CS6301 MACHINE LEARNING LAB WEEK 10 – DIMENSIONALITY REDUCTION SRIHARI. S – 2018103601

Date: 19-04-2021 Monday

Aim: To implement Principal Component Analysis and Linear Discriminant analysis and visualize datasets with a large number of features.

Principal Component Analysis:

PCA is a dimensionality-reduction method that is often used to reduce the dimensionality of large data sets, by transforming a large set of variables into a smaller one that still contains most of the information in the large set. It reduces the number of variables of a data set, while preserving as much information as possible.

Algorithm:

- Write N datapoints xi = (x1i, x2i, . . . , xMi) as row vectors
- Put these vectors into a matrix X (which will have size N ×M)
- Centre the data by subtracting off the mean of each column, putting it into matrix B
- Compute the covariance matrix $C = 1/N B^T B$
- Compute the eigenvalues and eigenvectors of C, so V^{-1} CV = D, where V holds the eigenvectors of C and D is the M ×M diagonal eigenvalue matrix.
- Sort the columns of D into order of decreasing eigenvalues, and apply the same order to the columns of V
- Reject those with eigenvalue less than some n (eta), leaving L dimensions in the data

Linear Discriminant Analysis:

It is a dimensionality reduction technique. It is used as a pre-processing step in Machine Learning and applications of pattern classification. The goal of LDA is to project the features in higher dimensional space onto a lowerdimensional space in order to avoid the curse of dimensionality and also reduce resources and dimensional costs. LDA is a supervised classification technique that is considered a part of crafting competitive machine learning models. This

category of dimensionality reduction is used in areas like image recognition and predictive analysis in marketing.

Algorithm:

LDA focuses primarily on projecting the features in higher dimension space to lower dimensions. You can achieve this in three steps:

- Firstly, you need to calculate the separability between classes which is the distance between the mean of different classes. This is called the between-class variance.
- Secondly, calculate the distance between the mean and sample of each class. It is also called the within-class variance.
- Finally, construct the lower-dimensional space which maximizes the between-class variance and minimizes the within-class variance. P is considered as the lowerdimensional space projection, also called Fisher's criterion.

Implementation of PCA:

Url: https://archive.ics.uci.edu/ml/datasets/breast+cancer+wisconsin+(diagnostic)

Dataset Description: Breast cancer wisconsin (diagnostic) dataset

	mean radius	mean texture	mean perimeter	mean	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809

5 rows × 30 columns

Data Set Characteristics:

• Number of Instances: 569

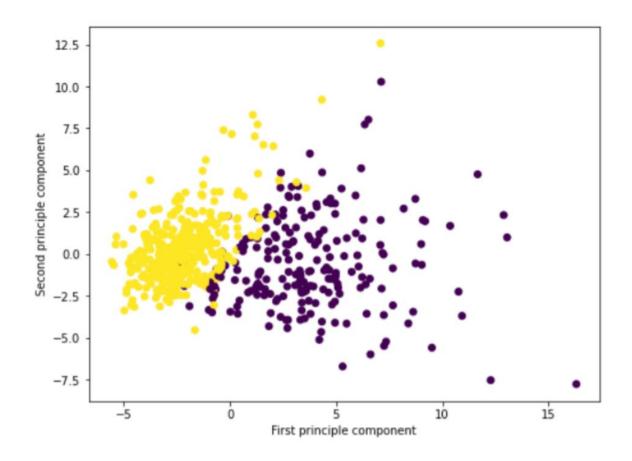
• Number of Attributes: 30 numeric, predictive attributes and the class

Attribute Information:

- radius (mean of distances from center to points on the perimeter)
- texture (standard deviation of gray-scale values)
- smoothness (local variation in radius lengths)

- compactness (perimeter^2 / area 1.0)
- concavity (severity of concave portions of the contour)
- concave points (number of concave portions of the contour)
- symmetry
- -fractal dimension ("coastline approximation" 1)
- The mean, standard error, and "worst" or largest (mean of the threeworst/largest values) of these features were computed for each image, resulting in 30 features. For instance, field 0 is Mean Radius, field 10 is Radius SE, field 20 is Worst Radius.
- Class
 - WDBC-Malignant
 - WDBC-Benign

OUTPUT:



Train accuracy 95.72 % Test accuracy 92.98 %

	precision	recall	f1-score	support
0	0.89	0.92	0.91	64
1	0.95	0.93	0.94	107
accuracy			0.93	171
macro avg	0.92	0.93	0.93	171
weighted avg	0.93	0.93	0.93	171

CODE:

```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
%matplotlib inline
from sklearn.datasets import load breast cancer
cancer=load_breast_cancer()
X=cancer.data
y=cancer.target
df=pd.DataFrame(cancer['data'],columns=cancer['feature names'])
df.head()
from sklearn.preprocessing import StandardScaler
scaler=StandardScaler()
scaler.fit(df)
scaled_data=scaler.transform(df)
from sklearn.decomposition import PCA
pca=PCA(n_components=2)
pca.fit(scaled_data)
x pca=pca.transform(scaled data)
scaled_data.shape
x_pca.shape
scaled data
x pca
plt.figure(figsize=(8,6))
```

```
plt.scatter(x_pca[:,0],x_pca[:,1],c=cancer['target'])
plt.xlabel('First principle component')
plt.ylabel('Second principle component')
X_train_new, X_test_new, y_train, y_test = train_test_split(x_pca, y, test_size = 0.3,
random_state=20, stratify=y)
knn_pca = KNeighborsClassifier(7)
knn_pca.fit(X_train_new,y_train)
print("Train Accuracy ",knn_pca.score(X_train_new,y_train)*100,"%")
print("Test Accuracy ",knn_pca.score(X_test_new,y_test) *100,"%")
```

Implementation Of LDA:

Dataset Used: bmd.csv (bone mineral density)

	age	weight_kg	height_cm	bmd	fracture
0	57.052768	64.0	155.5	0.8793	0
1	75.741225	78.0	162.0	0.7946	0
2	70.778900	73.0	170.5	0.9067	0
3	78.247175	60.0	148.0	0.7112	0
4	54.191877	55.0	161.0	0.7909	0
164	77.982543	74.0	164.0	0.7941	1
165	50.285303	59.0	161.0	0.7971	1
166	46.359721	67.0	169.0	0.8037	1
167	54.788368	70.0	166.0	0.8072	1
168	69.994822	68.5	165.0	0.8664	1

The file bmd.csv contains 169 records of bone densitometries (measurement of bone mineral density). The following variables were collected:

- id patient's number
- age patient's age
- fracture hip fracture (fracture / no fracture)
- weight_kg weight measured in Kg

- height_cm height measure in cm
- waiting_time time the patient had to wait for the densitometry (in minutes)
- bmd bone mineral density measure in the hip

```
#Import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model selection import train test split
from sklearn.neighbors import KNeighborsClassifier
#Load dataset
n components = 2
data = pd.read_csv('bmd.csv')
data = data[['age','weight kg','height cm','bmd','fracture']]
data
#Normalizing the attributes and encoding labels
from sklearn.preprocessing import StandardScaler
stdsc = StandardScaler()
X_train_std = stdsc.fit_transform(data.iloc[:,range(0,4)].values)
from sklearn.preprocessing import LabelEncoder
class le = LabelEncoder()
y = class le.fit transform(data['fracture'].values)
#Between class variance
S W = np.zeros((4,4))
for i in range(2):
 S_W += np.cov(X_train_std[y==i].T)
S W
#Distance between mean and sample of class
N=np.bincount(y)
vecs=[]
[vecs.append(np.mean(X train std[y==i],axis=0)) for i in range(2)]
mean_overall = np.mean(X_train_std, axis=0)
S_B=np.zeros((4,4))
for i in range(2):
 S_B += N[i]*(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_overall).reshape(4,1)).dot(((vecs[i]-mean_
mean_overall).reshape(1,4))))
S B
```

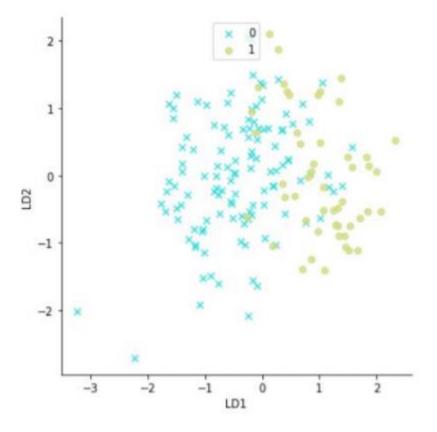
```
#Display eigen values
eigen vals, eigen vecs = np.linalg.eig(np.linalg.inv(S W).dot(S B))
                    [(np.abs(eigen vals[i]), eigen vecs[:,i]) for
eigen pairs
               =
                                                                             in
range(len(eigen vals))]
eigen_pairs = sorted(eigen_pairs,key=lambda k: k[0], reverse=True)
print('Eigenvalues in decreasing order:\n')
for eigen val in eigen pairs:
print(eigen_val[0])
#Finding LD1 & LD2
tot = sum(eigen vals.real)
discr = [(i / tot) for i in sorted(eigen vals.real, reverse=True)]
cum discr = np.cumsum(discr)
W=np.hstack((eigen pairs[0][1][:,].reshape(4,1),eigen pairs[1][1][:,
].reshape(4,1))).real
X train Ida = X train std.dot(W)
#Adding LD1 & LD2 Value to dataframe
data=pd.DataFrame(X_train_lda)
data['class']=y
data.columns=["LD1","LD2","class"]
data.head()
#Visualizing the data after LDA
import seaborn as sns
markers = ['x', 'o']
sns.lmplot(x="LD1", y="LD2", data=data, markers=markers,fit reg=False,
hue='class',
legend=False, palette='rainbow')
plt.legend(loc='upper center')
plt.show()
#KNN Classifier
X_train, X_test, y_train, y_test = train_test_split(data[['LD1','LD2']], data['class'],
test size=0.20)
knn= KNeighborsClassifier(n neighbors=3)
knn.fit(X_train, y_train)
y pred = knn.predict(X test)
print("Train accuracy ",knn.score(X train,y train)*100,"%")
print("Test accuracy ",knn.score(X test,y test)*100,"%")
```

OUTPUT

Between Class Variance

```
array([[ 1.9725685 , -0.04759746 , -0.42736814 , -0.30524193], [-0.04759746 , 1.78794962 , 0.71452081 , 0.59460869], [-0.42736814 , 0.71452081 , 2.03028906 , 0.56144434], [-0.30524193 , 0.59460869 , 0.56144434 , 1.0964439 ]])
```

Within class variance



Train accuracy 92.59 % Test accuracy 85.29 %

Implementation of PCA and LDA on a dataset having more than 100 columns:

Dataset: MNIST Dataset

The MNIST database is a large database of handwritten digits that is commonly used for training various image processing systems which contains 60,000 training images and 10,000 testing images. Half of the training set and half of the test set were taken from NIST's training dataset, while the other half of the training set and the other half of the test set were taken from NIST's testing dataset.

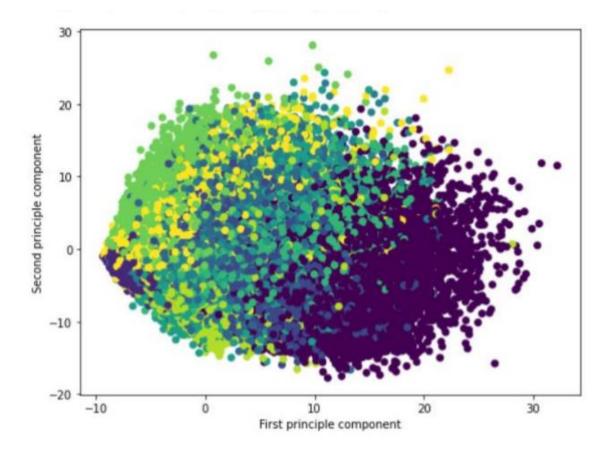
Input:

ile E	dit Fo	rmat	View	Help													
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	3	18	18	18	126	136	175	26	166	255
247	127	0	0	0	0	0	0	0	0	0	0	0	0	30	36	94	154
170	253	253	253	253	253	225	172	253	242	195	64	0	0	0	0	0	0
0	0	0	0	0	49	238	253	253	253	253	253	253	253	253	251	93	82
82	56	39	0	0	0	0	0	0	0	0	0	0	0	0	18	219	253
253	253	253	253	198	182	247	241	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	80	156	107	253	253	205	11	0	43	154
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	14	1	154	253	90	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	139	253	190	2	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	11	190	253	70	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	35	241
225	160	108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	81	240	253	253	119	25	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	e
0	0	45	186	253	253	150	27	0	0	0	0	0	0	0	0	0	e
0	0	0	0	0	0	0	0	0	0	0	0	0	16	93	252		187

PCA USING MNIST:

#Import Library
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier

```
%matplotlib inline
#Import dataset
data = pd.read csv("mnist train.csv")
X = data.drop('label', axis=1)
y = data.label
data.head()
#Normalizing Dataset using StandardScaler
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
scaled data=scaler.fit transform(X)
scaled data
#Initializing PCA
from sklearn.decomposition import PCA
pca=PCA(n components=2)
pca.fit(scaled_data)
x pca=pca.transform(scaled data)
scaled_data.shape
x_pca.shape
scaled data
x_pca
#Printing transformed data
#Visualizing data after applying PCA
plt.figure(figsize=(8,6))
plt.scatter(x_pca[:,0],x_pca[:,1],c=cancer['target'])
plt.xlabel('First principle component')
plt.ylabel('Second principle component')
#KNN Classifier
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3,
random state=20,
stratify=y)
knn = KNeighborsClassifier(3)
knn.fit(X_train,y_train)
print("Train Accuracy",knn.score(X_train,y_train)*100,"%")
print("Test Accuracy ",knn.score(X_test,y_test) *100,"%")
```



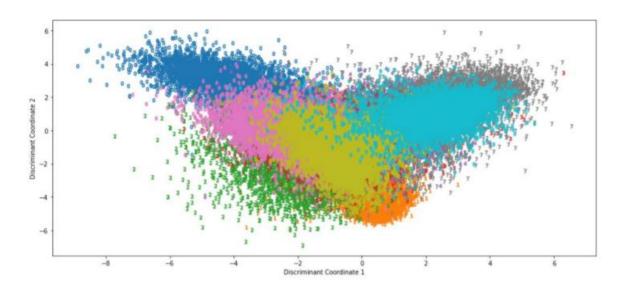
Train accuracy 98.5 % Test accuracy 96.95 %

LDA USING MNIST

#Import library
import matplotlib.pyplot as plt
from sklearn import datasets, svm, metrics
import pandas as pd
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
%matplotlib inline
#Loading data
data = pd.read_csv("mnist_train.csv")
X = data.drop('label', axis=1)
y = data.label

```
target names = data.label
data.head()
# Create a classifier: a Fisher's LDA classifier
Ida = LinearDiscriminantAnalysis(n components=2, solver='eigen',
shrinkage=0.1)
Ida = Ida.fit(X, y)
X r Ida = Ida.transform(X)
# Visualize transformed data on learnt discriminant coordinates
plt.figure(figsize=[13,6])
for i, target_name in zip([0,1,2,3,4,5,6,7,8,9], target_names):
plt.scatter(X_r_lda[y == i, 0], X_r_lda[y == i, 1], alpha=.8,label=target_name,
marker='$%.f$'%i)
plt.xlabel('Discriminant Coordinate 1')
plt.ylabel('Discriminant Coordinate 2')
plt.tight_layout()
#KNN Classifier
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3,
random_state=20,
stratify=y)
knn = KNeighborsClassifier(7)
knn.fit(X train,y train)
print("Train score ",knn.score(X_train,y_train),"%")
print("Test score ",knn.score(X test,y test),"%")
```

	precision	recall	f1-score	support
0	0.97	0.96	0.97	5335
1	0.96	0.98	0.97	6047
2	0.83	0.94	0.88	5352
3	0.92	0.89	0.91	5514
4	0.94	0.92	0.93	5266
5	0.92	0.90	0.91	4875
6	0.95	0.95	0.95	5331
7	0.93	0.92	0.93	5659
8	0.93	0.89	0.91	5264
9	0.92	0.91	0.91	5357



Train accuracy 97.63 % Test accuracy 96.68 %

TABULAR INFERENCE LINEAR DISCRIMINANT ANALYSIS

DATASET	Training Accuracy	Testing Accuracy
MNIST	97.63%	96.68%
BONE MINERAL	92.59%	85.29%
DENSITY		

PRINCIPAL COMPONENT ANALYSIS

DATASET	Training Accuracy	Testing Accuracy
MNIST	98.5%	96.95%
BREAST CANCER	95.72%	92.98%
DATASET		

DATASET	Precision	Recall	F1-Score
MNIST	0.95	0.94	0.94
BREAST CANCER	0.92	0.93	0.93
DATASET			

Inference: Thus, PCA and LDA are implemented and the performance metrics are recorded. The higher dimensional data has been visualized on a lower dimension.