In [53]:
```
#ML for cancer prediction
```

In [54]:
```
#import packages
```

In [137…
```
#data handeling
import pandas as pd
import numpy as np

#data viz
import matplotlib.pyplot as plt
import seaborn as sns

#preprocessing
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import label_binarize
from sklearn.preprocessing import MinMaxScaler

#feature selection
from sklearn.feature_selection import mutual_info_classif

#classification
from sklearn.multiclass import OneVsRestClassifier
from sklearn.ensemble import RandomForestClassifier

#performance metrics
from sklearn.metrics import balanced_accuracy_score,f1_score,precis
from sklearn.metrics import classification_report
from sklearn.metrics import plot_confusion_matrix
from sklearn.metrics import roc_curve, auc
from sklearn.metrics import roc_auc_score
```

In [56]:
```
#read data
```

In [57]:
```
file_path = "/Users/donu/Desktop/cancer_gene_expression.csv"

data = pd.read_csv(file_path)
```

In [58]:
```
#to check shape
print(data.shape)
```

```
(801, 8001)
```

In [59]:
```
#to check columns
print(data.columns[0:5])
```

```
Index(['gene_1', 'gene_2', 'gene_3', 'gene_4', 'gene_5'], dtype='ob
ject')
```

In [60]:
```
#to check last column
print(data.columns[-1])
```

```
Cancer_Type
```

In [61]:
```
#to check the missing value
datanul = data.isnull().sum()
g=[i for i in datanul if i>0]
print('columns with missing value:%d'%len(g))
```

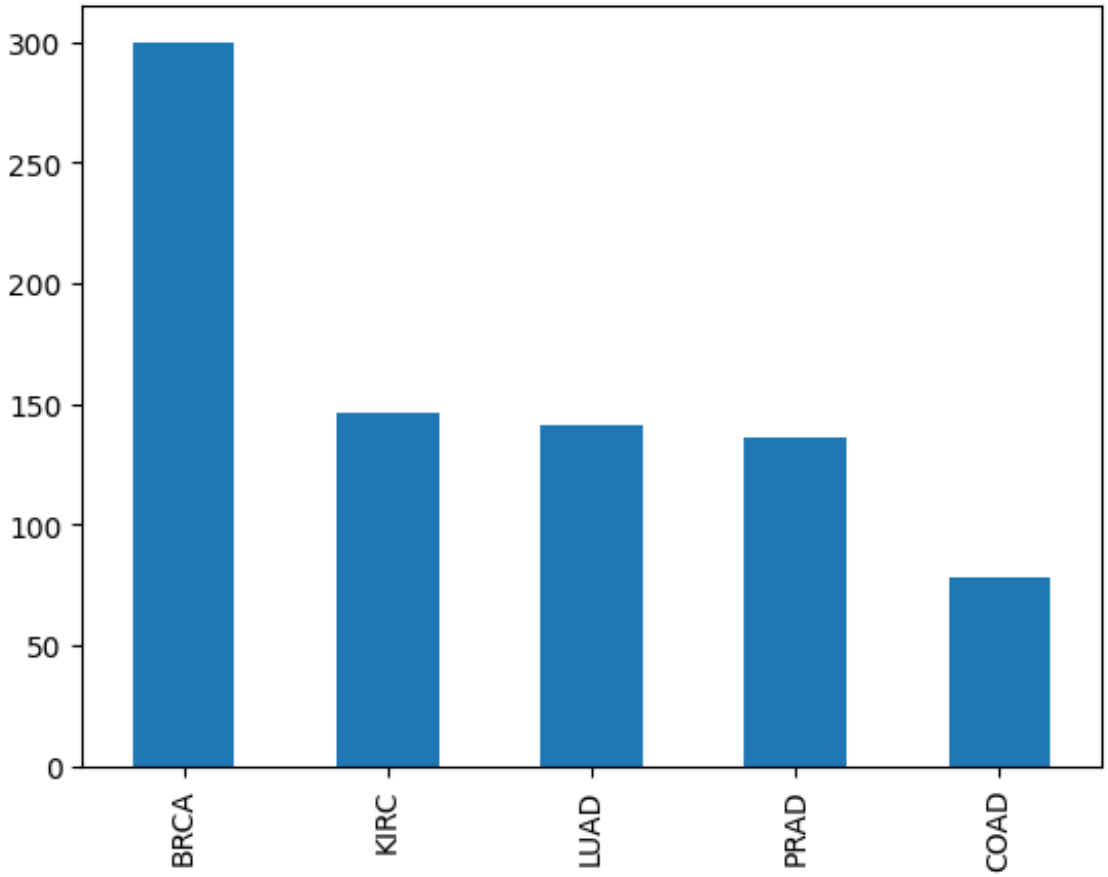
```
columns with missing value:0
```

In [62]:
```
#to check how many cancer types are present in the data

print(data['Cancer_Type'].value_counts())
```

```
BRCA    300
KIRC    146
LUAD    141
PRAD    136
COAD     78
Name: Cancer_Type, dtype: int64
```

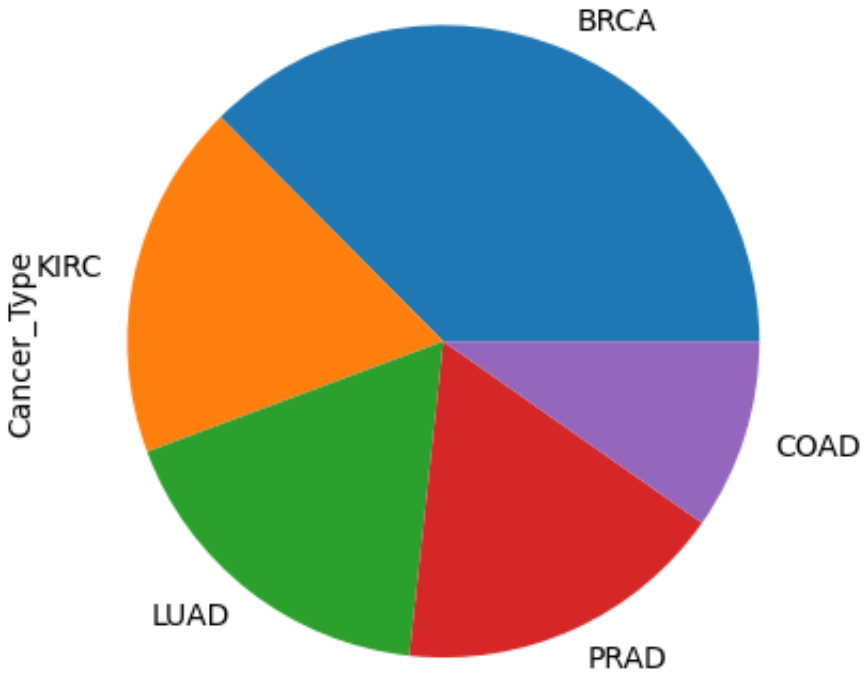
In [63]:
```
print(data['Cancer_Type'].value_counts().plot.bar())
```

```
Axes(0.125,0.11;0.775x0.77)
```



In [64]:
```
print(data['Cancer_Type'].value_counts().plot(kind='pie'))
```

```
Axes(0.22375,0.11;0.5775x0.77)
```



In [65]:
```
#data Preprocessing
```

In [66]:
```
X=data.iloc[:,0:-1]
Y=data.iloc[:,-1]

print(X.shape)
print(Y.shape)
```

```
(801, 8000)
(801,)
```

In [67]:
```
data.iloc[0:10].describe()
```

Out[67]:

	gene_1	gene_2	gene_3	gene_4	gene_5	gene_6	gene_7
count	10.0	10.000000	10.0	10.000000	10.000000	10.000000	10.000000
mean	0.0	0.092759	0.0	2.779896	0.053715	0.123462	0.123462
std	0.0	0.293331	0.0	1.067656	0.169861	0.390422	0.390422
min	0.0	0.000000	0.0	1.173191	0.000000	0.000000	0.000000
25%	0.0	0.000000	0.0	2.139328	0.000000	0.000000	0.000000
50%	0.0	0.000000	0.0	3.084558	0.000000	0.000000	0.000000
75%	0.0	0.000000	0.0	3.315225	0.000000	0.000000	0.000000
max	0.0	0.927593	0.0	4.746646	0.537147	1.234624	1.234624

8 rows × 8000 columns

In [68]:
```
#encoding
label_encoder = LabelEncoder()
label_encoder.fit(Y)
y_encoded = label_encoder.transform(Y)
labels = label_encoder.classes_
classes = np.unique(y_encoded)
```

In [69]:
```
print(labels)
print(classes)
```

```
['BRCA' 'COAD' 'KIRC' 'LUAD' 'PRAD']
[0 1 2 3 4]
```

In [70]:
```
#Data splitting
```

In [71]:
```
x_train,x_test,y_train,y_test = train_test_split(X,y_encoded,test_s
```

In [72]:
```
#Data Normalization

min_max_scaler = MinMaxScaler()
x_train_norm = min_max_scaler.fit_transform(x_train)
x_test_norm = min_max_scaler.fit_transform(x_test)
```

In [73]:
```
type(x_train)
```

Out[73]:
```
pandas.core.frame.DataFrame
```

In [74]:
```
x_train.iloc[0,3]
```

Out[74]:
```
2.18164326123
```

In [75]:
```
x_train_norm[0,3]
```

Out[75]:
```
0.4671305057022768
```

In [76]:
```
#feature selection

MI=mutual_info_classif(x_train_norm,y_train)
```

In [77]:
```
MI.shape
```

Out[77]:
```
(8000,)
```

In [78]:
```
MI[0:5]
```

Out[78]:
```
array([0.        , 0.04015616, 0.06819021, 0.05237047, 0.05047144])
```

In [79]:
```
feature=x_train.columns
```

In [80]:
```
feature.shape
```

Out[80]:
```
(8000,)
```

In [81]:
```
feature[0:5]
```

Out[81]:
```
Index(['gene_1', 'gene_2', 'gene_3', 'gene_4', 'gene_5'], dtype='ob
ject')
```

In [82]:
```
#now select feautures, lets say 300

n_features = 300
selected_score_indices=np.argsort(MI)[::-1][0:n_features]
```

In [83]:
```
x_train_selected = x_train_norm[:,selected_score_indices]
x_test_selected = x_test_norm[:,selected_score_indices]
```

In [84]:
```
x_train_selected.shape
```

Out[84]:
```
(640, 300)
```

In [85]:
```
x_test_selected.shape
```

Out[85]:
```
(161, 300)
```

In [86]:
```
#Random forest classifier

RF=OneVsRestClassifier(RandomForestClassifier(max_features=0.2))
RF.fit(x_train_selected,y_train)
y_pred = RF.predict(x_test_selected)
pred_prob = RF.predict_proba(x_test_selected)
```

In [87]:
```
#Model Evaluation

#accuracy
balanced_accuracy = np.round(balanced_accuracy_score(y_test, y_pred
print('balanced accuracy: %0.4f' % balanced_accuracy)

#precision
precision=np.round(precision_score(y_test,y_pred,average='weighted'
print('precision:%0.4f' %precision)

#recall
recall=np.round(recall_score(y_test,y_pred,average='weighted'),4)
print('recall:%0.4f' %recall)

#f1_score
f1score=np.round(f1_score(y_test,y_pred,average='weighted'),4)
print('f1score:%0.4f' %f1score)

report=classification_report(y_test,y_pred,target_names=labels)
print('\n')
print('classification_report\n\n')
print(report)
```

```
balanced accuracy: 0.9633
precision:0.9759
recall:0.9752
f1score:0.9750


classification_report
```

```
              precision    recall  f1-score   support

        BRCA       0.97      0.98      0.98        60
        COAD       1.00      0.88      0.93        16
        KIRC       1.00      1.00      1.00        28
        LUAD       0.92      0.96      0.94        24
        PRAD       1.00      1.00      1.00        33

    accuracy                           0.98       161
   macro avg       0.98      0.96      0.97       161
weighted avg       0.98      0.98      0.98       161
```

In [88]:
```
#generate confusion matrix
cm=confusion_matrix(y_test,y_pred)
cm_df=pd.DataFrame(cm,index=labels,columns=labels)
```

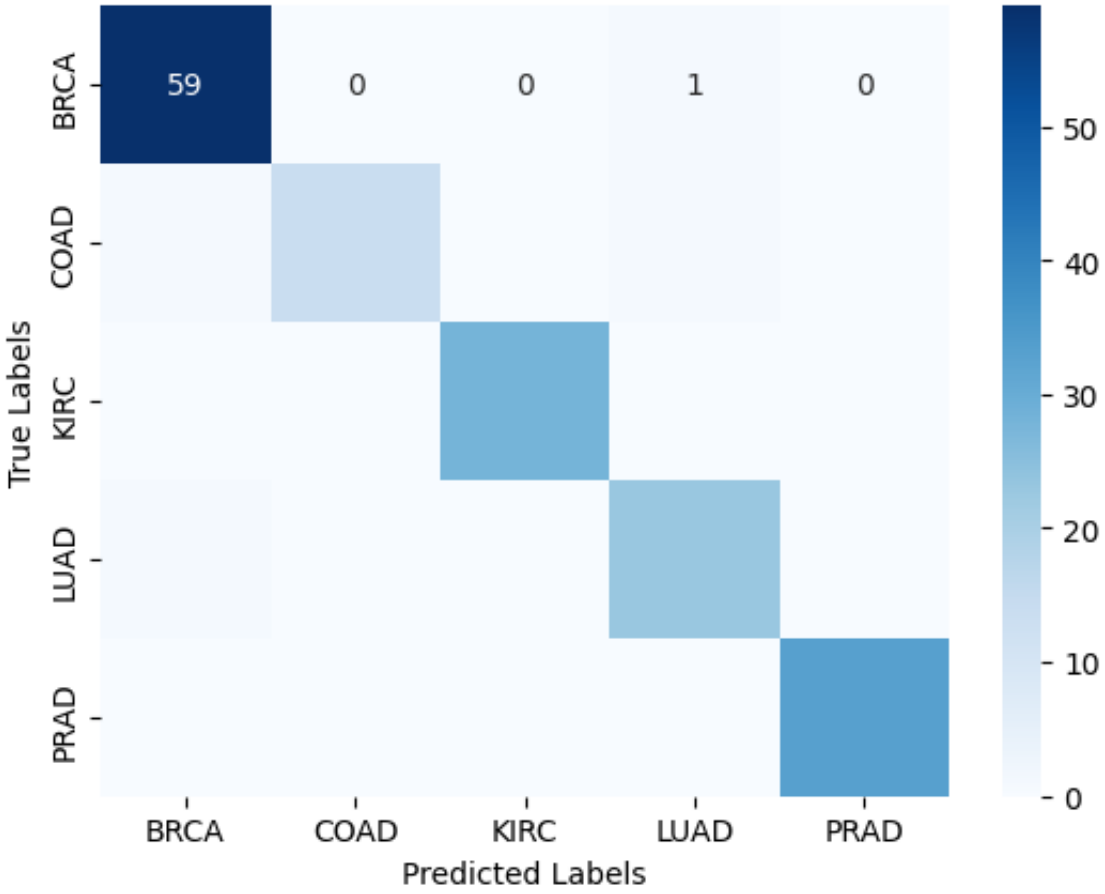
In [108…
```
cm_df
```

Out[108]:

	BRCA	COAD	KIRC	LUAD	PRAD
BRCA	59	0	0	1	0
COAD	1	14	0	1	0
KIRC	0	0	28	0	0
LUAD	1	0	0	23	0
PRAD	0	0	0	0	33

In [115…
```
#vizualize the confusion matrixusing seaborn

sns.heatmap(cm_df,annot=True,cmap="Blues")
plt.xlabel('Predicted Labels')
plt.ylabel('True Labels')
```

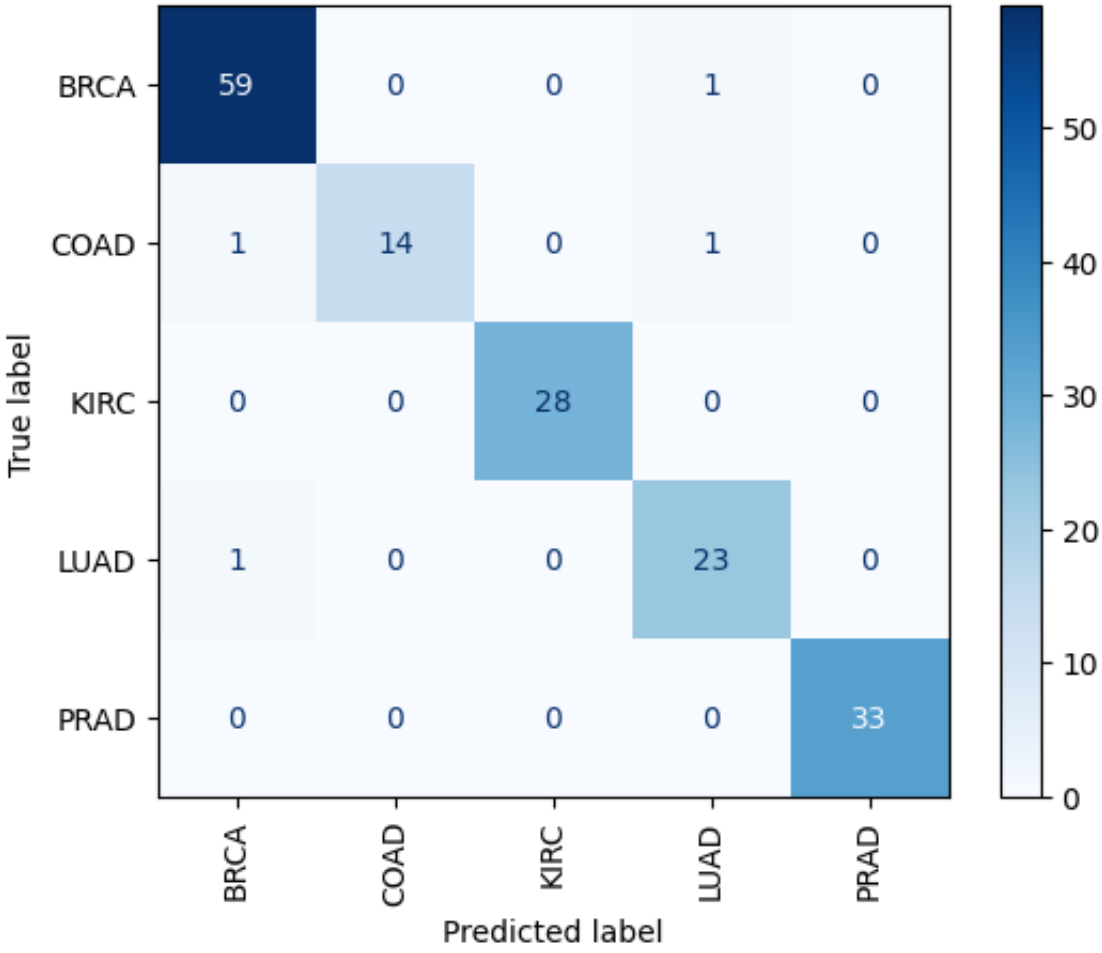
Out[115]:
```
Text(50.722222222222214, 0.5, 'True Labels')
```



In [132…

```
#vizualize the confusion matric directly

disp=plot_confusion_matrix(RF,x_test_selected,y_test,xticks_rotatio
```

```
/Users/donu/miniconda3/envs/twin/lib/python3.9/site-packages/sklear
n/utils/deprecation.py:87: FutureWarning: Function plot_confusion_m
atrix is deprecated; Function `plot_confusion_matrix` is deprecated
in 1.0 and will be removed in 1.2. Use one of the class methods: Co
nfusionMatrixDisplay.from_predictions or ConfusionMatrixDisplay.fro
m_estimator.
  warnings.warn(msg, category=FutureWarning)
```

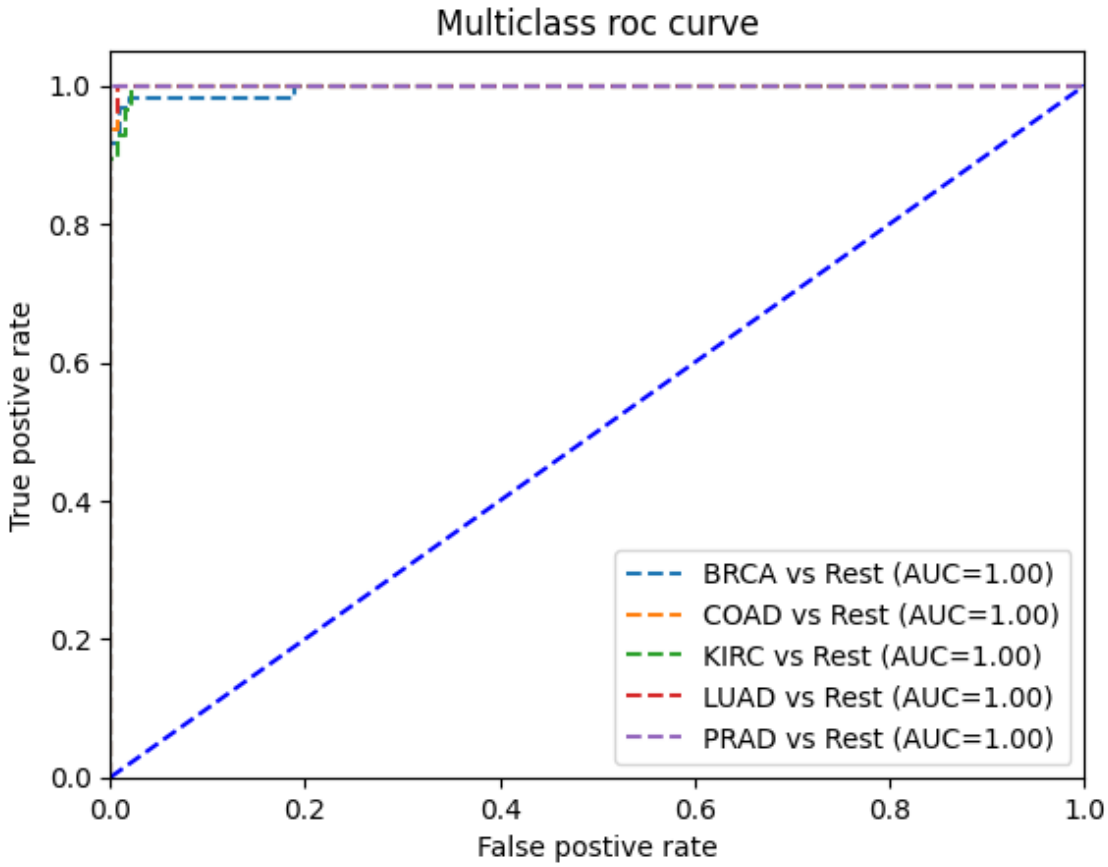


In [133…
```
pred_prob.shape
```

Out[133]: (161, 5)

In [150…

```
#roc curves will be generated for each classes
#we will therfore has to bonarize the y_test labels
#this is done because problities (pred_prob) are calculated for eac
#we therefore need to put y_test labels is same format as pred_prob

y_test_binarized=label_binarize(y_test,classes=classes)

#roc curve for classes
fpr = {}
tpr = {}
thresh = {}
roc_auc = dict()

n_class = classes.shape[0]

for i in range(n_class):
    fpr[i], tpr[i], thresh[i], = roc_curve(y_test_binarized[:,i], p
    roc_auc[i] = auc(fpr[i], tpr[i])

    #plotting

    plt.plot(fpr[i], tpr[i], linestyle='--',
             label='%s vs Rest (AUC=%0.2f)'%(labels[i],roc_auc[i])
            )

plt.plot([0, 1], [0, 1], 'b--')

plt.xlim([0,1])
plt.ylim([0,1.05])
plt.title('Multiclass roc curve')
plt.xlabel('False postive rate')
plt.ylabel('True postive rate')
plt.legend(loc = 'lower right')
plt.show()
```


Multiclass roc curve
True postive rate
False postive rate
0.0
0.2
0.4
0.6
0.8
1.0
BRCA vs Rest (AUC=1.00)
COAD vs Rest (AUC=1.00)
KIRC vs Rest (AUC=1.00)
LUAD vs Rest (AUC=1.00)
PRAD vs Rest (AUC=1.00)

In [ ]: