Homework 2 (MATH 6350)

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Name	Understanding the report	Coding	Interpretation
Thanh Hung Duong	100%	70%	30%
Hsien Hao Hsu	100%	30%	70%

```
# Import libraries
import time as tm
import numpy as np
import pandas as pd
from numpy import linalg as LA
import matplotlib
import matplotlib.pyplot as plt
matplotlib.use('nbagg')
from mpl_toolkits.mplot3d import Axes3D
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn import metrics
from scipy import stats
from sklearn.decomposition import PCA
from sklearn.linear_model import LogisticRegression
%matplotlib inline
```

PART 0: Preliminary treatment of the data set

0.1. Import data from 3 data files

```
start_time=tm.time()
url=('https://raw.githubusercontent.com/duonghung86/hello-world/master/COURIER.csv',
     'https://raw.githubusercontent.com/duonghung86/hello-world/master/CALIBRI.csv',
    'https://raw.githubusercontent.com/duonghung86/hello-world/master/TIMES.csv')
# creat an empty list of data frame
df={} # Data frame contain all data
nof=len(url) # number of input files
font_name=['COURIER','CALIBRI','TIMES']
for i in np.arange(nof):
  df[i] = pd.read_csv(url[i])
  #print('Display first 5 rows of data frame \n',df[i].head(5))
```

0.2. DISCARD the 9 columns listed below : fontVariant, m_label, orientation, m_top, m_left, originalH, originalW, h, w

- KEEP the 3 columns {font, strength, italic}
- KEEP the 400 columns named r0c0, r0c1,r0c2, ... , r19c18, r19c19

```
discard_columns=('fontVariant','m_label','orientation','m_top','m_left','originalH','originalW','h','w')
for j in np.arange(nof):
  for i in np.arange(len(discard_columns)):
    df[j]=df[j].drop(discard_columns[i],1)
  print('Display names of Data frame',font_name[j], 'after discarding \n',df[j].columns)
```

```
Display names of Data frame COURIER after discarding
 Index(['font', 'strength', 'italic', 'r0c0', 'r0c1', 'r0c2', 'r0c3', 'r0c4',
       'r0c5', 'r0c6',
       ...
       'r19c10', 'r19c11', 'r19c12', 'r19c13', 'r19c14', 'r19c15', 'r19c16',
       'r19c17', 'r19c18', 'r19c19'],
      dtype='object', length=403)
Display names of Data frame CALIBRI after discarding
 Index(['font', 'strength', 'italic', 'r0c0', 'r0c1', 'r0c2', 'r0c3', 'r0c4',
       'r0c5', 'r0c6',
       ...
       'r19c10', 'r19c11', 'r19c12', 'r19c13', 'r19c14', 'r19c15', 'r19c16',
       'r19c17', 'r19c18', 'r19c19'],
      dtype='object', length=403)
Display names of Data frame TIMES after discarding
 Index(['font', 'strength', 'italic', 'r0c0', 'r0c1', 'r0c2', 'r0c3', 'r0c4',
       'r0c5', 'r0c6',
       ...
       'r19c10', 'r19c11', 'r19c12', 'r19c13', 'r19c14', 'r19c15', 'r19c16',
       'r19c17', 'r19c18', 'r19c19'],
      dtype='object', length=403)
```

0.3. Define then three CLASSES of images of "normal" characters as follows

- CL1 = all rows of COURIER.csv file for which {row # >1 and strength = 0.4 and italic=0}
- CL2 = all rows of CALIBRI.csv file for which {row # >1 and strength = 0.4 and italic=0}
- CL3 = all rows of TIME.csv file for which {row # >1 and strength = 0.4 and italic=0}

Display their respective sizes n1, n2, n3

```
cl={}
N=0
for j in np.arange(nof):
  length_data=len(df[j])
  cl[j]=df[j][df[j].strength==0.4]
  cl[j]=cl[j][cl[j].italic==0]
  N+=len(cl[j])
  print('Size of CL',j+1,'is',len(cl[j]))
  print('Display first 5 rows of CL',j+1,'\n',cl[j].head(5))
print('Size of full data set DATA is',N)
```

```
Size of CL 1 is 4262
Display first 5 rows of CL 1
      font  strength  italic  r0c0  ...  r19c16  r19c17  r19c18  r19c19
0  COURIER       0.4       0     1  ...       1       1       1       1
1  COURIER       0.4       0     1  ...      34      26      22      22
2  COURIER       0.4       0     1  ...      64      45      30      23
3  COURIER       0.4       0     1  ...       1       1       1       1
4  COURIER       0.4       0   255  ...     255     255      86       1

[5 rows x 403 columns]
Size of CL 2 is 4768
Display first 5 rows of CL 2
      font  strength  italic  r0c0  ...  r19c16  r19c17  r19c18  r19c19
0  CALIBRI       0.4       0     1  ...       1       1       1       1
1  CALIBRI       0.4       0     1  ...       1       1     255     255
2  CALIBRI       0.4       0   255  ...       1       1      97     255
3  CALIBRI       0.4       0     1  ...       1       1       1       1
4  CALIBRI       0.4       0     1  ...       1       1     189     255

[5 rows x 403 columns]
Size of CL 3 is 4805
Display first 5 rows of CL 3
    font  strength  italic  r0c0  r0c1  ...  r19c15  r19c16  r19c17  r19c18  r19c19
0  TIMES       0.4       0     1     1  ...     255     255     255      86       1
1  TIMES       0.4       0     1    47  ...       1       1       1       1       1
2  TIMES       0.4       0   255   255  ...     255     255     255     255     255
3  TIMES       0.4       0     1     1  ...       5       4       4       4       4
4  TIMES       0.4       0     1     8  ...     214     211     204     170     153

[5 rows x 403 columns]
Size of full data set DATA is 13835
```

The full data set (denoted DATA) for the next questions will be the union of the three classes CL1 , CL2, CL3 and hence has size N= n1 +

```
data=pd.concat([cl[0],cl[1],cl[2]])
data_df=data # Data frame of DATA
data=np.array(data.loc[:,'r0c0':'r19c19'].values)
#print('Display first 5 rows of DATA \n',data[:5,:])

end_time=tm.time()
print(' The computing time for the preliminary treatment part is ' , round (end_time-start_time,2), 'second')
```

```
 The computing time for the preliminary treatment part is  4.07 second
```

PART 0

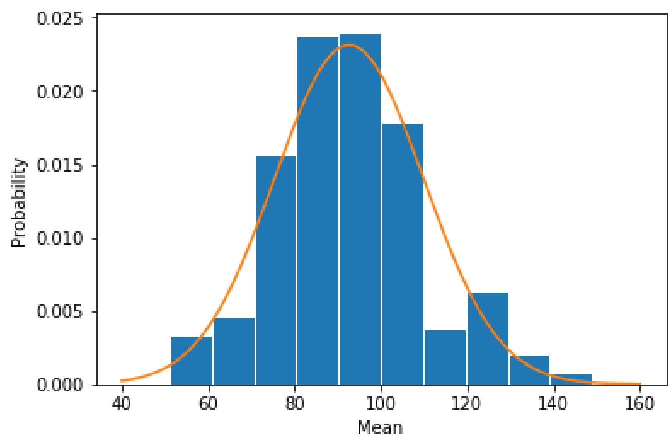
0.1. Compute the means m1 = mean(X1) ....mean(X400) = m400 and the standard deviations s1 = std(X1) s400

```
start_time=tm.time()
nofe=data.shape[1] #Number of features
mean_f=np.empty(nofe) # array contains means of all features
std_f=np.empty(nofe) # array contains standard deviation of all features
for i in np.arange(nofe):
    mean_f[i]=np.mean(data[:,i])
    std_f[i]=np.std(data[:,i])
#print('Display first 5 values of the mean array \n',mean_f[:5])
#print('Display first 5 values of the standard deviation array \n',std_f[:5])
```

0.1.1. Display

- Histogram of the means m1 m2 ... m400

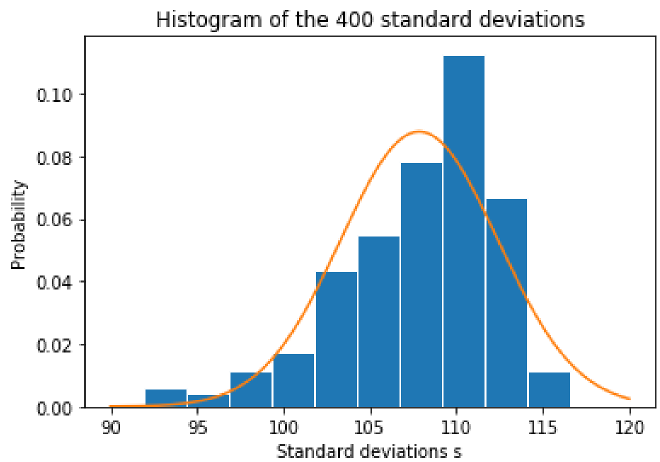
```
# Plot the histogram of the means
plt.hist(mean_f,edgecolor='white',density=True)
#plt.title('Histogram of the 400 means')
plt.xlabel('Mean')
plt.ylabel('Probability')
# Plot the norm distribution
#   Find minimum and maximum of xticks → Location of norm distribution
xt = plt.xticks()[0]
xmin, xmax = min(xt), max(xt)
lnspc = np.linspace(xmin, xmax, len(mean_f))
m, s = stats.norm.fit(mean_f) # get mean and standard deviation
pdf_g = stats.norm.pdf(lnspc, m, s) # get theoretical values in our interval
plt.plot(lnspc, pdf_g, label="Norm")
plt.show()
```



COMMENT: Values of means spreads well from 40 to 160. Their distribution match the norm distrubution closely. Means in the range be highest frequency

- Histogram of the standard deviations s1 s2 .... s400

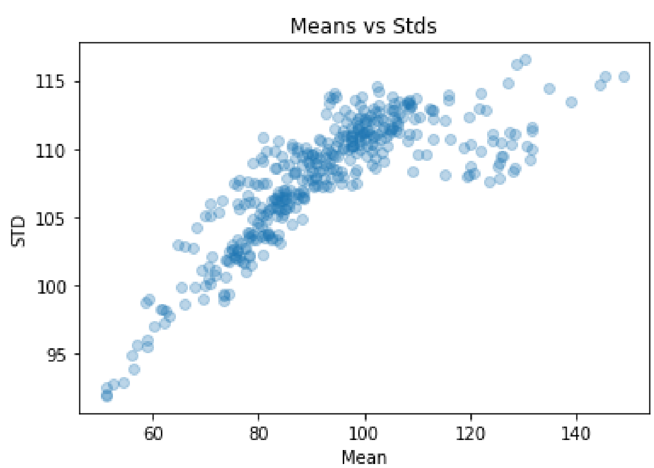
```
#Plot the histogram
plt.hist(std_f,edgecolor='white',density=True)
plt.title("Histogram of the 400 standard deviations")
plt.xlabel('Standard deviations s')
plt.ylabel('Probability')
xt = plt.xticks()[0]
xmin, xmax = min(xt), max(xt)
lnspc = np.linspace(xmin, xmax, len(std_f))
# Plot the norm distribution
#   Find minimum and maximum of xticks → Location of norm distribution
m, s = stats.norm.fit(std_f) # get mean and standard deviation
pdf_g = stats.norm.pdf(lnspc, m, s) # get theoretical values in our interval
plt.plot(lnspc, pdf_g, label="Norm")
plt.show() #std histogram
```



COMMENT: The values of 400 standard deviations spreads from 90 to around 120. Their histogram does not match with the norm distril around 110 have the highest frequency.

- Scatter plot of (m1 s1) , (m2,s2) , ... (m400,s400)

```
plt.scatter(mean_f,std_f,alpha=0.3)
plt.title("Means vs Stds")
plt.xlabel('Mean')
plt.ylabel('STD')
plt.show()
```



COMMENT: It can be seen clearly from the above figure that the mean is proportional with the std. When the mean increase, the std also distribution of the dots shape a curve or line like a function.

0.2. Standardize the features matrix DATA by centering and rescaling each random variable Xj into a new random v

The matrix DATA becomes a standardized data matrix SDATA, with coefficients given by SDATA(i,j) = (DATA(i,j) - mj)/sj

```
sdata = (data - mean_f)/std_f
print('Display first 5 rows of SDATA \n',np.round(sdata[:5,:5],3))
end_time=tm.time()
print(' The computing time for the part 0 is ' , round (end_time-start_time,2), 'second')
```

```
Display first 5 rows of SDATA
 [[-0.59  -0.658 -0.698 -0.743 -0.815]
 [-0.59  -0.583 -0.577 -0.613 -0.413]
 [-0.59  -0.64  -0.512 -0.324 -0.212]
 [-0.59  -0.658 -0.698 -0.743 -0.815]
 [ 1.977  1.74   1.667  1.62   1.504]]
 The computing time for the part 0 is  0.86 second
```

PART 1

1.1 Compute the correlation matrix COR of the 400 random variables Y1,..., Y400

```
start_time=tm.time()
cor_mtx=np.corrcoef(data.T)
print('Display first 5 rows of correlation matrix COR of DATA \n',np.round(cor_mtx[:5,:5],5))
```

```
Display first 5 rows of correlation matrix COR of DATA
 [[1.      0.92424 0.79024 0.62546 0.45097]
 [0.92424 1.      0.89406 0.70352 0.50868]
 [0.79024 0.89406 1.      0.86664 0.6432 ]
 [0.62546 0.70352 0.86664 1.      0.84092]
 [0.45097 0.50868 0.6432  0.84092 1.     ]]
```

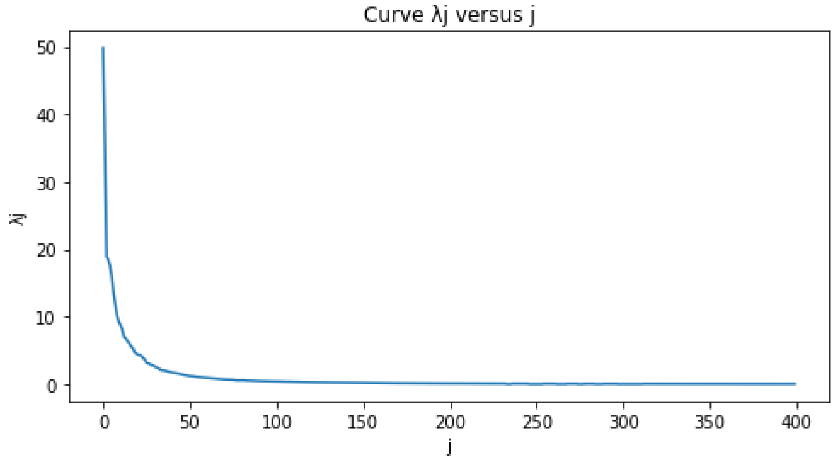
1.2. For the matrix COR , compute its 400 eigenvalues λ1 > λ2 > ... > λ400 > 0 , and its 400 eigenvectors v1, v2, ..., v

```
eig_val, eig_vec = LA.eig(cor_mtx)
print('Display first 5 eigen values \n',np.round(eig_val[:5],5))
print('Display first five eigen vectors \n',np.round(eig_vec[:5,:5],5))
```

```
Display first 5 eigen values
 [49.84356 35.38121 18.88504 18.40569 17.58024]
Display first five eigen vectors
 [[ 0.01826 -0.00925 -0.00363 -0.09989 -0.00793]
 [ 0.01324 -0.0111  -0.00464 -0.10357 -0.01645]
 [ 0.01605 -0.01334 -0.00087 -0.09573 -0.03043]
 [ 0.02208 -0.01475  0.0016  -0.07692 -0.04258]
 [ 0.02412 -0.01622 -0.00223 -0.05335 -0.04899]]
```

1.3. Plot the decreasing curve λj versus j for j=1 , 2, ..., 400

```
fig = plt.figure(figsize=(8,4))
ax = fig.add_subplot(111)

ax.plot(np.arange(400),eig_val)
ax.set(title='Curve \u03BBj versus j', ylabel='\u03BBj', xlabel='j')
plt.show()
```



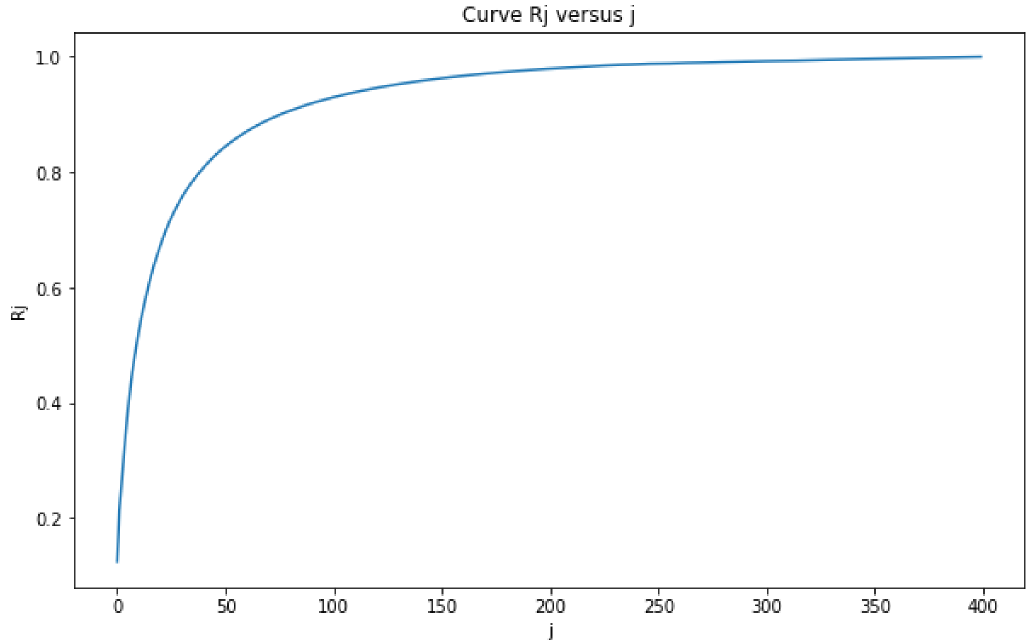
1.4. for j =1 ,2, ... ,400 compute the successive percentages Rj given by Rj = (λ1 + λ2 + ... + λj)/400

```
R=np.empty(400)
for i in np.arange(400):
  R[i]=sum(eig_val[:i+1])/400
print('Display first five values of Rj \n',np.round(R[:5],4))
```

```
Display first five values of Rj
 [0.1246 0.2131 0.2603 0.3063 0.3502]
```

1.5. Plot the increasing curve Rj versus j for j=1 , 2, ..., 400 and compute the smallest integer "r" such that Rr >90%

```
fig = plt.figure(figsize=(10,6))
ax = fig.add_subplot(111)
ax.plot(np.arange(400),R)
ax.set(title='Curve Rj versus j', ylabel='Rj', xlabel='j')
plt.show()
for i in np.arange(400):
    if R[i]>0.90:
        min_r=i+1
        break
print('The smallest integer "r" such that Rr > 90% is',min_r)
```




```
The smallest integer "r" such that Rr > 90% is 77
```

1.6) Explain the relationship between these computations and the PCA analysis of the set DATA

In part 0, we computed means, standard deviations of 400 features and the histogram shows that those features have a wide range of va standardlize the data, the PCA analysis of the set DATA will not be effective.

SDATA= $\frac{DATA - MEAN}{Std}$

By using the above formula, we can center the data and standardize the data's features onto unit scale (mean = 0 and variance = 1) whic optimal performance of many machine learning algorithms.

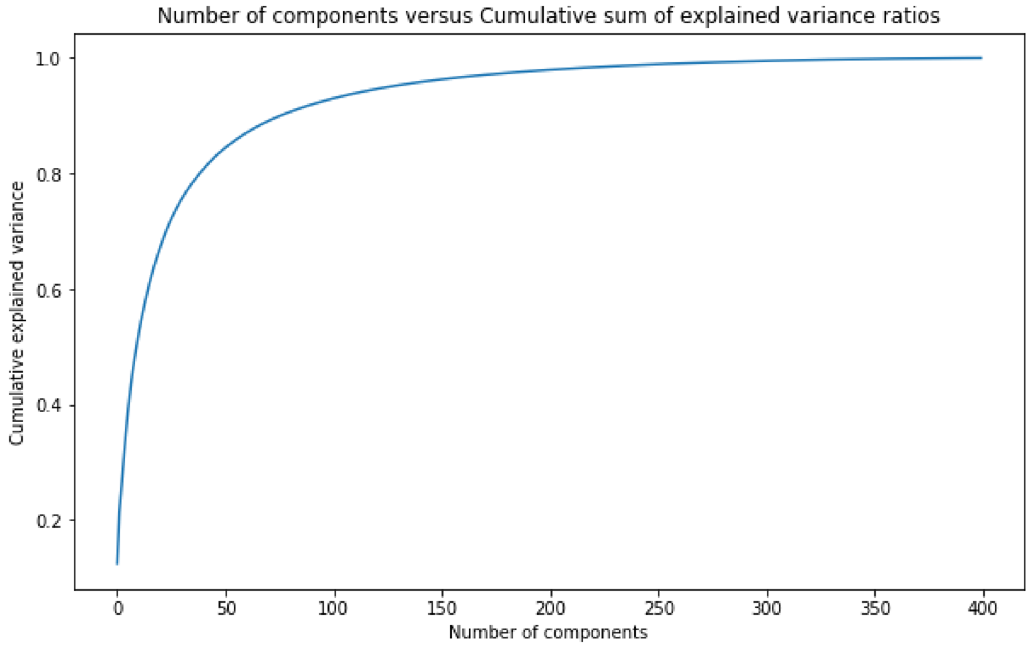
In part 1, we calculated the correlation matrix, eigen values and eigen vectors,\u03BBj and Rj. These computations help us to reduce the with a certain level of confidence

First, by using the correlation matrix, we can get the 400 eigenvalues. Then the smallest *j* which satisfies the condition Rj > 90% was obta which means that we can reduce the dimension of the set DATA to 77 features while we can still guarantee with 90% confident level that

1.7) Implement the PCA analysis of the rescaled data matrix SDATA either in R or in Python, or in Matlab; explain cl outputs of the pre-existing standard PCA functions you use

```
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
# Apply PCA analysis with number of features= 400
pca = PCA(n_components=400)
principalComponents = pca.fit_transform(sdata)
print('Example values of principal components array \n', np.round(principalComponents[:5,:5],3))
print('\n First five explained variance ratios \n', np.round(pca.explained_variance_ratio_[:5],3),'\n')
plt.figure(figsize=(10,6))
plt.plot(np.cumsum(pca.explained_variance_ratio_))
plt.title('Number of components versus Cumulative sum of explained variance ratios')
plt.xlabel('Number of components')
plt.ylabel('Cumulative explained variance')
```

```
Example values of principal components array
 [[-1.0370e+00  7.1650e+00 -5.5860e+00 -5.6400e-01  2.1840e+00]
 [ 1.2135e+01 -9.0360e+00  1.1520e+00  6.9000e-01  6.0000e-03]
 [ 9.8420e+00  4.4400e-01  8.3620e+00 -6.6770e+00 -3.3880e+00]
 [-9.7010e+00  1.3130e+00 -4.6680e+00  1.8420e+00 -4.3300e-01]
 [-3.0650e+00 -1.8350e+00 -1.5030e+00  1.2260e+00 -5.5670e+00]]

 First five explained variance ratios
 [0.125 0.088 0.047 0.046 0.044]

Text(0, 0.5, 'Cumulative explained variance')
```



Input and output of PCA functions

- ***PCA(n_components)***:
  - The **input** of PCA function within sklearn.decomposition pakage is the dimension you want to reduce to. For exampole, if yc to two dimensions so you can do the scatter plot to visualize it then you put n_components = 2 for input.
  - The **output** will be pca() we can use below.
- ***pca.fit_transform***: This function is a function chain rule denote by pca(fit_transform()). For fit_transform(), it can transfrom your or eual dimension by PCA analysis.
  - The **input** will be the original (untouched) data.
  - The **output** will be the rescale data transform by pca analysis with the dimension you want. In this homework, the output is SDATA
- ***pca.explained_variance_ratio_***: this function is a function chain rule too,can be denoted as pca(explained_variance_ratio_()).
  - This function requires no **input**
  - For the **output**, It will return the reliable confidence level persentage of each coordinate after pca transformation. Eventually will return 400 number represent the reliable confidence level for the 400 coordinates.

1.8) The standardized example # i is described by row "i" of SDATA .

After matrix transposition, this row becomes a column vector Ei in R400 . Compute the first three "scores" of example "i" by scor1 (i)= < E scor3 (i)= < Ei, v3>, These 3 numbers are the coordinates of a 3-dimensional vector Ui in R3.

The 2 numbers scor1 (i), scor2 (i) define a 2-dimensional vector Wi in R3. Explain the geometric relationship between Ei, Ui,Wi.

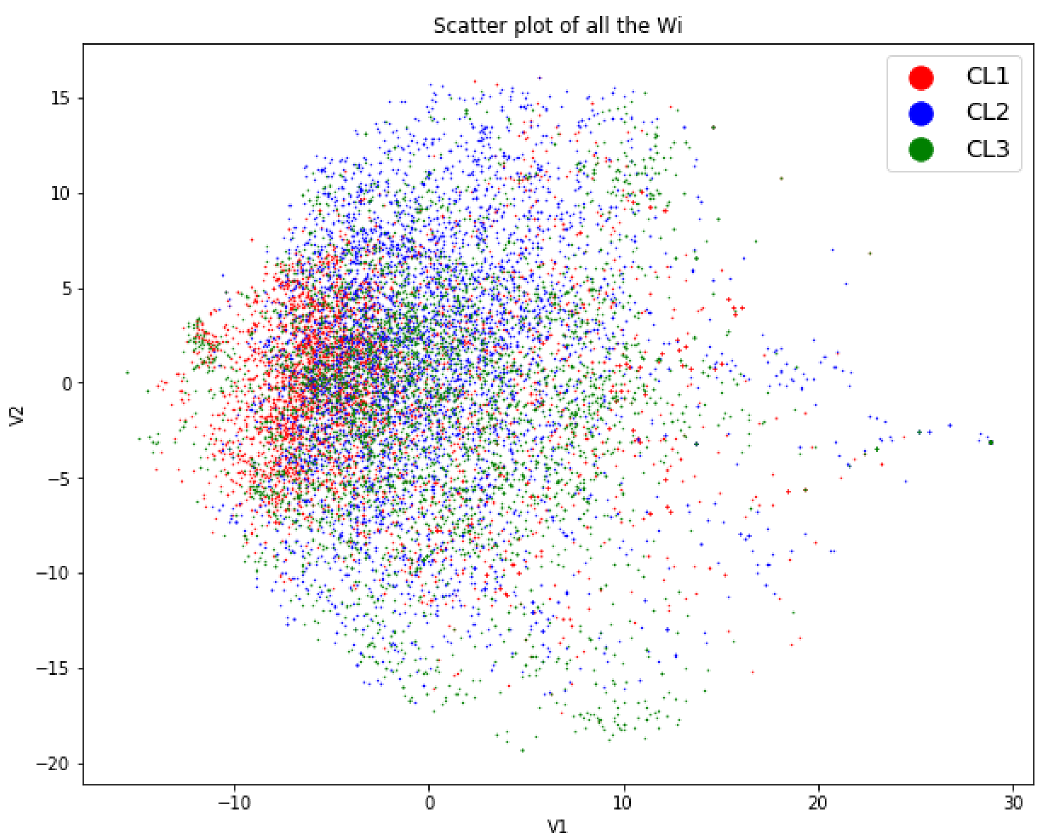
```
def proj_sca(a,b): #vector projection of a on b
    magn_b=np.sum(b**2)
```

```
    #print(magn_b)
    a_b=np.sum(a*b)
    #print(a_b)
    proj_a=(a_b/magn_b)
    return proj_a
noc=sdata.shape[0] #Number of cases
scor1=np.empty(noc)
scor2=np.empty(noc)
scor3=np.empty(noc)
for i in np.arange(noc):
  scor1[i]=proj_sca(sdata[i,:],eig_vec[:,0])
  scor2[i]=proj_sca(sdata[i,:],eig_vec[:,1])
  scor3[i]=proj_sca(sdata[i,:],eig_vec[:,2])
```

1.9) Display graphically the 2 dimensional scatterplot of all the Wi , i= 1,2,...,N , using 3 colors (1 for each class);

for instance red for CL1, blue for CL2 ; green for CL3. Interpret this display visually in terms of separability of the 3 classes

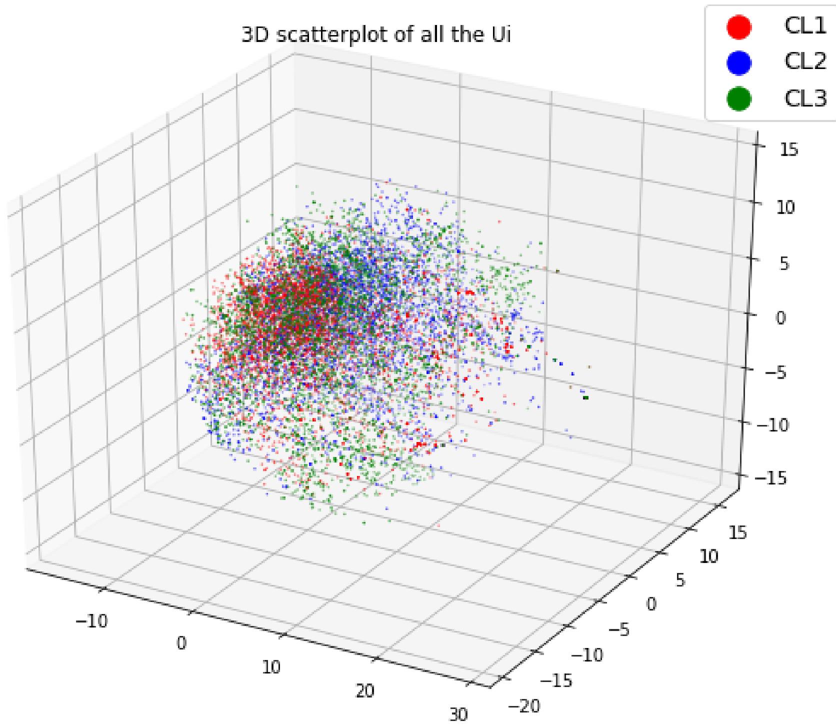
```
l_cl1=len(cl[0])
l_cl2=len(cl[0])+len(cl[1])
plt.figure(figsize=(10,8))
plt.scatter(scor1[:l_cl1],scor2[:l_cl1],color='red',s=0.2)
plt.scatter(scor1[l_cl1:l_cl2],scor2[l_cl1:l_cl2],color='blue',s=0.2)
plt.scatter(scor1[l_cl2:],scor2[l_cl2:],color='green',s=0.2)
plt.title('Scatter plot of all the Wi')
plt.legend(['CL1','CL2','CL3'],markerscale=30,fontsize='x-large')
plt.xlabel('V1')
plt.ylabel('V2')
plt.show()
```



1.10) Display graphically the 3 dimensional scatterplot of all the Ui , i= 1,2,...,N , with the same 3 colors;

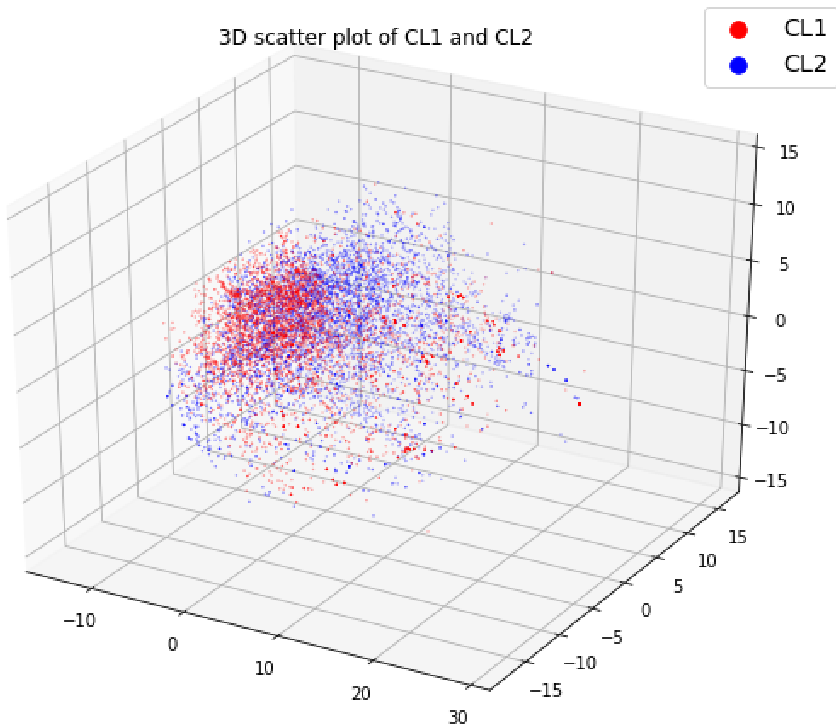
Interpret visually. To facilitate the visual interpretation generate a similar display but with only the two classes CL1 and CL2. Repeat this interpretation for CL1 and CL3, and then for CL2 and CL3

```
# Scatter plot of all Ui
fig = plt.figure(figsize=(10,8))
ax = fig.add_subplot(111, projection='3d')
plt.title('3D scatterplot of all the Ui')
ax.scatter(scor1[:l_cl1],scor2[:l_cl1],scor3[:l_cl1],color='red',s=0.2)
ax.scatter(scor1[l_cl1:l_cl2],scor2[l_cl1:l_cl2],scor3[l_cl1:l_cl2],color='blue',s=0.2)
ax.scatter(scor1[l_cl2:],scor2[l_cl2:],scor3[l_cl2:],color='green',s=0.2)
plt.legend(['CL1','CL2','CL3'],markerscale=30,fontsize='x-large')
plt.show()
```



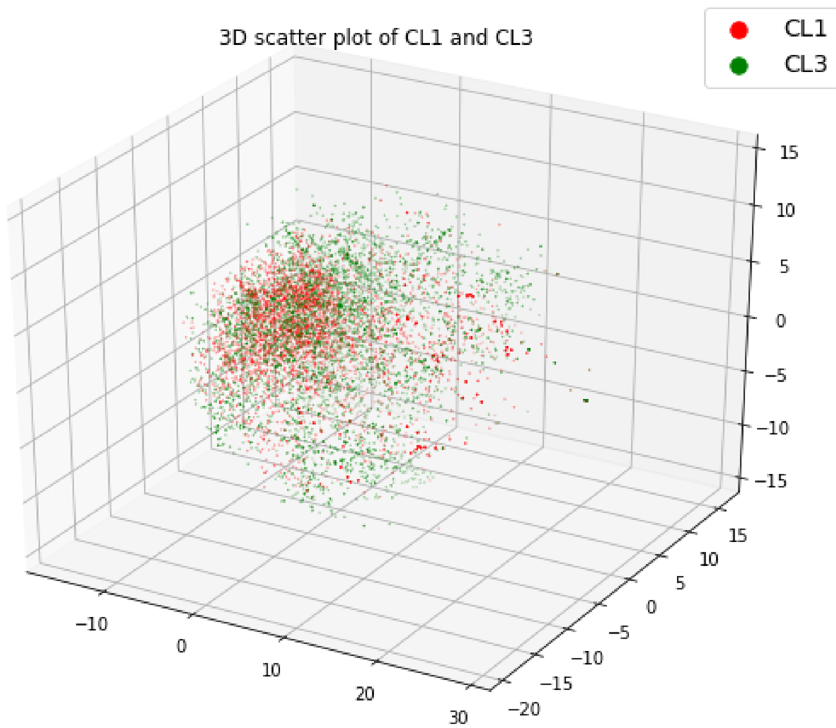
INTERPRET: Eventhough it seems that CL1, CL2 and CL3 mix together, we still can reluctantly conclude some informations from this gra
CL1 is much more concentrated than CL2 and CL3. Moreover, CL2 is slighty more concnetrated than CL3.

```
#Only CL1 and CL2
fig = plt.figure(figsize=(10,8))
ax = fig.add_subplot(111, projection='3d')
ax.scatter(scor1[:l_cl1],scor2[:l_cl1],scor3[:l_cl1],color='red',s=0.1)
ax.scatter(scor1[l_cl1:l_cl2],scor2[l_cl1:l_cl2],scor3[l_cl1:l_cl2],color='blue',s=0.1)
#ax.scatter(scor1[l_cl2:],scor2[l_cl2:],scor3[l_cl2:],color='green',s=0.1)
plt.title('3D scatter plot of CL1 and CL2')
plt.legend(['CL1','CL2'],markerscale=30,fontsize='x-large')
plt.show()
```



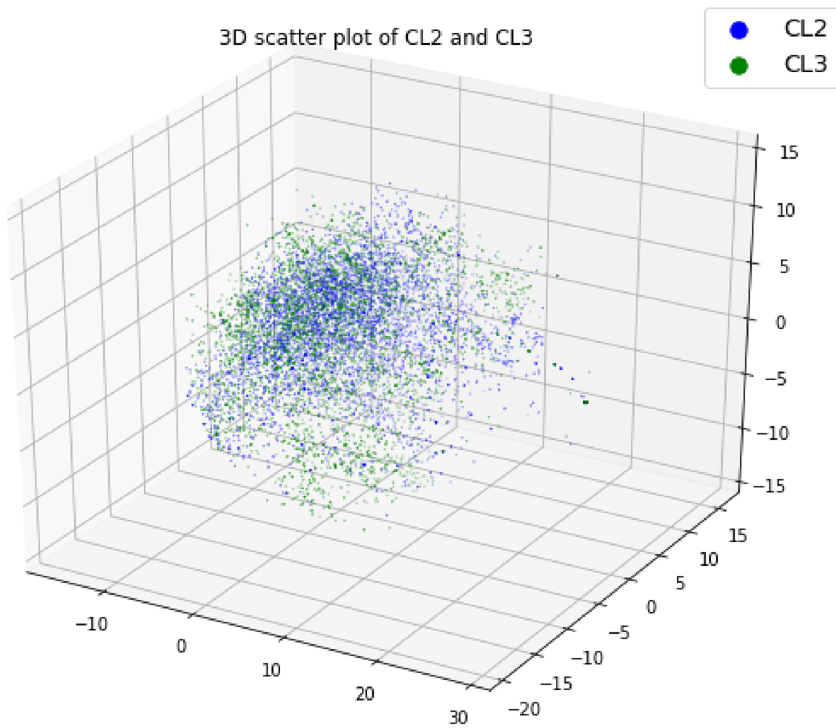
INTERPRET: The red dots concentrate in a small area while blue dots spread well over the space.We can conclude more clearly by this g that CL1 is much more concentrated than CL2

```
#Only CL1 and CL3
fig = plt.figure(figsize=(10,8))
ax = fig.add_subplot(111, projection='3d')
ax.scatter(scor1[:l_cl1],scor2[:l_cl1],scor3[:l_cl1],color='red',s=0.1)
#ax.scatter(scor1[l_cl1:l_cl2],scor2[l_cl1:l_cl2],scor3[l_cl1:l_cl2],color='blue',s=0.1)
ax.scatter(scor1[l_cl2:],scor2[l_cl2:],scor3[l_cl2:],color='green',s=0.1)
plt.title('3D scatter plot of CL1 and CL3')
plt.legend(['CL1','CL3'],markerscale=30,fontsize='x-large')
plt.show()
```



INTERPRET: This plot also displays the same situation as the previous plot. The distribution of CL1 is in a small volume but the one of C Therefore, it can be said that there is a significance discrimination between CL1 and CL3.

```
#Only CL2 and CL3
fig = plt.figure(figsize=(10,8))
ax = fig.add_subplot(111, projection='3d')
#ax.scatter(scor1[:l_cl1],scor2[:l_cl1],scor3[:l_cl1],color='red',s=0.1)
ax.scatter(scor1[l_cl1:l_cl2],scor2[l_cl1:l_cl2],scor3[l_cl1:l_cl2],color='blue',s=0.1)
ax.scatter(scor1[l_cl2:],scor2[l_cl2:],scor3[l_cl2:],color='green',s=0.1)
plt.title('3D scatter plot of CL2 and CL3')
plt.legend(['CL2','CL3'],markerscale=30,fontsize='x-large')
plt.show()
```



INTERPRET: In this plot, both the distributions of blue dots and green dots have a wide range. However it seems that the green dots spre blue dots. We can also conclude that there is a slight separation between CL2 and CL3. In summary, we can finally conclude that CL1 is and CL2 is more concentrated than CL3

```
end_time=tm.time()
print(' The computing time for the part 1 is ' , round (end_time-start_time,2), 'second')
```

```
 The computing time for the part 1 is  7.4 second
```

Part 2

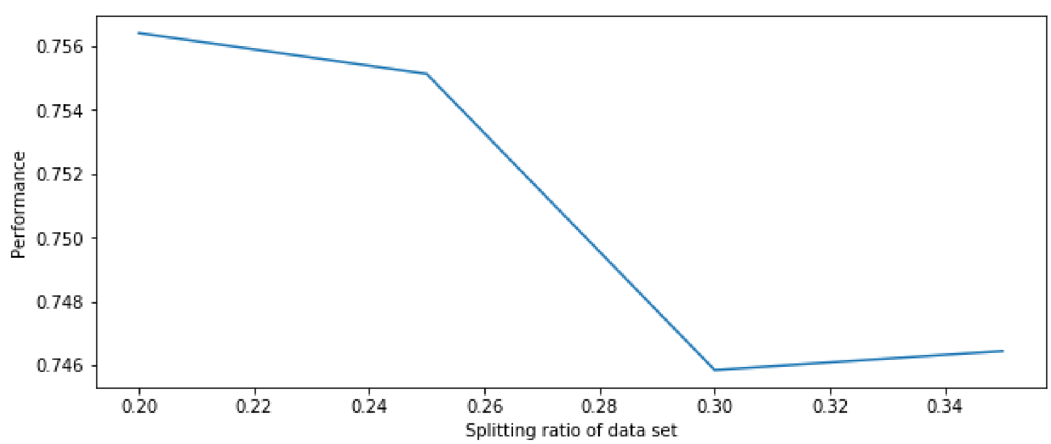
2.1) Fix k = 15. Use the standardized data matrix SDATA to apply the k nearest neighbor (kNN) algorithm

for the automatic classification of arbitrary examples into one of the three classes CL1 CL2 CL3. Compute the percentage per(15) of cor whole data set of N examples

```
start_time=tm.time()
k=15
#To avoid over-fitting, we will divide our dataset into training and test splits
#We splits the dataset into train data and test data with different ratios
#Percentage of test set is from 0.2 to 0.35
classifier = KNeighborsClassifier(n_neighbors=k)
score=np.empty(4)
for i in np.arange(4):
  tes_siz=np.round(0.2+i*0.05,2)
  sdata_train, sdata_test,font_train,font_test= train_test_split(sdata,data_df.font, test_size=tes_siz)
  classifier.fit(sdata_train, font_train)
  font_pred = classifier.predict(sdata_test)
  print('\n If the percentage of test set is',tes_siz,' then the confusion matrix is \n',confusion_matrix(font
  score[i]=metrics.accuracy_score(font_test, font_pred)
  print('\n And the performance is',np.round(score[i],3))
```

```
If the percentage of test set is 0.2  then the confusion matrix is
[[757  68 110]
[144 566 118]
[139  95 770]]

And the performance is 0.756

If the percentage of test set is 0.25  then the confusion matrix is
[[924 117 146]
[157 748 180]
[137 110 940]]

And the performance is 0.755

If the percentage of test set is 0.3  then the confusion matrix is
[[1126  107  180]
[ 195  845  254]
[ 185  134 1125]]

And the performance is 0.746

If the percentage of test set is 0.35  then the confusion matrix is
[[1300  137  236]
[ 219 1014  241]
[ 212  183 1301]]

And the performance is 0.746
```

```
plt.close()
plt.figure(figsize=(10,4))
plt.xlabel('Splitting ratio of data set')
plt.ylabel('Performance')
plt.plot(np.arange(4)*0.05+0.2,score)
plt.title=('Performance versus splitting ratio')
plt.show()
```



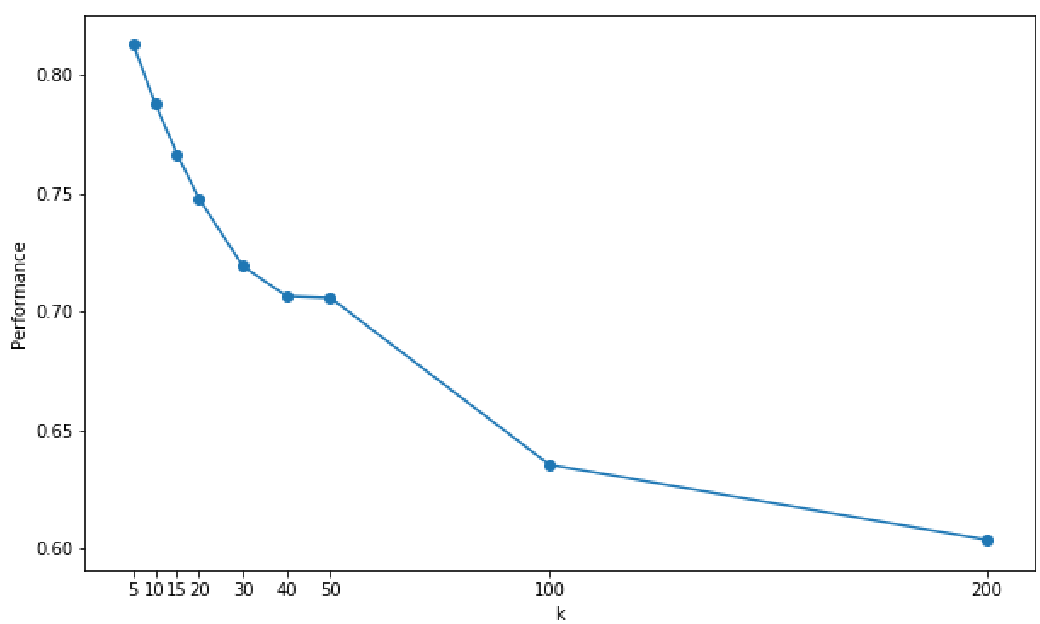
$\rightarrow$ **Based on the graph, it seems that the 80:20 ratio is the best one to attain the highest performance**

2.2) Repeat the preceding operation for k = 5, 10 , 15, 20, 30, 40, 50 ,100,200; and compute the percentages per(k) classifications on the whole data set of N examples

plot the curve per(k) versus k to try to identify a best range [A < k <B] of values for the integer k

```
k_vals=[5, 10 , 15, 20, 30, 40, 50 ,100,200]
```

```
per=np.empty(len(k_vals))
for i in np.arange(len(k_vals)):
  classifier = KNeighborsClassifier(n_neighbors=k_vals[i])
  sdata_train, sdata_test,font_train,font_test= train_test_split(sdata,data_df.font, test_size=0.2)
  classifier.fit(sdata_train, font_train)
  font_pred = classifier.predict(sdata_test)
  #print(confusion_matrix(font_test, font_pred))
  per[i]=metrics.accuracy_score(font_test, font_pred)


plt.figure(figsize=(10,6))
plt.plot(k_vals,per)
plt.scatter(k_vals,per)
plt.xticks(k_vals)
plt.title=('Performance versus k values')
plt.xlabel('k')
plt.ylabel('Performance')
plt.show()
print('Percentages of correct classifications for each k is \n', per)
```

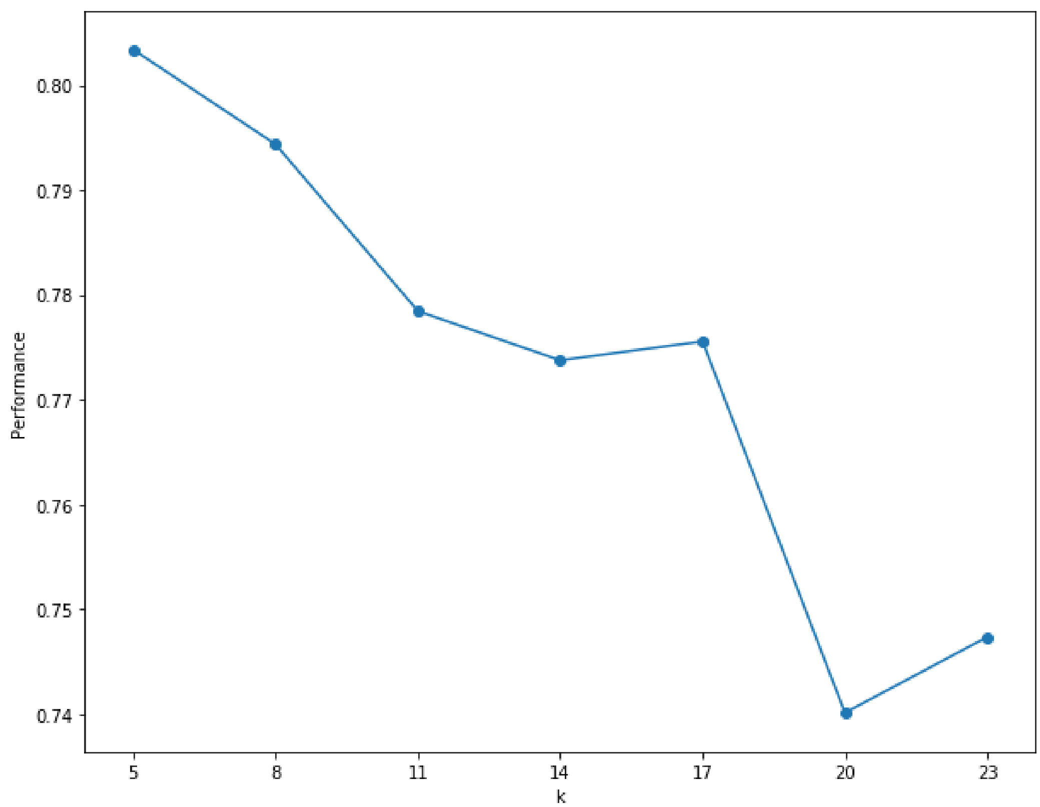



```
Percentages of correct classifications for each k is
 [0.81279364 0.78785688 0.76653415 0.74774124 0.71919046 0.70654138
 0.70581858 0.63534514 0.60354174]
```

2.3) Repeat the preceding exploration for a few more values of k within the range [A,B]. Conclude by selecting a "be integer k

```
k_vals_1=[5, 8, 11, 14, 17, 20, 23]
per1=np.empty(len(k_vals_1))
for i in np.arange(len(k_vals_1)):
  classifier = KNeighborsClassifier(n_neighbors=k_vals_1[i])
  sdata_train, sdata_test,font_train,font_test= train_test_split(sdata,data_df.font, test_size=0.2)
  classifier.fit(sdata_train, font_train)
  font_pred = classifier.predict(sdata_test)
  #print(confusion_matrix(font_test, font_pred))
  per1[i]=metrics.accuracy_score(font_test, font_pred)


plt.figure(figsize=(10,8))
plt.plot(k_vals_1,per1)
```

```
plt.scatter(k_vals_1,per1)
plt.xticks(k_vals_1)
plt.title=('Performance versus k values')
plt.xlabel('k')
plt.ylabel('Performance')
plt.show()
print(per1)
```




```
[0.80339718 0.79436213 0.77846043 0.7737622  0.77556921 0.74015179
 0.74737983]
```

We can conclude by the elbow theorem that k* = 8

2.4) Compute and interpret the 3x3 confusion matrix for kNN classification using the "best" k= k*

```
classifier = KNeighborsClassifier(n_neighbors=8)
sdata_train, sdata_test,font_train,font_test= train_test_split(sdata,data_df.font, test_size=0.2)
classifier.fit(sdata_train, font_train)
font_pred = classifier.predict(sdata_test)
print('Confusion matrix for k = 8 is \n',confusion_matrix(font_test, font_pred))
```

```
Confusion matrix for k = 8 is
 [[855  34  87]
 [121 633  97]
 [114  95 731]]
```

A confusion matrix is often used to describe the performance of a lassification model (or “classifier”) on a set of test data for which the

NA	Predicted CL1	Predicted CL2	Predicted CL3
True CL1	855	34	87
True CL2	121	633	97
True CL3	114	95	731

```
end_time=tm.time()
print(' The computing time for the part 2 is ' , round (end_time-start_time,2), 'second')
```

```
The computing time for the part 2 is  950.96 second
```