# **Evaluating classification models**

In this notebook we will learn about ways of evaluating classification models. Here's the methods we will see:

- I- Binary classification:
  - 1- Binary classification parameters
  - 2- ROC curve
- II- Multiclass classificatin:
  - 1- ROC curve
  - 2- Confusion Matrix

## **Binary classification**

## **Imports**

```
In [1]: import numpy as np
    import matplotlib.pyplot as plt
    import itertools
    from itertools import cycle
    from scipy import interp

from ConfusionMatrix import plot_confusion_matrix

from sklearn.metrics import confusion_matrix
    from sklearn import svm, datasets
    from sklearn.metrics import roc_curve, auc
    from sklearn.model_selection import train_test_split, cross_val_score
    from sklearn.multiclass import LabelBinarizer
    from sklearn.multiclass import OneVsRestClassifier
    from sklearn.naive_bayes import GaussianNB
    from sklearn.svm import SVC
    from sklearn.ensemble import RandomForestClassifier
```

Binary classification parameters:

Precision, also known as True Positive Rate:

 $\mathsf{TPR} = \mathsf{TP} \ / \ \mathsf{P}$ , where  $\mathsf{TP}$  is number of True Positive and P is number of all Positive In other words, the precision is the probability of catching a positive.

Recall, also known as False Positive Rate:

FPR = FP / N, where FP is number of False Positive and N is number of all Negative In other words, recall is the probability of missing a negative

Loading the breast cancer dataset from sklearn

```
In [2]: breast_cancer = datasets.load_breast_cancer()
    data = breast_cancer.data
    target = breast_cancer.target
    list(breast_cancer.target_names)

random_state = np.random.RandomState(0)
    n_samples, n_features = data.shape
```

We will use Gaussian Naive Bayes as our binary classifier since it is fast with high dimensions

```
In [3]: gnb = GaussianNB()
    score_gnb = cross_val_score(gnb, data, target, cv=10)
    print score_gnb

[0.94827586 0.87931034 0.89473684 0.92982456 0.94736842 0.98245614
    0.92982456 0.96428571 0.94642857 0.96428571]
```

Classification parameters

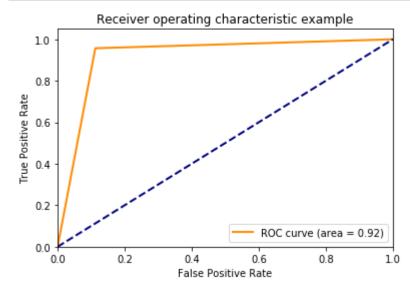
```
In [4]: # Splitting the dataset
        data_train, data_test, target_train, target_test = train_test_split(data, targ
        et, test_size=0.4)
        gnb = GaussianNB()
        gnb.fit(data_train, target_train)
        # Let's predic on the test
        target_predicted = gnb.predict(data_test)
        # Calculating TPR and FPR
        P = sum(target_test)
        N = target_test.size - P
        TP = sum(target_predicted * target_test)
        FP = np.where( (target_test - target_predicted) < 0 )[0].size</pre>
        TPR = float(TP) / P
        FPR = float(FP) / N
        print "Precision: ", TPR
        print "Recall: ", FPR
```

Precision: 0.956834532374 Recall: 0.112359550562

**ROC** 

Plotting the ROC curve

```
In [6]: fpr0, tpr0, t = roc_curve(target_test, target_predicted)
  roc_auc = auc(fpr0, tpr0)
  plot_roc_binary(fpr0, tpr0)
```



## **Multiclass classification**

```
In [7]: iris = datasets.load_iris()
    print "Number of features", iris.data.shape[1]
    print "Number of lables", np.unique(iris.target).shape[0]

X = iris.data
    y = iris.target

# Binarize the output
    lb = LabelBinarizer()
    lb.fit([0,1,2])
    y = lb.transform(y)
    # Transforms the 3 Labels classification problem to 3 binary classification problems (one vs all)
    n_classes = y.shape[1]
```

Number of features 4 Number of lables 3

Adding noise to the data

## **ROC Curve**

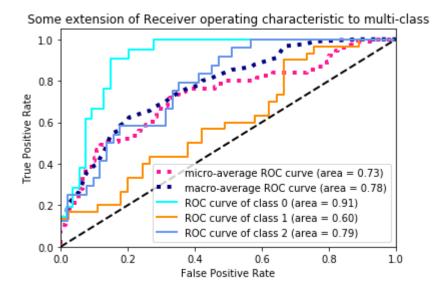
On the ROC curve, we plot the points (FPR, TPR) for different thresholds, going from 0 to 1.

#### One Vs Rest Classification

```
In [9]: # Learn to predict each class against the other
        classifier = OneVsRestClassifier(svm.SVC(kernel='linear', probability=True,
                                          random state=random state))
        # training the data
        classifier.fit(X train, y train)
        # testing the data
        y predicted = classifier.decision function(X test)
        # Compute ROC curve and ROC area for each class
        fpr = {} # False Positive Rate
        tpr = {} # True Positive Rate
        roc_auc = {} # Area under the curve
        for i in range(n classes):
            fpr[i], tpr[i], t = roc_curve(y_test[:, i], y_predicted[:, i])
            roc_auc[i] = auc(fpr[i], tpr[i])
        # Compute micro-average ROC curve and ROC area
        fpr["micro"], tpr["micro"], t = roc_curve(y_test.ravel(), y_predicted.ravel())
        roc auc["micro"] = auc(fpr["micro"], tpr["micro"])
```

Multiclass ROC curve

```
In [10]: # First aggregate all false positive rates
         all fpr = np.unique(np.concatenate([fpr[i] for i in range(n classes)]))
         # Then interpolate all ROC curves at this points
         mean tpr = np.zeros like(all fpr)
         for i in range(n_classes):
             mean tpr += 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()
         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)
         1w=2
         colors = cycle(['aqua', 'darkorange', 'cornflowerblue'])
         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.show()
```

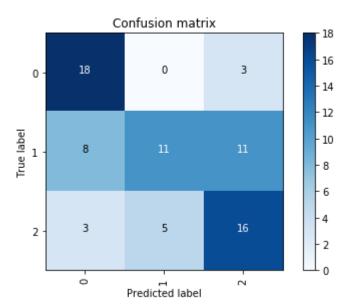


## **Confusion Matrix**

```
In [11]: y_predicted_labels = lb.inverse_transform(y_predicted)
y_true_labels = lb.inverse_transform(y_test)
```

In [12]: plot\_confusion\_matrix(y\_predicted\_labels, y\_true\_labels)

Confusion matrix, without normalization



Notice the match in accuracy between the confusion matrix and the roc plots for each label!