CS156 (Introduction to AI), Spring 2021

Homework Assignment #4 submission

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Reference:

https://scikit-

<u>learn.org/stable/tutorial/statistical_inference/model_selection.html</u> (https://scikit-

<u>learn.org/stable/tutorial/statistical_inference/model_selection.html)</u>

https://scikit-learn.org/stable/modules/cross_validation.html (https://scikit-learn.org/stable/modules/cross_validation.html)

https://intellipaat.com/community/12741/sklearn-metrics-for-multiclass-classification (https://intellipaat.com/community/12741/sklearn-metrics-for-multiclass-classification)

https://scikit-

<u>learn.org/stable/auto_examples/model_selection/plot_confusion_matrix.</u>| (https://scikit-

learn.org/stable/auto examples/model selection/plot confusion matrix.

Solution

In [41]: import numpy as np import pandas as pd import matplotlib.pyplot as plt import matplotlib.pyplot as plt from sklearn.decomposition import PCA from sklearn.preprocessing import StandardScaler from sklearn.model_selection import train_test_split, StratifiedKFold from sklearn.svm import LinearSVC from sklearn.svm import SVC from sklearn.metrics import accuracy_score, precision_score, recall_score from sklearn.model_selection import cross_val_score from sklearn.metrics import plot_confusion_matrix from collections import Counter from sklearn.metrics import classification report from sklearn.model_selection import GridSearchCV np.random.seed(42)

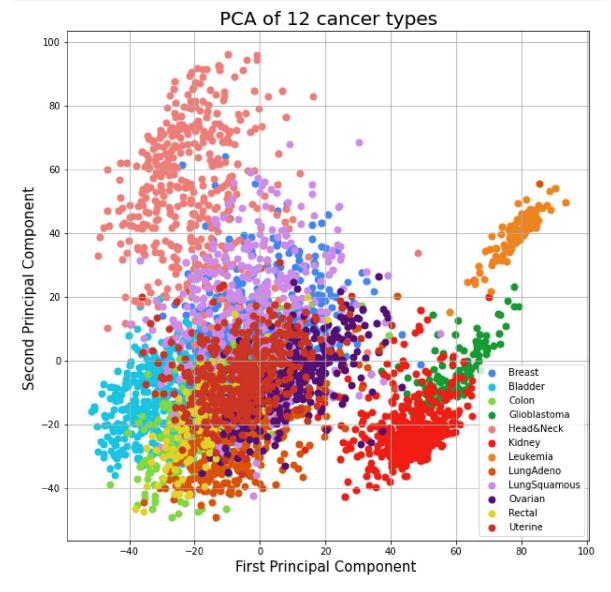
Out[42]:

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

5 rows × 3002 columns

```
In [43]:
         ▶ | pca = PCA(n_components=2)
             Y = dataSet['Class']
             X = dataSet.drop(['id'], axis =1).drop(['Class'], axis =1)
             x = X.values
             Principal_Component = pca.fit_transform(x)
             Principal_ComponentDf = pd.DataFrame(data = Principal_Component
                           , columns = ['First Principal Component', 'Second Principal Comp
             print(Principal ComponentDf)
             print(Y)
                    First Principal Component Second Principal Component
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                                    82.045989
                                                                 46.713045
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                                    76.722515
                                                                 37.919089
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                                    76.643204
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In [44]:
          ▶ | colors = {"Breast": '#4287f5',
               "Bladder": '#19c5e3',
               "Colon": '#80d941'.
               "Glioblastoma": '#179933',
               "Head&Neck": '#f07e78',
               "Kidney": '#f01e13',
               "Leukemia": '#f0841f',
              "LungAdeno": '#db5209',
               "LungSquamous": '#ce8ced',
               "Ovarian": '#551075',
               "Rectal": '#e3d329',
              "Uterine": '#cc3423'}
             finalDf = pd.concat([principalDf, Y], axis = 1)
```

```
fig = plt.figure(figsize = (10,10))
ax = fig.add_subplot(1,1,1)
ax.set_xlabel('First Principal Component ', fontsize = 15)
ax.set_ylabel('Second Principal Component ', fontsize = 15)
ax.set_title('PCA of 12 cancer types', fontsize = 20)
for target, color in colors.items():
    indicesToKeep = Y == target
    ax.scatter(finalDf.loc[indicesToKeep, 'principal component 1']
        , finalDf.loc[indicesToKeep, 'principal component 2']
        , c = color
        , s = 50)
ax.legend(colors.keys())
ax.grid()
```



Data preprocessing

```
In [16]: N
scaler = StandardScaler()
X_rescaled = scaler.fit_transform(X)

X_train, X_test, Y_train, Y_test = train_test_split(X_rescaled, Y, test_size=
X_train.shape, Y_train.shape, X_test.shape, Y_test.shape
Out[16]: ((3468, 3000), (3468,), (868, 3000), (868,))
```

Build an SVM model

Reporting/printing 5-fold cross-validation results

Mean cross validation accuracy: 0.9659763547371616

Perform systematic grid search for the regularization parameter that maximizes model accuracy

The best parameters are {'C': 0.7430147299885189} with a score of 96 Best estimator accuracy on test set 97.00

Test acuracy: 0.9700460829493087 Test precision: 0.9700460829493087 Test recall: 0.9700460829493087

Classification report

	precision	recall	f1-score	support
Bladder	1.00	1.00	1.00	66
Breast	0.98	1.00	0.99	175
Colon	0.86	0.89	0.87	74
Glioblastoma	1.00	0.91	0.95	23
Head&Neck	1.00	0.98	0.99	83
Kidney	1.00	1.00	1.00	84
Leukemia	1.00	1.00	1.00	20
LungAdeno	0.98	0.99	0.98	85
LungSquamous	0.97	0.97	0.97	78
Ovarian	1.00	1.00	1.00	68
Rectal	0.65	0.58	0.61	26
Uterine	1.00	1.00	1.00	86
accuracy			0.97	868
macro avg	0.95	0.94	0.95	868
weighted avg	0.97	0.97	0.97	868

Finally, let's transform the feature space by PCA prior to building an SVM model

```
In [35]:
               np.set_printoptions(precision=2)
               titles_options = [("Confusion matrix, without normalization", None),
                                    ("Normalized confusion matrix", 'true')]
               for title, normalize in titles options:
                    disp = plot_confusion_matrix(model, X_test, Y_test,
                                                      display_labels=np.unique(Y),
                                                      cmap=plt.cm.Blues,
                                                      normalize=normalize,
                                                     xticks_rotation='vertical')
                    disp.ax_.set_title(title)
                    print(title)
                    print(disp.confusion_matrix)
               plt.show()
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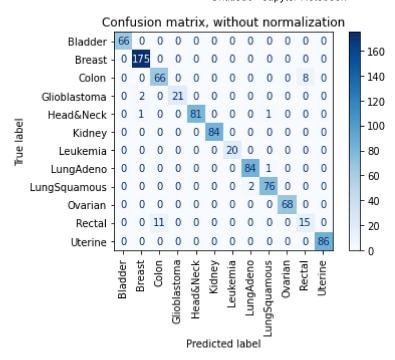
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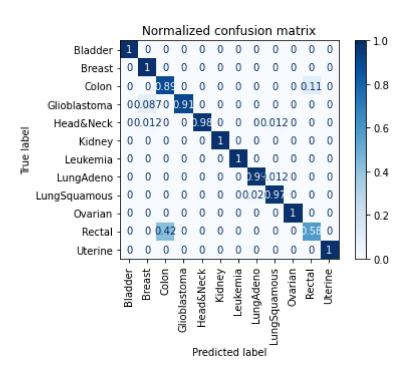
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