Using Survey Data as a Predictor of Pandemic Vaccination
3 - Clustering

Mark Patterson, March 2021

Clustering of h1n1 survey data
Following the classification modeling, the next step is to look for additional patterns that may help identify who did or did not get vaccinated. In this step we are seeing what clusters emerge from the survey data set. Will it group along types of questions in the survey? Or will it (hopefully) break into segments of people based combinations of factors? Or will it be able to detect vax versus non-vax recipients?

Import Libraries and Load Data

In [2]:
```
# Import the relevant libraries
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns

from sklearn.cluster import KMeans
from scipy import stats
from sklearn.cluster import AgglomerativeClustering
from sklearn.neighbors import KernelDensity
import scipy.cluster.hierarchy as sch
from sklearn.cluster import AgglomerativeClustering
from sklearn.neighbors import KernelDensity
from scipy.cluster.hierarchy import dendrogram, ward

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

Initial Clustering with Approach A Data
Recall that initial modeling was done with a dataset that did not use one-hot encoding, and instead reated all features as ordinal. I did several runs on Clustering u data-set - importing df5.csv. K-Means clustering with 4 clusters was used and then an HAC model with 2 clusters was also run. That approach was abandoned, and instead the Approach B data. This is described below.

In [45]:
```
# Creating 7 lists of conceptually similar features. For cycling through plotting
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']
pcols_4 = ['behavioral_antiviral_meds', 'behavioral_avoidance','behavioral_face_mask', 'behavioral_wash_hands','behavioral_large_gatherings', 'behavioral_outside_home
pcols_5 = ['sex_num', 'age_group', 'education', 'race', 'marital_status']
pcols_6 = ['employment_status', 'health_worker', 'income_poverty', 'rent_or_own']
pcols_7 = ['hhs_geo_region_num', 'household_adults', 'household_children']
```

In [ ]:

Attempt 2 with Clustering - Data Prep Approach B w/ cut down dataframe
For this round of clustering I am utilizing a dataframe that included both one-hot encoding of some categorical variables and column value encoding for other variable truly were ordinal). Then KNN Imputing was used to address the missing values. Standard Scaler was used to ensure the features were of the same magnitude. Finally, th with 72 features was cut down to the most important features (identified via Random Forest modeling) which includes 19 features.

In [61]:
```
# Load the previously shaped data and take a look.
df19C = pd.read_csv('data/df2_im_scal_19.csv')
print(df19C.shape)
df19C.head()
```

```
(26707, 20)
```

Out[61]:

	Unnamed: 0	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective
0	0	-0.679477	-2.043782	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-1.048700	-0.264324	-1.869153
1	1	1.519841	1.196063	-0.538812	-0.714456	-0.354921	0.429421	1.150052	1.296788	1.210360	-0.019914
2	2	-0.679477	-0.423859	-0.538812	-0.714456	-0.354921	-1.074749	-0.844586	-1.048700	-1.001667	-0.019914
3	3	-0.679477	-0.423859	-0.538812	1.477700	-0.354921	0.429421	-0.844586	0.514959	1.947702	0.904706
4	4	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	0.514959	-0.264324	-0.944533

In [62]:
```
# drop the unecesary first column.
df19C = df19C.drop(columns=['Unnamed: 0'], axis=1)
df19C.shape
```

Out[62]:
```
(26707, 19)
```

In [63]:
```
X_train = df19C.values
```

K-Means clustering with 3 clusters
Based on earlier runs of clustering I felt 3 was a reasonable number of clusters. NOTE that this run of clustering is with the full dataset - both those who got vacci and those that didnt.

In [64]:
```
k_means = KMeans(n_clusters=3)
k_means.fit(X_train)
predicted_clusters = k_means.predict(X_train)
print("The clusters are:", k_means.labels_)
print("The inertia score is:", k_means.inertia_)
```

```
The clusters are: [2 0 2 ... 0 2 2]
The inertia score is: 423478.39990249794
```

In [65]:
```
# Want to get a count of nuber of records per cluster
unique, counts = np.unique(predicted_clusters, return_counts=True)
counts = counts.reshape(1,3)
countscldf = pd.DataFrame(counts, columns=['cluster_0', 'cluster_1', 'cluster_2'])
countscldf
```

Out[65]:

	cluster_0	cluster_1	cluster_2
0	8113	6573	12021

In [66]:

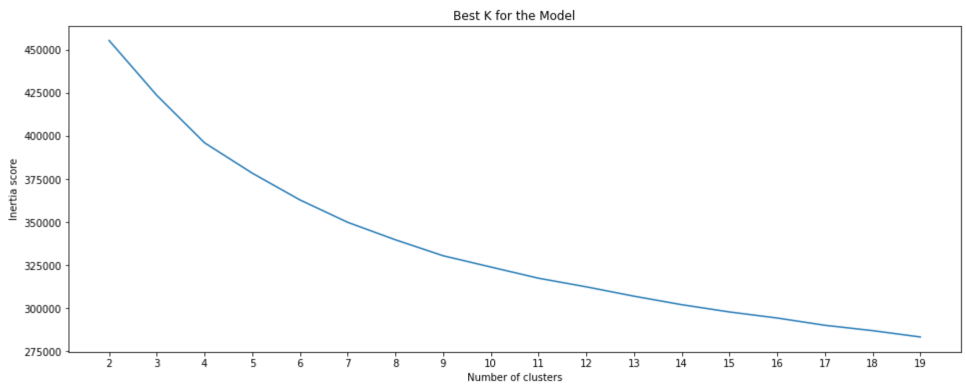
```
# Look at the inertia score for various values of k to identify best number of clusters.
no_of_clusters = range(2,20)
inertia = []

for f in no_of_clusters:
    kmeans = KMeans(n_clusters=f)
    kmeans = kmeans.fit(X_train)
    u = kmeans.inertia_
    inertia.append(u)
    print("The inerta for:", f, "clusters is:", u)
```

```
The inerta for: 2 clusters is: 455302.3504063671
The inerta for: 3 clusters is: 423479.2116751037
The inerta for: 4 clusters is: 395981.94809310965
The inerta for: 5 clusters is: 378375.0996337224
The inerta for: 6 clusters is: 362847.4341601973
The inerta for: 7 clusters is: 349870.0486879499
The inerta for: 8 clusters is: 339741.495400871
The inerta for: 9 clusters is: 330485.7205681158
The inerta for: 10 clusters is: 323942.93790775404
The inerta for: 11 clusters is: 317446.6205196062
The inerta for: 12 clusters is: 312461.29041765514
The inerta for: 13 clusters is: 307042.63585104473
The inerta for: 14 clusters is: 302110.6669158055
The inerta for: 15 clusters is: 297888.3569961508
The inerta for: 16 clusters is: 294386.29525038373
The inerta for: 17 clusters is: 290169.72176907776
The inerta for: 18 clusters is: 287065.3196844167
The inerta for: 19 clusters is: 283392.6874529617
```

In [67]:

```
# Plotting the inertia score for various K values
fig,(ax1)=plt.subplots(1, figsize=(16,6))
xx = np.arange(len(no_of_clusters))
ax1.plot(xx, inertia)
ax1.set_xticks(xx)
ax1.set_xticklabels(no_of_clusters)
plt.xlabel("Number of clusters")
plt.ylabel("Inertia score")
plt.title("Best K for the Model")
```

Out[67]: Text(0.5, 1.0, 'Best K for the Model')



Observations on this KMeans cluster attemp

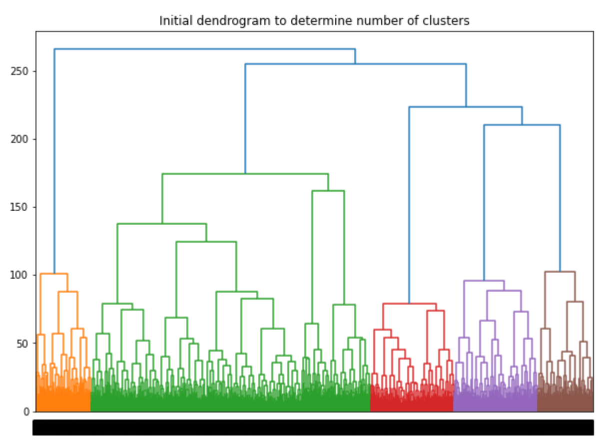
Based on a previous run of clustering, 4 seemed like too many clusters so this time went with 3. However, from looking at the inertia values and the elbow plot above like 4 is being suggested. Will also try plotting an HAC dendrogram to see if that is suggesting something different.

The HAC dendrogram (below) seems to be suggesting 5 clusters... but I could also see the 3 clusters on the right belonging together, and the one on the left may just outliers or misc group?

In [68]:

```
# Step to view dendrogram first, in order to see how many clusters to use for HAC
plt.figure(figsize=(10,7))
dendrogram = sch.dendrogram(sch.linkage(X_train, method='ward'))
plt.title('Initial dendrogram to determine number of clusters')
```

Out[68]: Text(0.5, 1.0, 'Initial dendrogram to determine number of clusters')



In [69]:

```
# Rerunning the K-Means with 4 clusters.
k_means = KMeans(n_clusters=4)
k_means.fit(X_train)
predicted_clusters = k_means.predict(X_train)
print("The clusters are:", k_means.labels_)
print("The inertia score is:", k_means.inertia_)
```

```
The clusters are: [0 0 2 ... 3 2 2]
The inertia score is: 395977.8975838526
```

In [70]:
```python
# Want to get a count of nuber of records per cluster
unique, counts = np.unique(predicted_clusters, return_counts=True)
counts = counts.reshape(1,4)
countscldf = pd.DataFrame(counts, columns=['cluster_0', 'cluster_1', 'cluster_2', 'cluster_3'])
countscldf
```

Out[70]:

	cluster_0	cluster_1	cluster_2	cluster_3
0	2726	6606	10122	7253

In [71]:
```python
# Attach the cluster labels back to the full df.
clusters = k_means.labels_
df19C['Clusters-B4'] = clusters
df19C.head(5)
```

Out[71]:

1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_seas_risk	opinion_seas_sick_from_vacc	age_group	education	household_adults	household_children	INC__75K_to_Poverty	INC__over_75K	INC__below_
1.048700	-0.264324	-1.869153	-1.245424	-0.090271	0.558480	-2.006398	-1.182000	-0.582158	-0.957721	-0.585032	2
1.296788	1.210360	-0.019914	-0.519056	1.420485	-0.813928	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2
1.048700	-1.001667	-0.019914	-1.245424	-0.090271	-1.500131	1.041938	1.481332	-0.582158	1.044146	-0.585032	-0
0.514959	1.947702	0.904706	0.933679	-0.845649	1.244684	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2
0.514959	-0.264324	-0.944533	-1.245424	1.420485	-0.127724	0.025826	0.149666	-0.582158	1.044146	-0.585032	-0

In [73]:
```python
# Load the df with Y features to reattach to this? NOTE this is just importated to grab the Y variables.
df_yforC = pd.read_csv('data/df2_all_numerical.csv')
print(df_yforC.shape)
df_yforC.head()
```

```
(26707, 75)
```

Out[73]:

	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	doctor
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 [74]:
```python
# Wondering if I can copy out 1 column and then do same as above with values?
y_h1n1 = df_yforC['h1n1_vaccine']
y_seasonal = df_yforC['seasonal_vaccine']
```

In [75]:
```python
# Attach the y back to the full df.
df19C['H1n1_vaccine'] = y_h1n1
df19C.head(5)
```

Out[75]:

	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_se
0	-0.679477	-2.043782	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-1.048700	-0.264324	-1.869153	-1
1	1.519841	1.196063	-0.538812	-0.714456	-0.354921	0.429421	1.150052	1.296788	1.210360	-0.019914	-0
2	-0.679477	-0.423859	-0.538812	-0.714456	-0.354921	-1.074749	-0.844586	-1.048700	-1.001667	-0.019914	-1
3	-0.679477	-0.423859	-0.538812	1.477700	-0.354921	0.429421	-0.844586	0.514959	1.947702	0.904706	0
4	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	0.514959	-0.264324	-0.944533	-1

In [78]:
```python
# Attach the y back to the full df.
df19C['Seasonal_vaccine'] = y_seasonal
df19C.head(5)
```

Out[78]:

vacc	opinion_seas_vacc_effective	opinion_seas_risk	opinion_seas_sick_from_vacc	age_group	education	household_adults	household_children	INC__75K_to_Poverty	INC__over_75K	INC__below_Poverty	Clusters-B4	H1n1_vaccine
4324	-1.869153	-1.245424	-0.090271	0.558480	-2.006398	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
0360	-0.019914	-0.519056	1.420485	-0.813928	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
1667	-0.019914	-1.245424	-0.090271	-1.500131	1.041938	1.481332	-0.582158	1.044146	-0.585032	-0.335154	2	0
7702	0.904706	0.933679	-0.845649	1.244684	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
4324	-0.944533	-1.245424	1.420485	-0.127724	0.025826	0.149666	-0.582158	1.044146	-0.585032	-0.335154	2	0

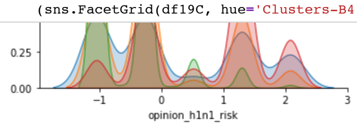
In [79]:
```
# Look at clusters in relation to each feature (mean values per cluster) and try and interpret.
result = df19C.groupby(["Clusters-B4"]).mean().transpose()
result
```

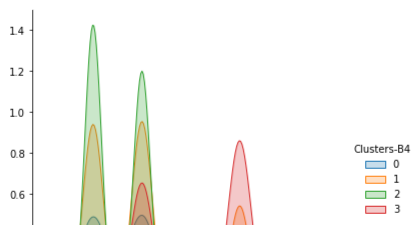
Out[79]:

Clusters-B4	0	1	2	3
h1n1_concern	0.217838	-0.074049	-0.447768	0.610458
h1n1_knowledge	-0.487801	0.357754	-0.189497	0.121951
doctor_recc_h1n1	0.030047	-0.023751	-0.365961	0.521061
doctor_recc_seasonal	-0.033488	-0.061986	-0.341733	0.545951
health_worker	-0.165161	0.156546	-0.146628	0.124122
health_insurance	-0.670566	0.302252	-0.102359	0.119586
opinion_h1n1_vacc_effective	-0.030780	0.149049	-0.367406	0.388553
opinion_h1n1_risk	0.214388	-0.013409	-0.549046	0.697864
opinion_h1n1_sick_from_vacc	0.292334	-0.139403	-0.358514	0.517423
opinion_seas_vacc_effective	-0.083545	0.059867	-0.333601	0.442434
opinion_seas_risk	0.107869	-0.015745	-0.565816	0.763429
opinion_seas_sick_from_vacc	0.323275	-0.167890	-0.239182	0.365205
age_group	-0.260635	-0.220277	0.053013	0.224603
education	-0.845585	0.596301	-0.093754	-0.094460
household_adults	0.073654	0.298879	-0.118035	-0.135174
household_children	0.267528	0.245439	-0.143433	-0.123924
INC__75K_to_Poverty	-0.957721	-0.957721	0.499477	0.535192
INC__over_75K	-0.585032	1.639498	-0.561685	-0.489501
INC__below_Poverty	2.944744	-0.335154	-0.334826	-0.334239
H1n1_vaccine	0.189288	0.239328	0.090595	0.366745
Seasonal_vaccine	0.360235	0.488344	0.321972	0.684958

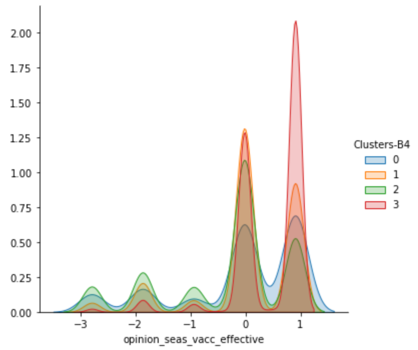
In [80]:
```
# Take a look at these clusters visually... cycle through a few sets of features.
# Creating lists of conceptually similar features.
pcols_a = ['h1n1_concern', 'h1n1_knowledge', 'opinion_h1n1_vacc_effective', 'opinion_h1n1_risk','opinion_h1n1_sick_from_vacc']
pcols_b = ['opinion_seas_vacc_effective','opinion_seas_risk', 'opinion_seas_sick_from_vacc']
pcols_c = ['doctor_recc_h1n1', 'doctor_recc_seasonal', 'health_worker', 'health_insurance']
pcols_d = ['age_group', 'education', 'household_adults', 'household_children', 'INC_75K_to_Poverty', 'INC_over_75K', 'INC_below_Poverty']
```

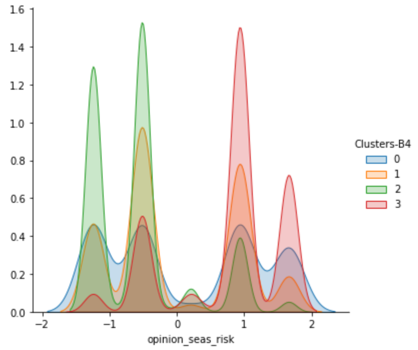
In [81]:
```
for p in pcols_a:
    (sns.FacetGrid(df19C, hue='Clusters-B4',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

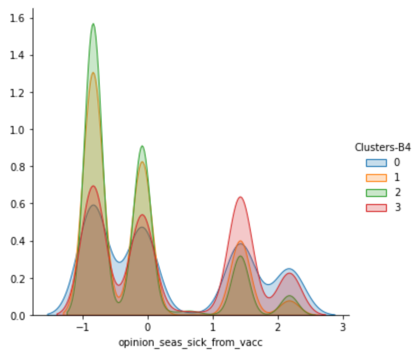




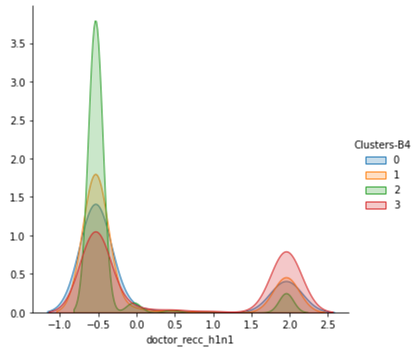
In [82]:
```
for p in pcols_b:
    (sns.FacetGrid(df19C, hue='Clusters-B4',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

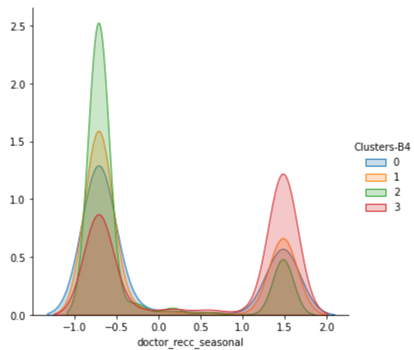


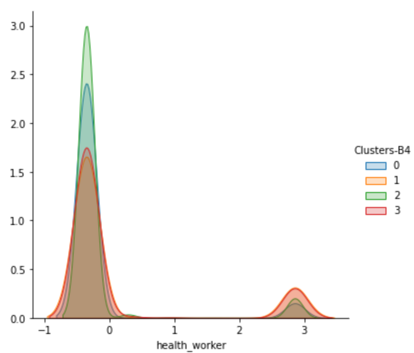


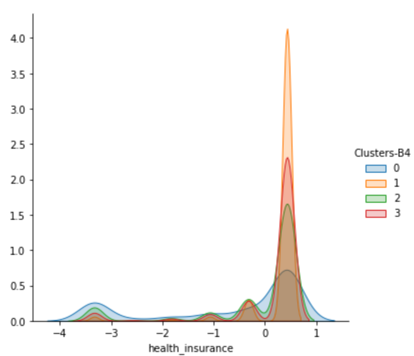


In [83]:
```python
for p in pcols_c:
    (sns.FacetGrid(df19C, hue='Clusters-B4',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```



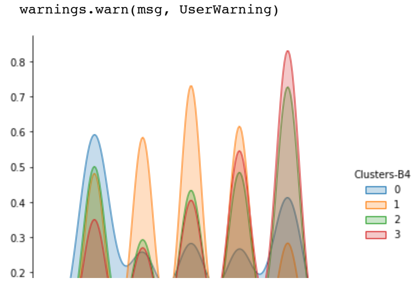






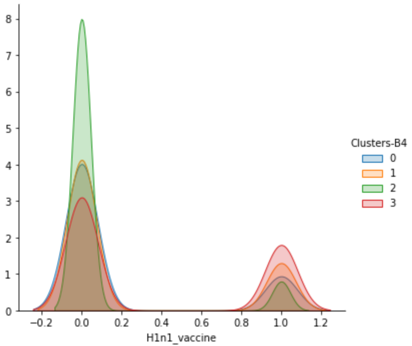
In [85]:
```python
pcols_d = ['age_group', 'education', 'household_adults', 'household_children', 'INC__75K_to_Poverty', 'INC__over_75K', 'INC__below_Poverty']
for p in pcols_d:
    (sns.FacetGrid(df19C, hue='Clusters-B4',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

```
/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/seaborn/distributions.py:306: UserWarning: Dataset has 0 variance; skipping density estimate.
  warnings.warn(msg, UserWarning)
/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/seaborn/distributions.py:306: UserWarning: Dataset has 0 variance; skipping density estimate.
  warnings.warn(msg, UserWarning)
```



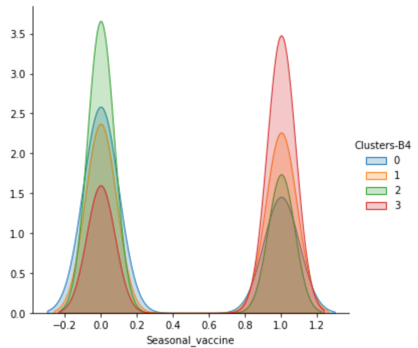
In [86]:
```
sns.FacetGrid(df19C, hue='Clusters-B4',height=5).map(sns.kdeplot, 'H1n1_vaccine', shade=True).add_legend()
```

Out[86]: `<seaborn.axisgrid.FacetGrid at 0x1a2a405908>`



In [87]:
```
sns.FacetGrid(df19C, hue='Clusters-B4',height=5).map(sns.kdeplot, 'Seasonal_vaccine', shade=True).add_legend()
```

Out[87]: `<seaborn.axisgrid.FacetGrid at 0x1a2ac5b978>`



Observations: Approach B with the full dataset

With 4 clusters the plots are difficult to interpret. Decided to focus down more to JUST the records of people that did not get the H1N1 vaccine (class = 0).

In [ ]:

Rerun the analysis with just the non-vax class (79% of dataset)

Decidded to focus on this subset of data. Perhaps there are other patterns once we remove the obvious ones from the full data set.

In [88]:
```
print(df19C.shape)
df19C.head(5)
```

```
(26707, 22)
```

Out[88]:

vacc	opinion_seas_vacc_effective	opinion_seas_risk	opinion_seas_sick_from_vacc	age_group	education	household_adults	household_children	INC__75K_to_Poverty	INC__over_75K	INC__below_Poverty	Clusters-B4	H1n1_vaccine
4324	-1.869153	-1.245424	-0.090271	0.558480	-2.006398	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
0360	-0.019914	-0.519056	1.420485	-0.813928	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
1667	-0.019914	-1.245424	-0.090271	-1.500131	1.041938	1.481332	-0.582158	1.044146	-0.585032	-0.335154	2	0
7702	0.904706	0.933679	-0.845649	1.244684	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
4324	-0.944533	-1.245424	1.420485	-0.127724	0.025826	0.149666	-0.582158	1.044146	-0.585032	-0.335154	2	0

In [89]:
```
df20C = df19C.loc[df19C['H1n1_vaccine'] == 0]
df20C.head()
```

Out[89]:

	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_se
0	-0.679477	-2.043782	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-1.048700	-0.264324	-1.869153	-1
1	1.519841	1.196063	-0.538812	-0.714456	-0.354921	0.429421	1.150052	1.296788	1.210360	-0.019914	-0
2	-0.679477	-0.423859	-0.538812	-0.714456	-0.354921	-1.074749	-0.844586	-1.048700	-1.001667	-0.019914	-1
3	-0.679477	-0.423859	-0.538812	1.477700	-0.354921	0.429421	-0.844586	0.514959	1.947702	0.904706	0
4	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	0.514959	-0.264324	-0.944533	-1

In [93]:
```
df20C['H1n1_vaccine'].value_counts()
```

Out[93]:
```
0    21033
Name: H1n1_vaccine, dtype: int64
```

In [94]:
```
# Cutting down the columns to eliminate target ariables and previosu cluster results.
columns_to_cut = ['Clusters-B4', 'H1n1_vaccine', 'Seasonal_vaccine']
df20C = df20C.drop(columns_to_cut, axis=1)
df20C.head()
```

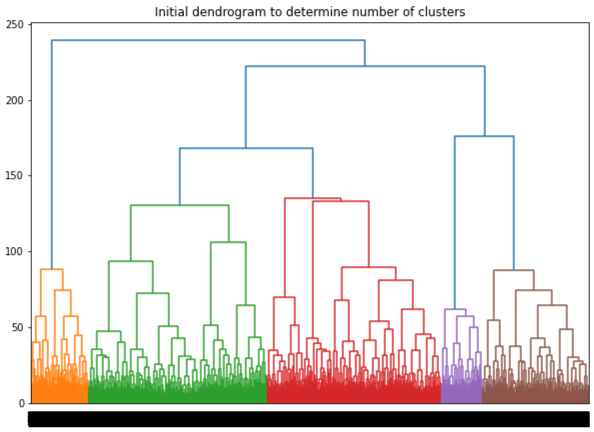
Out[94]:

	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_se
0	-0.679477	-2.043782	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-1.048700	-0.264324	-1.869153	-1
1	1.519841	1.196063	-0.538812	-0.714456	-0.354921	0.429421	1.150052	1.296788	1.210360	-0.019914	-0
2	-0.679477	-0.423859	-0.538812	-0.714456	-0.354921	-1.074749	-0.844586	-1.048700	-1.001667	-0.019914	-1
3	-0.679477	-0.423859	-0.538812	1.477700	-0.354921	0.429421	-0.844586	0.514959	1.947702	0.904706	0
4	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	0.514959	-0.264324	-0.944533	-1

In [95]:
```
X_train = df20C.values
```

In [96]:
```
# Step to view dendrogram first, in order to see how many clusters to use for HAC
plt.figure(figsize=(10,7))
dendrogram = sch.dendrogram(sch.linkage(X_train, method='ward'))
plt.title('Initial dendrogram to determine number of clusters')
```

Out[96]:
```
Text(0.5, 1.0, 'Initial dendrogram to determine number of clusters')
```



Observations on the dendrogram

It is suggesting 5 clusters, however the purple and orange clusters are fairly small. I am going to move forward with 3 clusters.

In [97]:
```
# K-Means clustering with 3 clusters (class 0 dataset)
k_means = KMeans(n_clusters=3)
k_means.fit(X_train)
predicted_clusters = k_means.predict(X_train)
print("The clusters are:", k_means.labels_)
print("The inertia score is:", k_means.inertia_)
```

```
The clusters are: [1 2 1 ... 2 1 1]
The inertia score is: 322195.6921531434
```

In [98]:
```
# Want to get a count of nuber of records per cluster
unique, counts = np.unique(predicted_clusters, return_counts=True)
counts = counts.reshape(1,3)
countscldf = pd.DataFrame(counts, columns=['cluster_0', 'cluster_1', 'cluster_2'])
countscldf
```

Out[98]:

	cluster_0	cluster_1	cluster_2
0	5057	10144	5832

In [99]:
```
df19C.head()
```

Out[99]:

vacc	opinion_seas_vacc_effective	opinion_seas_risk	opinion_seas_sick_from_vacc	age_group	education	household_adults	household_children	INC__75K_to_Poverty	INC__over_75K	INC__below_Poverty	Clusters-B4	H1n1_vaccine
4324	-1.869153	-1.245424	-0.090271	0.558480	-2.006398	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
0360	-0.019914	-0.519056	1.420485	-0.813928	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
1667	-0.019914	-1.245424	-0.090271	-1.500131	1.041938	1.481332	-0.582158	1.044146	-0.585032	-0.335154	2	0
7702	0.904706	0.933679	-0.845649	1.244684	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0
4324	-0.944533	-1.245424	1.420485	-0.127724	0.025826	0.149666	-0.582158	1.044146	-0.585032	-0.335154	2	0

In [100]:
```
df21C = df19C.loc[df19C['H1n1_vaccine'] == 0]
df21C.shape
```

Out[100]:
```
(21033, 22)
```

In [101]:
```
# Attach the cluster labels back to the full df.
clusters = k_means.labels_
df21C['Clusters-non-vac-3'] = clusters
df21C.head(5)
```

```
/Users/markp/opt/anaconda3/envs/learn-env/lib/python3.6/site-packages/ipykernel_launcher.py:3: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (http://pandas.pydata.org/pa
ble/user_guide/indexing.html#returning-a-view-versus-a-copy)
  This is separate from the ipykernel package so we can avoid doing imports until
```

Out[101]:

on_seas_vacc_effective	opinion_seas_risk	opinion_seas_sick_from_vacc	age_group	education	household_adults	household_children	INC__75K_to_Poverty	INC__over_75K	INC__below_Poverty	Clusters-B4	H1n1_vaccine	Seasonal_
-1.869153	-1.245424	-0.090271	0.558480	-2.006398	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0	
-0.019914	-0.519056	1.420485	-0.813928	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0	
-0.019914	-1.245424	-0.090271	-1.500131	1.041938	1.481332	-0.582158	1.044146	-0.585032	-0.335154	2	0	
0.904706	0.933679	-0.845649	1.244684	-0.990286	-1.182000	-0.582158	-0.957721	-0.585032	2.983703	0	0	
-0.944533	-1.245424	1.420485	-0.127724	0.025826	0.149666	-0.582158	1.044146	-0.585032	-0.335154	2	0	

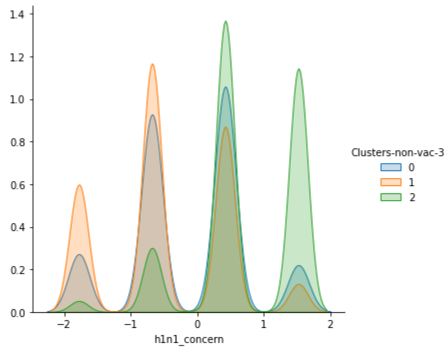
In [102]:
```
# Look at clusters in relation to each feature (means) and try and interpret.
result = df21C.groupby(["Clusters-non-vac-3"]).mean().transpose()
result
```

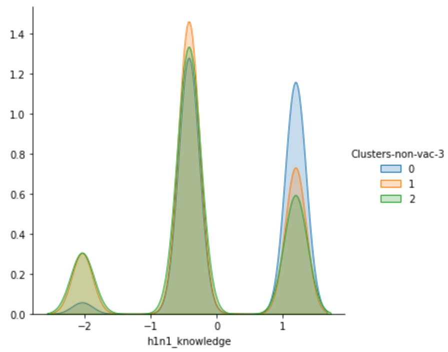
Out[102]:

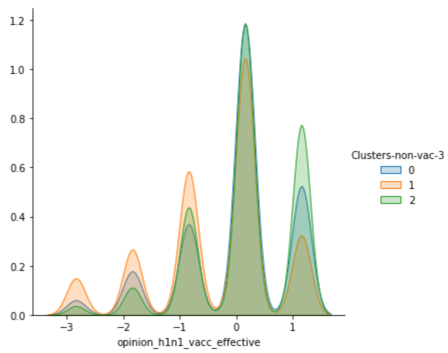
Clusters-non-vac-3	0	1	2
h1n1_concern	-0.135410	-0.467220	0.702262
h1n1_knowledge	0.290162	-0.147080	-0.216925
doctor_recc_h1n1	-0.213536	-0.336804	0.038623
doctor_recc_seasonal	-0.160369	-0.235570	0.153987
health_worker	0.013073	-0.137007	-0.089378
health_insurance	0.281146	-0.075627	-0.296357
opinion_h1n1_vacc_effective	-0.011508	-0.370663	0.151057
opinion_h1n1_risk	-0.239228	-0.572697	0.600649
opinion_h1n1_sick_from_vacc	-0.187339	-0.424092	0.758624
opinion_seas_vacc_effective	-0.054251	-0.304118	0.238479
opinion_seas_risk	-0.190130	-0.534752	0.610500
opinion_seas_sick_from_vacc	-0.163971	-0.306280	0.658372
age_group	-0.222438	0.108159	-0.072187
education	0.568422	-0.081675	-0.483136
household_adults	0.291917	-0.159385	0.010974
household_children	0.227896	-0.180926	0.124359
INC__75K_to_Poverty	-0.957721	0.462373	0.065867
INC__over_75K	1.636716	-0.580735	-0.517760
INC__below_Poverty	-0.327935	-0.100243	0.491146
Clusters-B4	1.032826	1.943415	2.105110
H1n1_vaccine	0.000000	0.000000	0.000000
Seasonal_vaccine	0.373344	0.321372	0.444102

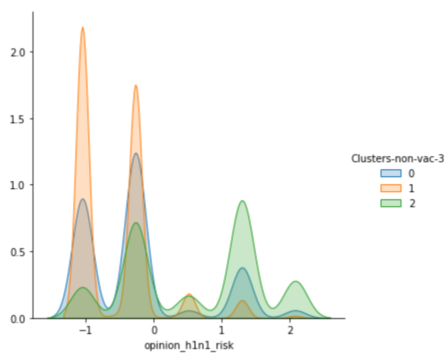
In [ ]:
```
# Also running the full series of plots for all features for visual interpretation.
```

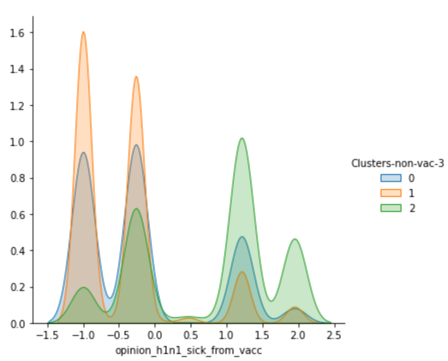
In [103]:
```python
for p in pcols_a:
    (sns.FacetGrid(df21C, hue='Clusters-non-vac-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```



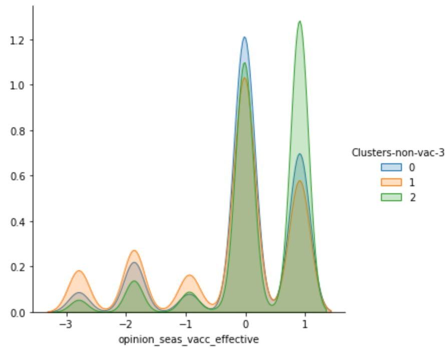


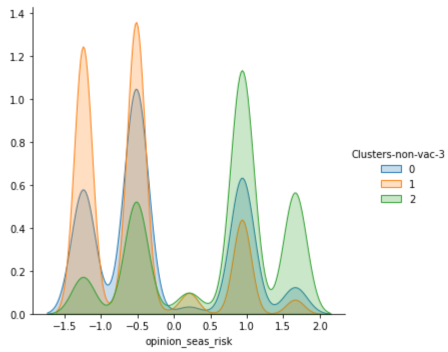


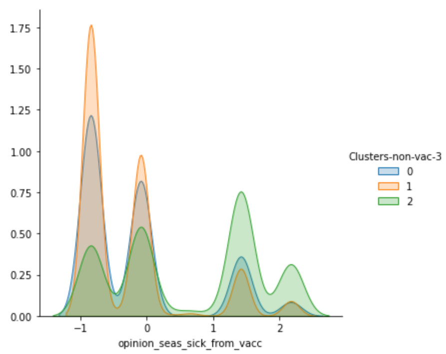




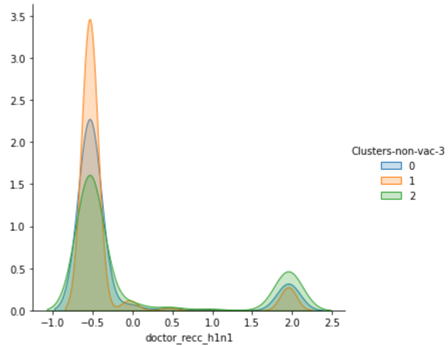
```
In [104]: for p in pcols_b:
              (sns.FacetGrid(df21C, hue='Clusters-non-vac-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

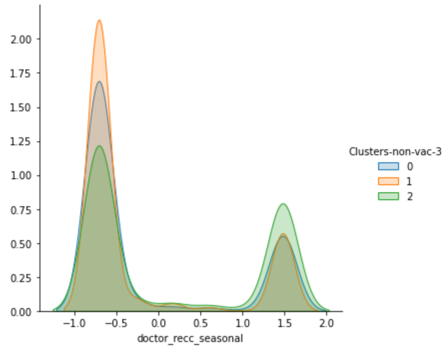


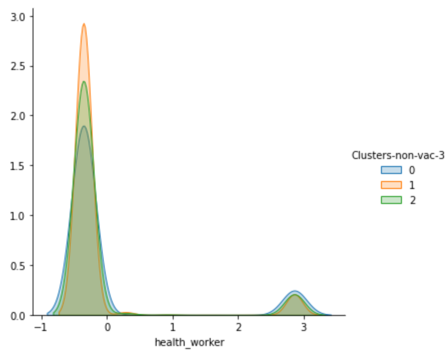


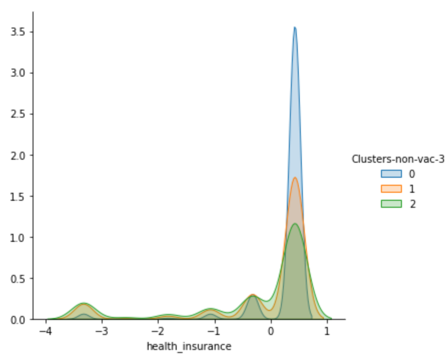


In [105]:
```
for p in pcols_c:
    (sns.FacetGrid(df21C, hue='Clusters-non-vac-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

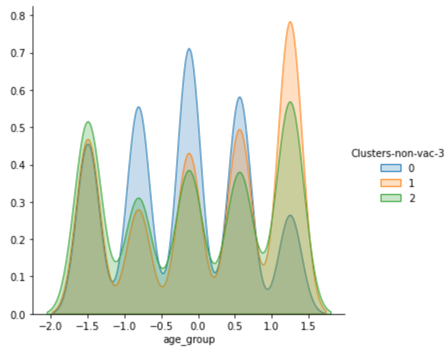


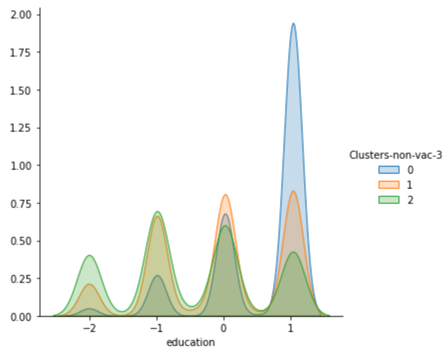


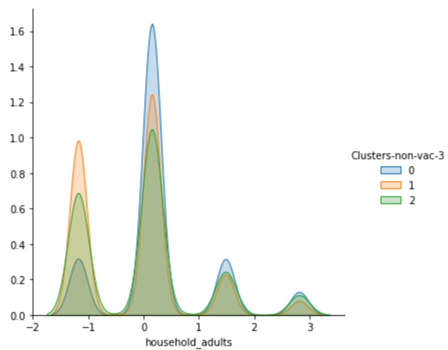


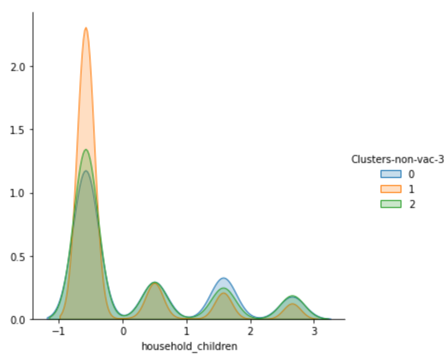


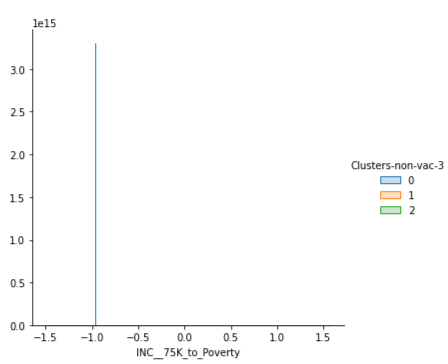
In [106]:
```
pcols_d = ['age_group', 'education', 'household_adults', 'household_children', 'INC__75K_to_Poverty', 'INC__over_75K', 'INC__below_Poverty']
for p in pcols_d:
    (sns.FacetGrid(df21C, hue='Clusters-non-vac-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

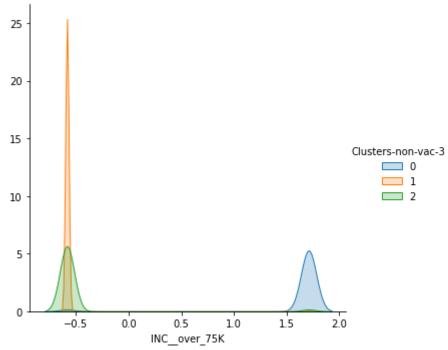


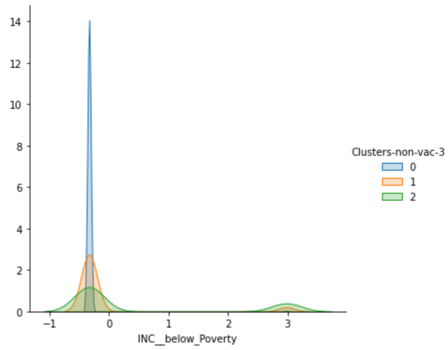






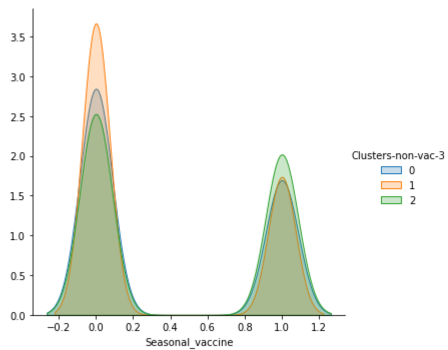






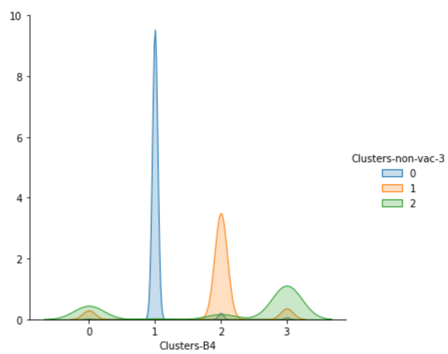
In [108]:
```
sns.FacetGrid(df21C, hue='Clusters-non-vac-3',height=5).map(sns.kdeplot, 'Seasonal_vaccine', shade=True).add_legend()
```

Out[108]: <seaborn.axisgrid.FacetGrid at 0x1a2c351518>



In [109]:
```
sns.FacetGrid(df21C, hue='Clusters-non-vac-3',height=5).map(sns.kdeplot, 'Clusters-B4', shade=True).add_legend()
```

Out[109]: <seaborn.axisgrid.FacetGrid at 0x1a2abf7400>



Observations on K-means clustering with 3 clusters
Looking at the plots shows some interesting distinctions between the clusters.
* Group 1: older, less contact with others, feel less at risk, lower doctor recommended
* Group 0: younger (18-34) more concerned about risks
* Group 2: more contact with others in home; higher income and education / knowledge; but lower to med on opinion questions.

Group 1 makes sense as people over 65 were less at risk of catching the H1N1 virus. These findings help to corroborate what we saw in the modeling - in terms of featu

```
![Cluster-results-3.JPG](attachment:Cluster-results-3.JPG)
```

In [ ]:

Also cluster with the subset of people who GOT Vaccinated for H1n1 (21%)
Interested to see if there are any big differences.

In [110]:
```python
print(df19C.shape)
df19C.head(5)
```

(26707, 22)

Out[110]:

	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_se
0	-0.679477	-2.043782	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-1.048700	-0.264324	-1.869153	-1
1	1.519841	1.196063	-0.538812	-0.714456	-0.354921	0.429421	1.150052	1.296788	1.210360	-0.019914	-0
2	-0.679477	-0.423859	-0.538812	-0.714456	-0.354921	-1.074749	-0.844586	-1.048700	-1.001667	-0.019914	-1
3	-0.679477	-0.423859	-0.538812	1.477700	-0.354921	0.429421	-0.844586	0.514959	1.947702	0.904706	0
4	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	0.514959	-0.264324	-0.944533	-1

In [111]:
```python
df21C = df19C.loc[df19C['H1n1_vaccine'] == 1]
df21C.head()
```

Out[111]:

vacc	opinion_seas_vacc_effective	opinion_seas_risk	opinion_seas_sick_from_vacc	age_group	education	household_adults	household_children	INC__75K_to_Poverty	INC__over_75K	INC__below_Poverty	Clusters-B4	H1n1_vaccine
1667	-0.019914	-0.519056	-0.845649	-0.127724	0.025826	1.481332	-0.582158	1.044146	-0.585032	-0.335154	2	1
4324	0.904706	0.933679	1.420485	-0.127724	-0.990286	1.481332	-0.582158	1.044146	-0.585032	-0.335154	2	1
4324	-0.019914	-0.519056	-0.845649	0.558480	1.041938	0.149666	1.576705	-0.957721	1.709308	-0.335154	1	1
1667	-0.019914	0.933679	-0.845649	1.244684	-0.990286	-1.182000	-0.582158	1.044146	-0.585032	-0.335154	3	1
0360	0.904706	1.660047	1.420485	-0.127724	1.041938	0.149666	1.576705	-0.957721	-0.585032	-0.335154	3	1

In [112]:
```python
df21C['H1n1_vaccine'].value_counts()
```

Out[112]:
```
1    5674
Name: H1n1_vaccine, dtype: int64
```

In [113]:
```python
# Cutting down the columns
columns_to_cut = ['Clusters-B4', 'H1n1_vaccine', 'Seasonal_vaccine']
df21C = df21C.drop(columns_to_cut, axis=1)
df21C.head()
```

Out[113]:

	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_s
7	-0.679477	-2.043782	1.953490	-0.714456	-0.354921	0.429421	1.150052	-0.266871	-1.001667	-0.019914	-
10	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	-3.331004	0.152733	-1.048700	-0.264324	0.904706	
11	-0.679477	1.196063	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-0.266871	-0.264324	-0.019914	-
16	0.420182	-0.423859	1.953490	1.477700	-0.354921	0.429421	-0.844586	-0.266871	-1.001667	-0.019914	
26	1.519841	-0.423859	1.953490	1.477700	-0.354921	0.429421	-0.844586	-0.266871	1.210360	0.904706	

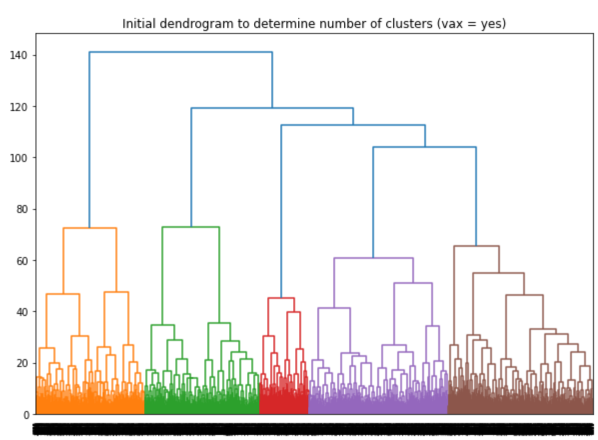
In [114]:
```python
df21C.shape
```

Out[114]: (5674, 19)

In [115]:
```python
X_train = df21C.values
```

In [116]:
```python
# Step to view dendrogram first, in order to see how many clusters to use for HAC
plt.figure(figsize=(10,7))
dendrogram = sch.dendrogram(sch.linkage(X_train, method='ward'))
plt.title('Initial dendrogram to determine number of clusters (vax = yes)')
```

Out[116]: Text(0.5, 1.0, 'Initial dendrogram to determine number of clusters (vax = yes)')



Observations on the dendrogram

Still suggesting 5 clusters, but distributed a bit differently. Here the red cluster is fairly small. There is also an interseting pattern to the way the branches gro
top level. More distinct groups moving from right to left.

In [117]:
```python
# Run K-Means clustering with 3 clusters - to make it more directly comparable to the other set of data (class = 0).
k_means = KMeans(n_clusters=3)
k_means.fit(X_train)
predicted_clusters = k_means.predict(X_train)
print("The clusters are:", k_means.labels_)
print("The inertia score is:", k_means.inertia_)
```

```
The clusters are: [1 1 1 ... 1 2 2]
The inertia score is: 88656.48567981855
```

In [118]:
```python
# Want to get a count of nuber of records per cluster
unique, counts = np.unique(predicted_clusters, return_counts=True)
counts = counts.reshape(1,3)
countscldf = pd.DataFrame(counts, columns=['cluster_0', 'cluster_1', 'cluster_2'])
countscldf
```

Out[118]:

	cluster_0	cluster_1	cluster_2
0	1186	2173	2315

In [119]:
```python
# Attach the cluster labels back to the full df.
clusters = k_means.labels_
df21C['Clusters-VAC-3'] = clusters
df21C.head(5)
```

Out[119]:

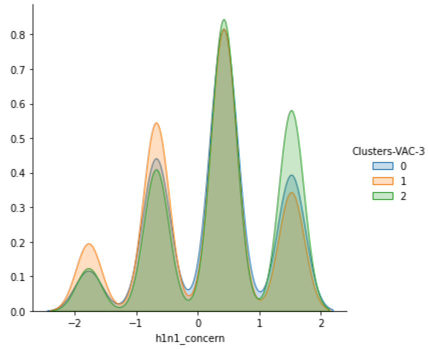
	h1n1_concern	h1n1_knowledge	doctor_recc_h1n1	doctor_recc_seasonal	health_worker	health_insurance	opinion_h1n1_vacc_effective	opinion_h1n1_risk	opinion_h1n1_sick_from_vacc	opinion_seas_vacc_effective	opinion_s
7	-0.679477	-2.043782	1.953490	-0.714456	-0.354921	0.429421	1.150052	-0.266871	-1.001667	-0.019914	-0
10	0.420182	-0.423859	-0.538812	-0.714456	-0.354921	-3.331004	0.152733	-1.048700	-0.264324	0.904706	0
11	-0.679477	1.196063	-0.538812	-0.714456	-0.354921	0.429421	-0.844586	-0.266871	-0.264324	-0.019914	-0
16	0.420182	-0.423859	1.953490	1.477700	-0.354921	0.429421	-0.844586	-0.266871	-1.001667	-0.019914	0
26	1.519841	-0.423859	1.953490	1.477700	-0.354921	0.429421	-0.844586	-0.266871	1.210360	0.904706	

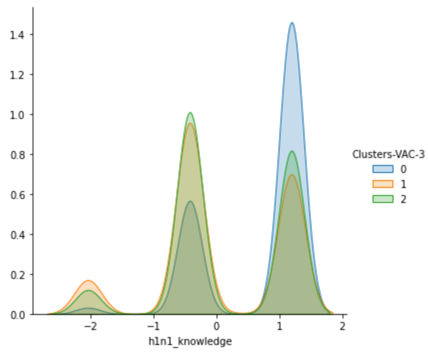
In [120]:
```python
# Look at clusters in relation to each feature (mean) and try and interpret.
result = df21C.groupby(["Clusters-VAC-3"]).mean().transpose()
result
```

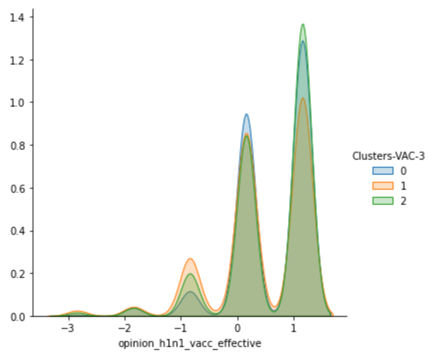
Out[120]:

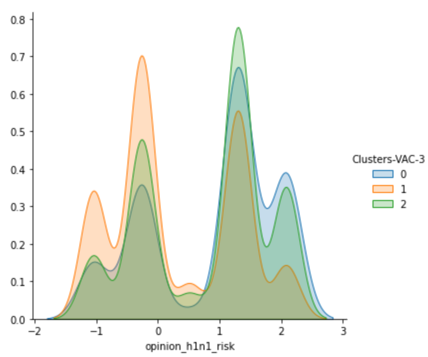
Clusters-VAC-3	0	1	2
h1n1_concern	0.245312	0.076165	0.376766
h1n1_knowledge	0.700525	0.046238	0.154834
doctor_recc_h1n1	0.688846	-0.380075	1.848845
doctor_recc_seasonal	0.367945	-0.461848	1.239641
health_worker	2.856957	-0.343980	-0.343818
health_insurance	0.258838	0.154960	0.185765
opinion_h1n1_vacc_effective	0.601106	0.413881	0.572339
opinion_h1n1_risk	0.900732	0.282029	0.792703
opinion_h1n1_sick_from_vacc	0.065179	0.016632	0.307394
opinion_seas_vacc_effective	0.351025	0.230538	0.454098
opinion_seas_risk	0.660893	0.213596	0.681474
opinion_seas_sick_from_vacc	-0.125683	-0.065451	0.167504
age_group	-0.187318	0.068695	0.225308
education	0.423703	0.107003	0.015819
household_adults	0.065903	0.022321	-0.021639
household_children	0.118289	-0.033352	-0.047618
INC__75K_to_Poverty	-0.066502	-0.072404	0.002137
INC__over_75K	0.380293	0.080147	0.003667
INC__below_Poverty	-0.172849	-0.043437	0.047626

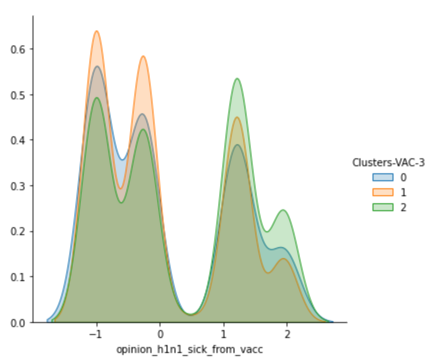
In [121]:
```python
# Also plotting all features for easier visual intepretation.
for p in pcols_a:
    (sns.FacetGrid(df21C, hue='Clusters-VAC-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```



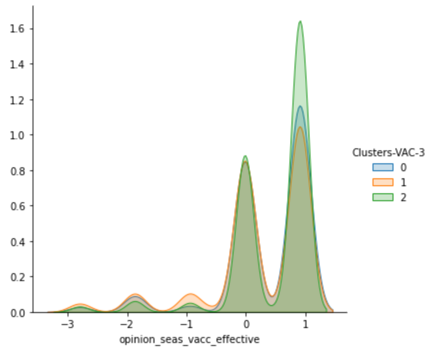


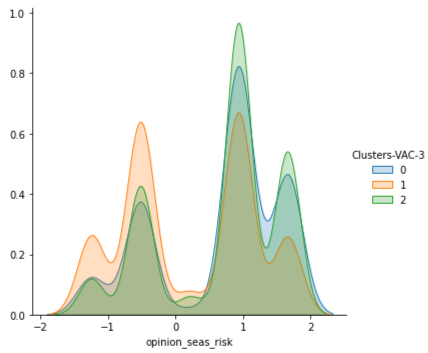


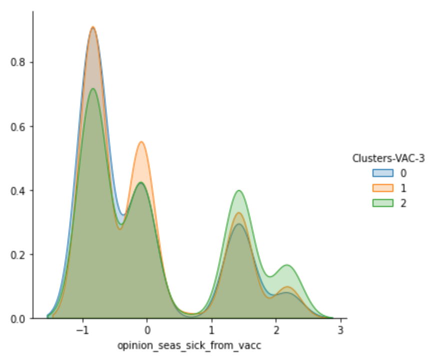




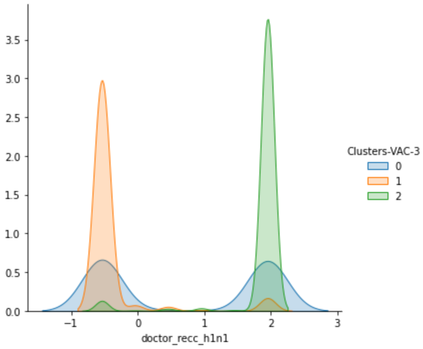
In [122]:
```
for p in pcols_b:
    (sns.FacetGrid(df21C, hue='Clusters-VAC-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

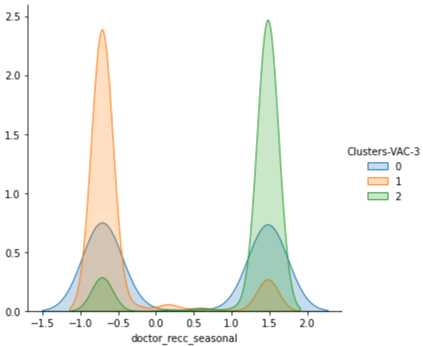


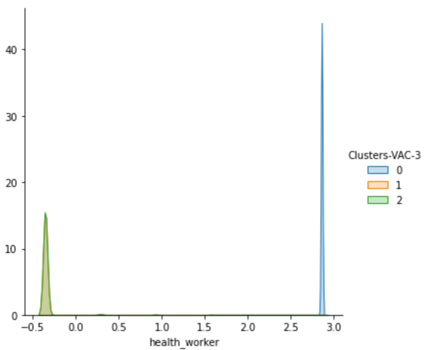


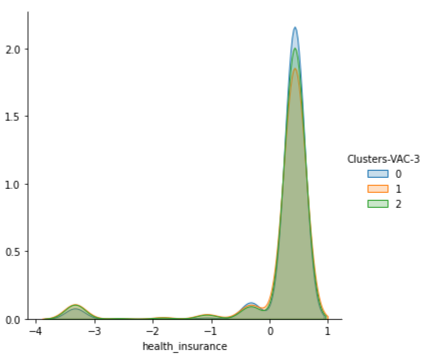


In [123]:
```
for p in pcols_c:
    (sns.FacetGrid(df21C, hue='Clusters-VAC-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

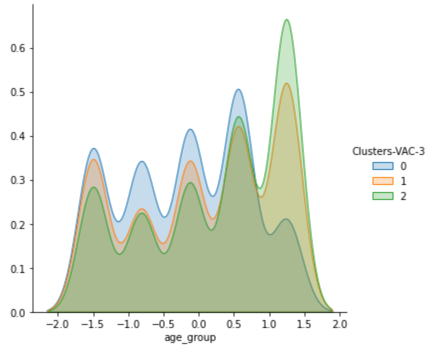


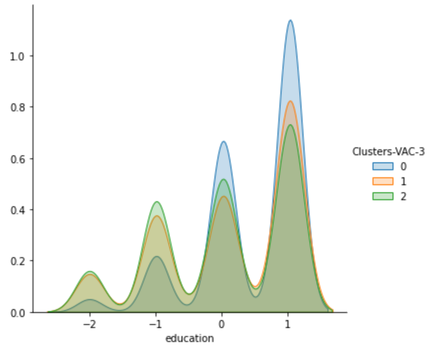


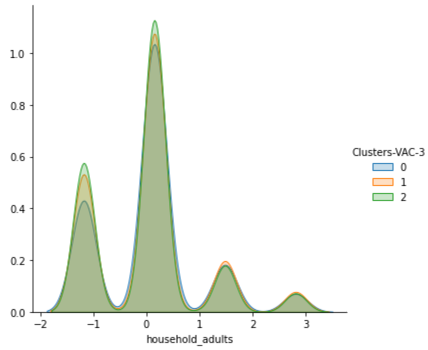


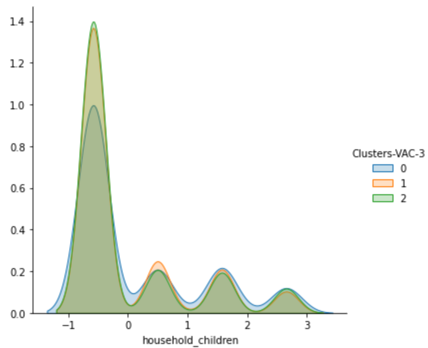


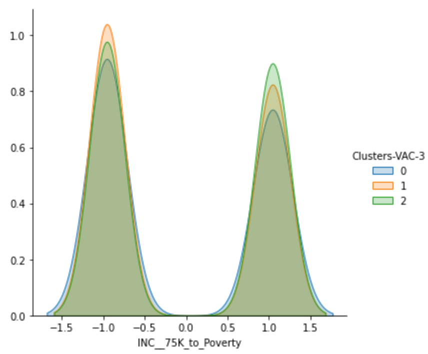
In [124]:
```
for p in pcols_d:
    (sns.FacetGrid(df21C, hue='Clusters-VAC-3',height=5).map(sns.kdeplot, p, shade=True).add_legend())
```

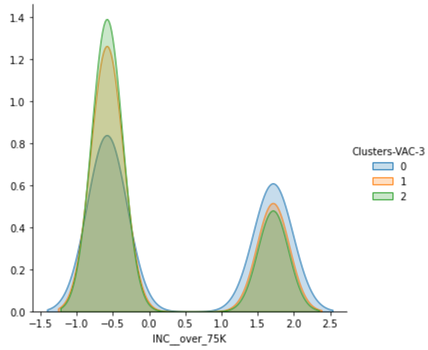


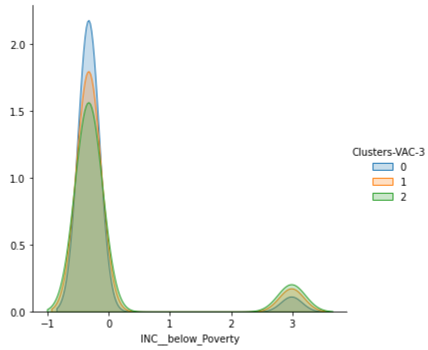












Observations on the clustering of class = 1 (people who got vaccinated)

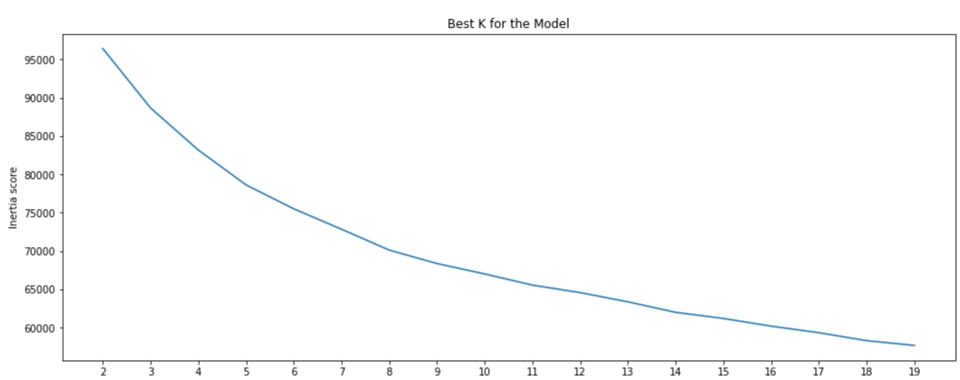
The results were similar to the non-vaccinated group, but the mean values were different. Similar things stood out:
* Age-based (older and less at risk)
* Doctor recommended and strong positive opinions, feel at risk
* Educated, knowledgeable about h1n1, health worker, younger age groups < 65

In [125]:
```
# Curious to see what the inertia scores would suggest for number of clusters,
# Look at the inertia score for various values of k to identify best number of clusters.
no_of_clusters = range(2,20)
inertia = []

for f in no_of_clusters:
    kmeans = KMeans(n_clusters=f)
    kmeans = kmeans.fit(X_train)
    u = kmeans.inertia_
    inertia.append(u)
    print("The inerta for:", f, "clusters is:", u)
```

```
The inerta for: 2 clusters is: 96407.05189269112
The inerta for: 3 clusters is: 88656.48567981855
The inerta for: 4 clusters is: 83171.31495269496
The inerta for: 5 clusters is: 78617.92106338264
The inerta for: 6 clusters is: 75498.23869006155
The inerta for: 7 clusters is: 72833.53475464947
The inerta for: 8 clusters is: 70108.33841676732
The inerta for: 9 clusters is: 68357.80374507113
The inerta for: 10 clusters is: 66997.35051318673
The inerta for: 11 clusters is: 65540.16280777409
The inerta for: 12 clusters is: 64562.817825088045
The inerta for: 13 clusters is: 63359.76103345601
The inerta for: 14 clusters is: 61989.793652077155
The inerta for: 15 clusters is: 61189.733942863604
The inerta for: 16 clusters is: 60184.18821283025
The inerta for: 17 clusters is: 59332.20045801561
The inerta for: 18 clusters is: 58294.02929757264
The inerta for: 19 clusters is: 57672.01555079321
```

In [126]:
```
# Plotting the inertia score for various K values
fig,(ax1)=plt.subplots(1, figsize=(16,6))
xx = np.arange(len(no_of_clusters))
ax1.plot(xx, inertia)
ax1.set_xticks(xx)
ax1.set_xticklabels(no_of_clusters)
plt.xlabel("Number of clusters")
plt.ylabel("Inertia score")
plt.title("Best K for the Model")
```

Out[126]: Text(0.5, 1.0, 'Best K for the Model')



Observations on the number of clusters

It appears that either 3 or 5 are suggested via the elbo plot.

In [ ]:

In [ ]:

APPENDIX

In [ ]:

In [46]:
```
import plotly.express as px
```

In [ ]:

In [ ]:
```
# Potentil solution for running a set of plots?
numeric_features=[x for x in data.columns if data[x].dtype!="object"]
#taking only the numeric columns from the dataframe.

for i in data[numeric_features].columns:
    plt.figure(figsize=(12,5))
    plt.title(i)
    sns.boxplot(data=data[i])
```

In [ ]:
```
# Another possible plotting option
profiles_file = 'data.csv'
df = pd.read_csv(profiles_file)

cols_to_plot = ['age', 'drinking', 'exercise', 'smoking']

fig, axs = plt.subplots(nrows=2, ncols=2)
fig.set_size_inches(20, 10)
fig.subplots_adjust(wspace=0.2)
fig.subplots_adjust(hspace=0.5)

for col, ax in zip(cols_to_plot, axs.flatten()):
    dftemp = df[col].value_counts()
    ax.bar(dftemp.index, list(dftemp))
    ax.set_title(col)
    ax.tick_params(axis='x', labelrotation=30)

plt.show()
```

In [ ]:

In [ ]:
```
# Try a different style of viz. Grouped bar.
```

In [31]:
```
# This code having trouble with countplot and catplot.
# fig, ax = plt.subplots()

# sns.countplot("h1n1_vaccine", hue="education", data=df5, kind="count",
#              palette={0:"blue",1:"yellow", 2:"orange", 3:"red"}, ax=ax)

# plt.close(2) # catplot creates an extra figure we don't need

# ax.legend(title="Education")
# ax.set_xticklabels(["not vacc", "vaccinated"])
# ax.set_xlabel("")

# fig.suptitle("Education vs. h1n1 vaccination");
```

In [ ]: