CS156 (Introduction to AI), Spring 2021

Assignment_4

Roster Name: GURSIMRAN SINGH

Preferred Name (if different): SIMRAN

Student ID: 015212210

Email address: gursimransingh@sjsu.edu

References and sources

https://www.geeksforgeeks.org/python-get-unique-values-list/

https://stackoverflow.com/questions/42521772/importerror-no-module-named-plotly-plotly-in-linuxmint17-3

https://towardsdatascience.com/pca-using-python-scikit-learn-e653f8989e60

https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#deprecate-loc-reindex-listlike

https://scikit-learn.org/stable/modules/generated/sklearn.model_selection.KFold.html

https://scikit-learn.org/stable/modules/generated/sklearn.metrics.plot_confusion_matrix.html#sklearn.metrics.plot_co

Solution

Code the solution

In [1]:
```
import pandas as pd
import numpy as np
```

importing the data

In [2]:
```
dt=pd.read_csv(r'C:\Users\gursi\Desktop\CS 156\CS 156\Assignment\Assignment 4\homework4_
dt.head()
```

Out[2]:

	id	ASS1	SPX	C6orf141	SP5	SP6	ITGA8	ATP2A1	ATP2A3	ITGA2	...

	id	ASS1	SPX	C6orf141	SP5	SP6	ITGA8	ATP2A1	ATP2A3	ITGA2	...
0	TCGA-AB-2828-03	3.935027	0.523329	0.0	0.000000	0.102277	2.686908	2.837357	7.444575	2.246715	...
1	TCGA-AB-2846-03	3.372801	0.000000	0.0	0.000000	0.116270	2.083429	5.567935	8.361999	3.626850	...
2	TCGA-AB-2870-03	4.198301	0.000000	0.0	0.000000	0.249176	1.546059	6.605116	9.138359	2.858430	...
3	TCGA-AB-2872-03	4.115014	0.000000	0.0	0.222018	0.632254	2.158989	6.858708	9.201254	2.295229	...
4	TCGA-AB-2881-03	3.662169	0.467823	0.0	0.000000	0.000000	1.183388	5.567935	9.040883	1.815837	...

5 rows × 3002 columns

In [3]:
```python
#to see all the different type of cancer

from collections import Counter

Counter(dt['Class'].tolist())

#in this there are 12 different type of cancer
```

Out[3]:
```
Counter({'Leukemia': 102,
         'Bladder': 327,
         'Breast': 875,
         'Colon': 370,
         'Glioblastoma': 117,
         'Head&Neck': 415,
         'Kidney': 420,
         'LungAdeno': 424,
         'LungSquamous': 390,
         'Ovarian': 337,
         'Rectal': 128,
         'Uterine': 431})
```

In [4]:
```python
dz= dt.drop(['id','Class'],axis=1)
```

In [5]:
```python
dz.head()
```

Out[5]:

	ASS1	SPX	C6orf141	SP5	SP6	ITGA8	ATP2A1	ATP2A3	ITGA2	ITGA3	.
0	3.935027	0.523329	0.0	0.000000	0.102277	2.686908	2.837357	7.444575	2.246715	0.202624	.
1	3.372801	0.000000	0.0	0.000000	0.116270	2.083429	5.567935	8.361999	3.626850	0.449673	.

	ASS1	SPX	C6orf141	SP5	SP6	ITGA8	ATP2A1	ATP2A3	ITGA2	ITGA3	.
2	4.198301	0.000000	0.0	0.000000	0.249176	1.546059	6.605116	9.138359	2.858430	1.624238	.
3	4.115014	0.000000	0.0	0.222018	0.632254	2.158989	6.858708	9.201254	2.295229	0.326149	.
4	3.662169	0.467823	0.0	0.000000	0.000000	1.183388	5.567935	9.040883	1.815837	1.658433	.

5 rows × 3000 columns

Pca

In [6]:
```
#visualizaztion of the data with original dimensions -  we use scatter plot matrix

import plotly.express as px  # install plotly first using pip install plotly
import numpy as np
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA

pca=PCA(n_components=2)
pca1_new=pca.fit_transform(dz)


#np.shape(pca1_new)[0]

#here we are creating a new dataframe of pca values
principalDf = pd.DataFrame(data = pca1_new, columns = ['PCA1', 'PCA2'])
principalDf.head()

Dz = pd.concat([principalDf, dt[['Class']]], axis = 1)

Dz.head()
```

Out[6]:

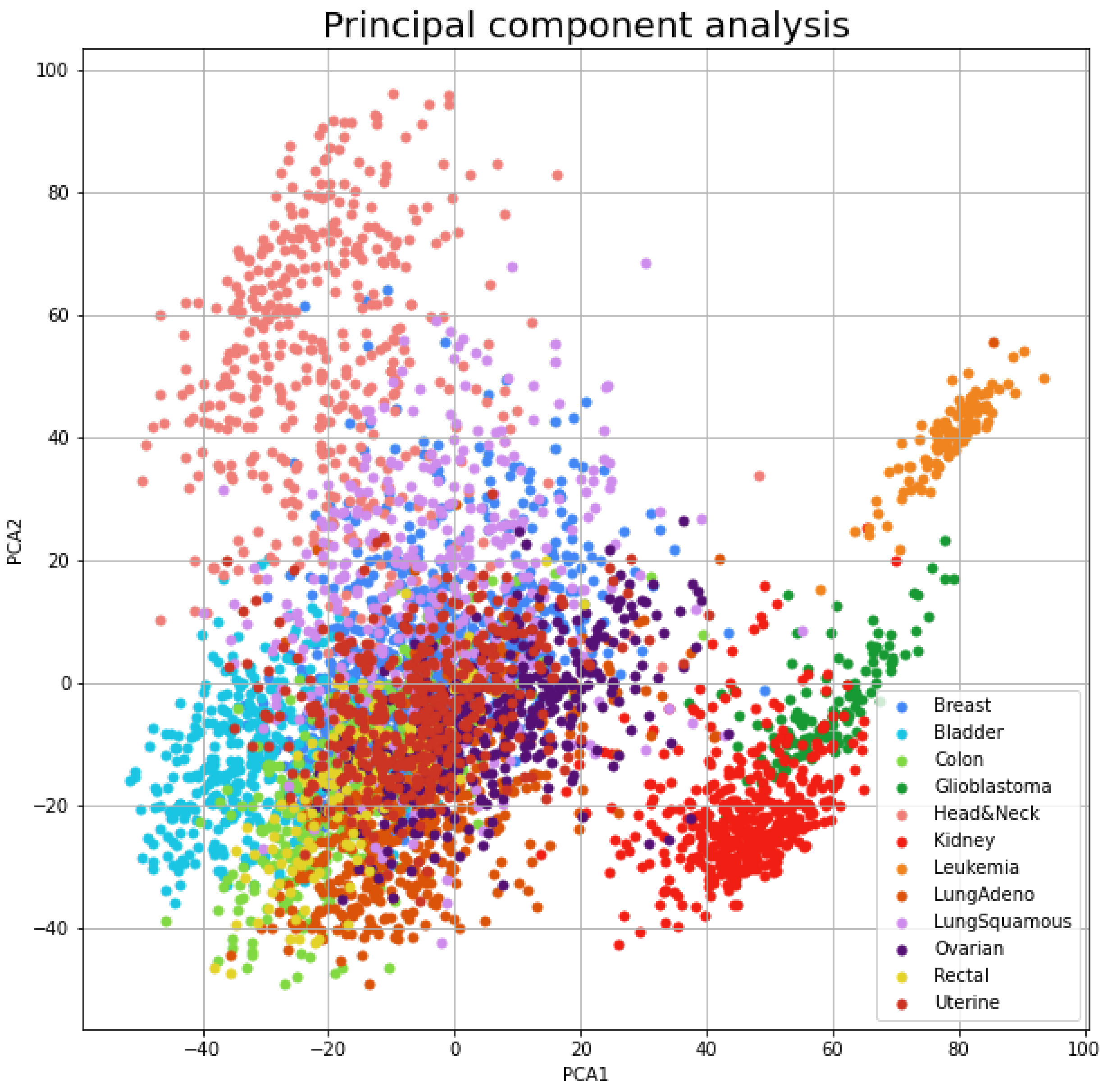
	PCA1	PCA2	Class
0	82.045989	46.713051	Leukemia
1	76.722516	37.919092	Leukemia
2	76.643207	39.867655	Leukemia
3	74.817224	36.351105	Leukemia
4	79.694765	43.781020	Leukemia

Plotting the PCA

In [7]:
```
Class = ["Breast", "Bladder", "Colon" ,"Glioblastoma","Head&Neck", "Kidney","Leukemia",

colors = ['#4287f5','#19c5e3', '#80d941','#179933','#f07e78','#f01e13','#f0841f','#db52
```

In [8]:
```
fig = plt.figure(figsize = (10,10))
ax = fig.add_subplot(1,1,1)
ax.set_xlabel('PCA1', fontsize = 10)
ax.set_ylabel('PCA2', fontsize = 10)
ax.set_title('Principal component analysis', fontsize = 20)

for class1, color in zip(Class,colors):
    print(class1)
    indicesToKeep = Dz['Class'] == class1  # here only those indices will come as true
    #print(indicesToKeep)
    ax.scatter(Dz.loc[indicesToKeep, 'PCA1'], Dz.loc[indicesToKeep, 'PCA2'] , c = color
ax.legend(Class)
ax.grid()
```

```
Breast
Bladder
Colon
Glioblastoma
Head&Neck
Kidney
Leukemia
LungAdeno
LungSquamous
Ovarian
Rectal
Uterine
```



Normalizing the data

In [9]:
```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

scaler=StandardScaler()
X_rescaled=scaler.fit_transform(dz)

print(len(X_rescaled))
```

```
4336
```

In [28]:
```
Xtrain,Xtest,Ytrain,Ytest=train_test_split(X_rescaled,dt['Class'],test_size =0.2 , rand
Xtrain.shape,Ytrain.shape

Xtrain.shape,Xtest.shape,Ytrain.shape,Ytest.shape
y1=Ytrain.to_numpy() # for cross validation we need Ytrain to be in numpy array
print(Xtrain.shape)
```

```
(3468, 3000)
```

Cross Validation

In [29]:
```
from sklearn.svm import LinearSVC
model = LinearSVC(multi_class='ovr',class_weight='balanced')
```

In [30]:
```
from sklearn.model_selection import KFold
# KFold(n_splits=10).get_n_splits(X_rescaled)
kfolds = KFold(n_splits =5)

for train_indices, validation_indices in kfolds.split(Xtrain):
    #print("Training indices: "+str(train_indices))
    #print("Validation indices: "+str(validation_indices))
    X_train_set, X_validation_set = Xtrain[train_indices], Xtrain[validation_indices]
   # Ytrain[validation_indices]
    Y_train_set, Y_validation_set = y1[train_indices], y1[validation_indices] #here pan
    model.fit( X_train_set,Y_train_set)
    print(model.score(X_validation_set,Y_validation_set))


# here KFold method divide the kinto kfolds and return 2 parameter : 1) indices of trai
```

```
0.9639769452449568
0.9654178674351584
0.9610951008645533
0.9624819624819625
0.9682539682539683
```

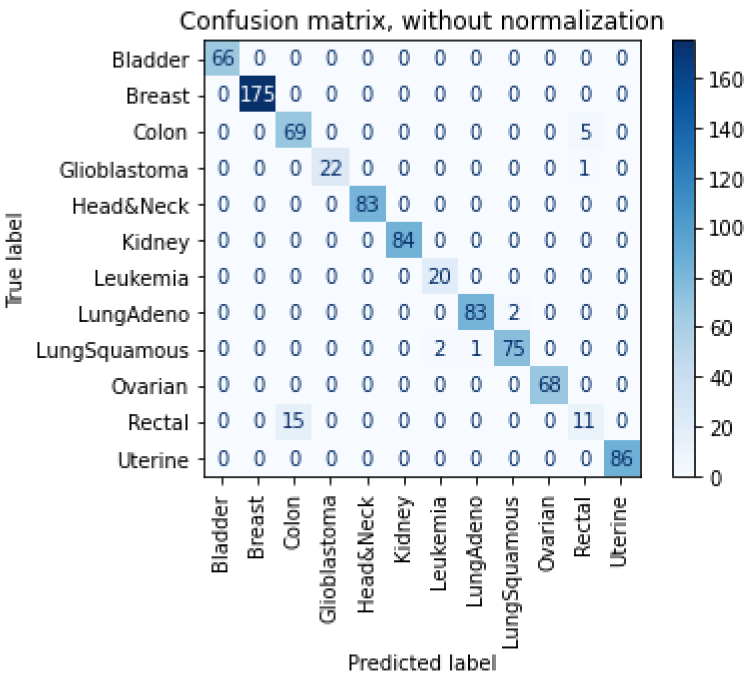
In [31]:
```
y_pred=model.predict(Xtest)
print(model.score(Xtest,Ytest))
```

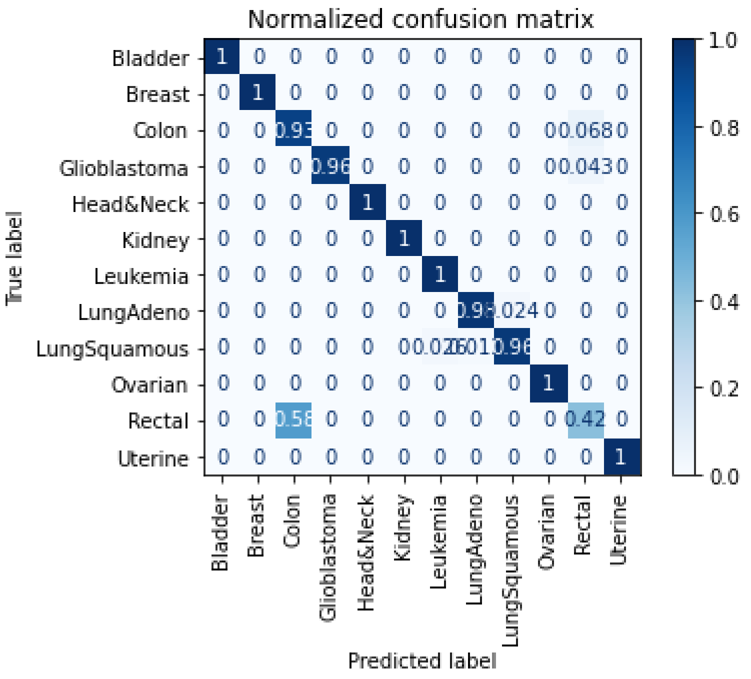
```
0.9700460829493087
```

In [32]:
```
from sklearn.metrics import plot_confusion_matrix

#print(plot_confusion_matrix(Ytest, y_pred))
```

In [33]:
```
plt.show()
```

In [34]:
```
np.set_printoptions(precision=2)
titles_options = [("Confusion matrix, without normalization", None), ("Normalized confu
for title, normalize in titles_options:
    disp = plot_confusion_matrix(model, Xtest, Ytest, cmap=plt.cm.Blues, normalize=norm
    disp.ax_.set_title(title)

    #print(title)
    #print(disp.confusion_matrix)

plt.show()
```





In [ ]:

In [ ]:

In [ ]: