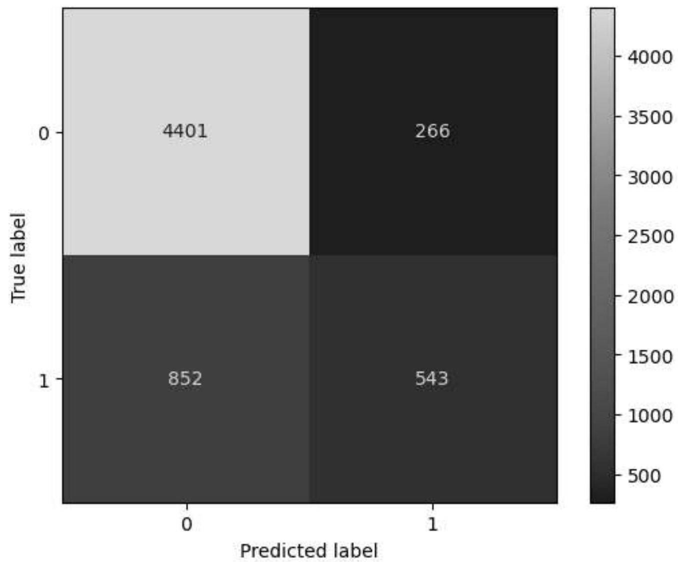
In [61]:
```
y_tepreds_t_big = tree_big.predict(X_test)
```

In [62]:
```
cm_t_big =  confusion_matrix(y_test, y_tepreds_t_big)
cm_t_big
```
Out[62]:
```
array([[4401,  266],
       [ 852,  543]], dtype=int64)
```

In [63]:

```
cmd= ConfusionMatrixDisplay(cm_t_big)
cmd=cmd.from_predictions(y_test,y_tepreds_t_big)
cmd
```

Out[63]: <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x212c777fc40>



The confusion matrix is similar for both iterations of the tree model (293 false positives vs. 286 in final), as expected given there was only a slight improvement in training accuracy. Compared to the baseline model, even though there are greater false positives, our greatest concern, our total correct predictions have increased. Thus even though the tree models would incorrectly classify more unvaccinated persons and therefore result in less resources for that population, given the higher accuracy on the test set of the big_tree model and the higher number of correct predictions (and lower false negatives) in our confusion matrix, resources would be better conserved and allocated by relying on the big_tree model.

Results, Recommendations, Limitations.

The results show that the big_tree model is the preferred model given its higher accuracy on the training and test sets compared to both the first tree iteration and the baseline logistic regression model. Given that this model performs better than the other models and better than the simple strategy of guessing the majority class for each prediction, it is recommended that this model be used to predict whether or not individuals have been given the a vaccine for any virus similar to H1N1, so that resources can be allocated efficiently based on one's vaccine status. More generally, the models show us that the three factors, presence of a doctor reccomendation, opinion of virus risk, and opinion of vaccine effectiveness, are significantly related to whether one has received the vaccine. This suggest that it would be beneficial to both increase outreach to those with low presence of these factors and to provide outreach that may could educate and provide resources so that such persons may become more likely to receive a vaccine.

The core limitation is that there is much room for improvement in the accuracy level of the final model. While the accuracy of the final model is 82%, a strategy of simply guessing that all persons have not received the vaccine would result in a similar 79% accuracy. Also note that iteratively, only slight improvement on models was made, given similar accuracies and only 1 more correct prediction in final model as compared to baseline.

In [ ]: