FinalRun

December 13, 2021

[1]:

```python
import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import cross_validate
from sklearn.preprocessing import MinMaxScaler
from sklearn.ensemble import ExtraTreesClassifier
from sklearn.model_selection import KFold
from sklearn.pipeline import make_pipeline
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import roc_curve, roc_auc_score

from sklearn.neural_network import MLPClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.preprocessing import MinMaxScaler

import xgboost
from xgboost import XGBClassifier
xgboost.set_config(verbosity=0)
from sklearn.model_selection import train_test_split
from sklearn import metrics

import sklearn
from sklearn.metrics import roc_curve, roc_auc_score
from sklearn.metrics import confusion_matrix
```

```
/home/shikha/snap/jupyter/common/lib/python3.7/site-
packages/joblib/_multiprocessing_helpers.py:45: UserWarning: [Errno 13]
Permission denied.  joblib will operate in serial mode
  warnings.warn('%s.  joblib will operate in serial mode' % (e,))
```

[4]:

```python
renamedf = pd.read_csv('../input/renamed.csv')
renamedf.drop(columns=['Unnamed: 0'], inplace = True)
renamedf
```

[4]:

```
     Age  Gender   BMI  Presence of Symptoms  Fever  Cough  Breathlessness  \
0     53       1  22.5                     1      1      1               1
1     26       0  25.7                     0      0      0               0
2     28       1  22.2                     0      0      0               0
3     73       1  21.5                     1      1      1               1
4     49       1  27.4                     1      1      1               0
..   …     …   …                   …    …    …             …
170   53       1  27.2                     1      1      1               1
171   33       1  26.0                     1      1      1               1
172   70       1  21.4                     1      1      0               1
173   65       0  22.4                     1      0      1               1
174   75       1  26.2                     1      1      0               1

     Travel History   Temp  SpO2  …  Potassium  Chloride  Total Bilirubin  \
0                 0   96.8    99  …        4.8     108.0              0.5
1                 0   98.7    98  …        4.1     108.0              0.3
2                 0   98.4    98  …       18.1       1.1              0.8
3                 0   98.0    98  …        4.2     104.0              2.4
4                 0  101.0    98  …        3.8      92.0              4.2
..              …    …   …  …        …       …              …
170               0   98.9    96  …        2.9      97.0              1.4
171               0   99.3    98  …        4.2     106.0              0.5
172               0   98.3    99  …        4.2     106.0              1.8
173               0   98.9    97  …        3.8     110.0              1.2
174               0   99.0    95  …        6.7      93.0              0.6

     Direct Bilirubin   SGOT   SGPT  Total proteins  Albumin  \
0                 0.2   81.3   70.0             5.9      3.8
1                 0.1   22.2   14.8             6.6      3.9
2                 0.3   19.3   12.8             7.0      4.2
3                 1.2   59.0   47.9             6.3      3.7
4                 2.1   44.6   55.5             5.9      3.1
..                …    …    …             …      …
170               0.5   43.8   38.8             6.2      3.7
171               0.2   80.6   42.6             6.6      3.8
172               0.6   77.0   27.9             5.9      3.3
173               0.6   56.2   43.2             5.6      3.4
174               0.3  474.2  157.9             6.6      3.3

     Alkaline Phosphatase  C-Reactive Proteins
0                    44.1                58.10
1                    58.5                 3.66
2                    86.0                10.17
3                   120.0               168.90
4                   177.0               164.00
..                    …                  …
170                  73.3               127.60
```

```
171                  57.4               138.15
172                  60.1               143.00
173                 216.0               124.00
174                 320.9               163.15

[175 rows x 35 columns]
```

[5]:

```
X = renamedf.drop(['Outcome','qSOFA score'],axis=1)
Y = renamedf['Outcome']
```

[9]:

```
renamedf[['Outcome']].value_counts()
```

[9]:

```
Outcome
0          151
1           24
dtype: int64
```

[9]:

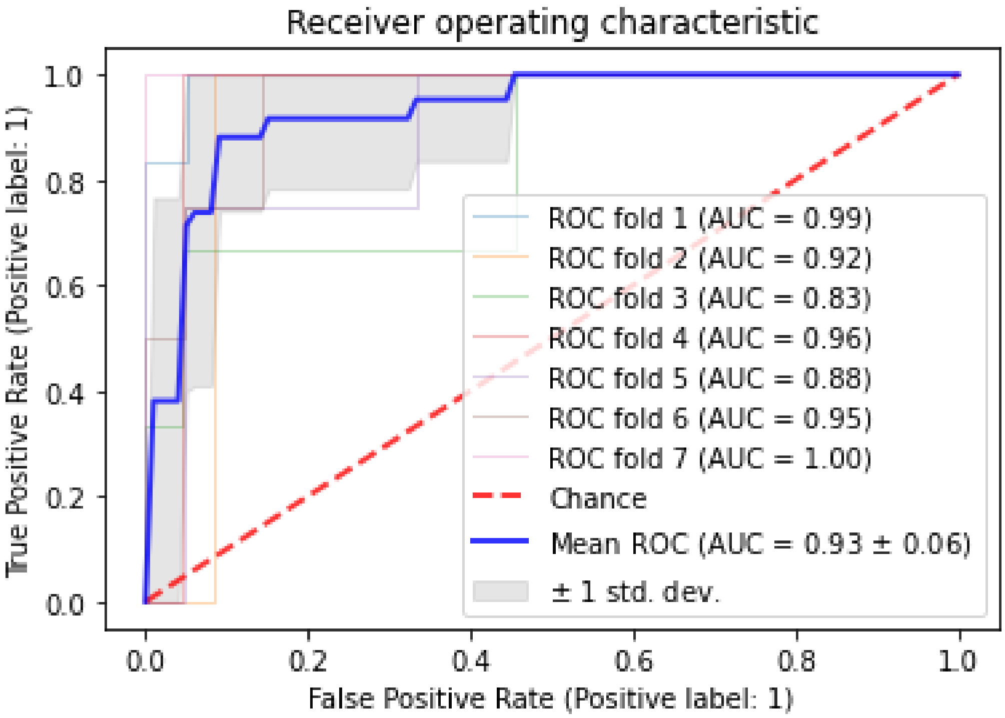
```
from scipy import interp
def nestedcv(pipeline,param_grid, X, Y):


    f1 = [0]*7
    roc = [0]*7
    prec = [0]*7
    rec = [0]*7
    acc = [0]*7


    cv_outer = KFold(n_splits=7, shuffle=True)
    i = 0

    tprs = []
    aucs = []
    mean_fpr = np.linspace(0, 1, 100)

    fig, ax = plt.subplots()

    for train_ix, test_ix in cv_outer.split(X):

        print(i+1)

        X_train = X.iloc[train_ix]
        X_test =  X.iloc[test_ix]
        y_train = Y.iloc[train_ix]
        y_test =  Y.iloc[test_ix]
        scaler = MinMaxScaler()
        model = ExtraTreesClassifier()
        model.fit(scaler.fit_transform(X_train),y_train)

        feat_importances = pd.Series(model.feature_importances_, index=X_train.
↪columns)
        x = feat_importances.nlargest(5)
        features = np.array(x.index)
        print(*features+',')

        gs = GridSearchCV(estimator=pipeline, param_grid = param_grid,
                     cv = 6, scoring = 'f1', n_jobs = -1, refit = True)

        result = gs.fit(X_train[features],y_train)
        print(result.best_params_)
        best_model = result.best_estimator_

        best_model.fit(X_train[features],y_train)
        y_hat = best_model.predict(X_test[features])
        f1[i] = metrics.f1_score(y_test, y_hat)
        prec[i] = metrics.precision_score(y_test, y_hat)
        rec[i] = metrics.recall_score(y_test,y_hat)
        acc[i] = metrics.accuracy_score(y_test,y_hat)


        viz = metrics.plot_roc_curve(best_model, X_test[features], y_test,
                             name='ROC fold {}'.format(i+1),
                             alpha=0.3, lw=1, ax=ax)
        interp_tpr = np.interp(mean_fpr, viz.fpr, viz.tpr)
        interp_tpr[0] = 0.0
        tprs.append(interp_tpr)
        aucs.append(viz.roc_auc)

        i+=1
        print()


        if i==6:
            cf_matrix = confusion_matrix(y_test, y_hat)

    ax.plot([0, 1], [0, 1], linestyle='--', lw=2, color='r',
        label='Chance', alpha=.8)

    mean_tpr = np.mean(tprs, axis=0)
    mean_tpr[-1] = 1.0
    mean_auc = metrics.auc(mean_fpr, mean_tpr)
    std_auc = np.std(aucs)
    ax.plot(mean_fpr, mean_tpr, color='b',
            label=r'Mean ROC (AUC = %0.2f $\pm$ %0.2f)' % (mean_auc, std_auc),
            lw=2, alpha=.8)

    std_tpr = np.std(tprs, axis=0)
    tprs_upper = np.minimum(mean_tpr + std_tpr, 1)
    tprs_lower = np.maximum(mean_tpr - std_tpr, 0)
    ax.fill_between(mean_fpr, tprs_lower, tprs_upper, color='grey', alpha=.2,
                    label=r'$\pm$ 1 std. dev.')

    ax.set(xlim=[-0.05, 1.05], ylim=[-0.05, 1.05],
           title="Receiver operating characteristic")
    ax.legend(loc="lower right")
    plt.show()

    arr = [np.mean(acc),np.mean(f1),mean_auc,np.mean(prec),np.mean(rec)]
    return arr, mean_fpr, mean_tpr, cf_matrix
```

[15]:

```
# Pipeline created using Logistic Regression and MinMaxScaler
pipeline = make_pipeline(MinMaxScaler(),LogisticRegression(max_iter=10000))

param_grid = {'logisticregression__solver' : ['newton-cg', 'lbfgs',␣
 ↪'liblinear','sag','saga'],
'logisticregression__penalty' : ['l2'],
'logisticregression__C' : [300, 100, 30, 10, 3, 1.0, 0.3, 0.1, 0.03, 0.01]}

lg, lr_fpr, lr_tpr, cf_lr = nestedcv(pipeline,param_grid,X,Y)
lg
```

```
1
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Total proteins,
{'logisticregression__C': 300, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'newton-cg'}

2
Respiratory rate(breaths per minute), Breathlessness, C-Reactive Proteins, Age,
Urea,
{'logisticregression__C': 10, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'newton-cg'}

3
Respiratory rate(breaths per minute), Breathlessness, C-Reactive Proteins, Age,
Total proteins,
{'logisticregression__C': 10, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'newton-cg'}

4
```

```
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Age,
{'logisticregression__C': 10, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'liblinear'}

5
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Platelet count,
{'logisticregression__C': 30, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'newton-cg'}

6
C-Reactive Proteins, Respiratory rate(breaths per minute), Breathlessness, Age,
TLC Count,
{'logisticregression__C': 100, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'newton-cg'}

7
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, SGOT,
Urea,
{'logisticregression__C': 300, 'logisticregression__penalty': 'l2',
'logisticregression__solver': 'newton-cg'}
```

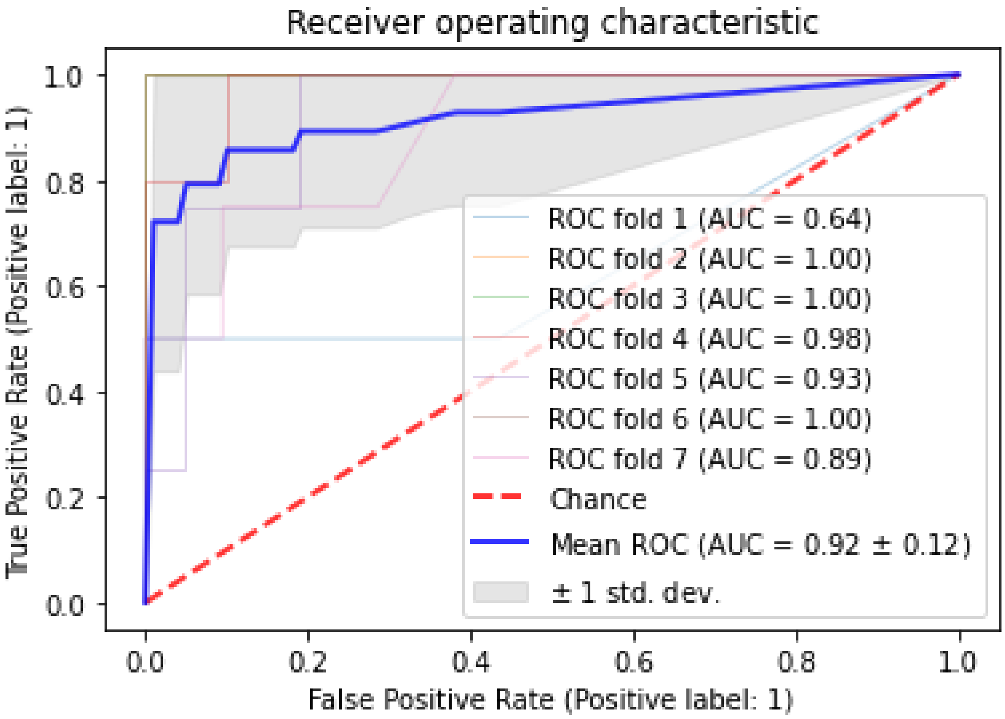


```
[15]: [0.8914285714285715,
       0.5197278911564626,
       0.9309764309764309,
       0.6904761904761905,
       0.4880952380952381]
```

```
[16]: # Pipeline created using Random Forest Classifier and MinMaxScaler
      pipeline = make_pipeline(MinMaxScaler(),
                               RandomForestClassifier())

      param_grid = {
          'randomforestclassifier__n_estimators': [400, 700],
          'randomforestclassifier__max_depth': [15,20],
          'randomforestclassifier__max_leaf_nodes': [50, 100]
      }

      rf, fpr_rf, tpr_rf, cf_rf = nestedcv(pipeline,param_grid,X,Y)
      rf
```

```
1
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Alkaline Phosphate,
{'randomforestclassifier__max_depth': 20,
'randomforestclassifier__max_leaf_nodes': 50,
'randomforestclassifier__n_estimators': 400}

2
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'randomforestclassifier__max_depth': 15,
'randomforestclassifier__max_leaf_nodes': 100,
'randomforestclassifier__n_estimators': 700}

3
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'randomforestclassifier__max_depth': 15,
'randomforestclassifier__max_leaf_nodes': 50,
'randomforestclassifier__n_estimators': 700}

4
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Age,
{'randomforestclassifier__max_depth': 20,
'randomforestclassifier__max_leaf_nodes': 100,
'randomforestclassifier__n_estimators': 700}
```

```
5
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Age,
{'randomforestclassifier__max_depth': 15,
'randomforestclassifier__max_leaf_nodes': 50,
'randomforestclassifier__n_estimators': 400}

6
C-Reactive Proteins, Respiratory rate(breaths per minute), Breathlessness, Age,
Platelet count,
{'randomforestclassifier__max_depth': 15,
'randomforestclassifier__max_leaf_nodes': 50,
'randomforestclassifier__n_estimators': 400}

7
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Urea,
Total proteins,
{'randomforestclassifier__max_depth': 20,
'randomforestclassifier__max_leaf_nodes': 100,
'randomforestclassifier__n_estimators': 400}
```



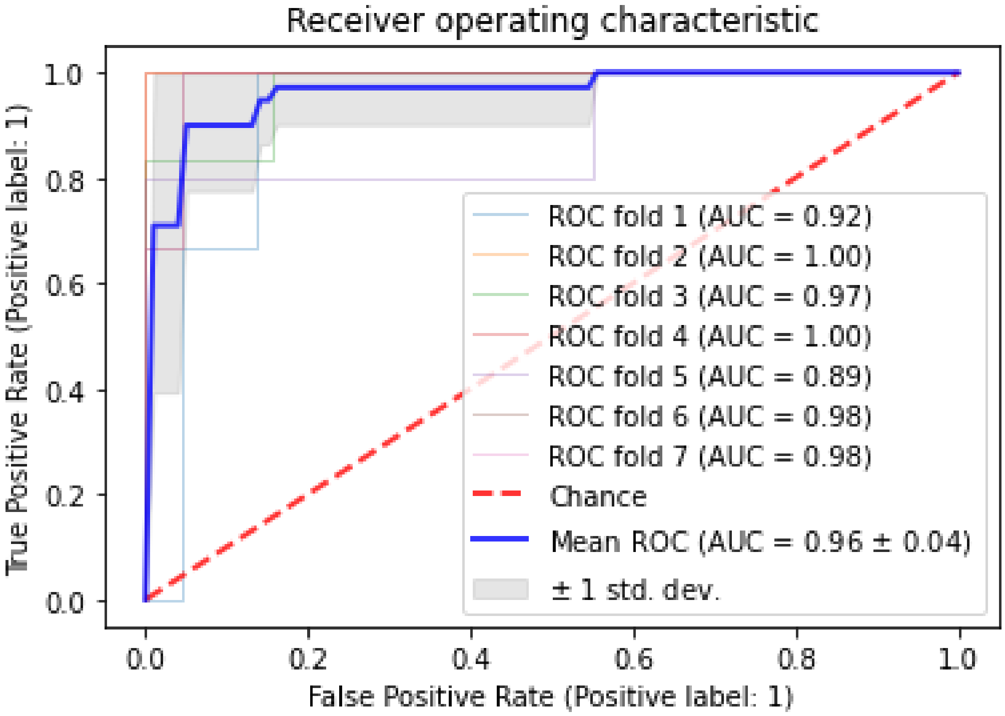
```
[16]: [0.9257142857142856,
       0.6998144712430427,
 0.917120225453559,
 0.8095238095238094,
 0.6738095238095239]
```

[12]:

```
# Pipeline created using MLP Classifier and MinMaxScaler
pipeline = make_pipeline(MinMaxScaler(),
                         MLPClassifier(max_iter=5000))

pipeline.get_params().keys()
param_grid = {
    'mlpclassifier__hidden_layer_sizes': [(50,), (100,)],
    'mlpclassifier__activation': ['relu','logistic'],
    'mlpclassifier__solver': ['lbfgs'],
    'mlpclassifier__alpha': [0.001, 0.003, 0.01, 0.03, 0.1, 0.3],
    'mlpclassifier__learning_rate': ['constant','adaptive'],
}

mlp, fpr_mlp, tpr_mlp, cf_mlp = nestedcv(pipeline,param_grid,X,Y)
mlp
```

```
1
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Urea,
{'mlpclassifier__activation': 'logistic', 'mlpclassifier__alpha': 0.001,
'mlpclassifier__hidden_layer_sizes': (50,), 'mlpclassifier__learning_rate':
'adaptive', 'mlpclassifier__solver': 'lbfgs'}

2
Respiratory rate(breaths per minute), Breathlessness, C-Reactive Proteins, Age,
TLC Count,
{'mlpclassifier__activation': 'logistic', 'mlpclassifier__alpha': 0.01,
'mlpclassifier__hidden_layer_sizes': (50,), 'mlpclassifier__learning_rate':
'constant', 'mlpclassifier__solver': 'lbfgs'}

3
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'mlpclassifier__activation': 'relu', 'mlpclassifier__alpha': 0.1,
'mlpclassifier__hidden_layer_sizes': (50,), 'mlpclassifier__learning_rate':
'adaptive', 'mlpclassifier__solver': 'lbfgs'}

4
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'mlpclassifier__activation': 'relu', 'mlpclassifier__alpha': 0.1,
'mlpclassifier__hidden_layer_sizes': (50,), 'mlpclassifier__learning_rate':
'constant', 'mlpclassifier__solver': 'lbfgs'}
```

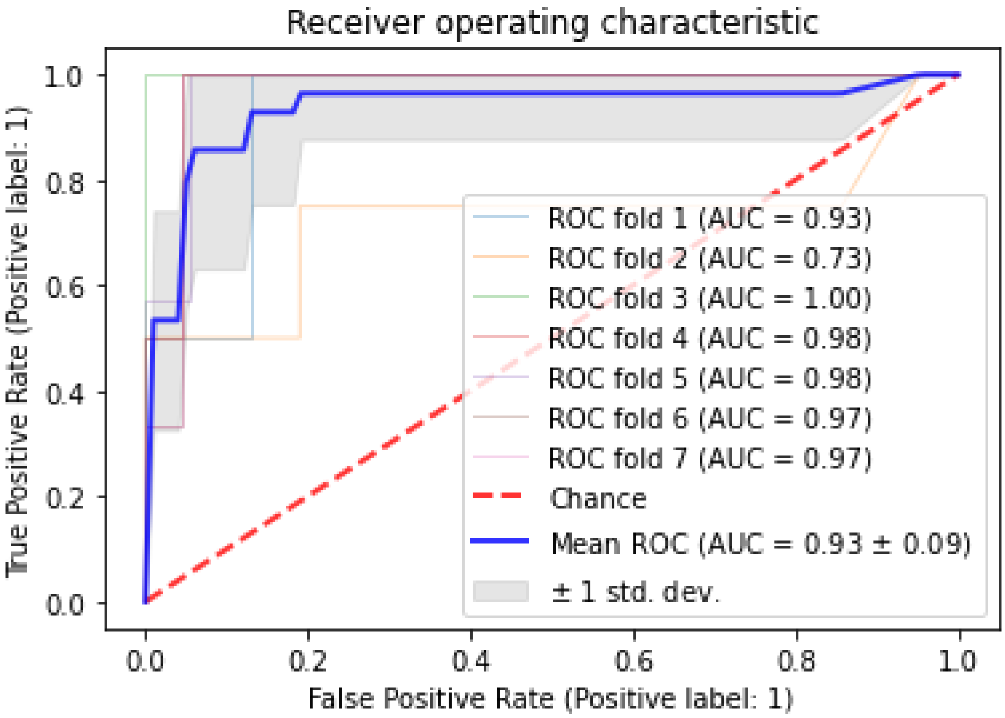
```
5
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'mlpclassifier__activation': 'logistic', 'mlpclassifier__alpha': 0.01,
'mlpclassifier__hidden_layer_sizes': (100,), 'mlpclassifier__learning_rate':
'adaptive', 'mlpclassifier__solver': 'lbfgs'}

6
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Urea,
Age,
{'mlpclassifier__activation': 'logistic', 'mlpclassifier__alpha': 0.01,
'mlpclassifier__hidden_layer_sizes': (50,), 'mlpclassifier__learning_rate':
'adaptive', 'mlpclassifier__solver': 'lbfgs'}

7
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Age,
{'mlpclassifier__activation': 'relu', 'mlpclassifier__alpha': 0.1,
'mlpclassifier__hidden_layer_sizes': (100,), 'mlpclassifier__learning_rate':
'adaptive', 'mlpclassifier__solver': 'lbfgs'}
```



```
[12]: [0.9428571428571428,
        0.7917748917748917,
        0.9618085618085619,
        0.8476190476190476,
        0.7761904761904762]
```

```
[17]: # Pipeline created using XGBoost and MinMaxScaler
      pipeline = make_pipeline(MinMaxScaler(),
                               XGBClassifier(use_label_encoder=False))

      param_grid = {
          'xgbclassifier__n_estimators': [400, 700],
          'xgbclassifier__colsample_bytree': [0.7, 0.8],
          'xgbclassifier__max_depth': [15,20],
          'xgbclassifier__reg_alpha': [1.1, 1.2],
          'xgbclassifier__reg_lambda': [1.1, 1.2],
          'xgbclassifier__subsample': [0.7, 0.8]
      }
      xgb, fpr_xgb, tpr_xgb, cf_xgb = nestedcv(pipeline,param_grid,X,Y)
      xgb
```

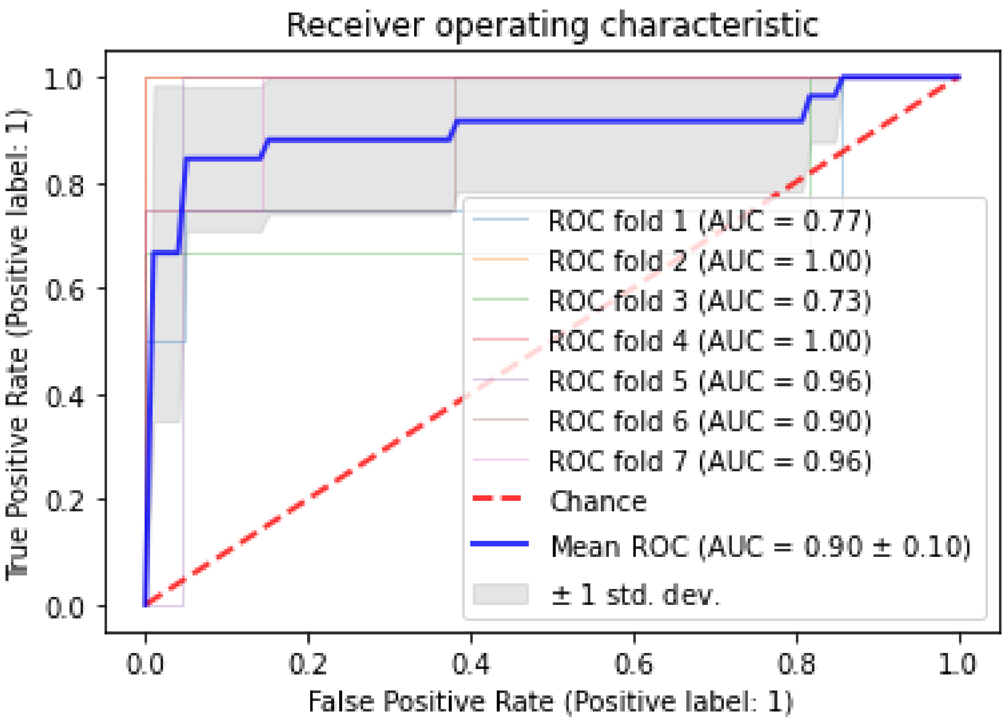
```
1
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Urea,
{'xgbclassifier__colsample_bytree': 0.8, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 400, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.1, 'xgbclassifier__subsample': 0.7}

2
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Age,
{'xgbclassifier__colsample_bytree': 0.7, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 400, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.1, 'xgbclassifier__subsample': 0.7}

3
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'xgbclassifier__colsample_bytree': 0.7, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 400, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.1, 'xgbclassifier__subsample': 0.8}

4
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Urea,
{'xgbclassifier__colsample_bytree': 0.7, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 400, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.1, 'xgbclassifier__subsample': 0.7}

5
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, TLC
Count, Age,
{'xgbclassifier__colsample_bytree': 0.7, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 400, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.1, 'xgbclassifier__subsample': 0.7}

6
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
SGOT,
{'xgbclassifier__colsample_bytree': 0.8, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 700, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.2, 'xgbclassifier__subsample': 0.7}

7
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Urea,
{'xgbclassifier__colsample_bytree': 0.8, 'xgbclassifier__max_depth': 15,
'xgbclassifier__n_estimators': 400, 'xgbclassifier__reg_alpha': 1.1,
'xgbclassifier__reg_lambda': 1.1, 'xgbclassifier__subsample': 0.7}
```



```
[17]: [0.9428571428571428,
       0.7692022263450834,
       0.9339897115871143,
       0.869047619047619,
       0.7482993197278912]
```

```
[19]: # Pipeline created using SVC and MinMaxScaler
      pipeline = make_pipeline(MinMaxScaler(),
                               SVC(probability=True))

      param_grid = {'svc__C': [0.1, 0.3, 1, 3, 10, 30, 100, 300, 1000],
                    'svc__gamma': [3, 1, 0.3, 0.1, 0.03, 0.01, 0.003, 0.001, 0.0003,␣
       ↪0.0001],
                    'svc__kernel': ['rbf','linear','sigmoid','poly']}


      svc, fpr_svc, tpr_svc, cf_svc = nestedcv(pipeline,param_grid,X,Y)
      svc
```

```
1
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'svc__C': 10, 'svc__gamma': 3, 'svc__kernel': 'rbf'}

2
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Urea,
{'svc__C': 300, 'svc__gamma': 1, 'svc__kernel': 'rbf'}

3
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'svc__C': 10, 'svc__gamma': 3, 'svc__kernel': 'rbf'}

4
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'svc__C': 30, 'svc__gamma': 3, 'svc__kernel': 'poly'}

5
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
TLC Count,
{'svc__C': 300, 'svc__gamma': 0.3, 'svc__kernel': 'rbf'}

6
Respiratory rate(breaths per minute), Breathlessness, C-Reactive Proteins, TLC
Count, Age,
{'svc__C': 3, 'svc__gamma': 3, 'svc__kernel': 'rbf'}

7
Respiratory rate(breaths per minute), C-Reactive Proteins, Breathlessness, Age,
Total proteins,
{'svc__C': 300, 'svc__gamma': 0.1, 'svc__kernel': 'sigmoid'}
```



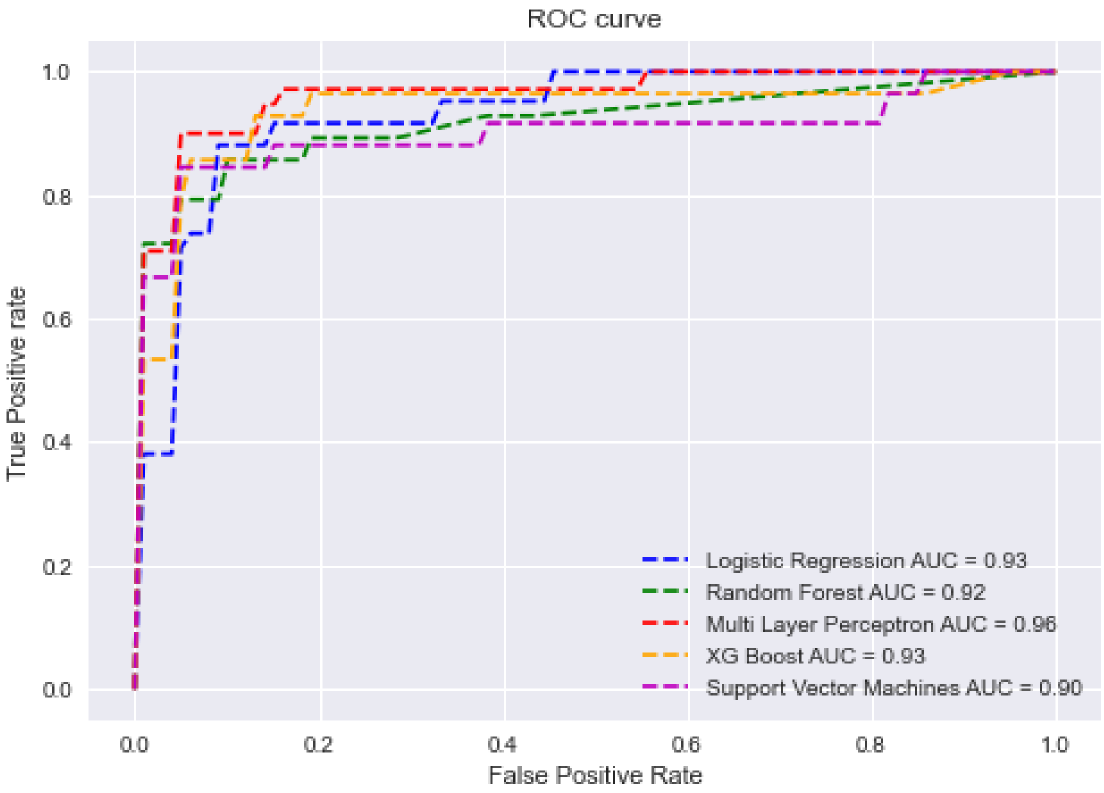
```
[19]: [0.9485714285714285,
       0.7931972789115648,
       0.9005531505531504,
       0.869047619047619,
       0.7738095238095237]
```

```
[20]: headings = ['Model','Accuracy Score','F1 Score','ROC AUC␣
       ↪Score','Precision','Recall']
      data = [['Logistic Regression', lg[0],lg[1], lg[2], lg[3], lg[4] ],
      ['Support Vector Machine', svc[0], svc[1], svc[2],svc[3],svc[4]],
      ['XGBoost',xgb[0],xgb[1],xgb[2],xgb[3],xgb[4]],
      ['Random Forest',rf[0],rf[1],rf[2],rf[3],rf[4]],
      ['Multi-Layer Perceptron',mlp[0],mlp[1],mlp[2],mlp[3], mlp[4]]]

      df = pd.DataFrame(data, columns = headings)
      df.to_csv('results.csv')
```

```
df
```

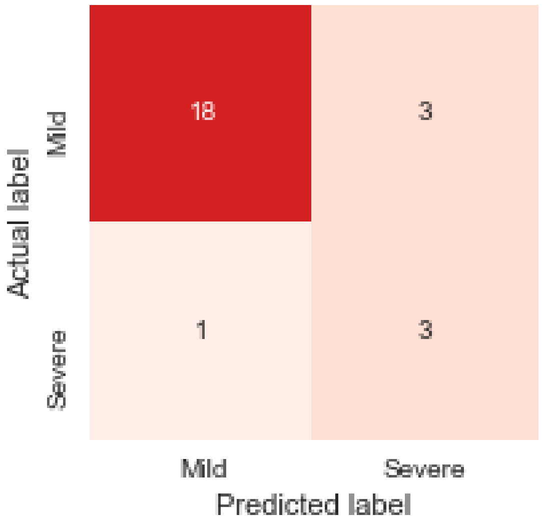
```
[20]:                        Model  Accuracy Score  F1 Score  ROC AUC Score  Precision  \
      0     Logistic Regression        0.891429  0.519728       0.930976   0.690476
      1  Support Vector Machine        0.948571  0.793197       0.900553   0.869048
      2                 XGBoost        0.942857  0.769202       0.933990   0.869048
      3           Random Forest        0.925714  0.699814       0.917120   0.809524
      4  Multi-Layer Perception        0.942857  0.791775       0.961809   0.847619

           Recall
      0  0.488095
      1  0.773810
      2  0.748299
      3  0.673810
      4  0.776190
```

```
[30]: import matplotlib.pyplot as plt
      plt.style.use('seaborn')

      plt.plot(lr_fpr, lr_tpr, linestyle='--',color='blue', label='Logistic␣
       ↪Regression AUC = 0.93')
      plt.plot(fpr_rf, tpr_rf, linestyle='--',color='green', label='Random Forest AUC␣
       ↪= 0.92')
      plt.plot(fpr_mlp, tpr_mlp, linestyle='--',color='red', label='Multi Layer␣
       ↪Perceptron AUC = 0.96')
      plt.plot(fpr_xgb, tpr_xgb, linestyle='--',color='orange', label='XG Boost AUC =␣
       ↪0.93')
      plt.plot(fpr_svc, tpr_svc, linestyle='--',color='m', label='Support Vector␣
       ↪Machines AUC = 0.90')

      plt.title('ROC curve')
      plt.xlabel('False Positive Rate')
      plt.ylabel('True Positive rate')

      plt.legend(loc='best')
      plt.savefig('ROC')
      plt.show()
```



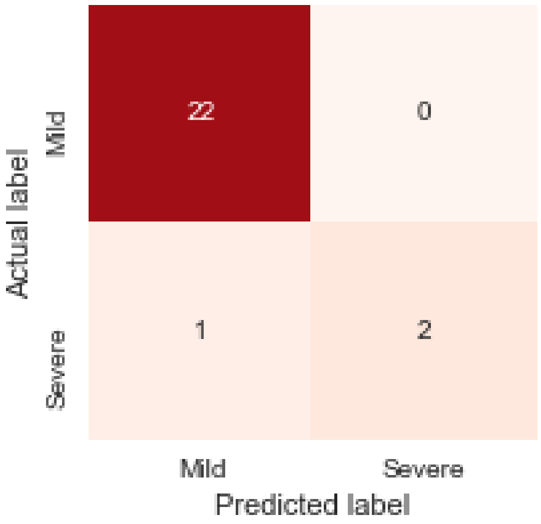
```
[22]: import seaborn as sns
      plt.figure
      fig, ax = plt.subplots(figsize=(3,3))

      sns.heatmap(cf_lr, cmap="Reds", annot=True, vmin = 0, vmax = 25, ax=␣
       ↪ax,cbar=False)

      ax.set_xticklabels(["Mild","Severe"])
      ax.set_yticklabels(["Mild","Severe"])

      plt.ylabel('Actual label')
      plt.xlabel('Predicted label')
```

```
[22]: Text(0.5, 7.0, 'Predicted label')
```



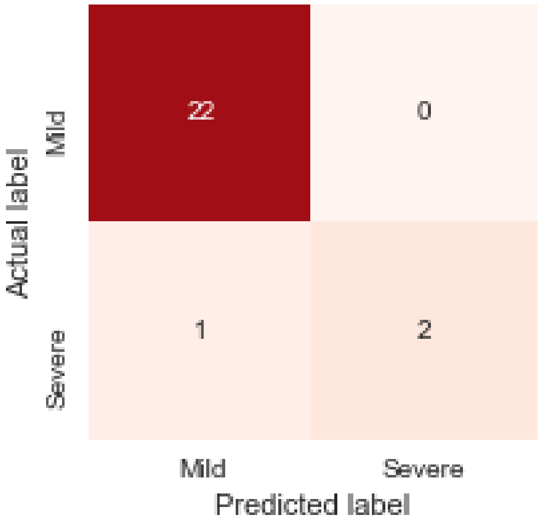
[23]:
```
import seaborn as sns
plt.figure
fig, ax = plt.subplots(figsize=(3,3))

sns.heatmap(cf_rf, cmap="Reds", annot=True, vmin = 0, vmax = 25, ax=␣
 ↪ax,cbar=False)

ax.set_xticklabels(["Mild","Severe"])
ax.set_yticklabels(["Mild","Severe"])

plt.ylabel('Actual label')
plt.xlabel('Predicted label')
```

[23]:
```
Text(0.5, 7.0, 'Predicted label')
```



[24]:
```
import seaborn as sns
plt.figure
fig, ax = plt.subplots(figsize=(3,3))

sns.heatmap(cf_mlp, cmap="Reds", annot=True, vmin = 0, vmax = 25, ax=␣
 ↪ax,cbar=False)

ax.set_xticklabels(["Mild","Severe"])
ax.set_yticklabels(["Mild","Severe"])
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
```

[24]:
```
Text(0.5, 7.0, 'Predicted label')
```

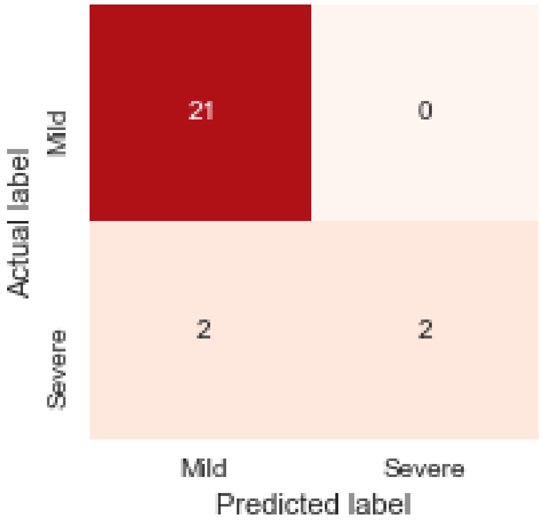


[25]:

```
import seaborn as sns
plt.figure
fig, ax = plt.subplots(figsize=(3,3))

sns.heatmap(cf_svc, cmap="Reds", annot=True, vmin = 0, vmax = 25, ax=␣
 ↪ax,cbar=False)

ax.set_xticklabels(["Mild","Severe"])
ax.set_yticklabels(["Mild","Severe"])
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
```

[25]:

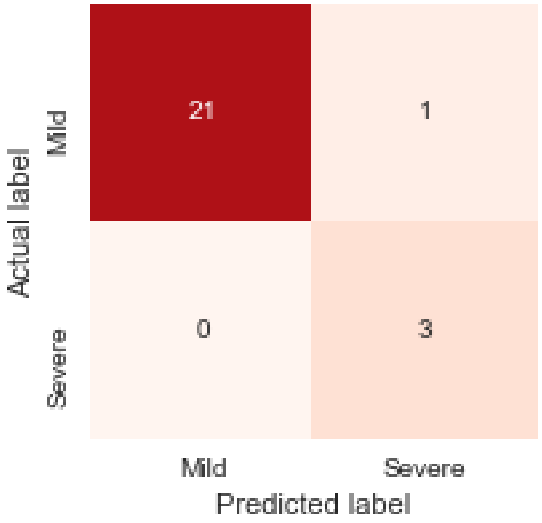
```
Text(0.5, 7.0, 'Predicted label')
```



[26]:

```
import seaborn as sns
plt.figure
fig, ax = plt.subplots(figsize=(3,3))

sns.heatmap(cf_xgb, cmap="Reds", annot=True, vmin = 0, vmax = 25, ax=␣
 ↪ax,cbar=False)

ax.set_xticklabels(["Mild","Severe"])
ax.set_yticklabels(["Mild","Severe"])
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
```

```
[26]: Text(0.5, 7.0, 'Predicted label')
```



```
[ ]:
```