PCA_Iris_Dataset

November 5, 2018

1 PCA on Iris Data Set

Why this notebook To have hands-on exercise on PCA using Python
Reference None. Since IRIS Dataset is easily available, chosen that to try PCA

```
In [1]: import numpy as np
        import matplotlib.pyplot as plt # for plotting
        import seaborn as sns
        import pandas as pd
        from sklearn.preprocessing import StandardScaler # for column standardization
        from scipy.linalg import eigh # for eigen value/vector calculation
```

1.1 Load Data Set

```
In [2]: df = pd.read_csv('../../../datasets/iris-dataset/iris.csv')
        df.head()
```

```
Out[2]:    sepal_length  sepal_width  petal_length  petal_width species
        0           5.1          3.5           1.4          0.2  setosa
        1           4.9          3.0           1.4          0.2  setosa
        2           4.7          3.2           1.3          0.2  setosa
        3           4.6          3.1           1.5          0.2  setosa
        4           5.0          3.6           1.4          0.2  setosa
```

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

```
Out[3]:        sepal_length  sepal_width  petal_length  petal_width
        count    150.000000   150.000000    150.000000   150.000000
        mean       5.843333     3.054000      3.758667     1.198667
        std        0.828066     0.433594      1.764420     0.763161
        min        4.300000     2.000000      1.000000     0.100000
        25%        5.100000     2.800000      1.600000     0.300000
        50%        5.800000     3.000000      4.350000     1.300000
        75%        6.400000     3.300000      5.100000     1.800000
        max        7.900000     4.400000      6.900000     2.500000
```

```
In [4]: # move labels to a seperate data frame
        df_labels = df['species']
        df_data = df.drop('species',axis=1)
```

```
In [5]: df_labels.shape
```

```
Out[5]: (150,)
```

```
In [6]: df_labels.head()
```

```
Out[6]: 0    setosa
        1    setosa
        2    setosa
        3    setosa
        4    setosa
        Name: species, dtype: object
```

```
In [7]: df_data.shape
```

```
Out[7]: (150, 4)
```

```
In [8]: df_data.head()
```

```
Out[8]:    sepal_length  sepal_width  petal_length  petal_width
        0           5.1          3.5           1.4          0.2
        1           4.9          3.0           1.4          0.2
        2           4.7          3.2           1.3          0.2
        3           4.6          3.1           1.5          0.2
        4           5.0          3.6           1.4          0.2
```

1.2 Column Standardize the Data

```
In [9]: # Column Standardize the data
        standardized_data = StandardScaler().fit_transform(df_data)
```

```
In [10]: standardized_data.shape
```

```
Out[10]: (150, 4)
```

```
In [11]: standardized_data[1:4]
```

```
Out[11]: array([[-1.14301691, -0.1249576 , -1.3412724 , -1.31297673],
                [-1.38535265,  0.33784833, -1.39813811, -1.31297673],
                [-1.50652052,  0.10644536, -1.2844067 , -1.31297673]])
```

1.3 Computing PCA manually

1.3.1 Compute Covariance Matrix

```
In [12]: # Compute covariance Matrix
         sample_data = standardized_data
         covar_matrix = np.matmul(sample_data.T,sample_data)
         covar_matrix.shape
```

```
Out[12]: (4, 4)
```

```
In [13]: covar_matrix
```

```
Out[13]: array([[150.        , -16.40538749, 130.7631236 , 122.69304501],
               [-16.40538749, 150.        , -63.07741446, -53.48161344],
               [130.7631236 , -63.07741446, 150.        , 144.41356456],
               [122.69304501, -53.48161344, 144.41356456, 150.        ]])
```

1.3.2 Compute Eigen Values and Eigen Vectors

```
In [14]: # calculate eignen values and eigen vectors
         eigen_values, eigen_vectors = eigh(covar_matrix)
```

```
In [15]: eigen_values.shape
```

```
Out[15]: (4,)
```

```
In [16]: eigen_vectors.shape
```

```
Out[16]: (4, 4)
```

```
In [17]: eigen_values
```

```
Out[17]: array([  3.09115609,  22.10299175, 138.18313961, 436.62271256])
```

```
In [18]: eigen_vectors
```

```
Out[18]: array([[ 0.26199559,  0.72101681, -0.37231836,  0.52237162],
               [-0.12413481, -0.24203288, -0.92555649, -0.26335492],
               [-0.80115427, -0.14089226, -0.02109478,  0.58125401],
               [ 0.52354627, -0.6338014 , -0.06541577,  0.56561105]])
```

1.3.3 2-D Visualization

```
In [19]: # Since we are going to do 2-D visualization, take last two eigen vectors having max
         eigen_2d = eigen_vectors[:,[-1,-2]]
         eigen_2d = eigen_2d.T
         eigen_2d.shape
```

```
Out[19]: (2, 4)
```

```
In [20]: # project data points into hyper plane
         new_data_matrix = np.matmul(eigen_2d,standardized_data.T)
```

```
In [21]: 'Resultant matrix {0} x {1} = {2}'.format(eigen_2d.shape,standardized_data.T.shape,ne
```

```
Out[21]: 'Resultant matrix (2, 4) x (4, 150) = (2, 150)'
```

```
In [22]: # Add label column
         new_data_matrix = np.vstack((new_data_matrix, df_labels))
```

```
In [23]: new_data_matrix.shape
```

Out[23]: (3, 150)

```
In [24]: # Transpose the matrix to have data points as rows
         new_data_matrix = new_data_matrix.T
         new_data_matrix.shape
```

Out[24]: (150, 3)

```
In [25]: new_data_matrix[:5]
```

```
Out[25]: array([[-2.2645417283949003, -0.5057039027737857, 'setosa'],
                [-2.08642550061616, 0.6554047293691359, 'setosa'],
                [-2.3679504490625267, 0.31847731084724806, 'setosa'],
                [-2.3041971611520102, 0.5753677125331943, 'setosa'],
                [-2.3887774935056423, -0.6747673967025166, 'setosa']], dtype=object)
```

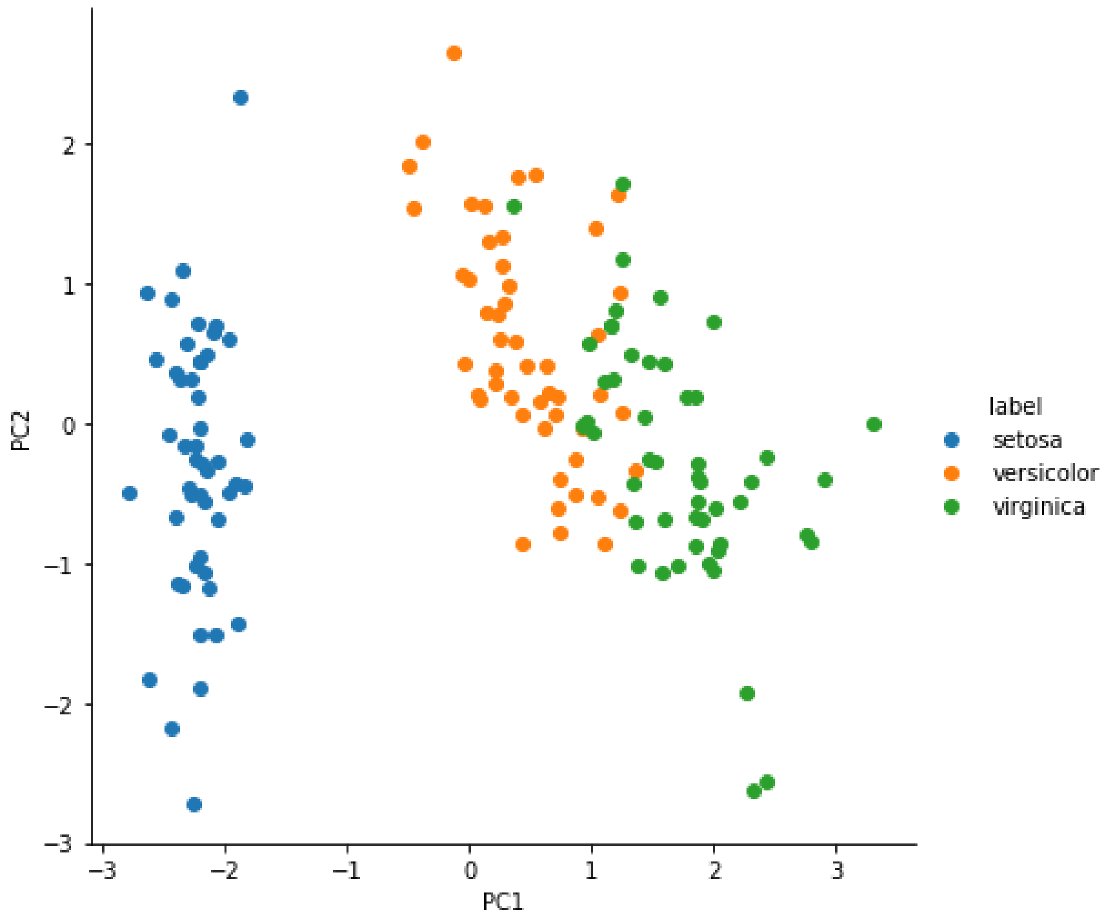
```
In [26]: # Create a data frame using new data matrix for plotting
         new_data_df = pd.DataFrame(data=new_data_matrix,columns=['PC1','PC2','label'])
         new_data_df.head()
```

Out[26]:

	PC1	PC2	label
0	-2.26454	-0.505704	setosa
1	-2.08643	0.655405	setosa
2	-2.36795	0.318477	setosa
3	-2.3042	0.575368	setosa
4	-2.38878	-0.674767	setosa

```
In [27]: sns.FacetGrid(data=new_data_df,hue='label',height=6).map(plt.scatter,'PC1','PC2').add_
```

Out[27]: <seaborn.axisgrid.FacetGrid at 0x7fc81357eef0>



1.4 PCA using SciKit-Learn

```
In [28]: # import required modules
         from sklearn import decomposition
```

```
In [29]: # init PCA
         pca = decomposition.PCA()
```

1.4.1 2-D Visualization

```
In [30]: # config required parameters
         pca.n_components = 2
         pca_data = pca.fit_transform(standardized_data)

         print('Size of PCA reducated data shape: ', pca_data.shape)
```

```
Size of PCA reducated data shape:  (150, 2)
```

In [31]:
```
# add labels to PCA new data matrix for plotting
pca_data = np.vstack((pca_data.T, df_labels)).T
print('New Projected Matrix shape : ', pca_data.shape)
```

```
New Projected Matrix shape :  (150, 3)
```

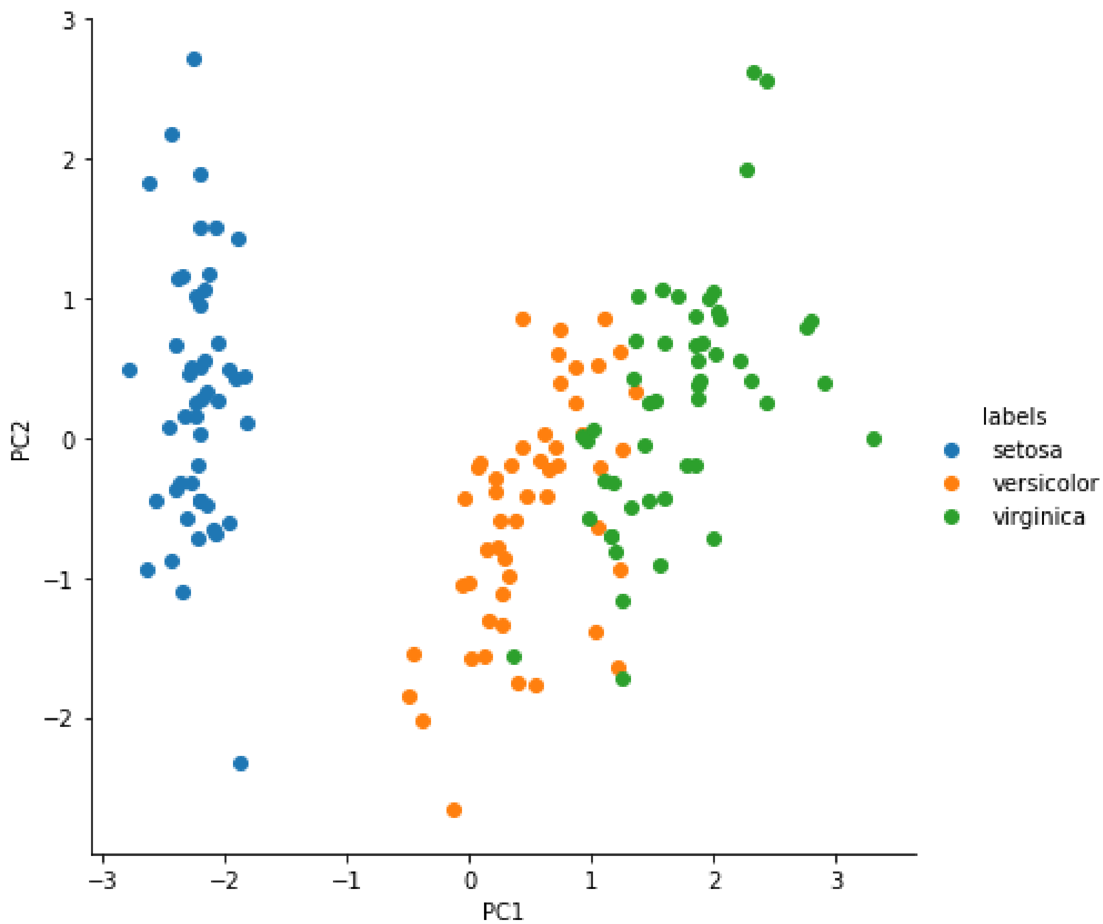
In [32]:
```
# create dataframe out of PCA Data
new_data_df = pd.DataFrame(data=pca_data, columns=['PC1','PC2','labels'])
new_data_df.head()
```

Out[32]:

	PC1	PC2	labels
0	-2.26454	0.505704	setosa
1	-2.08643	-0.655405	setosa
2	-2.36795	-0.318477	setosa
3	-2.3042	-0.575368	setosa
4	-2.38878	0.674767	setosa

In [33]:
```
# Plot the matrix
sns.FacetGrid(new_data_df, hue='labels',height=6).map(plt.scatter, 'PC1', 'PC2').add_l
```

Out[33]: <seaborn.axisgrid.FacetGrid at 0x7fc8128e54a8>



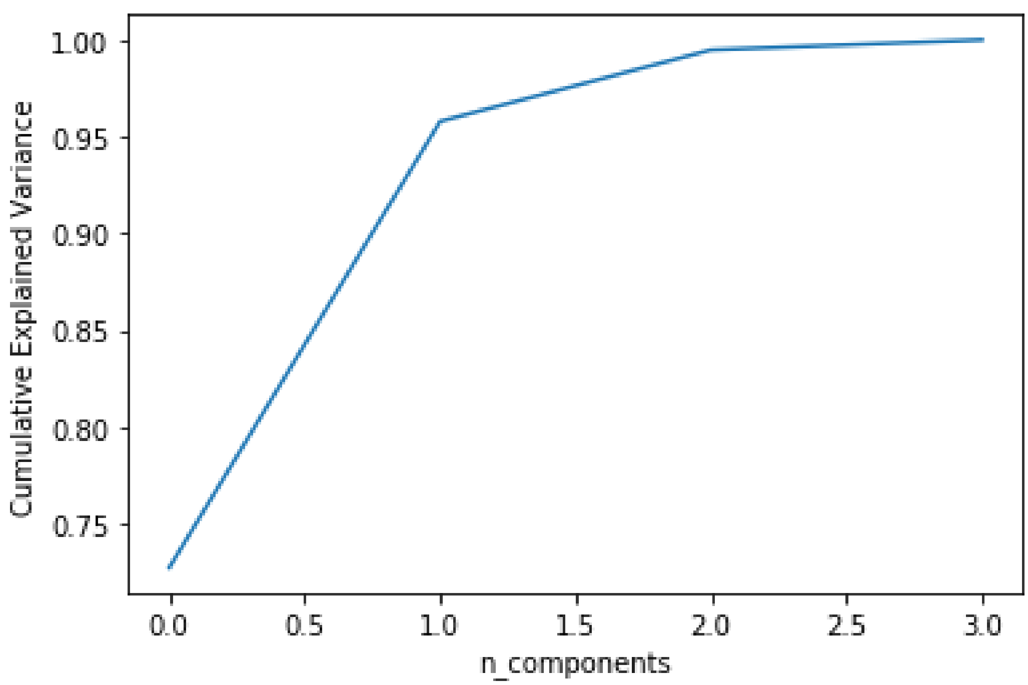
1.4.2 CDF of Data Variances

```
In [34]: pca.n_components = 4
         pca_data = pca.fit_transform(standardized_data)

         percentage_var_explained = pca.explained_variance_ / np.sum(pca.explained_variance_)
         print('Percentage of data explained: ',percentage_var_explained)

         cum_var_explained = np.cumsum(percentage_var_explained)

         print('Cumulative Sum of Vairances explained : ', cum_var_explained)
```

```
Percentage of data explained:  [0.72770452 0.23030523 0.03683832 0.00515193]
Cumulative Sum of Vairances explained :  [0.72770452 0.95800975 0.99484807 1.        ]
```

```
In [35]: plt.figure(1, figsize=(6,4))
         plt.plot(cum_var_explained)
         plt.xlabel('n_components')
         plt.ylabel('Cumulative Explained Variance')
```

```
Out[35]: Text(0, 0.5, 'Cumulative Explained Variance')
```



1.4.3 Pair Plot of all components

In [36]:
```
print(pca_data.T.shape, df_labels.shape)
pca_data = np.vstack((pca_data.T, df_labels))
pca_data = pca_data.T
print(pca_data.shape)
```

```
(4, 150) (150,)
(150, 5)
```

In [37]:
```
new_data_df = pd.DataFrame(data=pca_data,columns=['PC1','PC2','PC3','PC4','labels'])
new_data_df.head()
```

Out[37]:

	PC1	PC2	PC3	PC4	labels
0	-2.26454	0.505704	-0.121943	-0.0230733	setosa
1	-2.08643	-0.655405	-0.227251	-0.103208	setosa
2	-2.36795	-0.318477	0.0514796	-0.0278252	setosa
3	-2.3042	-0.575368	0.0988604	0.0663115	setosa
4	-2.38878	0.674767	0.0214278	0.0373973	setosa

In [38]:
```
sns.pairplot(new_data_df, hue='labels', vars=['PC1','PC2','PC3','PC4'],height=4)
```

```
/home/mlstudy/anaconda3/envs/mlstudy_1/lib/python3.6/site-packages/scipy/stats/stats.py:1713: F
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```

Out[38]: <seaborn.axisgrid.PairGrid at 0x7fc7ef767cc0>


```
In [39]: #plt.scatter(pca_data[:,0], pca_data[:,1],c=df_labels)
         df_labels.unique()
```

```
Out[39]: array(['setosa', 'versicolor', 'virginica'], dtype=object)
```

```
In [40]: # create map of labels to int for plotting
         targets = df_labels.unique()
         targets
```

```
Out[40]: array(['setosa', 'versicolor', 'virginica'], dtype=object)
```