Q3

May 10, 2024

0.1 Mahdi Anvari 610700002 Homework 2 of Machine Learning Question 3

[96]:

```python
# importing libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from sklearn.metrics import adjusted_rand_score
from sklearn import metrics
from sklearn.decomposition import PCA
```

a. Perform clustering (with 2 and 3 clusters) on the samples and compare the results to Project and Tissue label in the annotation file.

[97]:

```python
AnnotationDF = pd.read_csv("Leaf_Root_annotation.csv")
RawDF = pd.read_csv("Leaf_Root_raw_data.csv")
NormalizedDF = pd.read_csv("Leaf_Root_normalized_data.csv")
#print(AnnotationDF.shape)
#print(RawDF.shape)
#print(NormalizedDF.shape)

Projects = AnnotationDF.values[:,1]
Tissues = AnnotationDF.values[:,4]
print(Tissues)
print(Projects)

RawNP = RawDF.values
RawData = np.transpose(RawNP[:,1:])
NormalizedNP = NormalizedDF.values
NormalizedData = np.transpose(NormalizedNP[:,1:])
```

```
['Leaf' 'Leaf' 'Leaf' 'Leaf' 'Root' 'Root' 'Root' 'Root' 'Leaf' 'Root'
 'Leaf' 'Leaf' 'Root' 'Root' 'Root' 'Root' 'Root' 'Leaf' 'Leaf' 'Leaf'
 'Leaf' 'Leaf' 'Leaf' 'Root' 'Root' 'Root']
['PRJNA493167' 'PRJNA493167' 'PRJNA493167' 'PRJNA493167' 'PRJNA493167'
 'PRJNA493167' 'PRJNA493167' 'PRJNA493167' 'PRJNA661543' 'PRJNA661543'
 'PRJNA661543' 'PRJNA661543' 'PRJNA661543' 'PRJNA661543' 'PRJNA730337'
 'PRJNA730337' 'PRJNA730337' 'PRJNA730337' 'PRJNA730337' 'PRJNA730337'
 'PRJNA730337' 'PRJNA730337' 'PRJNA730337' 'PRJNA730337' 'PRJNA730337'
 'PRJNA730337']
```

[98]:

```
# for raw data
Kmeans2 = KMeans(n_clusters=2, n_init=10)
Kmeans3 = KMeans(n_clusters=3, n_init=10)
Clusters2 = Kmeans2.fit_predict(RawData)
Clusters3 = Kmeans3.fit_predict(RawData)
print(Clusters2)
print(Clusters3)
ari2 = adjusted_rand_score(Tissues,Clusters2)
ari3 = adjusted_rand_score(Projects,Clusters3)
print("For raw data:")
print("Adjusted Rand Index of Kmeans based on tissues is",ari2)
print("Adjusted Rand Index of Kmeans based on projects is",ari3)
```

```
[0 0 0 0 1 1 1 1 0 1 0 0 1 1 1 1 1 0 0 0 0 0 0 1 1 1]
[2 0 2 2 2 2 2 2 0 2 0 0 2 2 1 1 1 0 0 0 0 0 0 1 1 1]
For raw data:
Adjusted Rand Index of Kmeans based on tissues is 1.0
Adjusted Rand Index of Kmeans based on projects is 0.30347192456065153
```

[99]:

```
# for normalized data
Kmeans2 = KMeans(n_clusters=2, n_init=10)
Kmeans3 = KMeans(n_clusters=3, n_init=10)
Clusters2 = Kmeans2.fit_predict(NormalizedData)
Clusters3 = Kmeans3.fit_predict(NormalizedData)
print(Clusters2)
print(Clusters3)
ari2 = adjusted_rand_score(Tissues,Clusters2)
ari3 = adjusted_rand_score(Projects,Clusters3)
print("For normalized data:")
print("Adjusted Rand Index of Kmeans based on tissues is",ari2)
print("Adjusted Rand Indexof Kmeans based on projects is",ari3)
```

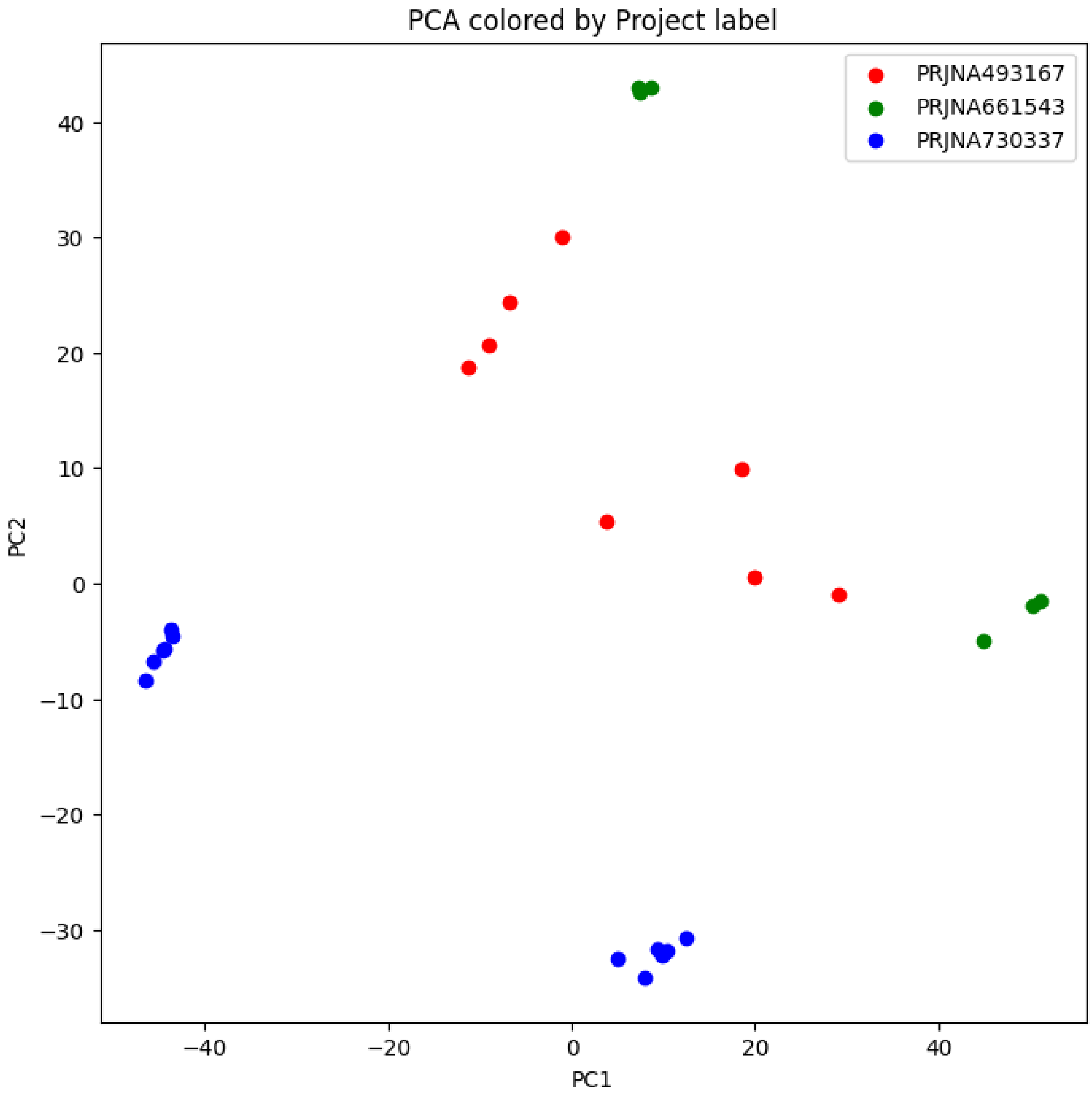
```
[1 1 1 1 0 0 0 0 1 0 1 1 0 0 0 0 0 1 1 1 1 1 1 0 0 0]
[0 0 0 0 1 1 1 1 0 1 0 0 1 1 2 2 2 0 0 0 0 0 0 2 2 2]
For normalized data:
Adjusted Rand Index of Kmeans based on tissues is 1.0
Adjusted Rand Indexof Kmeans based on projects is 0.1332969363542826
```

b. Perform PCA, and color the samples once with Project label and once with the Tissue label.

[100]:

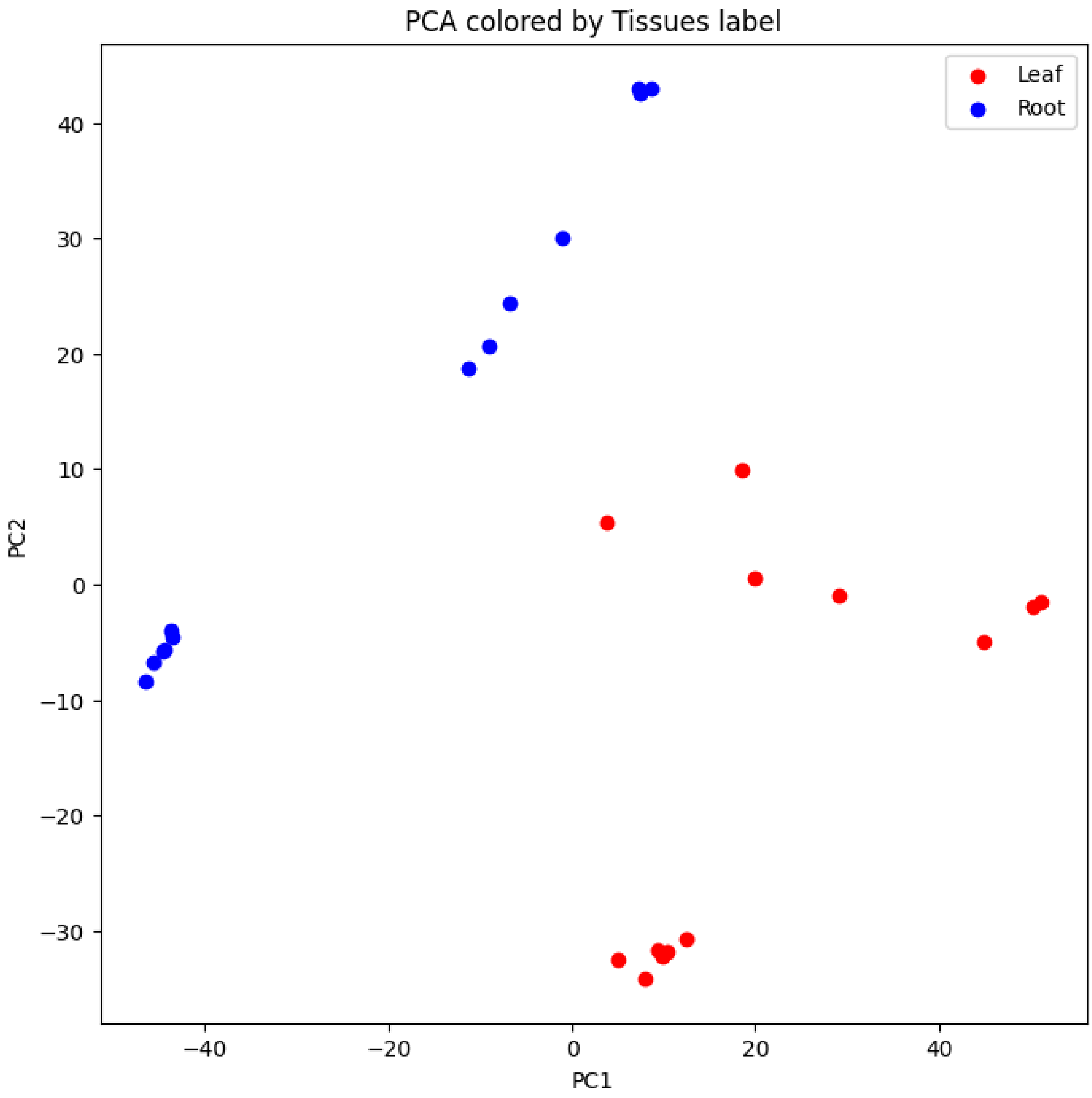
```
# for raw data
pca = PCA(n_components=20)
pcaResult = pca.fit_transform(RawData)
#print(pcaResult.shape)

plt.figure(figsize=(8, 8))
for project, color in zip(np.unique(Projects), ['r', 'g', 'b']):
    idx = AnnotationDF['Project'] == project
    plt.scatter(pcaResult[idx, 0], pcaResult[idx, 1], c=color, label=project)
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.title('PCA colored by Project label')
plt.legend()
plt.show()
```



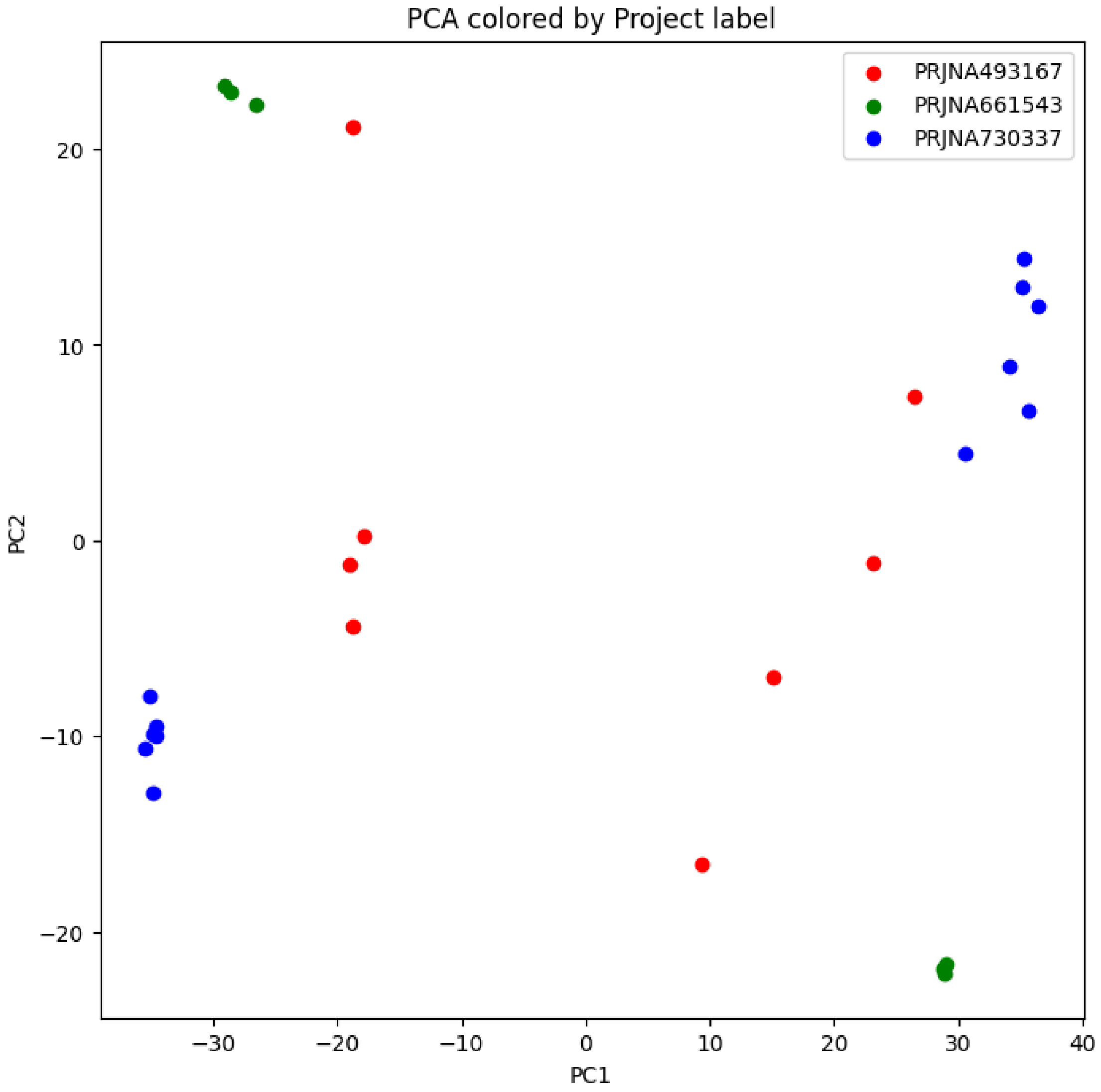
[101]:

```
# for raw data
plt.figure(figsize=(8, 8))
for tissue, color in zip(np.unique(Tissues), ['r', 'b']):
    idx = AnnotationDF['Tissue'] == tissue
    plt.scatter(pcaResult[idx, 0], pcaResult[idx, 1], c=color, label=tissue)
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.title('PCA colored by Tissues label')
plt.legend()
plt.show()
```



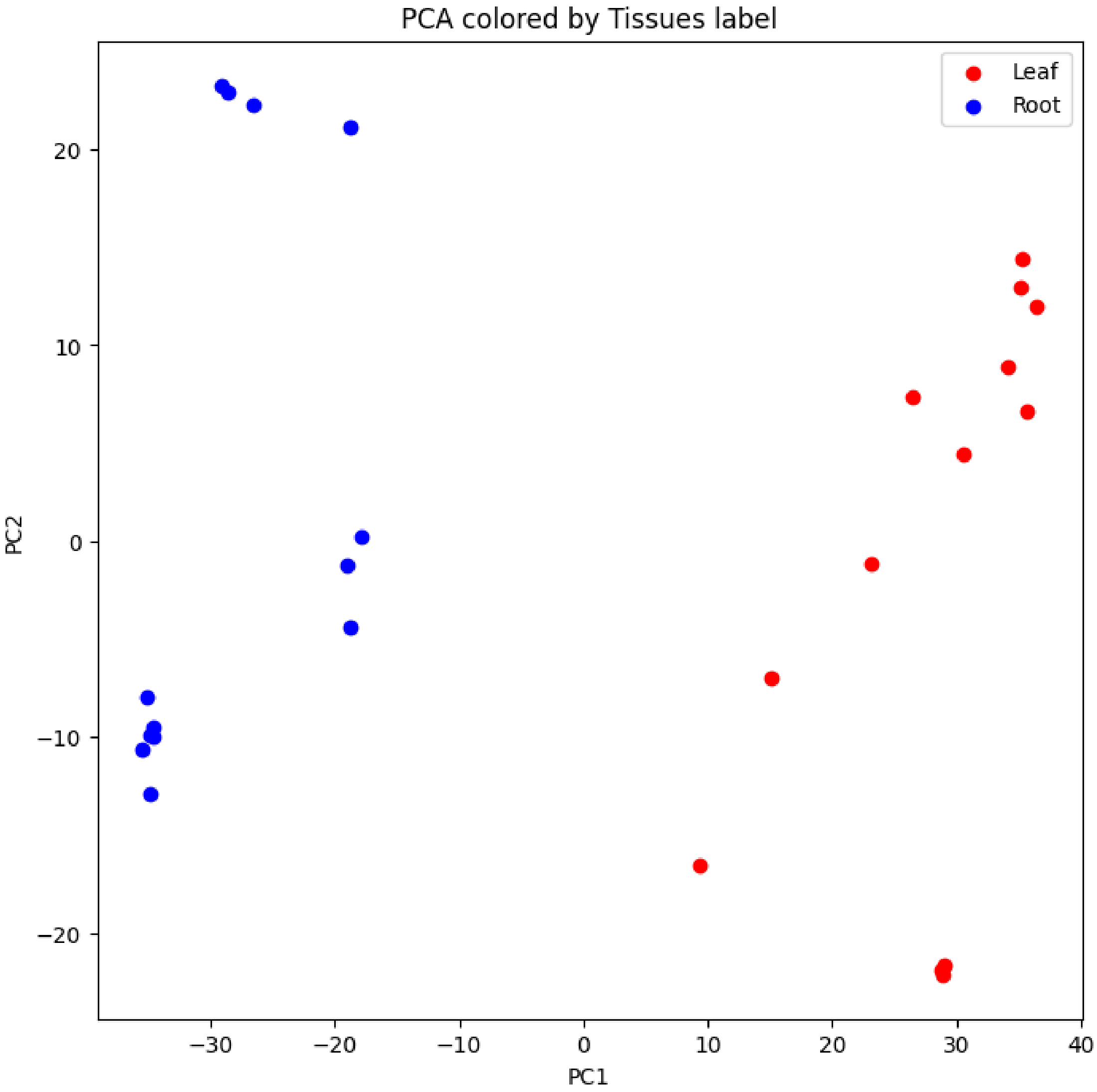
[102]:
```
# for normalized data
pca = PCA(n_components=20)
pcaResult = pca.fit_transform(NormalizedData)
#print(pcaResult.shape)
```

```python
plt.figure(figsize=(8, 8))
for project, color in zip(np.unique(Projects), ['r', 'g', 'b']):
    idx = AnnotationDF['Project'] == project
    plt.scatter(pcaResult[idx, 0], pcaResult[idx, 1], c=color, label=project)
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.title('PCA colored by Project label')
plt.legend()
plt.show()
```



[103]:

```python
# for normalized data
plt.figure(figsize=(8, 8))
for tissue, color in zip(np.unique(Tissues), ['r', 'b']):
    idx = AnnotationDF['Tissue'] == tissue
    plt.scatter(pcaResult[idx, 0], pcaResult[idx, 1], c=color, label=tissue)
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.title('PCA colored by Tissues label')
plt.legend()
plt.show()
```



[ ]:

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