Project: Data Representation and Clustering

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- Representing data into more interpretable formats.
- Well defined clustering so that data points are classified as per meaningful clusters and it's evaluation using the labels
- Transfer learning and image classification

Part 1: Clustering on Text Data

In [10]:

```
# Importing Libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import random
import re
import contractions
import nltk

from sklearn.model_selection import train_test_split
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.feature_extraction.text import TfidfTransformer
from nltk.stem import WordNetLemmatizer
from nltk.stem import PorterStemmer
from nltk.corpus import wordnet
from nltk.corpus import stopwords
from sklearn.pipeline import Pipeline
from sklearn.decomposition import TruncatedSVD

from sklearn.decomposition import NMF
from sklearn import datasets, metrics
from sklearn.model_selection import KFold
from sklearn.model_selection import GridSearchCV

from sklearn.metrics import plot_confusion_matrix, f1_score, accuracy_score, precisi

import pickle
import umap

import itertools
import matplotlib.colors as colors

from matplot import plot_mat
from sklearn.cluster import KMeans
from sklearn.metrics.cluster import contingency_matrix

from sklearn.metrics.cluster import homogeneity_score
from sklearn.metrics.cluster import completeness_score
from sklearn.metrics.cluster import v_measure_score
from sklearn.metrics.cluster import adjusted_rand_score
from sklearn.metrics.cluster import adjusted_mutual_info_score


from scipy.optimize import linear_sum_assignment
from sklearn.metrics import confusion_matrix
from sklearn.cluster import AgglomerativeClustering
from sklearn.cluster import DBSCAN

import hdbscan
```

In [11]:

```
# Fetching all data from 20newgroups
newsgroups_data = datasets.fetch_20newsgroups(subset='all', remove=('headers', 'foot
```

In [12]:

```
# One time imports
stopWords = set(stopwords.words('english'))
```

In [13]:

```
def getScores(true, predicted):
    scores = {}
    scores["Homogeneity"] = homogeneity_score(true, predicted)
    scores["Completeness"] = completeness_score(true, predicted)
    scores["V-measure"] = v_measure_score(true, predicted)
    scores["Adjusted Rand Index"] = adjusted_rand_score(true, predicted)
    scores["Adjusted mutual information score"] = adjusted_mutual_info_score(true, p

    return scores
```

In [14]:

```
# Raw data dimensions and visualizations
print("Number of classes in newgroups data: {}".format(len(newsgroups_data.target_na
print("Number of datapoints in newsgroups data: {}".format(len(newsgroups_data.data)
print("First newarticle:\n", newsgroups_data.data[0])
```

```
Number of classes in newgroups data: 20
Number of datapoints in newsgroups data: 18846
First newarticle:


I am sure some bashers of Pens fans are pretty confused about the lack
of any kind of posts about the recent Pens massacre of the Devils. Act
ually,
I am  bit puzzled too and a bit relieved. However, I am going to put a
n end
to non-PIttsburghers' relief with a bit of praise for the Pens. Man, t
hey
are killing those Devils worse than I thought. Jagr just showed you wh
y
he is much better than his regular season stats. He is also a lot
fo fun to watch in the playoffs. Bowman should let JAgr have a lot of
fun in the next couple of games since the Pens are going to beat the p
ulp out of Jersey anyway. I was very disappointed not to see the Islan
ders lose the final
regular season game.          PENS RULE!!!
```

In [15]:

```
#  Function to clean the raw HTML text

"""
- HTML artifacts removal
- Links removal
- quotes removal
- Special characters removal
- Extra spaces removal
- Changing the short forms to full forms using contractions
- Punctuations removal
- Changing all text to lower case
"""

def clean(text):
    text = re.sub(r'^https?:\/\/.*[\r\n]*', '', text, flags=re.MULTILINE)
    texter = re.sub(r"<br />", " ", text)
    texter = re.sub(r'http\S+', '', text)
    texter = re.sub(r"&quot;", "\"",texter)
    texter = re.sub('&#39;', "\"", texter)
    texter = re.sub('\n', " ", texter)
    texter = re.sub(' u '," you ", texter)
    texter = re.sub('`',"", texter)
    texter = re.sub(' +', ' ', texter)
    texter = re.sub(r"(!)\1+", r"!", texter)
    texter = re.sub(r"(\?)\1+", r"?", texter)
    texter = re.sub('&amp;', 'and', texter)
    texter = re.sub('\r', ' ',texter)
    clean = re.compile('<.*?>')
    texter = texter.encode('ascii', 'ignore').decode('ascii')
    texter = re.sub(clean, '', texter)
    texter = texter.strip()
    texter = contractions.fix(texter)
    texter = re.sub('''[!"#$%&'()*+,/;:-<=>?@[\]^_`{|}~-]''', '', texter)
    texter = texter.lower()
    texter = re.sub(' +', ' ', texter)
    if texter == "":
        texter = ""
    return texter

def removeStopwords(words, stopWords):
    return " ".join([word for word in words if word not in stopWords])

def preprocess(sample):
    sample = clean(sample)
    sample = sample.split('.')
    sample = [removeStopwords(nltk.word_tokenize(sentence), stopWords) for sentence
    sample = '.'.join(sample)
    return sample
```

In [247]:

```
def getSVD(n_comp, data):
    SVD = TruncatedSVD(n_components=n_comp, random_state=42)
    SVD.fit(data)
    return SVD

# NMF Non-negative Matrix Factorization
def getNMF(n_comp, data):
    NMFmodel = NMF(n_components=n_comp, init='random', max_iter=300, random_state=42
    NMFmodel.fit(data)
    return NMFmodel

def getLabels(true, predicted):
    size = len(true)
    incorrect = np.count_nonzero(true - predicted)

    if incorrect > (size/2):
        return 1 - predicted
    return predicted
```

In [17]:

```
data = newsgroups_data.data
labelNames = np.array(newsgroups_data.target_names)
labels = np.array(newsgroups_data.target)
stringLabels = np.array([labelNames[label] for label in labels])
```

In [18]:

```
# Constructing subset of data

class_1 = ['comp.graphics',  'comp.os.ms-windows.misc', 'comp.sys.ibm.pc.hardware',
class_2 = ['rec.autos', 'rec.motorcycles', 'rec.sport.baseball', 'rec.sport.hockey']


subsetData = []
subsetLabels = []
subsettrueLabels = []

for idx, label in enumerate(stringLabels):
    if label in class_1:
        subsetData.append(data[idx])
        subsetLabels.append(0)
        subsettrueLabels.append(label)

    elif label in class_2:
        subsetData.append(data[idx])
        subsetLabels.append(1)
        subsettrueLabels.append(label)
```

In [19]:

```
# Feature Extraction using CountVectorizer and TF-IDF transformation using Pipeline.
featurePipeline = Pipeline([
    ('count', CountVectorizer(preprocessor=preprocess, stop_words='english', min_df=
    ('tfidf', TfidfTransformer(smooth_idf=True, use_idf=True))
]).fit(subsetData)
```

In [20]:

```
features = featurePipeline.transform(subsetData)
```

In [21]:

```
print("Dimensions of TF-IDF matrix: {}".format(features.shape))
```

```
Dimensions of TF-IDF matrix: (7882, 21132)
```

Question 1

Dimensions of TF-IDF matrix of two classes as given : (7882, 21132)

In [22]:

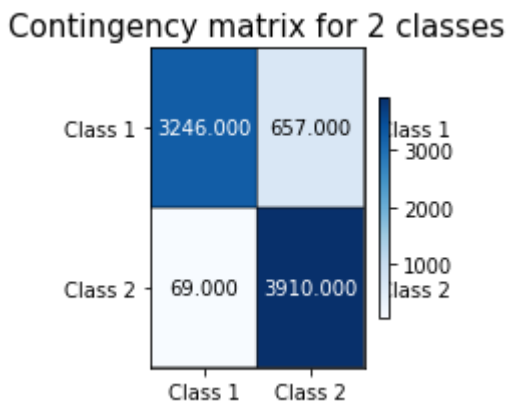
```
kmeans = KMeans(n_clusters=2, random_state=0, max_iter=3000, n_init=50).fit(features
predictedLabels = kmeans.labels_
```

In [23]:

```
Cmatrix = contingency_matrix(subsetLabels, 1 - predictedLabels)
predictedLabels = getLabels(subsetLabels, predictedLabels) # because the classes wer
```

In [24]:

```
plot_mat(Cmatrix, size=(3,3), title="Contingency matrix for 2 classes", xticklabels=
```



Question 2

The contingency matrix is plotted above.

No the contingency matrix is not always square. Example when the number of clusters formed are more than the no. of true classes.

Contingency matrix is square when its about classification problems and is referred as confusion matrix.

In [25]:

```
# Scores for two class clustering
scores = getScores(subsetLabels, predictedLabels)
scores
```

Out[25]:

```
{'Homogeneity': 0.5942490015150945,
 'Completeness': 0.6052721260505387,
 'V-measure': 0.5997099147063929,
 'Adjusted Rand Index': 0.6654594117635557,
 'Adjusted mutual information score': 0.5996729309950798}
```

Question 3

5 measures for K-means clustering:

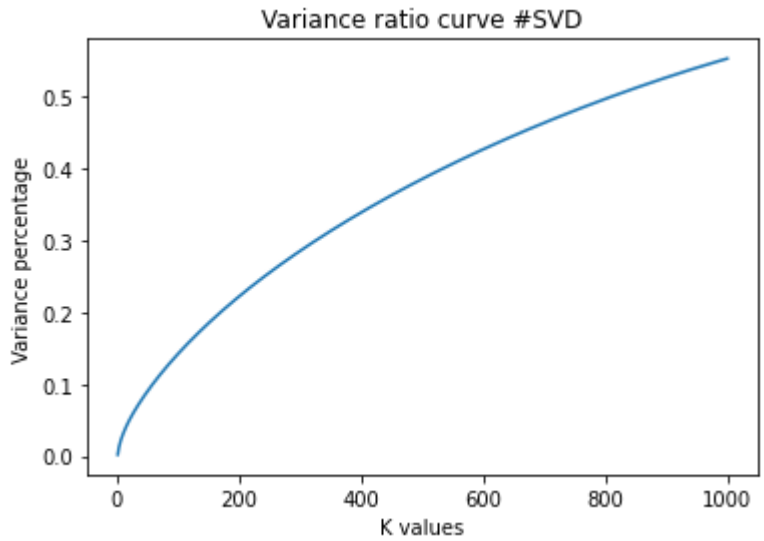
'Homogeneity': 0.5942490015150945,
'Completeness': 0.6052721260505387,
'V-measure': 0.5997099147063929,
'Adjusted Rand Index': 0.6654594117635557,
'Adjusted mutual information score': 0.5996729309950798

Dense representations for better k- means clustering

Question 4

In [26]:

```
# Plotting variance graph from 1000 top components from SVD decomposition

n_components = 1000
SVD = getSVD(n_components, features)
varianceRatios = SVD.explained_variance_ratio_
cumulativeVarianceRatios = np.cumsum(varianceRatios)


plt.plot(np.arange(1000) + 1, cumulativeVarianceRatios)
plt.xlabel("K values")
plt.ylabel("Variance percentage")
plt.title("Variance ratio curve #SVD")
plt.show()
```



Question 5

In [27]:

```
# For SVD decompositions

r = [1,2,3,5,10,20,50,100,300]

SVDScores_homogeneity = []
SVDScores_completeness = []
SVDScores_v_measure = []
SVDScores_adj_rand_idx = []
SVDScores_adj_mutual_inf_score = []


for k in r:
    SVD = getSVD(k, features)
    transformed = SVD.transform(features)
    kmeans = KMeans(n_clusters=2, random_state=0, max_iter=3000, n_init=50).fit(tran
    predictedLabels = kmeans.labels_
    predictedLabels = getLabels(subsetLabels, predictedLabels)
    scores = getScores(subsetLabels, predictedLabels)
    SVDScores_homogeneity.append(scores['Homogeneity'])
    SVDScores_completeness.append(scores['Completeness'])
    SVDScores_v_measure.append(scores['V-measure'])
    SVDScores_adj_rand_idx.append(scores['Adjusted Rand Index'])
    SVDScores_adj_mutual_inf_score.append(scores['Adjusted mutual information score'
```

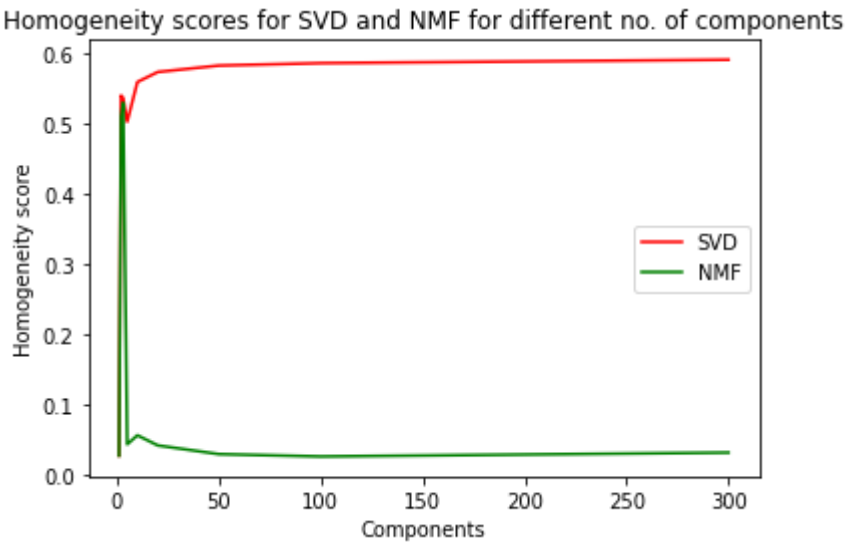
In [28]:

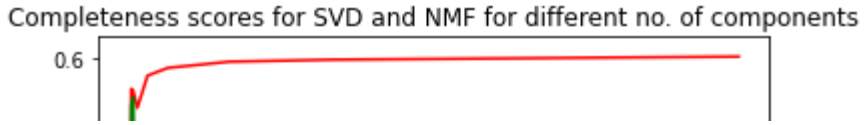
```
# For NMF

NMFScores_homogeneity = []
NMFScores_completeness = []
NMFScores_v_measure = []
NMFScores_adj_rand_idx = []
NMFScores_adj_mutual_inf_score = []

for k in r:
    NMFmodel = getNMF(k, features)
    transformed = NMFmodel.transform(features)
    kmeans = KMeans(n_clusters=2, random_state=0, max_iter=3000, n_init=50).fit(tran
    predictedLabels = kmeans.labels_
    predictedLabels = getLabels(subsetLabels, predictedLabels)
    scores = getScores(subsetLabels, predictedLabels)
    NMFScores_homogeneity.append(scores['Homogeneity'])
    NMFScores_completeness.append(scores['Completeness'])
    NMFScores_v_measure.append(scores['V-measure'])
    NMFScores_adj_rand_idx.append(scores['Adjusted Rand Index'])
    NMFScores_adj_mutual_inf_score.append(scores['Adjusted mutual information score'
```

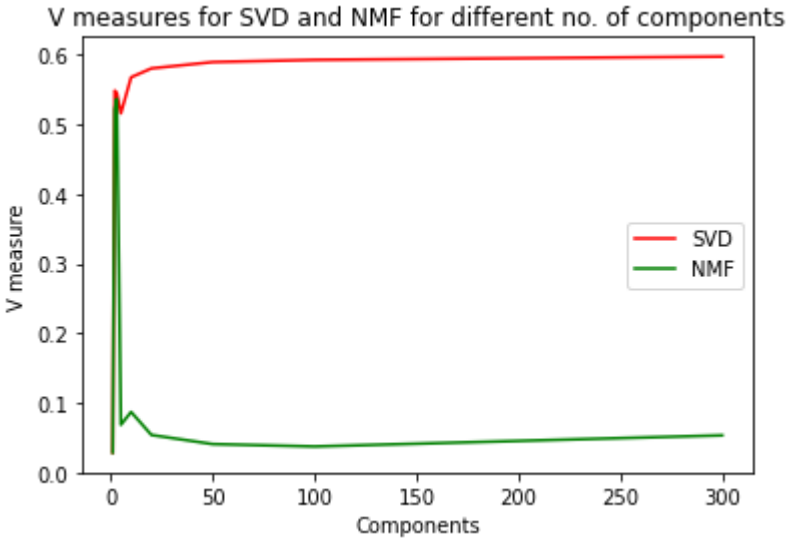
```
/Users/gauravsingh/miniforge3/envs/py38_torch/lib/python3.8/site-packa
ges/sklearn/decomposition/_nmf.py:1637: ConvergenceWarning: Maximum nu
mber of iterations 200 reached. Increase it to improve convergence.
  warnings.warn(
/Users/gauravsingh/miniforge3/envs/py38_torch/lib/python3.8/site-packa
ges/sklearn/decomposition/_nmf.py:1637: ConvergenceWarning: Maximum nu
mber of iterations 200 reached. Increase it to improve convergence.
  warnings.warn(
/Users/gauravsingh/miniforge3/envs/py38_torch/lib/python3.8/site-packa
ges/sklearn/decomposition/_nmf.py:1637: ConvergenceWarning: Maximum nu
mber of iterations 200 reached. Increase it to improve convergence.
  warnings.warn(
/Users/gauravsingh/miniforge3/envs/py38_torch/lib/python3.8/site-packa
ges/sklearn/decomposition/_nmf.py:1637: ConvergenceWarning: Maximum nu
mber of iterations 200 reached. Increase it to improve convergence.
  warnings.warn(
```

In [29]:

```
plt.plot(r, SVDScores_homogeneity, color='r', label='SVD')
plt.plot(r, NMFScores_homogeneity, color='g', label='NMF')

plt.xlabel("Components")
plt.ylabel("Homogeneity score")
plt.title("Homogeneity scores for SVD and NMF for different no. of components")

plt.legend()
plt.show()


plt.plot(r, SVDScores_completeness, color='r', label='SVD')
plt.plot(r, NMFScores_completeness, color='g', label='NMF')
plt.xlabel("Components")
plt.ylabel("Completeness score")
plt.title("Completeness scores for SVD and NMF for different no. of components")

plt.legend()
plt.show()

plt.plot(r, SVDScores_v_measure, color='r', label='SVD')
plt.plot(r, NMFScores_v_measure, color='g', label='NMF')
plt.xlabel("Components")
plt.ylabel("V measure")
plt.title("V measures for SVD and NMF for different no. of components")

plt.legend()
plt.show()
```

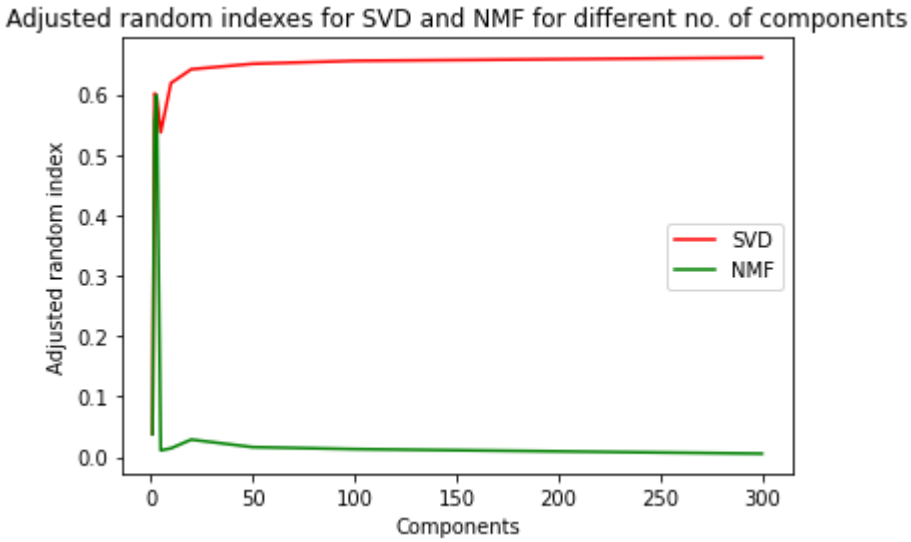


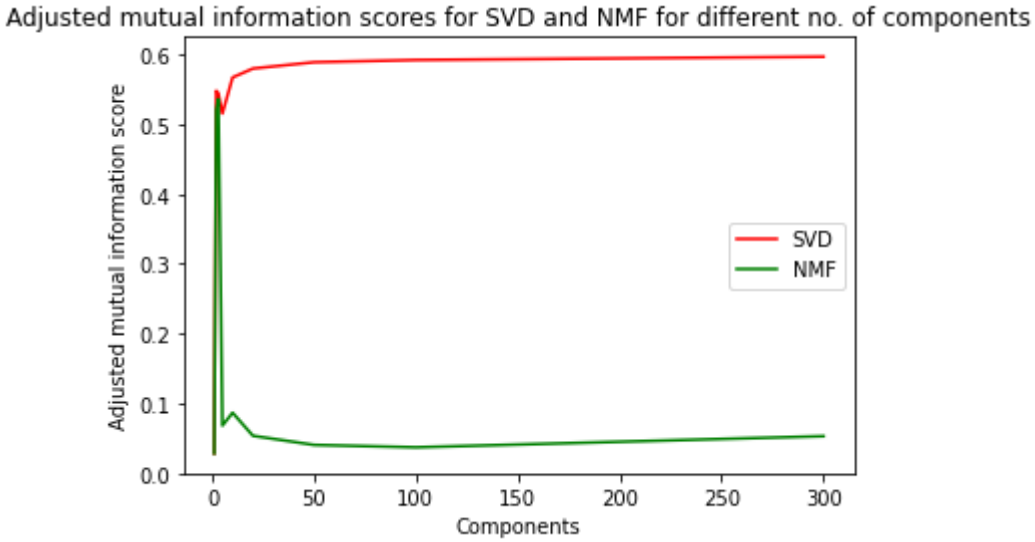

Completeness scores for SVD and NMF for different no. of components
0.6


V measures for SVD and NMF for different no. of components
V measure
Components
SVD
NMF
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
200
250
300

In [30]:

```
plt.plot(r, SVDScores_adj_rand_idx, color='r', label='SVD')
plt.plot(r, NMFScores_adj_rand_idx, color='g', label='NMF')

plt.xlabel("Components")
plt.ylabel("Adjusted random index")
plt.title("Adjusted random indexes for SVD and NMF for different no. of components")

plt.legend()
plt.show()



plt.plot(r, SVDScores_adj_mutual_inf_score, color='r', label='SVD')
plt.plot(r, NMFScores_adj_mutual_inf_score, color='g', label='NMF')

plt.xlabel("Components")
plt.ylabel("Adjusted mutual information score")
plt.title("Adjusted mutual information scores for SVD and NMF for different no. of c

plt.legend()
plt.show()
```





Answer 5

The best choice of r for NMF seems to be around 3-4 components.
For the SVD the best choice of r is around the same 3-4 components if we see the first peak.
After that the results fro SVD are increasing slowly. But since there is a tradeoff between higher dimensionality and the performance of K-means the first peak results are more meaningful hence chosing r = 2

Question 6

As r increases, the number of components increases. There is a tradeoff between the number of dimensions and the segregating power of K-means clustering. As the number of components were very low, the discriminative power of the algorithm was low since there is not much information in those components. The at certain number the information held by those components and the discriminative power of the K-means in the feature space attains its maxima. Then the algorithm starts to perform worse in not able to discriminate the distances between different clusters.

And thus the non monotonic behaviour is justified.

Question 7

On seeing the metrics of question 3 and to that of metrics with reduced dimesions, on average the reduced dimensions metrics with SVD are performing slightly better than that of full features with less time taken for clustering and delivering better results.

Visualising the clusters

In [31]:

```
# Visualisation using NMF reduction

# chosen r = 3
NMF_r = 3

NMFmodel = getNMF(NMF_r, features)

transformed = NMFmodel.transform(features)

kmeans = KMeans(n_clusters=2, random_state=0, max_iter=3000, n_init=50).fit(transfor
predictedLabelsNMF = kmeans.labels_

# Projecting 3 dimensional features onto 2D plane using NMF

SVDmodel = getSVD(2, transformed)
twoDimNMF = SVDmodel.transform(transformed)
```

In [32]:

```
# Visualisation using SVD reduction

# chosen r = 2
SVD_r = 2

SVDmodel = getSVD(SVD_r, features)

twoDimSVD = SVDmodel.transform(features)

kmeans = KMeans(n_clusters=2, random_state=0, max_iter=3000, n_init=50).fit(transfor
predictedLabelsSVD = kmeans.labels_
```

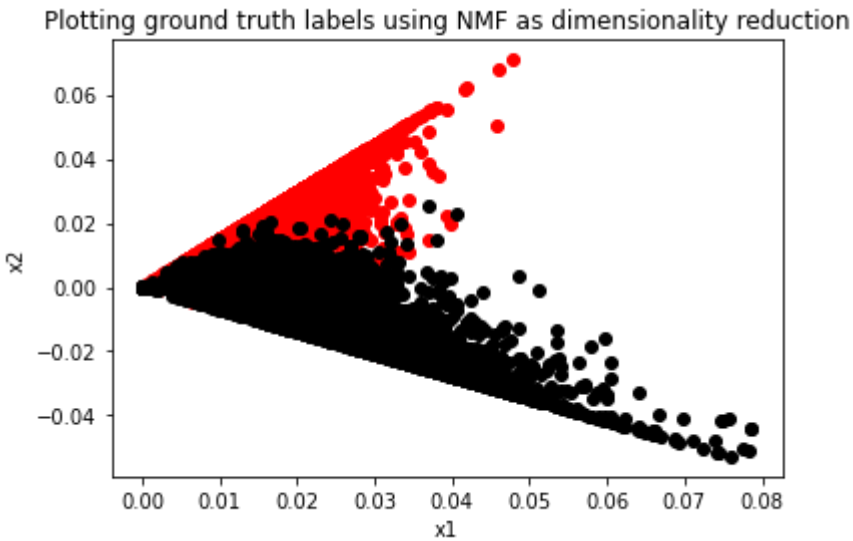
In [33]:

```
def plotScatter(data, labels):
    labels = np.array(labels)
    data = np.array(data)
    data1 = data[np.where(labels == 1)]
    data0 = data[np.where(labels == 0)]

    plt.scatter(data1[:,0] , data1[:,1] , color = 'red')
    plt.scatter(data0[:,0] , data0[:,1] , color = 'black')
    plt.show()
```

Question 8

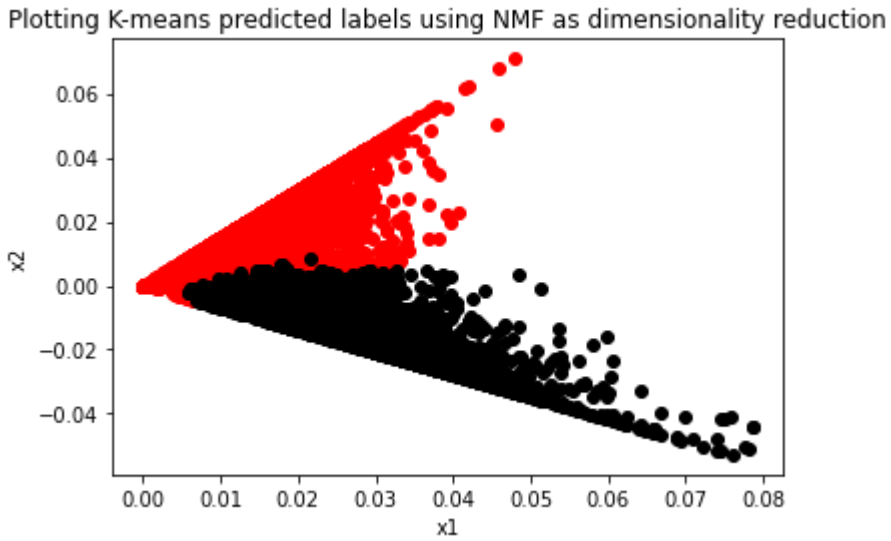
In [34]:

```
# Plotting scatter plots with ground truth labels and using NMF for dimensionality r
plt.title("Plotting ground truth labels using NMF as dimensionality reduction")
plt.xlabel("x1")
plt.ylabel("x2")
plotScatter(twoDimNMF, subsetLabels)
```



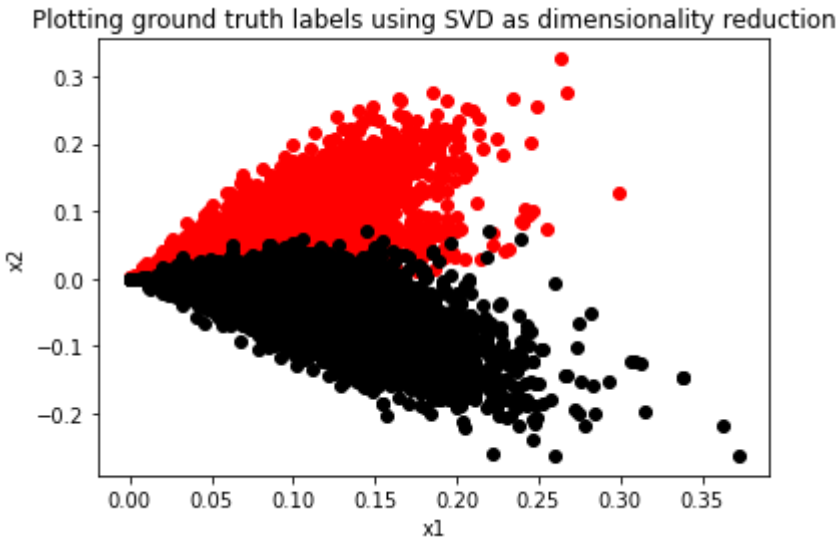
In [35]:

```
plt.title("Plotting K-means predicted labels using NMF as dimensionality reduction")
plt.xlabel("x1")
plt.ylabel("x2")
plotScatter(twoDimNMF, 1 - predictedLabelsNMF)
```



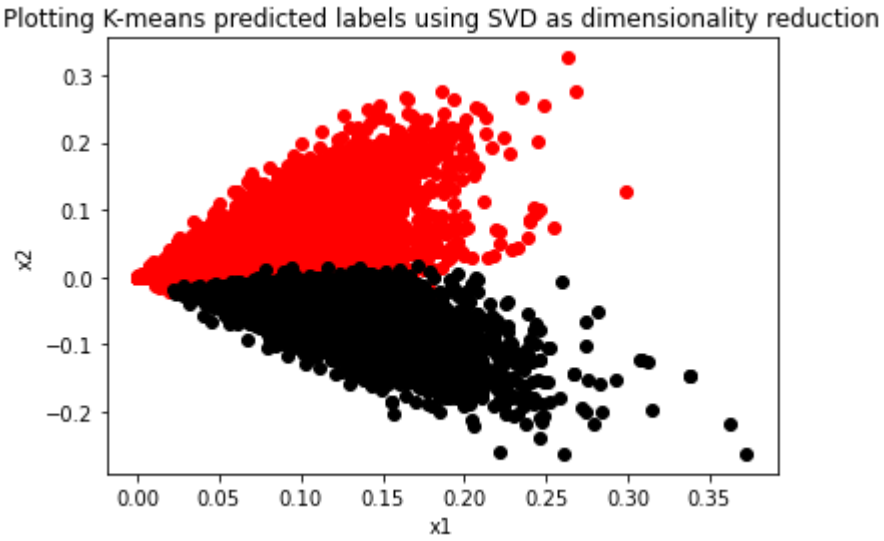
In [36]:

```
plt.title("Plotting ground truth labels using SVD as dimensionality reduction")
plt.xlabel("x1")
plt.ylabel("x2")
plotScatter(twoDimSVD, subsetLabels)
```



In [37]:

```
plt.title("Plotting K-means predicted labels using SVD as dimensionality reduction")
plt.xlabel("x1")
plt.ylabel("x2")
plotScatter(twoDimSVD, 1 - predictedLabelsSVD)
```



The dimensionality of the data was reduced by SVD and NMF as explained in question 5. And it was further reduced to two dimensions so as to visualise it via scatter plot.

I observe a clear boundary between the two clusters. Though they are not separated by a margin in this 2-D plot. I see a lot of commonality between the ground truth labels plot and the cluster assignments of the K-means clustering and there is a minute difference in the way the boundary separates the points.

One thing to notice is that the dimensionality reduction did help to visualise it but I am seeing a few outliers on the scatter plot which could have been mapped nearby to the riginal clusters.

The distribution is not very ideal for K-means clustering. Since its like wedge shaped and not like real ball shaped distribution which is very ideal for K-means algroithm to shine.

Working with full 20 classes

In [38]:

```
#  Creating the features using TF-IDF transformation

fullPipeline = Pipeline([
    ('count', CountVectorizer(preprocessor=preprocess, stop_words='english', min_df=
    ('tfidf', TfidfTransformer(smooth_idf=True, use_idf=True))
]).fit(data)

fullFeatures = fullPipeline.transform(data)
```

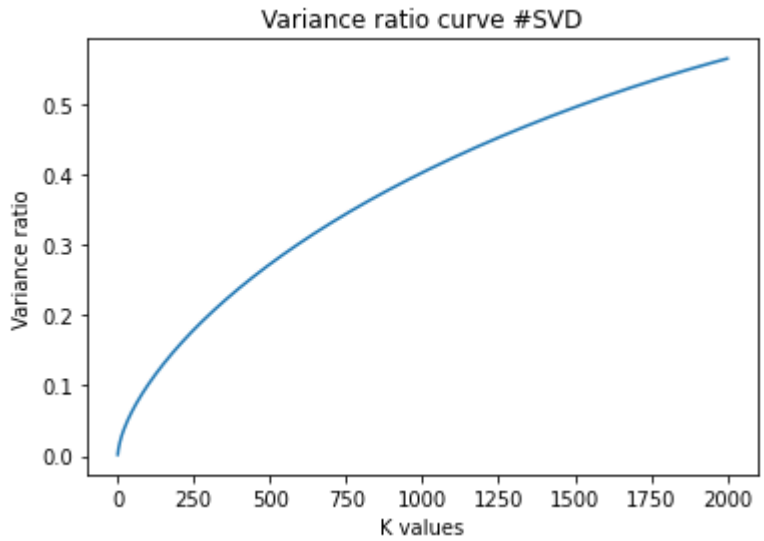
In [39]:

```
print("Dimensions of TF-IDF matrix: {}".format(fullFeatures.shape))
```

```
Dimensions of TF-IDF matrix: (18846, 43038)
```

In [40]:

```
# Dimensionality reduction of full data

# Choosing SVD as it performs well generally and is much faster.

# Choosing upper bound of n_components such that it works well with K means as well.
# is really absurd for Kmeans.

n_components = 2000
SVD = getSVD(n_components, fullFeatures)
varianceRatios = SVD.explained_variance_ratio_
cumulativeVarianceRatios = np.cumsum(varianceRatios)


plt.plot(np.arange(n_components) + 1, cumulativeVarianceRatios)
plt.xlabel("K values")
plt.ylabel("Variance ratio")
plt.title("Variance ratio curve #SVD")
plt.show()
```



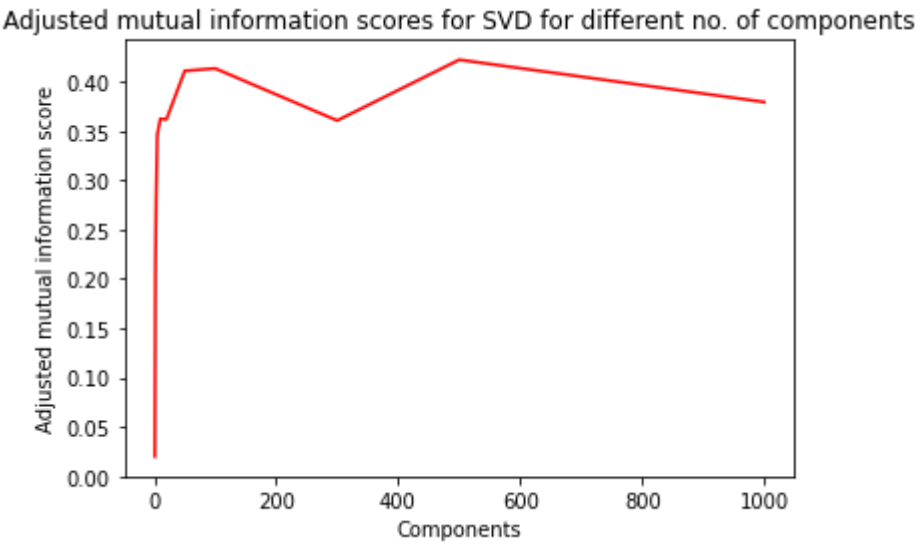
In [41]:

```
r = [1,2,3,5,10,20,50,100,300, 500, 1000]

SVDScores_homogeneity = []
SVDScores_completeness = []
SVDScores_v_measure = []
SVDScores_adj_rand_idx = []
SVDScores_adj_mutual_inf_score = []


for k in r:
    SVD = getSVD(k, fullFeatures)
    transformed = SVD.transform(fullFeatures)
    kmeans = KMeans(n_clusters=20, random_state=0, max_iter=3000, n_init=50).fit(tra
    predictedLabels = kmeans.labels_
#     predictedLabels = getLabels(subsetLabels, predictedLabels)
    scores = getScores(labels, predictedLabels)
    SVDScores_homogeneity.append(scores['Homogeneity'])
    SVDScores_completeness.append(scores['Completeness'])
    SVDScores_v_measure.append(scores['V-measure'])
    SVDScores_adj_rand_idx.append(scores['Adjusted Rand Index'])
    SVDScores_adj_mutual_inf_score.append(scores['Adjusted mutual information score'
```

Question 10

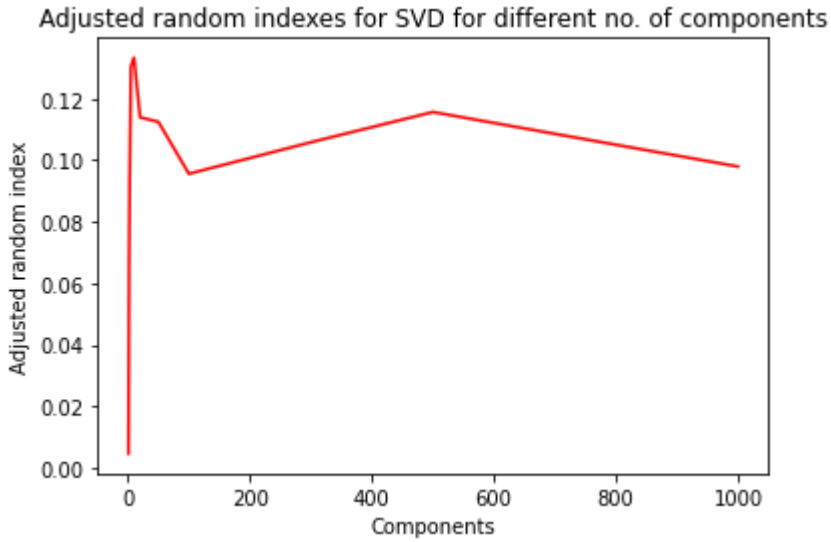
In [42]:

```
plt.plot(r, SVDScores_adj_mutual_inf_score, color='r')

plt.xlabel("Components")
plt.ylabel("Adjusted mutual information score")
plt.title("Adjusted mutual information scores for SVD for different no. of component

plt.show()
```



In [43]:

```
plt.plot(r, SVDScores_adj_rand_idx, color='r')

plt.xlabel("Components")
plt.ylabel("Adjusted random index")
plt.title("Adjusted random indexes for SVD for different no. of components")

plt.show()
```



In [44]:

```
# Choosing n components to be 50.

best_r = 50

SVD = getSVD(best_r, fullFeatures)
transformed = SVD.transform(fullFeatures)

kmeans = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(transfo
predictedLabels = kmeans.labels_

scores = getScores(labels, predictedLabels)
```

Answer 10:

The cluster scores are low for K-means run on dimensionality reduction done with SVD as shown below. There is a trend all the cluster scores are first increasing and then decreasing. Choosing the optimal components value for SVD is between 50 - 100 since most of the scores achieve their best value in that range. Adjusted random index takes its best value when n components = 10 but the value is very low compared to other scores.

Choosing K = 20, Dimensionality reduction method = SVD. No. of components chosen: 50.

The 5 clustering metrics and the contingency matrix (20 X 20) are given below:

In [45]:

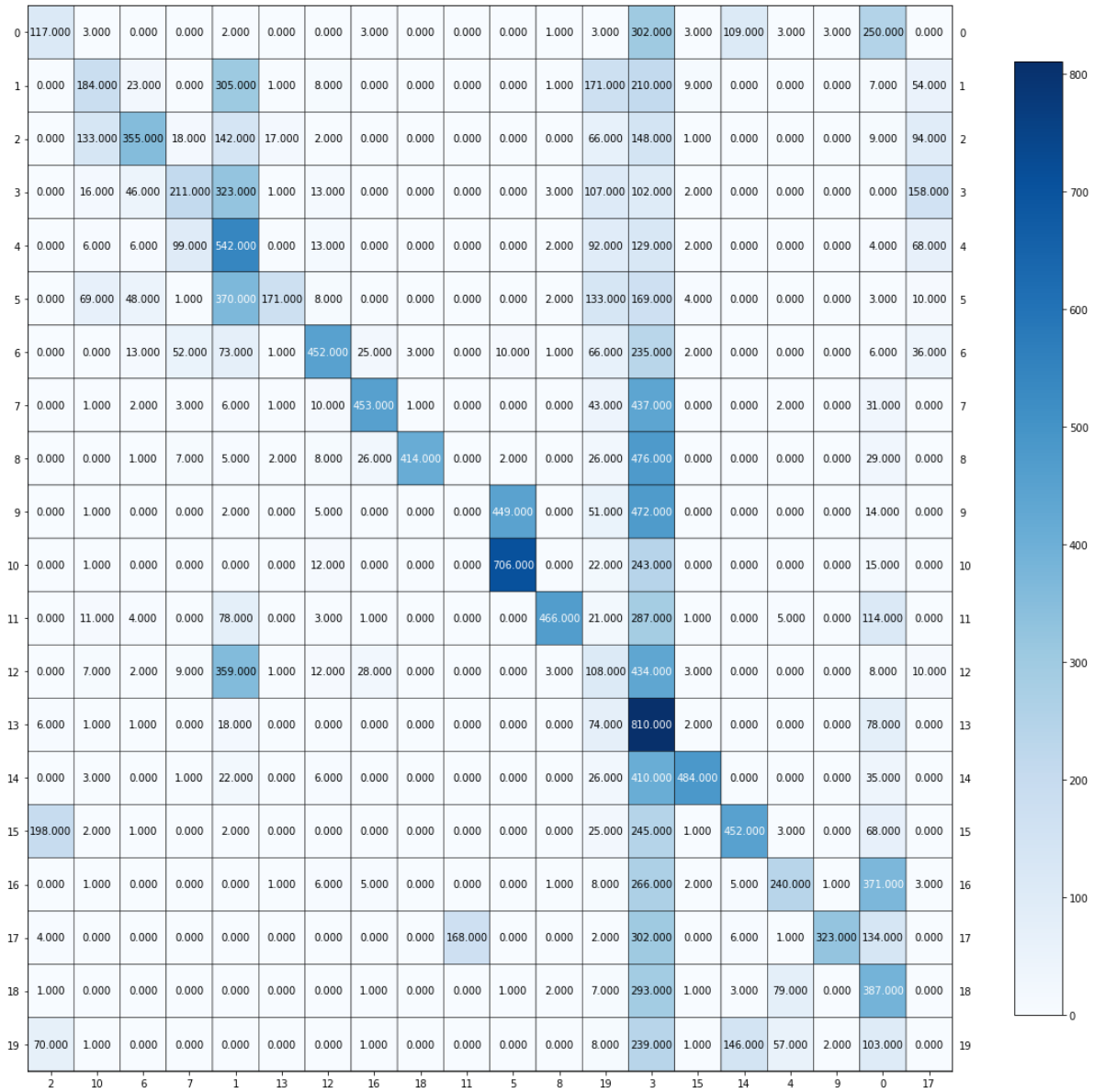
```
# Clustering scores
scores
```

Out[45]:

```
{'Homogeneity': 0.37586200944874926,
 'Completeness': 0.45857601184540586,
 'V-measure': 0.4131194813723549,
 'Adjusted Rand Index': 0.11244938656096547,
 'Adjusted mutual information score': 0.41102834776024916}
```

In [46]:

```
# Visualising contingency matrix
cm = confusion_matrix(labels, predictedLabels)
rows, cols = linear_sum_assignment(cm, maximize=True)
plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows, size=(15
```



UMAP

Question 11

In [47]:

```
# Dimensionality reduction using UMAP

umap_fit = umap.UMAP(n_components=20)
umap_features = umap_fit.fit_transform(fullFeatures)
```

In [48]:

```
# Kmeans clustering with UMAP 20 components.
kmeans = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(umap_fe
predictedLabels = kmeans.labels_

scores = getScores(labels, predictedLabels)
```

In [49]:

```
scores
```

Out[49]:

```
{'Homogeneity': 0.011915303439345229,
 'Completeness': 0.01282021964030221,
 'V-measure': 0.012351208962218677,
 'Adjusted Rand Index': 0.002696882412425153,
 'Adjusted mutual information score': 0.009065734404541063}
```

In [50]:

```
n_comp = [5, 10, 20, 30, 40, 50, 75, 100, 200]

UMAPScores_homogeneity = []
UMAPScores_completeness = []
UMAPScores_v_measure = []
UMAPScores_adj_rand_idx = []
UMAPScores_adj_mutual_inf_score = []


for k in n_comp:
    umap_fit = umap.UMAP(n_components=k)
    umap_features = umap_fit.fit_transform(fullFeatures)
    kmeans = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(uma
    predictedLabels = kmeans.labels_
    scores = getScores(labels, predictedLabels)
    UMAPScores_homogeneity.append(scores['Homogeneity'])
    UMAPScores_completeness.append(scores['Completeness'])
    UMAPScores_v_measure.append(scores['V-measure'])
    UMAPScores_adj_rand_idx.append(scores['Adjusted Rand Index'])
    UMAPScores_adj_mutual_inf_score.append(scores['Adjusted mutual information score
```

In [51]:

```
UMAPScores_adj_rand_idx
```

Out[51]:

```
[0.0016911562672956544,
 0.00209463040786006,
 0.0025241673639614308,
 0.002609746146537501,
 0.0024236433206437243,
 0.002972661683736763,
 0.00295061622086766,
 0.0024132056171847533,
 0.0026458874519850774]
```

The best Adjusted Rand index value for UMAP based Kmeans clustering happens at n_components = 100. Hence choosing it

In [52]:

```
# Setting metric with best n_components

best_umap_components = 100

umap_fit = umap.UMAP(n_components=best_umap_components, random_state=0, metric='eucl
umap_features = umap_fit.fit_transform(fullFeatures)

kmeans = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(umap_fe
predictedLabels = kmeans.labels_

scoresEucUMAP = getScores(labels, predictedLabels)
```

In [53]:

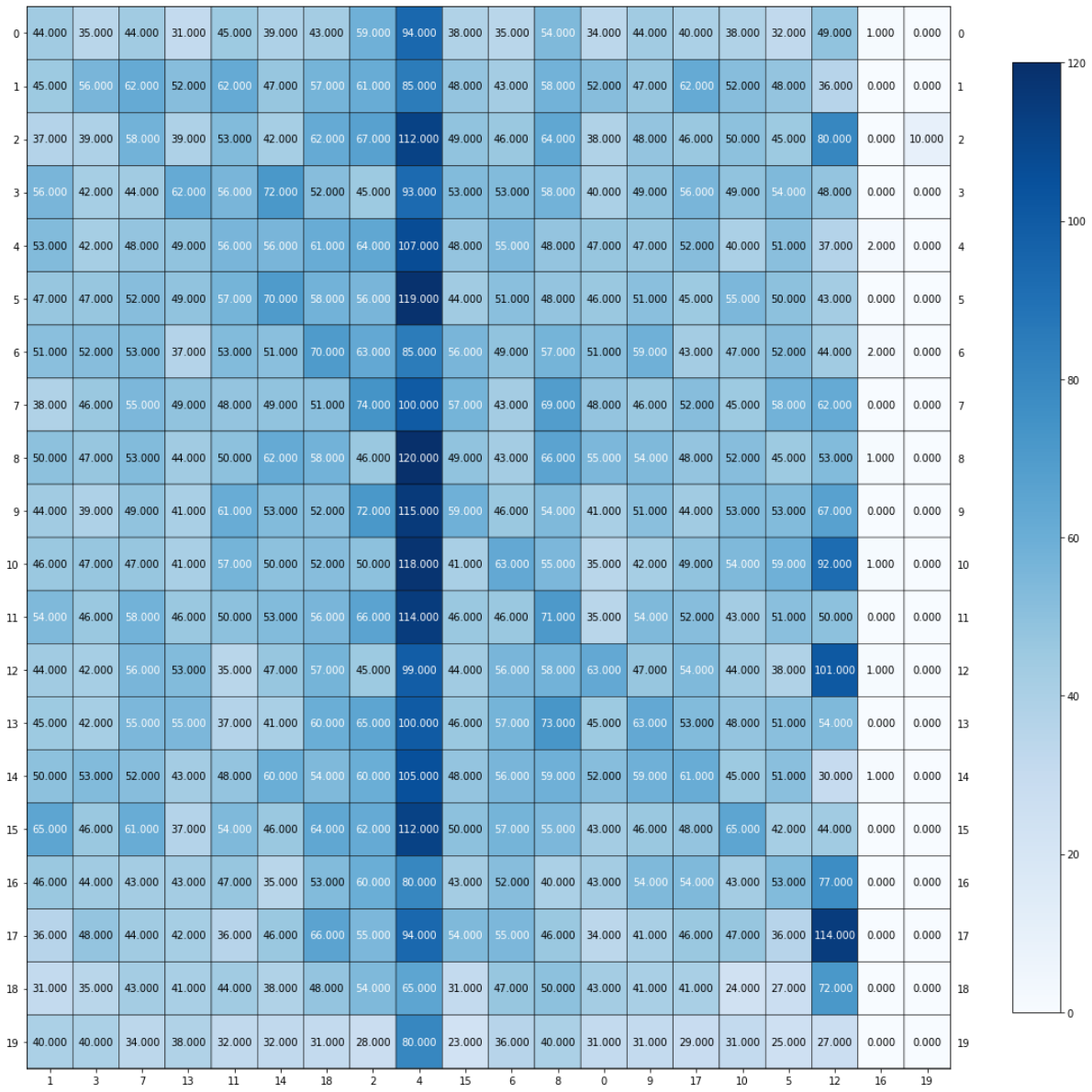
```
scoresEucUMAP
```

Out[53]:

```
{'Homogeneity': 0.004903617340411761,
 'Completeness': 0.0051039669481124,
 'V-measure': 0.005001786667008602,
 'Adjusted Rand Index': 0.00053799139140666,
 'Adjusted mutual information score': 0.0017245171021564687}
```

In [54]:

```
cmEUC = confusion_matrix(labels, predictedLabels)
rows, cols = linear_sum_assignment(cmEUC, maximize=True)
plot_mat(cmEUC[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows, size=
```



In [83]:

```
best_umap_components = 100

umap_fit = umap.UMAP(n_components=best_umap_components, random_state=0, metric='cosi
umap_features = umap_fit.fit_transform(fullFeatures)

kmeans = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(umap_fe
predictedLabels = kmeans.labels_

scoresCosUMAP = getScores(labels, predictedLabels)
```

In [84]:

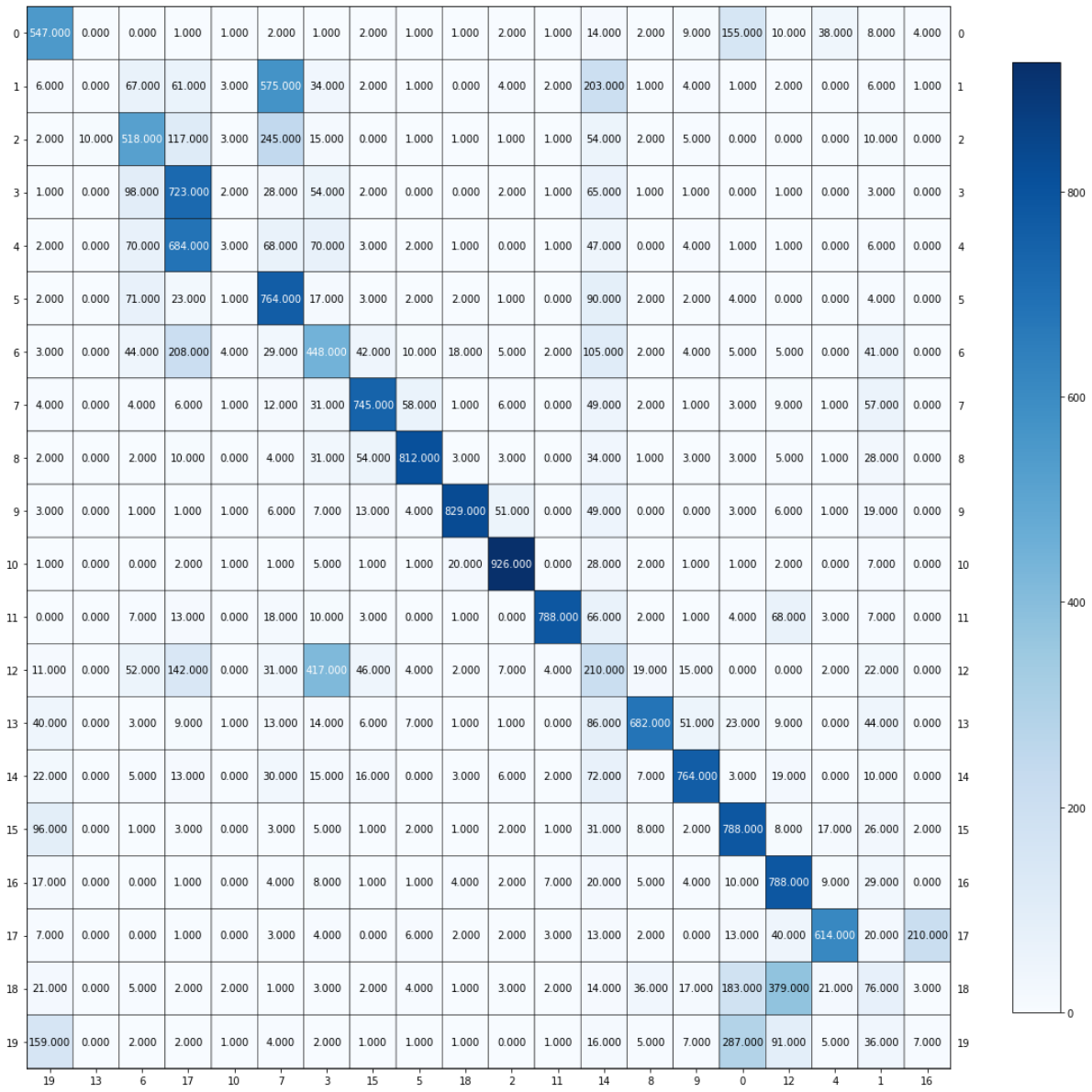
```
scoresCosUMAP
```

Out[84]:

```
{'Homogeneity': 0.5707173806276715,
 'Completeness': 0.6067497438785596,
 'V-measure': 0.588182238494506,
 'Adjusted Rand Index': 0.43891485058403334,
 'Adjusted mutual information score': 0.586797994256375}
```

In [85]:

```
cmCos = confusion_matrix(labels, predictedLabels)
rows, cols = linear_sum_assignment(cmCos, maximize=True)
plot_mat(cmCos[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows, size=
```



Answer 11

A linear search was done to find the number of components which perform best with K-means clustering in the range of:

[5, 10, 20, 30, 40, 50, 75, 100, 200].

Comparing the clustering scores it was found that n = 100 UMAP components is performing much better copared to others with K-means clustering. The Adjusted rand index scores for the search are given below:

[0.0016911562672956544, 0.00209463040786006, 0.0025241673639614308, 0.002609746146537501, 0.0024236433206437243, 0.002972661683736763, 0.0024132056171847533, 0.00295061622086766, 0.0026458874519850774]

Then with these 100 components, two UMAP metrics of distance were compared: 'eculidean' and 'cosine'

For "Euclidean" metric the clustering scores obtained with K-means were very low and the contingency matrix for the same is all radomly scattered in different clusters as shown above in the plot:

'Homogeneity': 0.004903617340411761,
'Completeness': 0.0051039669481124,
'V-measure': 0.005001786667008602,
'Adjusted Rand Index': 0.00053799139140666,
'Adjusted mutual information score': 0.0017245171021564687

For "Cosine" metric the clustering scores obtained with K-means were quite better with high clustering scores as shown below. The clustering assignment as shown above via the contingency matrix is good as well, with clear highly distinguishable allocations of data into clusters:

'Homogeneity': 0.5707173806276715,
'Completeness': 0.6067497438785596,
'V-measure': 0.588182238494506,
'Adjusted Rand Index': 0.43891485058403334,
'Adjusted mutual information score': 0.586797994256375

Answer 12

Analysing the contingency matrces above, I see that the Euclidean matrix did not do well with the clustering. The clusters formed are quite random and not much clearly distinguishable, it looks like more of a random cluster assignment.

For the cosine matrix, the clusters seems to are well formed with clear segregations and allocations. There seems to have some proper assigment based on underlying distance metric. There are a few points which are not able to be allocated well to a cluster and there are some clusters which have very low assignments which shows the outliers for Kmeans have to be managed well.

Answer 13

Based on the scores and contingency matrices shown in previous questions,:

UMAP with 100 components, metric = 'cosine' seems to perform much better with K-MEANS on the 20 newsgroup data.

The Adjusted Rand Index is as high as 0.43, with V-measure as 0.58 which is way higher than the SVD or NMF scores which ranged between (0.13, 0.21) and (0.41, 0.3) respectively.

The contingency matrices for the same shows the same that UMAP + Kmeans is better. Each cluster is having way more correct dense allocations of data points for UMAP then SVD or NMF with comparatively low wrong cluster allocations.

Agglomerative Clustering

Question 14

In [86]:

```
# Ward Agglomerative Clustering

n_components = [5, 20, 50, 100, 200]
clusters = 20
AggScores_homogeneity = []
AggScores_completeness = []
AggPScores_v_measure = []
AggScores_adj_rand_idx = []
AggScores_adj_mutual_inf_score = []


for comp in n_components:
    umap_fit = umap.UMAP(n_components=comp, metric='cosine')
    umap_features = umap_fit.fit_transform(fullFeatures)
    AggClustering = AgglomerativeClustering(n_clusters=clusters, linkage='ward').fit

    predictedLabels = AggClustering.labels_
    scores = getScores(labels, predictedLabels)

    AggScores_homogeneity.append(scores['Homogeneity'])
    AggScores_completeness.append(scores['Completeness'])
    AggPScores_v_measure.append(scores['V-measure'])
    AggScores_adj_rand_idx.append(scores['Adjusted Rand Index'])
    AggScores_adj_mutual_inf_score.append(scores['Adjusted mutual information score'
```

In [92]:

```
AggScores_adj_rand_idx
```

Out[92]:

```
[0.41217492442078074,
 0.41850328546214566,
 0.42512625114117725,
 0.4160045459802611,
 0.4173238010950882]
```

In [105]:

```
aggScores = np.vstack([AggScores_homogeneity, AggScores_completeness, AggPScores_v_m
aggScores = aggScores.T

print("Scores for Agglomerative Clustering for ward linkage")
pd.DataFrame(aggScores, columns=['Homogeneity', 'Completeness', 'Vmeasure', 'ARI', '
```

```
Scores for Agglomerative Clustering for ward linkage
```

Out[105]:

	Homogeneity	Completeness	Vmeasure	ARI	AMIS
0	0.556167	0.594698	0.574788	0.412175	0.573355
1	0.557389	0.591978	0.574163	0.418503	0.572733
2	0.560388	0.594437	0.576911	0.425126	0.575490
3	0.552100	0.583679	0.567451	0.416005	0.566005
4	0.559102	0.593432	0.575755	0.417324	0.574331

In [106]:

```
# Choosing best n_components = 100 as its giving lowest Adjusted rand index.

best_Ward_comp = 50
clusters = 20

umap_fit = umap.UMAP(n_components=best_Ward_comp, metric='cosine')
umap_features = umap_fit.fit_transform(fullFeatures)
AggClustering = AgglomerativeClustering(n_clusters=clusters, linkage='ward').fit(uma

predictedLabels = AggClustering.labels_
scores = getScores(labels, predictedLabels)

scores
```

Out[106]:

```
{'Homogeneity': 0.5532128999826028,
 'Completeness': 0.5868772124352711,
 'V-measure': 0.569548040262317,
 'Adjusted Rand Index': 0.4030347023439802,
 'Adjusted mutual information score': 0.5681037770844866}
```

In [107]:

```
n_components = [5, 20, 50, 100, 200]
clusters = 20
AggScoresSingle_homogeneity = []
AggScoresSingle_completeness = []
AggPScoresSingle_v_measure = []
AggScoresSingle_adj_rand_idx = []
AggScoresSingle_adj_mutual_inf_score = []


for comp in n_components:
    umap_fit = umap.UMAP(n_components=comp, metric='cosine')
    umap_features = umap_fit.fit_transform(fullFeatures)
    AggClustering = AgglomerativeClustering(n_clusters=clusters, linkage='single').f

    predictedLabels = AggClustering.labels_
    scores = getScores(labels, predictedLabels)

    AggScoresSingle_homogeneity.append(scores['Homogeneity'])
    AggScoresSingle_completeness.append(scores['Completeness'])
    AggPScoresSingle_v_measure.append(scores['V-measure'])
    AggScoresSingle_adj_rand_idx.append(scores['Adjusted Rand Index'])
    AggScoresSingle_adj_mutual_inf_score.append(scores['Adjusted mutual information
```

In [108]:

```
aggSingleScores = np.vstack([AggScoresSingle_homogeneity, AggScoresSingle_completene
                             , AggScoresSingle_adj_rand_idx, AggScoresSingle_adj_mut
aggSingleScores = aggSingleScores.T

print("Scores for Agglomerative Clustering for Single linkage")
pd.DataFrame(aggSingleScores, columns=['Homogeneity', 'Completeness', 'Vmeasure', 'A
```

```
Scores for Agglomerative Clustering for Single linkage
```

Out[108]:

	Homogeneity	Completeness	Vmeasure	ARI	AMIS
0	0.108424	0.695943	0.187619	0.020581	0.183878
1	0.095910	0.750839	0.170093	0.020068	0.166618
2	0.097546	0.718864	0.171782	0.019985	0.168048
3	0.006954	0.266164	0.013553	0.000083	0.009270
4	0.098007	0.714442	0.172368	0.020217	0.168451

In [229]:

```
# Choosing n_components to be 5 based on above adjusted rank index. All of them are

best_Single_comp = 5
clusters = 20

umap_fit = umap.UMAP(n_components=best_Single_comp, metric='cosine')
umap_features = umap_fit.fit_transform(fullFeatures)
AggClustering = AgglomerativeClustering(n_clusters=clusters, linkage='single').fit(u

predictedLabels = AggClustering.labels_
scores = getScores(labels, predictedLabels)

scores
```

Answer 14

For UMAP the number of components were searched which worked best with each type (ward, single) of linkage criteria for Agglomerative Clustering.

The range in which the components were searched for : [5, 20, 50, 100, 200]

The data frames holding 5 clustering metrics corresponding to each type of linkage are given above.

Best For Ward linkage:

n_components = 50
n_clusters = 20
metric = 'cosine'

Scores for Ward:

'Homogeneity': 0.5532128999826028,
'Completeness': 0.5868772124352711,
'V-measure': 0.569548040262317,
'Adjusted Rand Index': 0.4030347023439802,
'Adjusted mutual information score': 0.5681037770844866

Best For Single linkage:

n_components = 5
n_clusters = 20
metric = 'cosine'

'Homogeneity': 0.108424,
'Completeness': 0.695943,
'V-measure': 0.187619,
'Adjusted Rand Index': 0.020581,
'Adjusted mutual information score': 0.183878

Ward linkage is performing much much better.

In [110]:

```
# Creating a dict of UMAP features with different n_components

def getUMAP(n_components, data):
    umap_fit = umap.UMAP(n_components=n_components, metric='cosine')
    umap_features = umap_fit.fit_transform(data)
    return umap_features

UMAPDict = {}
components = [5, 20, 200]
for comp in components:
    UMAPDict[comp] = getUMAP(comp, fullFeatures)
```

In [115]:

```
SVDDict = {}
NMFDict = {}
components = [5, 20, 200]
for comp in components:
    svd = getSVD(comp, fullFeatures)
    SVDDict[comp] = svd.transform(fullFeatures)
    nf = getNMF(comp, fullFeatures)
    NMFDict[comp] = nf.transform(fullFeatures)
```

DBSCAN and HDBSCAN

In [126]:

```
n_components = [5, 20, 200]
cluster_size = [100, 200]
metric_types = [ 'euclidean', 'manhattan', 'cosine']
minsamples = [10, 20, 50, 100]
eps_vals = [0.5, 0.8, 5]

bestDBSCAN = []
bestHDBSCAN = []

bestavgDBScore = -1000
bestavgHDBScore = -1000

bestDBScores = {}
bestHDBScores = {}

bestDBLabels = []
bestHDBLabels = []

for comp in n_components:
    xdata = UMAPDict[comp]

    for ep in eps_vals:
        for samples in minsamples:
            for met in metric_types:
                for cluster in cluster_size:
                    DBS = DBSCAN(min_samples=samples, metric=met, eps=ep)
                    DBS.fit(xdata)
                    DBScore = getScores(labels, DBS.labels_)

                    HDB = hdbscan.HDBSCAN(min_cluster_size=cluster, min_samples=samp
                    HDB.fit(xdata)
                    HDBScore = getScores(labels, HDB.labels_)

                    avgDBScore = (DBScore["Homogeneity"] + DBScore["Completeness"] +
                    avgHDBScore = (HDBScore["Homogeneity"] + HDBScore["Completeness"

                    if avgDBScore > bestavgDBScore:
                        bestavgDBScore = avgDBScore
                        bestDBSCAN = DBS
                        bestDBScores = DBScore
                        bestDBLabels = DBS.labels_

                    if avgHDBScore > bestavgHDBScore:
                        bestavgHDBScore = avgHDBScore
                        bestHDBSCAN = HDB
                        bestHDBScores = HDBScore
                        bestHDBLabels = HDB.labels_
```

In [127]:

```
bestDBScores
```

Out[127]:

```
{'Homogeneity': 0.5235148929796238,
 'Completeness': 0.5426392854617677,
 'V-measure': 0.5329055650663066,
 'Adjusted Rand Index': 0.31171940870320614,
 'Adjusted mutual information score': 0.5237556916329063}
```

In [128]:

```
bestHDBScores
```

Out[128]:

```
{'Homogeneity': 0.37458825185751765,
 'Completeness': 0.6692492369359203,
 'V-measure': 0.48032937006425697,
 'Adjusted Rand Index': 0.19408884553341005,
 'Adjusted mutual information score': 0.47953777524015656}
```

In [201]:

```
print(bestDBSCAN)
print(bestHDBSCAN)
```

```
DBSCAN(eps=0.8, metric='manhattan', min_samples=100)
HDBSCAN(cluster_selection_epsilon=0.5, min_cluster_size=100, min_sampl
es=100)
```

Question 15

For DBSCAN with UMAP hyperparameter search grid is as follows:

n_components = [5, 20, 200]
metric = ['euclidean', 'manhattan', 'cosine']
min_samples = [10, 20, 50, 100]
eps valuess = [0.5, 0.8, 5]

The best DBSCAN hyperparameters are :

eps = 0.8,
metric = 'manhattan'
min_samples = 100
DBSCAN(eps=0.8, metric='manhattan', min_samples=100)
UMAP Components = 5

Scores:

'Homogeneity': 0.5235148929796238,
'Completeness': 0.5426392854617677,
'V-measure': 0.5329055650663066,
'Adjusted Rand Index': 0.31171940870320614,
'Adjusted mutual information score': 0.5237556916329063

For HDBSCAN with UMAP hyperparameter search grid is as follows:

n_components = [5, 20, 200]
min_samples = [10, 20, 50, 100]
cluster_size = [100, 200]
cluster_selection_epsilon = [0.5, 0.8, 5]

The best HDBSCAN hyperparameters are :

eps = 0.5,
min_samples = 100
min_cluster_size = 100
UMAP Components = 5

'Homogeneity': 0.37458825185751765,
'Completeness': 0.6692492369359203,
'V-measure': 0.48032937006425697,
'Adjusted Rand Index': 0.19408884553341005,
'Adjusted mutual information score': 0.47953777524015656

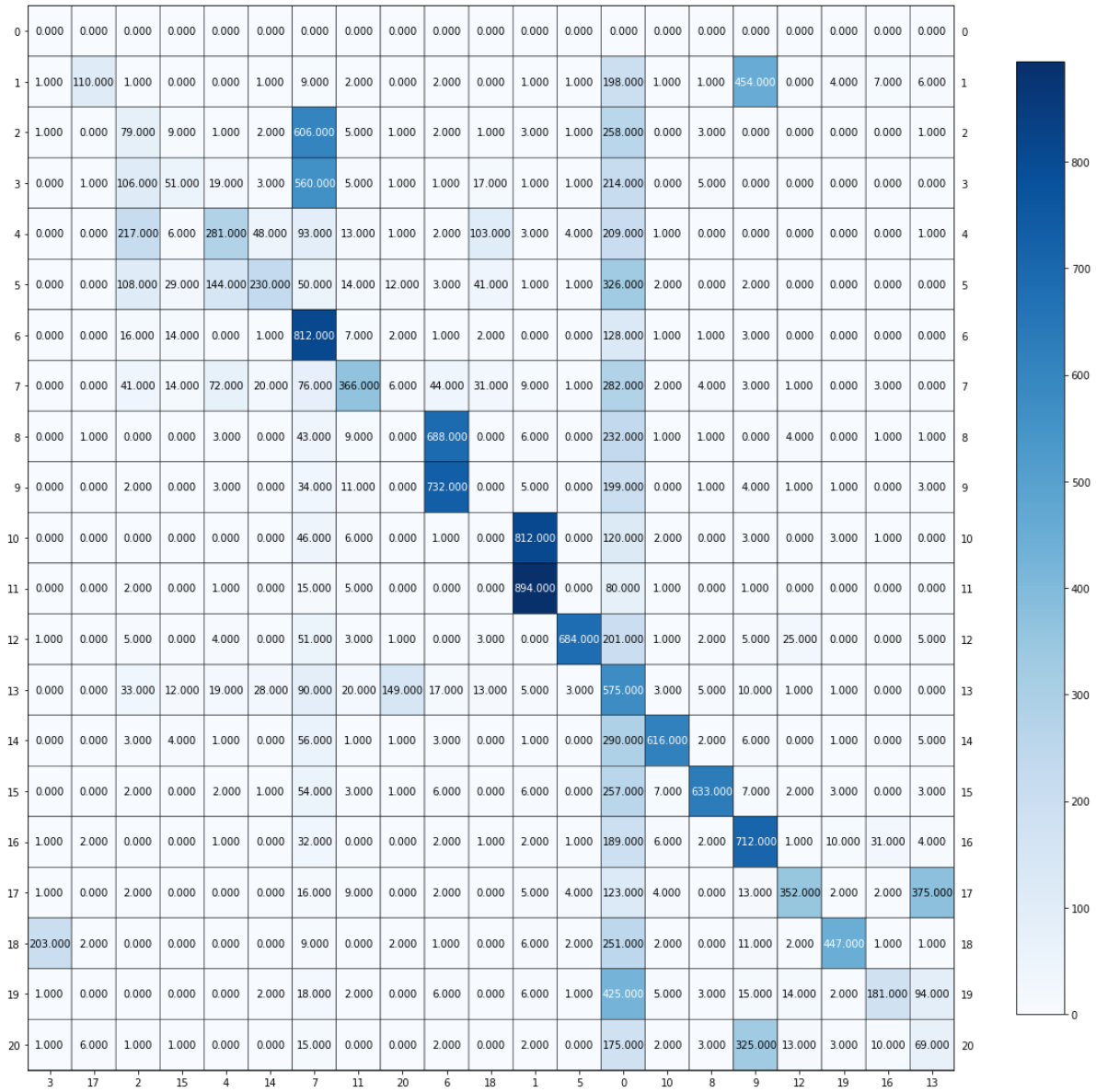
DBSCAN seems to perform better

Question 16

Contingency matrix for best DBSCAN

In [148]:

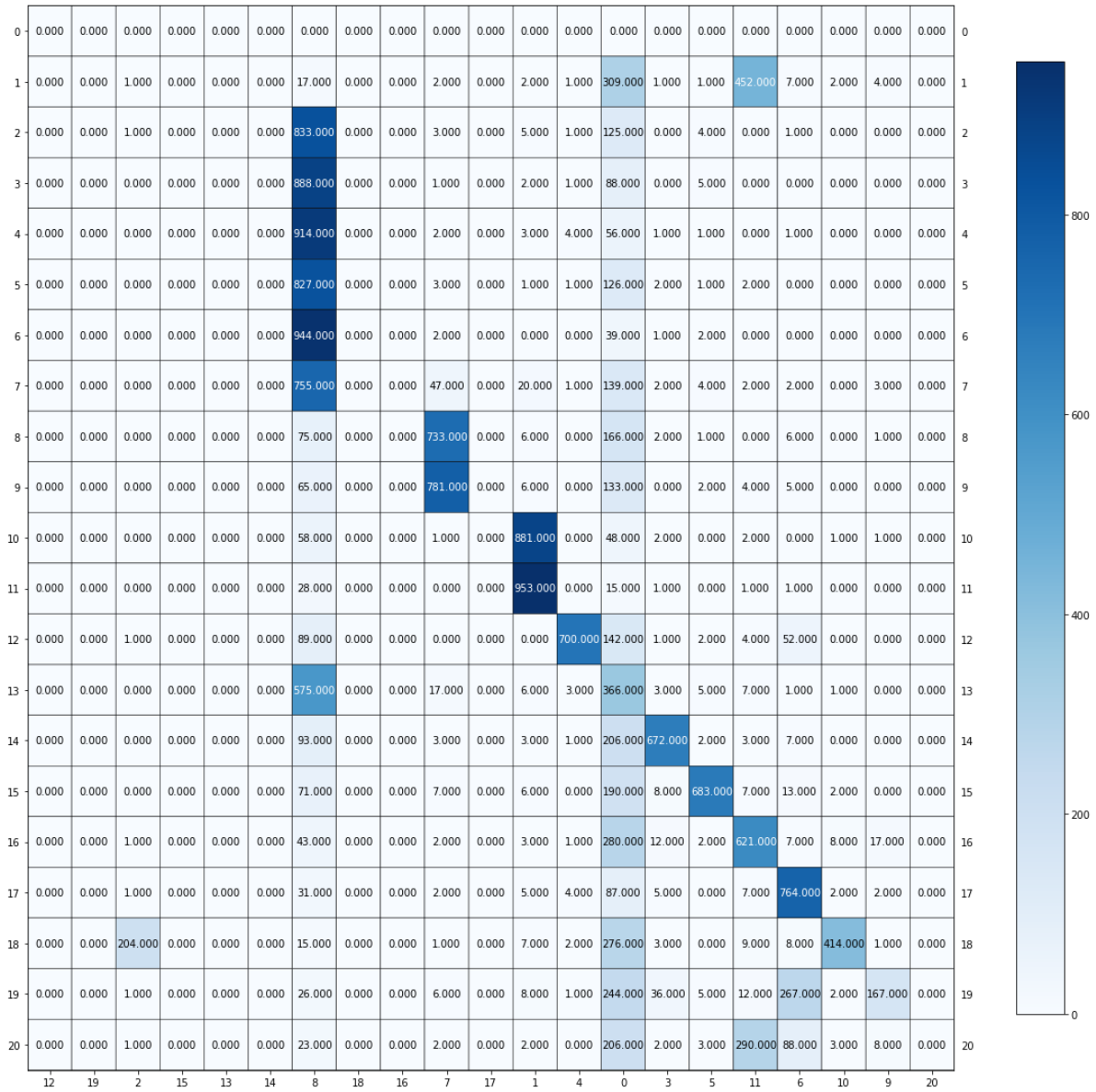
```
bestDBSCAN = DBSCAN(min_samples=100, eps=0.8, metric='manhattan')
bestDBSCAN.fit(UMAPDict[5])
bestDBLabels = mod.labels_

cmDB = confusion_matrix(labels, lab)
rows, cols = linear_sum_assignment(cmDB, maximize=True)
plot_mat(cmDB[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows, size=(
```



Contingency matrix for best HDBSCAN

In [200]:

```
bestHDBSCAN = hdbscan.HDBSCAN(cluster_selection_epsilon=0.5, min_cluster_size=100, m
bestHDBSCAN.fit(UMAPDict[5])
bestHDBLabels = mod.labels_

cmHDB = confusion_matrix(labels, bestHDBLabels)
rows, cols = linear_sum_assignment(cmHDB, maximize=True)
plot_mat(cmHDB[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows, size=
```



Answer 16

The contingency matrices for both best DBSCAN and HDBSCAN with UMAP components are plotted above.

"-1" for the clustering labels means the data points which are considered as outliers/ noisy samples by the clustering alogrithm. They dont belong to any cluster.

There are 21 clusters for formed for both HDBSCAN and DBSCAN. Though some data points are considered as outliers by the algorithms and those re neglected.

Seeing the scores and contingency matrix, DBSCAN seems to perform better.

In [202]:

```
redDICT = {
    'SVD': SVDDict,
    'NMF': NMFDict,
    'UMAP': UMAPDict
}
```

Question 17

In [203]:

```
# For K-means

bestKmeansScores = []
bestK = 10
bestRedK = 'None'
bestCompK = 5
reductions = ['None', 'SVD', 'NMF', 'UMAP']
components = [5, 20, 200]
bestARIK = 0
bestKMEANS = ""

clusters = [10, 20, 50]

for red in reductions:
    if red == 'None':
        for k in clusters:
            kmeans = KMeans(n_clusters=k, random_state=0, max_iter=3000, n_init=50).
            predictedLabels = kmeans.labels_
            scores = getScores(labels, predictedLabels)

            if scores['Adjusted Rand Index'] > bestARIK:
                bestARIK = scores['Adjusted Rand Index']
                bestRedK = 'None'
                bestKmeansScores = scores
                bestK = k
                bestKMEANS = kmeans
                bestCompK = 'All'
    else:
        for comp in components:
            xdata = redDICT[red][comp]
            for k in clusters:
                kmeans = KMeans(n_clusters=k, random_state=0, max_iter=3000, n_init=
                predictedLabels = kmeans.labels_
                scores = getScores(labels, predictedLabels)

                if scores['Adjusted Rand Index'] > bestARIK:
                    bestARIK = scores['Adjusted Rand Index']
                    bestRedK = red
                    bestKmeansScores = scores
                    bestK = k
                    bestKMEANS = kmeans
                    bestCompK = comp
```

In [205]:

```
print("Best KMeans Scores: " , bestKmeansScores)
print("Best Number of Clusters: ", bestK)
print("Best Reduction Method: ", bestRedK)
print("Best Components for the reduction method: ", bestCompK)
print("Best Clusterer: ", bestKMEANS)
```

```
Best KMeans Scores:  {'Homogeneity': 0.5806805815300556, 'Completenes
s': 0.6115249272650983, 'V-measure': 0.5957037570532415, 'Adjusted Ran
d Index': 0.4569803695125659, 'Adjusted mutual information score': 0.5
943523647530761}
Best Number of Clusters:  20
Best Reduction Method:  UMAP
Best Components for the reduction method:  200
Best Clusterer:  KMeans(max_iter=3000, n_clusters=20, n_init=50, rando
m_state=0)
```

In [207]:

```
# For agglomerative clustering
#  Choosing WARD as it was performing best.

bestAggloScores = []
bestKAgglo = 20
bestRedAgglo = 'None'
bestCompAgglo = 5
reductions = ['None', 'SVD', 'NMF', 'UMAP']
components = [5, 20, 200]
bestARIAgglo = 0
bestAGGLO = ""

clusters = [20]

for red in reductions:
    if red == 'None':
        for k in clusters:
            AggClustering = AgglomerativeClustering(n_clusters=k, linkage='ward').fi
            predictedLabels = AggClustering.labels_
            scores = getScores(labels, predictedLabels)

            if scores['Adjusted Rand Index'] > bestARIAgglo:
                bestARIAgglo = scores['Adjusted Rand Index']
                bestRedAgglo = 'None'
                bestAggloScores = scores
                bestKAgglo = k
                bestAGGLO = AggClustering
                bestCompAgglo = 'All'
    else:
        for comp in components:
            xdata = redDICT[red][comp]
            for k in clusters:
                AggClustering = AgglomerativeClustering(n_clusters=k, linkage='ward'
                predictedLabels = AggClustering.labels_
                scores = getScores(labels, predictedLabels)

                if scores['Adjusted Rand Index'] > bestARIAgglo:
                    bestARIAgglo = scores['Adjusted Rand Index']
                    bestRedAgglo = red
                    bestAggloScores = scores
                    bestKAgglo = k
                    bestAGGLO = AggClustering
                    bestCompAgglo = comp
```

In [208]:

```
print("Best Agglomerative Scores: " , bestAggloScores)
print("Best Number of Clusters: ", bestKAgglo)
print("Best Reduction Method: ", bestRedAgglo)
print("Best Components for the reduction method: ", bestCompAgglo)
print("Best Agglomerative Clusterer: ", bestAGGLO)
```

```
Best Agglomerative Scores:  {'Homogeneity': 0.5606966790260698, 'Compl
eteness': 0.5999114955884185, 'V-measure': 0.5796415890276118, 'Adjust
ed Rand Index': 0.41951672531146084, 'Adjusted mutual information scor
e': 0.5782252143043021}
Best Number of Clusters:  20
Best Reduction Method:  UMAP
Best Components for the reduction method:  200
Best Agglomerative Clusterer:  AgglomerativeClustering(n_clusters=20)
```

In [209]:

```
# For DBSCAN

bestDBScores = []
bestRedDB = 'SVD'
reductions = ['SVD', 'NMF', 'UMAP']
components = [5, 20, 200]
bestARIDB = 0
bestDB = ""
bestepsDB = 0.5
bestcompDB = 5

eps = [0.5, 5]

for red in reductions:
    for comp in components:
        xdata = redDICT[red][comp]
        for ep in eps:
            DBS = DBSCAN(eps=ep, metric='manhattan', min_samples=100)
            DBS.fit(xdata)
            scores = getScores(labels, DBS.labels_)

            if scores['Adjusted Rand Index'] > bestARIDB:
                bestARIDB = scores['Adjusted Rand Index']
                bestRedDB = red
                bestDBScores = scores
                bestepsDB = ep
                bestDB = DBS
                bestcompDB = comp
```

In [210]:

```
print("Best DBSCAN Scores: " , bestDBScores)
print("Best eps: ", bestepsDB)
print("Best Reduction Method: ", bestRedDB)
print("Best Components for the reduction method: ", bestcompDB)
print("Best DBSCAN: ", bestDB)
```

```
Best DBSCAN Scores:  {'Homogeneity': 0.33120205835686245, 'Completenes
s': 0.6945617362912734, 'V-measure': 0.44852485126850467, 'Adjusted Ra
nd Index': 0.16235616472721429, 'Adjusted mutual information score':
0.447892746623063}
Best eps:  5
Best Reduction Method:  UMAP
Best Components for the reduction method:  200
Best DBSCAN:  DBSCAN(eps=5, metric='manhattan', min_samples=100)
```

In [211]:

```
# For HDBScan

bestHDBScores = []
bestRedHDB = 'SVD'
reductions = ['SVD', 'NMF', 'UMAP']
components = [5, 20, 200]
bestARIHDB = 0
bestHDB = ""
bestcompHDB = 5
bestminClustersHDB = 100

clusters = [100, 200]

for red in reductions:
    for comp in components:
        xdata = redDICT[red][comp]
        for k in clusters:
            HDB = hdbscan.HDBSCAN(cluster_selection_epsilon=0.5, min_cluster_size=k,
            HDB.fit(xdata)
            scores = getScores(labels, HDB.labels_)

            if scores['Adjusted Rand Index'] > bestARIDB:
                bestARIHDB = scores['Adjusted Rand Index']
                bestRedHDB = red
                bestHDBScores = scores
                bestminClustersHDB = k
                bestHDB = HDB
                bestcompHDB = comp
```

In [212]:

```
print("Best HDBSCAN Scores: " , bestHDBScores)
print("Best min clusters: ", bestminClustersHDB)
print("Best Reduction Method: ", bestRedHDB)
print("Best Components for the reduction method: ", bestcompHDB)
print("Best DBSCAN: ", bestHDB)
```

```
Best HDBSCAN Scores:  {'Homogeneity': 0.4129198938992539, 'Completenes
s': 0.6174470134270562, 'V-measure': 0.49488420767373975, 'Adjusted Ra
nd Index': 0.19576297047983665, 'Adjusted mutual information score':
0.4937516237378393}
Best min clusters:  200
Best Reduction Method:  UMAP
Best Components for the reduction method:  200
Best DBSCAN:  HDBSCAN(cluster_selection_epsilon=0.5, min_cluster_size=
200, min_samples=100)
```

Answer 17

The following grid was followed to determine the best combination to perform the clustering task.

Module	Alternatives	Hyperparameters
Dimensionality Reduction	None	N/A
	SVD	r = [5,20,200]
	NMF	r = [5,20,200]
	UMAP	n_components = [5,20,200]
Clustering	K-Means	k = [10,20,50]
	Agglomerative Clustering	n_clusters = [20]
	DBSCAN	min_cluster_size = [100,200]
	HDBSCAN	min_cluster_size = [100,200]

Best KMeans Scores with hyperparameters:

'Homogeneity': 0.5806805815300556,
'Completeness': 0.6115249272650983,
'V-measure': 0.5957037570532415,
'Adjusted Rand Index': 0.4569803695125659,
'Adjusted mutual information score': 0.5943523647530761
Best Number of Clusters: 20
Best Reduction Method: UMAP
Best Components for the reduction method: 200
Best Clusterer: KMeans(max_iter=3000, n_clusters=20, n_init=50, random_state=0)

Best Agglomerative Scores with hyperparameters:

'Homogeneity': 0.5606966790260698,
'Completeness': 0.5999114955884185,
'V-measure': 0.5796415890276118,
'Adjusted Rand Index': 0.41951672531146084,
'Adjusted mutual information score': 0.5782252143043021}
Best Number of Clusters: 20

Best Reduction Method: UMAP
Best Components for the reduction method: 200
Best Agglomerative Clusterer: AgglomerativeClustering(n_clusters=20)

Best DBSCAN Scores with hyperparameters:
'Homogeneity': 0.33120205835686245,
'Completeness': 0.6945617362912734,
'V-measure': 0.44852485126850467,
'Adjusted Rand Index': 0.16235616472721429,
'Adjusted mutual information score': 0.447892746623063}
Best eps: 5
Best Reduction Method: UMAP
Best Components for the reduction method: 200
Best DBSCAN: DBSCAN(eps=5, metric='manhattan', min_samples=100)

Best HDBSCAN Scores with hyperparameters:
'Homogeneity': 0.4129198938992539,
'Completeness': 0.6174470134270562,
'V-measure': 0.49488420767373975,
'Adjusted Rand Index': 0.19576297047983665,
'Adjusted mutual information score': 0.4937516237378393}
Best min clusters: 200
Best Reduction Method: UMAP
Best Components for the reduction method: 200
Best DBSCAN: HDBSCAN(cluster_selection_epsilon=0.5, min_cluster_size=200, min_samples=100)

From above results, the best combinations in decreasing order of average clustering measures:

1). KMeans + UMAP

2). Agglomerative clustering + UMAP

3). DBSCAN + UMAP

4). HDBSCAN + UMAP

The reason why UMAP is best compared to other dimensionality reduction techniques is because UMAP learns the global data structure and is less dependent on random initiators compared to NMF. Also UMAP with cosine similarity is performing much well because of the fact that sparse text document matrices are difficult to work with using SVD and NMF whereas cosine similarity measure is not much effected by it.

KMeans is performing well because, it uses the fact of prior number of clusters unlike DBSCAN and HDBSCAN which are highly sensitive to other parameters like eps and min_cluster_size. In Agglomerative clustering there is no such minimization happening in terms of intra cluster distances which is being performed extensively in KMeans optimization.

Question 18

In [234]:

```
umap_mod = umap.UMAP(n_components=50)
UMAPFeat = umap_mod.fit_transform(fullFeatures)

svdmod = getSVD(50, fullFeatures)
svdFeat = svdmod.transform(fullFeatures)
```

In [248]:

```
nmfmod = getNMF(50, fullFeatures)
nmfFeat = nmfmod.transform(fullFeatures)
```

In [243]:

```
crossed = np.multiply(UMAPFeat, svdFeat)
```

In [244]:

```
clusterer = KMeans(n_clusters=20, random_state=0, max_iter=3000, n_init=50).fit(cros
clustLabs = clusterer.labels_
```

In [245]:

```
getScores(labels, clustLabs)
```

Out[245]:

```
{'Homogeneity': 0.27836989706305004,
 'Completeness': 0.3335059715132977,
 'V-measure': 0.30345378116014127,
 'Adjusted Rand Index': 0.08149556694266143,
 'Adjusted mutual information score': 0.3009870693322971}
```

In [259]:

```
# Keeping header and footers of data

data = datasets.fetch_20newsgroups(subset='all')
```

In [260]:

```
fullData = data.data
labelNames = np.array(data.target_names)
fullDataLabels = np.array(data.target)
stringLabels = np.array([labelNames[label] for label in fullDataLabels])
```

In [263]:

```
pipe = Pipeline([
    ('count', CountVectorizer(preprocessor=preprocess, stop_words='english', min_df=
    ('tfidf', TfidfTransformer(smooth_idf=True, use_idf=True))
]).fit(fullData)

newsData3df = pipe.transform(fullData)
```

In [264]:

```
pipe = Pipeline([
    ('count', CountVectorizer(preprocessor=preprocess, stop_words='english', min_df=
    ('tfidf', TfidfTransformer(smooth_idf=True, use_idf=True))
]).fit(fullData)

newsData5df = pipe.transform(fullData)
```

In [311]:

```
umap_mod = umap.UMAP(n_components=100, random_state=42)
UMAPFeat3 = umap_mod.fit_transform(newsData3df)

svdmod = getSVD(100, newsData3df)
svdFeat3 = svdmod.transform(newsData3df)

umap_mod = umap.UMAP(n_components=100, random_state=42)
UMAPFeat5 = umap_mod.fit_transform(newsData5df)

svdmod = getSVD(100, newsData5df)
svdFeat5 = svdmod.transform(newsData5df)
```

In [329]:

```
clusterer = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(UMAP
clustLabs = clusterer.labels_
getScores(labels, clustLabs)
```

Out[329]:

```
{'Homogeneity': 0.5377529918200834,
 'Completeness': 0.5696767485293908,
 'V-measure': 0.5532547388430132,
 'Adjusted Rand Index': 0.43050889147870935,
 'Adjusted mutual information score': 0.5517557788353247}
```

In [330]:

```
clusterer = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(svdF
clustLabs = clusterer.labels_
getScores(labels, clustLabs)
```

Out[330]:

```
{'Homogeneity': 0.3744111494089925,
 'Completeness': 0.46459306903108544,
 'V-measure': 0.41465542403778416,
 'Adjusted Rand Index': 0.13739295602486884,
 'Adjusted mutual information score': 0.41252473959983915}
```

In [331]:

```
clusterer = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(UMAP
clustLabs = clusterer.labels_
getScores(labels, clustLabs)
```

Out[331]:

```
{'Homogeneity': 0.5267248371135923,
 'Completeness': 0.553470030490929,
 'V-measure': 0.5397663336506847,
 'Adjusted Rand Index': 0.41868703780435773,
 'Adjusted mutual information score': 0.5382405122437159}
```

In [332]:

```
clusterer = KMeans(n_clusters=20, random_state=0, max_iter=5000, n_init=50).fit(svdF
clustLabs = clusterer.labels_
getScores(labels, clustLabs)
```

Out[332]:

```
{'Homogeneity': 0.3275364431703451,
 'Completeness': 0.41027035386490357,
 'V-measure': 0.3642647180349287,
 'Adjusted Rand Index': 0.1351860325744043,
 'Adjusted mutual information score': 0.3619497993048606}
```

Answer 18

Two approaches are tried:

- Using a combination of SVD and UMAP. The 50 dimensionally reduced features were taken from both and multiplied together element wise. The idea was may be the feature representation with this maps the data points far away in the combined reduced space of SVD and UMAP representation.

The above approach failed big time. The scores of which are given below.

'Homogeneity': 0.27836989706305004,
'Completeness': 0.3335059715132977,
'V-measure': 0.30345378116014127,
'Adjusted Rand Index': 0.08149556694266143,
'Adjusted mutual information score': 0.3009870693322971

- Making the changes in the data itself.

1). Using the full data from 20 news group without removing the header and footers.

Two variations were tried for this and best combination from previous results i.e UMAP with K-means and SVD with K-Means were tried.

n_components for both SVD and UMAP = 50
n_clusters = 20.
n_init = 50
max_iter = 5000

- Using min_df = 3 with TF-IDF representation.

a). UMAP + KMeans:
'Homogeneity': 0.5377529918200834,
'Completeness': 0.5696767485293908,
'V-measure': 0.5532547388430132,
'Adjusted Rand Index': 0.43050889147870935,
'Adjusted mutual information score': 0.5517557788353247

b). SVD + Kmeans:
'Homogeneity': 0.3744111494089925,
'Completeness': 0.46459306903108544,
'V-measure': 0.41465542403778416,
'Adjusted Rand Index': 0.13739295602486884,
'Adjusted mutual information score': 0.41252473959983915

- Using min_df = 5 with TF-IDF representation.

a).UMAP + Kmeans:
'Homogeneity': 0.5267248371135923,
'Completeness': 0.553470030490929,
'V-measure': 0.5397663336506847,
'Adjusted Rand Index': 0.41868703780435773,
'Adjusted mutual information score': 0.5382405122437159

b). SVD + Kmeans:

'Homogeneity': 0.3275364431703451,
'Completeness': 0.41027035386490357,
'V-measure': 0.3642647180349287,
'Adjusted Rand Index': 0.1351860325744043,
'Adjusted mutual information score': 0.3619497993048606

The Adjusted Rand index of this approach were almost equivalent to the results without header and footer but on average the results of all the metrics were improved a little bit.

In [ ]:

Part 2 - Deep Learning and Clustering of Image Data

In [28]:

```
import torch
import torch.nn as nn
from torchvision import transforms, datasets
from torch.utils.data import DataLoader, TensorDataset
import numpy as np
import matplotlib.pyplot as plt

from tqdm import tqdm
import requests
import os
import tarfile

from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans
from sklearn.metrics import confusion_matrix, adjusted_rand_score, adjusted_mutual_i
from sklearn.pipeline import Pipeline
from sklearn.base import TransformerMixin

# !pip install hdbscan
from hdbscan import HDBSCAN

from sklearn.manifold import TSNE

from sklearn.model_selection import train_test_split
# !pip install umap-learn[plot]
# !pip install holoviews
# !pip install -U ipykernel

import umap
import umap.plot

from sklearn.metrics import f1_score
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
from sklearn.metrics import accuracy_score
from sklearn.metrics import plot_confusion_matrix
from sklearn.metrics.cluster import rand_score


from sklearn.cluster import KMeans
from sklearn.metrics.cluster import contingency_matrix

from sklearn.metrics.cluster import homogeneity_score
from sklearn.metrics.cluster import completeness_score
from sklearn.metrics.cluster import v_measure_score
from sklearn.metrics.cluster import adjusted_rand_score
from sklearn.metrics.cluster import adjusted_mutual_info_score


from scipy.optimize import linear_sum_assignment
from sklearn.metrics import confusion_matrix
from sklearn.cluster import AgglomerativeClustering
from sklearn.cluster import DBSCAN
from sklearn.decomposition import TruncatedSVD
```

Flowers Dataset and VGG Features

Question 19

If the VGG network is trained on a dataset with different classes as targets, the features derived from that model are expected to have discriminative power for a custom dataset is quite true only when the VGG netowrk is trained on a relatively large dataset compared to the custom data in consideration and also the dataset on which VGG was trained has to be of some relevance to the custom dataset. One can't expect the features extracted from a VGG network trained on a Speech data to perform and to be used on a custom dataset of images.

Also given the above conditions are met one can expect the VGG extracted features to have a discriminative power for custom dataset because the features learned by the network are generalized features for a class of data which are universal for the object.

In [2]:

```
filename = './flowers_features_and_labels.npz'

if os.path.exists(filename):
    file = np.load(filename)
    f_all, y_all = file['f_all'], file['y_all']

else:
    if not os.path.exists('./flower_photos'):
        # download the flowers dataset and extract its images
        url = 'http://download.tensorflow.org/example_images/flower_photos.tgz'
        with open('./flower_photos.tgz', 'wb') as file:
            file.write(requests.get(url).content)
        with tarfile.open('./flower_photos.tgz') as file:
            file.extractall('./')
        os.remove('./flower_photos.tgz')

    class FeatureExtractor(nn.Module):
        def __init__(self):
            super().__init__()

            vgg = torch.hub.load('pytorch/vision:v0.10.0', 'vgg16', pretrained=True)

            # Extract VGG-16 Feature Layers
            self.features = list(vgg.features)
            self.features = nn.Sequential(*self.features)
            # Extract VGG-16 Average Pooling Layer
            self.pooling = vgg.avgpool
            # Convert the image into one-dimensional vector
            self.flatten = nn.Flatten()
            # Extract the first part of fully-connected layer from VGG16
            self.fc = vgg.classifier[0]

        def forward(self, x):
            # It will take the input 'x' until it returns the feature vector called
            out = self.features(x)
            out = self.pooling(out)
            out = self.flatten(out)
            out = self.fc(out)
            return out

    # Initialize the model
    assert torch.cuda.is_available()
    feature_extractor = FeatureExtractor().cuda().eval()

    dataset = datasets.ImageFolder(root='./flower_photos',
                                   transform=transforms.Compose([transforms.Resize(2
                                                                 transforms.CenterCr
                                                                 transforms.ToTensor
                                                                 transforms.Normaliz
    dataloader = DataLoader(dataset, batch_size=64, shuffle=True)

    # Extract features and store them on disk
    f_all, y_all = np.zeros((0, 4096)), np.zeros((0,))
    for x, y in tqdm(dataloader):
        with torch.no_grad():
            f_all = np.vstack([f_all, feature_extractor(x.cuda()).cpu()])
            y_all = np.concatenate([y_all, y])
    np.savez(filename, f_all=f_all, y_all=y_all)
```

```
Using cache found in /root/.cache/torch/hub/pytorch_vision_v0.10.0
100%|██████████| 58/58 [00:55<00:00,  1.04it/s]
```

In [3]:

```
print(f_all.shape, y_all.shape)
num_features = f_all.shape[1]
```

```
(3670, 4096) (3670,)
```

Question 20

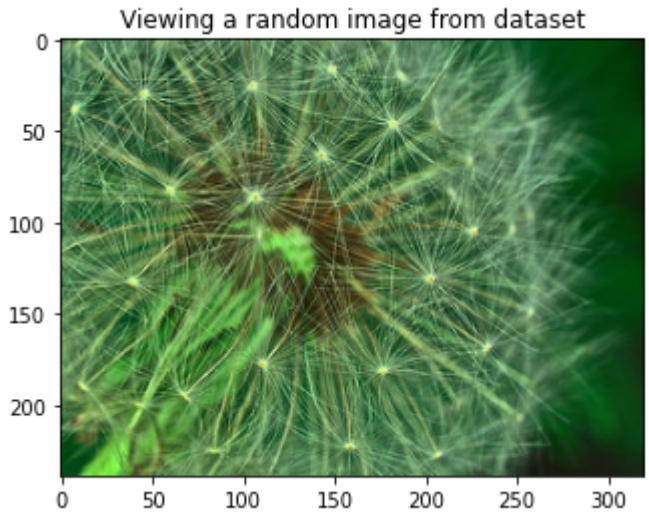
How features are extracted:

- The custom dataset is loaded via dataloader from the directory.
- While being loaded each image is preprocessed with resizing and cropping (for same size of images), then they are converted to tensors and normalized for faster convergence.
- Then all the code is doing is to pass these images in batches to the Feature extractor which is initialized with VGG extracted features, leaving the dense layers which do the predictions.
- Each image does a forward pass through the VGG features, then it's passed through pooling layer and flattened and appened to a numpy array as (1 X 4096) size row vector.
- When the forward pass of image is done, the pretrained model extracts the features from the image.

In [4]:

```
# Finding the size of original images.
# Fetching a few from the original dataset saved under folder flower_photos

imageData = datasets.ImageFolder(root='./flower_photos')
print("Size of dataset: ", len(imageData))

print("Classes in dataset", imageData.classes)

print("Viewing a random image::: ")

image, label = imageData[np.random.randint(len(imageData))]
plt.imshow(image)

plt.title("Viewing a random image from dataset")

print("Size of original image 1: ", image.size)

# More rrandomly selected image.
image, label = imageData[np.random.randint(len(imageData))]
print("Size of original image 2: ", image.size)

image, label = imageData[np.random.randint(len(imageData))]
print("Size of original image 3: ", image.size)

image, label = imageData[np.random.randint(len(imageData))]
print("Size of original image 4: ", image.size)
```

```
Size of dataset:  3670
Classes in dataset ['daisy', 'dandelion', 'roses', 'sunflowers', 'tuli
ps']
Viewing a random image:::
Size of original image 1:  (320, 239)
Size of original image 2:  (500, 334)
Size of original image 3:  (500, 375)
Size of original image 4:  (500, 331)
```



Question 21

There are varying amount of pixels in the original dataset.

The sizes are all different, each image has three channels and different dimensions as shown above(320, 239), (500, 334), (500, 375) etc.. thats why while being loaded by dataloader, the cropping and resisizing is done to make them of same size.

For each image 4096 features are extracted.

Each image then is represented as a (1 x 4096) row vector.

```
Question 22
```

In [5]:

```
TFIDFRepresentations = np.array(fullFeatures.toarray())
averageZeros = np.mean((TFIDFRepresentations.shape[1] - np.count_nonzero(TFIDFRepres
sparsity = averageZeros * 100/ TFIDFRepresentations.shape[1]
print("On average every TFIDF Representation of news data is {} % sparse".format(spa
```

```
On average every TFIDF Representation of news data is 99.9230158439087
3 % sparse
```

In [6]:

```
# Sparsity check of VGG Features.
averageZerosVGG = np.mean((f_all.shape[1] - np.count_nonzero(f_all, axis=0)))
print(averageZerosVGG * 100/ f_all.shape[1])
```

```
10.400390625
```

In [7]:

```
print("On average every Image feature Representation is {} % sparse".format(10.40039
```

```
On average every Image feature Representation is 10.400390625 % sparse
```

Answer 22

The extracted features are around 10.400 % sparse i.e. around ~410 zeros per 4096 entries. We can't call these sparse but somewhat dense.

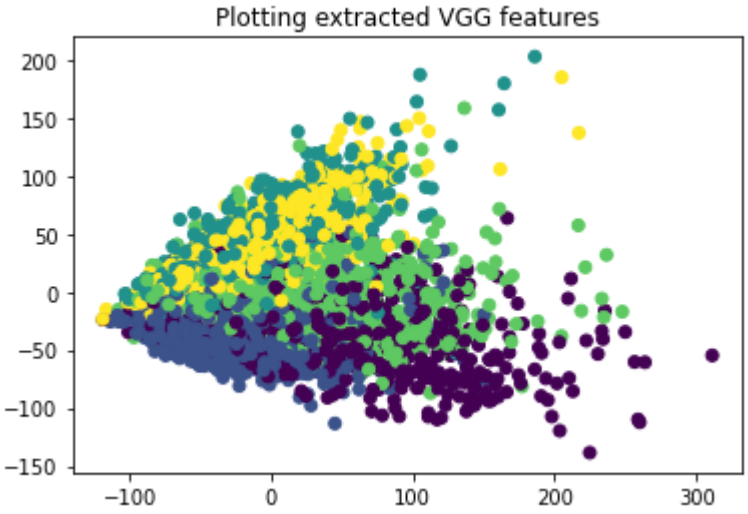
For the TF-IDF representations of the news data: They are 99.92 % sparse. Which is huge and highly sparse.

In [8]:

```
f_pca = PCA(n_components=2).fit_transform(f_all)
plt.scatter(*f_pca.T, c=y_all)
plt.title("Plotting extracted VGG features")
```

Out[8]:

```
Text(0.5, 1.0, 'Plotting extracted VGG features')
```



Question 23

In [9]:

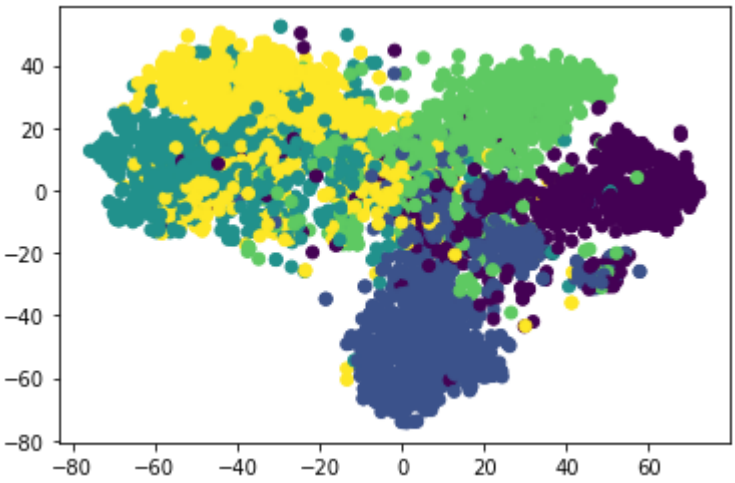
```
# Visualisation using TSNE

tsneMod = TSNE(n_components=2, n_iter=2000, init='random', learning_rate='auto')
tsne_results = tsneMod.fit_transform(f_all)
```

In [10]:

```
plt.scatter(*tsne_results.T, c=y_all)
```

Out[10]:

```
<matplotlib.collections.PathCollection at 0x7f7316168f10>
```



Answer 23

The TSNE representation of the flower data is shown above.

We can see that the extracted features are quite well separated in the 2-D space mapping done by TSNE.

MLP Classifier

In [47]:

```
class MLP(torch.nn.Module):
    def __init__(self, num_features):
        super().__init__()
        self.model = nn.Sequential(
            nn.Linear(num_features, 1280),
            nn.ReLU(True),
            nn.Linear(1280, 640),
            nn.ReLU(True),
            nn.Linear(640, 5),
            nn.LogSoftmax(dim=1)
        )
        self.cuda()


    def forward(self, X):
        return self.model(X)

    def train(self, X, y):
        X = torch.tensor(X, dtype=torch.float32, device='cuda')
        y = torch.tensor(y, dtype=torch.int64, device='cuda')
        lossHistory = []
        self.model.train()

        criterion = nn.NLLLoss()
        optimizer = torch.optim.Adam(self.parameters(), lr=1e-3, weight_decay=1e-5)

        dataset = TensorDataset(X, y)
        dataloader = DataLoader(dataset, batch_size=128, shuffle=True)

        for epoch in tqdm(range(100)):
            for (X_, y_) in dataloader:
                out=self.forward(X_)
                loss=criterion(out,y_)
                lossHistory.append(loss)
                loss.backward()
                optimizer.step()
                optimizer.zero_grad()
        return self, lossHistory

    def eval(self, X_test, y_test):
      X_tensor = torch.tensor(X_test, dtype=torch.float32, device='cuda')
      y_tensor = torch.tensor(y_test, dtype=torch.int64, device='cuda')
      scores = self.forward(X_tensor)
      print(scores.shape)
      _, pred = torch.max(scores.data, 1)
      pred = pred.cpu().detach().numpy()
      print(pred.shape)
      print("Accuracy:", accuracy_score(y_test, pred))
      print("Precision:", precision_score(y_test, pred,average='macro'))
      print("Recall:", recall_score(y_test, pred, average='macro'))
      print("F1 Score:", f1_score(y_test, pred, average='macro'))
      acc=accuracy_score(y_test, pred)
      return {
          'accuracy': acc,
          'predictions': pred
      }
```

Autoencoder

In [12]:

```
class Autoencoder(torch.nn.Module, TransformerMixin):
    def __init__(self, n_components):
        super().__init__()
        self.n_components = n_components
        self.n_features = None  # to be determined with data
        self.encoder = None
        self.decoder = None

    def _create_encoder(self):
        return nn.Sequential(
            nn.Linear(4096, 1280),
            nn.ReLU(True),
            nn.Linear(1280, 640),
            nn.ReLU(True), nn.Linear(640, 120), nn.ReLU(True), nn.Linear(120, self.r

    def _create_decoder(self):
        return nn.Sequential(
            nn.Linear(self.n_components, 120),
            nn.ReLU(True),
            nn.Linear(120, 640),
            nn.ReLU(True),
            nn.Linear(640, 1280),
            nn.ReLU(True), nn.Linear(1280, 4096))

    def forward(self, X):
        encoded = self.encoder(X)
        decoded = self.decoder(encoded)
        return decoded

    def fit(self, X):
        X = torch.tensor(X, dtype=torch.float32, device='cuda')
        self.n_features = X.shape[1]
        self.encoder = self._create_encoder()
        self.decoder = self._create_decoder()
        self.cuda()
        self.train()

        criterion = nn.MSELoss()
        optimizer = torch.optim.Adam(self.parameters(), lr=1e-3, weight_decay=1e-5)

        dataset = TensorDataset(X)
        dataloader = DataLoader(dataset, batch_size=128, shuffle=True)

        for epoch in tqdm(range(100)):
            for (X_,) in dataloader:
                X_ = X_.cuda()
                # ===================forward====================
                output = self(X_)
                loss = criterion(output, X_)
                # ===================backward====================
                optimizer.zero_grad()
                loss.backward()
                optimizer.step()

        return self

    def transform(self, X):
        X = torch.tensor(X, dtype=torch.float32, device='cuda')
        self.eval()
```

```
        with torch.no_grad():
            return self.encoder(X).cpu().numpy()
```

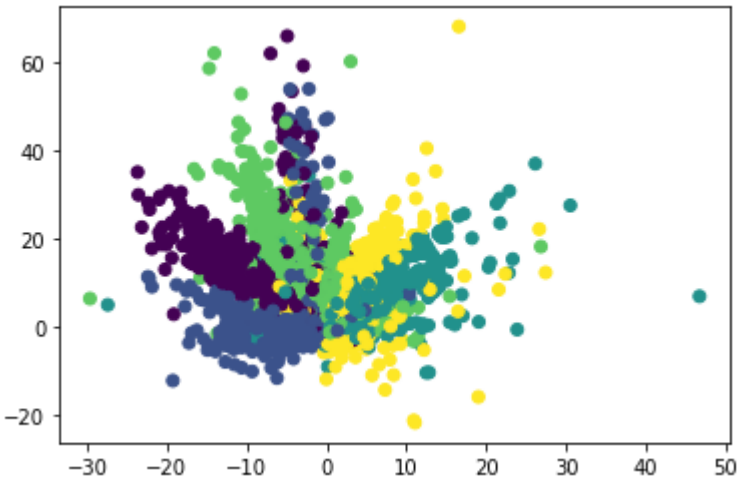
In [13]:

```
X_em =Autoencoder(2).fit_transform(f_all)
plt.scatter(*X_em.T, c=y_all)
```

```
100%|██████████| 100/100 [00:48<00:00,  2.05it/s]
```

Out[13]:

```
<matplotlib.collections.PathCollection at 0x7f7311892b90>
```



Question 24

Clustering the Images via VGG Extracted features

In [29]:

```
def getScores(true, predicted):
    scores = {}
    scores["Homogeneity"] = homogeneity_score(true, predicted)
    scores["Completeness"] = completeness_score(true, predicted)
    scores["V-measure"] = v_measure_score(true, predicted)
    scores["Adjusted Rand Index"] = adjusted_rand_score(true, predicted)
    scores["Adjusted mutual information score"] = adjusted_mutual_info_score(true, p
    scores["Rand Score"] = rand_score(true, predicted)

    return scores

def getSVD(n_comp, data):
    SVD = TruncatedSVD(n_components=n_comp, random_state=42)
    SVD.fit(data)
    return SVD
```

In [15]:

```
VGGFeatures = f_all

# Dimensionality reduction using SVD, Autoencoder, UMAP to 50 components

SVDVGG = getSVD(50, VGGFeatures).transform(VGGFeatures)
UMAPVGG = umap.UMAP(n_components=50, random_state=42, metric='cosine').fit_transform
AutoVGG = Autoencoder(50).fit_transform(VGGFeatures)
```

```
/usr/local/lib/python3.7/dist-packages/numba/np/ufunc/parallel.py:363:
NumbaWarning: The TBB threading layer requires TBB version 2019.5 or l
ater i.e., TBB_INTERFACE_VERSION >= 11005. Found TBB_INTERFACE_VERSION
= 9107. The TBB threading layer is disabled.
  warnings.warn(problem)
100%|██████████| 100/100 [00:48<00:00,  2.05it/s]
```

In [16]:

```
reductionMap = {
    0: VGGFeatures,
    1: SVDVGG,
    2: UMAPVGG,
    3: AutoVGG
}
```

In [30]:

```
# Kmeans clustering

KmeanScores = {}

for i in range(len(reductionMap)):
  VGGkmeans = KMeans(n_clusters=5, random_state=42, max_iter=5000, n_init=50)
  VGGkmeans.fit(reductionMap[i])

  labels = VGGkmeans.labels_

  KmeanScores[i] = getScores(y_all, labels)
```

In [31]:

```
KmeanScores
```

Out[31]:

```
{0: {'Homogeneity': 0.32900498422322894,
  'Completeness': 0.3647476844761788,
  'V-measure': 0.3459555878942219,
  'Adjusted Rand Index': 0.1909980740775149,
  'Adjusted mutual information score': 0.34501522579192423,
  'Rand Score': 0.7028579534103762},
 1: {'Homogeneity': 0.33000487503166903,
  'Completeness': 0.3654963545562431,
  'V-measure': 0.346845048372751,
  'Adjusted Rand Index': 0.19274636767379966,
  'Adjusted mutual information score': 0.34590641140835016,
  'Rand Score': 0.7037911717809499},
 2: {'Homogeneity': 0.47828781665544173,
  'Completeness': 0.49429203168034336,
  'V-measure': 0.4861582460856243,
  'Adjusted Rand Index': 0.39803638259161356,
  'Adjusted mutual information score': 0.48544437660805734,
  'Rand Score': 0.7971381105261477},
 3: {'Homogeneity': 0.28887124749043513,
  'Completeness': 0.31848384786762535,
  'V-measure': 0.30295564206911507,
  'Adjusted Rand Index': 0.2051647001076375,
  'Adjusted mutual information score': 0.30195569753477,
  'Rand Score': 0.7147583814015802}}
```

In [32]:

```
# Agglomerative clustering
# Using ward as its better
AggloScores = {}

for i in range(4):
  VGGAgglo = AgglomerativeClustering(n_clusters=5, linkage='ward')
  VGGAgglo.fit(reductionMap[i])

  labels = VGGAgglo.labels_

  AggloScores[i] = getScores(y_all, labels)
```

In [33]:

```
AggloScores
```

Out[33]:

```
{0: {'Homogeneity': 0.357423727296284,
  'Completeness': 0.41402546658906453,
  'V-measure': 0.3836481433561248,
  'Adjusted Rand Index': 0.18855278251971858,
  'Adjusted mutual information score': 0.3827433388813023,
  'Rand Score': 0.6862000871875192},
 1: {'Homogeneity': 0.337935008027874,
  'Completeness': 0.3725478151154862,
  'V-measure': 0.35439829026356473,
  'Adjusted Rand Index': 0.20355368611320795,
  'Adjusted mutual information score': 0.3534724748241373,
  'Rand Score': 0.7127723774491783},
 2: {'Homogeneity': 0.46289484728283964,
  'Completeness': 0.48520405989530135,
  'V-measure': 0.47378698046331336,
  'Adjusted Rand Index': 0.375806793954751,
  'Adjusted mutual information score': 0.473050766884461,
  'Rand Score': 0.7861848627910552},
 3: {'Homogeneity': 0.3357871451429153,
  'Completeness': 0.3506824651172434,
  'V-measure': 0.34307320252318935,
  'Adjusted Rand Index': 0.257130769678637,
  'Adjusted mutual information score': 0.34215574432201706,
  'Rand Score': 0.7475399974601251}}
```

In [34]:

```
# HDBSCAN Clustering

UMAPVGG = umap.UMAP(n_components=50).fit_transform(VGGFeatures)
reductionMap = {
    0: VGGFeatures,
    1: SVDVGG,
    2: UMAPVGG,
    3: AutoVGG
}

minClusters = [200]
minSamples = [20, 40]

HDBScores = {}

for i in range(4):
  for cluster in minClusters:
    for sample in minSamples:
      VGGHDB = HDBSCAN(min_cluster_size=cluster, min_samples=sample)
      VGGHDB.fit(reductionMap[i])

      labels = VGGHDB.labels_

      key = 'R:' + str(i) + ":" + 'C:' + str(cluster) + 'S:' + str(sample)

      HDBScores[key] = getScores(y_all, labels)
```

In [35]:

```
HDBScores
```

Out[35]:


```
{'R:0:C:200S:20': {'Homogeneity': 1.3876720518042915e-16,
  'Completeness': 1.0,
  'V-measure': 2.7753441036085825e-16,
  'Adjusted Rand Index': 0.0,
  'Adjusted mutual information score': 5.0062065300172974e-17,
  'Rand Score': 0.20358404572368982},
 'R:0:C:200S:40': {'Homogeneity': 1.3876720518042915e-16,
  'Completeness': 1.0,
  'V-measure': 2.7753441036085825e-16,
  'Adjusted Rand Index': 0.0,
  'Adjusted mutual information score': 5.0062065300172974e-17,
  'Rand Score': 0.20358404572368982},
 'R:1:C:200S:20': {'Homogeneity': 1.3876720518042915e-16,
  'Completeness': 1.0,
  'V-measure': 2.7753441036085825e-16,
  'Adjusted Rand Index': 0.0,
  'Adjusted mutual information score': 5.0062065300172974e-17,
  'Rand Score': 0.20358404572368982},
 'R:1:C:200S:40': {'Homogeneity': 1.3876720518042915e-16,
  'Completeness': 1.0,
  'V-measure': 2.7753441036085825e-16,
  'Adjusted Rand Index': 0.0,
  'Adjusted mutual information score': 5.0062065300172974e-17,
  'Rand Score': 0.20358404572368982},
 'R:2:C:200S:20': {'Homogeneity': 0.4795458497901656,
  'Completeness': 0.4545916769800998,
  'V-measure': 0.46673545553549106,
  'Adjusted Rand Index': 0.3471197403721511,
  'Adjusted mutual information score': 0.4658479882162801,
  'Rand Score': 0.7892772719069782},
 'R:2:C:200S:40': {'Homogeneity': 0.42880090833124035,
  'Completeness': 0.4459129279435399,
  'V-measure': 0.4371895369876539,
  'Adjusted Rand Index': 0.3183117345479725,
  'Adjusted mutual information score': 0.43640521810959215,
  'Rand Score': 0.7688379626638386},
 'R:3:C:200S:20': {'Homogeneity': 1.3876720518042915e-16,
  'Completeness': 1.0,
  'V-measure': 2.7753441036085825e-16,
  'Adjusted Rand Index': 0.0,
  'Adjusted mutual information score': 5.0062065300172974e-17,
  'Rand Score': 0.20358404572368982},
 'R:3:C:200S:40': {'Homogeneity': 1.3876720518042915e-16,
  'Completeness': 1.0,
  'V-measure': 2.7753441036085825e-16,
  'Adjusted Rand Index': 0.0,
  'Adjusted mutual information score': 5.0062065300172974e-17,
  'Rand Score': 0.20358404572368982}}
```


Answer 24

Module	Alternatives	Hyperparameters
Dimensionality Reduction	None	N/A
	SVD	r = 50
	UMAP	n_components = 50
	Autoencoder	num_features = 50
Clustering	K-Means	k = 5
	Agglomerative Clustering	n_clusters = 5
	HDBSCAN	min_cluster_size & min_samples

Using the grid above, the best results for different clustering algorithms with different dimensionality reduction techniques on the extracted image features are shown below:

The grid for HDBSCAN:
minClusters = [200]
minSamples = [20, 40]

*** The full results for each combination can be viewed in above cells ***

Best KMEANS scores:

'Homogeneity': 0.47828781665544173,
'Completeness': 0.49429203168034336,
'V-measure': 0.4861582460856243,
'Adjusted Rand Index': 0.39803638259161356,
'Adjusted mutual information score': 0.48544437660805734,
'Rand Score': 0.7971381105261477

Dimensionality reduction method: UMAP
No. of components: 50
Cluster: 5

Best AGGLOMERATIVE CLUSTERING scores:

'Homogeneity': 0.46289484728283964, 'Completeness': 0.48520405989530135,
'V-measure': 0.47378698046331336,
'Adjusted Rand Index': 0.375806793954751,
'Adjusted mutual information score': 0.473050766884461,
'Rand Score': 0.7861848627910552},

Dimensionality reduction method: UMAP
No. of components: 50
Cluster: 5

Best HDBSCAN scores:

'Homogeneity': 0.4795458497901656,
'Completeness': 0.4545916769800998,
'V-measure': 0.46673545553549106,
'Adjusted Rand Index': 0.3471197403721511,
'Adjusted mutual information score': 0.4658479882162801,
'Rand Score': 0.7892772719069782

Dimensionality reduction method: UMAP
No. of components: 50
min_samples: 20

min_cluster_size: 200

Out of the three best combinations,

KMEANS with UAMP seems to better, then AGGLOMERATIVE CLUSTERING with UMAP and then HDBSCAN with UMAP.

All comparisons are done using Adjusted Rand index and Rand Scores

Question 25

In [48]:

```
# Using full VGG features
X_train, X_test, y_train, y_test = train_test_split(f_all, y_all, test_size=0.2)
mlpClf = MLP(f_all.shape[1])
_, lossHistory = mlpClf.train(X_train, y_train)
results = mlpClf.eval(X_test, y_test)
```

```
100%|██████████| 100/100 [00:18<00:00,  5.45it/s]

torch.Size([734, 5])
(734,)
Accuracy: 0.885558583106267
Precision: 0.8851169609829797
Recall: 0.8804573088633741
F1 Score: 0.8824354514357271
```

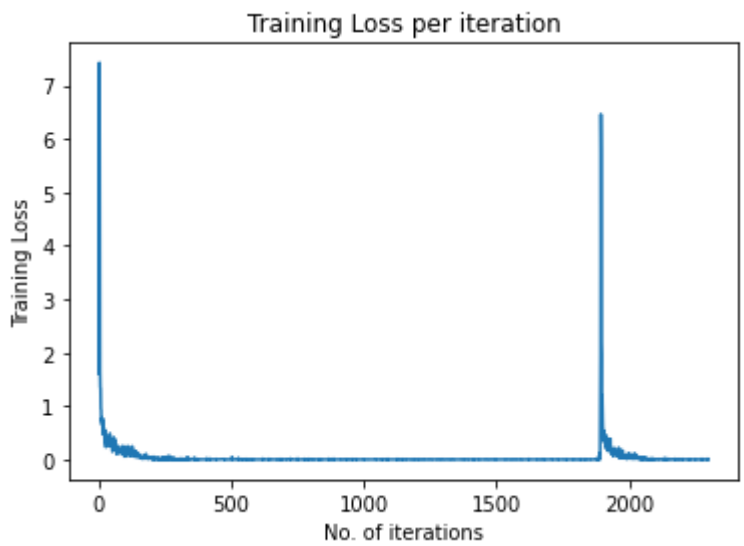
In [50]:

```
print(len(lossHistory))
plt.title("Training Loss per iteration")
plt.xlabel("No. of iterations")
plt.ylabel("Training Loss")
plt.plot(np.asarray(lossHistory))
```

```
2300
```

Out[50]:

```
[<matplotlib.lines.Line2D at 0x7f72f75d6490>]
```



In [43]:

```
# Working with dimensinality reduced features.
# All of the lcustering algorithms perform better with UMAP so choosing it.
redFeatures = umap.UMAP(n_components=50, random_state=42, metric='cosine').fit_trans
```

In [51]:

```
X_train, X_test, y_train, y_test = train_test_split(redFeatures, y_all, test_size=0.
mlpClf2 = MLP(redFeatures.shape[1])
_, lossHistory = mlpClf2.train(X_train, y_train)
```

```
100%|██████████| 100/100 [00:15<00:00,  6.52it/s]
```

In [52]:

```
results2 = mlpClf2.eval(X_test, y_test)
```

```
torch.Size([734, 5])
(734,)
Accuracy: 0.8174386920980926
Precision: 0.836476174133052
Recall: 0.819305812573243
F1 Score: 0.8155649804246113
```

In [54]:

```
# Using clustering to see the labels.
# Using KMeans as it gave beter results in terms of rand score and adjusted rand
#  index compared to other clusterers.

classify = KMeans(n_clusters=5, random_state=42, max_iter=5000, n_init=50)
classify.fit(X_train)

preds = classify.predict(X_test)
```

In [56]:

```
scores = getScores(y_test, preds)
scores
```

Out[56]:

```
{'Homogeneity': 0.5307977061484846,
 'Completeness': 0.539075917630815,
 'V-measure': 0.5349047853101441,
 'Adjusted Rand Index': 0.46554180782117577,
 'Adjusted mutual information score': 0.5316506767024964,
 'Rand Score': 0.8224459222857058}
```

Answer 25

*** Test accuracy of the MLP classifier on the original VGG features: *** Accuracy: 0.885558583106267
Precision: 0.8851169609829797
Recall: 0.8804573088633741
F1 Score: 0.8824354514357271

*** Test accuracy of the MLP classifier on the reduced VGG features: ***

UMAP chosen since its the best performing method till the end of the project.

Dimensionality reduction method: UMAP
Metric: cosine
components: 50

Accuracy: 0.8174386920980926
Precision: 0.836476174133052
Recall: 0.819305812573243
F1 Score: 0.8155649804246113

The performance of the classifier is reduced when dimensionality reduction of the features was done. There is a drop of ~7-8 % which is quite significant

Correlation with clustering results

Using the best combination i.e KMeans with UMAP, the scores of clustering with reduced dimensions are:

'Homogeneity': 0.5307977061484846,
'Completeness': 0.539075917630815,
'V-measure': 0.5349047853101441,
'Adjusted Rand Index': 0.46554180782117577,
'Adjusted mutual information score': 0.5316506767024964,
'Rand Score': 0.8224459222857058

Comparing the scores I found that K-means clustering is giving 82.24 % similarity compared to 81.74 % accuracy of the MLP classifier on the test set using dimensionality reduced features