Cervical Cancer Behavior Risk

February 26, 2023

1 Unsupervised Learning on Cervical Cancer Behavior Risk

The dataset was retrieved from the UC Irvine Machine Learning Repository. Courtesy goes to Dr. Sobar, Professor Rizanda Machmud and (Dr.) Adi Wijaya for providing the dataset to the repository.

Sobar, Machmud, R., & Wijaya, A. (2016). Cervical Cancer Behavior Risk Data Set. Link

1.1 Table of Contents

1.2 Background

Cancer is the uncontrollable growth of cells; cervical cancer is thus, the uncontrollable growth of cells in the cervix of women. According to the CDC page for cervical cancer, "human papillomavirus(HPV) is the main cause of cervical cancer. HPV is a common virus that is passed from one person to another during sex. At least half of sexually active people will have HPV at some point in their lives, but few women will get cervical cancer".

Accordingly, there are screening tests to detect HPV and there is the HPV vaccine which can help with cervical cancer prevention. Screening tests include the pap smear (looks for precancers, cells changes) and the HPV test (looks for presence of HPV). When detected early on, the cancer is treatable.

The dataset provided by the UC Irvine Machine Learning Repository includes data from surveys conducted by the researchers, mentioned above, in Indonesia. The dataset is the result of the response of 72 respondents. The goal of the dataset was to attempt to predict cervical risk through behavioral measures. Sobar et al. used supervised learning methods, i.e. logistic regression, to determine cervical risk. More information can be found in their paper here. As the title says, this notebook is going try to use unsupervised learning to see whether we can detect signs of cervical cancer risks through cluster models.

1.2.1 Goal

To reiterate, the goal of this notebook is going to be using unsupervised learning, more specifically clustering, to see whether we can differentiate groups that are susceptible to cervical cancer based on their behavioral determinants. The clustering model comparison will consist of 3 feature modifications: using the original data, using scaled data, and using post-PCA data. The models used will be hierarchical and K-means clustering.

[1]:

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

from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.cluster import AgglomerativeClustering, KMeans
from sklearn.metrics import confusion_matrix
```

1.3 Exploratory Data Analysis

[2]:

```
data = pd.read_csv('sobar-72.csv')
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 72 entries, 0 to 71
Data columns (total 20 columns):
 #   Column                      Non-Null Count  Dtype
---  ------                      --------------  -----
 0   behavior_sexualRisk         72 non-null     int64
 1   behavior_eating             72 non-null     int64
 2   behavior_personalHygine     72 non-null     int64
 3   intention_aggregation       72 non-null     int64
 4   intention_commitment        72 non-null     int64
 5   attitude_consistency        72 non-null     int64
 6   attitude_spontaneity        72 non-null     int64
 7   norm_significantPerson      72 non-null     int64
 8   norm_fulfillment            72 non-null     int64
 9   perception_vulnerability    72 non-null     int64
 10  perception_severity         72 non-null     int64
 11  motivation_strength         72 non-null     int64
 12  motivation_willingness      72 non-null     int64
 13  socialSupport_emotionality  72 non-null     int64
 14  socialSupport_appreciation  72 non-null     int64
 15  socialSupport_instrumental  72 non-null     int64
 16  empowerment_knowledge       72 non-null     int64
 17  empowerment_abilities       72 non-null     int64
 18  empowerment_desires         72 non-null     int64
 19  ca_cervix                   72 non-null     int64
```

```
dtypes: int64(20)
memory usage: 11.4 KB
```

Initial inspection shows 72 data points and none of the columns seem to have null values. There are 20 columns total. The goal is going to be trying to use unsupervised learning to identify the ca_cervix column, i.e. the presence or absence of cervical cancer.

According to the background information provided by the dataset, there are 19 attributes that come from 8 variables. The variables is written as the first part of the attribute name - behavior, intention, attitude, norm, perception, motivation, socialSupport, and empowerment.

[3]:

```
data.describe()
```

[3]:

```
       behavior_sexualRisk  behavior_eating  behavior_personalHygine  \
count            72.000000        72.000000                72.000000
mean              9.666667        12.791667                11.083333
std               1.186782         2.361293                 3.033847
min               2.000000         3.000000                 3.000000
25%              10.000000        11.000000                 9.000000
50%              10.000000        13.000000                11.000000
75%              10.000000        15.000000                14.000000
max              10.000000        15.000000                15.000000

       intention_aggregation  intention_commitment  attitude_consistency  \
count              72.000000             72.000000             72.000000
mean                7.902778             13.347222              7.180556
std                 2.738148              2.374511              1.522844
min                 2.000000              6.000000              2.000000
25%                 6.000000             11.000000              6.000000
50%                10.000000             15.000000              7.000000
75%                10.000000             15.000000              8.000000
max                10.000000             15.000000             10.000000

       attitude_spontaneity  norm_significantPerson  norm_fulfillment  \
count             72.000000               72.000000         72.000000
mean               8.611111                3.125000          8.486111
std                1.515698                1.845722          4.907577
min                4.000000                1.000000          3.000000
25%                8.000000                1.000000          3.000000
50%                9.000000                3.000000          7.000000
75%               10.000000                5.000000         14.000000
max               10.000000                5.000000         15.000000

       perception_vulnerability  perception_severity  motivation_strength  \
count                 72.000000            72.000000            72.000000
mean                   8.513889             5.388889            12.652778
std                    4.275686             3.400727             3.207209
min                    3.000000             2.000000             3.000000
```

```
25%                    5.000000             2.000000            11.000000
50%                    8.000000             4.000000            14.000000
75%                   13.000000             9.000000            15.000000
max                   15.000000            10.000000            15.000000

       motivation_willingness  socialSupport_emotionality  \
count               72.000000                   72.000000   
mean                 9.694444                    8.097222   
std                  4.130406                    4.243171   
min                  3.000000                    3.000000   
25%                  7.000000                    3.000000   
50%                 11.000000                    9.000000   
75%                 13.000000                   11.250000   
max                 15.000000                   15.000000   

       socialSupport_appreciation  socialSupport_instrumental  \
count                   72.000000                   72.000000   
mean                     6.166667                   10.375000   
std                      2.897303                    4.316485   
min                      2.000000                    3.000000   
25%                      3.750000                    6.750000   
50%                      6.500000                   12.000000   
75%                      9.000000                   14.250000   
max                     10.000000                   15.000000   

       empowerment_knowledge  empowerment_abilities  empowerment_desires  \
count              72.000000              72.000000            72.000000   
mean               10.541667               9.319444            10.277778   
std                 4.366768               4.181874             4.482273   
min                 3.000000               3.000000             3.000000   
25%                 7.000000               5.000000             6.750000   
50%                12.000000              10.000000            11.000000   
75%                15.000000              13.000000            15.000000   
max                15.000000              15.000000            15.000000   

       ca_cervix  
count  72.000000  
mean    0.291667  
std     0.457719  
min     0.000000  
25%     0.000000  
50%     0.000000  
75%     1.000000  
max     1.000000  
```

```
[4]: data.head()
```

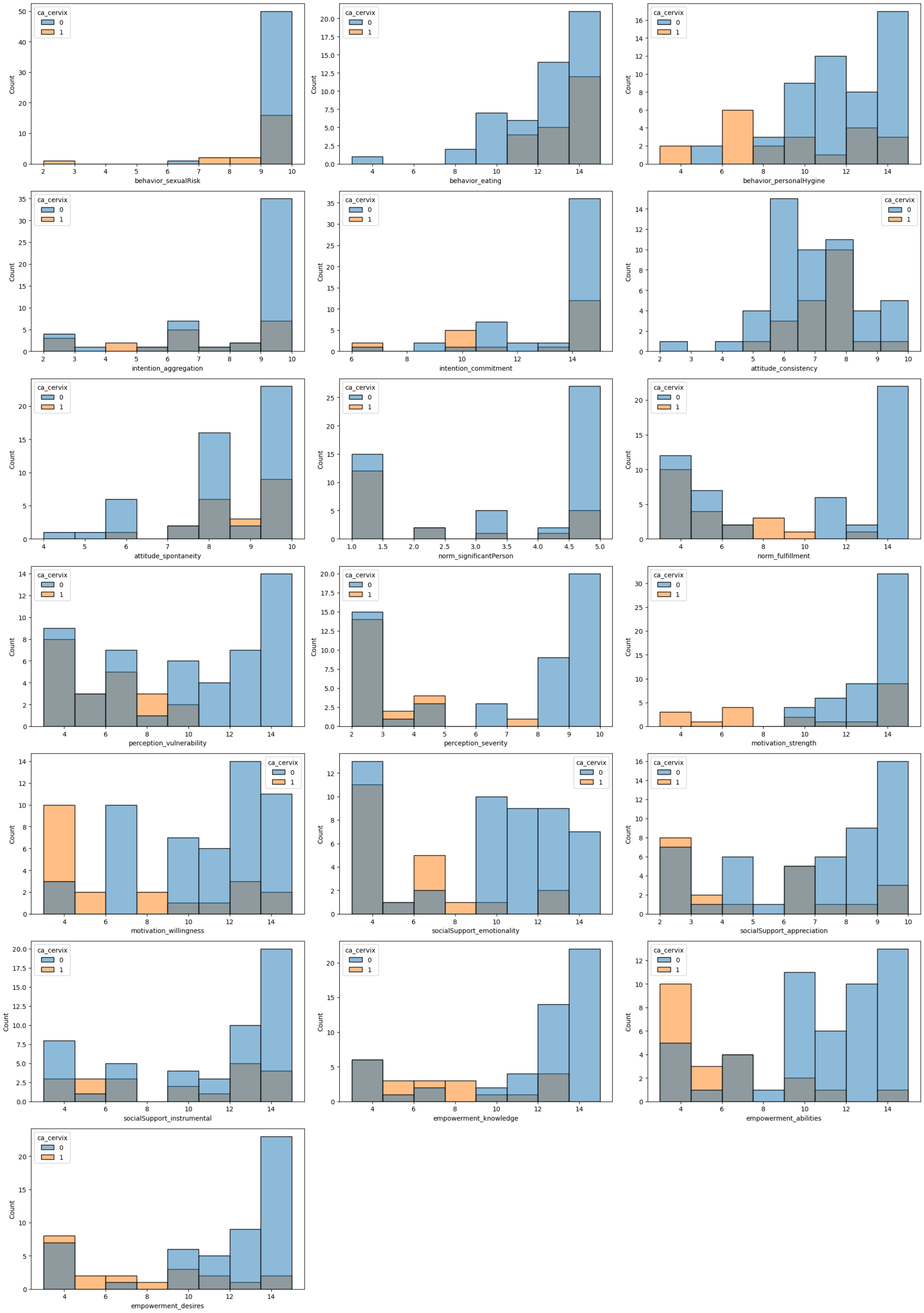
[4]:

```
   behavior_sexualRisk  behavior_eating  behavior_personalHygine  \
0                   10               13                       12
1                   10               11                       11
2                   10               15                        3
3                   10               11                       10
4                    8               11                        7

   intention_aggregation  intention_commitment  attitude_consistency  \
0                      4                     7                     9
1                     10                    14                     7
2                      2                    14                     8
3                     10                    15                     7
4                      8                    10                     7

   attitude_spontaneity  norm_significantPerson  norm_fulfillment  \
0                    10                       1                 8
1                     7                       5                 5
2                    10                       1                 4
3                     7                       1                 5
4                     8                       1                 5

   perception_vulnerability  perception_severity  motivation_strength  \
0                         7                    3                   14
1                         4                    2                   15
2                         7                    2                    7
3                         4                    2                   15
4                         3                    2                   15

   motivation_willingness  socialSupport_emotionality  \
0                       8                           5
1                      13                           7
2                       3                           3
3                      13                           7
4                       5                           3

   socialSupport_appreciation  socialSupport_instrumental  \
0                           7                          12
1                           6                           5
2                           6                          11
3                           4                           4
4                           6                          12

   empowerment_knowledge  empowerment_abilities  empowerment_desires  \
0                     12                     11                    8
1                      5                      4                    4
2                      3                      3                   15
3                      4                      4                    4
```

```
4                       5                       4                      7

   ca_cervix
0          1
1          1
2          1
3          1
4          1
```

Looking at the description and a subset of the dataset, the values are related to each respondents' answers to the questionaire. But, it isn't clear what the values represent in terms of context. It is unclear what the measure of the values are; are they representing awareness, their thoughts towards each attribute, or something else?

[5]:
```
# removing the classification col for attribute eda.
columns = list(data.columns.values)
columns.remove('ca_cervix')

fig = plt.figure(figsize=(20, 40))
rows, cols = 10, 3

# subplots for each attribute
for i, col in enumerate(columns):
    ax = fig.add_subplot(rows, cols, i+1)
    sns.histplot(data=data, x=col, hue='ca_cervix')
    ax.set_xlabel(col)

fig.tight_layout()
plt.show()
```

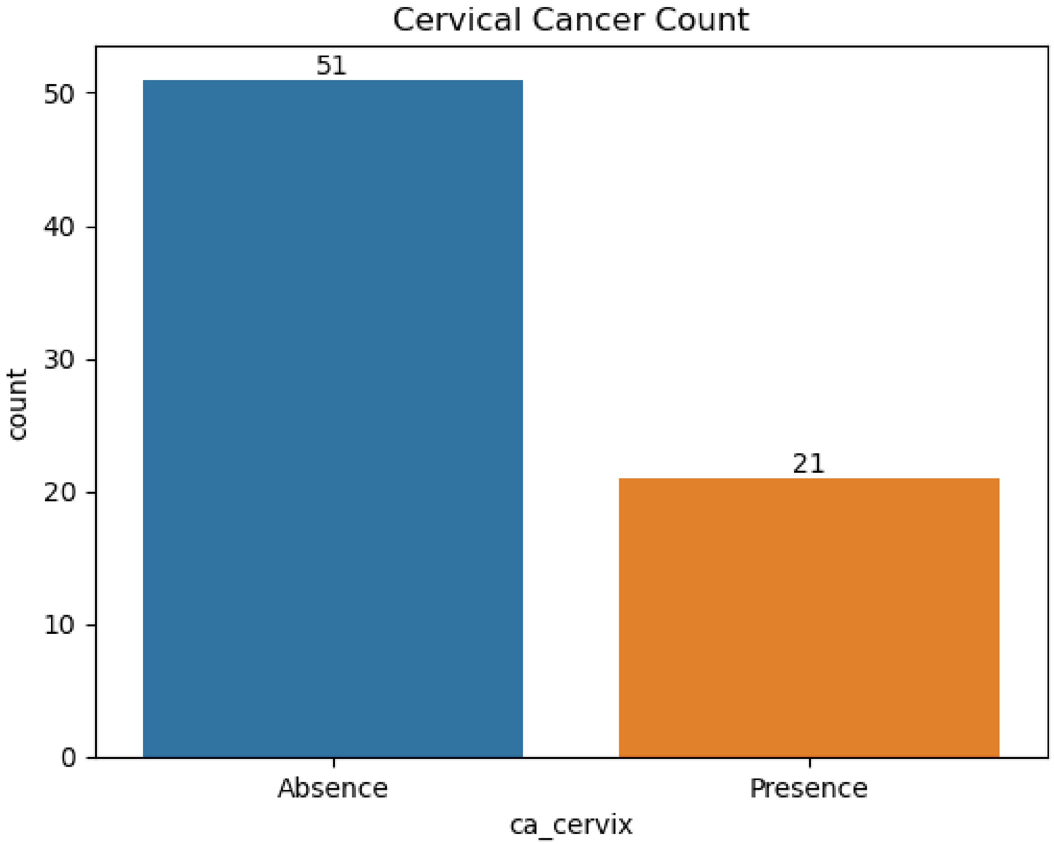

ca_cervix
0
1
Count
behavior_sexualRisk
behavior_eating
behavior_personalHygine
intention_aggregation
intention_commitment
attitude_consistency
attitude_spontaneity
norm_significantPerson
norm_fulfillment
perception_vulnerability
perception_severity
motivation_strength
motivation_willingness
socialSupport_emotionality
socialSupport_appreciation
socialSupport_instrumental
empowerment_knowledge
empowerment_abilities
empowerment_desires

In the plots above, we can see that there is a range of data and the attributes don't look normal. I think it's necessary for it to be normal for unsupervised learning methods. From the histogram, we also notice some points that could outliers; for example in the behavior_sexualRisk plot, most points are under 10 whereas theres a lone point at 2. The same pattern can be seen in the intention_commitment plot. We are not going to remove the outliers however, because they may be useful in the clustering differentiation process.

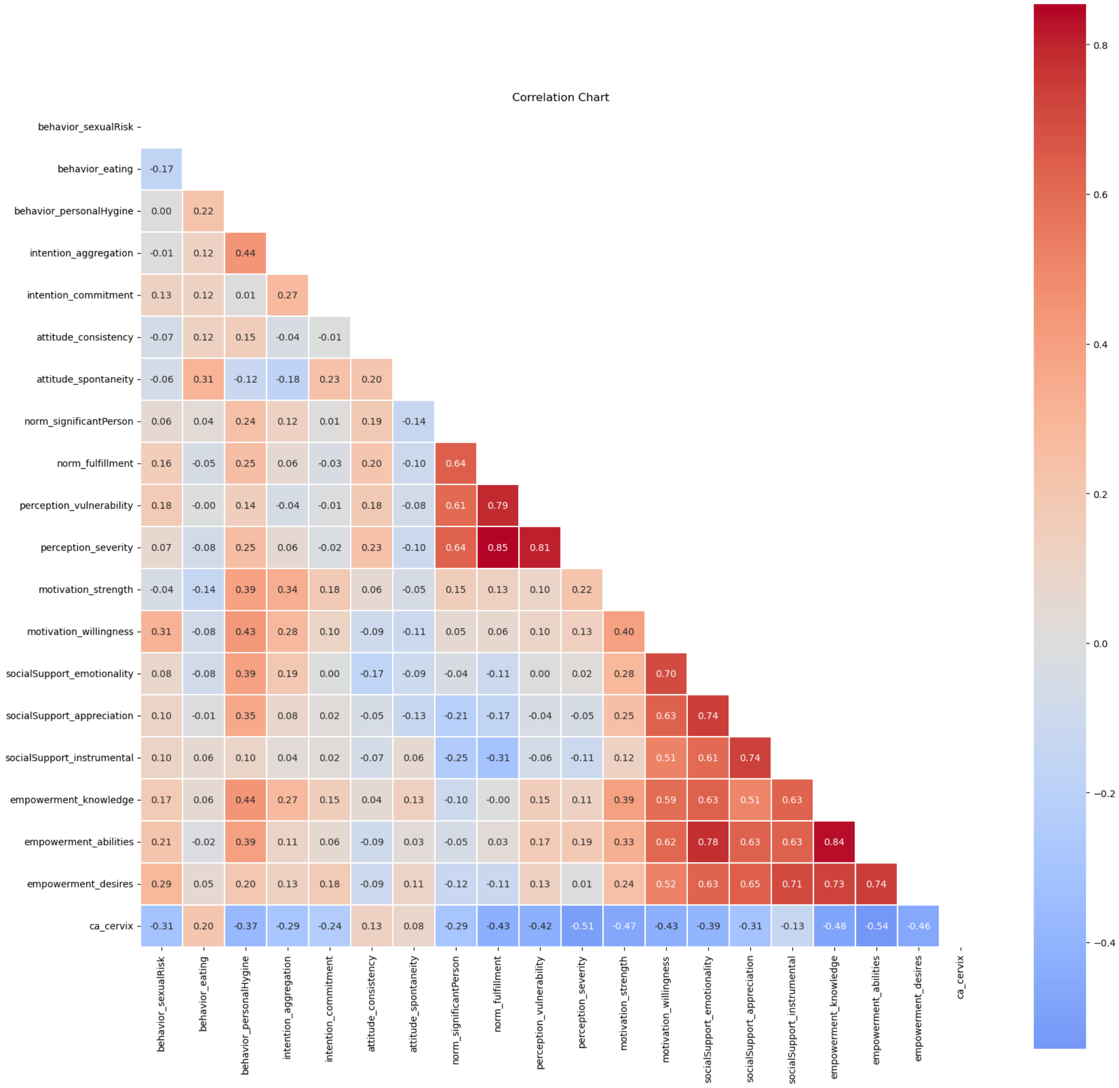
We do see some small trends for example in the percception_vulnerability chart, we see that respondents with cervical cancer tend to have mid-low answers to the related questions and none of the higher answers has cervical cancer. There is also the empowerment_abilities plot that shows low scores tend to have the cancer.

[6]:

```python
ax = sns.countplot(data=data, x='ca_cervix')

# find the count labels
for i in ax.containers:
    ax.bar_label(i,)

ax.set_xticklabels(['Absence','Presence'])
plt.title('Cervical Cancer Count')
plt.show()
```



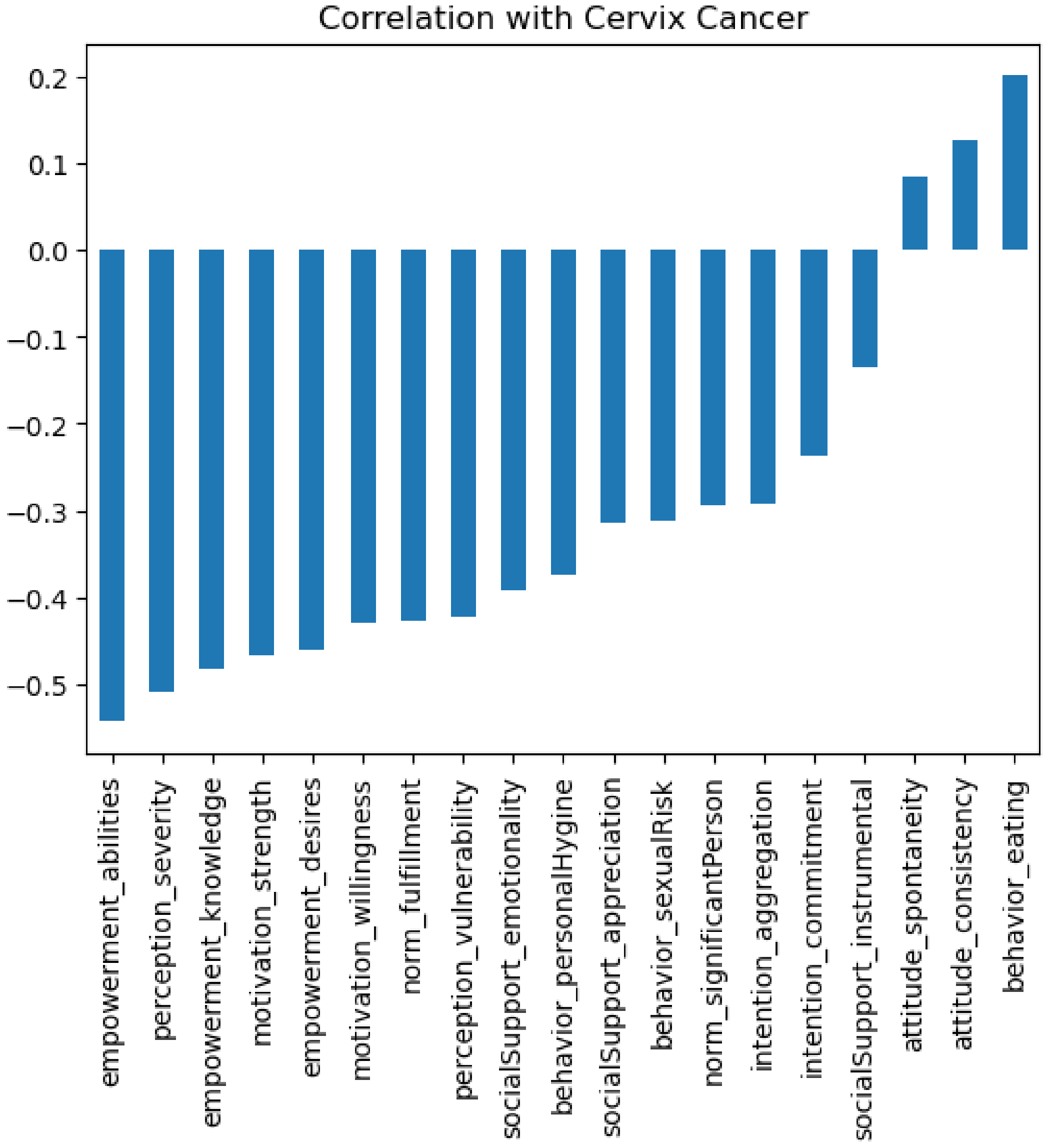
```
[7]: corr = data.corr()
     # used to take the top half of the correlation chart away for easier viewing
     mask = np.triu(np.ones_like(corr, dtype=bool))

     plt.figure(figsize=(20,20))
     sns.heatmap(corr, linewidths=0.05, center=0, cmap='coolwarm', mask=mask,␣
       ↪square=True, annot=True, fmt=".2f")
     plt.title('Correlation Chart')
     plt.show()
```



We see from the correlation plot that some attributes are highly correlated with each other. For example, perception_severity and norm_fulfillment are highly correlated at 0.85. Another notable one is empowerment_abilities and empowerment_knowledge at 0.84. This one you can reason out that the more knowledge someone has on the cancer, the more they feel they are in control of preventing it.

In the plot below is the correlation of cervical cancer against all the attributes. We see that the highest correlation is a negative correlation with empowerment_abilities at -0.54.

[8]:
```
# correlation with the presence/absence of cancer
data.corr()['ca_cervix'][:-1].sort_values().plot(kind='bar')
plt.title('Correlation with Cervix Cancer')
plt.show()
```



Because we are going to be using unsupervised learning methods, the apparent relationships we see from the plots above is good to note but won't be useful in the clustering process. Unsupervised learning is trying to find latent patterns to separate the respondents into groups - presence of absence of cervical cancer.

Because the labels are given to us, we are going to use it to compare with the cluster models.

Below we scale the data between 0 and 1 using the standard scaler function. This will be the scaled features used for modeling. I choose to scale the data because as seen in the description of the dataset, the features have different min and max values. This corresponds to questions that had answers ranging from 0 to 10, 0 to 15, etc. Scaling the features would put them all on the same footing for model development.

[9]:
```
features = data.drop(['ca_cervix'], axis=1)
```

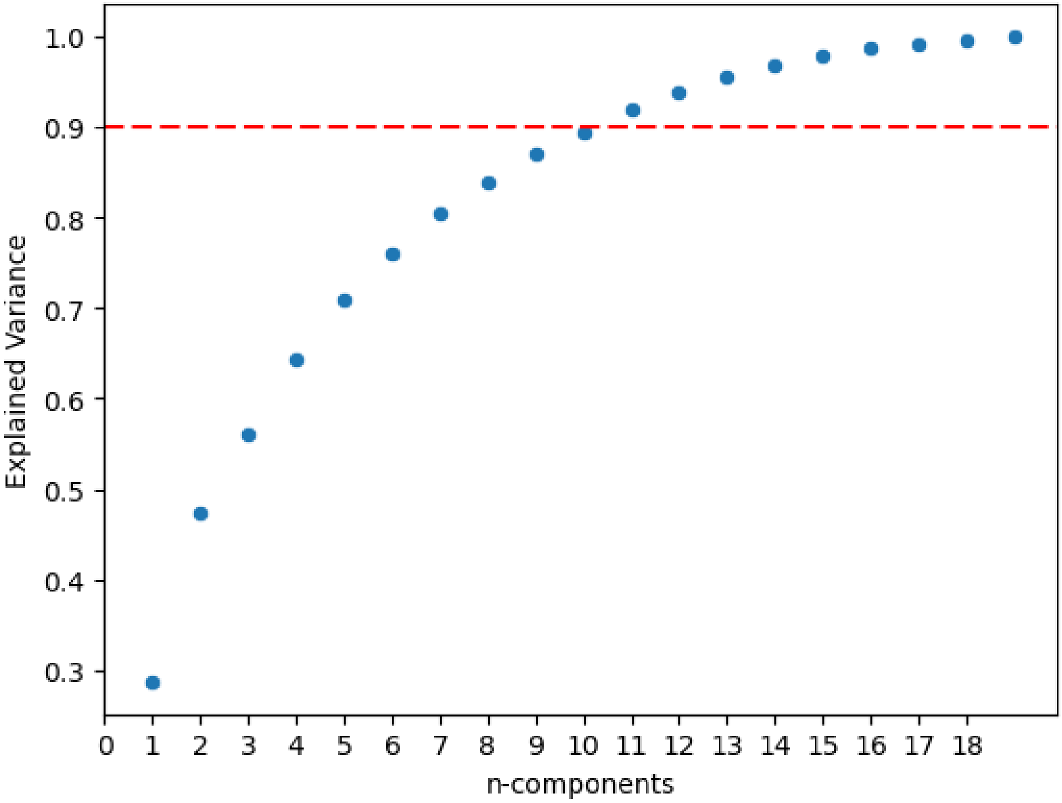
[10]:
```
scaler = StandardScaler()
scaler.fit(features)

features_scaled = pd.DataFrame(scaler.transform(features), columns=features.
  ↪columns)
```

Finally, all that's left is the PCA feature set. Why choose to do a PCA when the number of features isn't overly large or sparse? I chose to perform a PCA feature just to reduce the number of dimensions and also to try to reduce the correlation present between the features which may lead to some unknown interactions. Instead PCA will just create a number of features that explains the most variance in the dataset.

[11]:
```
explained_var = []
for i in range(1,20):
    pca = PCA(n_components=i).fit(features_scaled)
    explained_var.append(sum(pca.explained_variance_ratio_))
```

The chosen cutoff for PCA is going to be around 90% explained variance. This seems to be around 10-features so that's what is going to be used for the PCA features part of the model development.

[12]:
```
ax = sns.scatterplot(x=range(1, 20), y=explained_var)
ax.set_xticks(range(len(explained_var)), labels=range(0,19))
ax.axhline(.9, color='red', dashes=(5, 2))
plt.xlabel('n-components')
plt.ylabel('Explained Variance')
plt.show()
```



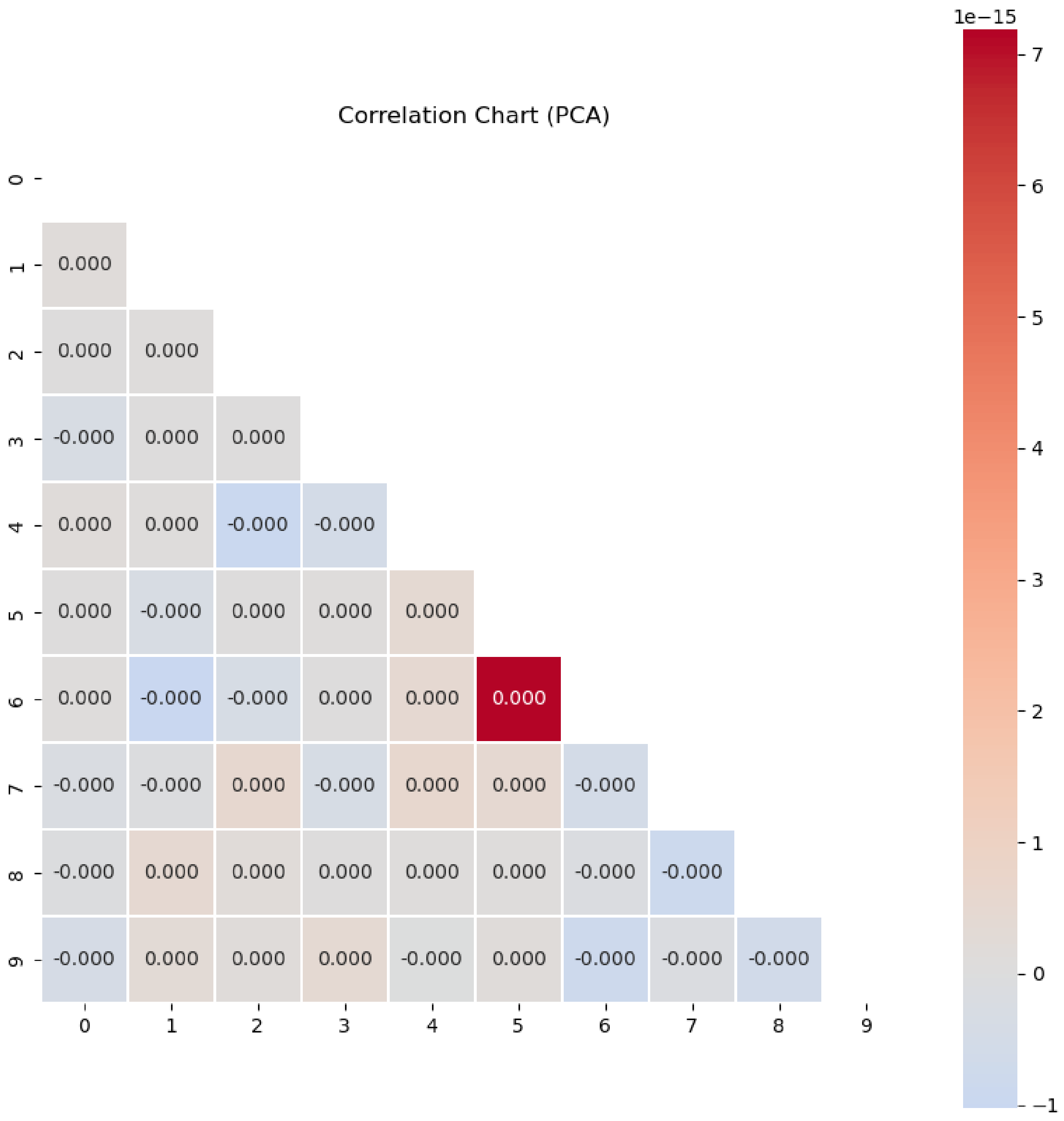
```
[13]: pca = PCA(n_components=10).fit(features_scaled)
      pca_features = pca.transform(features_scaled)
```

```
[14]: pca_features[0]
```

```
[14]: array([ 0.34259186, -0.93663453,  0.44628193,  1.25042552,  2.13653477,
              1.04437742, -1.49113714, -1.74232282, -0.24873946,  0.98933645])
```

```
[15]: pca_df = pd.DataFrame(pca_features)
```

```
[16]: corr_pca = pca_df.corr()
      mask = np.triu(np.ones_like(corr_pca, dtype=bool))
      plt.figure(figsize=(10,10))
      sns.heatmap(corr_pca, linewidths=0.05, center=0, cmap='coolwarm', mask=mask,␣
       ↪square=True, annot=True, fmt=".3f")
      plt.title('Correlation Chart (PCA)')
      plt.show()
```



You see that after the PCA, the features chosen have basically 0 correlation with each other.

1.4 Model Development

1.4.1 Using Original Data

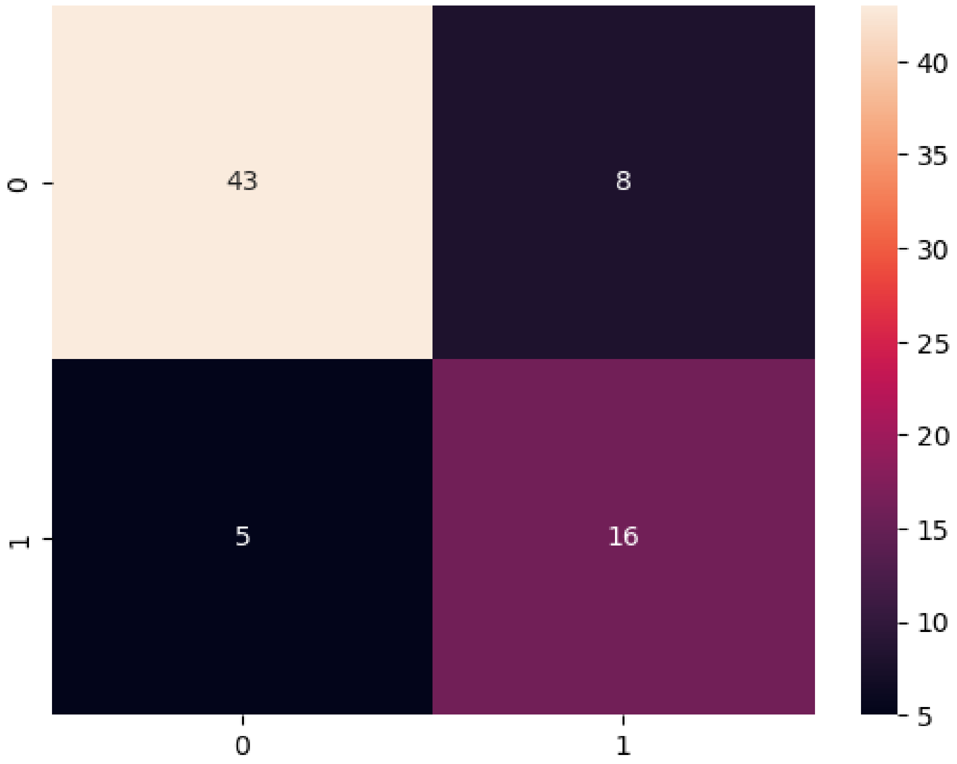
Running an initial hierarchical clustering method. 'n_clusters' is set at 2 because that's what we are hoping to separate into presence and absence of cancer.

[17]:
```
# intial test run of the model
model = AgglomerativeClustering(n_clusters=2, linkage='average').fit(features)
model.labels_
```

```
[17]: array([0, 1, 1, 1, 1, 1, 1, 0, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 0,
              0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0,
              0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 1, 1, 0, 0,
              0, 0, 0, 0, 0, 0], dtype=int64)
```

```
[18]: n = len(data)

      # compares the model labels against the dataset classification
      print('accuracy:', sum(model.labels_ == np.array(data.ca_cervix)) / n)

      sns.heatmap(confusion_matrix(y_pred=model.labels_, y_true=np.array(data.
        ↪ca_cervix)), annot=True)
      plt.show()
```

```
accuracy: 0.8194444444444444
```



We have here that the accuracy of the clusters to the labels are around 82%. This is pretty decent. Looking at the confusion matrix we see that the cluster does relatively well. It has a precision of (16/24) = 67% and a true positive rate of (16/21) = 76% and a false negative (5/21) = 24%.

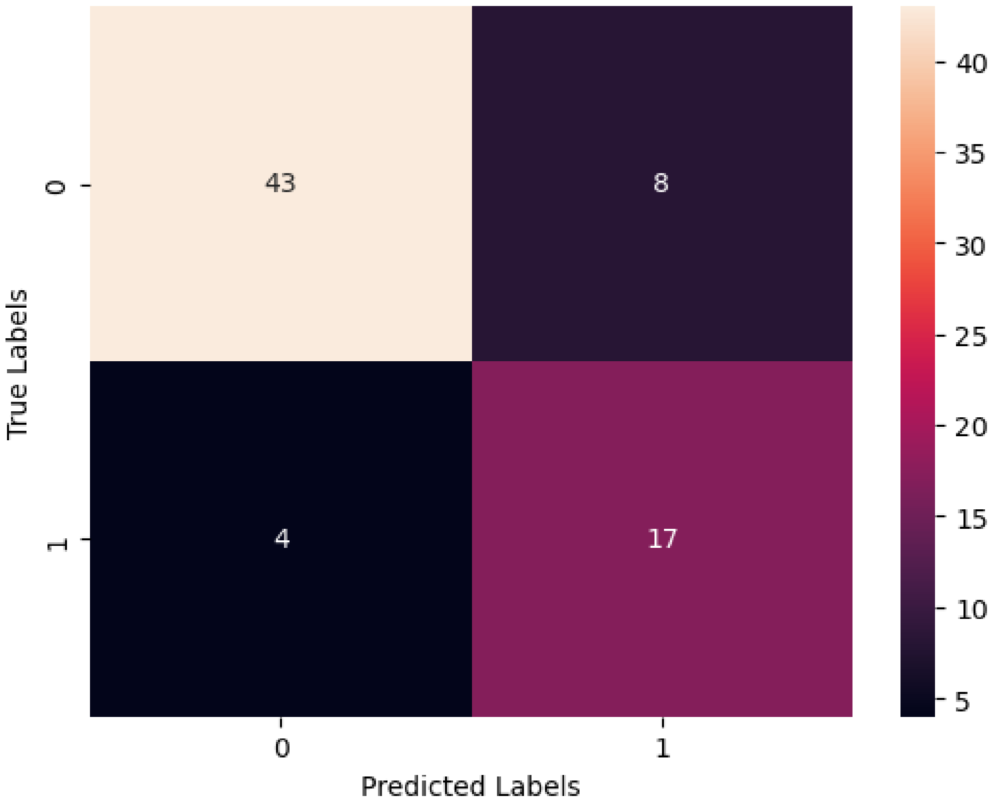
Cancer in general is a detrimental disease to have, thus it's important to discern whether a person has it or not. As a result, it's important to look at the accuracy of the model and the false negative rate and hopefully have the FNR as low as possible.

Next, we are going to see whether an adjustment to the hierarchical cluster model can improve those metrics.

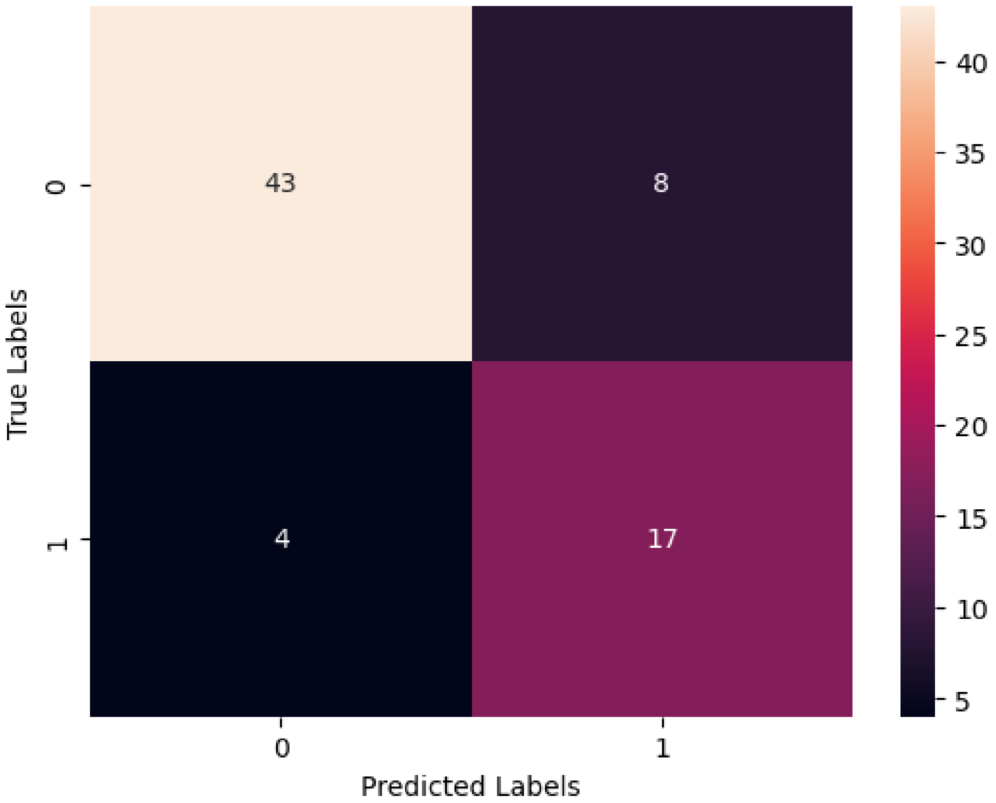
[19]:
```
# tests given iteration of agglomerative clustering and prints combination/
 ↪accuracy and confusion matrix.
# prints highest and increasing accuracy only.
def agcluster(feature_df, n):
    acc=0
    for i in ['ward', 'complete', 'average', 'single']:
        for j in ['euclidean', 'manhattan', 'l1', 'l2', 'cosine']:
            try:
                mod = AgglomerativeClustering(n_clusters=2, linkage=i,␣
 ↪affinity=j).fit(feature_df)
                total = max(sum(mod.labels_ == np.array(data.ca_cervix)),␣
 ↪sum(mod.labels_ != np.array(data.ca_cervix)))
                acc_mod = total/n
                if acc_mod >= acc:
                    acc = acc_mod
                    print(i, j, round(acc, 5))
                    sns.heatmap(confusion_matrix(y_pred=mod.labels_, y_true=np.
 ↪array(data.ca_cervix)), annot=True)
                    plt.ylabel('True Labels')
                    plt.xlabel('Predicted Labels')
                    plt.show()

            except:
                continue
```

[20]:
```
agcluster(features, n)
```

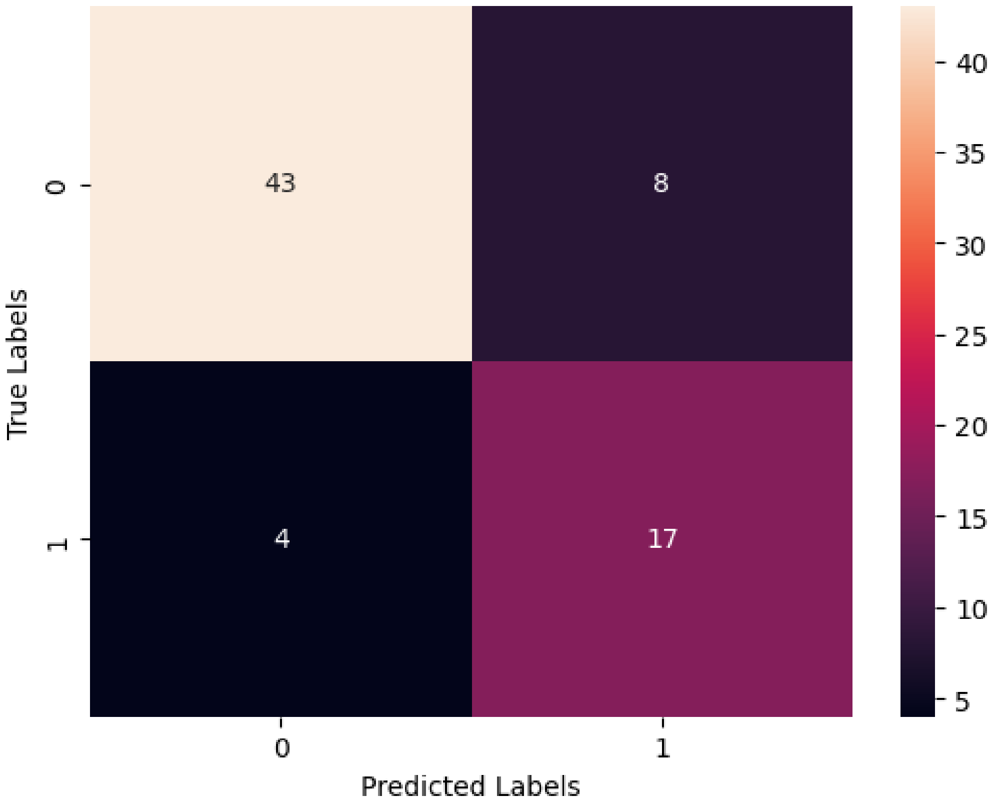
```
ward euclidean 0.83333
```



```
average manhattan 0.83333
```



```
average l1 0.83333
```



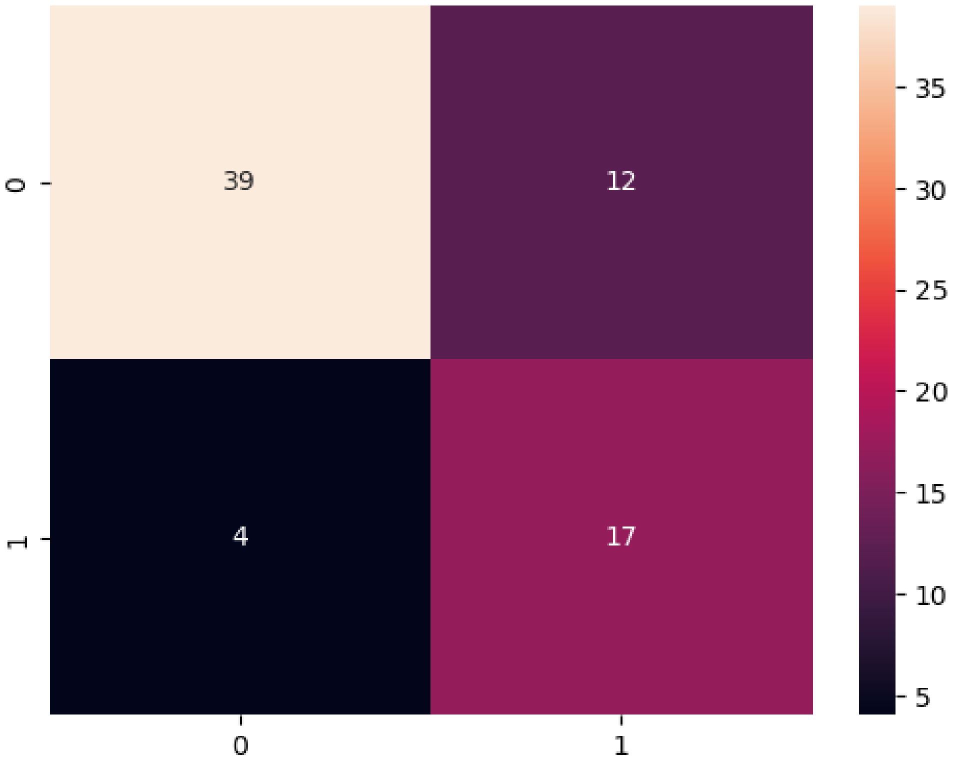
We see that the linkage-metric combination that yielded the highest accuracy is [ward, euclidean], [average, manhattan], and [average, l1] at 83%. We see that these models yield the same result with 1 less false negative (19% FNR) compared to the initial model.

Next, we are going to try the K-means clustering method to see whether there is any differences.

[21]:

```
# inital kmeans test run.
kmeans = KMeans(n_clusters=2, random_state=41).fit(features)

# max was done here to find whether the 0 label = 0 or 0 label = 1.
print('accuracy:', max(sum(kmeans.labels_ == data.ca_cervix), sum(kmeans.
 ↪labels_!=data.ca_cervix)) / n)

sns.heatmap(confusion_matrix(y_pred=kmeans.labels_, y_true=np.array(data.
 ↪ca_cervix)), annot=True)
plt.show()
```

```
accuracy: 0.7777777777777778
```



- Accuracy: 78%
- FNR: 19%

The initial K-means model yielded a lower accuracy, 5% less, than the best hiearchical model.

Let's see if there can be any further adjustments to be made.

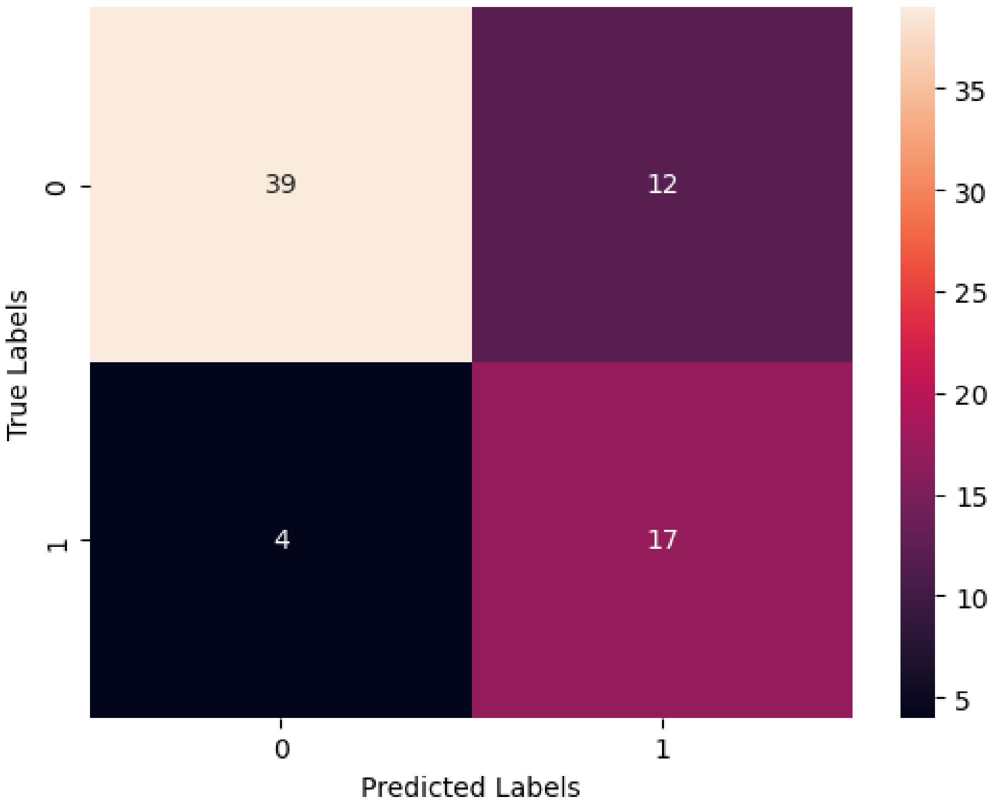
[22]:

```python
# prints kmeans combination/accuracy and confusion matrix
# prints only the best and increasingly higher accuracy models.
def kmeanscluster(features_df, n):
    acc = 0
    for i in ['auto', 'elkan']:
        for j in ['k-means++', 'random']:
            km_mod = KMeans(n_clusters=2, init=j, algorithm=i, random_state=41).fit(features_df)
            total = max(sum(km_mod.labels_ == np.array(data.ca_cervix)), sum(km_mod.labels_ != np.array(data.ca_cervix)))
            acc_mod = total/n
            if acc_mod >= acc:
                acc = acc_mod
                print(i, j, round(acc, 5))
                sns.heatmap(confusion_matrix(y_pred=km_mod.labels_, y_true=np.array(data.ca_cervix)), annot=True)
                plt.ylabel('True Labels')
                plt.xlabel('Predicted Labels')
                plt.show()
```

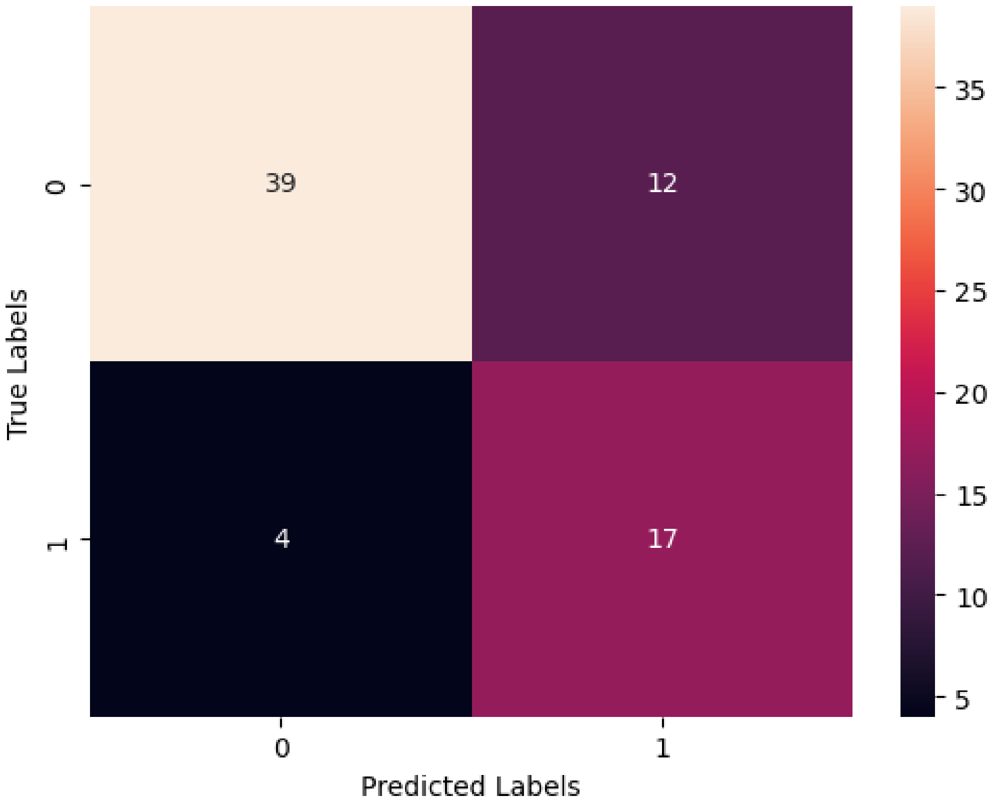
[23]:

```
kmeanscluster(features, n)
```

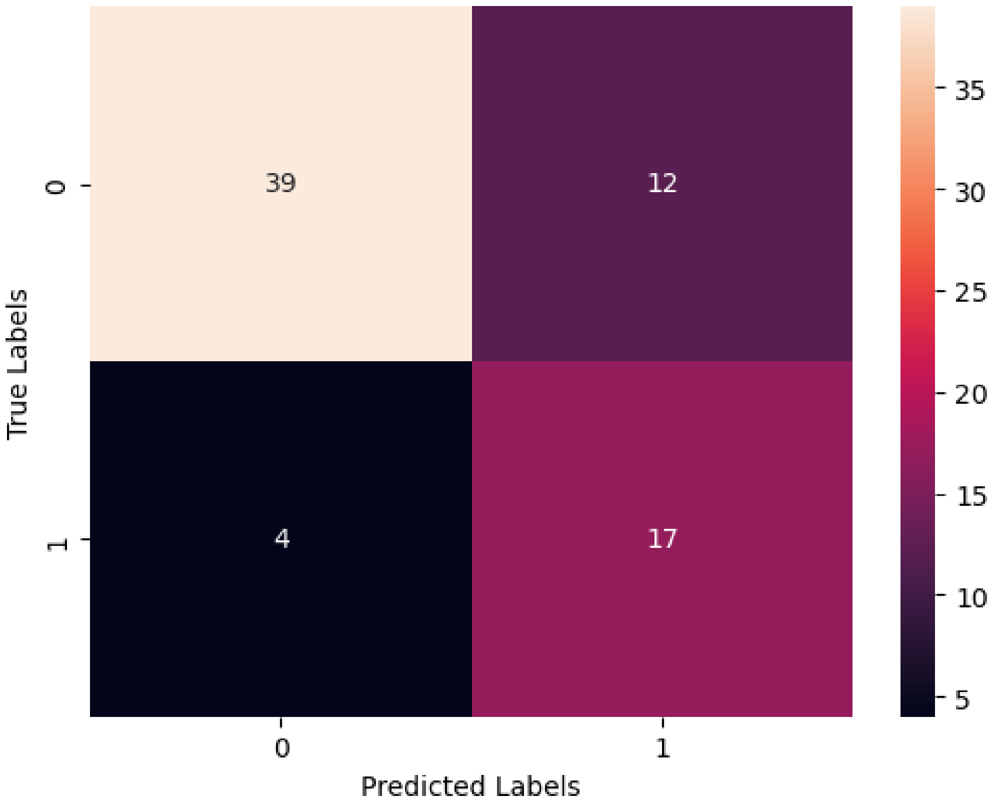
```
auto k-means++ 0.77778
```



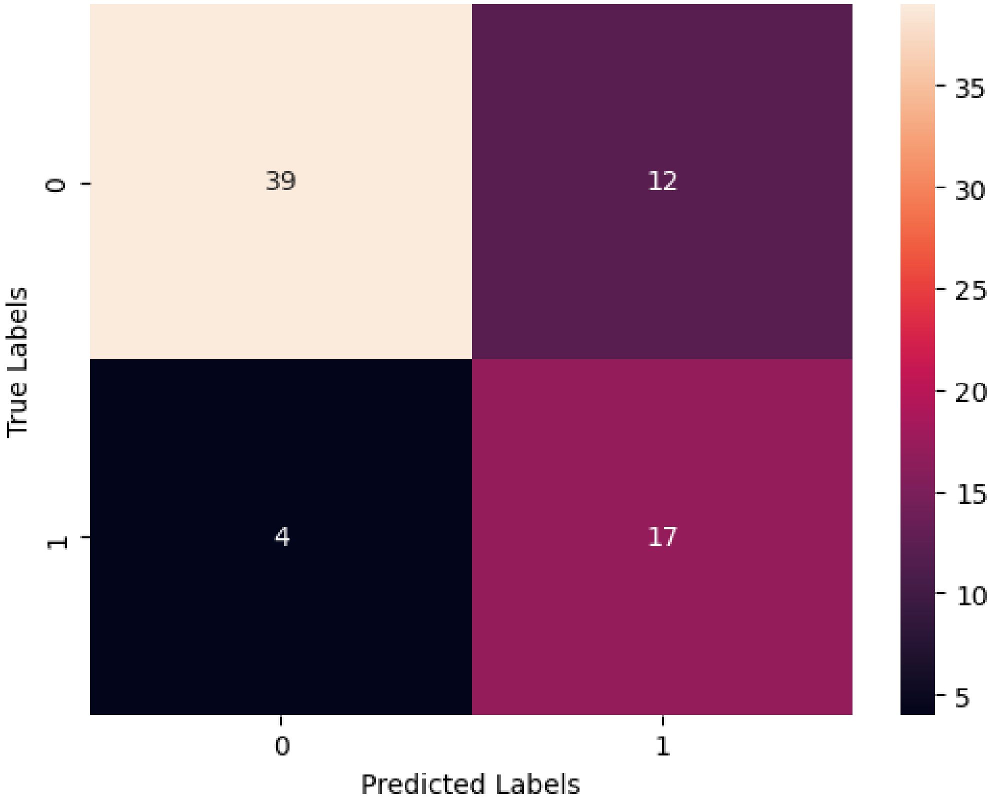
```
auto random 0.77778
```



```
elkan k-means++ 0.77778
```



```
elkan random 0.77778
```

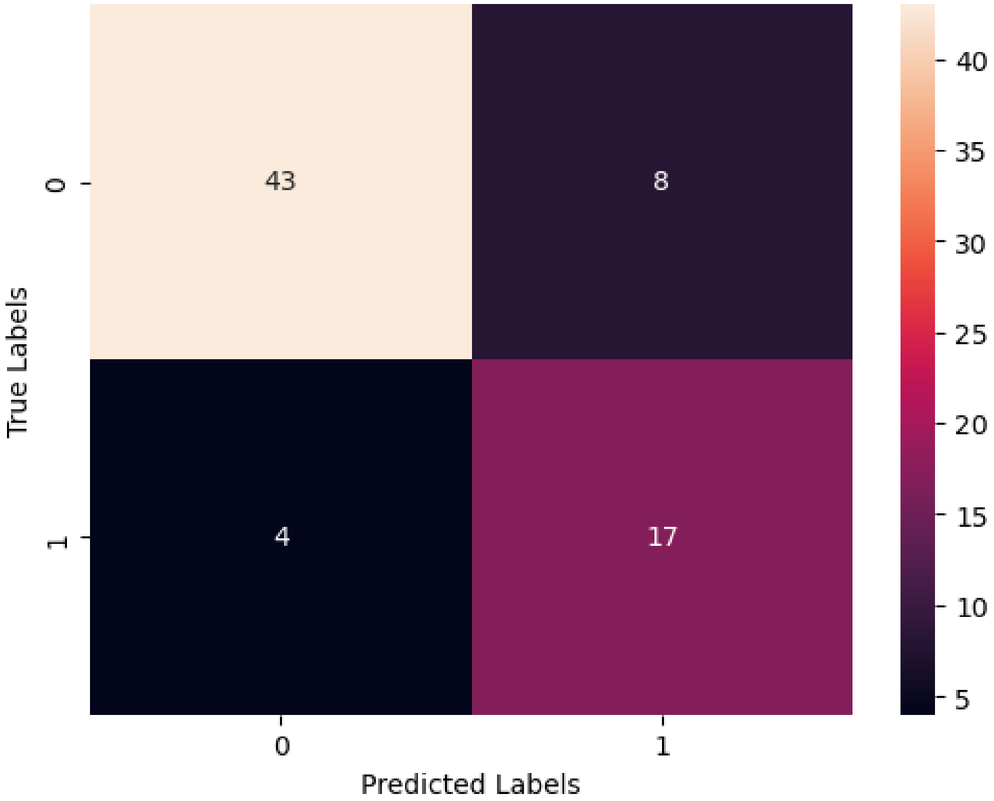


Looks like nothing changed even with different parameters.

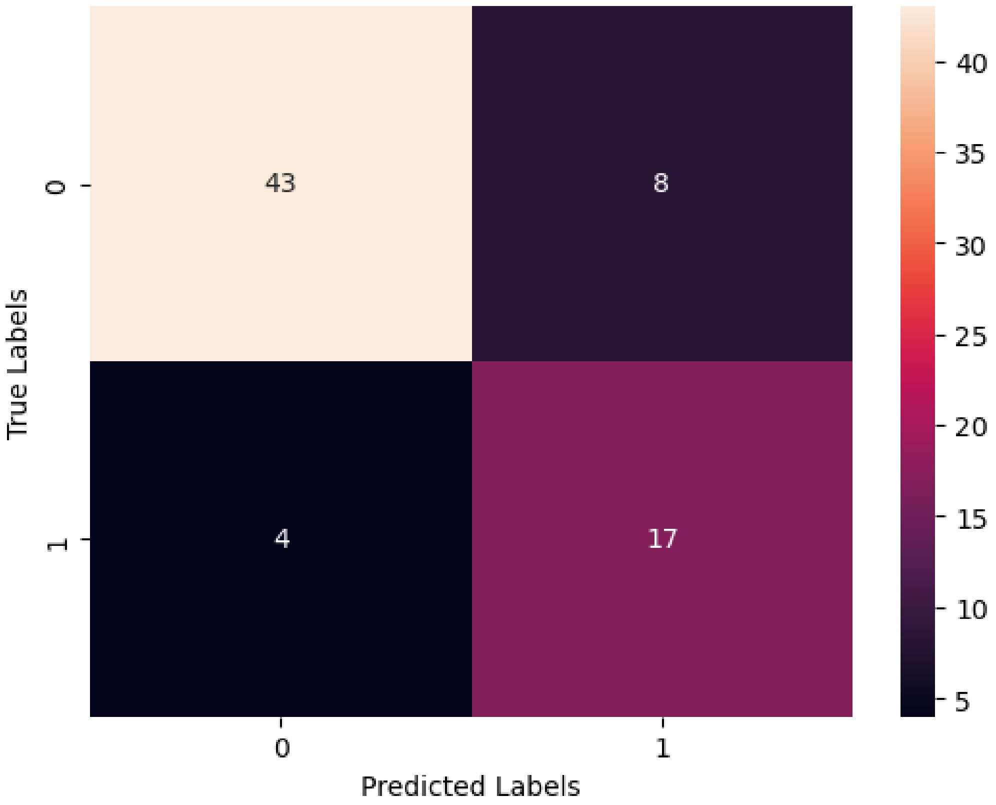
1.4.2 Using Scaled Features

```
[24]: agcluster(features_scaled, n)
```

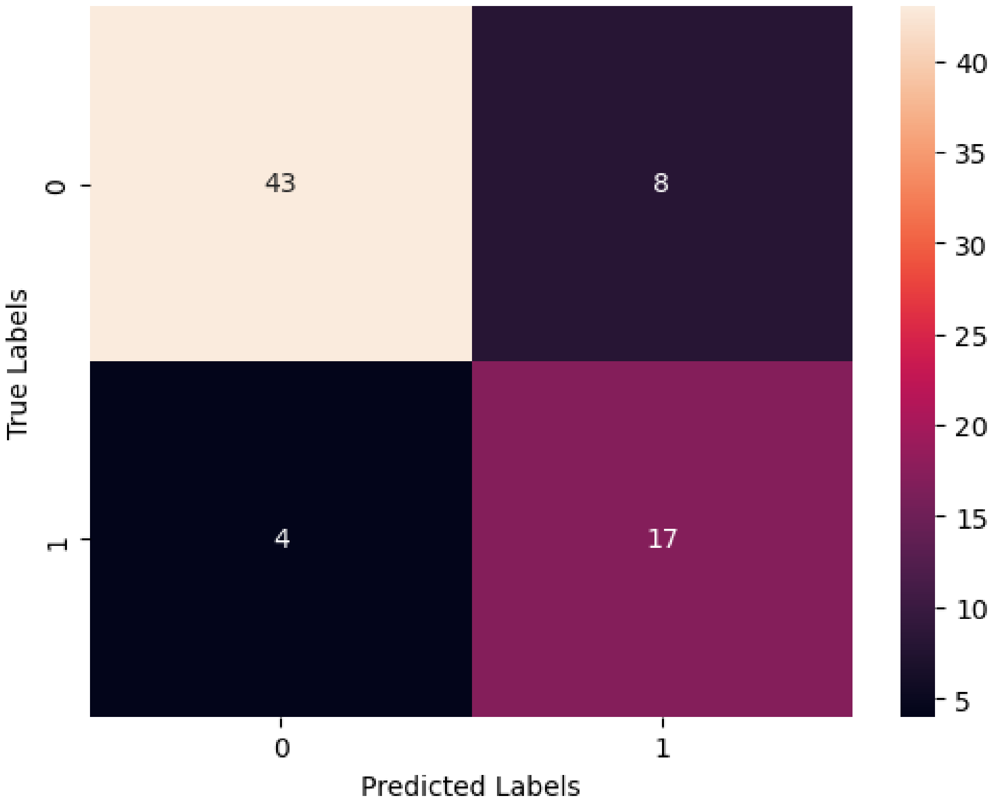
```
ward euclidean 0.83333
```



```
complete manhattan 0.83333
```



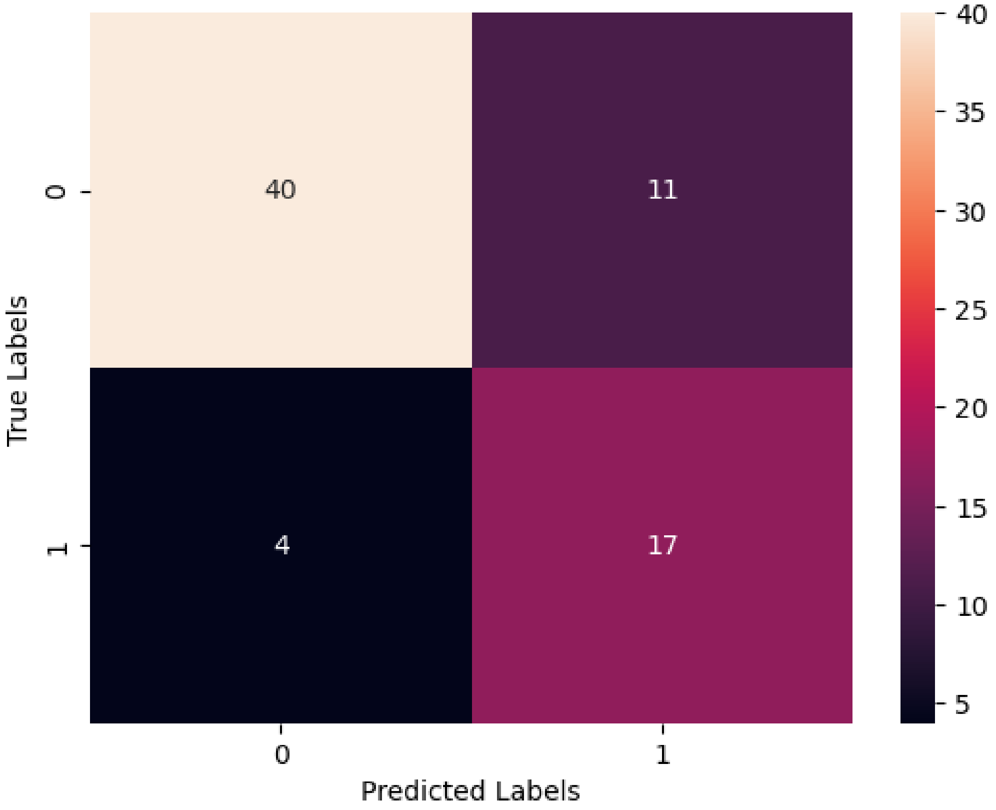
```
complete l1 0.83333
```



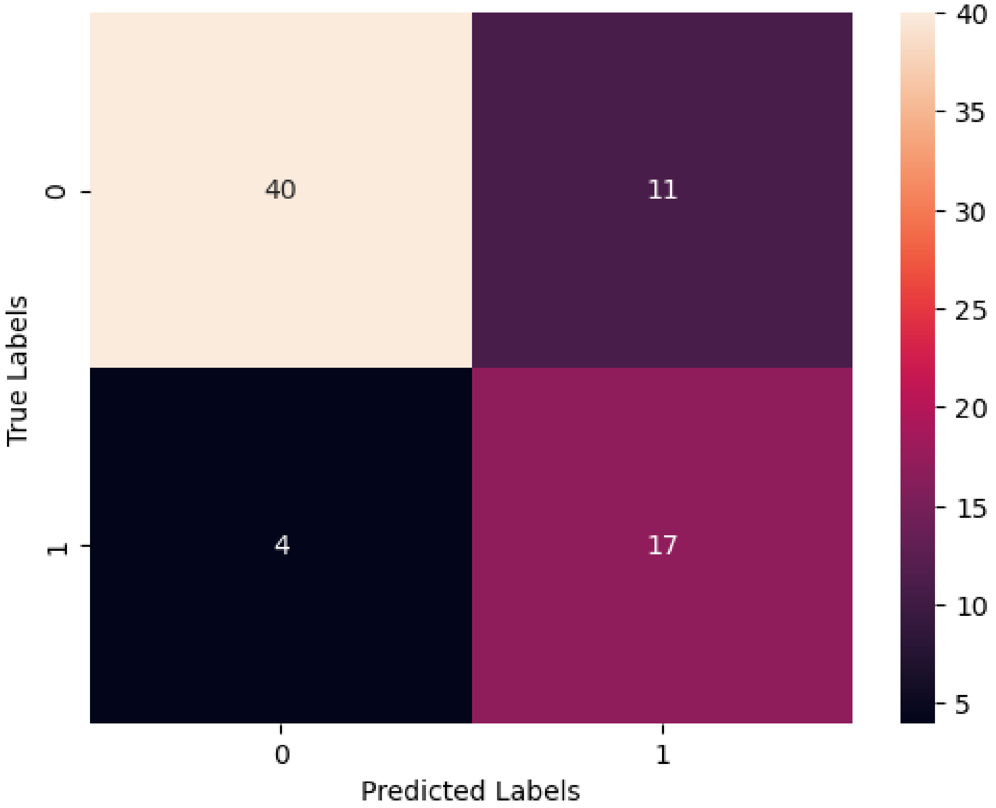
Nothing changed from the hierarchical model.

[25]:
```
kmeanscluster(features_scaled, n)
```

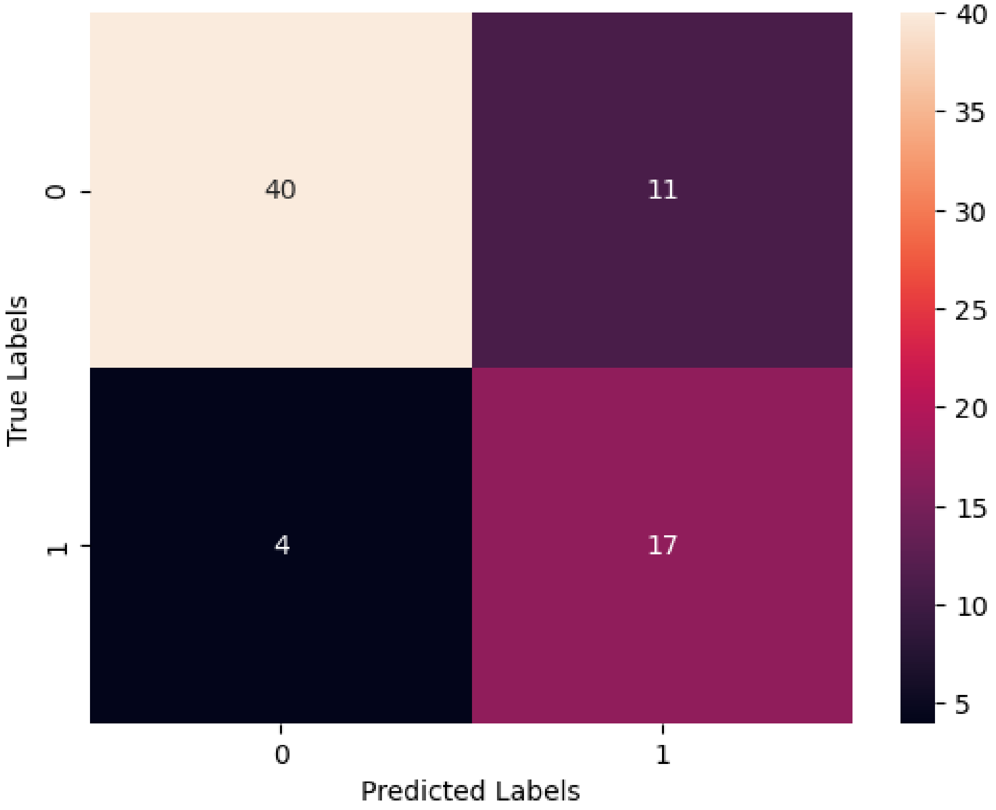
```
auto k-means++ 0.79167
```



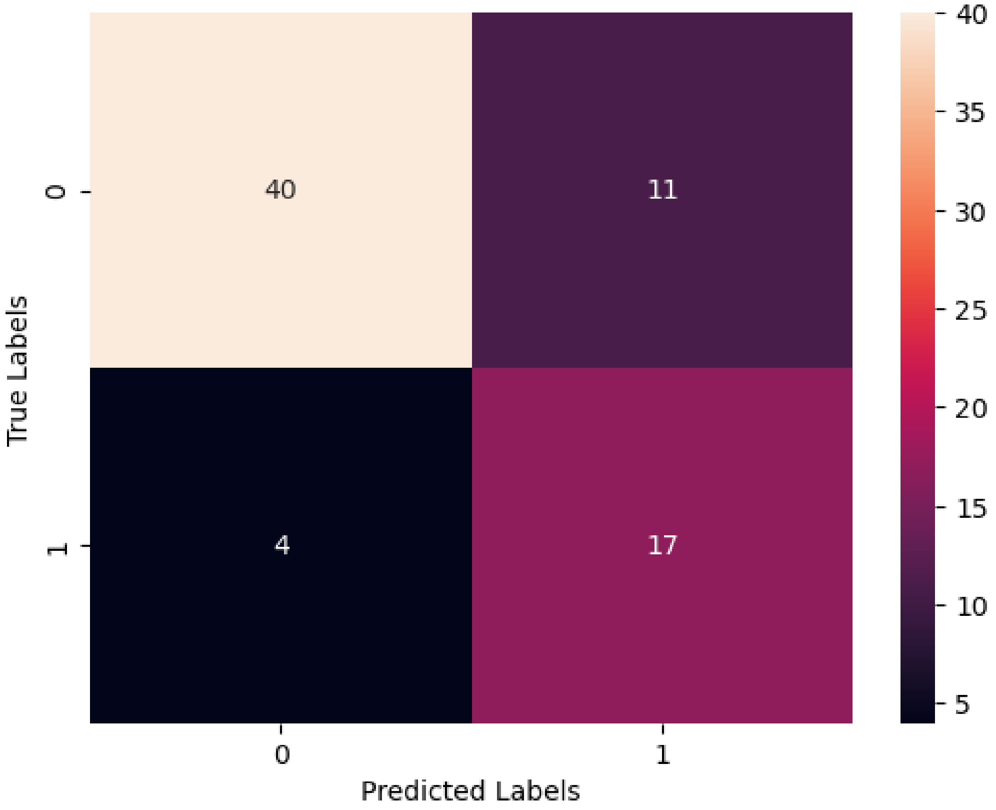
```
auto random 0.79167
```



```
elkan k-means++ 0.79167
```



```
elkan random 0.79167
```

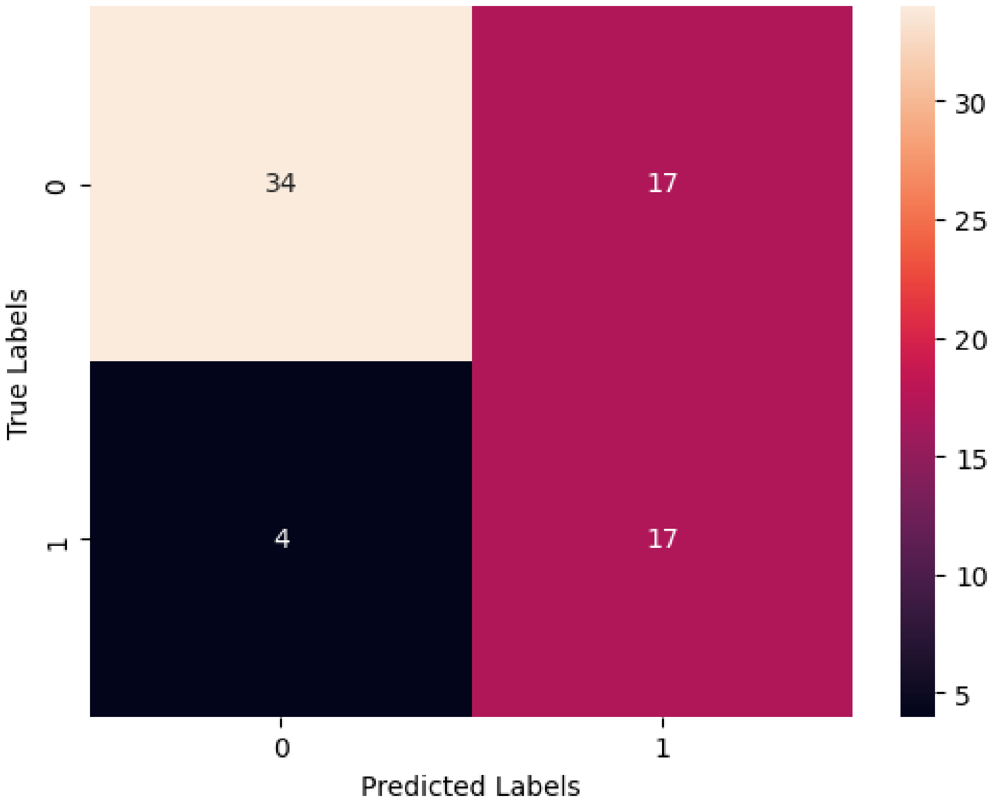


The K-means model does see a very small improvement in their accuracy - 78% to 79%. The FNR remains the same.

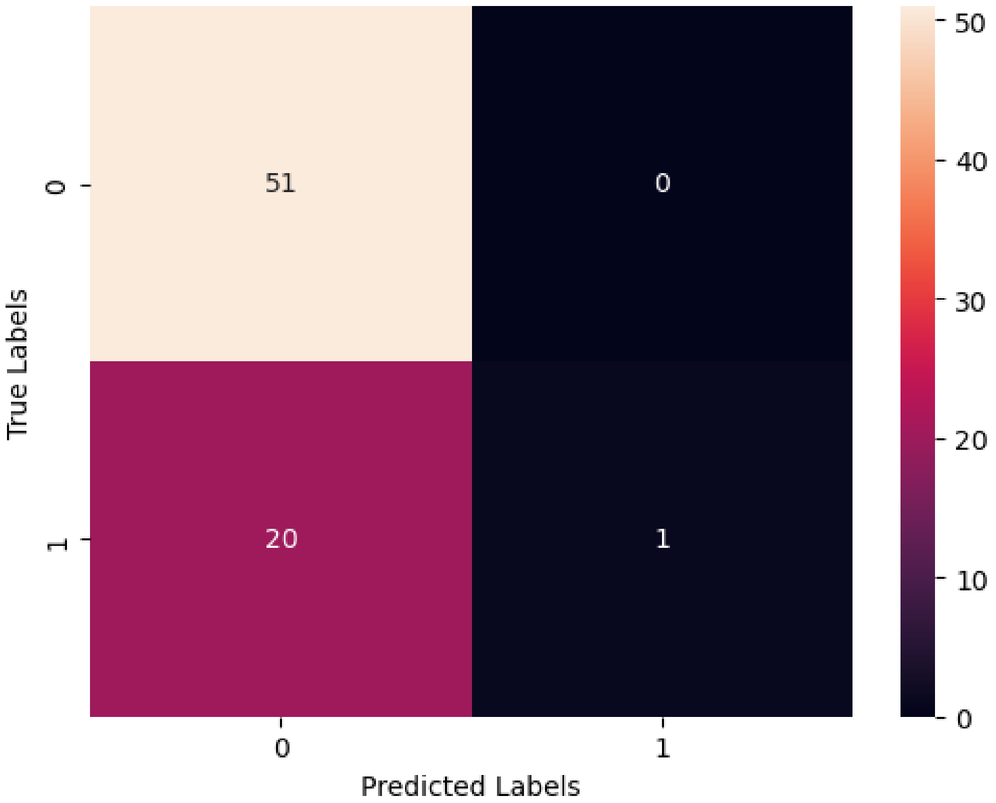
1.4.3 Using PCA Features

```
[26]: agcluster(pca_features, n)
```

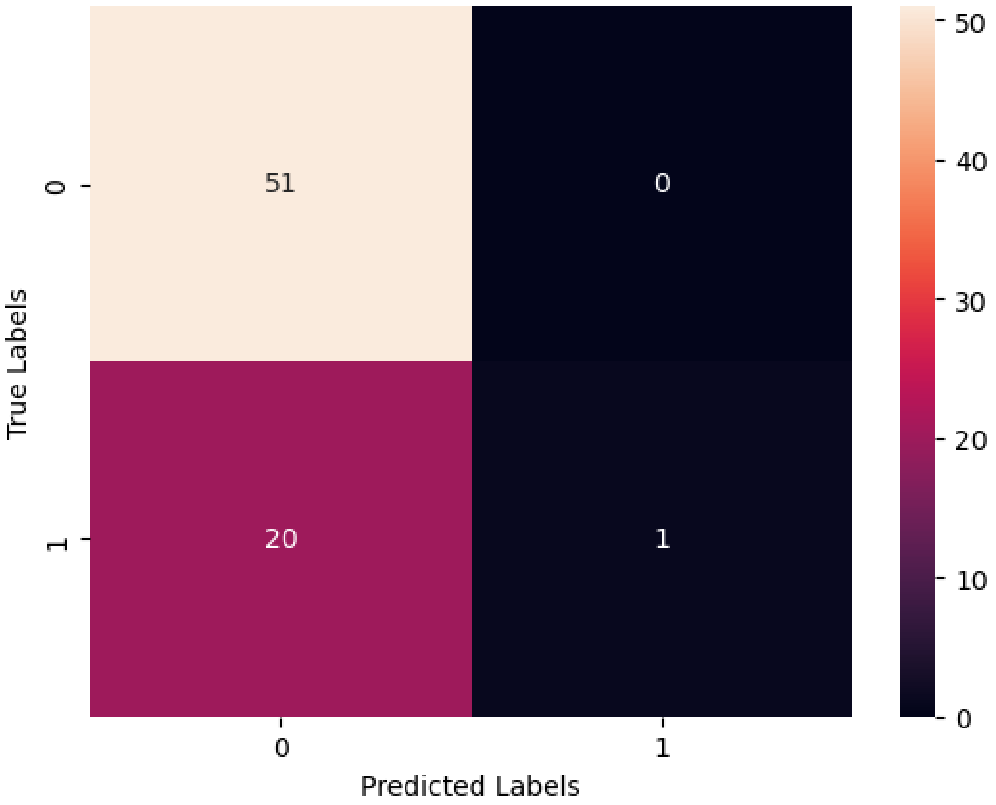
```
ward euclidean 0.70833
```



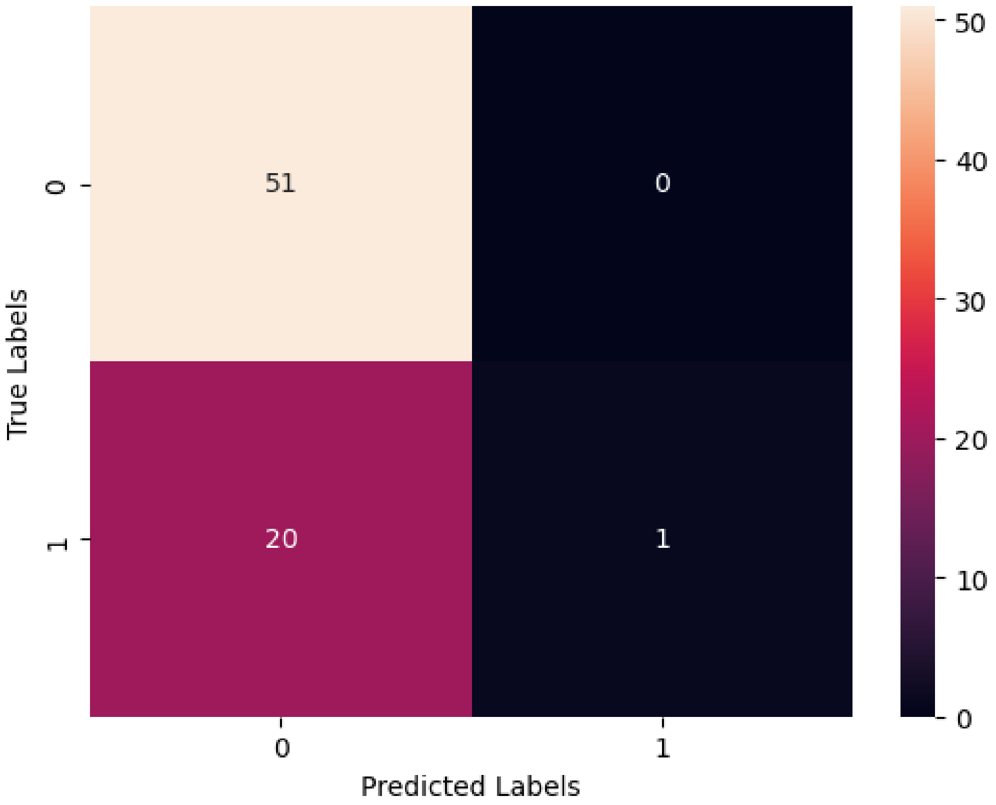
```
complete euclidean 0.72222
```



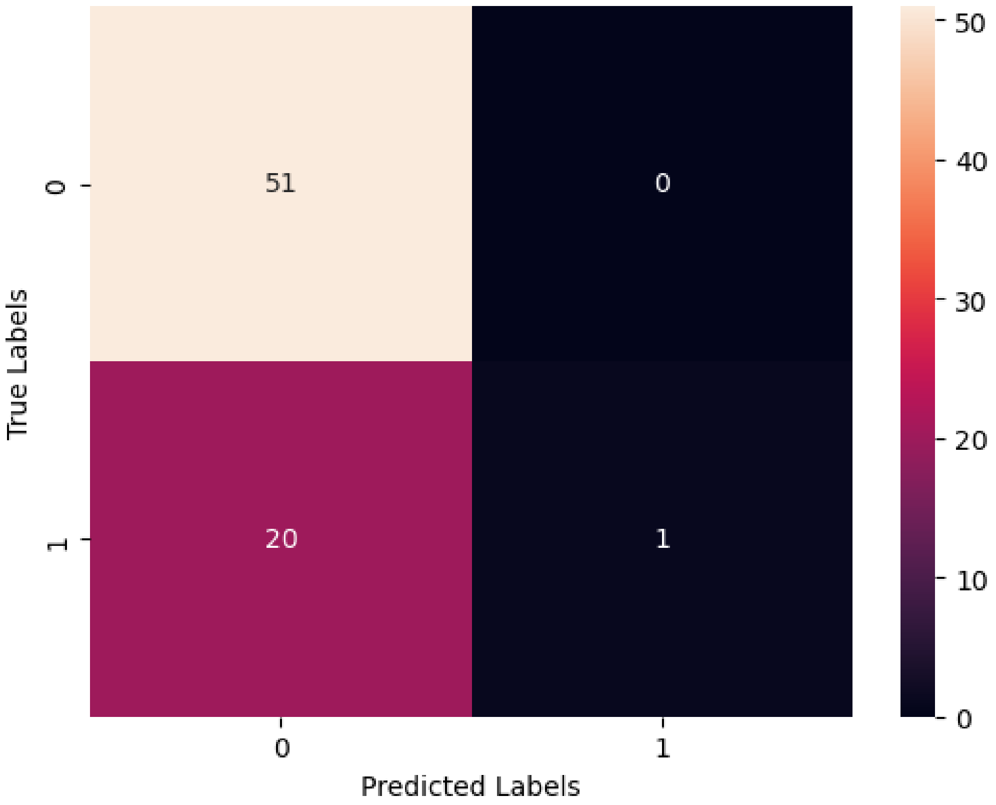
```
complete manhattan 0.72222
```



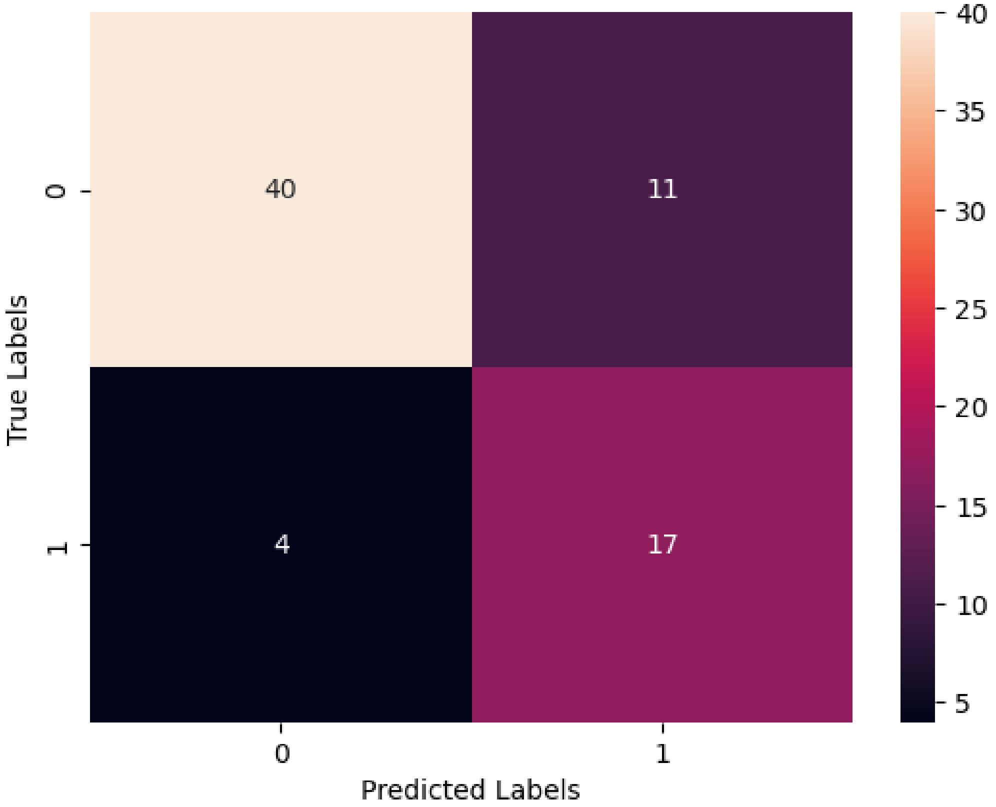
```
complete l1 0.72222
```



```
complete l2 0.72222
```

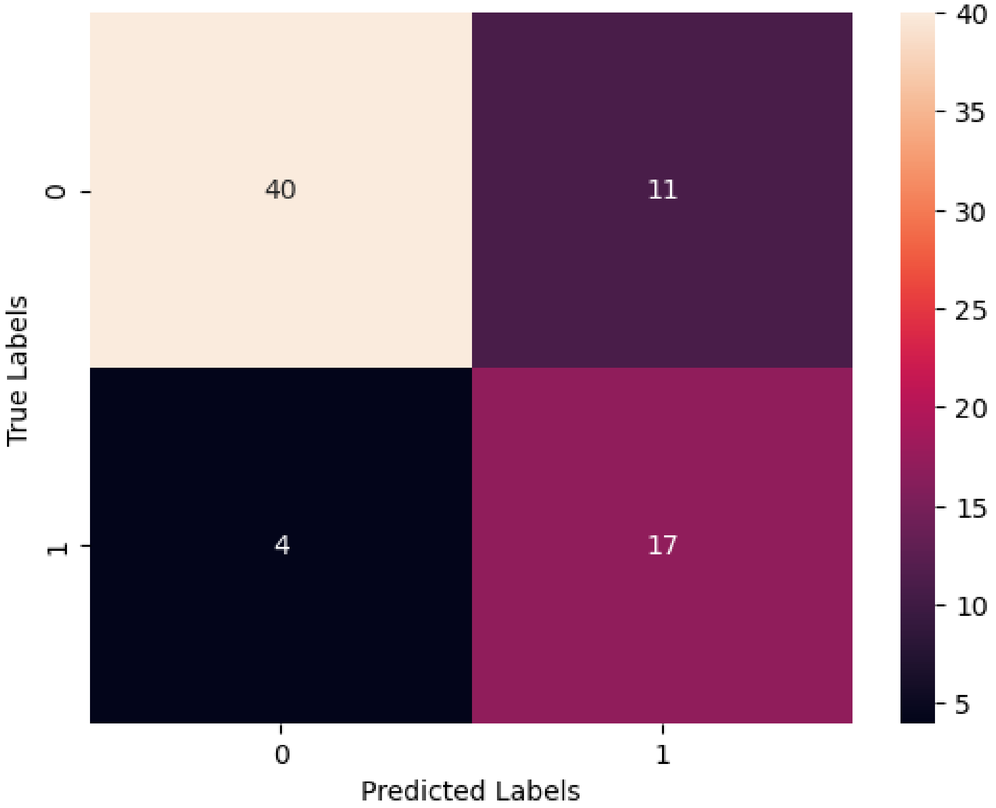


```
complete cosine 0.79167
```

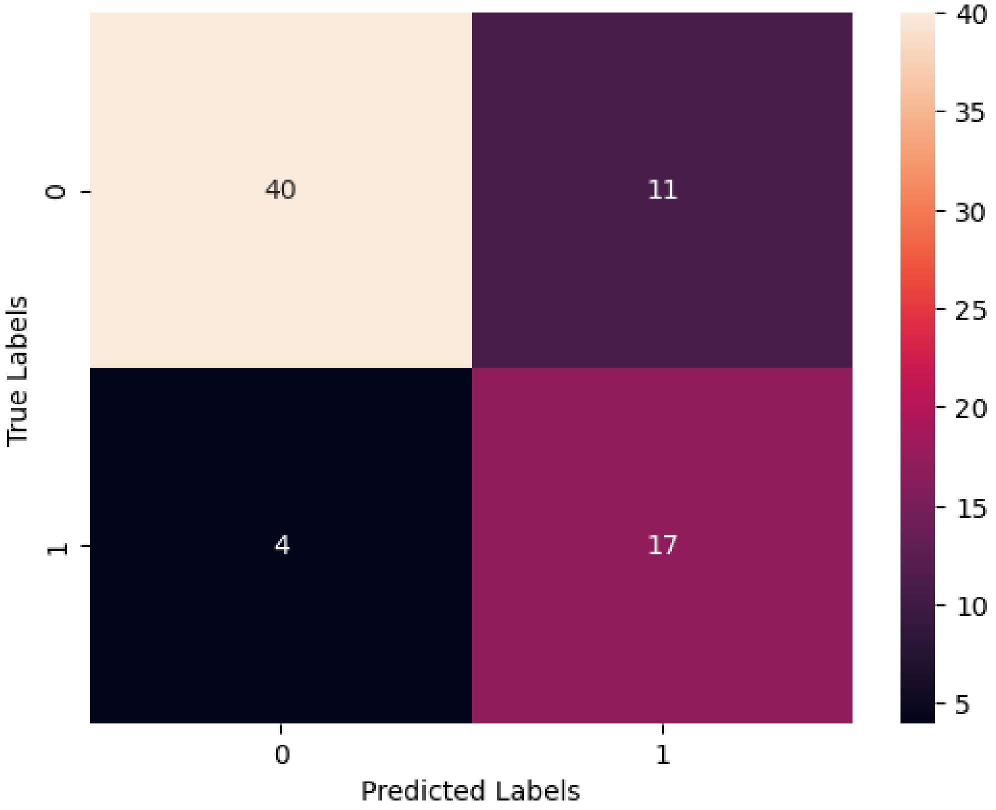


```
[27]: kmeanscluster(pca_features, n)
```

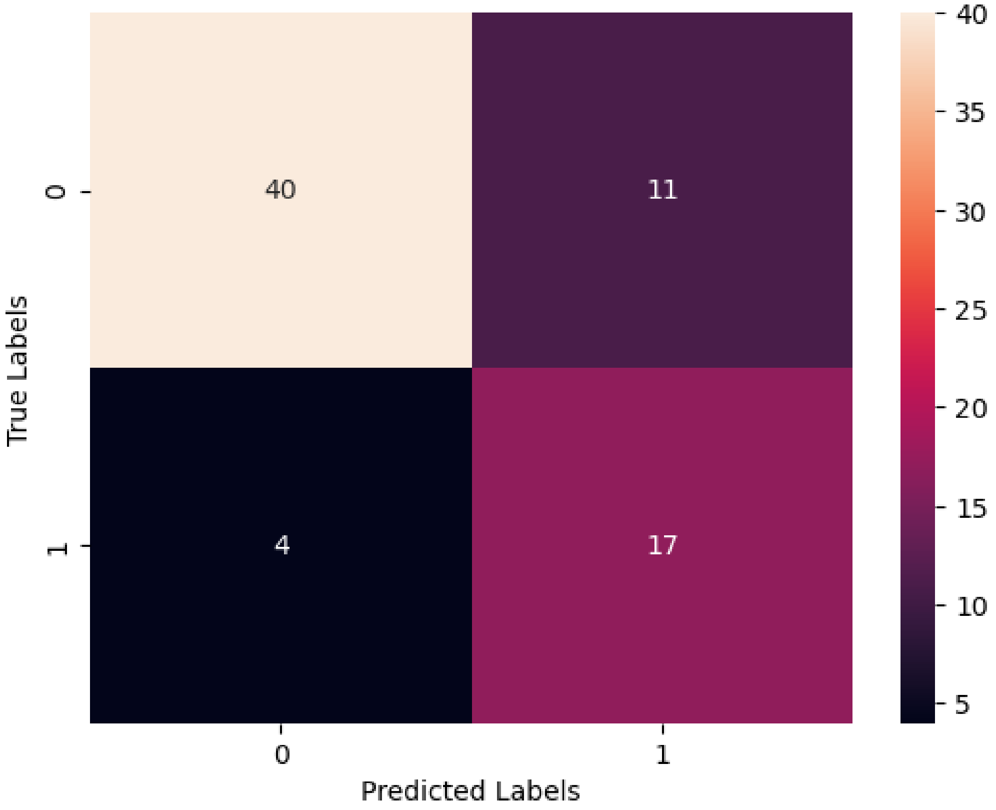
```
auto k-means++ 0.79167
```



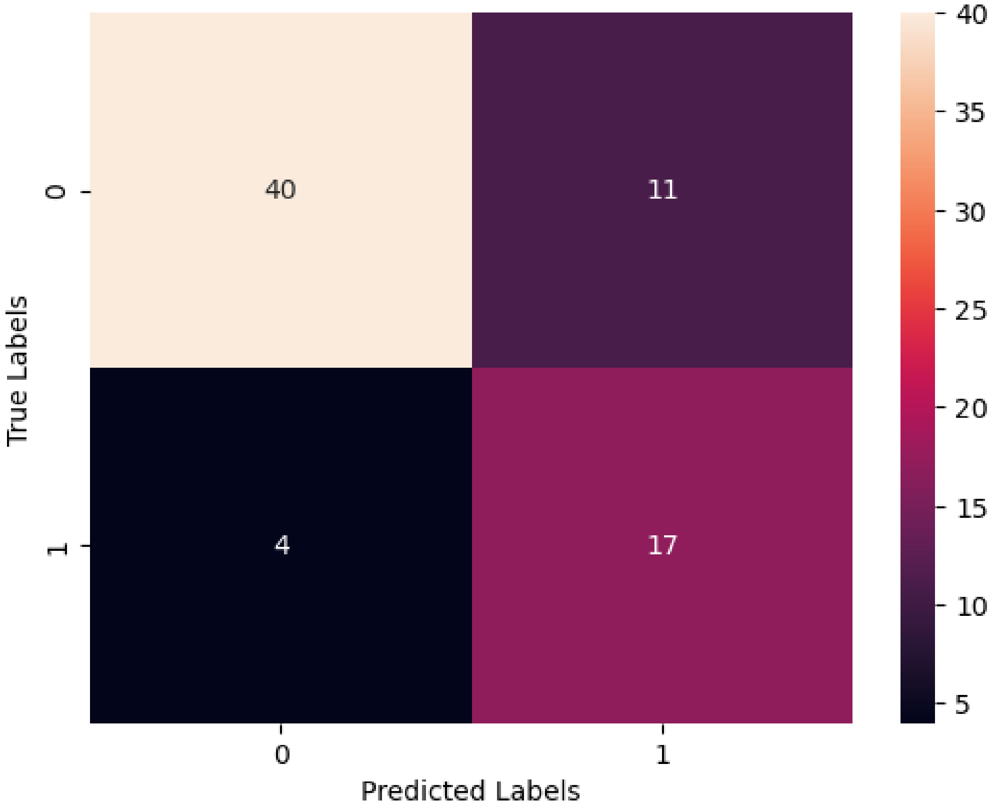
```
auto random 0.79167
```



```
elkan k-means++ 0.79167
```



```
elkan random 0.79167
```



1.4.4 Summary

Method	Original Features	Scaled Features	PCA Features
Hiearchical Clustering	0.833	0.833	0.792
KMeans Clustering	0.778	0.792	0.792

In summary we see that scaling the features increased the K-means result and that performing pca on the scaled features yielded the same result. In contrast, the hierarchical clustering yielded the highest accuracy on the original dataset and after scaling it. The FNR is not shown but it was the same for all best models under each category at 19%.

The hiearchical clustering yielded the highest accuracy using the original dataset probably because there was more context involved in the clustering which helped group certain points together. K-means didn't do as well there because the scaling was different very some features which may have caused some points to be further away then should be. Also K-means is highly susceptible to the effects of outliers and remember, there were some points that were outliers which may have caused the mean centroids to shift in certain directions that would miss some points. You do see it improve after scaling.

In general, it would be best to scale the features for clustering and in this case, hierarchical clustering is the best model.

1.5 Discussion

Cervical cancer is one of the cancers that when found early, can be treatable. It is important to find methods to be able to detect it early on. Previously mentioned, there are screening tests that can help detect the presence of the HPV itself and signs of cell changing but these are pretty much after the fact. If we were able to use behavior determinants to find people at risk of cervical cancer, prventative measures can given to the people.

As we see from the results, clustering can help determine the presence/absence of cervical cancer with an overall accuracy of 83% and a false negative rate of 19%. It is a decent model and can be used as possible precursory test to find people at risk of cervical cancer.

It is important to consider that the data was obtained via a questionaire. Questionaires are subject and the phrasing of questions may cause different understanding of what is asked of the respondents. We also don't know what was asked for each behavioral determinant in the questionaire. Another consideration is the location of the survey. The dataset values originally came from responses from Indonesian women. Not to say they are not important, but due to the culture, the data may not be representative for the entire women population.

For future works, hopefully there would be more data available and perhaps more variety in the data. Variety in terms of the nationality of the women so we can see a more representative response and thus a more representative model.

1.6 Conclusion

Hierarchical modeling is a viable method for determining women at risk of cervical cancer based on their behavioral determinants. The model yield a decent accuracy of 83% and a false negative rate of 19%. It seems relatively high for some but the result came from a dataset with 72 points and fewer examples of true positives. There are some improvements that could be done but in the context of women in Indonesia, this hierarchical modeling is potential screening method for cervical cancer.