

L13 fork from PCA - IRIS

February 17, 2023

```
[ ]: from sklearn import datasets
      #we use iris data
      iris = datasets.load_iris()
      iris_X=iris.data
```

```
[ ]: len(iris_X[0]) #first let us see the dimension of the feature
```

```
[ ]: 4
```

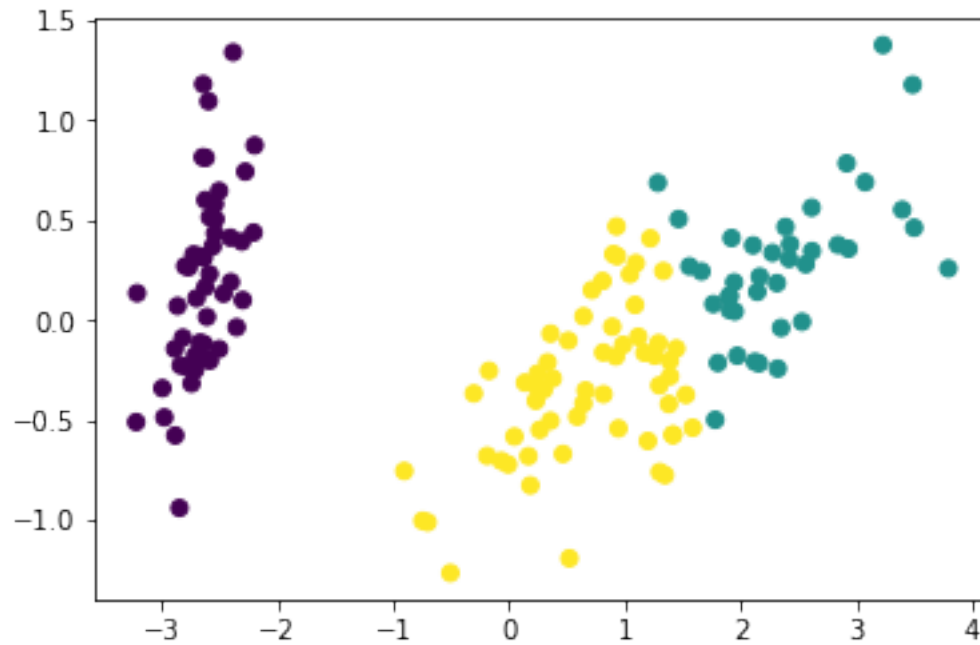
```
[ ]: from sklearn.decomposition import PCA
      #let us use PCA to compress the data to 2 dimensions
      pca_2 = PCA(n_components=2) #define the PCA model
      pca_iris=pca_2.fit_transform(iris_X) #use the PCA model to fit and transform
      ↪ the original data to 2-dimension data
```

```
[ ]: from sklearn.cluster import KMeans
      #we use clustering to cluster the transformed data
      kmeans = KMeans(n_clusters=3, random_state=0) #define the cluster model
      cluster_pca=kmeans.fit(pca_iris) #fit the model with transformed data
      labels_pca=kmeans.labels_ #generate the label
```

```
[ ]: import matplotlib.pyplot as plt
      %matplotlib inline

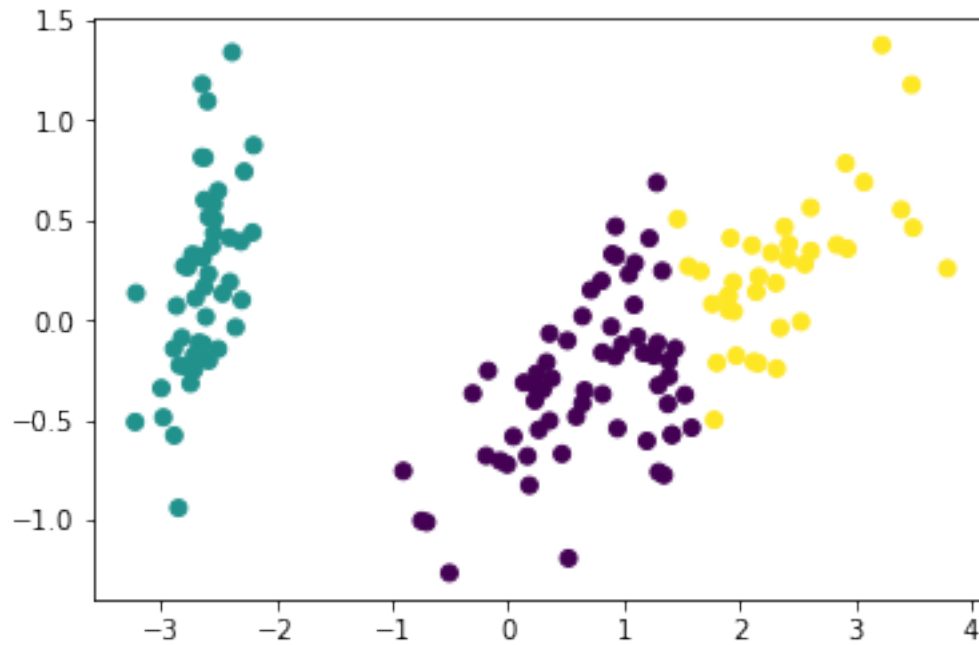
      #let use plot the clustered data
      plt.scatter(pca_iris[:, 0], pca_iris[:, 1], c=labels_pca)
```

```
[ ]: <matplotlib.collections.PathCollection at 0x1a259590cd0>
```



```
[ ]: #we want to cluster the original data  
cluster_pca=kmeans.fit(iris.data)  
labels_ori=kmeans.labels_  
plt.scatter(pca_iris[:, 0], pca_iris[:, 1], c=labels_ori)  
#very similar to the result with PCA
```

```
[ ]: <matplotlib.collections.PathCollection at 0x1a259693970>
```



```
[ ]: #check the label
print(labels_pca)
print(labels_ori)
print(iris.target)
```

```
[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 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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2 2]
```

```
[ ]: #reorganize the label
import numpy as np

clu_pca_0=np.where(labels_pca==0)
```

```
clu_ori_0=np.where(labels_ori==1)
clu_pca_1=np.where(labels_pca==2)
clu_ori_1=np.where(labels_ori==0)
clu_pca_2=np.where(labels_pca==1)
clu_ori_2=np.where(labels_ori==2)
```

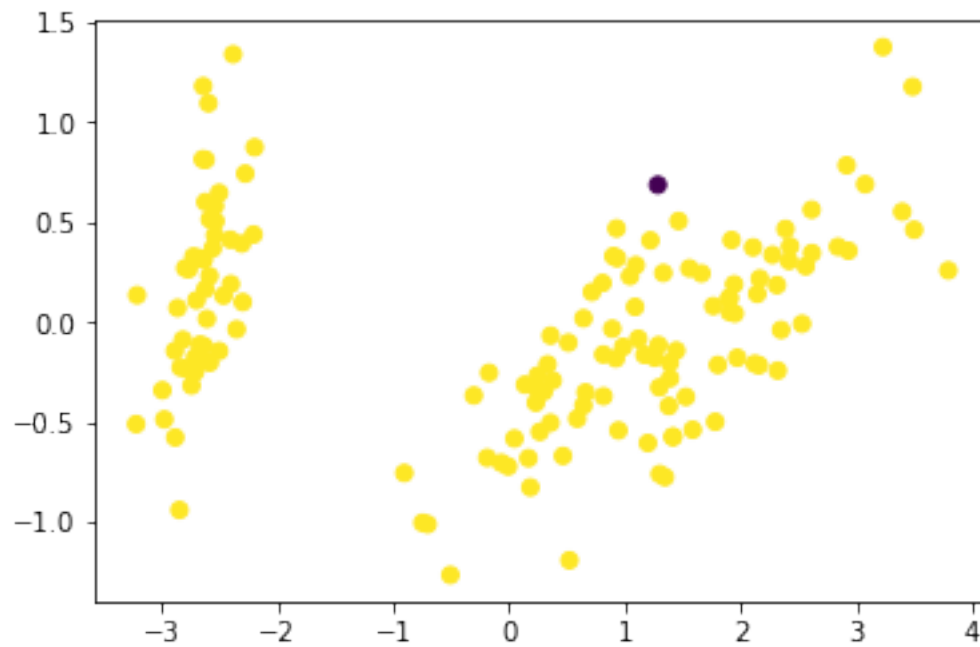
```
[ ]: labels_pca[clu_pca_0]=0
labels_pca[clu_pca_1]=1
labels_pca[clu_pca_2]=2
labels_ori[clu_ori_0]=0
labels_ori[clu_ori_1]=1
labels_ori[clu_ori_2]=2
```

```
[ ]: print(labels_pca)
print(labels_ori)
print(iris.target)
```

```
[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 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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2 2 1 1 2 2 2 2 1 2 1 2 1 2 2 1 1 2 2 2 2 2 1 2 2 2 2 1 2 2 2 1 2 2 2 1 2
2 1]
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2 1]
[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
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
2 2]
```

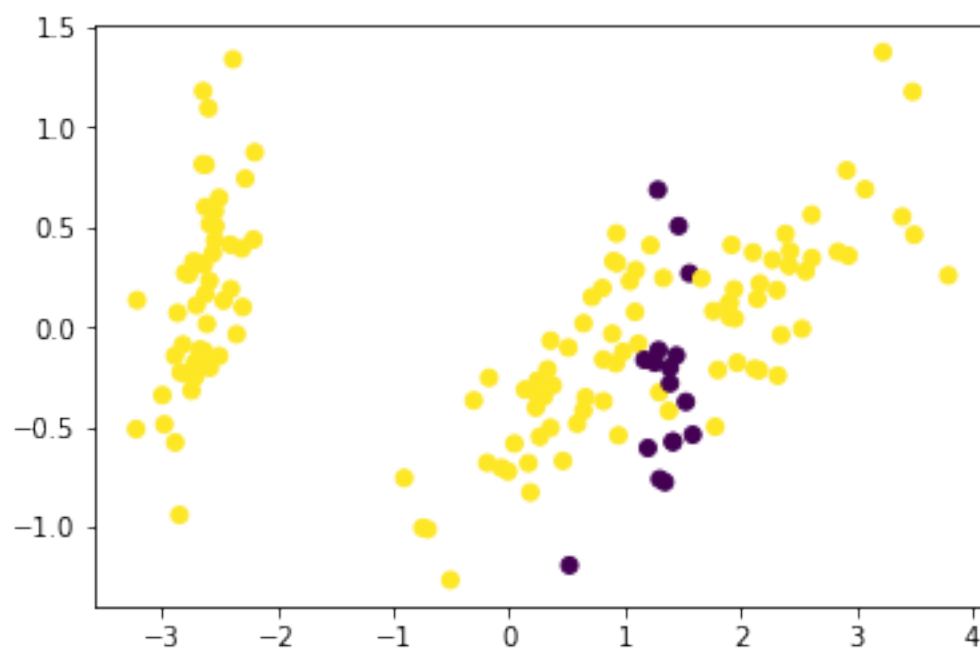
```
[ ]: same_diff=(labels_ori==labels_pca) #let us check which data points have
↳ different label with/without PCA
plt.scatter(pca_iris[:, 0], pca_iris[:, 1], c=same_diff)
#only one data point
```

```
[ ]: <matplotlib.collections.PathCollection at 0x1a259704eb0>
```



```
[ ]: #let us see how many data points are clustered correctly after PCA
pca_true=(iris.target==labels_pca)
plt.scatter(pca_iris[:, 0], pca_iris[:, 1], c=pca_true)
```

```
[ ]: <matplotlib.collections.PathCollection at 0x1a25976fa60>
```



```
[ ]: #new part
      #obtain the eigenvalues and eigenvectors
      #let us conduct PCA without dimension reduction
      pca_4 = PCA(n_components=4)
      pca_4.fit(iris_X)
```

```
[ ]: PCA(n_components=4)
```

```
[ ]: #get the covariance matrix, the eigenvalues and eigenvector
      cov_M=pca_4.get_covariance()
      e_M=pca_4.components_
      lambda_V=pca_4.explained_variance_
```

```
[ ]: e_M
```

```
[ ]: array([[ 0.36138659, -0.08452251,  0.85667061,  0.3582892 ],
            [ 0.65658877,  0.73016143, -0.17337266, -0.07548102],
            [-0.58202985,  0.59791083,  0.07623608,  0.54583143],
            [-0.31548719,  0.3197231 ,  0.47983899, -0.75365743]])
```

```
[ ]: lambda_V
```

```
[ ]: array([4.22824171, 0.24267075, 0.0782095 , 0.02383509])
```

```
[ ]: #let us check  $Q e_i = \lambda_i e_i$ 
      print(np.dot(cov_M,e_M[0,:]))
      print(np.dot(lambda_V[0],e_M[0,:]))
```

```
[ 1.52802986 -0.35738162  3.62221038  1.51493333]
[ 1.52802986 -0.35738162  3.62221038  1.51493333]
```

```
[ ]: #calculate the covariance matrix by ourself
      mat_X=np.mat(iris_X-np.mean(iris_X,0))
      Q=np.dot(mat_X.T,mat_X) #here we do not divide it by N-1, then we will see it
      →will not influence the results in general
```

```
[ ]: eigval, eigvec = np.linalg.eig(Q) #solve the eigenvalues and eigenvectors
```

```
[ ]: eigvec #same as pca_4.components_.T
```

```
[ ]: matrix([[ 0.36138659, -0.65658877, -0.58202985,  0.31548719],
            [-0.08452251, -0.73016143,  0.59791083, -0.3197231 ],
            [ 0.85667061,  0.17337266,  0.07623608, -0.47983899],
            [ 0.3582892 ,  0.07548102,  0.54583143,  0.75365743]])
```

```
[ ]: eigval #different from pca_4.components_
```

```
[ ]: array([630.0080142 , 36.15794144, 11.65321551, 3.55142885])
```

```
[ ]: eigval/149 #devided by N-1, it becomes same as pca_4.components_  
      #Whether to devide by N-1 will not influence the results
```

```
[ ]: array([4.22824171, 0.24267075, 0.0782095 , 0.02383509])
```

```
[ ]: print(np.dot(Q,eigvec[:,0])) #Qe_1  
      print(eigval[0]*eigvec[:,0]) #lambda_1e_1
```

```
[[227.67644905]  
 [-53.24986124]  
 [539.70934728]  
 [225.72506561]]  
[[227.67644905]  
 [-53.24986124]  
 [539.70934728]  
 [225.72506561]]
```

```
[ ]:
```