

# FuzzyDeepLearningOralCancer\_RF

April 17, 2024

```
[171]: #Importing Libraries
import numpy as np
import pandas as pd
import joblib
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix

# from sklearn.externals import joblib
print('Libraries Imported')
```

Libraries Imported

```
[172]: dataset = pd.read_csv("Data_RF_SVM/9.Training_oral_cancer.csv", header = None)
dataset.columns = [
    'gender', 'age_fuzzy', 'primary_tumor', 'pT_stage', 'pN_stage', 'Staging', 'Patho', 'lymph_metastasis'
]
print('Shape of the dataset: ' + str(dataset.shape))
dataset.head()
```

Shape of the dataset: (1253, 14)

```
[172]:   gender  age_fuzzy  primary_tumor  pT_stage  pN_stage  Staging  Patho \
0        1          3            1          3          3          4          1
1        1          2            1          4          1          4          1
2        2          6            6          2          3          4          1
3        1          3            1          3          6          3          1
4        2          5            1          3          6          3          1

      lymph_metastasis  positive_margin  extranodal_extension  vascular_invasion \
0                  1                  2                  2                  2
1                  1                  1                  2                  2
2                  1                  2                  2                  2
3                  2                  1                  1                  2
4                  2                  2                  2                  2

  perineural_invasion  five_year_surv  target
0                  2                  1          1
1                  1                  1          1
```

```
2          2          1          1
3          2          1          1
4          2          1          1
```

```
[173]: factor = pd.factorize(dataset['target'])
dataset.target = factor[0]
definitions = factor[1]
print(dataset.target.head())
print(definitions)
```

```
0    0
1    0
2    0
3    0
4    0
Name: target, dtype: int64
Index([1, 2, 3, 4, 5, 6], dtype='int64')
```

```
[174]: X_train = dataset.iloc[:,0:13].values
y_train = dataset.iloc[:,13].values
print('The independent features set: ')
print(X_train[:14,:])
print('The dependent variable: ')
print(y_train[:14])
```

The independent features set:

```
[[1 3 1 3 3 4 1 1 2 2 2 2 1]
 [1 2 1 4 1 4 1 1 1 2 1 1 1]
 [2 6 6 2 3 4 1 1 2 2 2 2 1]
 [1 3 1 3 6 3 1 2 1 2 2 2 1]
 [2 5 1 3 6 3 1 2 2 2 2 2 1]
 [1 4 2 1 6 1 1 2 2 2 2 2 1]
 [1 2 1 2 6 2 1 2 2 2 2 2 1]
 [2 3 1 3 3 4 1 1 2 1 1 1 1]
 [1 3 1 2 3 4 3 1 1 1 1 1 1]
 [2 4 3 4 6 4 1 2 2 2 2 2 1]
 [2 2 1 4 6 4 2 2 2 2 1 2 1]
 [2 4 1 2 3 4 1 1 2 1 2 2 1]
 [1 3 1 2 3 4 1 1 2 1 1 1 1]
 [2 4 1 2 3 4 1 1 2 1 1 2 1]]
```

The dependent variable:

```
[0 0 0 0 0 0 0 0 0 0 0 0 0]
```

```
[175]: dataset_test = pd.read_csv("Data_RF_SVM/5.test_oral_cancer.csv", header = None)
dataset_test.columns =
    ['gender', 'age_fuzzy', 'primary_tumor', 'pT_stage', 'pN_stage', 'Staging', 'Patho', 'lymph_metast
print('Shape of the dataset: ' + str(dataset_test.shape))
dataset_test.head()
```

```
Shape of the dataset: (116, 14)
```

```
[175]:    gender  age_fuzzy  primary_tumor  pT_stage  pN_stage  Staging  Patho  \
0          2          2              4          4          6          4          1
1          1          3              7          3          3          4          2
2          2          3              6          3          6          3          1
3          1          2              7          4          3          4          1
4          1          3              1          3          3          4          2

      lymph_metastasis  positive_margin  extranodal_extension  vascular_invasion  \
0                  2                  1                      1                  1          1
1                  1                  2                      2                  2          2
2                  2                  2                      2                  2          2
3                  1                  1                      1                  2          2
4                  1                  2                      2                  2          2

  perineural_invasion  five_year_surv  target
0                  1                  1          1
1                  2                  1          1
2                  2                  1          1
3                  2                  1          1
4                  2                  1          1
```

```
[176]: factor_test = pd.factorize(dataset_test['target'])
dataset_test.target = factor_test[0]
definitions = factor_test[1]
print(dataset_test.target.head())
print(definitions)
```

```
0    0
1    0
2    0
3    0
4    0
Name: target, dtype: int64
Index([1, 2, 3, 4, 5, 6], dtype='int64')
```

```
[177]: X_test = dataset_test.iloc[:,0:13].values
y_test = dataset_test.iloc[:,13].values
print('The independent features set: ')
print(X[:14,:])
print('The dependent variable: ')
print(y[:14])
```

```
The independent features set:
```

```
[[5.1 3.5 1.4 0.2]
 [4.9 3.  1.4 0.2]
 [4.7 3.2 1.3 0.2]
 [4.6 3.1 1.5 0.2]]
```

```
[5.  3.6 1.4 0.2]
[5.4 3.9 1.7 0.4]
[4.6 3.4 1.4 0.3]
[5.  3.4 1.5 0.2]
[4.4 2.9 1.4 0.2]
[4.9 3.1 1.5 0.1]
[5.4 3.7 1.5 0.2]
[4.8 3.4 1.6 0.2]
[4.8 3.  1.4 0.1]
[4.3 3.  1.1 0.1]]
```

The dependent variable:

```
[[1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]
 [1 0 0 0 0 0]]
```

```
[178]: from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

```
[179]: classifier = RandomForestClassifier(n_estimators = 10, criterion = 'entropy',
                                          random_state = 42)
classifier.fit(X_train, y_train)
```

```
[179]: RandomForestClassifier(criterion='entropy', n_estimators=10, random_state=42)
```

```
[180]: y_pred = classifier.predict(X_test)
reversefactor = dict(zip(range(6),definitions))
print(pd.crosstab(y_test, y_pred, rownames=['Actual Species'],
                  colnames=['Predicted Species']))
```

Predicted Species	0	1	2	3	5
Actual Species					
0	21	6	2	2	0
1	9	4	0	0	0
2	6	1	0	0	0
3	1	3	0	0	0

$$\begin{array}{rccccc} 4 & & 1 & 0 & 0 & 0 & 0 \\ 5 & & 0 & 0 & 0 & 0 & 60 \end{array}$$

```
[181]: from sklearn.metrics import confusion_matrix,classification_report  
print(classification_report(y_test, y_pred))
```

	precision	recall	f1-score	support
0	0.55	0.68	0.61	31
1	0.29	0.31	0.30	13
2	0.00	0.00	0.00	7
3	0.00	0.00	0.00	4
4	0.00	0.00	0.00	1
5	1.00	1.00	1.00	60
accuracy			0.73	116
macro avg	0.31	0.33	0.32	116
weighted avg	0.70	0.73	0.71	116

```
/Users/rachasaksomyanonthanakul/anaconda3/lib/python3.11/site-  
packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning:  
Precision and F-score are ill-defined and being set to 0.0 in labels with no  
predicted samples. Use `zero_division` parameter to control this behavior.  
    _warn_prf(average, modifier, msg_start, len(result))  
/Users/rachasaksomyanonthanakul/anaconda3/lib/python3.11/site-  
packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning:  
Precision and F-score are ill-defined and being set to 0.0 in labels with no  
predicted samples. Use `zero_division` parameter to control this behavior.  
    _warn_prf(average, modifier, msg_start, len(result))  
/Users/rachasaksomyanonthanakul/anaconda3/lib/python3.11/site-  
packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning:  
Precision and F-score are ill-defined and being set to 0.0 in labels with no  
predicted samples. Use `zero_division` parameter to control this behavior.  
    _warn_prf(average, modifier, msg_start, len(result))
```

```
[185]: y_test
y_test = label_binarize(y_test, classes=[0, 1, 2, 3, 4, 5])
```

[186] : v test





```
[188]: y_pred = label_binarize(y_pred, classes=[0, 1, 2, 3, 4, 5])
        y_score = y_pred
        y_score
```



```
[189]: n_classes = y_score.shape[1]
        n_classes
```

[189] : 6

```
[221]: import numpy as np
from scipy import interp
import matplotlib.pyplot as plt
from itertools import cycle
from sklearn.metrics import roc_curve, auc

n_classes = 6
lw = 2
fpr = dict()
tpr = dict()
roc_auc = dict()
for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test[:, i], y_score[:, i])
    #fpr[i], tpr[i], _ = roc_curve(y_test[:, i], y_score[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

fpr["micro"], tpr["micro"], _ = roc_curve(y_test.ravel(), y_score.ravel())
roc_auc["micro"] = auc(fpr["micro"], tpr["micro"])

all_fpr = np.unique(np.concatenate([fpr[i] for i in range(n_classes)]))

mean_tpr = np.zeros_like(all_fpr)
for i in range(n_classes):
    mean_tpr += np.interp(all_fpr, fpr[i], tpr[i])

# Finally average it and compute AUC
mean_tpr /= n_classes

fpr["macro"] = all_fpr
tpr["macro"] = mean_tpr
roc_auc["macro"] = auc(fpr["macro"], tpr["macro"])

# Plot all ROC curves
plt.figure(1)
plt.grid(True)
plt.plot(fpr["micro"], tpr["micro"],
          label='micro-average ROC curve (area = {0:0.2f})'
                  ''.format(roc_auc["micro"]),
          color='deeppink', linestyle=':', linewidth=4)

plt.plot(fpr["macro"], tpr["macro"],
          label='macro-average ROC curve (area = {0:0.2f})'
                  ''.format(roc_auc["macro"]),
          color='navy', linestyle=':', linewidth=4)

colors = cycle(['aqua', 'darkorange', 'cornflowerblue', 'red', 'yellow', 'blue'])
for i, color in zip(range(n_classes), colors):
```

```

plt.plot(fpr[i], tpr[i], color=color, lw=lw,
         label='ROC curve of class {0} (area = {1:0.2f})'
         ''.format(i, roc_auc[i]))

plt.plot([0, 1], [0, 1], 'k--', lw=lw)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Some extension of Receiver operating characteristic to multi-class')
plt.legend(loc="lower right")
plt.savefig('ROC_RF_1.tiff')
plt.show()

# Zoom in view of the upper left corner.
plt.figure(2)

plt.grid(True)

plt.xlim(0, 0.2)
plt.ylim(0.8, 1)
plt.plot(fpr["micro"], tpr["micro"],
         label='micro-average ROC curve (area = {0:0.2f})'
         ''.format(roc_auc["micro"]),
         color='deeppink', linestyle=':', linewidth=4)

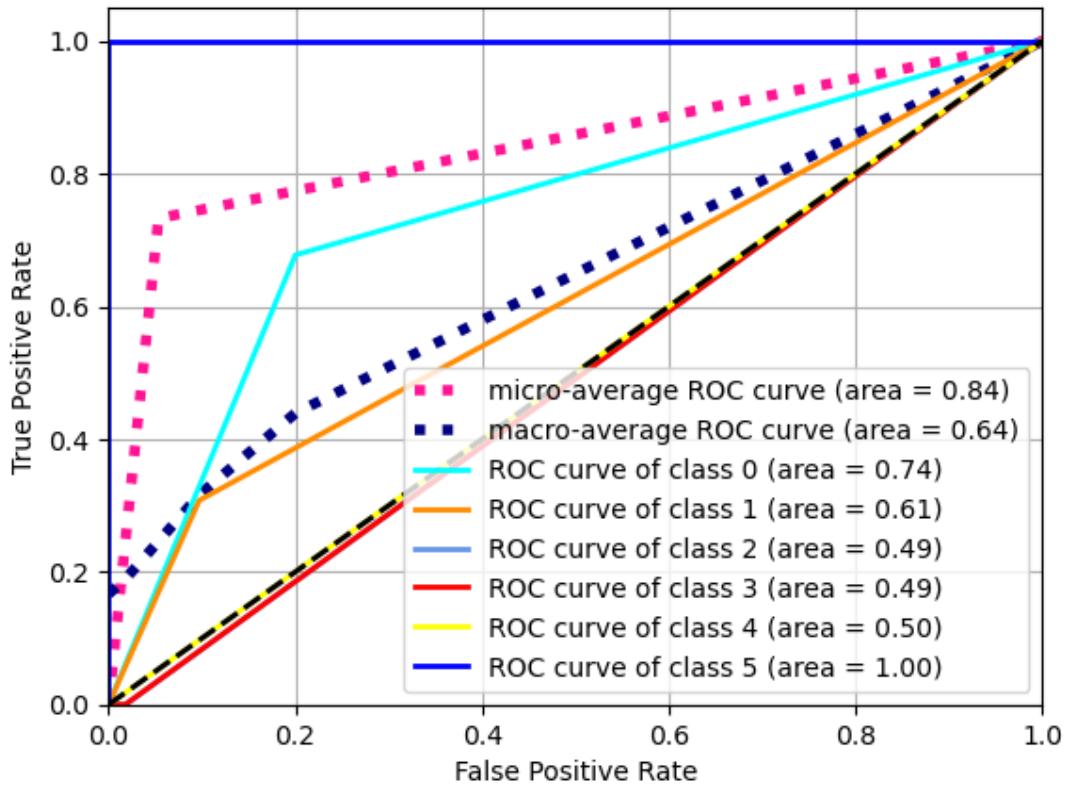
plt.plot(fpr["macro"], tpr["macro"],
         label='macro-average ROC curve (area = {0:0.2f})'
         ''.format(roc_auc["macro"]),
         color='navy', linestyle=':', linewidth=4)

colors = cycle(['aqua', 'darkorange', 'cornflowerblue', 'red', 'yellow', 'blue'])
for i, color in zip(range(n_classes), colors):
    plt.plot(fpr[i], tpr[i], color=color, lw=lw,
             label='ROC curve of class {0} (area = {1:0.2f})'
             ''.format(i, roc_auc[i]))

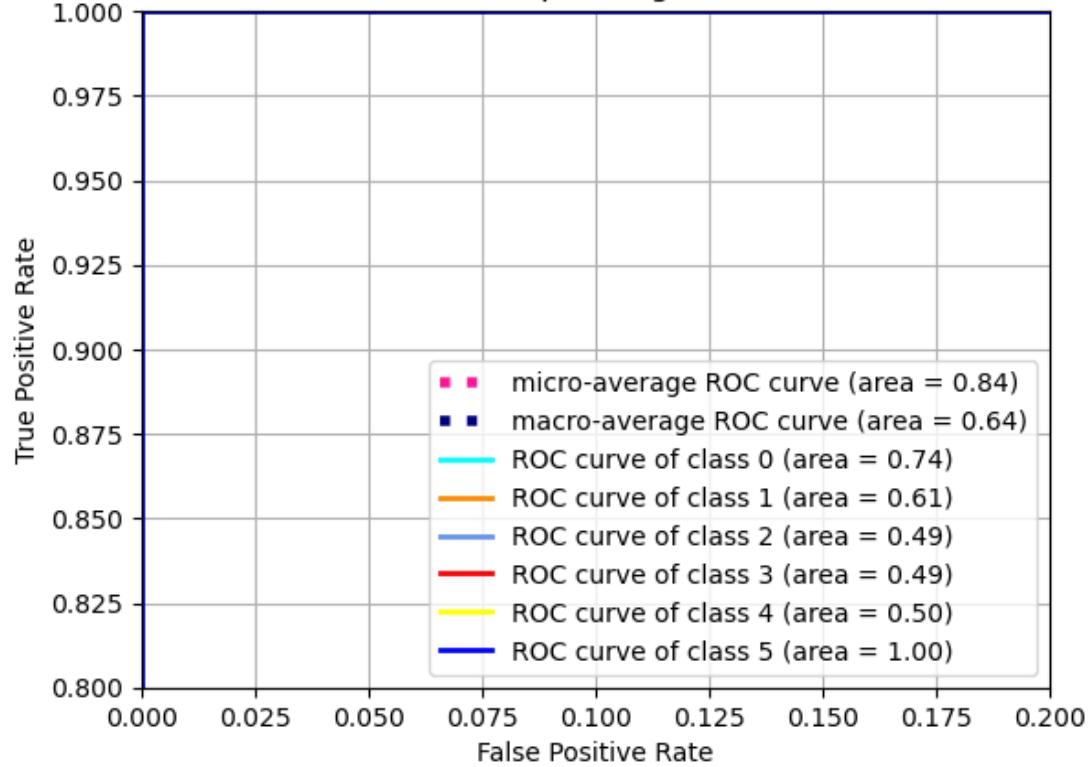
plt.plot([0, 1], [0, 1], 'k--', lw=lw)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Some extension of Receiver operating characteristic to multi-class')
plt.legend(loc="lower right")
plt.savefig('ROC_RF_2.pdf')
plt.show()

```

### Some extension of Receiver operating characteristic to multi-class



### Some extension of Receiver operating characteristic to multi-class



[ ]: