visualize

May 8, 2022

[1]:
```python
from sklearn.cluster import KMeans
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn import metrics
from sklearn.cluster import AgglomerativeClustering

from collections import Counter
import csv
```

[2]:
```python
# rawcount
from collections import Counter
import csv

def rawcount(filename, vocab, output):
    word_i = {}
    with open(vocab, 'r') as v:
        i = -1
        for word in v:
            if i == -1:
                i += 1
                continue
            word = word.strip()
            word_i[word.split(',')[1]] = i
            i += 1

    with open(output, 'w') as out:
        wr = csv.writer(out)

        with open(filename, 'r') as f:
            i = -1
            for line in f:
            # ignore the header
                if i == -1:
                    i += 1
                    continue
                # remove \n
                line = line.strip()

                words = line.split(',')
                p, seq = words[0], words[1:]
                counter = Counter(seq)
                p_rep = [0]*len(word_i)

                for key, freq in dict(counter).items():
                    p_rep[word_i[key]] = freq

                wr.writerow([p]+p_rep)
```

1 Cluster Cohorts of Patients in Synthetic Data

[3]:
```
convae_data_1 = pd.read_csv('synthetic/TRconvae-avg_vect_1.csv', header=None)
convae_data_1 = convae_data_1.drop(columns=[0])
convae_data_1.head()
```

[3]:
```
        1         2         3         4         5         6         7    \
0 -0.245492 -1.723636 -0.217432  1.412599  2.090927  3.460979  3.219759
1 -0.177317  0.581434 -0.233557 -0.819438 -0.856149  1.534644  0.902444
2 -0.086251  0.289699 -0.127992 -0.498970 -0.148464  1.362606  0.810772
3 -0.650934 -0.204592 -0.168182 -1.271896 -0.134454  1.193196  0.795659
4  0.338212  1.027026  0.182270 -1.075088 -0.242471  0.488513  1.398482

        8         9         10   …       91        92        93        94   \
0  2.154350  1.517181  2.821212  … -1.767284 -1.005675 -1.898477 -2.506755
1  0.126829  0.291722  0.764937  … -0.202243  0.865371 -0.551938 -0.140060
2 -0.163232 -0.435123  1.222380  … -0.430280  0.629954 -0.565389  0.090852
3  0.319215 -0.724538  1.937363  … -0.066636 -0.058400 -1.086811 -0.447154
4 -0.588494  0.183105  0.659151  … -0.729216  1.467192  0.488018 -0.057133

        95        96        97        98        99        100
0  2.391586  1.796674  0.014357 -1.714161 -1.905629 -2.658079
1  0.598072  0.185291  1.061913 -0.093946  0.092072  0.465387
2  0.130159  0.272310  0.473577 -0.101833 -0.001948  0.319315
3  0.839730  0.917877  0.798910 -0.865329 -0.244640 -0.172857
4 -0.086303 -0.434823  1.025620  0.104759  0.261447  0.593806

[5 rows x 100 columns]
```

[4]:
```
convae_data_2 = pd.read_csv('synthetic/TRconvae-avg_vect_2.csv', header=None)
convae_data_2 = convae_data_2.drop(columns=[0])
convae_data_2.head()
```

```
[4]:          1         2         3         4         5         6         7    \
     0  3.460280 -1.165073  0.043982 -0.209492  0.691597 -0.023895  0.588930
     1  0.094355 -0.269476 -0.896734 -0.336747 -0.741758  0.211373 -0.197271
     2 -0.016761 -0.525858 -0.926781  0.099622 -1.112849  0.558424  0.014202
     3  0.121185  0.093348 -0.813224 -0.549337 -0.322482  0.427428 -0.452533
     4  3.246645 -0.045888  0.005351  0.497746 -0.444151  0.366363  1.445255

             8         9        10  …        91        92        93        94   \
     0 -0.065933 -0.062688 -2.780302  …  3.837300  1.916883 -0.023542 -0.230170
     1 -1.365462 -0.121160  0.344159  …  0.956573  0.295175  0.096312 -0.467132
     2 -1.164957  0.400407  0.595222  …  0.879721  0.042045  0.250709 -0.459051
     3 -0.515359 -0.242799  0.266890  …  0.112507 -0.083479  0.149594 -0.693066
     4  0.271684 -0.220651 -2.101012  …  3.391958  0.269805  0.052752  0.763482

             95        96        97        98        99        100
     0 -2.105041  3.084079 -1.048391 -1.242677 -1.625257  1.863790
     1 -0.473703  0.175847  0.034651 -0.062616  0.048358  0.423669
     2 -0.395686  0.296956  0.533112 -0.158044 -0.388362  0.519822
     3  0.206137 -0.243773  0.206056 -0.331201 -0.546232  0.411023
     4 -2.929876  1.655250 -0.830859 -1.148471 -2.996922  2.726214

     [5 rows x 100 columns]
```

```
[5]: ## run only when first time generates the raw count of the synthetic data
     # rawcount('synthetic/cohort-ehrseq.csv', 'synthetic/cohort-vocab.csv',␣
      ↪'synthetic/rawcount.csv')
```

```
[6]: rc_data = pd.read_csv('synthetic/rawcount.csv', header=None)
     rc_data = rc_data.drop(columns=[0])
     rc_data.head()
```

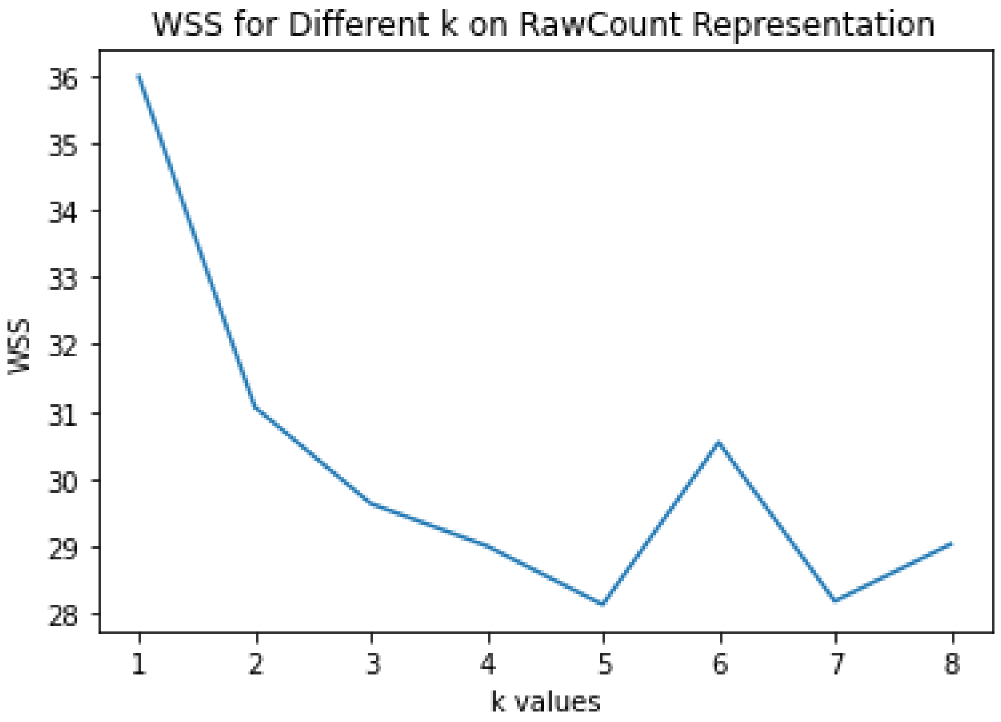
```
[6]:    1    2    3    4    5    6    7    8    9    10   …   191  192  193  194  \
     0    0    1    0    0    0    1    0    0    0    0  …     0    0    1    1
     1    0    0    0    0    0    1    0    0    1    0  …     0    0    0    0
     2    0    0    0    1    0    0    0    1    0    0  …     0    0    1    1
     3    0    0    0    0    0    0    0    0    1    0  …     0    0    0    1
     4    0    0    0    0    0    0    1    1    1    0  …     1    0    0    0

        195  196  197  198  199  200
     0    0    1    0    1    0    0
     1    0    0    0    0    1    0
     2    0    0    0    0    0    0
     3    0    0    0    1    0    0
     4    0    0    0    0    0    0

     [5 rows x 200 columns]
```

```
[7]: rc_data = rc_data.values
     convae_data_1 = convae_data_1.values
     convae_data_2 = convae_data_2.values
```

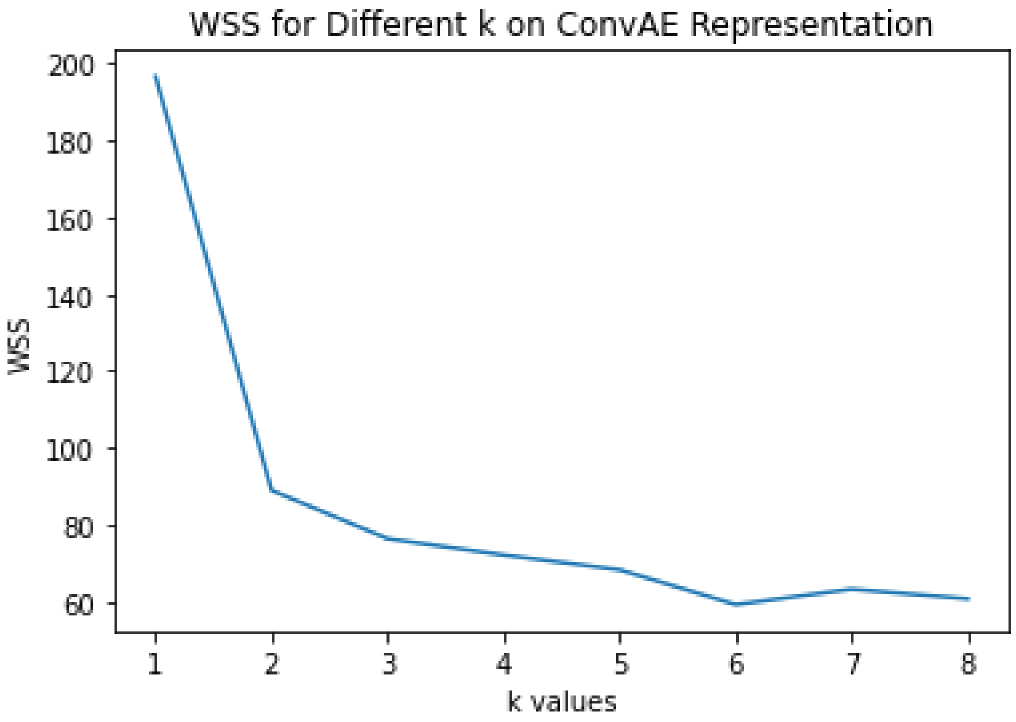
```
[8]: def calculate_WSS(points, kmax):
         sse = []
         for k in range(1, kmax+1):
             kmeans = KMeans(n_clusters = k, random_state=1234).fit(points)
             centroids = kmeans.cluster_centers_
             pred_clusters = kmeans.predict(points)
             curr_sse = 0

             # calculate square of Euclidean distance of each point from its cluster␣
      ↪center and add to current WSS
             for i in range(len(points)):
                 curr_center = centroids[pred_clusters[i]]
                 curr_sse += (points[i, 0] - curr_center[0]) ** 2 + (points[i, 1] -␣
      ↪curr_center[1]) ** 2

             sse.append(curr_sse)
         return sse
```

```
[9]: wss_score = calculate_WSS(rc_data, 8)
     plt.plot(range(1, 9), wss_score)
     plt.title("WSS for Different k on RawCount Representation")
     plt.ylabel('WSS')
     plt.xlabel('k values')
```

```
[9]: Text(0.5, 0, 'k values')
```



```
[10]: wss_score = calculate_WSS(convae_data_1, 8)
      plt.plot(range(1, 9), wss_score)
      plt.title("WSS for Different k on ConvAE Representation")
      plt.ylabel('WSS')
      plt.xlabel('k values')

[10]: Text(0.5, 0, 'k values')
```



```
[11]: pca = PCA(2)

      rc_data_2 = pca.fit_transform(rc_data)
      convae_data_12 = pca.fit_transform(convae_data_1)
      convae_data_22 = pca.fit_transform(convae_data_2)
```

1.1 k=2 clustering

```
[12]: cn = 2
      km_rc = KMeans(cn).fit(rc_data)
      km_convae1 = KMeans(cn).fit(convae_data_1)
      km_convae2 = KMeans(cn).fit(convae_data_2)
```

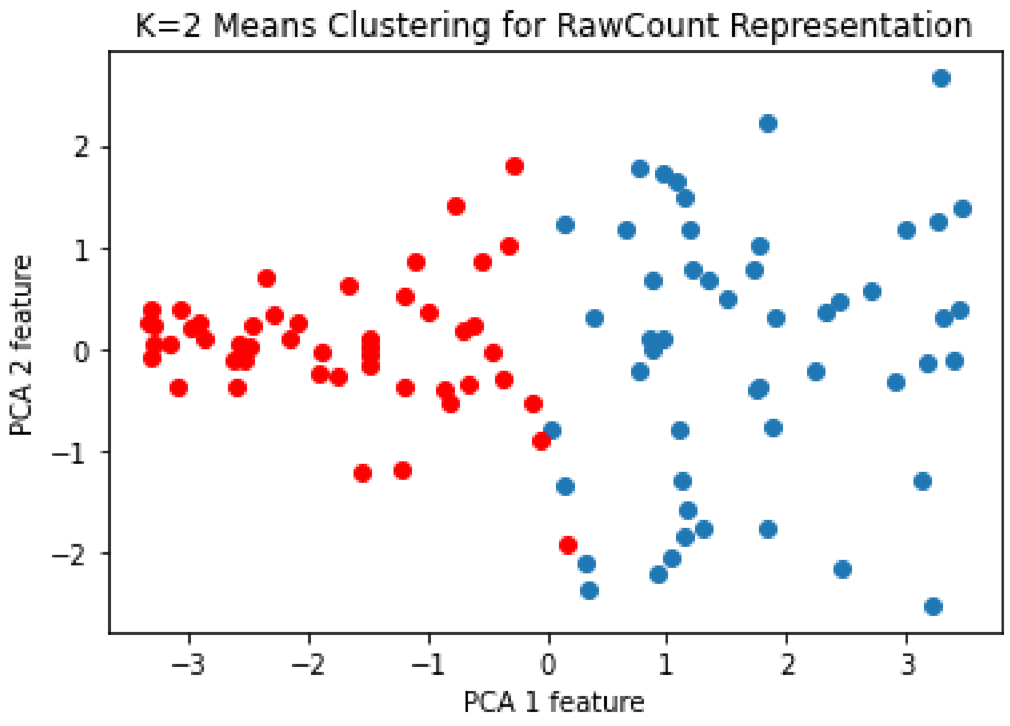
```
[13]: print(metrics.silhouette_score(convae_data_1, km_convae1.labels_))
      print(metrics.silhouette_score(convae_data_2, km_convae2.labels_))
      print(metrics.silhouette_score(rc_data, km_rc.labels_))
```

```
0.6171488014869471
0.6804293786556501
0.08214529130164738
```

```
[14]: rc_label1 = rc_data_2[km_rc.labels_ == 0]

      plt.scatter(rc_label1[:, 0], rc_label1[:, 1])
```

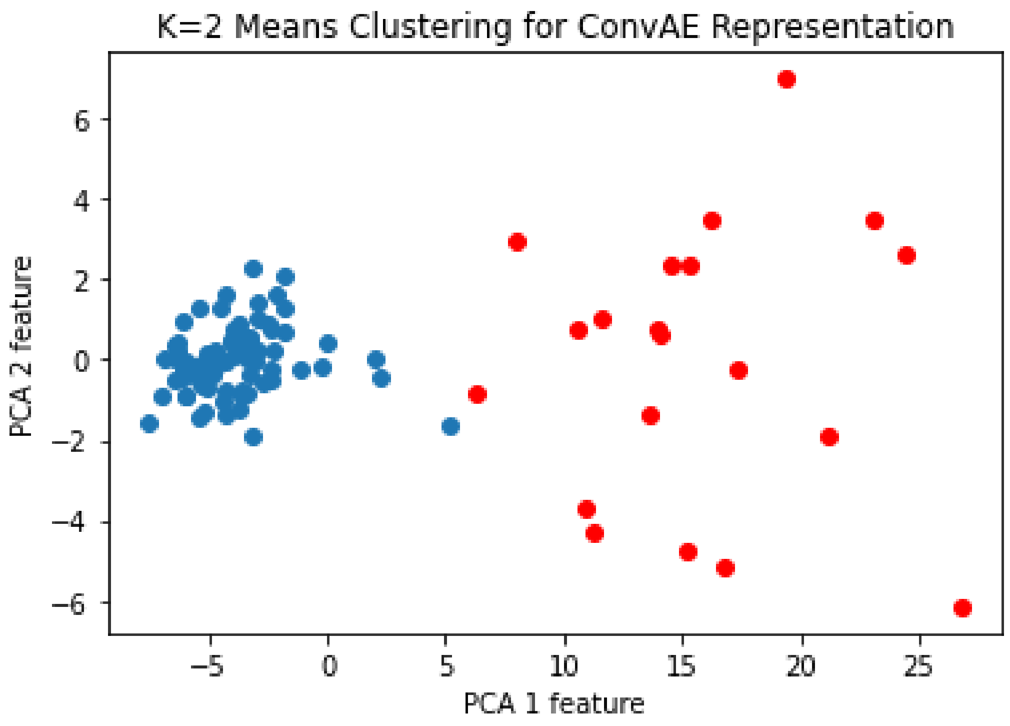
```
rc_label2 = rc_data_2[km_rc.labels_ == 1]
plt.scatter(rc_label2[:, 0], rc_label2[:, 1], color='red')
plt.title('K=2 Means Clustering for RawCount Representation')
plt.xlabel('PCA 1 feature')
plt.ylabel('PCA 2 feature')
```

[14]:
```
Text(0, 0.5, 'PCA 2 feature')
```



[15]:
```
convae_label1 = convae_data_12[km_convae1.labels_ == 0]

plt.scatter(convae_label1[:, 0], convae_label1[:, 1])
convae_label2 = convae_data_12[km_convae1.labels_ == 1]
plt.scatter(convae_label2[:, 0], convae_label2[:, 1], color='red')
plt.title('K=2 Means Clustering for ConvAE Representation')
plt.xlabel('PCA 1 feature')
plt.ylabel('PCA 2 feature')
```

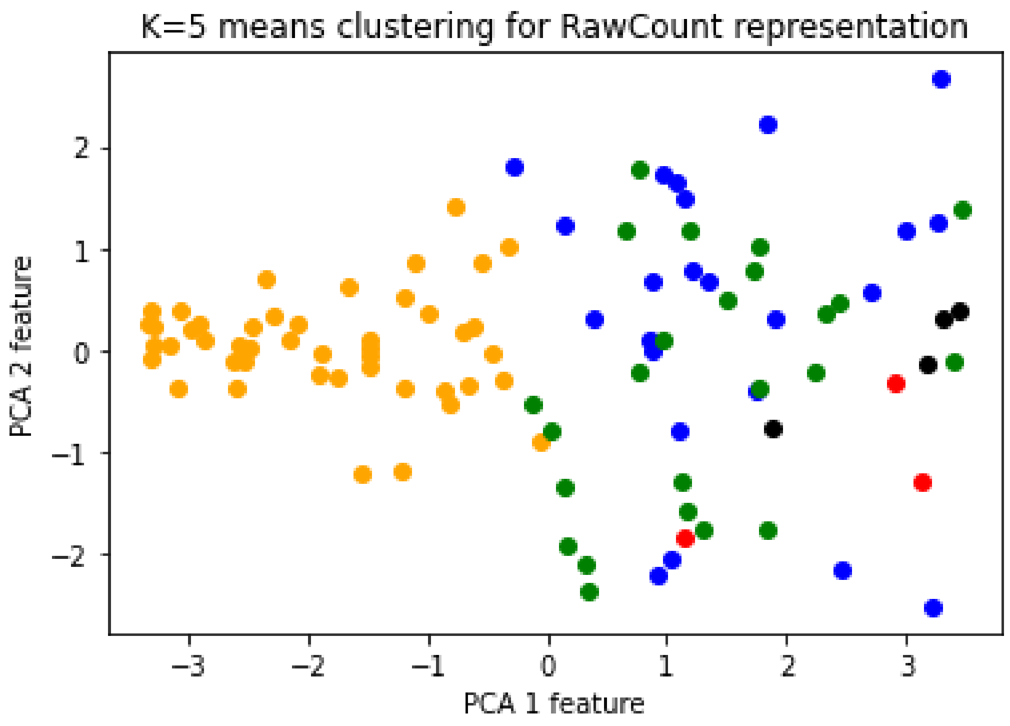
[15]:
```
Text(0, 0.5, 'PCA 2 feature')
```



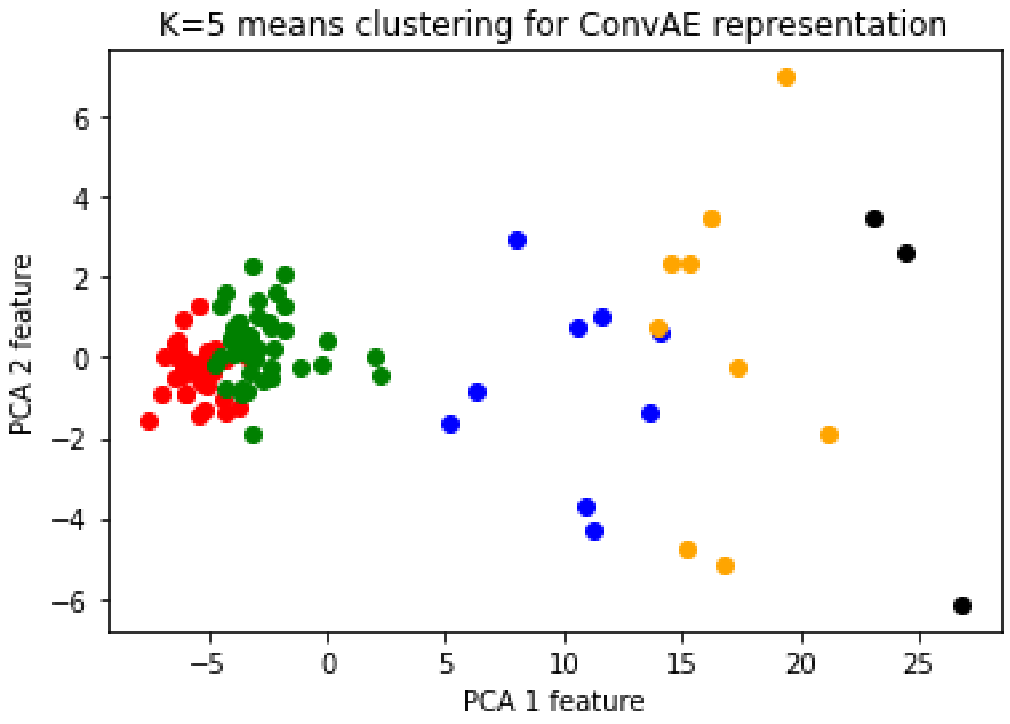
1.2 k=5 clustering

[16]:
```
cn = 5
km_rc = KMeans(cn).fit(rc_data)
km_convae_12 = KMeans(cn).fit(convae_data_1)
km_convae_22 = KMeans(cn).fit(convae_data_2)
```

[17]:
```
colors = ['red', 'blue', 'orange', 'black', 'green']
for label in range(5):
    rc_label = rc_data_2[km_rc.labels_ == label]
    plt.scatter(rc_label[:, 0], rc_label[:, 1], color=colors[label])

plt.title('K=5 means clustering for RawCount representation')
plt.xlabel('PCA 1 feature')
plt.ylabel('PCA 2 feature')
plt.show()
```



[18]:
```
colors = ['red', 'blue', 'orange', 'black', 'green']
for label in range(5):
    convae_label = convae_data_12[km_convae_12.labels_ == label]
    plt.scatter(convae_label[:, 0], convae_label[:, 1], color=colors[label])

plt.title('K=5 means clustering for ConvAE representation')
plt.xlabel('PCA 1 feature')
plt.ylabel('PCA 2 feature')
plt.show()
```



2 Suicide Risk Assessment based on Reddit Posts

2.1 Data Preprocess(no need to run this when evaluating the model)

```
[19]: import re
      import collections

      data = suicide_data = pd.read_csv('500_Reddit_users_posts_labels.csv')

      posts = []
      vocabulary = {}

      for userpost in data.Post.values:
          posts.append([])
          for post in userpost[2:-2].split('\','):
              posts[-1].append(re.sub('[^a-zA-Z0-9 \n]', '', post).lower())


              for word in posts[-1][-1].split(' '):
                  if word not in vocabulary:
                      vocabulary[word] = len(vocabulary)
          posts[-1] = ''.join(posts[-1])
```

```
train_idx = np.random.choice(len(posts), int(0.7*len(posts)), replace=False)
test_idx = np.array(list(set(range(len(posts))).difference(set(train_idx))))
train_posts = np.array(posts)[train_idx]
test_posts = np.array(posts)[test_idx]

with open('cohort-ehrseq.csv', 'w') as train_out:
    train_out.write('MRN,EHRseq\n')

    for i, p in enumerate(train_posts):
        word_list = p.split(' ')
        word_emb = [str(vocabulary[w]) for w in word_list]
        word_str = ','.join(word_emb)
        train_out.write(f'pat_{train_idx[i]},{word_str}\n')

with open('cohort_test-ehrseq.csv', 'w') as test_out:
    test_out.write('MRN,EHRseq\n')

    for i, p in enumerate(test_posts):
        word_list = p.split(' ')
        word_emb = [str(vocabulary[w]) for w in word_list]
        word_str = ','.join(word_emb)
        test_out.write(f'pat_{test_idx[i]},{word_str}\n')

with open('cohort-vocab.csv', 'w') as vocab_out:
    vocab_out.write('LABEL,CODE\n')

    for key in vocabulary:
        vocab_out.write(f'{key},{vocabulary[key]}\n')

np.save(
    open('train_idx.txt', 'wb'),
    train_idx
)
np.save(
    open('test_idx.txt', 'wb'),
    test_idx
)
```

2.2 Visualize Clustering

[20]:
```
convae_data_1 = pd.read_csv('suicide/TRconvae-avg_vect_1.csv', header=None)
convae_data_1 = convae_data_1.drop(columns=[0])
convae_data_1.head()
```

[20]:
```
          1         2         3         4         5         6         7   \
0  4.792002 -4.182917  0.504329  1.034935  6.722288  2.965201 -7.597964
1  3.031826 -2.228876  0.723921  1.243128  0.335348  0.966756 -2.259586
```

```
2  4.347315  0.317548   9.783994  1.039316 -6.086713 -3.634538 -2.878214
3  4.722687  1.320996  12.259055  0.045357 -7.071722 -4.573728 -3.511061
4  2.957799 -2.804701  -1.197343  1.118323  2.548878  1.793160 -3.890705

         8         9         10  …        91        92        93        94   \
0  6.288152  1.327902 -3.691782  … -4.469840 -0.809733  2.743039  2.791558
1  2.042837  1.677121 -2.544549  … -2.905806 -1.389448  1.969885  0.689893
2  2.623119  0.926128 -3.325168  … -2.733623 -2.882202  4.613301 -1.638416
3  2.502617  0.535087 -2.168540  … -2.568284 -2.593325  6.170129 -3.251006
4  1.929259  1.277872 -2.188694  … -2.946431 -0.506851  1.684679  1.369734

         95        96        97        98        99        100
0  3.434430  5.926430 -1.437946 -2.517109  5.947384  3.499781
1 -0.540738  2.790236  0.998298 -2.344237  3.917216  1.695267
2 -0.787181  1.801085  2.008439 -2.242496  3.588685  0.511575
3 -0.783794  1.943220  1.631231 -3.375519  3.806715 -0.969864
4  0.733448  3.910773  0.118717 -2.856843  4.061832  1.492922

[5 rows x 100 columns]
```

```
[21]: convae_data_2 = pd.read_csv('suicide/TRconvae-avg_vect_2.csv', header=None)
      convae_data_2 = convae_data_2.drop(columns=[0])
      convae_data_2.head()
```

```
[21]:         1         2         3         4         5         6         7    \
0 -0.265760  1.819030  2.114592 -1.503902  1.709242  1.080806  2.508768
1 -0.111605  2.074826  2.444105 -1.740146  1.859789  0.832969  2.819070
2 -1.081815  4.426412  3.382702 -3.064773  1.503283  2.644223  3.081339
3 -1.153381  2.246483  1.979828 -1.829293  1.712191  1.823514  2.249827
4 -0.747093  3.698134  2.605899 -3.106969  1.862821  2.313798  2.278987

         8         9         10  …        91        92        93        94   \
0  2.006261 -2.160024  1.149742  … -0.761870  0.483298  2.443803 -0.542755
1  2.144344 -2.465429  1.165465  … -0.809549  0.820165  2.769438 -0.086744
2  1.536571 -4.454443  0.523732  … -0.469871  0.311442  2.297619  0.251516
3  1.622034 -2.578066  0.850274  … -0.643407 -0.029906  1.923287 -0.989684
4  1.505187 -3.374255  0.680390  … -1.077267 -0.205817  1.848762  0.063171

         95        96        97        98        99        100
0  0.534815 -1.088351 -2.180832 -2.487342 -1.508296 -1.993607
1  0.541063 -1.366083 -2.689430 -2.858235 -1.534366 -2.045888
2 -0.340333 -2.125811 -5.249793 -2.501698 -1.029516 -1.661276
3  0.266016 -1.610323 -2.569872 -2.158781 -1.231015 -1.765235
4 -0.293556 -1.952785 -4.631961 -2.074854 -1.011812 -1.770192

[5 rows x 100 columns]
```

[22]:
```
rc_data = pd.read_csv('suicide/suicide_rawcount.csv', header=None)
rc_data = rc_data.drop(columns=[0])
rc_data.head()
```

[22]:
```
   1      2      3      4      5      6      7      8      9      10     …  \
0      6      7     22      0      2     38      3     15      0     10  …
1      0      1      2      0      0      1      0      0      0      0  …
2      4      4     27      0      0     26      2     10      0     18  …
3      0     11     42      0      0     76      1     26      0     18  …
4      0      1      2      0      0      8      0      1      0      2  …

   22920  22921  22922  22923  22924  22925  22926  22927  22928  22929
0      0      0      0      0      0      0      0      0      0      0
1      0      0      0      0      0      0      0      0      0      0
2      0      0      0      0      0      0      0      0      0      0
3      0      0      0      0      0      0      0      0      0      0
4      0      0      0      0      0      0      0      0      0      0

[5 rows x 22929 columns]
```

[23]:
```
convae_data1 = convae_data_1.values
convae_data2 = convae_data_2.values
rc_data = rc_data.values
```

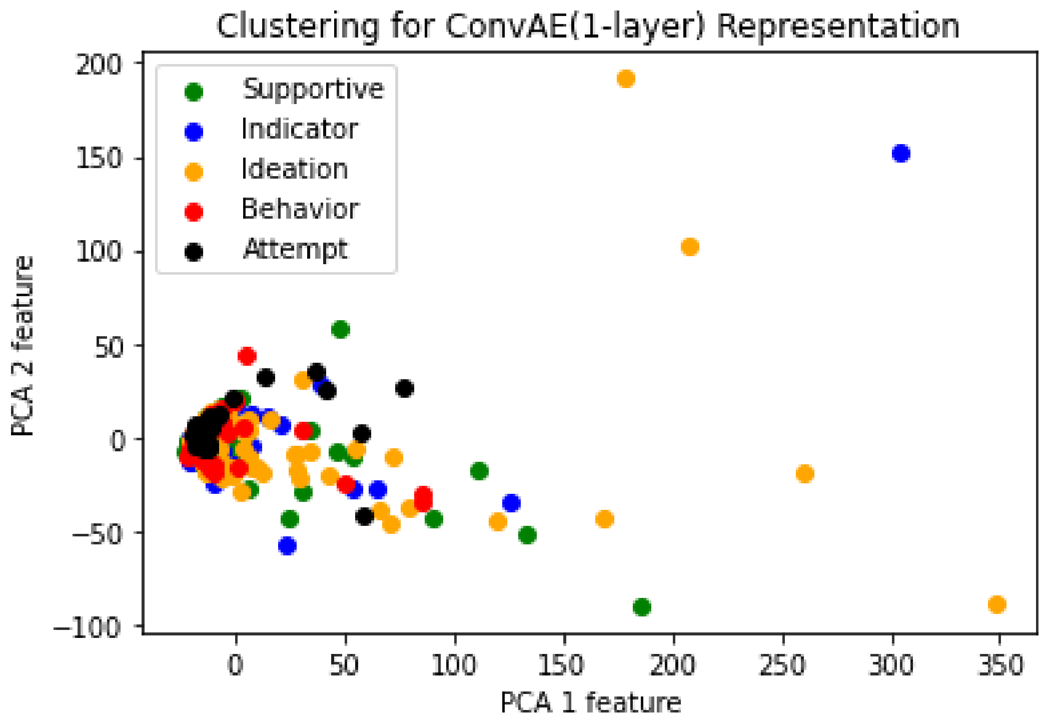
[24]:
```
pca = PCA(2)

rc_data_2 = pca.fit_transform(rc_data)
convae_data_12 = pca.fit_transform(convae_data1)
convae_data_22 = pca.fit_transform(convae_data2)
```

[25]:
```
# generate labels
suicide_label_map = {'Supportive':0, 'Indicator':1, 'Ideation':2, 'Behavior':3,␣
 ↪'Attempt':4}
mapLabel = np.vectorize(lambda x: suicide_label_map[x])

suicide_data = pd.read_csv('suicide/500_Reddit_users_posts_labels.csv')
suicide_label = mapLabel(suicide_data.Label)

train_idx = np.load('suicide/train_idx.txt')
test_idx = np.load('suicide/test_idx.txt')
```

[26]:
```
suicide_train_label = suicide_label[train_idx]
```

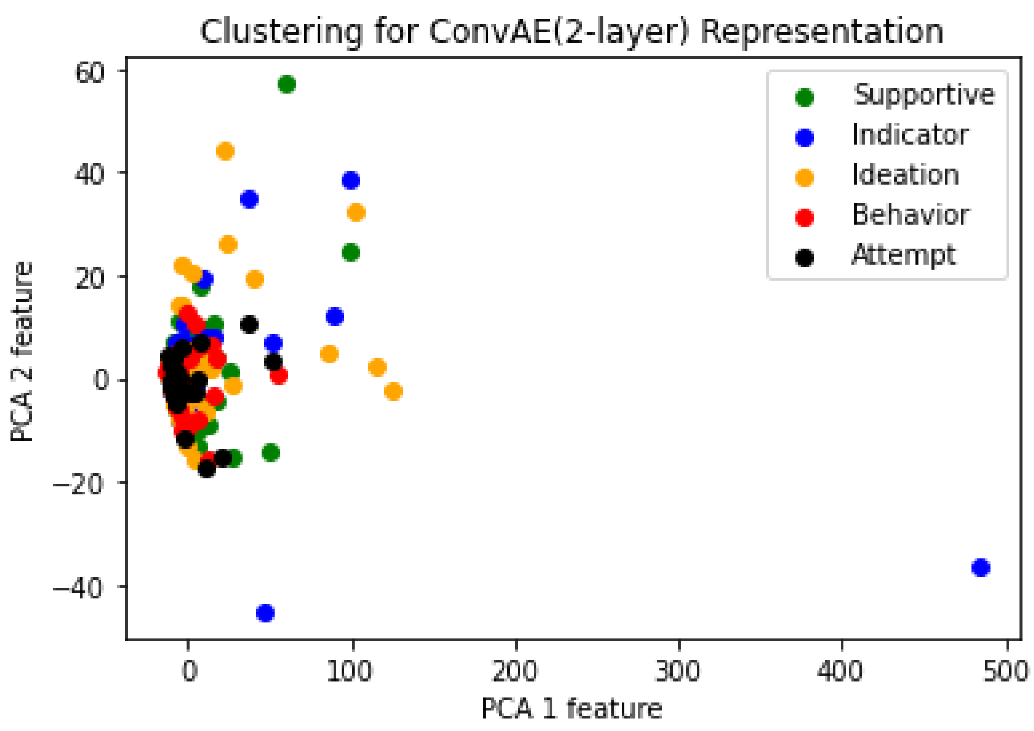
[27]:
```
colors = ['green', 'blue', 'orange', 'red', 'black']
labels = ['Supportive', 'Indicator', 'Ideation', 'Behavior', 'Attempt']
for label in range(5):
    convae_labeli = convae_data_12[suicide_train_label == label]
    plt.scatter(convae_labeli[:, 0], convae_labeli[:, 1], color=colors[label],␣
 ↪label=labels[label])
plt.title('Clustering for ConvAE(1-layer) Representation')
plt.xlabel('PCA 1 feature')
plt.ylabel('PCA 2 feature')
plt.legend()
```

```
[27]: <matplotlib.legend.Legend at 0x137caca30>
```



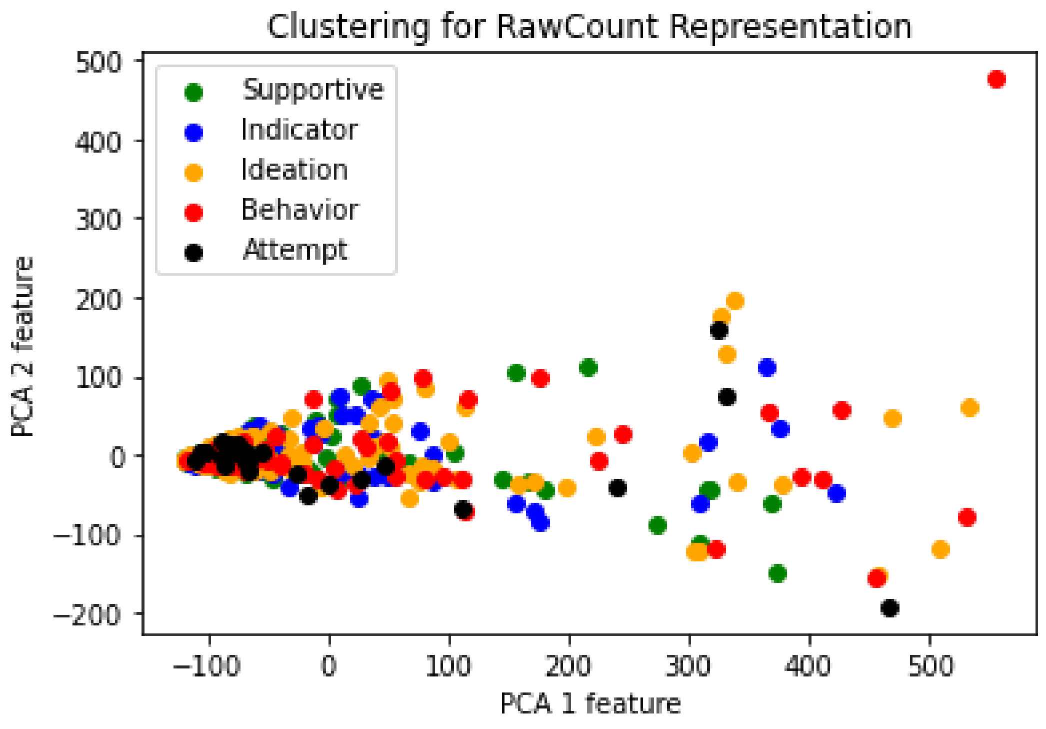
```
[28]: colors = ['green', 'blue', 'orange', 'red', 'black']
labels = ['Supportive', 'Indicator', 'Ideation', 'Behavior', 'Attempt']
for label in range(5):
    convae_labeli = convae_data_22[suicide_train_label == label]
    plt.scatter(convae_labeli[:, 0], convae_labeli[:, 1], color=colors[label],␣
 ↪label=labels[label])
plt.title('Clustering for ConvAE(2-layer) Representation')
plt.xlabel('PCA 1 feature')
plt.ylabel('PCA 2 feature')
plt.legend()
```

```
[28]: <matplotlib.legend.Legend at 0x13853d100>
```



```
[29]: import matplotlib.pyplot as plt

      colors = ['green', 'blue', 'orange', 'red', 'black']
      for label in range(5):
          rc_labeli = rc_data_2[suicide_train_label == label]
          plt.scatter(rc_labeli[:, 0], rc_labeli[:, 1], color=colors[label],␣
       ↪label=labels[label])
      plt.title('Clustering for RawCount Representation')
      plt.xlabel('PCA 1 feature')
      plt.ylabel('PCA 2 feature')
      plt.legend()
```

```
[29]: <matplotlib.legend.Legend at 0x1368afca0>
```



2.3 Hierarchical Clustering

[30]:
```
def purity_score(y_true, y_pred):
    contingency_matrix = metrics.cluster.contingency_matrix(y_true, y_pred)
    return np.sum(np.amax(contingency_matrix, axis=0)) / np.
  ↪sum(contingency_matrix)
```

[31]:
```
rc_hierarchical = AgglomerativeClustering(n_clusters=5).fit(rc_data)
convae1_hierarchical = AgglomerativeClustering(n_clusters=5).fit(convae_data_1)
convae2_hierarchical = AgglomerativeClustering(n_clusters=5).fit(convae_data_2)
```

[32]:
```
print(f'Purity for ConvAE with 1-layer CNN is␣
  ↪{purity_score(convae1_hierarchical.labels_, suicide_train_label)}')
print(f'Purity for ConvAE with 2-layer CNN is␣
  ↪{purity_score(convae2_hierarchical.labels_, suicide_train_label)}')
```

```
Purity for ConvAE with 1-layer CNN is 0.62
Purity for ConvAE with 2-layer CNN is 0.84
```

[33]:
```
print(f'Entropy for ConvAE with 1-layer CNN is {metrics.
  ↪homogeneity_score(convae1_hierarchical.labels_, suicide_train_label)}')
print(f'Entropy for ConvAE with 2-layer CNN is {metrics.
  ↪homogeneity_score(convae2_hierarchical.labels_, suicide_train_label)}')
```

```
Entropy for ConvAE with 1-layer CNN is 0.0219725368773614
Entropy for ConvAE with 2-layer CNN is 0.03837413298317611
```

[ ]:

```

```