Principal Component Analysis on MNIST Dataset

For this task I have downloaded the data from kaggle

https://www.kaggle.com/c/digit-recognizer/data?select=train.csv (https://www.kaggle.com/c/digit-recognizer/data?select=train.csv)

We know that MNIST data set is a dataset containing information abaout hand written numerical character in which each pixel is of 28x28 which is present in 784 dimensions. For training data we have 42000 such data points which in result give a matrix of 42000x784.

In [1]:
```
# Importing libraries

import pandas as pd
import numpy as np
import seaborn as sn
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler
from scipy.linalg import eigh
```

Loading the data

In [2]:
```
df=pd.read_csv("mnist_train.csv")
```

In [3]:
```
df.head()
```

Out[3]:

	label	pixel0	pixel1	pixel2	pixel3	pixel4	pixel5	pixel6	pixel7	pixel8	...	pixel774	pixel775
0	1	0	0	0	0	0	0	0	0	0	...	0	0
1	0	0	0	0	0	0	0	0	0	0	...	0	0
2	1	0	0	0	0	0	0	0	0	0	...	0	0
3	4	0	0	0	0	0	0	0	0	0	...	0	0
4	0	0	0	0	0	0	0	0	0	0	...	0	0

5 rows × 785 columns

In [4]:
```
## Since in above case we can see that label is also given for each of the data p
df_l=df['label']
data=df.drop('label' , axis=1)
```

In [5]:
```
data.head()
```

Out[5]:

	pixel0	pixel1	pixel2	pixel3	pixel4	pixel5	pixel6	pixel7	pixel8	pixel9	...	pixel774	pixel77
0	0	0	0	0	0	0	0	0	0	0	...	0	
1	0	0	0	0	0	0	0	0	0	0	...	0	
2	0	0	0	0	0	0	0	0	0	0	...	0	
3	0	0	0	0	0	0	0	0	0	0	...	0	
4	0	0	0	0	0	0	0	0	0	0	...	0	

5 rows × 784 columns

We know have separate 784 features for each data points. Also we have separate data for labels so that we can verify our results.

In [6]:
```
data.shape
```

Out[6]:
```
(42000, 784)
```

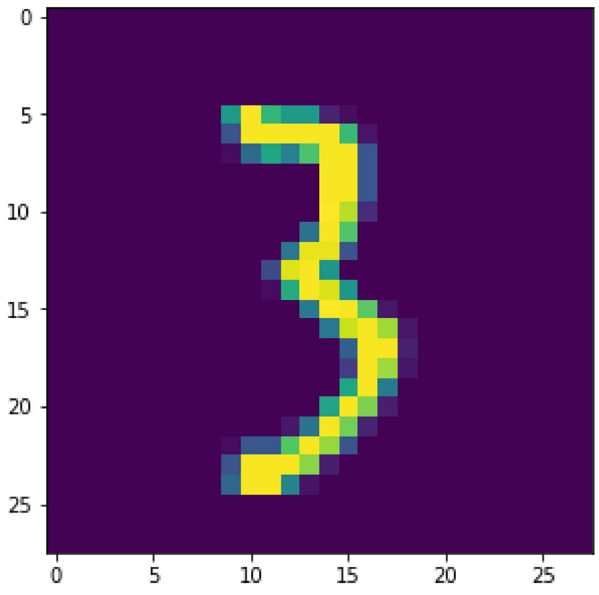
We can see that we have a dataset with large dimensions so visualization methods like pair plot, scatter plot etc., for 2d or 3d will not work here, so for this we will use Principal Component Ananlysis.

In [7]:
```
## Before proceeding further we will first test our data is correct and also we h

## For checking purpose we will take data point at any index and check if it matc

plt.figure(figsize=(5,5))
index_value=234
fig_data=data.iloc[index_value].to_numpy().reshape(28,28)
plt.imshow(fig_data)
plt.show()


print("Label for this data point is : {}".format(df_l[index_value]))
```



```
Label for this data point is : 3
```

Applying PCA

Instead of direct using sklearn library I will first do the custom implementation by finding coavariance matrix, eigen value and eigen vectors and then I will compare the result with the result using sklearn library.

In [8]:
```
## Standardizing the data
labels = df_l
data = data
print("the shape of sample data = ", data.shape)
standardized_data=StandardScaler().fit_transform(data)
standardized_data.shape
```

```
the shape of sample data =  (42000, 784)
```

Out[8]:
```
(42000, 784)
```

In [9]:
```
#find the co-variance matrix
sample_data = standardized_data

# matrix multiplication using numpy
covar_matrix = np.matmul(sample_data.T , sample_data)
covar_matrix=(covar_matrix/data.shape[0])

print ( "The shape of variance matrix = ", covar_matrix.shape)
```

```
The shape of variance matrix =  (784, 784)
```

In [10]:
```
## finding eigen value and corresponding eigen vectors

## we know that 70%-75% of the total variance of data is explained by first 2 pri

values, vectors = eigh(covar_matrix, eigvals=(782,783))
```

In [11]:
```
print("Shape of eigen vectors = ",vectors.shape)
# converting the eigen vectors into (2,d) shape for easyness of further computati
vectors = vectors.T

print("Updated shape of eigen vectors = ",vectors.shape)
# here the vectors[1] represent the eigen vector corresponding 1st principal eige
# here the vectors[0] represent the eigen vector corresponding 2nd principal eige
```

```
Shape of eigen vectors =  (784, 2)
Updated shape of eigen vectors =  (2, 784)
```

In [12]:
```
# multiplying obtained eigen vectors with sample data to obtain the new coordinat

new_coordinates=np.matmul(vectors,sample_data.T)
new_coordinates.shape
```

Out[12]:
```
(2, 42000)
```

In [13]:
```
## adding labels to the newly obtained data points

new_data=np.vstack((new_coordinates,labels)).T
```

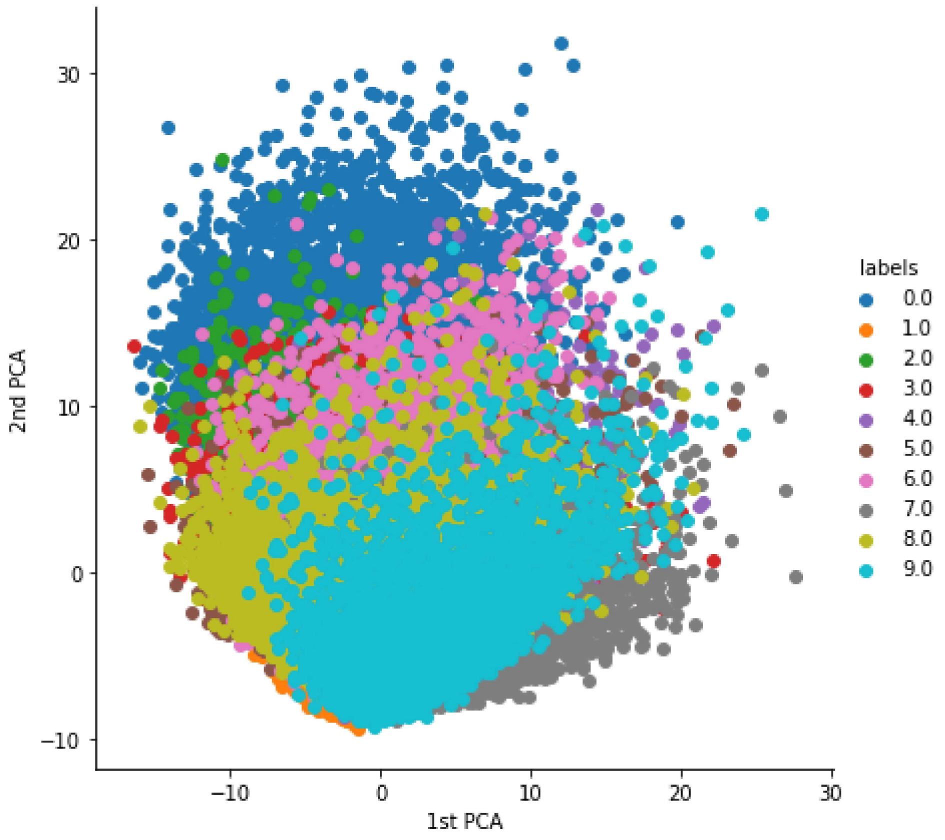
In [14]:
```
## converting this data to a new dataframe

dataframe=pd.DataFrame(new_data,columns=("1st PCA","2nd PCA","labels"))
dataframe.head()
```

Out[14]:

	1st PCA	2nd PCA	labels
0	-5.226445	-5.140478	1.0
1	6.032996	19.292332	0.0
2	-1.705813	-7.644503	1.0
3	5.836139	-0.474207	4.0
4	6.024818	26.559574	0.0

In [15]:
```
## Creating visualization
sn.FacetGrid(dataframe, hue="labels", height=6).map(plt.scatter, '1st PCA', '2nd
plt.show()
```



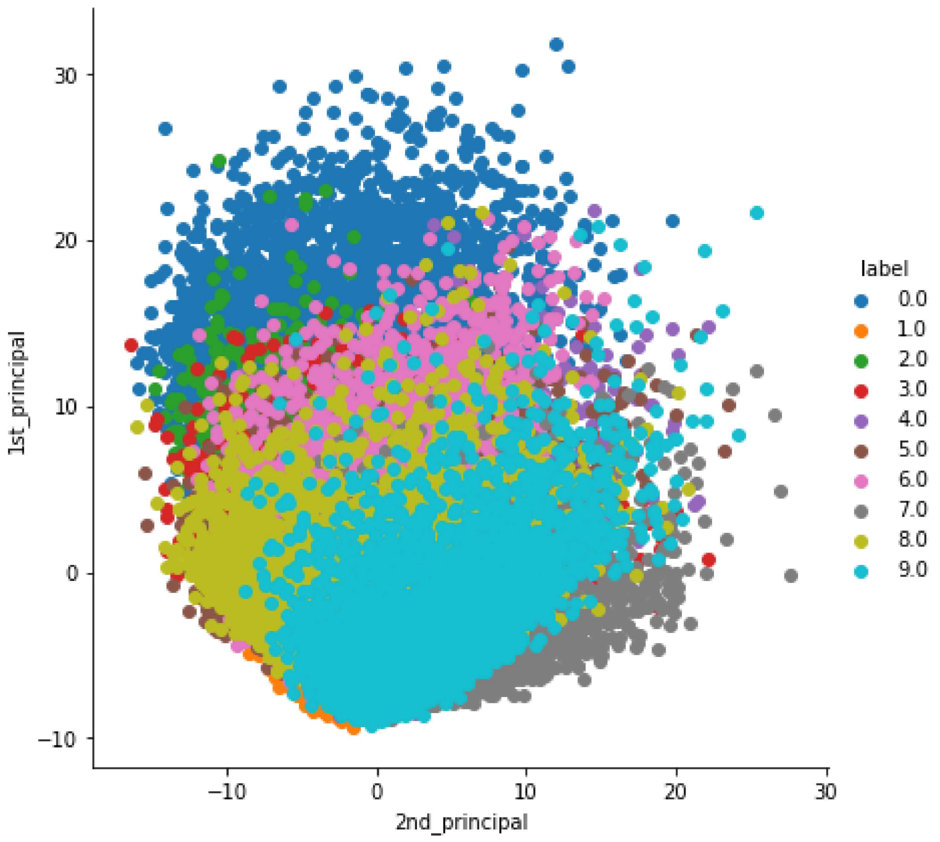
Comparing our custom implementation with scikit learn results

In [16]:
```
# initializing the pca
from sklearn import decomposition
pca = decomposition.PCA()
```

In [17]:
```
## fitting the data
pca.n_components = 2  ## since we are considering only 2 principal components to
pca_data = pca.fit_transform(sample_data)
pca_data.shape
```

Out[17]:
```
(42000, 2)
```

In [18]:
```
## creating the plot
pca_data = np.vstack((pca_data.T, labels)).T
pca_df = pd.DataFrame(data=pca_data, columns=("1st_principal", "2nd_principal", '
sn.FacetGrid(pca_df, hue="label", height=6).map(plt.scatter, '2nd_principal', '1s
plt.show()
```



Observations

So we have reduced dimensions of data from 784 to 2 dimensions and created visulization for the dataset. We can observe that data are partially separated but not completely separated so we cannot make clear assumptions about the data from the above graph but consequently we observe that data points for same digits are grouped together like all points of 0 digit lie only in the upper part with blue dots similarly all points for digit 7 are groped below in grey dots and so on for other digits.

PCA for dimensionality reduction

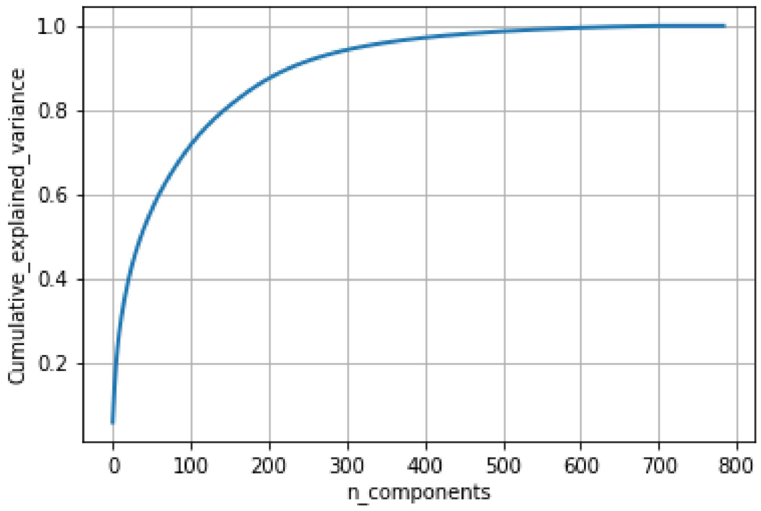
In [19]:
```
## finding all principal components
pca.n_components = 784
pca_data = pca.fit_transform(sample_data)


## calculating the percentage of variance explained by each component
percentage_var_explained = pca.explained_variance_ / np.sum(pca.explained_varianc

## finding the cummulattive sum to plot the graph
cum_var_explained = np.cumsum(percentage_var_explained)

# Plot the PCA spectrum
plt.figure(1, figsize=(6, 4))

plt.clf()
plt.plot(cum_var_explained, linewidth=2)
plt.axis('tight')
plt.grid()
plt.xlabel('n_components')
plt.ylabel('Cumulative_explained_variance')
plt.show()
```



Observation

From the above plot we can see that when we take almost 200 principal components instead of 784 components then 90% of the total variance is explained, so we can consider 200 components only for getting insights of the data which can save our time upto a large extenct.