EC ENGR 219

2023 Winer

Project 2:

Data Representations and Clustering

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QUESTION 1

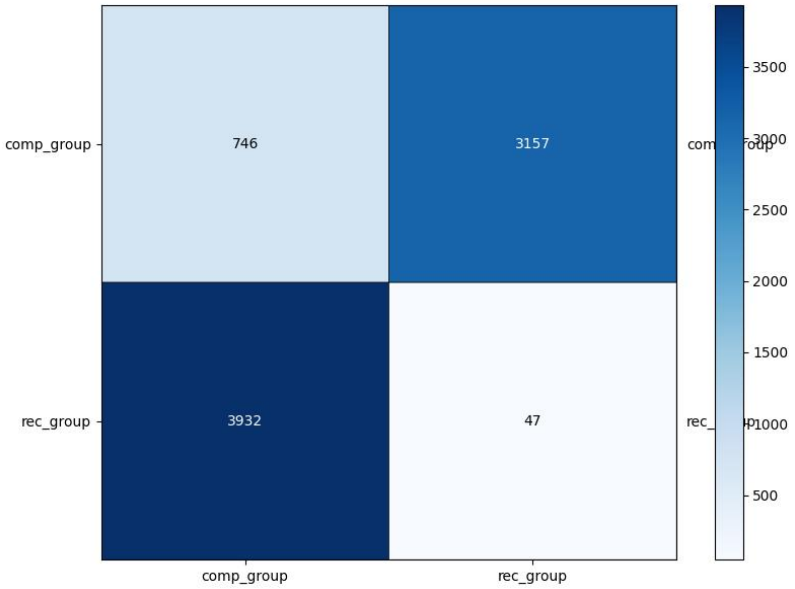
Report the dimensions of the TF-IDF matrix you obtain.

n_samples: 7882, n_features: 23522
data tf-idf matrix shape: (7882, 23522)
Therefore, the **dimensions** of the TF-IDF matrix we obtained is **(7882, 23522)**.

QUESTION 2

Report the contingency table of your clustering result. You may use the provided plotmat.py to visualize the matrix. Does the contingency matrix have to be square-shaped?

The contingency table visualized matrix of our clustering result has shown below,



Each value of the contingency matrix, M is given by Mij such that i is the true class and j is the predicted class/cluster. As can be observed, 3157 documents of Comp class were assigned to a single cluster which we can assume is the comp cluster. Similarly, 3932 of the rec documents are clustered together. As can be seen the comp cluster has 47 of the rec documents and rec cluster has 746 of the comp class documents.

Observing the contingency matrix, we can conclude that the clustering algorithm has worked accurately in categorizing majority of the sample points to their corresponding clusters

From the result, we can conclude that the dimension of the contingency matrix **has to be square-shaped**.This is because we have 2 classes and the k-means algorithm has 2 clusters. Contingency matrix is a broader extension of Confusion matrix's idea, where we have rows showing the number of samples in ground truth clusters while columns depict the number of samples segregated to those clusters by the clustering algorithm.

QUESTION 3

Report the 5 clustering measures explained in the introduction for Kmeans clustering.

Homogeneity: 0.579 ± 0.000
Completeness: 0.594 ± 0.000
V-measure: 0.587 ± 0.000
Adjusted Rand-Index: 0.638 ± 0.000
Adjusted_mutual_info_score: 0.587 ± 0.000

Homogeneity is a measure of how "pure" the clusters are. If each cluster contains only data points from a single class, the homogeneity is satisfied. Homogeneity metric of 57.9% indicates that 42.1% of the samples on an average are not from the assigned corresponding ground truth label.

Completeness indicates how much of the data points of a class are assigned to the same cluster. Completeness of 59.4 % shows that 59.4 % of the samples for a given class label are part of the same cluster.

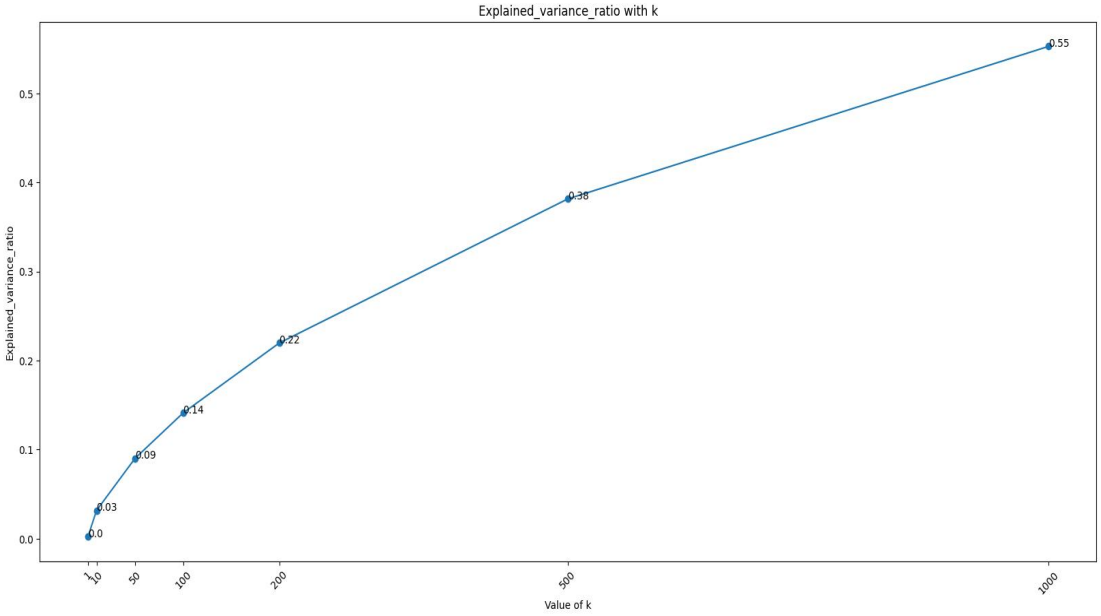
V-measure is the harmonic average of homogeneity score and completeness score. V-measure metric value of 58.7% stands at the harmonic mean of both Homogeneity and completeness, being a symmetric metric which is independent of the absolute values of the labels.

Adjusted Rand Index is similar to accuracy, which computes similarity between the clustering labels and ground truth labels. This method counts all pairs of points that both fall either in the same cluster and the same class or in different clusters and different classes.

Adjusted mutual information score measures the mutual information between the cluster label distribution and the ground truth label distributions.

● QUESTION 4

Report the plot of the percentage of variance that the top r principle components retain v.s. r, for r = 1 to 1000.

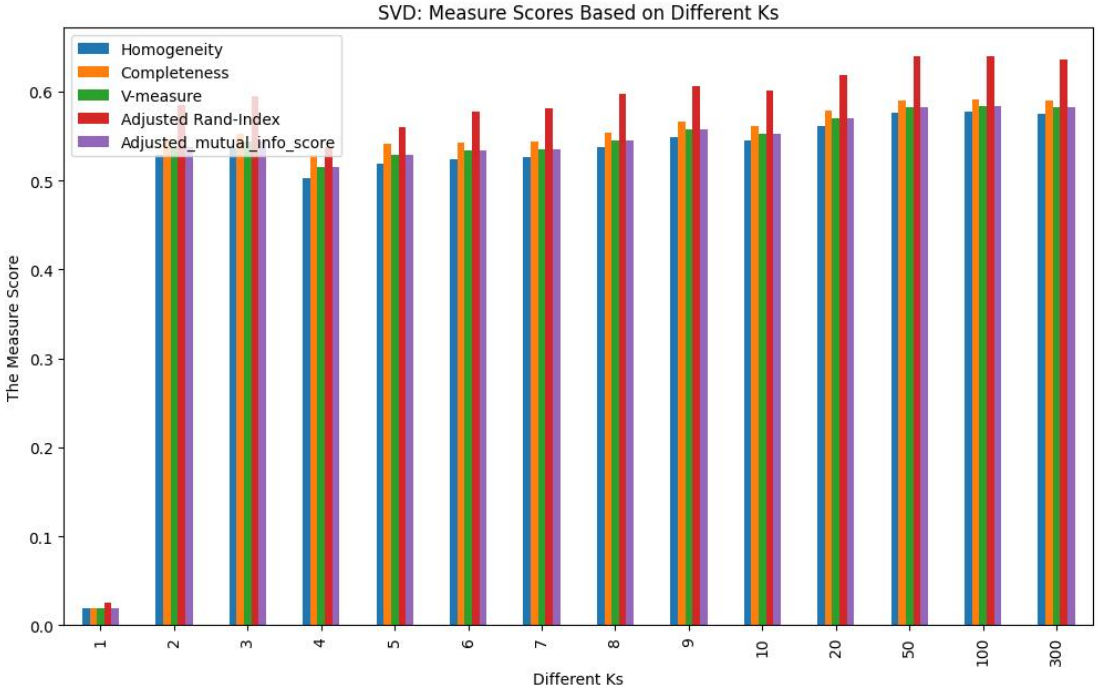


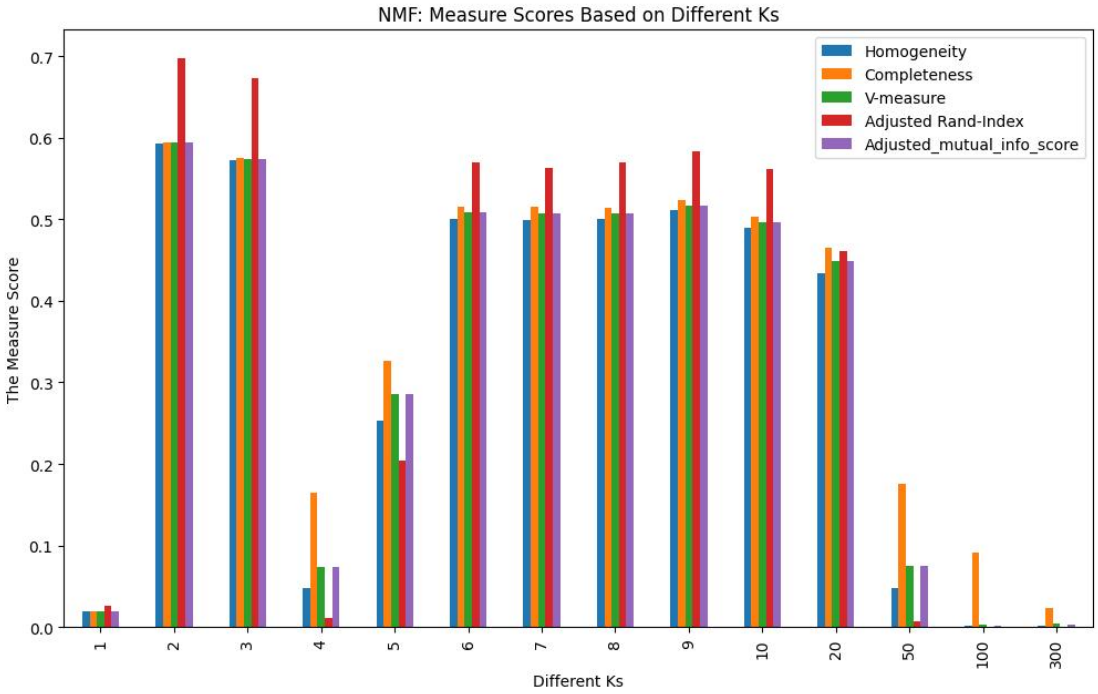
For a given r, Truncated SVD/LSI selects the first r principal components in descending order variance preserved by the components. 55% of the variance covered by about 1000 features. The larger the r, the slower the curve.

● QUESTION 5

Let r be the dimension that we want to reduce the data to (i.e. n components). Try r = 1 − 10, 20, 50, 100, 300, and plot the 5 measure scores v.s. r for both SVD and NMF. Report a good choice of r for SVD and NMF respectively. Note: In the choice of r, there is a trade-off between the information preservation, and better performance of k-means in lower dimensions.

We tried r = 1 through 10, 20, 50, 100, 300 and plotted five evaluation metrics scores for SVD and NMF respectively as below:





best r for svd is 100, the average score is: 0.595

best r for nmf is 2, the average score is: 0.614

According to the results, There is a trade-off between the information preservation, and better performance of k-means in lower dimensions observed in case of NMF very clearly and r = 2 is the best choice considering the two factors. But in the case of SVD we observe that the information preservation poor performance of k-means in higher dimensions even at r = 100.we find **the best r=100 for both SVD and NMF is 2**.

QUESTION 6

How do you explain the non-monotonic behavior of the measures as r increases?

When r increases, the original data information can be preserved more in the higher dimension. However, the performance of K means will be better in a low dimension. So the **trade-off** between **information preservation** and **performance of K means** along with increasing dimensions leads to the non-monotonic behavior of the measures.

QUESTION 7

Are these measures on average better than those computed in Question 3?

Yes, these measures on average are better than the results in Question 3. We can see from the figures in Question 5 that the average scores for all of five evaluated measures are higher than the scores in Question 3. Therefore, even though there is a tradeoff between information preservation and performance of K means, both NMF and SVD still perform better on average.

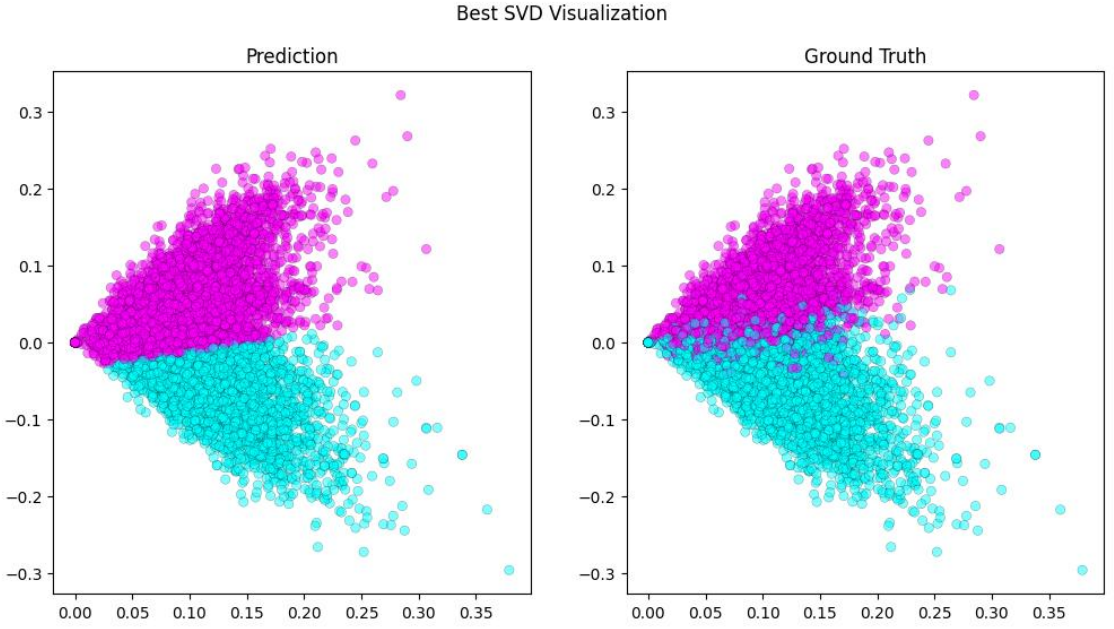
● QUESTION 8

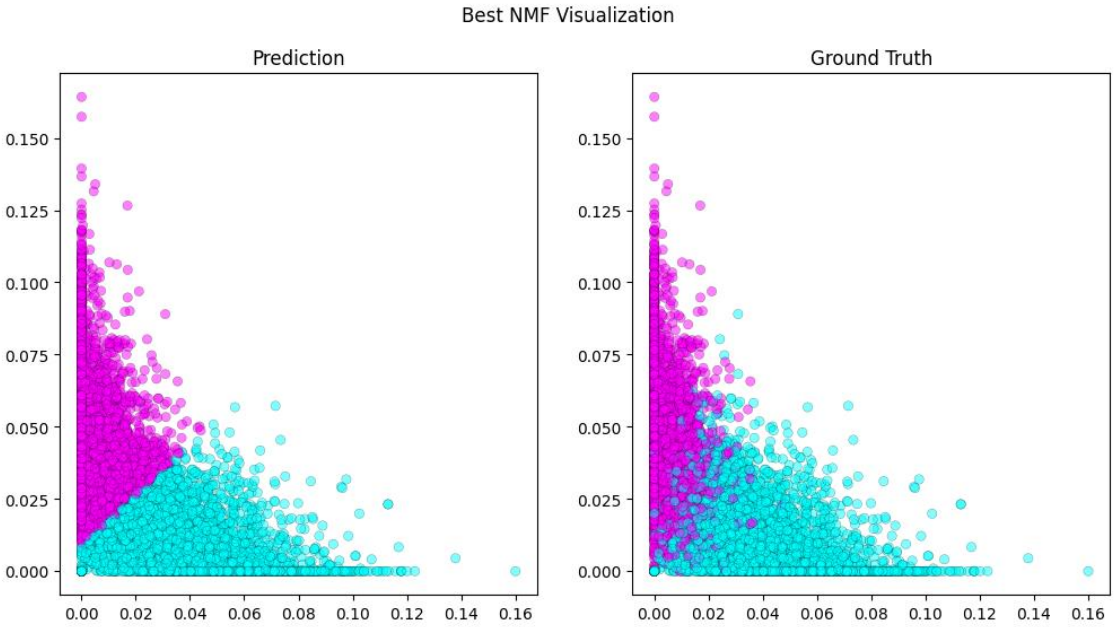
Visualize the clustering results for:

- **SVD with your optimal choice of r for K-Means clustering;**
- **NMF with your choice of r for K-Means clustering.**

To recap, you can accomplish this by first creating the dense representations and then once again projecting these representations into a 2-D plane for visualization.

We plotted SVD and NMF visualized clustering results as shown below respectively,





● QUESTION 9

What do you observe in the visualization? How are the data points of the two classes distributed? Is distribution of the data ideal for K-Means clustering?

Based on the results from question 8, we can observe that the K means clustering with ground truth labels is performing **well** on both SVD and NMF. There is a distinct separation line between two clusters, which means that the data points are distributed well using this method. However, there still exists some ambiguous boundary in the ground truth labels plot. Two different colors of the data points are mixed together in the boundary line, and this will result in a poor distinction in that area. The data points of the two classes are distributed clearly separate both on SVD and NMF.

However, since the boundary between two clusters are sort of ambiguous, K means clustering will become tricky and difficult when the test data point appears near or next to the boundary line. In that case, the accuracy of K means clustering will be decreased and highly depends on the value of K for predicting. Besides, the results will also become unaccountable. Therefore, distribution of the data **is not ideal** for K means clustering.

● QUESTION 10

Load documents with the same configuration as in Question 1, but for ALL 20 categories. Construct the TF-IDF matrix, reduce its dimensionality using BOTH NMF and SVD (specify settings you choose and why), and perform K-Means clustering with k=20 .
Visualize the contingency matrix and report the five clustering metrics (DO BOTH NMF AND SVD).
There is a mismatch between cluster labels and class labels. For example, the cluster #3 may correspond to the class #8. As a result, the high-value entries of the 20 × 20 contingency matrix can be scattered around, making it messy to inspect, even if the clustering result is not bad.
One can use scipy.optimize.linear_sum_assignment to identify the best-matching cluster-class pairs, and permute the columns of the contingency matrix accordingly. See below for an example:

```
import numpy as np
from plotmat import plot_mat
from scipy.optimize import linear_sum_assignment
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(labels, clustering_labels)
rows, cols = linear_sum_assignment(cm, maximize=True)
plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols,
yticklabels=rows, size=(15,15))
```

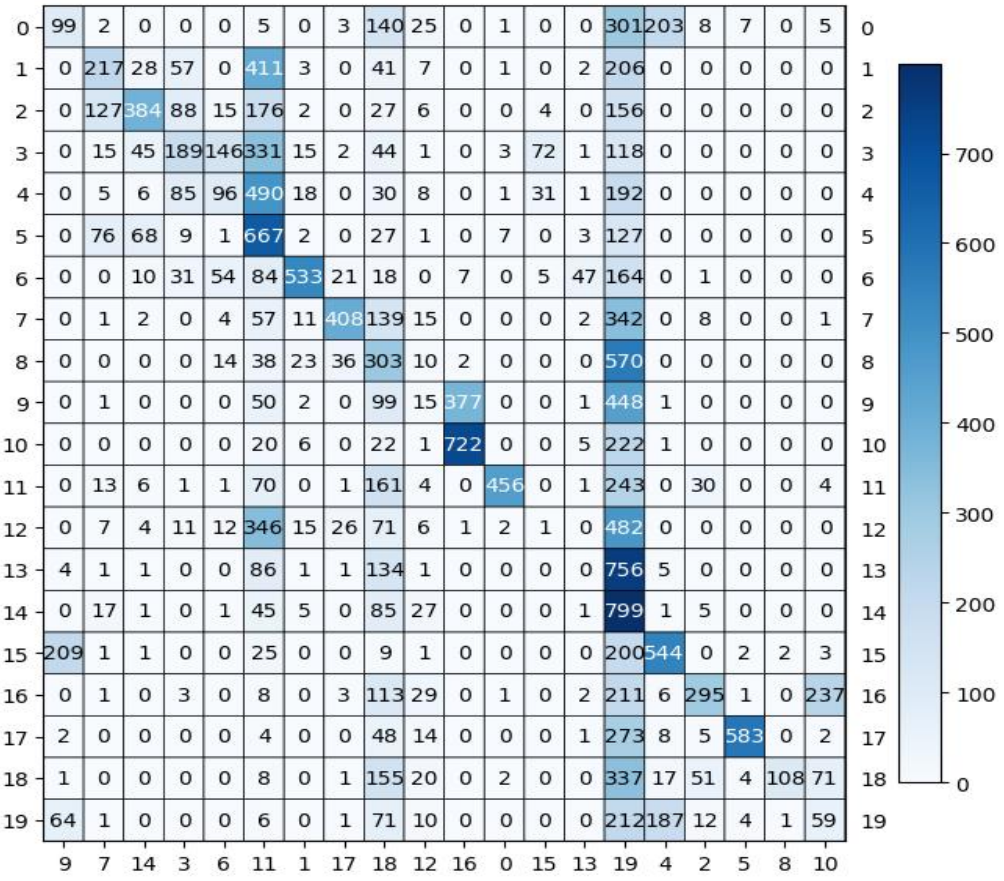
Here we constructed the TF-IDF matrix and obtained the TF-IDF matrix dimension is **(18846, 45365)**, where (n_samples = 18846) and (n_features = 45365).

After that, we firstly used **SVD** to reduce the dimensions of matrix and perform K means with k = 20. The **settings** we did here as follows:

```
kmeans20_svd = KMeans(max_iter=1000, n_clusters=20, n_init=30, random_state=0)
svd_t = TruncatedSVD(n_components=best_svd_r, random_state=42)
data_svd = svd_t.fit_transform(data_tf_idf3)
kmeans20_svd.fit(data_svd)
cm = confusion_matrix(dataset.target, kmeans20_svd.labels_)
rows, cols = linear_sum_assignment(cm, maximize=True)
plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols,
 yticklabels=rows)
```

The reason we chose this setting: Referred to the question, we set k = 20 using K means. We set **"best_svd_r"** from Question 5 as our n components and set random_state = 42. Based on our construction, we used a visualized plot to get our contingency matrix results.

Here we showed the visualized results as below:



And the five clustering evaluation metrics for **SVD** we got the following results:

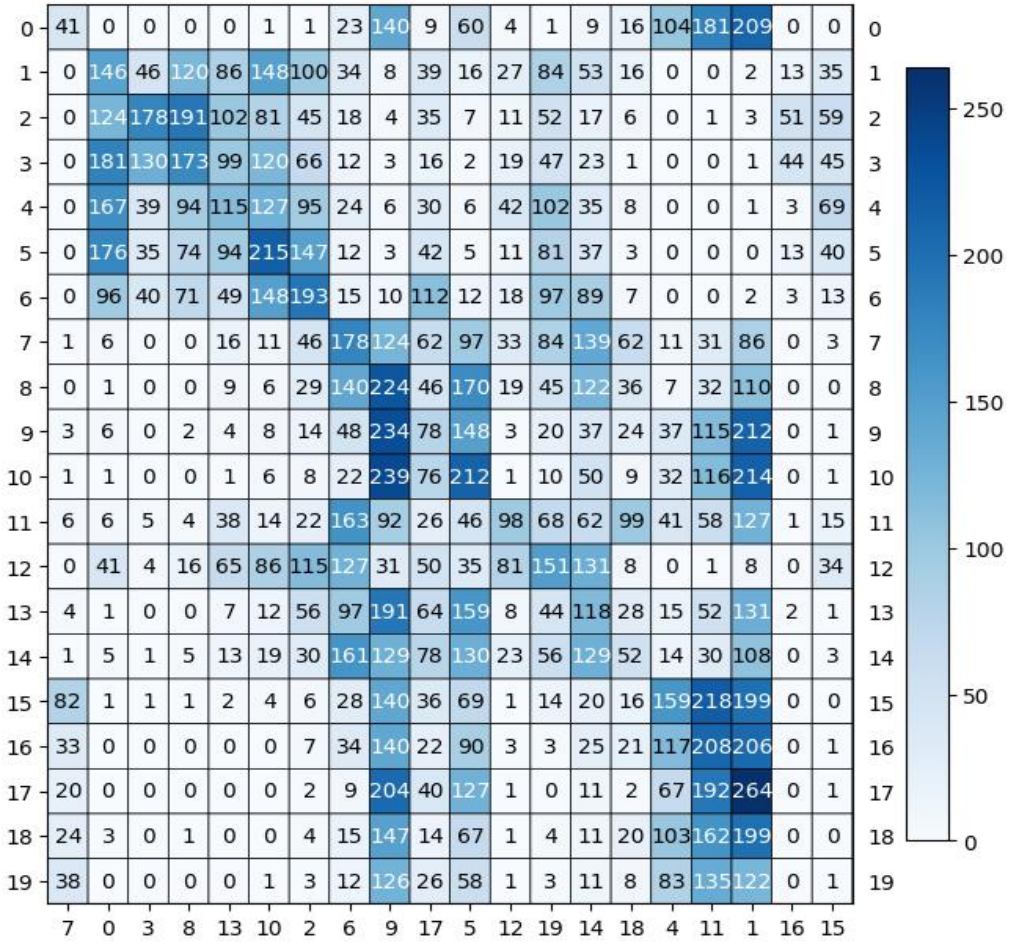
Homogeneity: 0.331 ± 0.000
Completeness: 0.227 ± 0.000
V-measure: 0.270 ± 0.000
Adjusted Rand-Index: 0.098 ± 0.000
Adjusted_mutual_info_score: 0.269 ± 0.000

Then we used **NMF** to reduce the dimension of the matrix obtained from TF-IDF still with k = 20 using K means. The **settings** code will be shown as follows:

```
1.   kmeans20_nmf = KMeans(init='k-
   means++', max_iter=1000, n_clusters=20, n_init=30, random_s
   tate=0)
2.   nmf_t = NMF(n_components=best_nmf_r, random_state=42)
3.   data_nmf = nmf_t.fit_transform(data_tf_idf3)
4.   kmeans20_nmf.fit(data_nmf)
5.
6.   cm = confusion_matrix(dataset.target, kmeans20_nmf.labels
   _)
7.   rows, cols = linear_sum_assignment(cm, maximize=True)
8.   plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols,
    yticklabels=rows)
```

The reason we chose this setting: Here we used **"best_nmf_r"** accordingly resulting from question 5 to be our n components in NMF and set random_state = 42.

As for K means, we set k = 20 meeting the question's requirements. Then we decided to visualize our contingency matrix shown as follows:



And the five clustering evaluation metrics for **NMF** we got the following results:

Homogeneity: 0.194 ± 0.000
Completeness: 0.110 ± 0.000
V-measure: 0.141 ± 0.000
Adjusted Rand-Index: 0.054 ± 0.000
Adjusted_mutual_info_score: 0.140 ± 0.000

● QUESTION 11

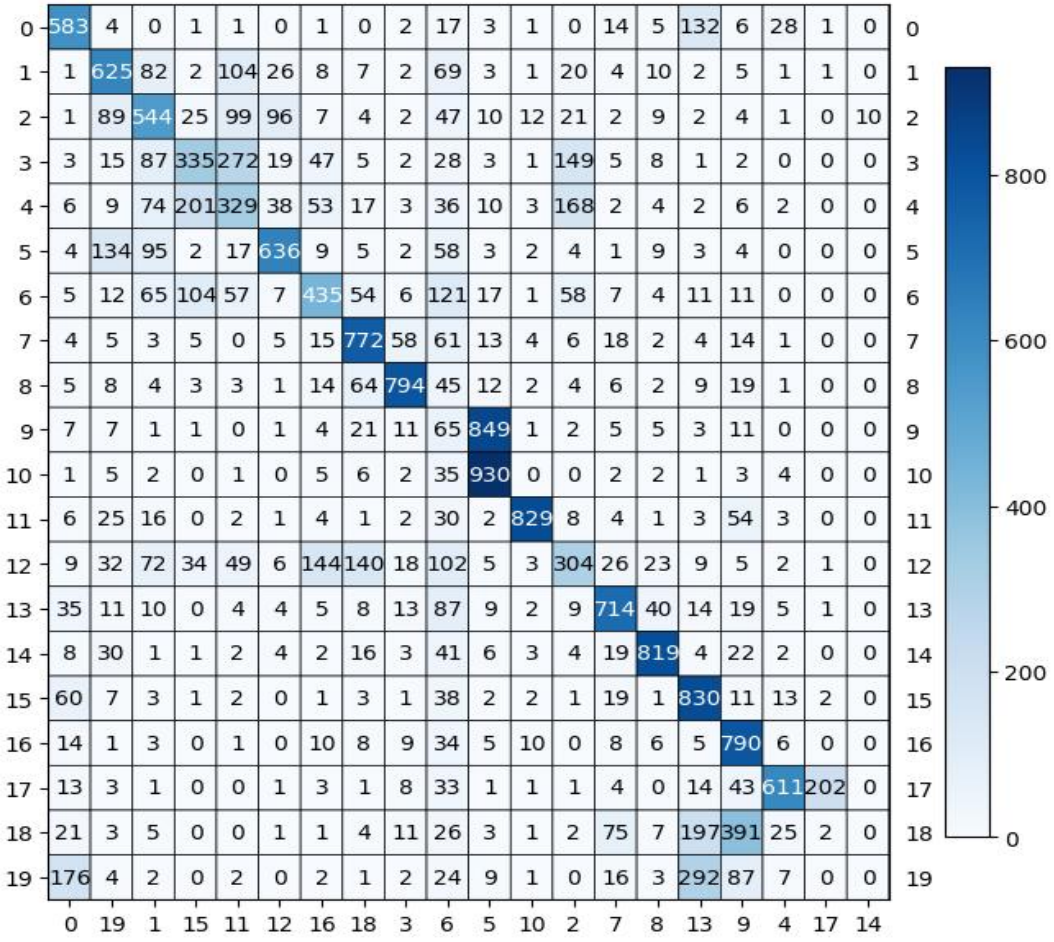
Reduce the dimension of your dataset with UMAP. Consider the following settings: n components = [5, 20, 200], metric = ”cosine” vs. ”euclidean”. If ”cosine” metric fails, please look at the FAQ at the end of this spec.
Report the permuted contingency matrix and the five clustering evaluation metrics for the different combinations (6 combinations).

First Combination: n components = 5 with metric = “cosine”

The clustering evaluation metrics are shown below,

Homogeneity: 0.533 ± 0.000
Completeness: 0.297 ± 0.000
V-measure: 0.381 ± 0.000
Adjusted Rand-Index: 0.216 ± 0.000
Adjusted_mutual_info_score: 0.381 ± 0.000

The permuted contingency matrix is plotted as below,

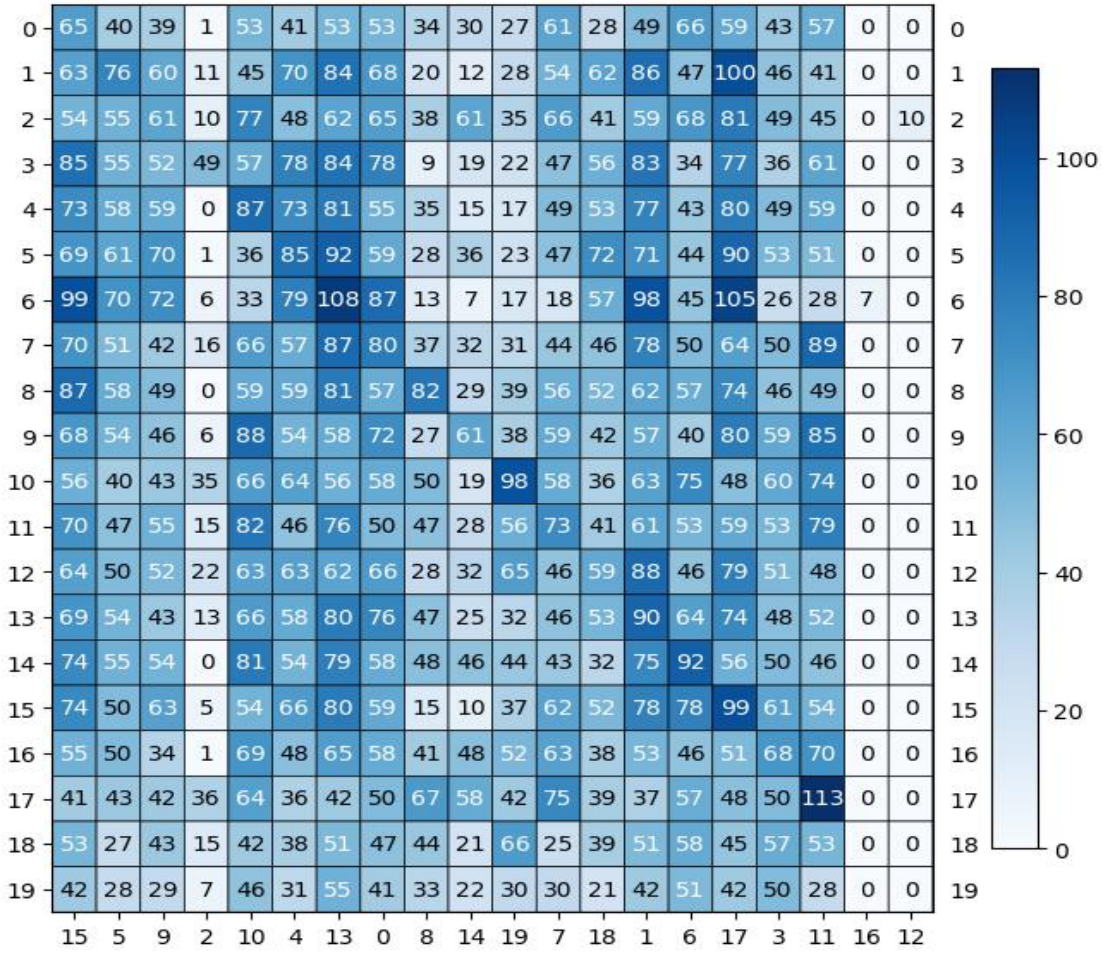


Second Combination: n components = 5 with metric = “euclidean”

The clustering evaluation metrics are shown below,

Homogeneity: 0.009 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.007 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.006 ± 0.000

The permuted contingency matrix is plotted as below,

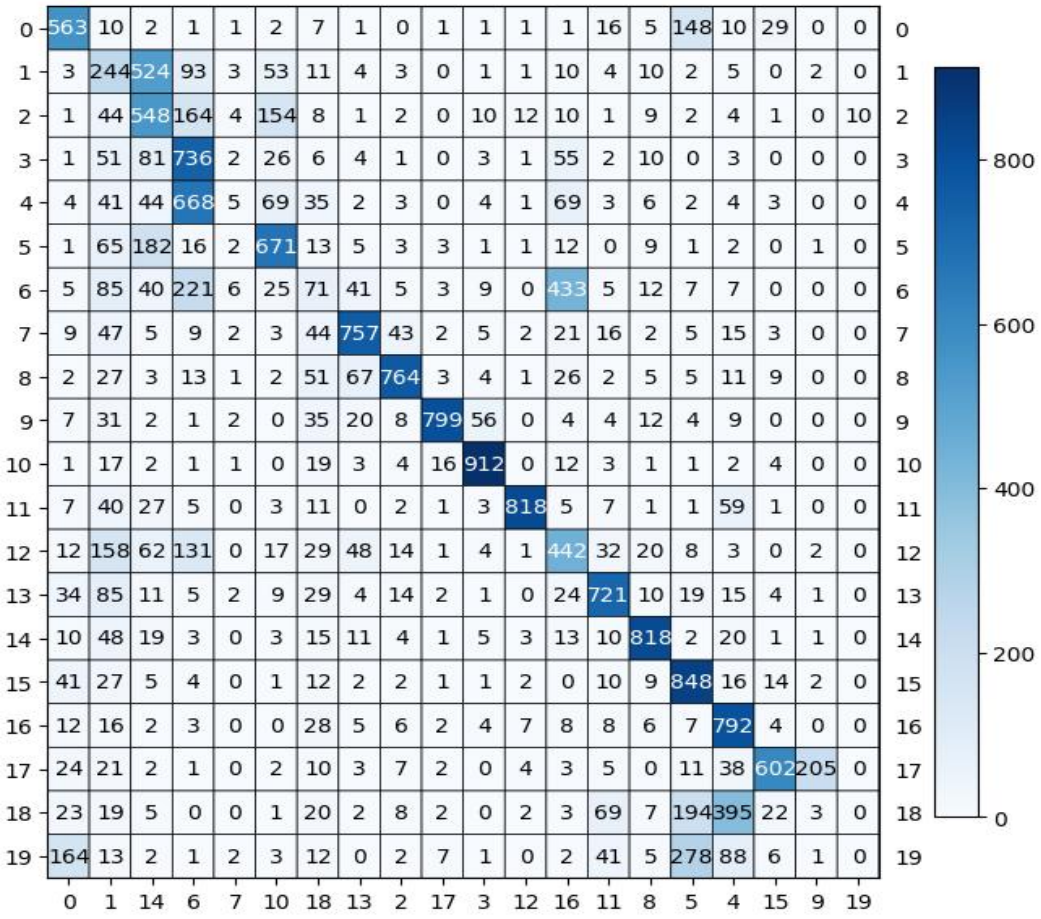


Third Combination: n components = 20 with metric = “cosine”

The clustering evaluation metrics are shown below,

Homogeneity: 0.534 ± 0.000
Completeness: 0.304 ± 0.000
V-measure: 0.387 ± 0.000
Adjusted Rand-Index: 0.205 ± 0.000
Adjusted_mutual_info_score: 0.387 ± 0.000

The permuted contingency matrix is plotted as below,

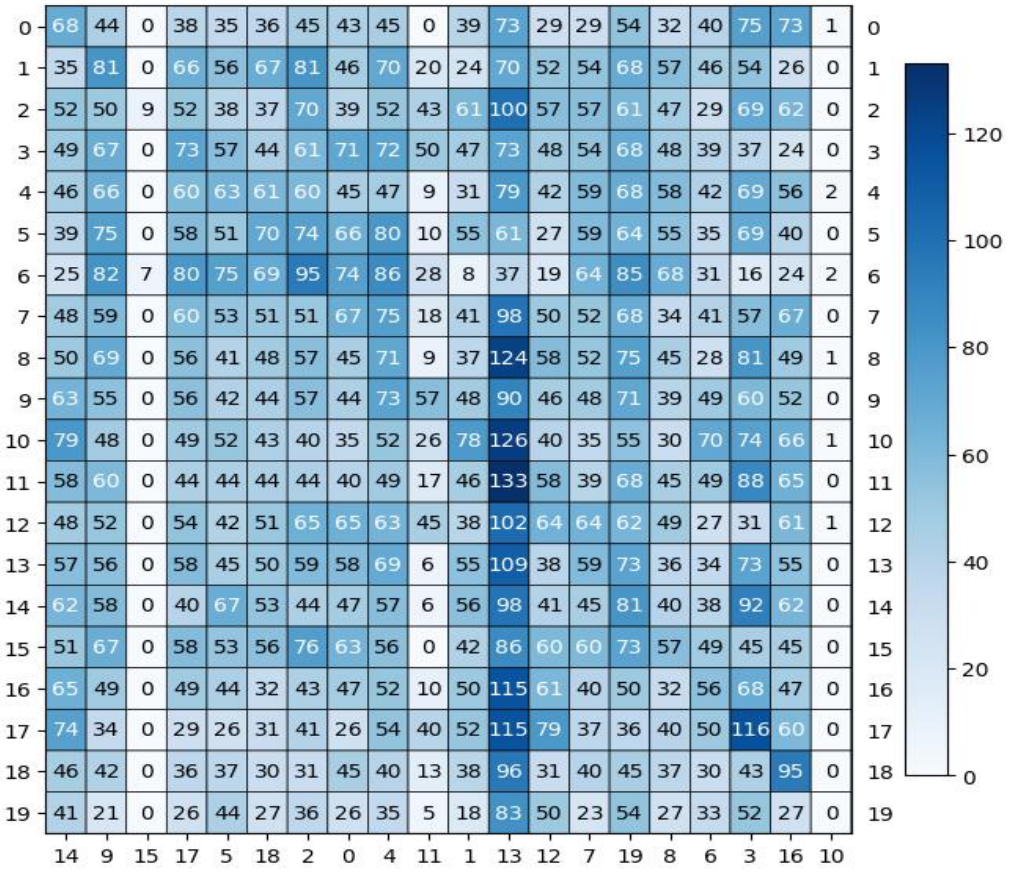


Fourth Combination: n components = 20 with metric = "euclidean"

The clustering evaluation metrics are shown below,

Homogeneity: 0.008 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.006 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.005 ± 0.000

The permuted contingency matrix is plotted as below,

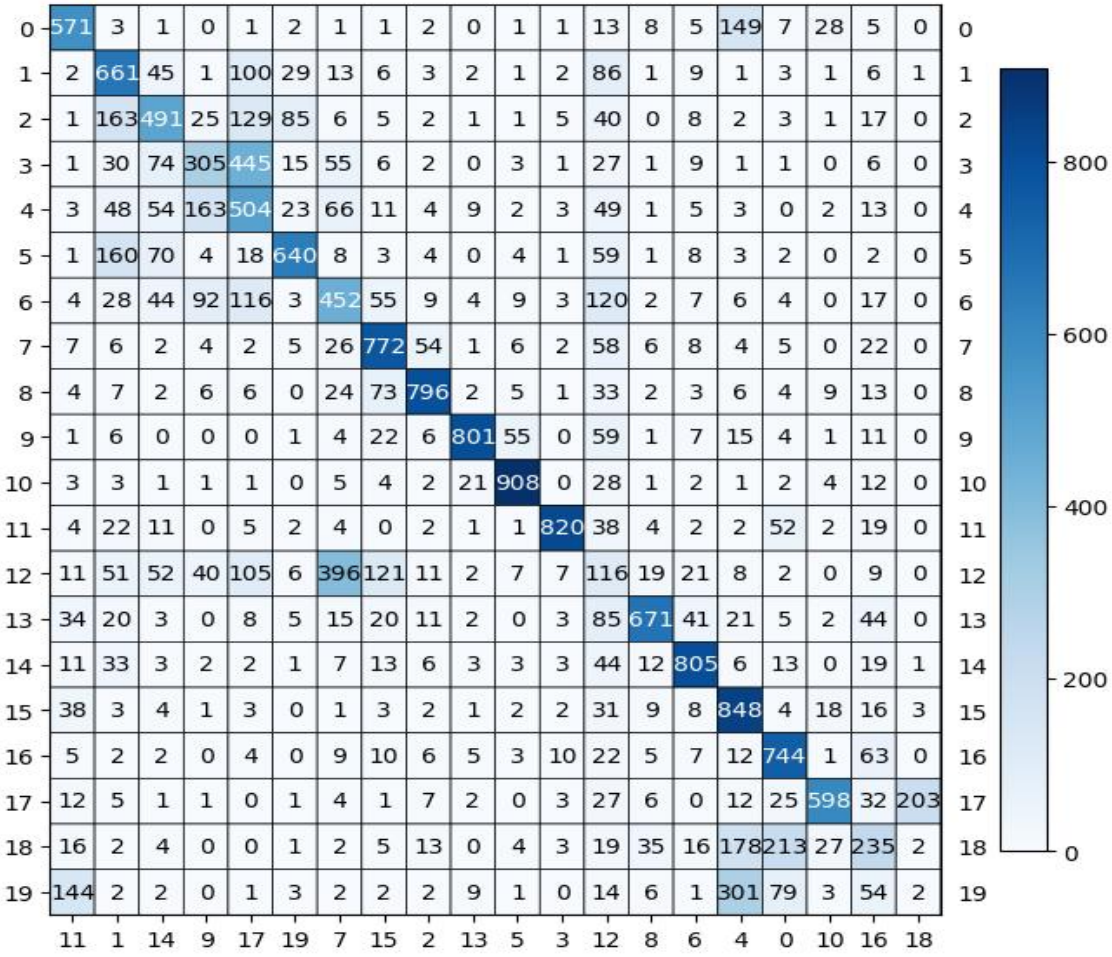


Fifth Combination: n components = 200 with metric = “cosine”

The clustering evaluation metrics are shown below,

Homogeneity: 0.534 ± 0.000
Completeness: 0.292 ± 0.000
V-measure: 0.377 ± 0.000
Adjusted Rand-Index: 0.184 ± 0.000
Adjusted_mutual_info_score: 0.377 ± 0.000

The permuted contingency matrix is plotted as below,

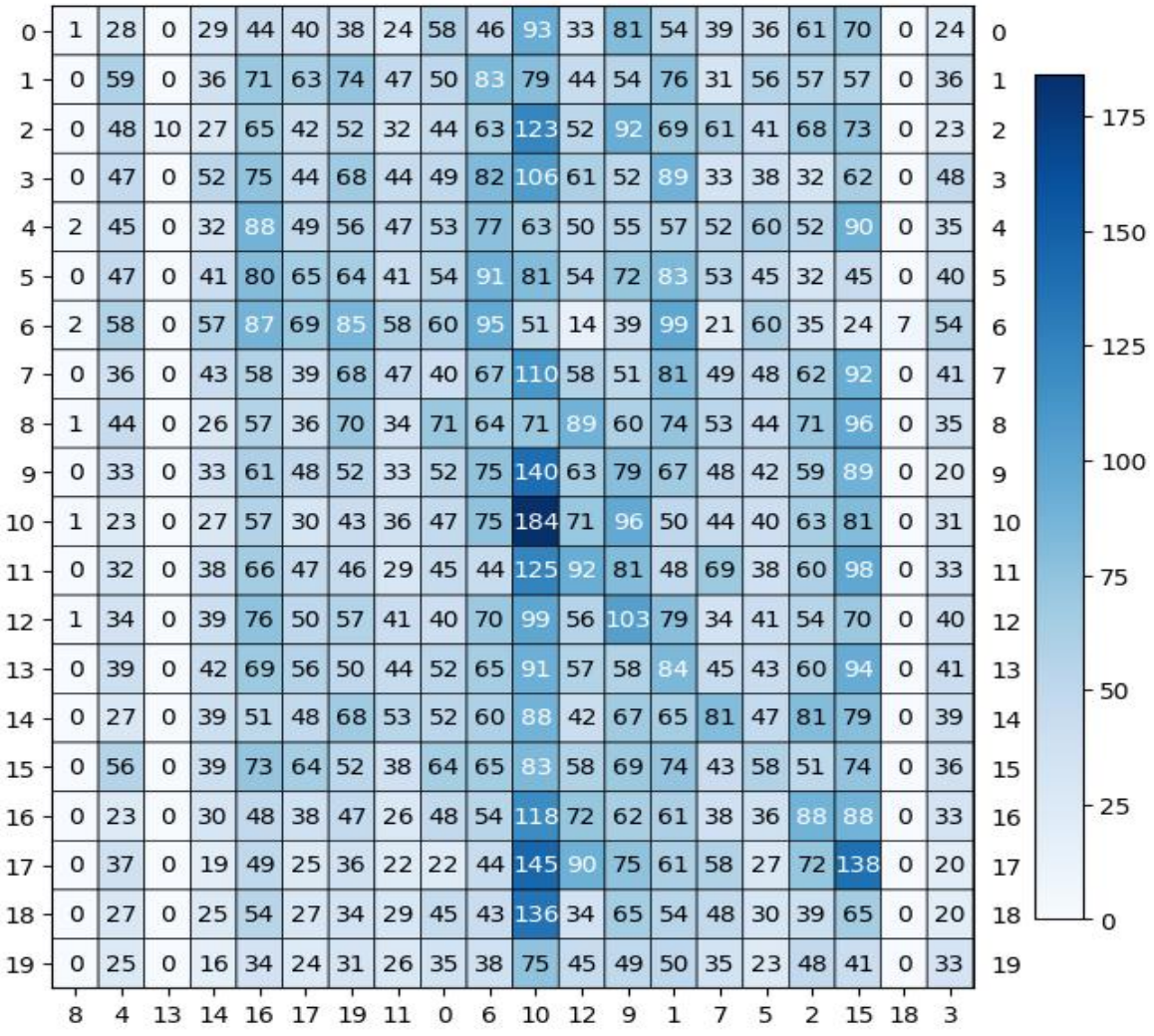


Sixth Combination: n components = 200 with metric = “euclidean”

The clustering evaluation metrics are shown below,

Homogeneity: 0.009 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.006 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.005 ± 0.000

The permuted contingency matrix is plotted as below,



best r for cosine is 20, the average score is: 0.363
best r for euclidean is 5, the average score is: 0.006

● QUESTION 12

Analyze the contingency matrices. Which setting works best and why? What about for each metric choice?

By analyzing the contingency matrices, we got the following scores for best r in two metrics respectively,

Best r for "**cosine**" is **20**, the average score is: 0.363.

Best r for "**euclidean**" is **5**, the average score is: 0.006.

Above all, comparing two average scores for two metrics, it can be concluded that the cosine **metric works best** because we can clearly see a diagonal line in the contingency matrix and the average score for cosine is obviously higher.

● QUESTION 13

So far, we have attempted K-Means clustering with 4 different representation learning techniques:sparse TF-IDF representation, PCA-reduced, NMF-reduced, UMAP-reduced. Compare and contrast the clustering results across the 4 choices, and suggest an approach that is best for the K-Means clustering task on the 20-class text data. Choose any choice of clustering metrics for your comparison.

Sparse TF-IDF representation:

Homogeneity: 0.357 ± 0.000
Completeness: 0.222 ± 0.000
V-measure: 0.274 ± 0.000
Adjusted Rand-Index: 0.097 ± 0.000
Adjusted_mutual_info_score: 0.273 ± 0.000

SVD/PCA-reduced(r = 100):

Homogeneity: 0.331 ± 0.000
Completeness: 0.227 ± 0.000
V-measure: 0.270 ± 0.000
Adjusted Rand-Index: 0.098 ± 0.000
Adjusted_mutual_info_score: 0.269 ± 0.000

NMF-reduced(r = 2):

Homogeneity: 0.194 ± 0.000
Completeness: 0.110 ± 0.000
V-measure: 0.141 ± 0.000
Adjusted Rand-Index: 0.054 ± 0.000
Adjusted_mutual_info_score: 0.140 ± 0.000

UMAP-reduced(n_components = 20, metric = “cosine”):

Homogeneity: 0.534 ± 0.000
Completeness: 0.304 ± 0.000
V-measure: 0.387 ± 0.000
Adjusted Rand-Index: 0.205 ± 0.000
Adjusted_mutual_info_score: 0.387 ± 0.000

According to the comparison above, we can conclude that the best approach for K means is **UMAP-reduced(n_components = 20, metric = “cosine”).**

● QUESTION 14

Use UMAP to reduce the dimensionality properly, and perform Agglom-erative clustering with n_clusters=20. Compare the performance of "ward" and "single" linkage criteria.
Report the five clustering evaluation metrics for each case.

umap use cosine n_componets = 20 and ward agglomerativeClustering

Homogeneity: 0.538 ± 0.000
Completeness: 0.299 ± 0.000
V-measure: 0.384 ± 0.000
Adjusted Rand-Index: 0.197 ± 0.000
Adjusted_mutual_info_score: 0.383 ± 0.000

umap use euclidean n_componets = 5 and ward agglomerativeClustering

Homogeneity: 0.010 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.007 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.006 ± 0.000

umap use cosine n_componets = 20 and single agglomerativeClustering

Homogeneity: 0.021 ± 0.000
Completeness: 0.182 ± 0.000
V-measure: 0.037 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.035 ± 0.000

umap use euclidean n_componets = 5 and single agglomerativeClustering

Homogeneity: 0.008 ± 0.000
Completeness: 0.165 ± 0.000
V-measure: 0.016 ± 0.000
Adjusted Rand-Index: -0.000 ± 0.000
Adjusted_mutual_info_score: 0.013 ± 0.000

Here, we can notice that **ward performs better** than single.

● QUESTION 15

Apply HDBSCAN on UMAP-transformed 20-category data.
Use min_cluster_size=100 .
Vary the min cluster size among 20, 100, 200 and report your findings in terms of the five clustering evaluation metrics - you will plot the best contingency matrix in the next question. Feel free to try modifying other parameters in HDBSCAN to get better performance.

We used the following code to apply HDBSCAN on UMAP-transformed 20-category data with min_cluster_size = 100.

```
hdbscan_model = hdbscan.HDBSCAN(min_cluster_size= 100)
hdb_ = hdbscan_model.fit(best_cos_data)
evaluate(hdb_, data_tf_idf3, Y_binary, name="KMeans\non tf-
   idf vectors")
```

And this is five clustering evaluation metrics we found,

Homogeneity: 0.419 ± 0.000
Completeness: 0.332 ± 0.000
V-measure: 0.370 ± 0.000
Adjusted Rand-Index: 0.210 ± 0.000
Adjusted_mutual_info_score: 0.370 ± 0.000

Next, we varied the min cluster size through 20, 100 to 200 and found the following five evaluation metrics results,

min_clusters: 20

Homogeneity: 0.000 ± 0.000
Completeness: 0.038 ± 0.000
V-measure: 0.001 ± 0.000
Adjusted Rand-Index: -0.000 ± 0.000
Adjusted_mutual_info_score: 0.000 ± 0.000

min_clusters: 100

Homogeneity: 0.419 ± 0.000
Completeness: 0.332 ± 0.000
V-measure: 0.370 ± 0.000
Adjusted Rand-Index: 0.210 ± 0.000
Adjusted_mutual_info_score: 0.370 ± 0.000

min_clusters: 200

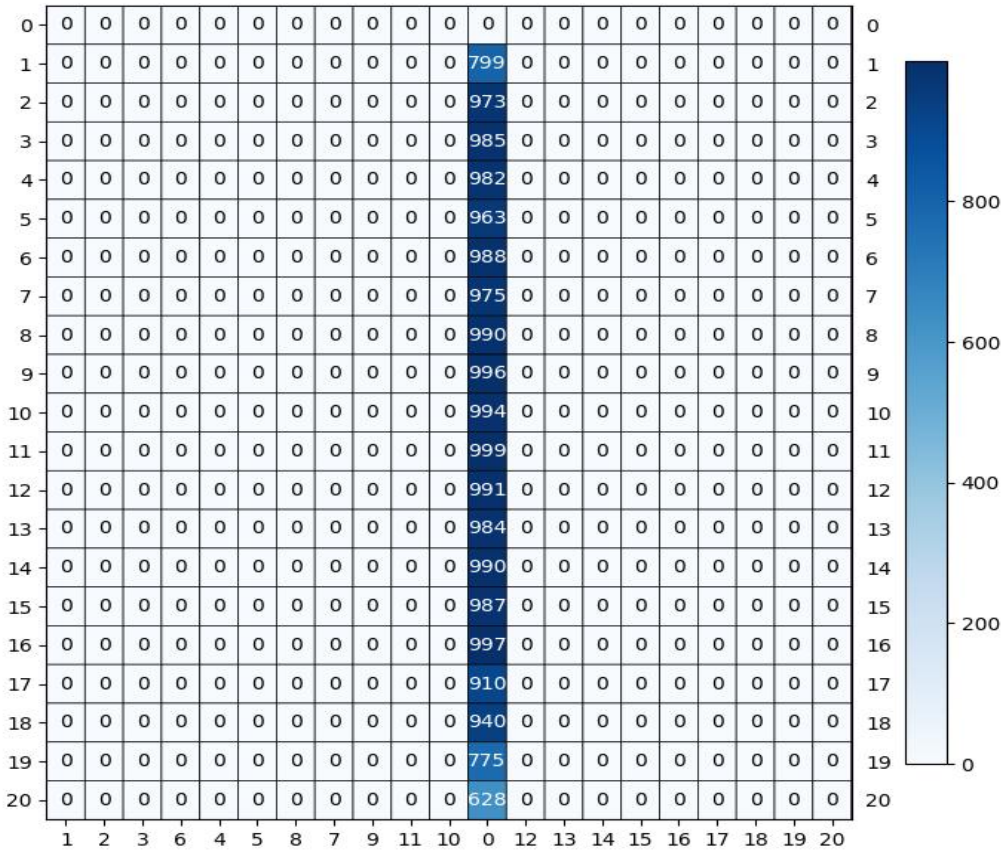
Homogeneity: 0.413 ± 0.000
Completeness: 0.327 ± 0.000
V-measure: 0.365 ± 0.000
Adjusted Rand-Index: 0.210 ± 0.000
Adjusted_mutual_info_score: 0.364 ± 0.000

Here we got the best performance is:
min_clusters = 100, the average score = 0.340.

● QUESTION 16

Contingency matrix
Plot the contingency matrix for the best clustering model from Question 15.
How many clusters are given by the model? What does "-1" mean for the clustering labels?
Interpret the contingency matrix considering the answer to these questions.

Here we used **100 min cluster size** as the best performance concluded from question 15. "-1" here means **noisy samples** for the clustering labels. By using 100 clusters, we plotted the contingency matrix as below,



From the plot, we found that there is no "-1" label in our contingency matrix, which means that our clustering labels were interpreted correctly without the noisy samples.

● QUESTION 17

Based on your experiments, which dimensionality reduction technique and clustering methods worked best together for 20-class text data and why? Follow the table below. If
UMAP takes too long to converge, consider running it once and saving the intermediate results in a pickle file.
Hint: DBSCAN and HDBSCAN do not accept the number of clusters as an input parameter. So pay close attention to how the different clustering metrics are being computed for these methods.

Dimensionality Reduction	Clustering Method	r	k	Result
None	K-means	None	**10**	**0.1230**
			20	0.0766
			30	0.0583
SVD	K-means	5	10	0.1150
			20	0.0904
			50	0.0481
		20	10	0.1030
			20	0.0723
			50	0.0565
		200	**10**	**0.1242**
			20	0.0852
			50	0.0559
NMF	K-means	**5**	**10**	**0.0767**
			20	0.0667
			50	0.0425
		20	10	0.0632
			20	0.0659
			50	0.0517
		200	10	0.0028
			20	0.0151
			50	0.0195
UMAP	K-means	5	10	0.2218
			20	0.2069
			50	0.1217
		20	10	0.2271
			20	0.2239
			50	0.1405
		200	10	0.2416
			20	**0.2426**
			50	0.1306

Dimensionality Reduction	Clustering Method	r	Result
SVD	Agglomerative Clustering	5	0.0920
		20	0.0927
		200	**0.0934**
NMF	Agglomerative Clustering	5	0.0732
		20	**0.0966**
		200	0.0085
UMAP	Agglomerative Clustering	5	0.2146
		20	**0.2281**
		200	0.2242

Dimensionality Reduction: UMAP
Clustering Method: HDBSCAN
min_cluster_size=100

Homogeneity	Completeness	V-measure	Adjusted Rand-Index	Adjusted mutual info score	mean	r	Result
0.430	0.335	0.376	0.229	0.359	0.346	**5**	**0.3458**
0.414	0.334	0.370	0.231	0.365	0.343	20	0.3426
0.411	0.322	0.361	0.195	0.275	0.313	200	0.3127

Best dimensionality reduction technique and clustering method:
Clustering method: HDBSCAN
Dimensionality reduction: UMAP

The choice of dimensionality reduction technique and clustering method depends on the specific characteristics of the data and the desired outcome. In general, UMAP is a good choice for dimensionality reduction because it is able to preserve the local structure of the data, making it suitable for clustering tasks. For clustering, both DBSCAN and HDBSCAN can be effective as they do not require prior knowledge of the number of clusters. DBSCAN is sensitive to the choice of epsilon and minimum number of samples, while HDBSCAN is more robust and can automatically determine the number of clusters.
For text data, it is also common to use clustering algorithms such as k-means or hierarchical clustering, which do accept the number of clusters as an input parameter. In these cases, it may be helpful to use a dimensionality reduction technique such as PCA or t-SNE to reduce the dimensionality of the data before clustering.
Ultimately, the best combination of dimensionality reduction and clustering methods will depend on the specific characteristics of the data and the desired outcome. It may be helpful to try multiple combinations and compare the results using metrics such as silhouette score or adjusted Rand index.

QUESTION 19

In a brief paragraph discuss: If the VGG network is trained on a dataset with perhaps totally different classes as targets, why would one expect the features derived from such a network to have discriminative power for a custom dataset?

The VGG network, pre-trained on a large dataset, has learned to extract generic and robust features that capture important visual patterns and variations in images. These features, learned through the convolutional and dense layers, can be useful for a wide range of visual recognition tasks even if the original training dataset and target classes are different from the custom dataset. This is because these features are designed to have strong discriminative power and can be adapted to new tasks through fine-tuning or transfer learning. As a result, one can expect the VGG network to provide useful features for a custom dataset, leading to improved performance for the target task.

QUESTION 20

In a brief paragraph explain how the helper code base is performing feature extraction.

The helper code base for feature extraction typically uses a pre-trained deep neural network, such as VGG, as a feature extractor. This is done by removing the final classification layer(s) of the network and using the activations from one or several intermediate layers as features for a new task. The process involves feeding input images through the network, which then outputs activations from the selected layer(s) as feature maps. These feature maps are then flattened and possibly transformed into a compact representation, such as PCA, before being used as input to a classifier or another machine learning model. This approach allows the feature extractor to leverage the prior knowledge learned on the original dataset to improve performance on the new task.

- **QUESTION 21**

How many pixels are there in the original images? How many features does the VGG network extract per image; i.e what is the dimension of each feature vector for an image sample?

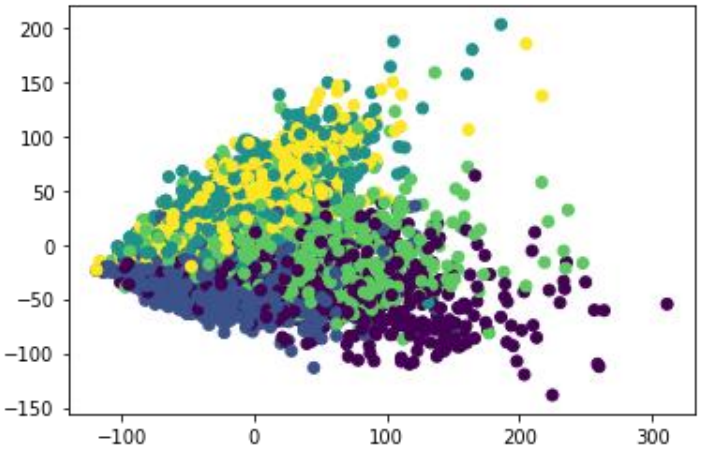
```
(f_all.shape, y_all.shape) = (3670, 4096)
```

The number of pixels in the original images depends on the size of the images. For example, an image with the size of 256×256 pixels would have 256×256 = 65,536 pixels. The dimension of the feature vector extracted by the VGG network for each image sample depends on the architecture of the network and the layer from which the features are extracted. The VGG network is a deep convolutional neural network that typically extracts features from the output of one or several intermediate layers. These feature maps can have thousands or millions of activations, resulting in a high-dimensional feature vector for each image. For example, the VGG16 network has a final feature vector of size 4096, while the VGG19 network has a final feature vector of size 512×7×7 = 25088.

QUESTION 22

Are the extracted features dense or sparse? (Compare with sparse TF-IDF features in text.)

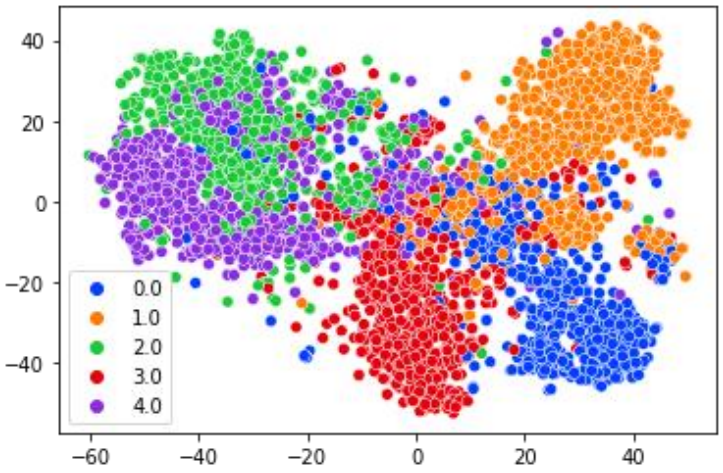
The features extracted from the VGG network are typically dense features. This means that the feature vectors have a relatively large number of non-zero elements and a high dimensionality. This is in contrast to sparse features, such as those obtained through TF-IDF in text analysis, where the feature vectors have a relatively small number of non-zero elements and a lower dimensionality. In text analysis, the sparsity of the features reflects the fact that only a small fraction of the words in the text are relevant to a specific task or document, while in image analysis, dense features reflect the complex and nuanced visual information contained in the images.



Scatter plot of mapped feature vectors for PCA

QUESTION 23

• In order to inspect the high-dimensional features, t-SNE is a popular off-the-shelf choice for visualizing Vision features. Map the features you have extracted onto 2 dimensions with t-SNE. Then plot the mapped feature vectors along x and y axes. Color-code the data points with ground-truth labels. Describe your observation.



Scatter plot of mapped feature vectors for t-SNE

T-SNE is a dimensionality reduction technique that maps high-dimensional data into a low-dimensional space, such as 2D, for visualization purposes. When applied to high-dimensional feature vectors extracted from images, t-SNE can reveal patterns and structures in the data that are not immediately apparent in the raw feature vectors. When the data points are color-coded with ground-truth labels, the t-SNE visualization can provide insight into how well the features are able to discriminate between different classes in the data. The observations from a t-SNE visualization of features extracted from images can help to identify issues with the features or the classification algorithm and inform further experimentation or improvement.

QUESTION 24

Report the best result (in terms of rand score) within the table below. For HDBSCAN, introduce a conservative parameter grid over min cluster size and min samples.

Clustering Method	Dimensionality Reduction	Results
K-means	None	0.1928
	SVD	0.1920
	UMAP	0.4669
	Autoencoder	0.2360
Agglomerative Clustering	None	0.1886
	SVD	0.2693
	UMAP	**0.4686**
	Autoencoder	0.2935

We notice that the best result was obtained from, Agglomerative Clustering with UMAP dimension reduction.

HDBSCAN w/o dimension reduction	**None**			**SVD**			**AutoEncoder**		
min_cluster_size	10	10	10	10	10	10	10	10	10
min_samples	1	2	3	1	2	3	1	2	3
homogeneity_score	0.014	0.014	0.021	0.033	0.027	0.026	0.022	0.029	0.025
Completeness	0.042	0.042	0.058	0.080	0.071	0.064	0.053	0.075	0.071
V-measure	0.021	0.021	0.030	0.047	0.039	0.037	0.032	0.042	0.037
Adjusted Rand-Index	0.015	0.015	0.008	0.017	0.010	0.016	0.030	0.015	0.010
Silhouette Coefficient	0.174	0.174	0.076	0.123	0.106	0.061	0.043	0.123	0.134
mean	0.053	0.053	0.008	0.011	0.008	0.016	0.036	0.008	0.002

QUESTION 25

• Report the test accuracy of the MLP classifier on the original VGG features. Report the same when using the reduced-dimension features (you have freedom in choosing the dimensionality reduction algorithm and its parameters). Does the performance of the model suffer with the reduced-dimension representations? Is it significant? Does the success in classification make sense in the context of the clustering results obtained for the same features in Question 24.

Techniques	Feature Accuracy
VGG	0.9305
SVD with 50 components	0.3038
UMAP with 50 components	0.2262
AutoEncoder	0.2262

The accuracy depends on the dimensionality reduction technique used and the data. Some dimensionality reduction techniques can preserve the relevant information in the data, while others may lose important information.
If the reduced-dimension representations accurately capture the structure of the data, then the performance of the MLP classifier on the reduced-dimension features may not suffer significantly. On the other hand, if the dimensionality reduction technique discards important information, the performance of the MLP classifier may suffer.
It's also important to consider the trade-off between dimensionality reduction and the performance of the MLP classifier. Reducing the dimensionality of the data can lead to faster and more efficient training and prediction times, but it may come at the cost of reduced accuracy. It is often necessary to experiment with different dimensionality reduction techniques and find the best balance between computational efficiency and accuracy.

Conclusion

we explore the concepts of feature extraction and clustering together. In an ideal world, all we need are data points – encoded using certain features– and AI should be able to find what is important to learn, or more specifically, determine what are the underlying modes or categories in the dataset. This is the ultimate goal of General AI: the machine is able to bootstrap a knowledge base, acting as its own teacher and interacting with the outside world to explore to be able to operate autonomously in an environment.

Since we learn how to store memory of transformer, it only takes 15 minutes for the overall project code to run, we also encapsulate functions as much as possible makes our code clearer, easier to understand, and easier to reuse.
Also,in the dimension reduction field, we store the pickle and reload it to different clustering methods, which saved lots of time.

This is the pickle we store.
https://drive.google.com/drive/folders/1Y6HbWVh2z20LRhPT2DSPLKMS4HpbB9Cg?usp=sharing

Work Distribution

Our group members are evenly distributed.

Project 2: Data Representations and Clustering

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0 pre-install packages

In [1]:
```
# !pip install nltk
# !pip install sklearn
# !pip install pandas
# !pip install numpy
# !pip install matplotlib
# !pip install scikit-learn
# !pip install seaborn
# !pip install umap-learn
# !pip install umap-learn[plot]
# !pip install annoy==1.17.0
# !pip install cython==0.29.21
# !pip install fuzzywuzzy==0.18.0
# !pip install hdbscan==0.8.26
# !pip install joblib==1.0.0
# !pip install kiwisolver==1.3.1
# !pip install llvmlite==0.35.0
# !pip install matplotlib==3.3.2
# !pip install numba==0.52.0
# !pip install pandas==1.1.2
# !pip install pillow==8.1.0
# !pip install pyarrow==1.0.1
# !pip install python-levenshtein==0.12.1
# !pip install pytz==2021.1
# !pip install scikit-learn==0.24.1
# !pip install scipy==1.6.0
# !pip install six==1.15.0
# !pip install threadpoolctl==2.1.0
# !pip install tqdm==4.50.0
# !pip install torch
```

In [2]:
```
import warnings
warnings.filterwarnings('ignore')
```

Question 1

In [12]:
```
from sklearn.datasets import fetch_20newsgroups
import numpy as np
import random
import pandas as pd
from sklearn.cluster import KMeans, AgglomerativeClustering, DBSCAN
from sklearn.metrics.cluster import adjusted_mutual_info_score
from sklearn.feature_extraction.text import CountVectorizer, TfidfTransformer
import itertools
import matplotlib.pyplot as plt
from sklearn.metrics.cluster import contingency_matrix
from collections import defaultdict
from sklearn import metrics
```

```
from time import time
from sklearn.decomposition import TruncatedSVD
from sklearn.utils.extmath import randomized_svd
from sklearn.decomposition import NMF
from tqdm import tqdm, trange
from scipy.optimize import linear_sum_assignment
from sklearn.metrics import confusion_matrix
import umap.plot as uplot
import umap.umap_ as umap
from sklearn.model_selection import train_test_split
import hdbscan
from sklearn.manifold import TSNE
import seaborn as sns
import pickle
import os
import requests
import torch
from torch import nn

np.random.seed(0)
random.seed(0)
```

In [4]:
```
categories = ['comp.graphics','comp.os.ms-windows.misc','comp.sys.ibm.pc.hardware', 'com
              'rec.autos','rec.motorcycles','rec.sport.baseball','rec.sport.hockey']
dataset = fetch_20newsgroups(subset = 'all', categories = categories,shuffle = True, ran
```

In [5]:
```
dataset.target
```

Out[5]:
```
array([6, 4, 1, ..., 0, 4, 6], dtype=int64)
```

In [6]:
```
dataset.keys()
```

Out[6]:
```
dict_keys(['data', 'filenames', 'target_names', 'target', 'DESCR'])
```

In [7]:
```
labels = dataset.target
unique_Y_binary, category_sizes = np.unique(dataset.target, return_counts=True)
true_k = len(unique_Y_binary)
print(f"{len(dataset.data)} documents - {true_k} categories")
```

```
7882 documents - 8 categories
```

In [8]:
```
dataset.target_names
```

Out[8]:
```
['comp.graphics',
 'comp.os.ms-windows.misc',
 'comp.sys.ibm.pc.hardware',
 'comp.sys.mac.hardware',
 'rec.autos',
 'rec.motorcycles',
 'rec.sport.baseball',
 'rec.sport.hockey']
```

In [5]:
```
comp_class = ['comp.graphics','comp.os.ms-windows.misc','comp.sys.ibm.pc.hardware','comp
rec_class = ['rec.autos','rec.motorcycles','rec.sport.baseball','rec.sport.hockey']
```

In [6]:
```
Y_binary = [i // 4 for i in dataset.target]
```

In [7]:
```
from sklearn.feature_extraction.text import CountVectorizer, TfidfTransformer

count_vectorizer = CountVectorizer(stop_words="english", min_df=3)
tfidf_tranformer = TfidfTransformer(use_idf=True)

data_count_vectorizer = count_vectorizer.fit_transform(dataset.data)
```

```
print(f"n_samples: {data_count_vectorizer .shape[0]}, n_features: {data_count_vectorizer

data_tf_idf3 = tfidf_tranformer.fit_transform(data_count_vectorizer)
data_tf_idf3_ar = data_tf_idf3.toarray()
print('data tf-idf matrix shape:', data_tf_idf3_ar.shape)

dataset_pd = pd.DataFrame(data=data_tf_idf3_ar , columns = count_vectorizer.get_feature_
```

```
n_samples: 7882, n_features: 23522
data tf-idf matrix shape: (7882, 23522)
```

Question 2

In [8]:
```
kmeans = KMeans(n_clusters=2, random_state=0)
kmeans.fit(dataset_pd)
```

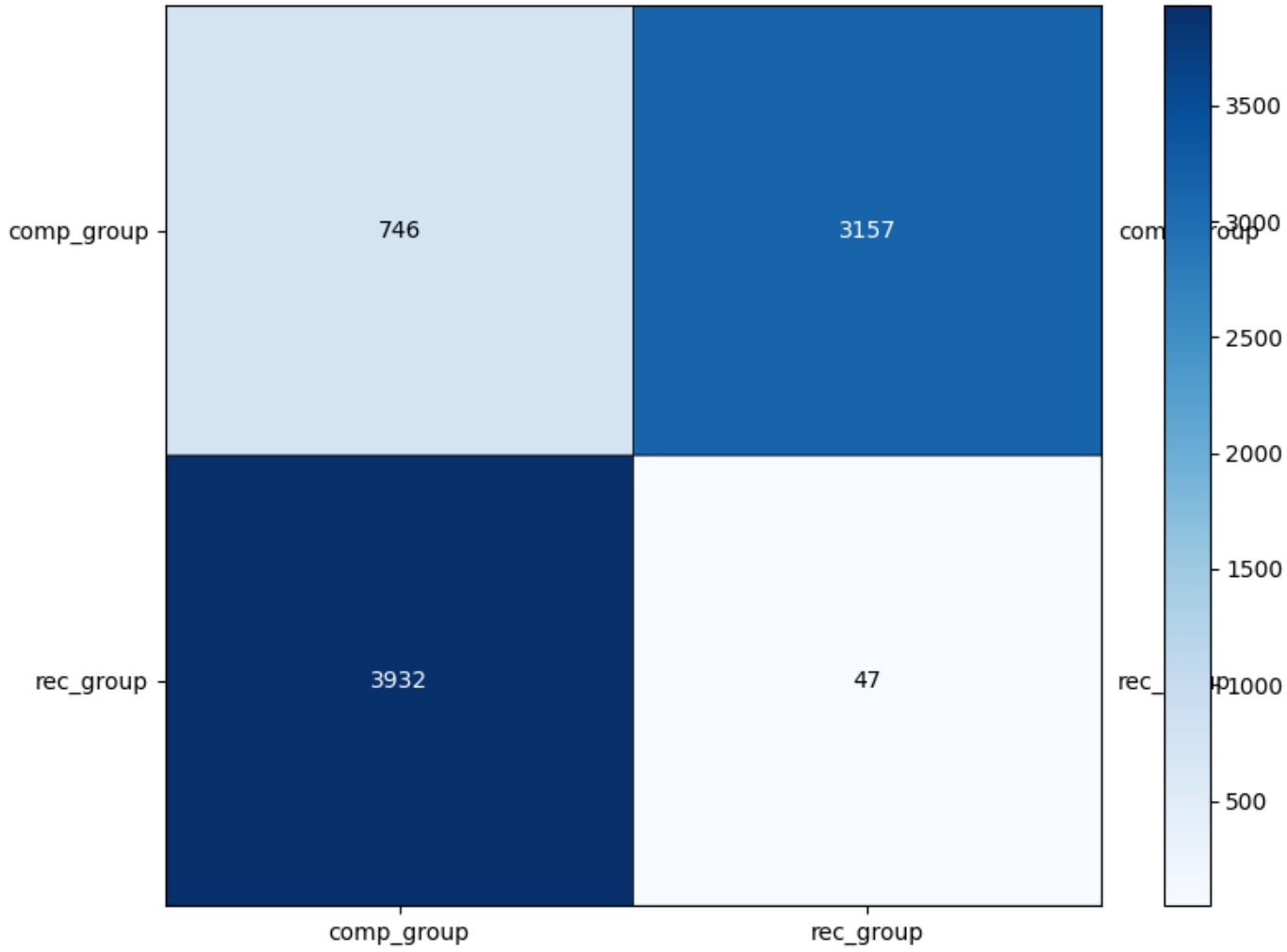
Out[8]:
```
KMeans(max_iter=1000, n_clusters=2, n_init=30, random_state=0)
```

In [9]:
```
import itertools
import matplotlib
import matplotlib.pyplot as plt
import numpy as np

def plot_mat(mat, xticklabels = None, yticklabels = None, pic_fname = None, size=(-1,-1)
             colorbar = True, grid = 'k', xlabel = None, ylabel = None, title = None, vm
    if size == (-1, -1):
        size = (mat.shape[1] / 3, mat.shape[0] / 3)

    fig = plt.figure(figsize=size)
    ax = fig.add_subplot(1,1,1)

    # im = ax.imshow(mat, cmap=plt.cm.Blues)
    im = ax.pcolor(mat, cmap=plt.cm.Blues, linestyle='-', linewidth=0.5, edgecolor=grid,

    if colorbar:
        plt.colorbar(im,fraction=0.046, pad=0.06)
    # tick_marks = np.arange(len(classes))
    # Ticks
    lda_num_topics = mat.shape[0]
    nmf_num_topics = mat.shape[1]
    yticks = np.arange(lda_num_topics)
    xticks = np.arange(nmf_num_topics)
    ax.set_xticks(xticks + 0.5)
    ax.set_yticks(yticks + 0.5)
    if xticklabels is None:
        xticklabels = [str(i) for i in xticks]
    if yticklabels is None:
        yticklabels = [str(i) for i in yticks]
    ax.set_xticklabels(xticklabels)
    ax.set_yticklabels(yticklabels)

    # Minor ticks
    # ax.set_xticks(xticks, minor=True);
    # ax.set_yticks(yticks, minor=True);
    # ax.set_xticklabels([], minor=True)
    # ax.set_yticklabels([], minor=True)

    # ax.grid(which='minor', color='k', linestyle='-', linewidth=0.5)

    # tick labels on all four sides
    ax.tick_params(labelright = True, labeltop = False)

    if ylabel:
        plt.ylabel(ylabel, fontsize=15)
```

```
    if xlabel:
        plt.xlabel(xlabel, fontsize=15)
    if title:
        plt.title(title, fontsize=15)

    # im = ax.imshow(mat, interpolation='nearest', cmap=plt.cm.Blues)
    ax.invert_yaxis()

    # thresh = mat.max() / 2

    def show_values(pc, fmt="%.0f", **kw):
        pc.update_scalarmappable()
        ax = pc.axes
        for p, color, value in itertools.zip_longest(pc.get_paths(), pc.get_facecolors()
            x, y = p.vertices[:-2, :].mean(0)
            if np.all(color[:3] > 0.5):
                color = (0.0, 0.0, 0.0)
            else:
                color = (1.0, 1.0, 1.0)
            ax.text(x, y, fmt % value, ha="center", va="center", color=color, **kw, font

    if if_show_values:
        show_values(im)
    # for i, j in itertools.product(range(mat.shape[0]), range(mat.shape[1])):
    #     ax.text(j, i, "{:.2f}".format(mat[i, j]), fontsize = 4,
    #             horizontalalignment="right",
    #             color="white" if mat[i, j] > 0.05 else "black")

    plt.tight_layout()
    if pic_fname:
        plt.savefig(pic_fname, dpi=300, transparent=True)
    plt.show()
    plt.close()
```

In [10]:

```
from sklearn.metrics.cluster import contingency_matrix

plot_mat(contingency_matrix(Y_binary, kmeans.labels_), size = (8,6), xticklabels = ['com
```



Question 3

In [27]:

```
from collections import defaultdict
from sklearn import metrics
from time import time

evaluations = []
evaluations_std = []

def evaluate(km, X, Y_binary, name=None, n_runs=5):
    name = km.__class__.__name__ if name is None else name

    train_times = []
    scores = defaultdict(list)
    for seed in range(n_runs):
        t0 = time()
        train_times.append(time() - t0)
        scores["Homogeneity"].append(metrics.homogeneity_score(Y_binary, km.labels_))
        scores["Completeness"].append(metrics.completeness_score(Y_binary, km.labels_))
        scores["V-measure"].append(metrics.v_measure_score(Y_binary, km.labels_))
        scores["Adjusted Rand-Index"].append(
            metrics.adjusted_rand_score(Y_binary, km.labels_)
        )
        scores["Adjusted_mutual_info_score"].append(
            adjusted_mutual_info_score(Y_binary, km.labels_)
        )
    train_times = np.asarray(train_times)

    print(f"clustering done in {train_times.mean():.2f} ± {train_times.std():.2f} s ")
    evaluation = {
        "estimator": name,
```

```
        "train_time": train_times.mean(),
    }
    evaluation_std = {
        "estimator": name,
        "train_time": train_times.std(),
    }
    for score_name, score_values in scores.items():
        mean_score, std_score = np.mean(score_values), np.std(score_values)
        print(f"{score_name}: {mean_score:.3f} ± {std_score:.3f}")
        evaluation[score_name] = mean_score
        evaluation_std[score_name] = std_score
    evaluations.append(evaluation)
    evaluations_std.append(evaluation_std)
```

In [28]:
```
evaluate(kmeans, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
```

```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.579 ± 0.000
Completeness: 0.594 ± 0.000
V-measure: 0.587 ± 0.000
Adjusted Rand-Index: 0.638 ± 0.000
Adjusted_mutual_info_score: 0.587 ± 0.000
```

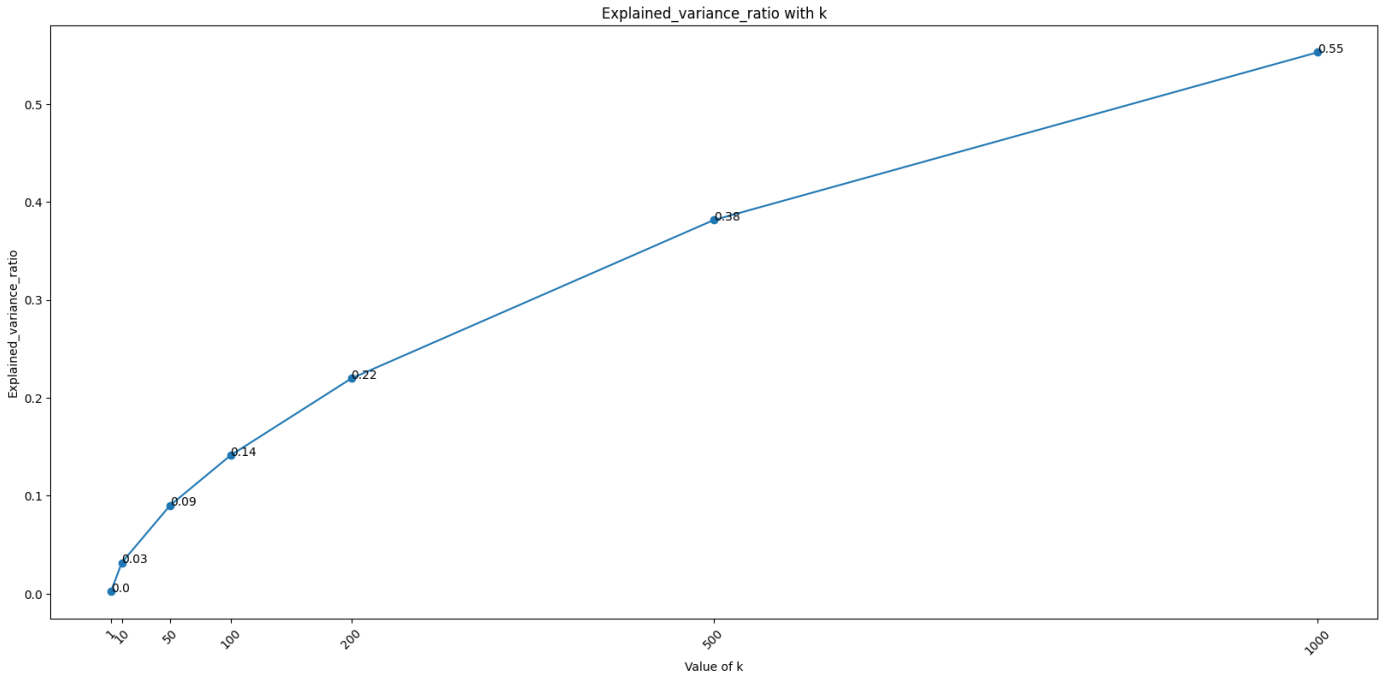
Question 4

In [17]:
```
from sklearn.decomposition import TruncatedSVD
from tqdm import tqdm, trange

k = [1, 10, 50, 100, 200, 500, 1000]
explained_variance_ratio = []

def plot_figure_for_each_k(k, svd_t):
    exp_var_pca = svd_t.explained_variance_ratio_
    cum_sum_eigenvalues = np.cumsum(exp_var_pca)

    plt.bar(range(0,len(exp_var_pca)), exp_var_pca, alpha=0.5, align='center', label='In
    plt.step(range(0,len(cum_sum_eigenvalues)), cum_sum_eigenvalues, where='mid',label='
    plt.title(f"Explained_variance_ratio when k = {k}")
    plt.ylabel('Explained variance ratio')
    plt.xlabel('Principal component index')
    plt.legend(loc='best')
    plt.tight_layout()
    plt.show()


for i in trange(len(k)):
    svd_t = TruncatedSVD(n_components=k[i], random_state=42)
    svd_t.fit(data_tf_idf3)
    # plot_figure_for_each_k(kcomponents[i], svd_t)
    explained_variance_ratio.append(sum(svd_t.explained_variance_ratio_))
```

```
100%|██████████| 7/7 [00:24<00:00,  3.52s/it]
```

In [18]:
```
plt.figure(figsize=(20,9))
plt.title('Explained_variance_ratio with k')
plt.xlabel("Value of k")
plt.ylabel("Explained_variance_ratio")

plt.xticks(k, rotation = 45)

plt.plot(k, explained_variance_ratio, ls="-", marker="o", label="points")

for ks, exp in zip(k, explained_variance_ratio):
```

```
      plt.text(ks, exp, str(round(exp, 2)))
plt.show()
```



Question 5

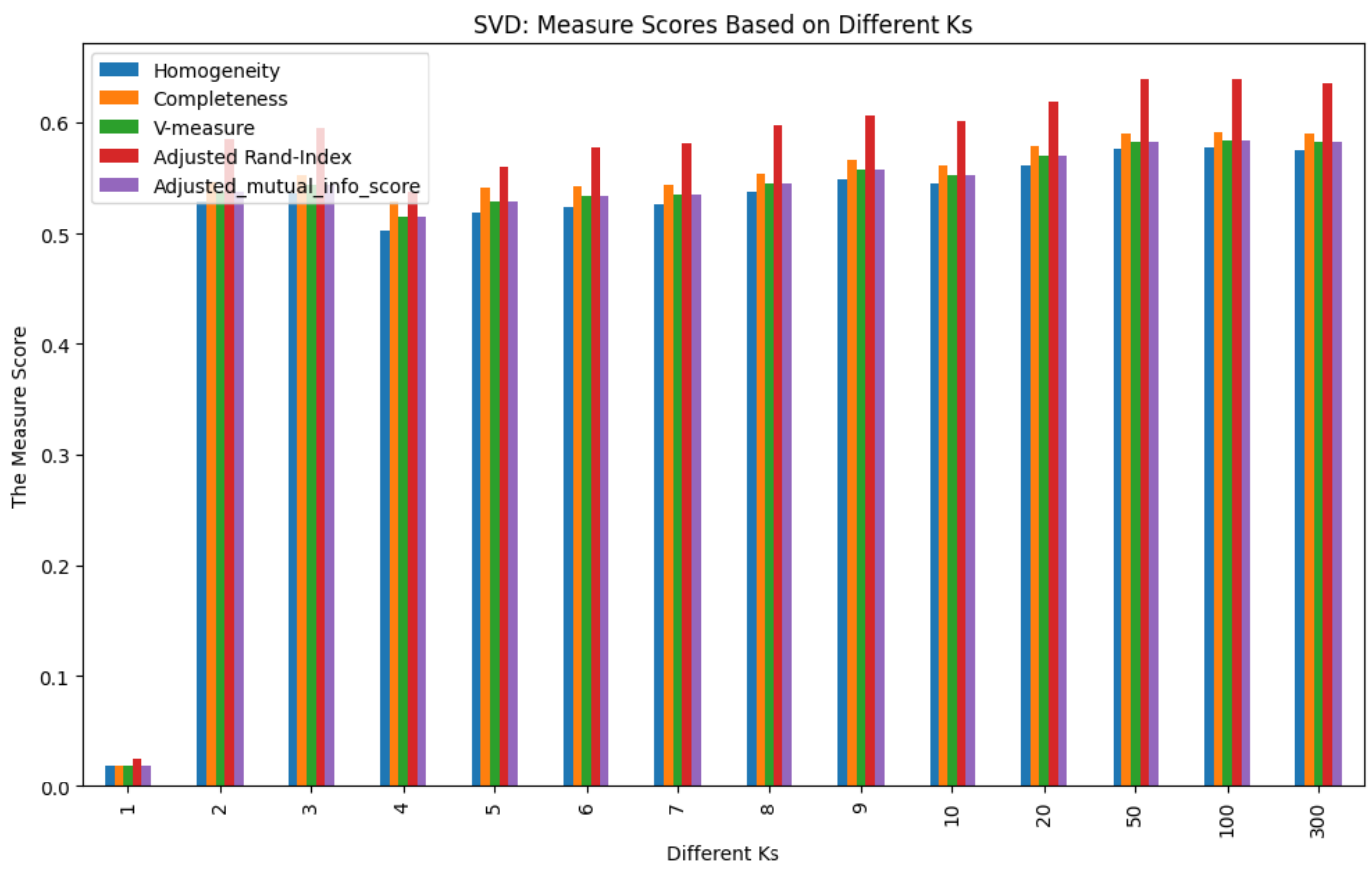
In [34]:
```
from sklearn.utils.extmath import randomized_svd
from sklearn.decomposition import NMF
from sklearn.decomposition import TruncatedSVD
from tqdm import tqdm, trange

r_ = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 50, 100, 300]
SVD_results = defaultdict(list)
NMF_results = defaultdict(list)

best_svd = 0
best_nmf = 0
best_svd_r = 0
best_nmf_r = 0

for r in r_:
    print('n_componets: ' + str(r))

    model_svd = TruncatedSVD(n_components=r)
    svd_data = model_svd.fit_transform(data_tf_idf3)
    km = KMeans(n_clusters=2, random_state=0)
    km.fit(svd_data)

    SVD_results["Homogeneity"].append(metrics.homogeneity_score(Y_binary, km.labels_))
    SVD_results["Completeness"].append(metrics.completeness_score(Y_binary, km.labels_))
    SVD_results["V-measure"].append(metrics.v_measure_score(Y_binary, km.labels_))
    SVD_results["Adjusted Rand-Index"].append(metrics.adjusted_rand_score(Y_binary, km.l
    SVD_results["Adjusted_mutual_info_score"].append(adjusted_mutual_info_score(Y_binary

    avg_svd_score = (SVD_results["Homogeneity"][-1] + SVD_results["Completeness"][-1] \
    + SVD_results["V-measure"][-1] + SVD_results["Adjusted Rand-Index"][-1]  \
    + SVD_results["Adjusted_mutual_info_score"][-1]) / 5.0

    if(avg_svd_score > best_svd):
        best_svd = avg_svd_score
        best_svd_r = r
        best_svd_kmeans = km
        best_svd_data = svd_data
```

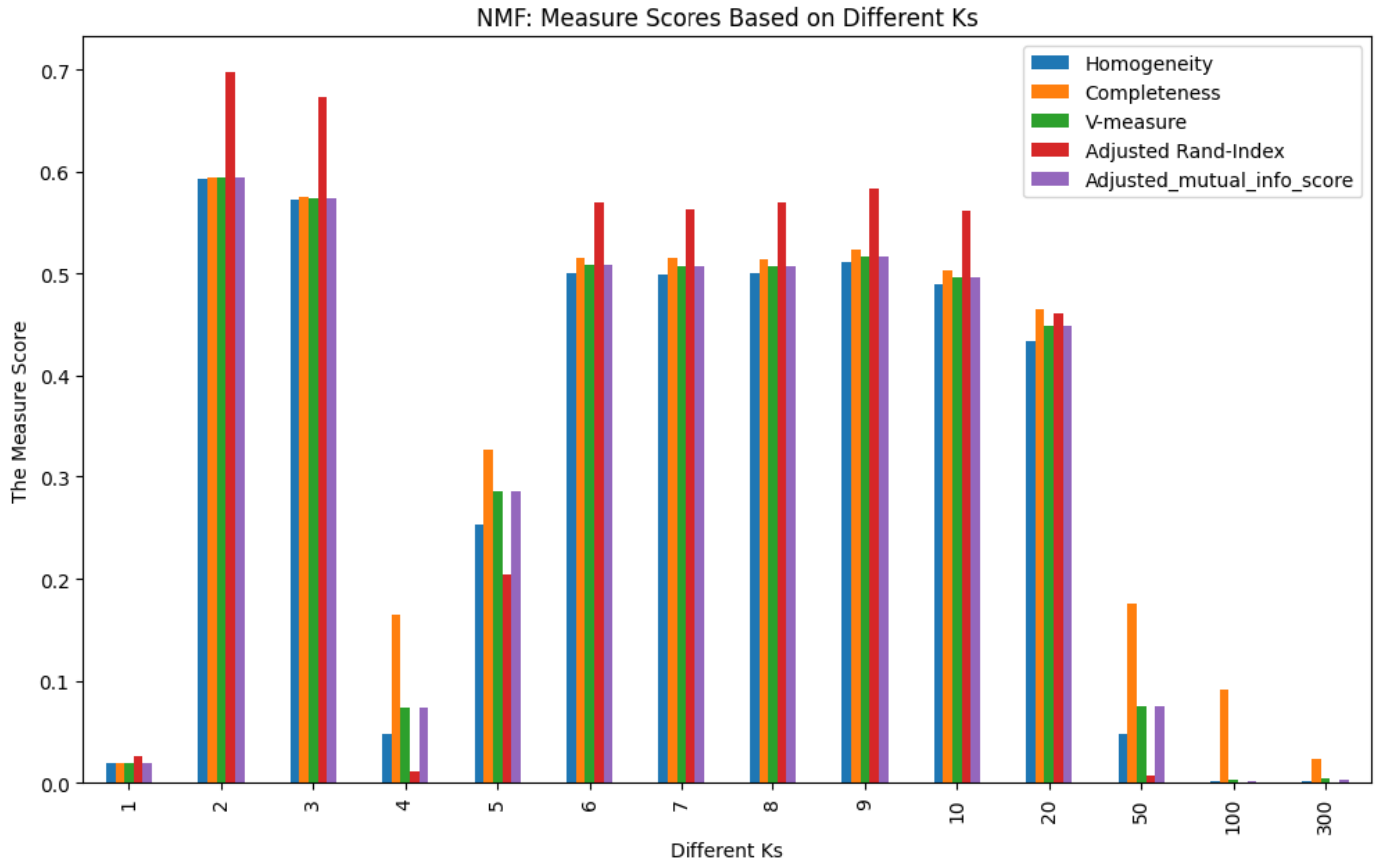
```
    model_nmf = NMF(n_components=r)
    nmf_data = model_nmf.fit_transform(data_tf_idf3)
    km = KMeans(n_clusters=2, random_state=0)
    km.fit(nmf_data)

    NMF_results["Homogeneity"].append(metrics.homogeneity_score(Y_binary, km.labels_))
    NMF_results["Completeness"].append(metrics.completeness_score(Y_binary, km.labels_))
    NMF_results["V-measure"].append(metrics.v_measure_score(Y_binary, km.labels_))
    NMF_results["Adjusted Rand-Index"].append(metrics.adjusted_rand_score(Y_binary, km.l
    NMF_results["Adjusted_mutual_info_score"].append(adjusted_mutual_info_score(Y_binary

    avg_nmf_score = (NMF_results["Homogeneity"][-1] + NMF_results["Completeness"][-1] \
    + NMF_results["V-measure"][-1] + NMF_results["Adjusted Rand-Index"][-1]  \
    + NMF_results["Adjusted_mutual_info_score"][-1]) / 5.0

    if(avg_nmf_score > best_nmf):
        best_nmf = avg_nmf_score
        best_nmf_r = r
        best_nmf_kmeans = km
        best_nmf_data = nmf_data


print(f"best r for svd is {best_svd_r}, the average score is: {best_svd:.3f}")
print(f"best r for nmf is {best_nmf_r}, the average score is: {best_nmf:.3f}")
```

```
n_componets: 1
n_componets: 2
n_componets: 3
n_componets: 4
n_componets: 5
n_componets: 6
n_componets: 7
n_componets: 8
n_componets: 9
n_componets: 10
n_componets: 20
n_componets: 50
n_componets: 100
n_componets: 300
best r for svd is 100, the average score is: 0.595
best r for nmf is 2, the average score is: 0.614
```

In [32]:
```
def plot_measure(results, r_, model_name):
  results_df = pd.DataFrame(
      data = results,
      index = r_
  )

  results_df.plot(
      kind = 'bar',
      title = "{}: Measure Scores Based on Different Ks".format(model_name),
      xlabel = "Different Ks",
      ylabel = "The Measure Score",
      figsize = (12, 7)
  )
```

In [35]:
```
plot_measure(SVD_results, r_, "SVD")
plot_measure(NMF_results, r_, "NMF")
```





Question6 and Question 7 are stated on our Report

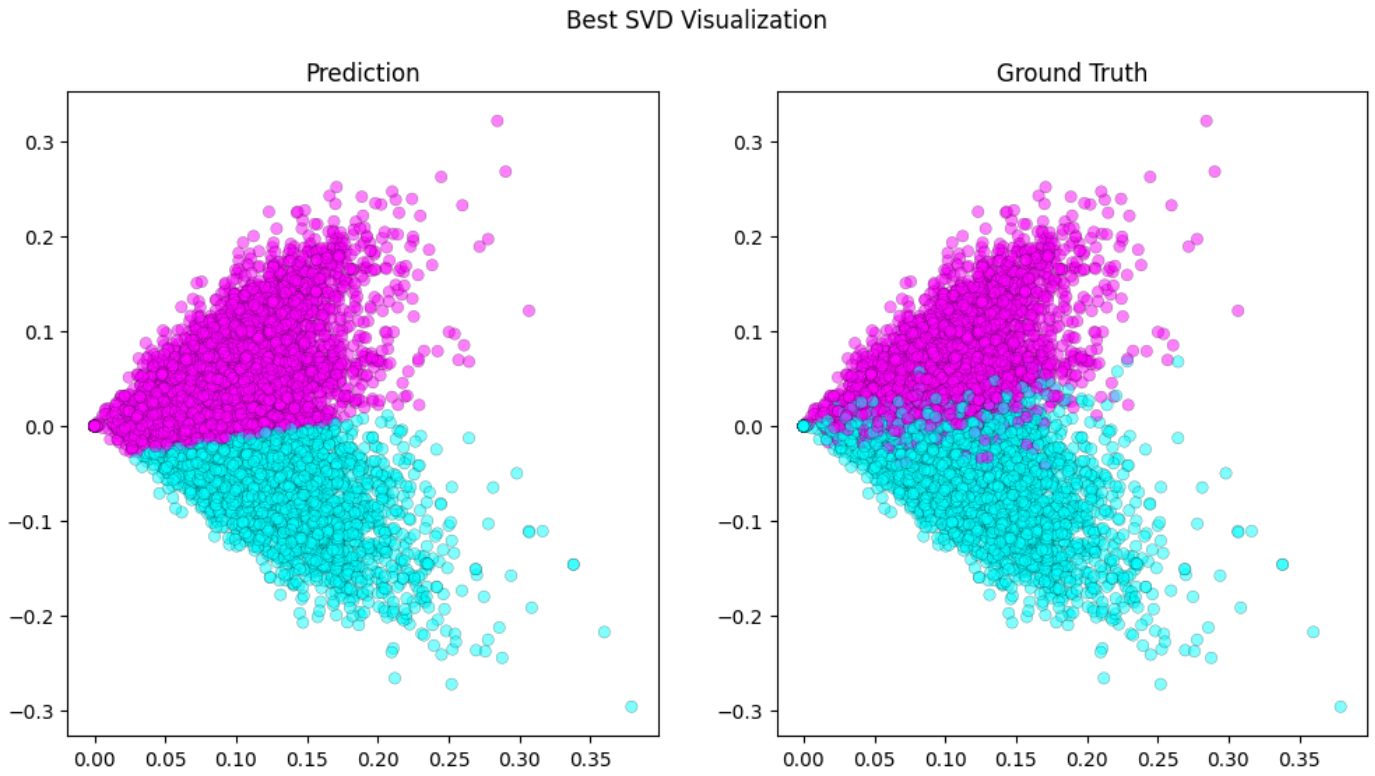
Question8

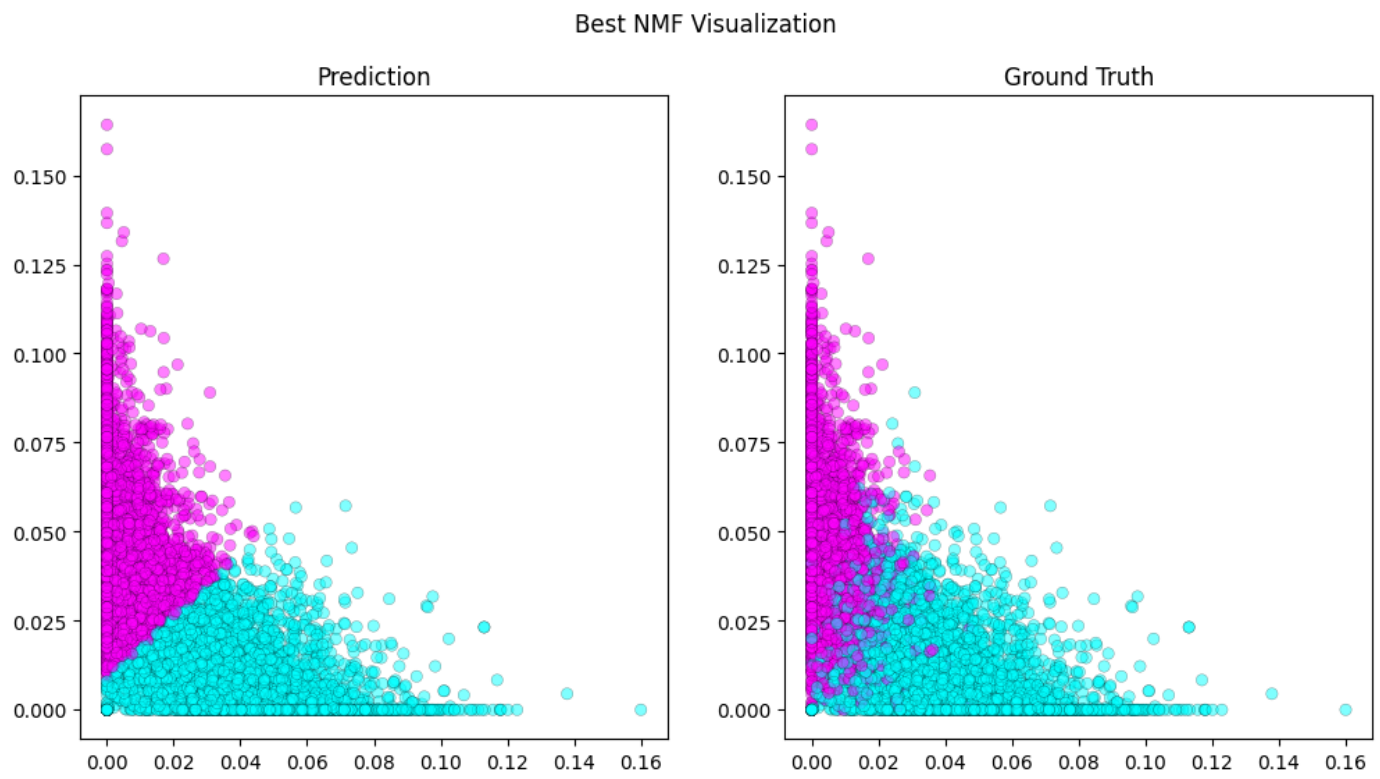
In [22]:

```
def plot_kmeans_clusters(km, data, truth, model_name):

  fig = plt.figure(figsize=(12, 6))
```

```
  ax1 = fig.add_subplot(1, 2, 1)
  ax2 = fig.add_subplot(1, 2, 2)

  predicted_labels = km.labels_
  if np.mean(km.labels_ == truth) > 0.5:
    predicted_labels = km.labels_
  else:
    predicted_labels = [1-x for x in km.labels_]
  ax1.scatter(
      x = data[: ,0],
      y = data[: ,1],
      c = predicted_labels,
      edgecolors='k',
      linewidth=0.25,
      cmap='cool',
      alpha=0.5
  )
  ax1.set_title("Prediction")

  ax2.scatter(
      x = data[: ,0],
      y = data[: ,1],
      c = truth,
      edgecolors='k',
      linewidth=0.25,
      cmap='cool',
      alpha=0.5
  )
  ax2.set_title("Ground Truth")
  fig.suptitle("Best {} Visualization".format(model_name))
  plt.show()
```

In [23]:
```
plot_kmeans_clusters(best_svd_kmeans, best_svd_data, Y_binary, "SVD")
plot_kmeans_clusters(best_nmf_kmeans, best_nmf_data, Y_binary, "NMF")
```





Question9 is stated on our Report

Question10

In [46]:
```
import numpy as np
from scipy.optimize import linear_sum_assignment
from sklearn.metrics import confusion_matrix

dataset = fetch_20newsgroups(subset = 'all', shuffle = True, random_state = 0,remove=('h
Y_binary = [i // 4 for i in dataset.target]

count_vectorizer = CountVectorizer(stop_words="english", min_df=3)
tfidf_tranformer = TfidfTransformer(use_idf=True)

data_count_vectorizer = count_vectorizer.fit_transform(dataset.data)
print(f"n_samples: {data_count_vectorizer .shape[0]}, n_features: {data_count_vectorizer

data_tf_idf3 = tfidf_tranformer.fit_transform(data_count_vectorizer)
# data_tf_idf3_ar = data_tf_idf3.toarray()
print('data tf-idf matrix shape:', data_tf_idf3.shape)
```

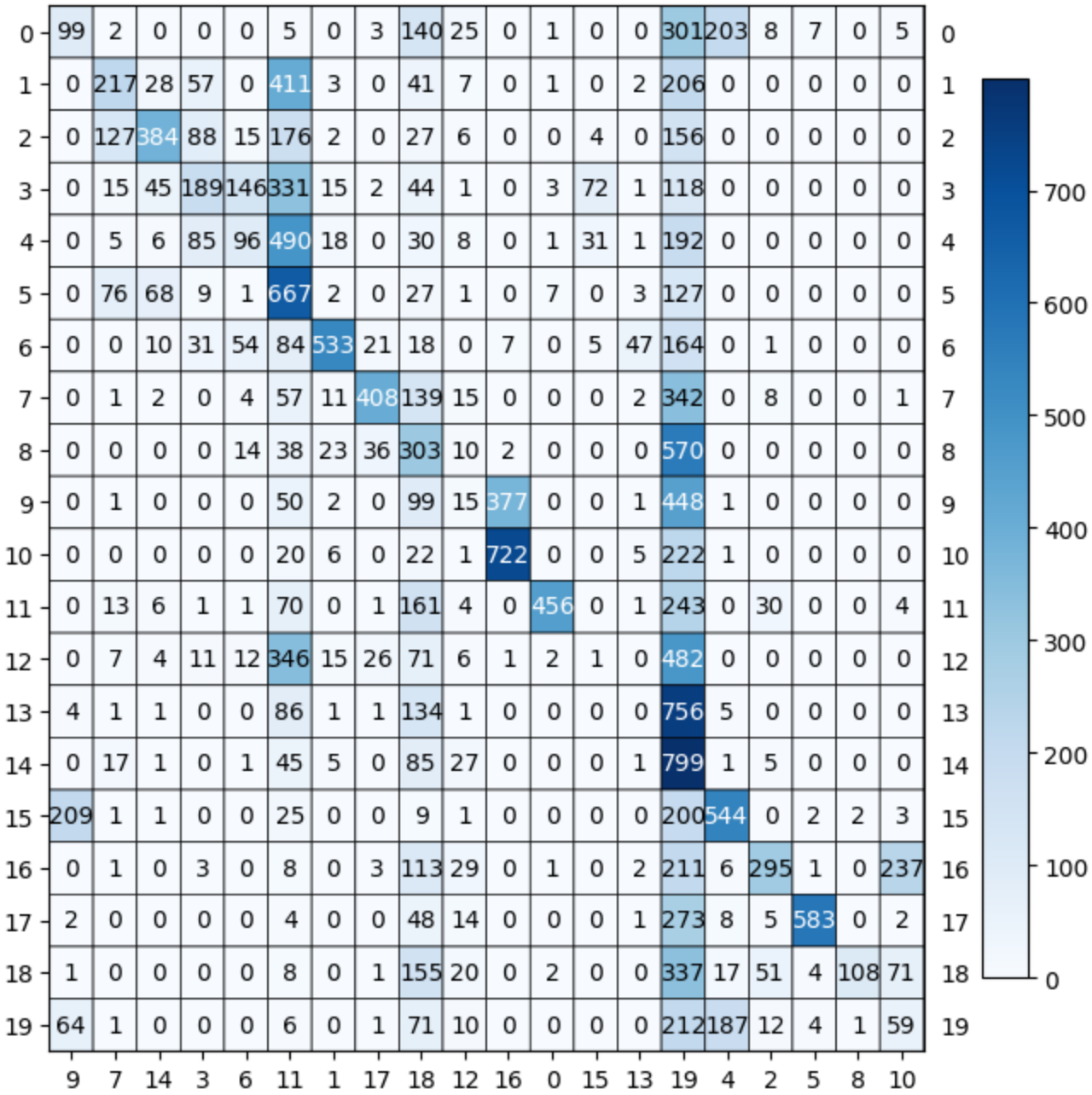
```
n_samples: 18846, n_features: 45365
data tf-idf matrix shape: (18846, 45365)
```

In [50]:
```
kmeans20_ = KMeans(n_clusters=20, random_state=0)
kmeans20_.fit(data_tf_idf3)
evaluate(kmeans20_, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
```

```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.357 ± 0.000
Completeness: 0.222 ± 0.000
V-measure: 0.274 ± 0.000
Adjusted Rand-Index: 0.097 ± 0.000
Adjusted_mutual_info_score: 0.273 ± 0.000
```

In [47]:
```
kmeans20_svd = KMeans(n_clusters=20, random_state=0)
svd_t = TruncatedSVD(n_components=best_svd_r, random_state=42)
data_svd = svd_t.fit_transform(data_tf_idf3)
```

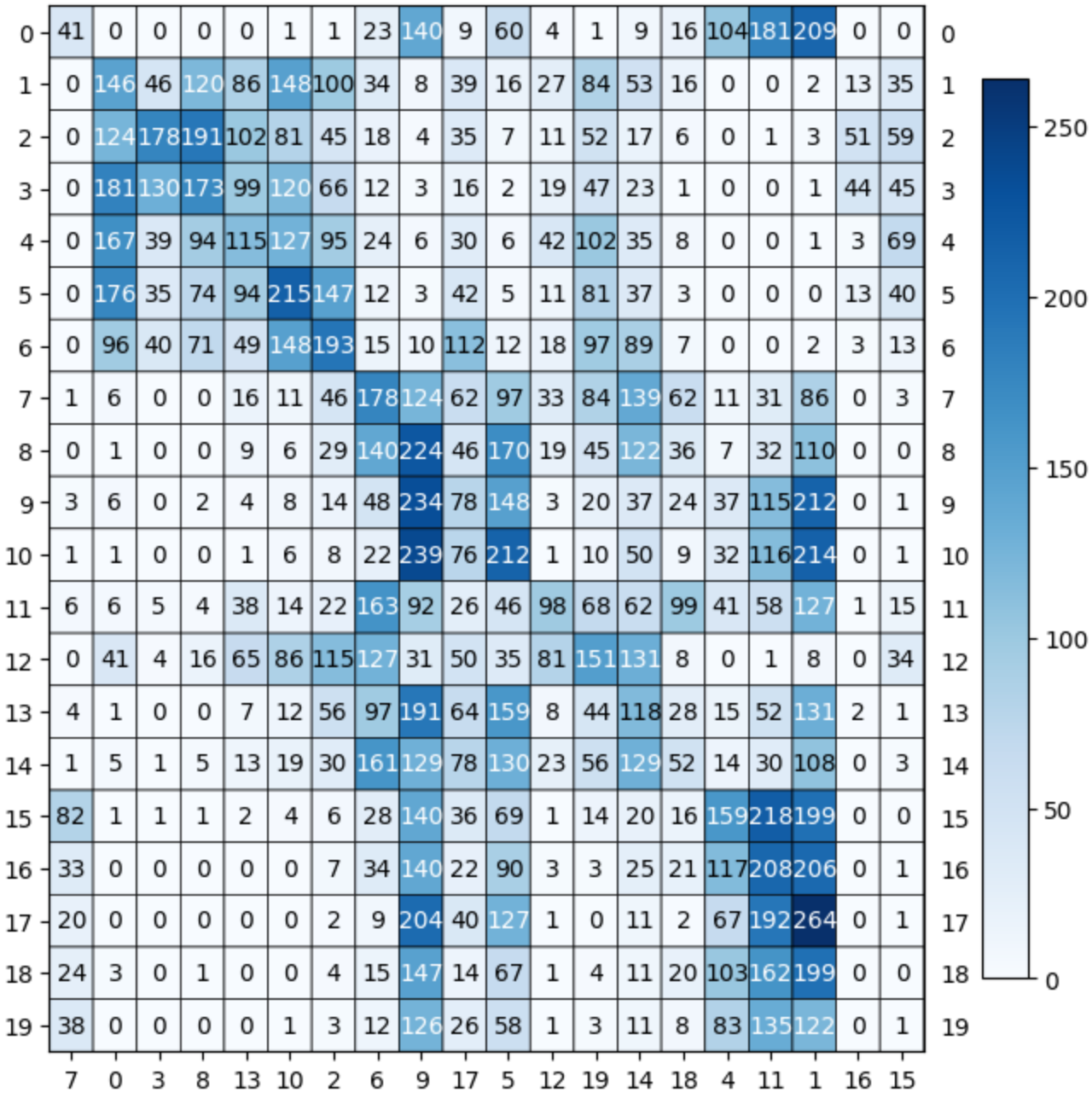
```
kmeans20_svd.fit(data_svd)

cm = confusion_matrix(dataset.target, kmeans20_svd.labels_)
rows, cols = linear_sum_assignment(cm, maximize=True)
plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows)
```



In [42]:
```
evaluate(kmeans20_svd, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
```

```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.331 ± 0.000
Completeness: 0.227 ± 0.000
V-measure: 0.270 ± 0.000
Adjusted Rand-Index: 0.098 ± 0.000
Adjusted_mutual_info_score: 0.269 ± 0.000
```

In [48]:
```
kmeans20_nmf = KMeans(n_clusters=20, random_state=0)
nmf_t = NMF(n_components=best_nmf_r, random_state=42)
data_nmf = nmf_t.fit_transform(data_tf_idf3)
kmeans20_nmf.fit(data_nmf)

cm = confusion_matrix(dataset.target, kmeans20_nmf.labels_)
rows, cols = linear_sum_assignment(cm, maximize=True)
plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows)
```



In [43]:
```
evaluate(kmeans20_nmf, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
```

```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.194 ± 0.000
Completeness: 0.110 ± 0.000
V-measure: 0.141 ± 0.000
Adjusted Rand-Index: 0.054 ± 0.000
Adjusted_mutual_info_score: 0.140 ± 0.000
```

Question11

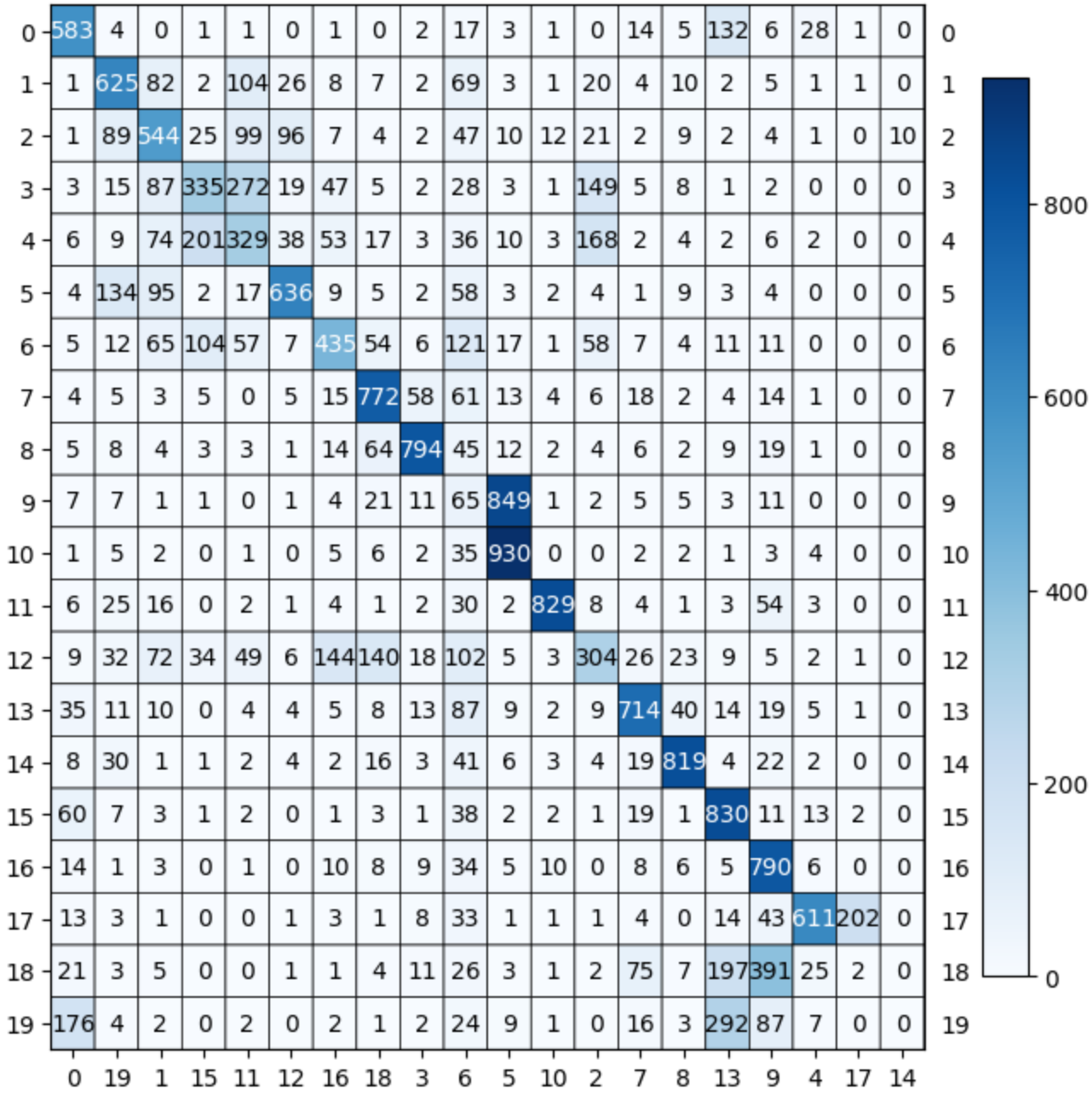
In [39]:
```
import umap.plot as uplot
import umap.umap_ as umap
```

In [44]:
```
n_comp = [5,20,200]
COS_results = defaultdict(list)
EUC_results = defaultdict(list)

best_cos = 0
best_euc = 0
best_cos_r = 0
best_euc_r = 0
```

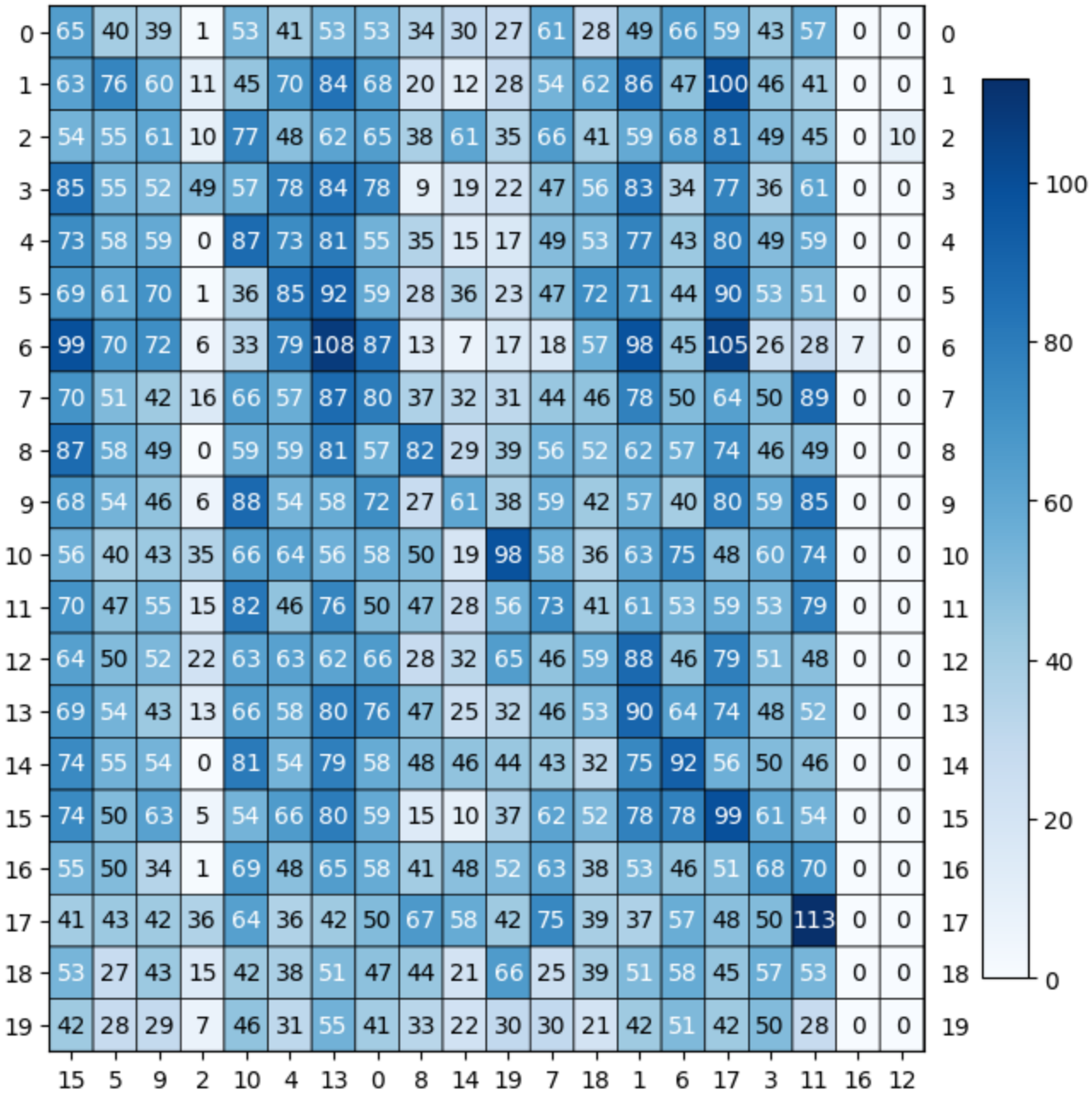
```
for r in n_comp:
    print('n_componets: ' + str(r))

    umap_cos = umap.UMAP(n_components=r, metric='cosine')
    cos_data = umap_cos.fit_transform(data_tf_idf3)
    km = KMeans(n_clusters=20, random_state=0)
    km.fit(cos_data)

    COS_results["Homogeneity"].append(metrics.homogeneity_score(Y_binary, km.labels_))
    COS_results["Completeness"].append(metrics.completeness_score(Y_binary, km.labels_))
    COS_results["V-measure"].append(metrics.v_measure_score(Y_binary, km.labels_))
    COS_results["Adjusted Rand-Index"].append(metrics.adjusted_rand_score(Y_binary, km.l
    COS_results["Adjusted_mutual_info_score"].append(adjusted_mutual_info_score(Y_binary

    avg_cos_score = (COS_results["Homogeneity"][-1] + COS_results["Completeness"][-1] \
    + COS_results["V-measure"][-1] + COS_results["Adjusted Rand-Index"][-1]  \
    + COS_results["Adjusted_mutual_info_score"][-1]) / 5.0

    evaluate(km, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
    cm = confusion_matrix(dataset.target, km.labels_)
    rows, cols = linear_sum_assignment(cm, maximize=True)
    plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows)

    if(avg_cos_score > best_cos):
        best_cos = avg_cos_score
        best_cos_r = r
        best_cos_kmeans = km
        best_cos_data = cos_data

    umap_euc = umap.UMAP(n_components=r, metric='euclidean')
    euc_data = umap_euc.fit_transform(data_tf_idf3)
    km = KMeans(n_clusters=20, random_state=0)
    km.fit(euc_data)

    EUC_results["Homogeneity"].append(metrics.homogeneity_score(Y_binary, km.labels_))
    EUC_results["Completeness"].append(metrics.completeness_score(Y_binary, km.labels_))
    EUC_results["V-measure"].append(metrics.v_measure_score(Y_binary, km.labels_))
    EUC_results["Adjusted Rand-Index"].append(metrics.adjusted_rand_score(Y_binary, km.l
    EUC_results["Adjusted_mutual_info_score"].append(adjusted_mutual_info_score(Y_binary

    avg_euc_score = (EUC_results["Homogeneity"][-1] + EUC_results["Completeness"][-1] \
    + EUC_results["V-measure"][-1] + EUC_results["Adjusted Rand-Index"][-1]  \
    + EUC_results["Adjusted_mutual_info_score"][-1]) / 5.0


    evaluate(km, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
    cm = confusion_matrix(dataset.target, km.labels_)
    rows, cols = linear_sum_assignment(cm, maximize=True)
    plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows)


    if(avg_euc_score > best_euc):
        best_euc = avg_euc_score
        best_euc_r = r
        best_euc_kmeans = km
        best_euc_data = euc_data


print(f"best r for cosine is {best_cos_r}, the average score is: {best_cos:.3f}")
print(f"best r for euclidean is {best_euc_r}, the average score is: {best_euc:.3f}")
```

```
n_componets: 5
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.533 ± 0.000
Completeness: 0.297 ± 0.000
```

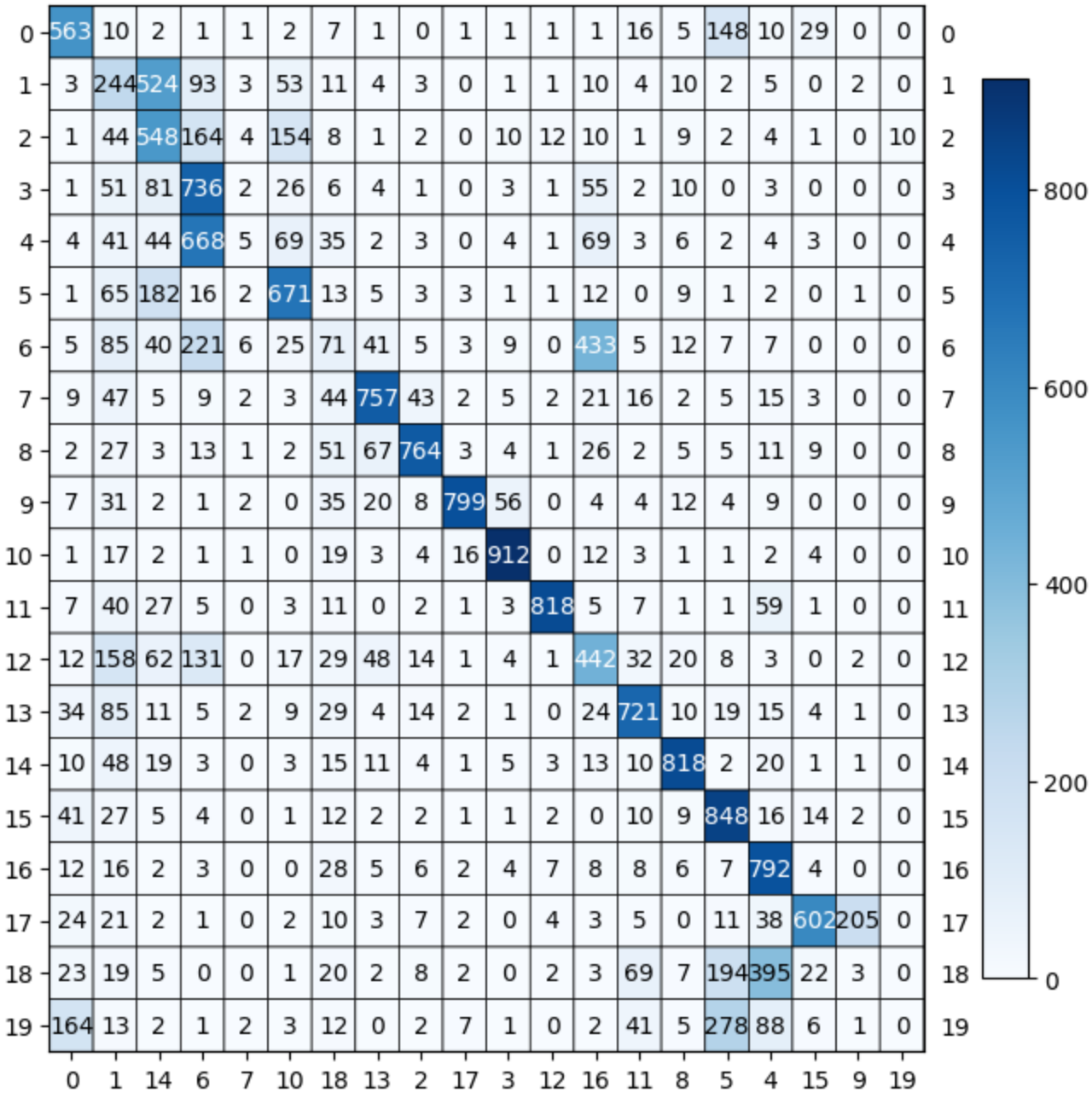
V-measure: 0.381 ± 0.000
Adjusted Rand-Index: 0.216 ± 0.000
Adjusted_mutual_info_score: 0.381 ± 0.000



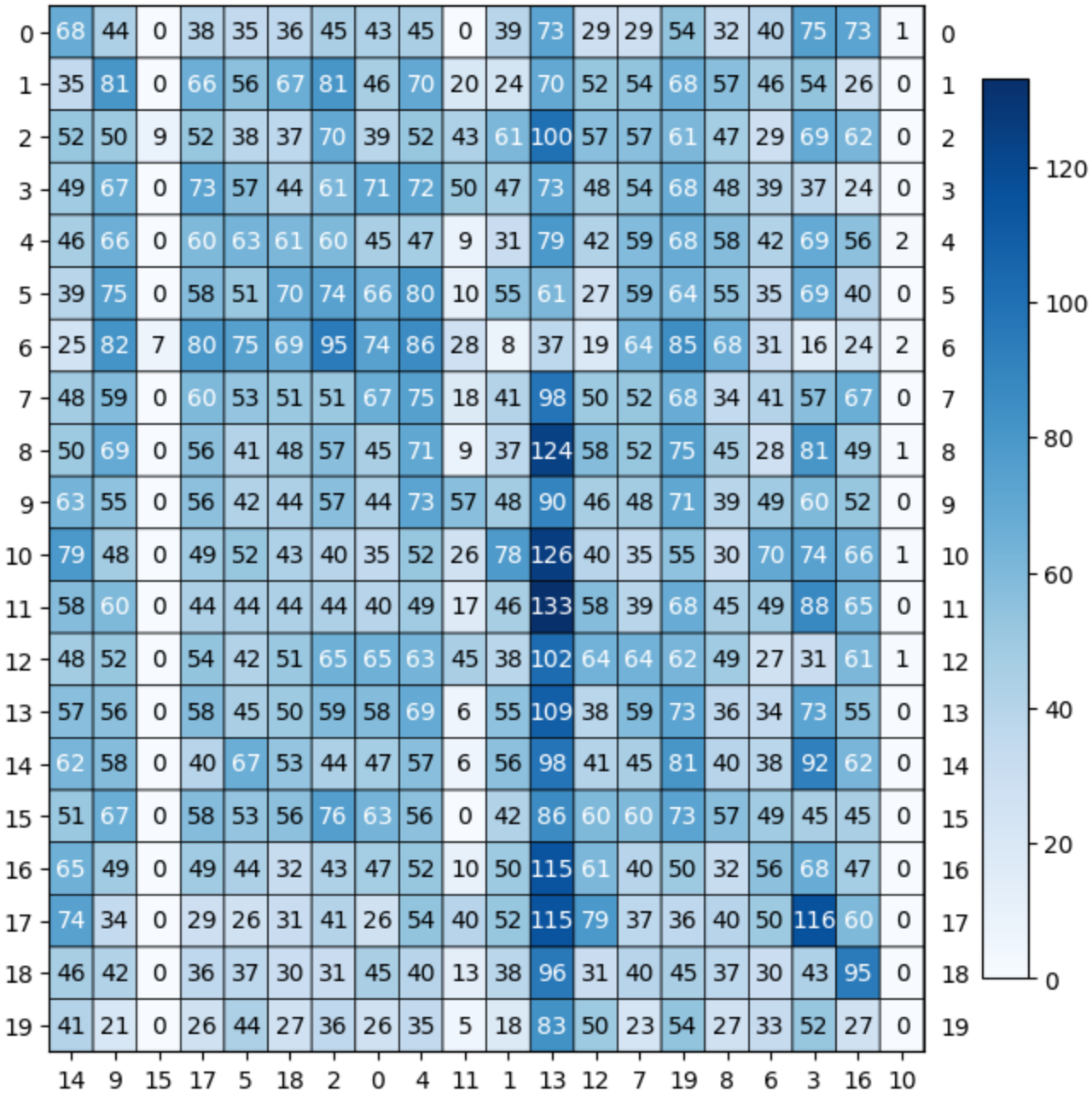
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.009 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.007 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.006 ± 0.000



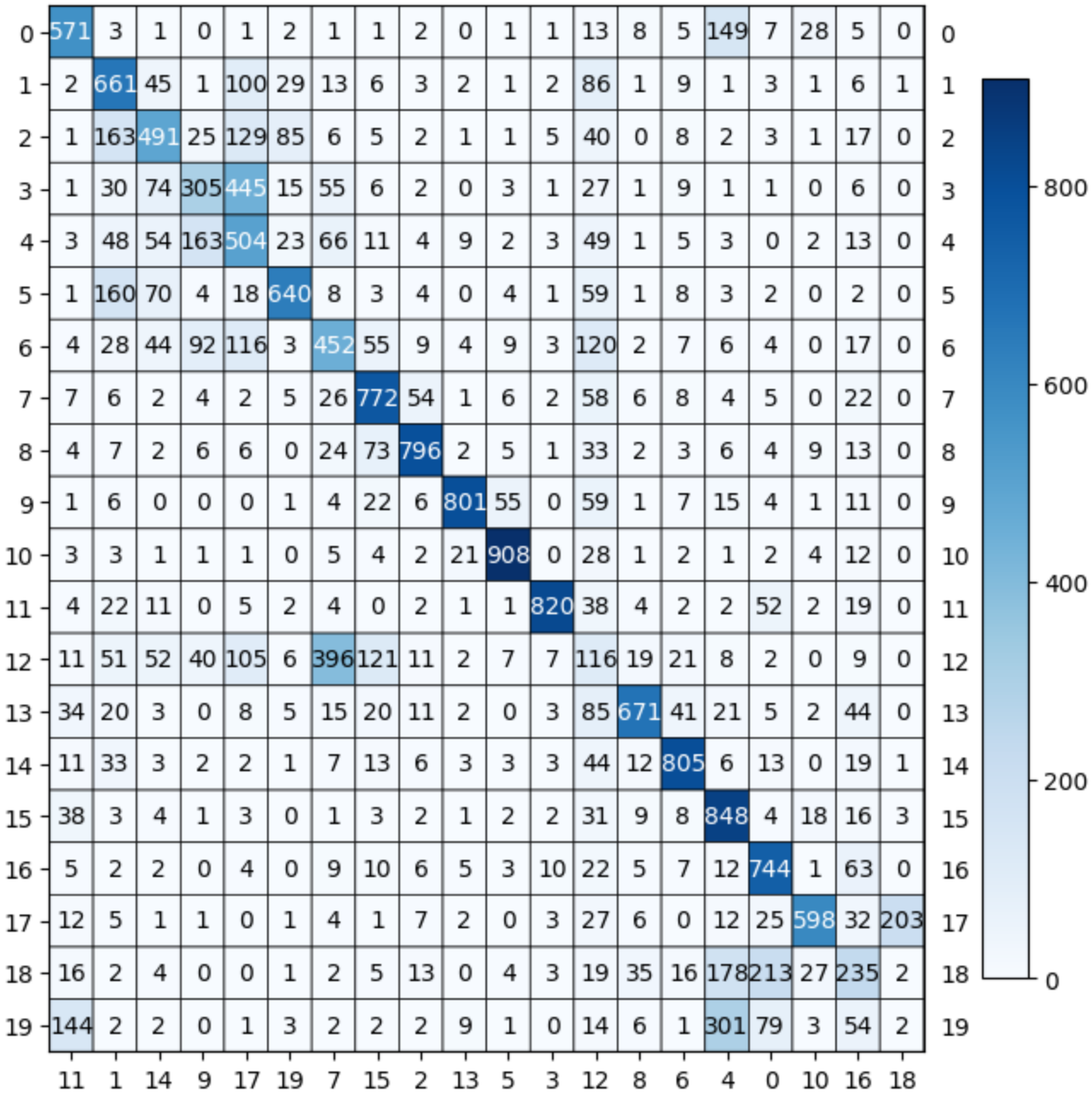
n_componets: 20
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.534 ± 0.000
Completeness: 0.304 ± 0.000
V-measure: 0.387 ± 0.000
Adjusted Rand-Index: 0.205 ± 0.000
Adjusted_mutual_info_score: 0.387 ± 0.000



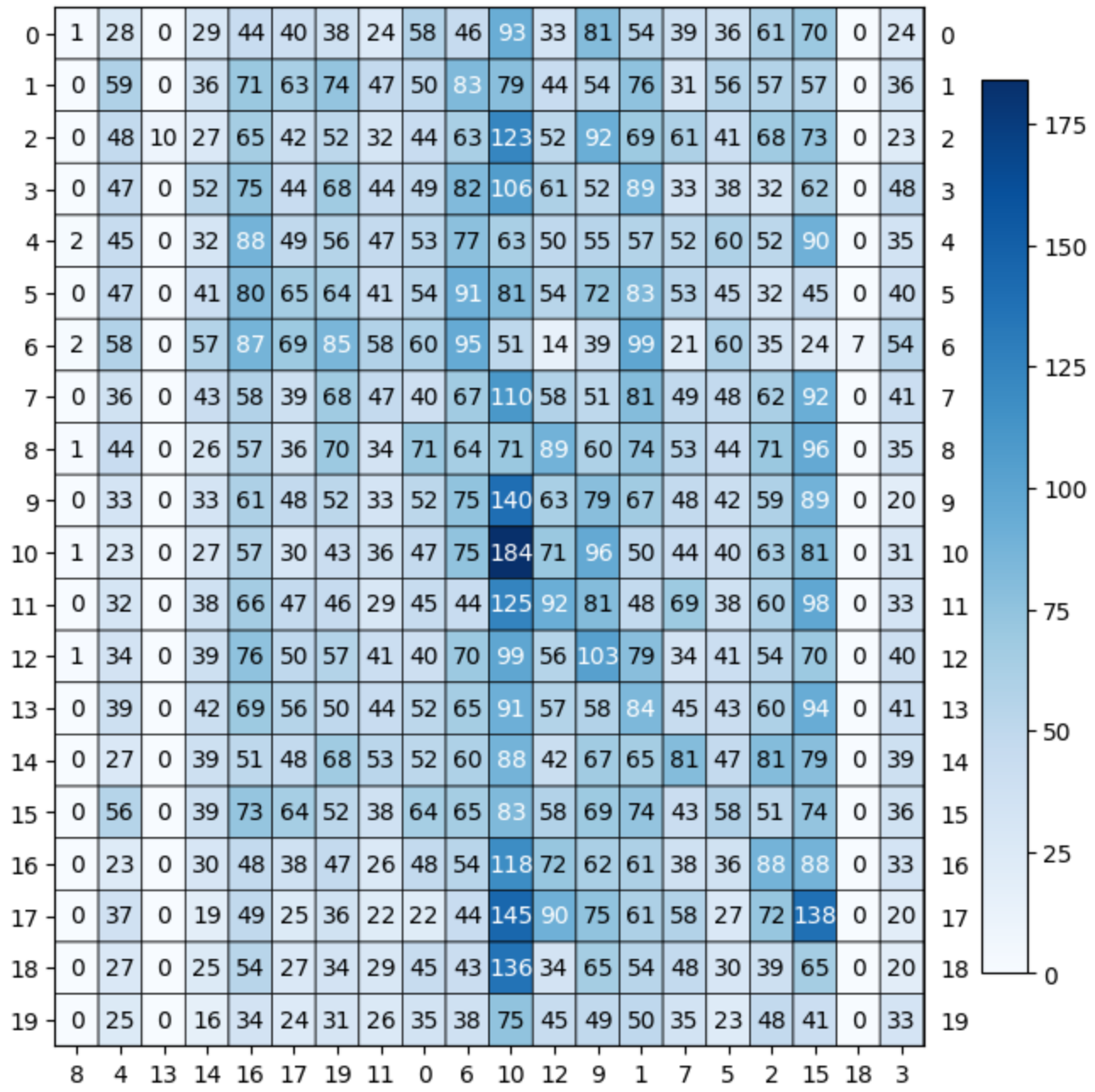

```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.008 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.006 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.005 ± 0.000
```



n_componets: 200
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.534 ± 0.000
Completeness: 0.292 ± 0.000
V-measure: 0.377 ± 0.000
Adjusted Rand-Index: 0.184 ± 0.000
Adjusted_mutual_info_score: 0.377 ± 0.000




```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.009 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.006 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.005 ± 0.000
```




```
best r for cosine is 20, the average score is: 0.363
best r for euclidean is 5, the average score is: 0.006
```

Question12 and Question 13 is stated on our report

Question14

In [49]:

```
from sklearn.cluster import AgglomerativeClustering
agg_ward = AgglomerativeClustering(n_clusters= 20,linkage='ward')
agg_single = AgglomerativeClustering(n_clusters= 20,linkage='single')

# use the best n_componets for umap
print(f"umap use cosine n_componets = {best_cos_r} and ward agglomerativeClustering")
agg_ward_ = agg_ward.fit(best_cos_data)
evaluate(agg_ward_, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")

print(f"umap use euclidean n_componets = {best_euc_r} and ward agglomerativeClustering")
agg_ward_ = agg_ward.fit(best_euc_data)
evaluate(agg_ward_, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")

print(f"umap use cosine n_componets = {best_cos_r} and single agglomerativeClustering")
agg_single_ = agg_single.fit(best_cos_data)
```

```
evaluate(agg_single_, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")

print(f"umap use euclidean n_componets = {best_euc_r} and single agglomerativeClustering
agg_single_ = agg_single.fit(best_euc_data)
evaluate(agg_single_, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
```

```
umap use cosine n_componets = 20 and ward agglomerativeClustering
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.538 ± 0.000
Completeness: 0.299 ± 0.000
V-measure: 0.384 ± 0.000
Adjusted Rand-Index: 0.197 ± 0.000
Adjusted_mutual_info_score: 0.383 ± 0.000
umap use euclidean n_componets = 5 and ward agglomerativeClustering
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.010 ± 0.000
Completeness: 0.005 ± 0.000
V-measure: 0.007 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.006 ± 0.000
umap use cosine n_componets = 20 and single agglomerativeClustering
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.021 ± 0.000
Completeness: 0.182 ± 0.000
V-measure: 0.037 ± 0.000
Adjusted Rand-Index: 0.002 ± 0.000
Adjusted_mutual_info_score: 0.035 ± 0.000
umap use euclidean n_componets = 5 and single agglomerativeClustering
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.008 ± 0.000
Completeness: 0.165 ± 0.000
V-measure: 0.016 ± 0.000
Adjusted Rand-Index: -0.000 ± 0.000
Adjusted_mutual_info_score: 0.013 ± 0.000
```

Question15

In [51]:
```
from sklearn.cluster import KMeans, AgglomerativeClustering, DBSCAN
import hdbscan
hdbscan_model = hdbscan.HDBSCAN(min_cluster_size= 100)
hdb_ = hdbscan_model.fit(best_cos_data)
evaluate(hdb_, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")
```

```
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.419 ± 0.000
Completeness: 0.332 ± 0.000
V-measure: 0.370 ± 0.000
Adjusted Rand-Index: 0.210 ± 0.000
Adjusted_mutual_info_score: 0.370 ± 0.000
```

In [52]:
```
min_cluster = [20,100,200]
clu_results = defaultdict(list)

best_clu = 0
best_clu_r = 0

for r in min_cluster:
    print('min_clusters: ' + str(r))

    hdbscan_model = hdbscan.HDBSCAN(min_cluster_size= r)
    hdb_label= hdbscan_model.fit_predict(best_cos_data)
    clu_results["Homogeneity"].append(metrics.homogeneity_score(Y_binary, hdb_label))
    clu_results["Completeness"].append(metrics.completeness_score(Y_binary, hdb_label))
    clu_results["V-measure"].append(metrics.v_measure_score(Y_binary, hdb_label))
    clu_results["Adjusted Rand-Index"].append(metrics.adjusted_rand_score(Y_binary, hdb_
```

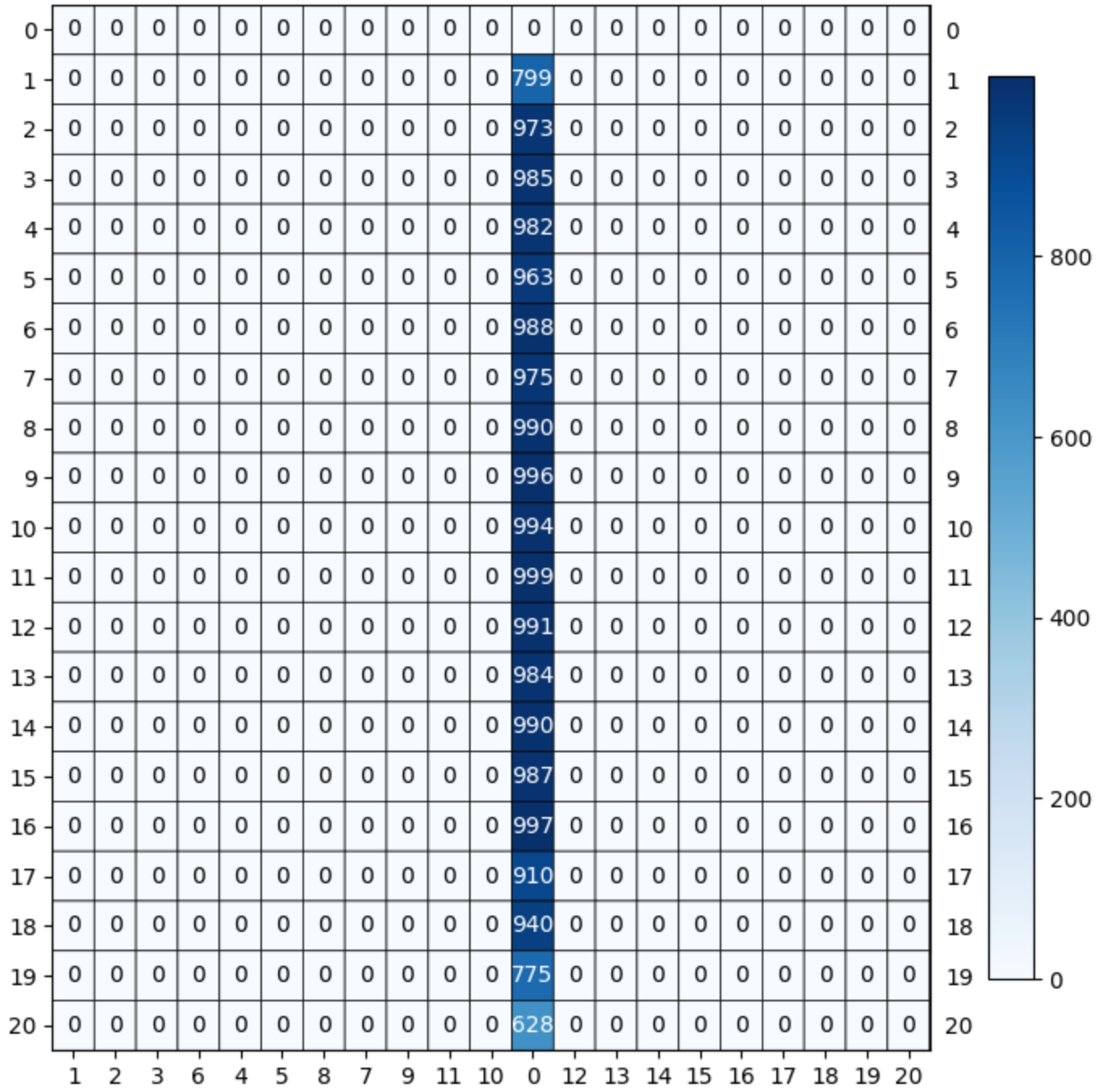
```
    clu_results["Adjusted_mutual_info_score"].append(adjusted_mutual_info_score(Y_binary

    avg_clu_score = (clu_results["Homogeneity"][-1] + clu_results["Completeness"][-1] \
    + clu_results["V-measure"][-1] + clu_results["Adjusted Rand-Index"][-1]  \
    + clu_results["Adjusted_mutual_info_score"][-1]) / 5.0

    evaluate(hdbscan_model, data_tf_idf3, Y_binary, name="KMeans\non tf-idf vectors")

    if(avg_clu_score > best_clu):
        best_clu = avg_clu_score
        best_clu_r = r

print(f"best min_clusters is {best_clu_r}, the average score is: {best_clu:.3f}")
```

```
min_clusters: 20
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.000 ± 0.000
Completeness: 0.038 ± 0.000
V-measure: 0.001 ± 0.000
Adjusted Rand-Index: -0.000 ± 0.000
Adjusted_mutual_info_score: 0.000 ± 0.000
min_clusters: 100
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.419 ± 0.000
Completeness: 0.332 ± 0.000
V-measure: 0.370 ± 0.000
Adjusted Rand-Index: 0.210 ± 0.000
Adjusted_mutual_info_score: 0.370 ± 0.000
min_clusters: 200
clustering done in 0.00 ± 0.00 s
Homogeneity: 0.413 ± 0.000
Completeness: 0.327 ± 0.000
V-measure: 0.365 ± 0.000
Adjusted Rand-Index: 0.210 ± 0.000
Adjusted_mutual_info_score: 0.364 ± 0.000
best min_clusters is 100, the average score is: 0.340
```

Question16

In [8]:

```
hdbscan_best = hdbscan.HDBSCAN(min_cluster_size= best_clu_r)
hdb_data = hdbscan_best.fit(data_tf_idf3)
cm = confusion_matrix(dataset.target, hdbscan_best.labels_)
rows, cols = linear_sum_assignment(cm, maximize=True)
plot_mat(cm[rows[:, np.newaxis], cols], xticklabels=cols, yticklabels=rows)
```



Question17

In [ ]:
```
import pickle
## dumping umap
for r in [5, 20, 200]:
  file = open(f'umap_{r}.obj', 'wb')
  umap_ = umap.UMAP(n_components=r, metric='cosine')
  X_svd = umap_.fit_transform(data_tf_idf3)
  X_svd = np.nan_to_num(X_svd)
  pickle.dump(X_svd, file)
  file.close()
```

In [ ]:
```
import pickle
## dumping svd
for r in [5, 20, 200]:
  file = open(f'svd_{r}.obj', 'wb')
  svd_ = TruncatedSVD(n_components=r)
  X_svd = svd_.fit_transform(data_tf_idf3)
  X_svd = np.nan_to_num(X_svd)
```

```
  pickle.dump(X_svd, file)
  file.close()
```

In [ ]:
```
import pickle
## dumping nmf
for r in [5, 20, 200]:
  file = open(f'nmf_{r}.obj', 'wb')
  nmf_ = NMF(n_components=r)
  X_svd = nmf_.fit_transform(data_tf_idf3)
  X_svd = np.nan_to_num(X_svd)
  pickle.dump(X_svd, file)
  file.close()
```

In [ ]:
```
#1 Using k-means without dimensinality reduction [k=10,20,50]
best_k = 0
best_result = 0
for k in [10,20,50]:
  km_ = KMeans(n_clusters=k,random_state=0,max_iter=1000,n_init=30)
  y_pred = km_.fit_predict(data_tf_idf3)
  result = metrics.adjusted_rand_score(Y_binary,y_pred)
  if result > best_result:
    best_k = k
    best_result = result
  print(f"Without Dimensionality Reduction, Clustering Method: K-means, k = {k} ", resul

print(f"Without Dimensionality Reduction, Clustering Method: K-means, best_k = {best_k}
```

```
Without Dimensionality Reduction, Clustering Method: K-means, k = 10  0.1229848087194413
5
Without Dimensionality Reduction, Clustering Method: K-means, k = 20  0.0765714911014780
5
Without Dimensionality Reduction, Clustering Method: K-means, k = 50  0.0583233930657275
56
Without Dimensionality Reduction, Clustering Method: K-means, best_k = 10 , best_result
= 0.12298480871944135
```

In [ ]:
```
#2 Using k-means with SVD reduction [k=10,20,50] [r=5,20,200]
best_r = 0
best_k = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'svd_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
  # svd_ = TruncatedSVD(n_components=r)
  # X_svd = svd_.fit_transform(data_tf_idf3)
  for k in [10,20,50]:
    km_ = KMeans(n_clusters=k,random_state=0,max_iter=1000,n_init=30)
    y_pred = km_.fit_predict(X_svd)
    result = metrics.adjusted_rand_score(Y_binary,y_pred)
    if result > best_result:
      best_r = r
      best_k = k
      best_result = result
    print(f"With SVD Dimensionality Reduction r = {r}, Clustering Method: K-means, k = {

print(f"With SVD Dimensionality Reduction best_r = {best_r}, Clustering Method: K-means,
```

```
With SVD Dimensionality Reduction r = 5, Clustering Method: K-means, k = 10  0.114996156
04359621
With SVD Dimensionality Reduction r = 5, Clustering Method: K-means, k = 20  0.090414215
13942735
With SVD Dimensionality Reduction r = 5, Clustering Method: K-means, k = 50  0.048143867
89830855
With SVD Dimensionality Reduction r = 20, Clustering Method: K-means, k = 10  0.10296792
```

```
705153543
With SVD Dimensionality Reduction r = 20, Clustering Method: K-means, k = 20  0.07229439
755949905
With SVD Dimensionality Reduction r = 20, Clustering Method: K-means, k = 50  0.05645572
2750361634
With SVD Dimensionality Reduction r = 200, Clustering Method: K-means, k = 10  0.1242324
0533402541
With SVD Dimensionality Reduction r = 200, Clustering Method: K-means, k = 20  0.0851988
0201681075
With SVD Dimensionality Reduction r = 200, Clustering Method: K-means, k = 50  0.0558718
07089970034
With SVD Dimensionality Reduction best_r = 200, Clustering Method: K-means, best_k = 10
, best_result = 0.12423240533402541
```

In [ ]:
```
#3 Using k-means with NMF reduction [k=10,20,50] [r=5,20,200]

best_r = 0
best_k = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'nmf_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
  # nmf_ = NMF(n_components=r)
  # X_nmf = nmf_.fit_transform(data_tf_idf3)
  for k in [10,20,50]:
    km_ = KMeans(n_clusters=k,random_state=0,max_iter=1000,n_init=30)
    y_pred = km_.fit_predict(X_svd)
    result = metrics.adjusted_rand_score(Y_binary,y_pred)
    if result > best_result:
      best_r = r
      best_k = k
      best_result = result
    print(f"With NMF Dimensionality Reduction r = {r}, Clustering Method: K-means, k = {

print(f"With NMF Dimensionality Reduction best_r = {best_r}, Clustering Method: K-means,
```

```
With NMF Dimensionality Reduction r = 5, Clustering Method: K-means, k = 10  0.076690213
27115816
With NMF Dimensionality Reduction r = 5, Clustering Method: K-means, k = 20  0.066714800
98168675
With NMF Dimensionality Reduction r = 5, Clustering Method: K-means, k = 50  0.042497918
64312421
With NMF Dimensionality Reduction r = 20, Clustering Method: K-means, k = 10  0.06342211
981938245
With NMF Dimensionality Reduction r = 20, Clustering Method: K-means, k = 20  0.06558078
90543427
With NMF Dimensionality Reduction r = 20, Clustering Method: K-means, k = 50  0.05170191
2816332816
With NMF Dimensionality Reduction r = 200, Clustering Method: K-means, k = 10  0.0027881
39578746605
With NMF Dimensionality Reduction r = 200, Clustering Method: K-means, k = 20  0.0151440
1931605396
With NMF Dimensionality Reduction r = 200, Clustering Method: K-means, k = 50  0.0195490
3417500828
With NMF Dimensionality Reduction best_r = 5, Clustering Method: K-means, best_k = 10 ,
best_result = 0.07669021327115816
```

In [ ]:
```
#4 Using k-means with UMAP reduction [k=10,20,50] [r=5,20,200]

best_r = 0
best_k = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'umap_{r}.obj', 'rb')
  X_svd = pickle.load(file)
```

```
  file.close()
  # umap_ = umap.UMAP(n_components=r, metric='cosine')
  # X_svd = umap_.fit_transform(data_tf_idf3)
  for k in [10,20,50]:
    km_ = KMeans(n_clusters=k,random_state=0,max_iter=1000,n_init=30)
    y_pred = km_.fit_predict(X_svd)
    result = metrics.adjusted_rand_score(Y_binary,y_pred)
    if result > best_result:
      best_r = r
      best_k = k
      best_result = result
    print(f"With UMAP Dimensionality Reduction r = {r}, Clustering Method: K-means, k =

print(f"With UMAP Dimensionality Reduction best_r = {best_r}, Clustering Method: K-means
```

```
With UMAP Dimensionality Reduction r = 5, Clustering Method: K-means, k = 10  0.22183715
096452636
With UMAP Dimensionality Reduction r = 5, Clustering Method: K-means, k = 20  0.20691564
611526206
With UMAP Dimensionality Reduction r = 5, Clustering Method: K-means, k = 50  0.12171406
066731445
With UMAP Dimensionality Reduction r = 20, Clustering Method: K-means, k = 10  0.2271224
74521217
With UMAP Dimensionality Reduction r = 20, Clustering Method: K-means, k = 20  0.2239373
9514220942
With UMAP Dimensionality Reduction r = 20, Clustering Method: K-means, k = 50  0.1405408
861078544
With UMAP Dimensionality Reduction r = 200, Clustering Method: K-means, k = 10  0.241580
88102041522
With UMAP Dimensionality Reduction r = 200, Clustering Method: K-means, k = 20  0.242556
63256252014
With UMAP Dimensionality Reduction r = 200, Clustering Method: K-means, k = 50  0.130550
04081977653
With UMAP Dimensionality Reduction best_r = 200, Clustering Method: K-means, best_k = 20
, best_result = 0.24255663256252014
```

In [ ]:
```
#5 Using AgglomerativeClustering without dimensinality reduction [k=20]
# causing too much time, not run
from sklearn.cluster import AgglomerativeClustering
agg_ward = AgglomerativeClustering(n_clusters=20,linkage='ward')
y_pred = agg_ward.fit_predict(data_tf_idf3.toarray())
result = metrics.adjusted_rand_score(Y_binary,y_pred)
print(f"Without Dimensionality Reduction, Clustering Method: K-means, k = 20 ", result)
```

In [ ]:
```
#6 Using AgglomerativeClustering with SVD reduction [r=5,20,200]
from sklearn.cluster import AgglomerativeClustering
best_r = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'svd_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
  # svd_ = TruncatedSVD(n_components=r)
  # X_svd = svd_.fit_transform(data_tf_idf3)
  agg_ward = AgglomerativeClustering(n_clusters=20,linkage='ward')
  y_pred = agg_ward.fit_predict(X_svd)
  result = metrics.adjusted_rand_score(Y_binary,y_pred)
  if result > best_result:
    best_r = r
    best_result = result
  print(f"With SVD Dimensionality Reduction r = {r}, Clustering Method: AgglomerativeClu

print(f"With SVD Dimensionality Reduction best_r = {best_r}, Clustering Method: Agglomer
```

```
With SVD Dimensionality Reduction r = 5, Clustering Method: AgglomerativeClustering, r =
5  0.09203719648907432
```

```
With SVD Dimensionality Reduction r = 20, Clustering Method: AgglomerativeClustering, r
= 20  0.09274187811699038
With SVD Dimensionality Reduction r = 200, Clustering Method: AgglomerativeClustering, r
= 200  0.09341058654516633
With SVD Dimensionality Reduction best_r = 200, Clustering Method: AgglomerativeClusteri
ng, best_result = 0.09341058654516633
```

In [ ]:
```
#7 Using AgglomerativeClustering with NMF reduction [r=5,20,200]
from sklearn.cluster import AgglomerativeClustering
best_r = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'nmf_{r}.obj', 'rb')
  X_nmf = pickle.load(file)
  file.close()
  # nmf_ = NMF(n_components=r)
  # X_nmf = nmf_.fit_transform(data_tf_idf3)
  agg_ward = AgglomerativeClustering(n_clusters=20,linkage='ward')
  y_pred = agg_ward.fit_predict(X_nmf)
  result = metrics.adjusted_rand_score(Y_binary,y_pred)
  if result > best_result:
    best_r = r
    best_result = result
  print(f"With NMF Dimensionality Reduction r = {r}, Clustering Method: AgglomerativeClu

print(f"With NMF Dimensionality Reduction best_r = {best_r}, Clustering Method: Agglomer
```

```
With NMF Dimensionality Reduction r = 5, Clustering Method: AgglomerativeClustering, r =
5  0.07315663293267735
With NMF Dimensionality Reduction r = 20, Clustering Method: AgglomerativeClustering, r
= 20  0.09652612630921366
With NMF Dimensionality Reduction r = 200, Clustering Method: AgglomerativeClustering, r
= 200  0.008523940255761885
With NMF Dimensionality Reduction best_r = 20, Clustering Method: AgglomerativeClusterin
g, best_result = 0.09652612630921366
```

In [ ]:
```
#8 Using AgglomerativeClustering with UMAP reduction [r=5,20,200]
from sklearn.cluster import AgglomerativeClustering
best_r = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'umap_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
  # umap_ = umap.UMAP(n_components=r, metric='cosine')
  # X_svd = umap_.fit_transform(data_tf_idf3)
  agg_ward = AgglomerativeClustering(n_clusters=20,linkage='ward')
  y_pred = agg_ward.fit_predict(X_svd)
  result = metrics.adjusted_rand_score(Y_binary,y_pred)
  if result > best_result:
    best_r = r
    best_result = result
  print(f"With UMAP Dimensionality Reduction r = {r}, Clustering Method: AgglomerativeCl
print(f"With UMAP Dimensionality Reduction best_r = {best_r}, Clustering Method: Agglome
```

```
With UMAP Dimensionality Reduction r = 5, Clustering Method: AgglomerativeClustering, r
= 5  0.21456619768075202
With UMAP Dimensionality Reduction r = 20, Clustering Method: AgglomerativeClustering, r
= 20  0.22808879369491192
With UMAP Dimensionality Reduction r = 200, Clustering Method: AgglomerativeClustering,
r = 200  0.2242264674981165
With UMAP Dimensionality Reduction best_r = 20, Clustering Method: AgglomerativeClusteri
ng, best_result = 0.22808879369491192
```

In [7]:
```
import hdbscan
min_cluster_size_list = [100,200]
```

```
def hdbscan_compare(X_umap,label,min_cluster_size_list):
  for mcs in min_cluster_size_list:
    hdbscan_model = hdbscan.HDBSCAN(min_cluster_size=mcs)
    y_pred_hdbscan = hdbscan_model.fit_predict(X_umap)

    homo = metrics.homogeneity_score(label,y_pred_hdbscan)
    comp = metrics.completeness_score(label,y_pred_hdbscan)
    v = metrics.v_measure_score(label,y_pred_hdbscan)
    adj = metrics.adjusted_rand_score(label,y_pred_hdbscan)
    sic = adjusted_mutual_info_score(label,y_pred_hdbscan)

    mean_ = (homo + comp + v + adj + sic) / 5.0

    print(f"HDBSCAN min_cluster_size={mcs},homogeneity_score={homo:.3f},Completeness={co
    return mean_
```

In [5]:
```
#9 Using HDBSCAN without dimensinality reduction [min_cluster=100,200]
hdbscan_compare(data_tf_idf3,Y_binary,min_cluster_size_list)
```

```
HDBSCAN min_cluster_size=100,homogeneity_score=0.000,Completeness=1.000,V-measure=0.000,
Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 0.19999999999999984
HDBSCAN min_cluster_size=200,homogeneity_score=0.000,Completeness=1.000,V-measure=0.000,
Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 0.19999999999999984
```

In [2]:
```
#10 Using HDBSCAN with SVD reduction [min_cluster=100,200] [r=5,20,200]
# not run cause Number of labels is 1. Valid values are 2 to n_samples - 1 (inclusive)
best_r = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'svd_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
  # svd_ = TruncatedSVD(n_components=r)
  # X_svd = svd_.fit_transform(data_tf_idf3)
  result = hdbscan_compare(X_svd,Y_binary,min_cluster_size_list)
  if result > best_result:
    best_r = r
    best_result = result
  print(f"With SVD Dimensionality Reduction r = {r}, Clustering Method: HDBSCAN, r = {r}
print(f"With SVD Dimensionality Reduction best_r = {best_r}, Clustering Method: HDBSCAN,
```

```
HDBSCAN min_cluster_size=100,homogeneity_score=0.000,Completeness=1.000,V-measure=0.000,
Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 With SVD Dimensionality Reduction r = 5, Clustering Method: HDBSCAN, r = 5  0.199999999
99999984
 HDBSCAN min_cluster_size=100,homogeneity_score=0.000,Completeness=1.000,V-measure=0.00
0,Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 With SVD Dimensionality Reduction r = 20, Clustering Method: HDBSCAN, r = 20  0.1999999
9999999984
 HDBSCAN min_cluster_size=100,homogeneity_score=0.000,Completeness=1.000,V-measure=0.00
0,Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 With SVD Dimensionality Reduction r = 200, Clustering Method: HDBSCAN, r = 200  0.19999
999999999984
 With SVD Dimensionality Reduction best_r = 5, Clustering Method: HDBSCAN, best_result =
0.19999999999999984
```

In [4]:
```
#11 Using HDBSCAN with NMF reduction [min_cluster=100,200] [r=5,20,200]
best_r = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'nmf_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
```

```
  # nmf_ = NMF(n_components=r)
  # X_nmf = nmf_.fit_transform(data_tf_idf3)
  result = hdbscan_compare(X_svd,Y_binary,min_cluster_size_list)
  if result > best_result:
    best_r = r
    best_result = result
  print(f"With NMF Dimensionality Reduction r = {r}, Clustering Method: HDBSCAN, r = {r}
print(f"With NMF Dimensionality Reduction best_r = {best_r}, Clustering Method: HDBSCAN,
```

```
HDBSCAN min_cluster_size=100,homogeneity_score=0.049,Completeness=0.122,V-measure=0.070,
Adjusted Rand-Index=0.040, Adjusted_mutual_info_score=0.070, mean=0.070
 With NMF Dimensionality Reduction r = 5, Clustering Method: HDBSCAN, r = 5  0.070054563
18209
 HDBSCAN min_cluster_size=100,homogeneity_score=0.000,Completeness=1.000,V-measure=0.00
0,Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 With NMF Dimensionality Reduction r = 20, Clustering Method: HDBSCAN, r = 20  0.1999999
9999999984
 HDBSCAN min_cluster_size=100,homogeneity_score=0.000,Completeness=1.000,V-measure=0.00
0,Adjusted Rand-Index=0.000, Adjusted_mutual_info_score=-0.000, mean=0.200
 With NMF Dimensionality Reduction r = 200, Clustering Method: HDBSCAN, r = 200  0.19999
999999999984
 With NMF Dimensionality Reduction best_r = 20, Clustering Method: HDBSCAN, best_result
= 0.19999999999999984
```

In [3]:
```
#12 Using HDBSCAN with UMAP reduction [min_cluster=100,200] [r=5,20,200]
best_r = 0
best_result = 0
for r in [5,20,200]:
  file = open(f'umap_{r}.obj', 'rb')
  X_svd = pickle.load(file)
  file.close()
  # umap_ = umap.UMAP(n_components=r, metric='cosine')
  # X_svd = umap_.fit_transform(data_tf_idf3)
  result = hdbscan_compare(X_svd,Y_binary,min_cluster_size_list)
  if result > best_result:
    best_r = r
    best_result = result
  print(f"With UMAP Dimensionality Reduction r = {r}, Clustering Method: HDBSCAN, r = {r
print(f"With UMAP Dimensionality Reduction best_r = {best_r}, Clustering Method: HDBSCAN
```

```
HDBSCAN min_cluster_size=100,homogeneity_score=0.430,Completeness=0.335,V-measure=0.376,
Adjusted Rand-Index=0.229, Adjusted_mutual_info_score=0.376, mean=0.349
 With UMAP Dimensionality Reduction r = 5, Clustering Method: HDBSCAN, r = 5  0.34924730
58590584
 HDBSCAN min_cluster_size=100,homogeneity_score=0.414,Completeness=0.334,V-measure=0.37
0,Adjusted Rand-Index=0.231, Adjusted_mutual_info_score=0.369, mean=0.344
 With UMAP Dimensionality Reduction r = 20, Clustering Method: HDBSCAN, r = 20  0.343515
83450504447
 HDBSCAN min_cluster_size=100,homogeneity_score=0.411,Completeness=0.322,V-measure=0.36
1,Adjusted Rand-Index=0.195, Adjusted_mutual_info_score=0.361, mean=0.330
 With UMAP Dimensionality Reduction r = 200, Clustering Method: HDBSCAN, r = 200  0.3299
164275939991
 With UMAP Dimensionality Reduction best_r = 5, Clustering Method: HDBSCAN, best_result
= 0.3492473058590584
```

Question19

Question20,21,22 are stated on Our Report

In [6]:
```
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
            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(224),
                                                                 transforms.CenterCrop(2
                                                                 transforms.ToTensor(),
                                                                 transforms.Normalize(me
    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)
```

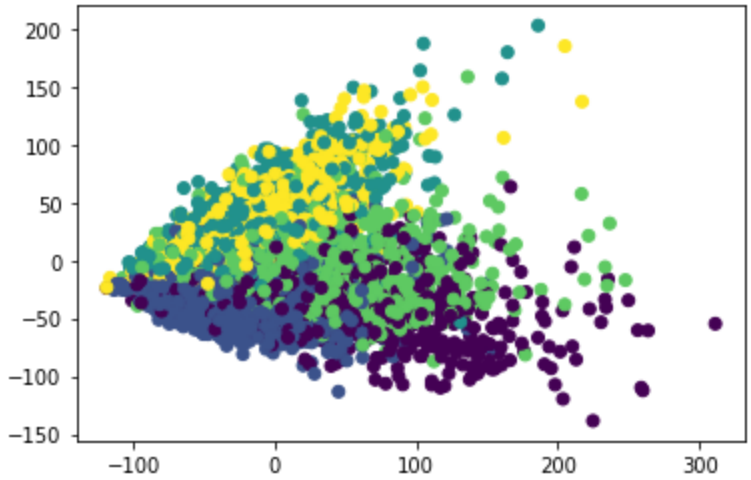
```
Downloading: "https://github.com/pytorch/vision/zipball/v0.10.0" to /root/.cache/torch/h
ub/v0.10.0.zip
Downloading: "https://download.pytorch.org/models/vgg16-397923af.pth" to /root/.cache/to
rch/hub/checkpoints/vgg16-397923af.pth
HBox(children=(HTML(value=''), FloatProgress(value=0.0, max=553433881.0), HTML(value
='')))

100%|██████████| 58/58 [00:42<00:00,  1.35it/s]
```

In [7]:
```
print(f_all.shape, y_all.shape)
num_features = f_all.shape[1]
```

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

In [8]:
```
f_pca = PCA(n_components=2).fit_transform(f_all)
plt.scatter(*f_pca.T, c=y_all)
```

Out[8]:
```
<matplotlib.collections.PathCollection at 0x7f58ac8b13d0>
```

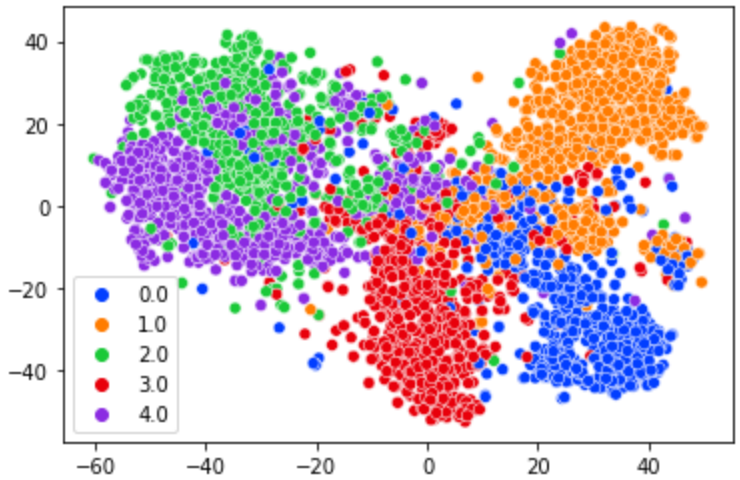


Question23

In [ ]:
```
from sklearn.manifold import TSNE
import seaborn as sns
f_tSNE = TSNE(n_components=2, learning_rate='auto',init='random').fit_transform(f_all)
palette = sns.color_palette("bright", 5)
sns.scatterplot(f_tSNE[:,0], f_tSNE[:,1], hue=y_all, legend='full', palette=palette)
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass th
e following variables as keyword args: x, y. From version 0.12, the only valid positiona
l argument will be `data`, and passing other arguments without an explicit keyword will
result in an error or misinterpretation.
  FutureWarning
```

Out[ ]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7f05770a0310>
```



Question24

In [10]:
```
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.n_com

    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 [8]:

```
#Using k-means without dimensinality reduction
km_5 = KMeans(n_clusters=5,random_state=0,max_iter=1000,n_init=30)
y_pred = km_5.fit_predict(f_all)
result = metrics.adjusted_rand_score(y_all,y_pred)
print("Without Dimensionality Reduction, Clustering Method: K-means", result)
```

```
Without Dimensionality Reduction, Clustering Method: K-means 0.19178888830300925
```

In [9]:

```
#Using k-means with SVD dimension reduction
```

```
km_5 = KMeans(n_clusters=5,random_state=0,max_iter=1000,n_init=30)
svd_ = TruncatedSVD(n_components=50)
X_svd = svd_.fit_transform(f_all)
y_pred = km_5.fit_predict(X_svd)

result = metrics.adjusted_rand_score(y_all,y_pred)
print("With SVD Dimensionality Reduction, Clustering Method: K-means", result)
```

```
With SVD Dimensionality Reduction, Clustering Method: K-means 0.19203019903753804
```

In [10]:
```
#Using k-means with umap dimension reduction
km_5 = KMeans(n_clusters=5,random_state=0,max_iter=1000,n_init=30)
umap_ = umap.UMAP(n_components=50, metric='cosine')
X_umap = umap_.fit_transform(f_all)
y_pred = km_5.fit_predict(X_umap)

result = metrics.adjusted_rand_score(y_all,y_pred)
print("With UMAP Dimensionality Reduction, Clustering Method: K-means", result)
```

```
With UMAP Dimensionality Reduction, Clustering Method: K-means 0.4668755531759629
```

In [11]:
```
#Using k-means with Autoencoder dimension reduction
km_5 = KMeans(n_clusters=5,random_state=0,max_iter=1000,n_init=30)
auto_ = Autoencoder(50)
X_auto = auto_.fit_transform(f_all)
y_pred = km_5.fit_predict(X_auto)

result = metrics.adjusted_rand_score(y_all,y_pred)
print("With Autoencoder Dimensionality Reduction, Clustering Method: K-means", result)
```

```
100%|██████████| 100/100 [00:25<00:00,  3.92it/s]
With Autoencoder Dimensionality Reduction, Clustering Method: K-means 0.2360001210989823
3
```

In [12]:
```
from sklearn.cluster import AgglomerativeClustering
#Using AgglomerativeClustering without dimensinality reduction
agg_ward = AgglomerativeClustering(n_clusters=5,linkage='ward')
y_pred = agg_ward.fit_predict(f_all)
result = metrics.adjusted_rand_score(y_all,y_pred)
print("Without Dimensionality Reduction, Clustering Method: AgglomerativeClustering", re
```

```
Without Dimensionality Reduction, Clustering Method: AgglomerativeClustering 0.188552782
51971858
```

In [24]:
```
from sklearn.cluster import AgglomerativeClustering
#Using AgglomerativeClustering with SVD dimension reduction
agg_ward = AgglomerativeClustering(n_clusters=5,linkage='ward')
svd_ = TruncatedSVD(n_components=50)
X_svd = svd_.fit_transform(f_all)
y_pred = agg_ward.fit_predict(X_svd)
result = metrics.adjusted_rand_score(y_all,y_pred)
print("with SVD dimension reduction, Clustering Method: AgglomerativeClustering", result
```

```
with SVD dimension reduction, Clustering Method: AgglomerativeClustering 0.2692890655209
4006
```

In [23]:
```
from sklearn.cluster import AgglomerativeClustering
#Using AgglomerativeClustering with umap dimension reduction
agg_ward = AgglomerativeClustering(n_clusters=5,linkage='ward')
umap_ = umap.UMAP(n_components=50, metric='cosine')
X_umap = umap_.fit_transform(f_all)
y_pred = agg_ward.fit_predict(X_umap)
result = metrics.adjusted_rand_score(y_all,y_pred)
print("with UMAP dimension reduction, Clustering Method: AgglomerativeClustering", resul
```

```
with UMAP dimension reduction, Clustering Method: AgglomerativeClustering 0.468634823586
84355
```

In [22]:
```
from sklearn.cluster import AgglomerativeClustering
#Using AgglomerativeClustering with Autoencoder dimension reduction
agg_ward = AgglomerativeClustering(n_clusters=5,linkage='ward')
auto_ = Autoencoder(50)
X_auto = auto_.fit_transform(f_all)
y_pred = agg_ward.fit_predict(X_auto)
result = metrics.adjusted_rand_score(y_all,y_pred)
print("with Autoencoder dimension reduction, Clustering Method: AgglomerativeClustering"
```

```
100%|██████████| 100/100 [00:22<00:00,  4.48it/s]
with Autoencoder dimension reduction, Clustering Method: AgglomerativeClustering 0.29353
08417813973
```

In [ ]:
```
import hdbscan
min_cluster_size_list = [10,50,100]
min_samples_list = [1,2,3]

def hdbscan_compare(X_umap,label,min_cluster_size_list,min_samples_list):
  for mcs in min_cluster_size_list:
    for ms in min_samples_list:
      hdbscan_model = hdbscan.HDBSCAN(min_cluster_size=mcs,min_samples=ms)
      y_pred_hdbscan = hdbscan_model.fit_predict(X_umap)

      homo = metrics.homogeneity_score(label,y_pred_hdbscan)
      comp = metrics.completeness_score(label,y_pred_hdbscan)
      v = metrics.v_measure_score(label,y_pred_hdbscan)
      adj = metrics.adjusted_rand_score(label,y_pred_hdbscan)
      sic = adjusted_mutual_info_score(label,y_pred_hdbscan)
      mean_ = (homo + comp + v + adj + sic) / 5.0

      print(f"HDBSCAN min_cluster_size={mcs},min_samples={ms},homogeneity_score={homo:.3
```

In [ ]:
```
print("with no dimension reduction, Clustering Method: HDBSCAN")
hdbscan_compare(f_all,y_all,min_cluster_size_list,min_samples_list)
```

```
with no dimension reduction, Clustering Method: HDBSCAN
 HDBSCAN min_cluster_size=10,min_samples=1,homogeneity_score=0.014,Completeness=0.042,V-
measure=0.021,Adjusted Rand-Index=0.015, Silhouette Coefficient=0.174, mean=0.053
 HDBSCAN min_cluster_size=10,min_samples=2,homogeneity_score=0.014,Completeness=0.042,V-
measure=0.021,Adjusted Rand-Index=0.015, Silhouette Coefficient=0.174, mean=0.053
 HDBSCAN min_cluster_size=10,min_samples=3,homogeneity_score=0.021,Completeness=0.058,V-
measure=0.030,Adjusted Rand-Index=0.008, Silhouette Coefficient=-0.076, mean=0.008
```

In [ ]:
```
print("with SVD dimension reduction, Clustering Method: HDBSCAN")
svd_ = TruncatedSVD(n_components=50)
X_svd = svd_.fit_transform(f_all)
hdbscan_compare(X_svd,y_all,min_cluster_size_list,min_samples_list)
```

```
with SVD dimension reduction, Clustering Method: HDBSCAN
 HDBSCAN min_cluster_size=10,min_samples=1,homogeneity_score=0.033,Completeness=0.080,V-
measure=0.047,Adjusted Rand-Index=0.017, Silhouette Coefficient=-0.123, mean=0.011
 HDBSCAN min_cluster_size=10,min_samples=2,homogeneity_score=0.027,Completeness=0.071,V-
measure=0.039,Adjusted Rand-Index=0.010, Silhouette Coefficient=-0.106, mean=0.008
 HDBSCAN min_cluster_size=10,min_samples=3,homogeneity_score=0.026,Completeness=0.064,V-
measure=0.037,Adjusted Rand-Index=0.016, Silhouette Coefficient=-0.061, mean=0.016
```

In [ ]:
```
print("with AutoEncoder dimension reduction, Clustering Method: HDBSCAN")
auto_ = Autoencoder(50)
X_auto = auto_.fit_transform(f_all)
hdbscan_compare(X_auto,y_all,min_cluster_size_list,min_samples_list)
```

```
with AutoEncoder dimension reduction, Clustering Method: HDBSCAN
 HDBSCAN min_cluster_size=10,min_samples=1,homogeneity_score=0.022,Completeness=0.053,V-
measure=0.032,Adjusted Rand-Index=0.030, Silhouette Coefficient=0.043, mean=0.036
 HDBSCAN min_cluster_size=10,min_samples=2,homogeneity_score=0.029,Completeness=0.075,V-
```

```
measure=0.042,Adjusted Rand-Index=0.015, Silhouette Coefficient=-0.123, mean=0.008
 HDBSCAN min_cluster_size=10,min_samples=3,homogeneity_score=0.025,Completeness=0.071,V-
measure=0.037,Adjusted Rand-Index=0.010, Silhouette Coefficient=-0.134, mean=0.002
```

In [ ]:
```
print("with UMAP dimension reduction, Clustering Method: HDBSCAN")
umap_ = umap.UMAP(n_components=50, metric='cosine')
X_umap = umap_.fit_transform(f_all)
hdbscan_compare(X_umap,y_all,min_cluster_size_list,min_samples_list)
```

```
HDBSCAN min_cluster_size=10,min_samples=1,homogeneity_score=0.179,Completeness=0.635,V-m
easure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=10,min_samples=2,homogeneity_score=0.179,Completeness=0.635,V-m
easure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=10,min_samples=3,homogeneity_score=0.179,Completeness=0.635,V-m
easure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=50,min_samples=1,homogeneity_score=0.179,Completeness=0.635,V-m
easure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=50,min_samples=2,homogeneity_score=0.179,Completeness=0.635,V-m
easure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=50,min_samples=3,homogeneity_score=0.179,Completeness=0.635,V-m
easure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=100,min_samples=1,homogeneity_score=0.179,Completeness=0.635,V-
measure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=100,min_samples=2,homogeneity_score=0.179,Completeness=0.635,V-
measure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
HDBSCAN min_cluster_size=100,min_samples=3,homogeneity_score=0.179,Completeness=0.635,V-
measure=0.280,Adjusted Rand-Index=0.095, Silhouette Coefficient=0.549, mean=0.348
```

Question25

In [34]:
```
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')

        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:
                X_ = X_.cuda()
                output = self(X_)
                loss = criterion(output,y_.cuda())
                optimizer.zero_grad()
```

```
                loss.backward()
                optimizer.step()
        return self

    def eval(self, X_test, y_test):
        X_pred = self(torch.tensor(X_test,dtype=torch.float32, device='cuda'))
        logit = X_pred.argmax(dim=1)
        acc = torch.sum(logit == torch.tensor(y_test,dtype=torch.float32, device='cuda')
        with torch.no_grad():
          acc = acc.cpu().numpy()
        return acc
```

In [28]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(f_all, y_all, test_size=0.2, random_
```

In [ ]:
```
model = MLP(4096)
model.train(X_train, y_train)
acc = model.eval(X_test, y_test)
```

In [36]:
```
print(f"the VGG feature accuracy={acc}")
```

```
the VGG feature accuracy=0.9305176734924316
```

In [41]:
```
# Using SVD
svd_ = TruncatedSVD(n_components=50)
X_train_ = svd_.fit_transform(X_train)
X_test_ = svd_.fit_transform(X_test)
model = MLP(50)
model.train(X_train_, y_train)
acc = model.eval(X_test_, y_test)
print(f"the SVD and MLP feature accuracy={acc}")
```

```
100%|██████████| 100/100 [00:06<00:00, 15.85it/s]
the SVD and MLP feature accuracy=0.30381470918655396
```

In [43]:
```
# Using UMAP
umap_ = umap.UMAP(n_components=50, metric='cosine')
X_train_ = umap_.fit_transform(X_train)
X_test_ = umap_.fit_transform(X_test)
model = MLP(50)
model.train(X_train_, y_train)
acc = model.eval(X_test_, y_test)
print(f"the UMAP and MLP feature accuracy={acc}")
```

```
100%|██████████| 100/100 [00:06<00:00, 15.82it/s]
the UMAP and MLP feature accuracy=0.2261580377817154
```

In [44]:
```
# Using Autoencoder
auto_ = Autoencoder(50)
X_train_ = auto_.fit_transform(X_train)
X_test_ = auto_.fit_transform(X_test)
model = MLP(50)
model.train(X_train_, y_train)
acc = model.eval(X_test_, y_test)
print(f"the AutoEncoder and MLP feature accuracy={acc}")
```

```
100%|██████████| 100/100 [00:17<00:00,  5.67it/s]
100%|██████████| 100/100 [00:04<00:00, 21.94it/s]
100%|██████████| 100/100 [00:06<00:00, 15.57it/s]
the AutoEncoder and MLP feature accuracy=0.2261580377817154
```